# Contents

## I General

<table>
<thead>
<tr>
<th>Chapter 1.</th>
<th>Introduction</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chapter 2.</td>
<td>Shared Concepts</td>
<td>7</td>
</tr>
</tbody>
</table>

## II Statistics

<table>
<thead>
<tr>
<th>Chapter 3.</th>
<th>The CORRELATION Procedure</th>
<th>87</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chapter 4.</td>
<td>The FREQTAB Procedure</td>
<td>111</td>
</tr>
<tr>
<td>Chapter 5.</td>
<td>The GAMMOD Procedure</td>
<td>295</td>
</tr>
<tr>
<td>Chapter 6.</td>
<td>The GENSELECT Procedure</td>
<td>355</td>
</tr>
<tr>
<td>Chapter 7.</td>
<td>The KCLUS Procedure</td>
<td>419</td>
</tr>
<tr>
<td>Chapter 8.</td>
<td>The LOGSELECT Procedure</td>
<td>455</td>
</tr>
<tr>
<td>Chapter 9.</td>
<td>The NLMOD Procedure</td>
<td>519</td>
</tr>
<tr>
<td>Chapter 10.</td>
<td>The PCA Procedure</td>
<td>549</td>
</tr>
<tr>
<td>Chapter 11.</td>
<td>The PHSELECT Procedure</td>
<td>587</td>
</tr>
<tr>
<td>Chapter 12.</td>
<td>The PLISMOD Procedure</td>
<td>631</td>
</tr>
<tr>
<td>Chapter 13.</td>
<td>The QTRSELECT Procedure</td>
<td>671</td>
</tr>
<tr>
<td>Chapter 14.</td>
<td>The REGSELECT Procedure</td>
<td>725</td>
</tr>
<tr>
<td>Chapter 15.</td>
<td>The SPC Procedure</td>
<td>773</td>
</tr>
<tr>
<td>Chapter 16.</td>
<td>The TREESPLIT Procedure</td>
<td>839</td>
</tr>
</tbody>
</table>

## III Utility

<table>
<thead>
<tr>
<th>Chapter 17.</th>
<th>The ASSESS Procedure</th>
<th>907</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chapter 18.</td>
<td>The BINNING Procedure</td>
<td>927</td>
</tr>
<tr>
<td>Chapter 19.</td>
<td>The CARDINALITY Procedure</td>
<td>951</td>
</tr>
<tr>
<td>Chapter 20.</td>
<td>The PARTITION Procedure</td>
<td>969</td>
</tr>
<tr>
<td>Chapter 21.</td>
<td>The VARIMPUTE Procedure</td>
<td>985</td>
</tr>
<tr>
<td>Chapter 22.</td>
<td>The VARREDUCE Procedure</td>
<td>995</td>
</tr>
</tbody>
</table>

## Subject Index

| Subject Index | 1025 |

## Syntax Index

| Syntax Index | 1047 |
Part I

General
Chapter 1
Introduction

Contents

| Overview of SAS Visual Statistics Procedures | 3 |
| About This Book | 3 |
| Chapter Organization | 3 |
| Typographical Conventions | 4 |
| Options Used in Examples | 5 |
| Where to Turn for More Information | 5 |
| Online Documentation | 5 |
| SAS Technical Support Services | 5 |

Overview of SAS Visual Statistics Procedures

SAS Visual Statistics procedures provide predictive modeling tools that have been specially developed to take advantage of the distributed environment that SAS Viya provides. Methods include linear regression, logistic regression, quantile regression, generalized linear models, generalized additive models, reduced-rank models, nonlinear models, clustering, and decision trees. The procedures provide model selection, dimension reduction, and identification of important variables whenever this identification is appropriate for the analysis.

This book also describes utility procedures, which can be used together with any SAS Viya procedures.

**NOTE:** When you license SAS Visual Statistics, you also have access to SAS/STAT software. For more information about SAS/STAT procedures, see *SAS/STAT User’s Guide*.

About This Book

This book assumes that you are familiar with Base SAS software and with the books *SAS Language Reference: Concepts* and *SAS Visual Data Management and Utility Procedures Guide*. It also assumes that you are familiar with basic SAS System concepts, such as using the DATA step to create SAS data sets and using Base SAS procedures (such as the PRINT and SORT procedures) to manipulate SAS data sets.

Chapter Organization

This book is divided into three major parts. Part I contains the following chapters:
Chapter 1, this chapter, provides an overview of SAS Visual Statistics procedures and summarizes related information, products, and services.

Chapter 2 provides information about topics that are common to multiple procedures. Topics include how to use SAS Cloud Analytic Services (CAS) sessions and how to load a SAS data set onto a CAS server. This chapter also documents the following statements that are used across a number of procedures: CLASS, CODE, EFFECT, PARTITION, and SELECTION.

Part II describes the statistical procedures and Part III describes the utility procedures. In each of these parts, the chapters appear in alphabetical order by procedure name and are organized as follows:

- The “Overview” section briefly describes the analysis provided by the procedure.
- The “Getting Started” section provides a quick introduction to the procedure through a simple example.
- The “Syntax” section describes the SAS statements and options that control the procedure.
- The “Details” section discusses methodology and other topics, such as ODS tables.
- The “Examples” section contains examples that use the procedure.
- The “References” section contains references for the methodology.

**Typographical Conventions**

This book uses several type styles for presenting information. The following list explains the meaning of the typographical conventions used in this book:

- **roman** is the standard type style used for most text.
- **UPPERCASE ROMAN** is used for SAS statements, options, and other SAS language elements when they appear in text. However, you can enter these elements in your own SAS programs in lowercase, uppercase, or a mixture of the two.
- **UPPERCASE BOLD** is used in the “Syntax” sections’ initial lists of SAS statements and options.
- **oblique** is used in the syntax definitions and in text to represent arguments for which you supply a value.
- **VariableName** is used for the names of variables and data sets when they appear in text.
- **bold** is used for matrices and vectors.
- **italic** is used for terms that are defined in text, for emphasis, and for references to publications.
- **monospace** is used for example code. In most cases, this book uses lowercase type for SAS code.
Options Used in Examples

The HTMLBLUE style is used to create the graphs and the HTML tables that appear in the online documentation. The PEARLJ style is used to create the PDF tables that appear in the documentation. A style template controls stylistic elements such as colors, fonts, and presentation attributes. You can specify a style template in an ODS destination statement as follows:

```sas
ods html style=HTMLBlue;
ods html close;
ods pdf style=PearlJ;
ods pdf close;
```

Most of the PDF tables are produced by using the following SAS System option:

```sas
options papersize=(6.5in 9in);
```

If you run the examples, you might get slightly different output. This is a function of the SAS System options that are used and the precision that your computer uses for floating-point calculations.

Where to Turn for More Information

Online Documentation

You can access the documentation by going to http://support.sas.com/documentation.

SAS Technical Support Services

The SAS Technical Support staff is available to respond to problems and answer technical questions regarding the use of procedures in this book. Go to http://support.sas.com/techsup for more information.
# Chapter 2

## Shared Concepts

**Contents**

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Introduction to Shared Concepts</td>
<td>8</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>8</td>
</tr>
<tr>
<td>Loading a SAS Data Set onto a CAS Server</td>
<td>9</td>
</tr>
<tr>
<td>Syntax Common to SAS Visual Statistics Procedures</td>
<td>10</td>
</tr>
<tr>
<td><strong>CLASS Statement</strong></td>
<td>10</td>
</tr>
<tr>
<td><strong>CODE Statement</strong></td>
<td>14</td>
</tr>
<tr>
<td><strong>DISPLAY Statement</strong></td>
<td>17</td>
</tr>
<tr>
<td><strong>DISPLAYOUT Statement</strong></td>
<td>18</td>
</tr>
<tr>
<td><strong>EFFECT Statement</strong></td>
<td>19</td>
</tr>
<tr>
<td>Collection Effects</td>
<td>21</td>
</tr>
<tr>
<td>Multimember Effects</td>
<td>21</td>
</tr>
<tr>
<td>Polynomial Effects</td>
<td>23</td>
</tr>
<tr>
<td>Spline Effects</td>
<td>26</td>
</tr>
<tr>
<td>Splines and Spline Bases</td>
<td>29</td>
</tr>
<tr>
<td>ODS Table Names</td>
<td>33</td>
</tr>
<tr>
<td><strong>PARTITION Statement</strong></td>
<td>34</td>
</tr>
<tr>
<td><strong>SELECTION Statement</strong></td>
<td>34</td>
</tr>
<tr>
<td>Optimization Options</td>
<td>42</td>
</tr>
<tr>
<td>Details for SAS Visual Statistics Procedures</td>
<td>47</td>
</tr>
<tr>
<td><strong>Levelization of Classification Variables</strong></td>
<td>47</td>
</tr>
<tr>
<td>Specification and Parameterization of Model Effects</td>
<td>49</td>
</tr>
<tr>
<td><strong>Effect Operators</strong></td>
<td>50</td>
</tr>
<tr>
<td>GLM Parameterization of Classification Variables and Effects</td>
<td>52</td>
</tr>
<tr>
<td>Nonsingular Parameterization</td>
<td>56</td>
</tr>
<tr>
<td>Class Variable Parameterization with Unbalanced Designs</td>
<td>59</td>
</tr>
<tr>
<td><strong>Model Selection Methods</strong></td>
<td>60</td>
</tr>
<tr>
<td>Full Model Fitted</td>
<td>60</td>
</tr>
<tr>
<td>Forward Selection</td>
<td>60</td>
</tr>
<tr>
<td>Backward Elimination</td>
<td>62</td>
</tr>
<tr>
<td>Stepwise Selection</td>
<td>63</td>
</tr>
<tr>
<td>Forward-Swap Selection</td>
<td>65</td>
</tr>
<tr>
<td>Least Angle Regression</td>
<td>65</td>
</tr>
<tr>
<td>LASSO Selection</td>
<td>66</td>
</tr>
<tr>
<td>Adaptive LASSO Selection</td>
<td>67</td>
</tr>
<tr>
<td>Group LASSO Selection</td>
<td>67</td>
</tr>
</tbody>
</table>
Introduction to Shared Concepts

SAS Visual Statistics procedures run on SAS Viya. One component of SAS Viya is SAS Cloud Analytic Services (CAS), which is the analytic server and associated cloud services. The following subsections describe how to set up and use CAS sessions.

The section “Syntax Common to SAS Visual Statistics Procedures” on page 10 describes the common syntax elements that are supported by some of the procedures in this book. In some cases, individual procedures implement these common elements in slightly different ways. When this occurs, the differences are described in the respective procedure chapters.

The section “Details for SAS Visual Statistics Procedures” on page 47 provides details that are common to some of the procedures in this book.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:
In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS statement and the LIBNAME statement, see *SAS Cloud Analytic Services: Language Reference*. For general information about CAS and CAS sessions, see *SAS Cloud Analytic Services: Fundamentals*.

### Loading a SAS Data Set onto a CAS Server

Procedures in this book require the input data to reside on a CAS server. To work with a SAS data set, you must first load the data set onto the CAS server. Data loaded on the CAS server are called *data tables*. This section lists three methods of loading a SAS data set onto a CAS server. In this section, `mycas` is the name of the caslib that is connected to the `mysess` CAS session.

- You can use a single DATA step to create a data table on the CAS server as follows:

  ```
  data mycas.Sample;
  input y x @@;
  datalines;
  .46 1 .47 2 .57 3 .61 4 .62 5 .68 6 .69 7
  ;
  ```

  Note that DATA step operations might not work as intended when you perform them on the CAS server instead of the SAS client.

- You can create a SAS data set first, and when it contains exactly what you want, you can use another DATA step to load it onto the CAS server as follows:

  ```
  data Sample;
  input y x @@;
  datalines;
  .46 1 .47 2 .57 3 .61 4 .62 5 .68 6 .69 7 .78 8
  ```
data mycas.Sample;
set Sample;
run;

- You can use the CASUTIL procedure as follows:

   proc casutil sessref=mysess;
   load data=Sample casout="Sample";
   quit;

The CASUTIL procedure can load data onto a CAS server more efficiently than the DATA step. For more information about the CASUTIL procedure, see SAS Cloud Analytic Services: Language Reference.

The mycas caslib stores the Sample data table, which can be distributed across many machine nodes. You must use a caslib reference in procedures in this book to enable the SAS client machine to communicate with the CAS session. For example, the following REGSELECT procedure statements use a data table that resides in the mycas caslib:

   proc regselect data = mycas.Sample;
   ...statements...
   run;

You can delete your data table by using the DELETE procedure as follows:

   proc delete data = mycas.Sample;
   run;

The Sample data table is accessible only in the mysess session. When you terminate the mysess session, the Sample data table is no longer accessible from the CAS server. If you want your Sample data table to be available to other CAS sessions, then you must promote your data table. For more information about data tables, see SAS Cloud Analytic Services: User’s Guide.

Syntax Common to SAS Visual Statistics Procedures

CLASS Statement

CLASS variable <(options)>...< variable <(options)>> < / global-options >;

This section applies to the following procedures: GAMMOD, GENSELECT, LOGSELECT, PLSMOD, QTRSELECT, REGSELECT, and TREESPLIT.

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. These variables enter the analysis not through their values, but through levels to which the unique values
are mapped. For more information about these mappings, see the section “Levelization of Classification Variables” on page 47.

If the procedure permits a classification variable as a response (dependent variable or target), the response does not need to be specified in the CLASS statement.

You can specify options either as individual variable options, by enclosing the options in parentheses after the variable name, or as global-options, by placing them after a slash (/). Global-options are applied to all variables that are specified in the CLASS statement. If you specify more than one CLASS statement, the global-options that are specified in any one CLASS statement apply to all CLASS statements. However, individual CLASS variable options override the global-options.

Table 2.1 summarizes the values you can use for either an option or a global-option. The options are described in detail in the list that follows Table 2.1.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>

**DESCENDING**

**DESC**

reverses the sort order of the classification variable. If both the DESCENDING and ORDER= options are specified, the procedure orders the categories according to the ORDER= option and then reverse that order.

**MISSING**

treats missing values ("." , "A", … , "Z" for numeric variables and blanks for character variables) as valid values for the CLASS variable.

If you do not specify the MISSING option, observations that have missing values for CLASS variables are removed from the analysis.

**ORDER=FORMATTED | FREQ | INTERNAL**

specifies the sort order for the levels of classification variables. This ordering determines which parameters in the model correspond to each level in the data.

The following table shows how values of the ORDER= option are interpreted.
Chapter 2: Shared Concepts

Value of ORDER= Levels Sorted By

<table>
<thead>
<tr>
<th>ORDER= Value</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMATTED</td>
<td>External formatted values, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) values. The sort order is machine-dependent. For numeric variables for which you have supplied no explicit format, the levels are ordered by their internal values.</td>
</tr>
<tr>
<td>FREQ</td>
<td>Descending frequency count (levels that have more observations come earlier in the order)</td>
</tr>
<tr>
<td>INTERNAL</td>
<td>Unformatted value. The sort order is machine-dependent.</td>
</tr>
</tbody>
</table>

For more information about sort order, see the chapter about the SORT procedure in SAS Visual Data Management and Utility Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts. By default, ORDER=FORMATTED.

PARAM=keyword

specifies the parameterization method for the classification variable or variables. You can specify any of the keywords shown in the following table; design matrix columns are created from CLASS variables according to the corresponding coding schemes.

Table 2.2 Value of PARAM=

<table>
<thead>
<tr>
<th>Value of PARAM=</th>
<th>Coding</th>
</tr>
</thead>
<tbody>
<tr>
<td>EFFECT</td>
<td>Effect coding. The REF= option in the CLASS statement determines the reference level.</td>
</tr>
<tr>
<td>GLM</td>
<td>Less-than-full-rank reference cell coding. This keyword can be used only as a global-option and is applied to all CLASS variables; all other individual variable parameterization specifications are ignored. The REF= option in the CLASS statement indirectly determines the reference level through the order of levels.</td>
</tr>
<tr>
<td>ORDINAL</td>
<td>THERMOMETER</td>
</tr>
<tr>
<td>POLYNOMIAL</td>
<td>POLY</td>
</tr>
<tr>
<td>REFERENCE</td>
<td>REF</td>
</tr>
<tr>
<td>ORTHOEFFECT</td>
<td>Orthogonalizes PARAM=EFFECT coding. The REF= option in the CLASS statement determines the reference level.</td>
</tr>
<tr>
<td>ORTHORDINAL</td>
<td>ORTHOTHERM</td>
</tr>
<tr>
<td>ORTHPOLY</td>
<td>Orthogonalizes PARAM=POLYNOMIAL coding. If the classification variable is numeric, then the ORDER= option in the CLASS statement is ignored, and the internal unformatted values are used.</td>
</tr>
</tbody>
</table>
Table 2.2  continued

<table>
<thead>
<tr>
<th>Value of PARAM=</th>
<th>Coding</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORTHREF</td>
<td>Orthogonalizes PARAM=REFERENCE coding. The REF= option in the CLASS statement determines the reference level.</td>
</tr>
</tbody>
</table>

All parameterizations are full rank, except for the GLM parameterization. If you specify a full rank parameterization for any CLASS variable, then every CLASS variable without a specified coding is given the EFFECT coding.

By default, PARAM=GLM. For more information about how parameterization of classification variables affects the construction and interpretation of model effects, see the section “Specification and Parameterization of Model Effects” on page 49.

**REF=’level’ | keyword**

**REFERENCE=’level’ | keyword**
specifies the reference level that is used when you specify a nonsingular parameterization. You can specify the following values:

- ‘level’ specifies the level of the variable to use as the reference level. Specify the formatted value of the variable if a format is assigned. You can specify this value only for an individual variable option.
- **FIRST** designates the first ordered level as reference. You can specify this value either for an individual variable option or for a global-option.
- **LAST** designates the last ordered level as reference. You can specify this value either for an individual variable option or for a global-option.

By default, REF=LAST.

**SPLIT**
specifies that design matrix columns that correspond to any effect that contains a split classification variable can be selected to enter or leave a model independently of the other design columns of that effect.

Suppose that the variable temp has three levels ('hot', 'warm', and 'cold'), that the variable gender has two levels ('M' and 'F'), and that the variables are used in a PROC REGSELECT run as follows:

```plaintext
proc regselect;
   class temp gender / split;
   model y = gender gender*temp;
run;
```

The two effects in the MODEL statement are split into eight independent effects. The effect “gender” is split into two effects that are labeled “gender_M” and “gender_F”. The effect “gender*temp” is split into six effects that are labeled “gender_M*temp_hot”, “gender_F*temp_hot”, “gender_M*temp_warm”, “gender_F*temp_warm”, “gender_M*temp_cold”, and “gender_F*temp_cold”. The previous PROC REGSELECT step is equivalent to the following:
Chapter 2: Shared Concepts

```sas
proc regselect;
   model y = gender_M gender_F
gender_M*temp_hot  gender_F*temp_hot
gender_M*temp_warm gender_F*temp_warm
gender_M*temp_cold gender_F*temp_cold;
run;
```

The SPLIT option can be used on individual classification variables. For example, consider the following PROC REGSELECT step:

```sas
proc regselect;
   class temp(split) gender;
   model y = gender gender*temp;
run;
```

In this case, the effect “gender” is not split and the effect “gender*temp” is split into three effects, which are labeled “gender*temp_hot”, “gender*temp_warm”, and “gender*temp_cold”. Furthermore, each of these three split effects now has two parameters that correspond to the two levels of “gender.” The PROC REGSELECT step is equivalent to the following:

```sas
proc regselect;
   class gender;
   model y = gender gender*temp_hot gender*temp_warm gender*temp_cold;
run;
```

CODE Statement

```sas
CODE <options> ;
```

This section applies to the following procedures: GENSELECT, KCLUS, LOGSELECT, PCA, PHSELECT, QTRSELECT, REGSELECT, and TREESPLIT.

The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a file, to a catalog entry, or to a CAS table. For survival procedures, the predicted values include survival probabilities and cumulative hazards at specific time points. To score new data, you can then include the file or the catalog entry in a DATA step, or you can specify the CAS table in the runCodeTable action in the dataStep action set.

Table 2.3 summarizes the options that you can specify in the CODE statement.
Table 2.3  CODE Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>CUMHAZ</td>
<td>Generates cumulative hazard values at specified time points</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>IPROB</td>
<td>Computes individual predicted probabilities for ordinal response models</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOSURVIVAL</td>
<td>Suppresses the generation of survival probabilities</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
<tr>
<td>PCATALL</td>
<td>Generates probabilities for all levels of categorical response variables</td>
</tr>
<tr>
<td>SHOWTIME</td>
<td>Creates variables that contain the time points at which predictions are made</td>
</tr>
<tr>
<td>TIMEPOINT=</td>
<td>Specifies the time points at which survival probabilities or cumulative hazards are predicted</td>
</tr>
</tbody>
</table>

If you do not specify the FILE= option or the OUT= option and if your SAS client has a default path, then the SAS scoring code is written to an external file named _code_. You can specify the following options in the CODE statement.

COMMENT

adds comments to the generated code.

CUMHAZ

generates SAS code to predict the cumulative hazard function at the time points that you specify in the TIMEPOINT= option. This option applies to the PHSELECT procedure.

FILE=filename

names the external file that saves the generated code. When enclosed in a quoted string (for example, FILE="c:\mydir\scorecode.sas"), this option specifies the path and filename for writing the code to an external file. If you do not specify a path but your SAS client has a default path, then the code is written to an external file named filename at that location. You can also specify an unquoted filename of no more than eight characters. If the filename is assigned as a fileref in a Base SAS FILENAME statement, the file specified in the FILENAME statement is opened; otherwise, if your SAS client has a default path, an external file named filename is created. This option cannot be specified with the OUT= option.

FORMATWIDTH=width

specifies the width to use in formatting derived numbers such as parameter estimates. You can specify a value in the range 12 to 32; the default is 20.

INDENTSIZE=n

specifies the number of spaces to indent the generated code. You can specify a value in the range 0 to 10; the default is 3.
IPROB computes the individual predicted probabilities for ordinal response models. This option applies to the following procedures: GENSELECT and LOGSELECT. For a response variable $Y$ with three levels, 1, 2, and 3, the individual probabilities are $\Pr(Y = 1)$, $\Pr(Y = 2)$, and $\Pr(Y = 3)$.

**LABELID=**value

specifies a number used to construct array names and statement labels in the generated code. You can specify a value in the range 0 to 1024; the default is randomly chosen.

**LINESIZE=**value

**LS=**value

specifies the line size for the generated code. You can specify a value in the range 64 to 254; the default is 120.

**NOSURVIVAL**

suppresses SAS code for survival probabilities prediction. This option applies to the PHSELECT procedure. If you do not specify this option, survival procedures generate SAS code to predict survival probabilities at the time points that you specify in the **TIMEPOINT=** option.

**NOTRIM**

bases comparisons of formatted values on the full format width, including blank padding. By default, blanks at the beginning and end of strings are ignored.

**OUT=**CAS-libref.data-table

creates a CAS table that contains the score code. *CAS-libref.data-table* is a two-level name, where *CAS-libref* refers to the caslib and session identifier, and *data-table* specifies the name of the output data table. For more information about this two-level name, see the section “Using CAS Sessions and CAS Engine Librefs” on page 8. You can specify this CAS table in the **runCodeTable** action in the **dataStep** action set to score another data table; for more information, see SAS Viya: System Programming Guide. This option cannot be specified with the **FILE=** option.

**PCATALL**

generates probabilities for all levels of categorical response variables. This option applies to the following procedures: GENSELECT and LOGSELECT.

**SHOWTIME**

creates variables that contain the time points at which predictions are made. This option applies to the PHSELECT procedure. If $T$ is the name of the failure time variable, these time point variables are named $T_1$, $T_2$, and so on.

**TIMEPOINT=**list | QUANTILE(probability-list)

**TIME=list | QUANTILE(probability-list)**

specifies the time points at which survival probabilities or cumulative hazards are predicted. This option applies to the PHSELECT procedure. You can specify a list of numbers that represent exact time points. For example:

```plaintext
code cumhaz timepoint = 40 to 60 by 10;
```
If $T$ is the name of the failure time variable, the preceding specification requests the predicted cumulative hazard and survival probability at the time points $T=40$, $T=50$, and $T=60$. If you also specify the SHOWTIME option, these time points are saved in the variables $T_1$, $T_2$, and $T_3$, respectively. The predicted variables are named and labeled as shown in Table 2.4.

<table>
<thead>
<tr>
<th>T</th>
<th>Name</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>40</td>
<td>C_T_1</td>
<td>Cumulative Hazard at $T_1$</td>
</tr>
<tr>
<td>50</td>
<td>C_T_2</td>
<td>Cumulative Hazard at $T_2$</td>
</tr>
<tr>
<td>60</td>
<td>C_T_3</td>
<td>Cumulative Hazard at $T_3$</td>
</tr>
<tr>
<td>40</td>
<td>S_T_1</td>
<td>Survival Probability at $T_1$</td>
</tr>
<tr>
<td>50</td>
<td>S_T_2</td>
<td>Survival Probability at $T_2$</td>
</tr>
<tr>
<td>60</td>
<td>S_T_3</td>
<td>Survival Probability at $T_3$</td>
</tr>
</tbody>
</table>

Alternatively, you can use the keyword QUANTILE to specify a list of quantile probabilities. For example:

```
code timepoint = quantile(.2, .5, .8);
```

Survival procedures compute the 20th, 50th, and 80th percentiles from the Kaplan-Meier curve (or the Breslow curve if you also specify the ENTRY= option in the MODEL statement) and use them as the time points for the prediction.

By default, TIMEPOINT=QUANTILE(0.25, 0.50, 0.75).

**DISPLAY Statement**

```
DISPLAY <table-list> < / options >;
```

This section applies to the following procedures: ASSESS, BINNING, CARDINALITY, CORRELATION, GAMMOD, GENSELECT, KCLUS, LOGSELECT, NLMOD, PARTITION, PCA, PHSELECT, PLSMOD, QTRSELECT, REGSELECT, TREESPLIT, VARIMPUTE, and VARREDUCE.

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE
statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the *table-list* as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the specific procedure chapters. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying `/*/tions/*` selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying `!/tions/*` selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following *options* after a slash (/):

- **CASESENSITIVE**
  - performs a case-sensitive comparison of table names in the *table-list* to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the *table-list* in quotation marks.

- **EXCLUDE**
  - displays all display tables except those that you specify in the *table-list*.

- **EXCLUDEALL**
  - suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  - displays the display table names, labels, and paths.

### DISPLAYOUT Statement

```plaintext
DISPLAYOUT statement < / options > ;
```

This section applies to the following procedures: ASSESS, BINNING, CARDINALITY, CORRELATION, GAMMOD, GENSELECT, KCLUS, LOGSELECT, NLMOD, PARTITION, PCA, PHSELECT, PLSMOD, QTRSELECT, REGSELECT, TREESPLIT, VARIMPUTE, and VARREDUCE.

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

The *table-spec-list* specifies a list of CAS output tables to create. Each entry in the list has either a *key=value* format or a *key* format:
key=value specifies key as the ODS table name, path, or partial pathname, and specifies value as the CAS output table name.

key specifies key as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

EFFECT Statement

EFFECT effect-name = effect-type (var-list < / effect-options> ) ;

This section applies to the following procedures: GENSELECT, LOGSELECT, PLSMOD, QTRSELECT, and REGSELECT.

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are called constructed effects to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52. For example, the terms A, B, x, A*x, and A*B in the following statements define fixed effects of the usual type in a generalized linear model:

proc genselect;
   class A B;
   model y = A B x A*x;
run;

A constructed effect, on the other hand, is assigned through the EFFECT statement. For example, in the following program, the EFFECT statement defines a constructed effect named spl:

proc genselect;
   class A B;
   effect spl = spline(x);
   model y = A B A*spl;
run;
The columns of \( x \) are formed from the data set variable \( x \) as a cubic B-spline basis with three equally spaced interior knots.

Each constructed effect corresponds to a collection of columns that are referred to by the name you supply. You can specify multiple EFFECT statements, and all EFFECT statements must precede the MODEL statement.

You must specify the following arguments:

**effect-name**

names the effect. This name can appear in only one EFFECT statement and cannot be the name of a variable in the input data set.

**effect-type**

specifies the type of effect. You can specify the following **effect-types**:

- **COLLECTION**: specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference. For more information, see the section “Collection Effects” on page 21.

- **MULTIMEMBER | MM**: specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement. For more information, see the section “Multimember Effects” on page 21.

- **POLYNOMIAL | POLY**: specifies a multivariate polynomial effect in the specified numeric variables. For more information, see the section “Polynomial Effects” on page 23.

- **SPLINE**: specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables. For more information, see the section “Spline Effects” on page 26.

**var-list**

specifies a list of variables that are used in constructing the effect. You can also specify any of the **effect-options** that are shown in Table 2.5 after a slash following the **var-list**.

### Table 2.5 EFFECT Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
</tbody>
</table>
### Table 2.5  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
<tr>
<td><strong>Polynomial Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the polynomial</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays details of the specified polynomial</td>
</tr>
<tr>
<td>MDEGREE=</td>
<td>Specifies the maximum degree of any variable in a term of the polynomial</td>
</tr>
<tr>
<td>NOSEPARATE</td>
<td>Treats the polynomial as a single effect with multiple degrees of freedom</td>
</tr>
<tr>
<td>STANDARDIZE=</td>
<td>Specifies centering and scaling suboptions for the variables that define the polynomial</td>
</tr>
<tr>
<td><strong>Spline Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>BASIS=</td>
<td>Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect</td>
</tr>
<tr>
<td>DATABOUNDARY</td>
<td>Uses the extremes of the data as boundary knots for a B-spline basis</td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the spline effect</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the knots and locations for each spline basis function</td>
</tr>
<tr>
<td>KNOTMAX=</td>
<td>Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value</td>
</tr>
<tr>
<td>KNOTMETHOD=</td>
<td>Specifies how to construct the knots for the spline effect</td>
</tr>
<tr>
<td>KNOTMIN=</td>
<td>Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value</td>
</tr>
<tr>
<td>NATURALCUBIC</td>
<td>Specifies a natural cubic spline basis for the spline effect</td>
</tr>
<tr>
<td>SEPARATE</td>
<td>Treats the spline basis for each variable as a separate effect when multiple variables are specified</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Treats each design matrix column as a separate effect for selection methods</td>
</tr>
</tbody>
</table>

**Collection Effects**

**EFFECT effect-name=COLLECTION (var-list < / DETAILS >) ;**

You use a collection effect to define a set of variables that are treated as a single effect that has multiple degrees of freedom. The variables in var-list can be continuous or classification variables. Columns in the design matrix that are contributed by a collection effect are the design columns of its constituent variables in the order in which they appear in the definition of the collection effect. If you specify the DETAILS option, then a table that shows the constituents of the collection effect is displayed.

**Multimember Effects**

**EFFECT effect-name=MULTIMEMBER (var-list < / mm-options >) ;**

**EFFECT effect-name=MM (var-list < / mm-options >) ;**
A multimember effect is formed from one or more classification variables in such a way that each observation can be associated with one or more levels of the union of the levels of the classification variables. In other words, a multimember effect is a classification-type effect with possibly more than one nonzero column entry for each observation. Multimember effects are useful, for example, in modeling the following:

- nurses’ effects on patient recovery in hospitals
- teachers’ effects on student scores
- lineage effects in genetic studies

The levels of a multimember effect consist of the union of formatted values of the variables that define this effect. Each such level contributes one column to the design matrix. For each observation, the value that corresponds to each level of the multimember effect in the design matrix is the number of times that this level occurs for the observation.

For example, the following data provide teacher information and end-of-year test scores for students after two semesters:

<table>
<thead>
<tr>
<th>Student</th>
<th>Score</th>
<th>Teacher1</th>
<th>Teacher2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mary</td>
<td>87</td>
<td>Tobias</td>
<td>Cohen</td>
</tr>
<tr>
<td>Tom</td>
<td>89</td>
<td>Rodriguez</td>
<td>Tobias</td>
</tr>
<tr>
<td>Fred</td>
<td>82</td>
<td>Cohen</td>
<td>Cohen</td>
</tr>
<tr>
<td>Jane</td>
<td>88</td>
<td>Tobias</td>
<td>.</td>
</tr>
<tr>
<td>Jack</td>
<td>99</td>
<td>.</td>
<td>.</td>
</tr>
</tbody>
</table>

For example, Mary had different teachers in the two semesters, Fred had the same teacher in both semesters, and Jane received instruction only in the first semester.

You can model the effect of the teachers on student performance by specifying a multimember effect as follows:

```
CLASS teacher1 teacher2;
EFFECT teacher = MM(teacher1 teacher2);
```

The levels of the teacher effect are Cohen, Rodriguez, and Tobias, and the associated design matrix columns are as follows:

<table>
<thead>
<tr>
<th>Student</th>
<th>Cohen</th>
<th>Rodriguez</th>
<th>Tobias</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mary</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Tom</td>
<td>0</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Fred</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Jane</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Jack</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
</tbody>
</table>

You can specify the following `mm-options` after a slash (/):

---

*Note: The content provided is a natural representation of the document text.*
DETAILS
displays a table that shows the levels of the multimember effect.

NOEFFECT
specifies that, for observations of the multimember variables whose levels are all missing, the values in
the corresponding design matrix columns be set to 0. If, in the preceding example, the teacher effect is
defined by the following statement, then the associated design matrix columns’ values for Jack are all
0:

\[
\text{EFFECT teacher = MM(teacher1 teacher2 / noeffect);}\]

This statement enables you to include Jack in the analysis even though there is no effect of teachers on
his performance.

A situation where it is important to designate observations as having no effect that can be attributed to
a classification variable is the analysis of crossover designs, where lagged treatment levels are used to
model the carryover effects of treatments between periods. Because there is no carryover effect for the
first period, the treatment lag effect in a crossover design can be modeled by using a multimember
effect that consists of a single classification variable and the NOEFFECT option, as in the following
statements:

\[
\text{CLASS Treatment lagTreatment;}
\text{EFFECT Carryover = MM(lagTreatment / noeffect);}\]

The \text{lagTreatment} variable contains a missing value for the first period. Otherwise, it contains the value
of the treatment variable for the preceding period.

STDIZE
specifies that for each observation, the entries in the design matrix that corresponds to the multimember
effect be scaled to have a sum of 1.

WEIGHT=\text{weight-list}
specifies numeric variables used to weigh the contributions of each of the classification effects that
define the constructed multimember effect. The number of variables in \text{weight-list} must match the
number of classification variables that define the effect.

Polynomial Effects

\[
\text{EFFECT effect-name=POLYNOMIAL (var-list / polynomial-options);}\]

\[
\text{EFFECT effect-name=POLY (var-list / polynomial-options);}\]

The variables in \text{var-list} must be numeric. A design matrix column is generated for each term of the specified
polynomial. By default, each of these terms is treated as a separate effect for the purpose of model building.
For example, the following two PROC GENSELECT steps yield the identical analysis:

\[
\text{proc genselect;}
\text{\hspace{1cm}effect MyPoly = polynomial(x1-x3/degree=2);}
\text{\hspace{1cm}model y = MyPoly;}
\text{run;}
\]
proc genselect;
  model y = x1 x2 x3 x1*x1 x1*x2 x1*x3 x2*x2 x2*x3 x3*x3;
run;

You can specify the following *polynomial-options* after a slash (/):

**DEGREE=n**

specifies the degree of the polynomial, where n must be a positive integer and is typically a small integer, such as 1, 2, or 3. By default, DEGREE=1.

**DETAILS**

displays a table that shows the details of the specified polynomial, including the number of terms generated. If you also specify the STANDARDIZE option, then a table that shows the standardization details is also produced.

**MDEGREE=n**

specifies the maximum degree of any variable in a term of the polynomial, where n must be a positive integer. The default is the degree of the specified polynomial. For example, the following statement generates the terms $x_1$, $x_2$, $x_1^2$, $x_1x_2$, $x_2^2$, $x_1^2x_2$, $x_1x_2^2$ and $x_1^2x_2^2$:

```plaintext
EFFECT MyPoly=POLYNOMIAL(x1 x2/degree=4 MDEGREE=2);
```

**NOSEPARATE**

treats the polynomial as a single effect that has multiple degrees of freedom. The *effect-name* that you specify is used as the constructed effect name, and the labels of the terms are used as labels of the corresponding parameters.

**STANDARDIZE < (centerscale-opts) > <= standardize-opt >**

standardizes the variables that define the polynomial. By default, the standardized variables receive prefix “s_” in the variable names.

You can use the following *centerscale-opts* to specify how the center and scale are estimated:

**METHOD=MOMENTS**

estimates the center by the variable mean and the scale by the standard deviation. If a weight variable is specified using a WEIGHT statement, the weights are not used in the computation of the mean and standard deviation, and observations that have invalid weights are ignored. Only observations that are used in performing the analysis are used for the standardization.

**METHOD=RANGE**

estimates the center by the midpoint of the variable range and the scale as half the variable range. Any observation that has a missing value for any regressor used in the model is ignored when the range of variables in a polynomial effect is computed. Observations that have valid regressor values but missing or invalid values of frequency variables, weight variables, or dependent variables are used in computing variable ranges. By default, METHOD=RANGE.

**METHOD=WMOMENTS**

is the same as METHOD=MOMENTS except that weighted means and weighted standard deviations are used.
**PREFIX=NONE | quoted-string**

specifies the prefix that is appended to standardized variables when forming the term labels. You can specify the following values:

- **quoted-string** specifies the prefix
- **NONE** does not apply a prefix

By default, PREFIX="s_".

Let

\[
\begin{align*}
    n &= \text{number of observations used in the analysis} \\
    w &= \text{weight variable} \\
    f &= \text{frequency variable} \\
    x &= \text{variable to be standardized} \\
    x_{(n)} &= \text{Max}_{i=1}^{n} (x_i) \\
    x_{(1)} &= \text{Min}_{i=1}^{n} (x_i) \\
    F &= \text{sum of frequencies} \\
    &= \sum_{i=1}^{n} f_i \\
    \text{WF} &= \text{sum of weighted frequencies} \\
    &= \sum_{i=1}^{n} w_i f_i
\end{align*}
\]

Table 2.6 shows how the center and scale are computed for each of the supported methods.

<table>
<thead>
<tr>
<th>Method</th>
<th>Center</th>
<th>Scale</th>
</tr>
</thead>
<tbody>
<tr>
<td>RANGE</td>
<td>((x_{(n)} + x_{(1)})/2)</td>
<td>((x_{(n)} - x_{(1)})/2)</td>
</tr>
<tr>
<td>MOMENTS</td>
<td>(\bar{x} = \sum_{i=1}^{n} f_i x_i / F)</td>
<td>(\sqrt{\sum_{i=1}^{n} f_i (x_i - \bar{x})^2 / (F - 1)})</td>
</tr>
<tr>
<td>WMOMENTS</td>
<td>(\bar{x}<em>w = \sum</em>{i=1}^{n} w_i f_i x_i / \text{WF})</td>
<td>(\sqrt{\sum_{i=1}^{n} w_i f_i (x_i - \bar{x}_w)^2 / (F - 1)})</td>
</tr>
</tbody>
</table>

You can control whether the standardization is to center, scale, or both center and scale by specifying one of the following `standardize-opts`:

**CENTER**

centers but does not scale the variables. For a variable \(x\),

\[
s_x = x - \text{center}
\]

**CENTERSCALE**

centers and scales the variables. This is the default if you do not specify a `standardization-opt`. For a variable \(x\),

\[
s_x = \frac{x - \text{center}}{\text{scale}}
\]
NONE
performs no standardization.

SCALE
scales but does not center the variables. For a variable $x$,

$$s_x = \frac{x}{\text{scale}}$$

Spline Effects

This section discusses the construction of spline effects through the EFFECT statement. A spline effect expands variables into spline bases whose form depends on the options that you specify. For more information about regression splines and spline bases, see the section “Splines and Spline Bases” on page 29. You request a spline effect with the syntax

```
EFFECT name=SPLINE (var-list < / spline-options> ) ;
```

The variables in `var-list` must be numeric. Design matrix columns are generated separately for each of these variables, and the set of columns is collectively referred to with the specified name. By default, the spline basis that is generated for each variable is a cubic B-spline basis that has three equally spaced knots positioned between the minimum and maximum values of that variable. This yields by default seven design matrix columns for each of the variables in the SPLINE effect.

You can specify the following `spline-options` after a slash (/):

- **BASIS=BSPLINE**
  uses a B-spline basis for the spline expansion. For splines of degree $d$ that are defined with $n$ knots, this basis consists of $n + d + 1$ columns. In order to completely specify the B-spline basis, $d$ left-side boundary knots and $\max\{d, 1\}$ right-side boundary knots are also required. For information about how to specify the positions of both the internal and boundary knots, see the KNOTMETHOD=, DATABOUNDARY, KNOTMIN=, and KNOTMAX= suboptions.

- **BASIS=TPF(options)**
  specifies a truncated power function basis for the spline expansion. For splines of degree $d$ that are defined with $n$ knots for a variable $x$, this basis consists of an intercept, polynomials $x, x^2, \ldots, x^d$, and one truncated power function for each of the $n$ knots. Unlike the B-spline basis, no boundary knots are required. For information about how you can specify the position of the internal knots, see the KNOTMETHOD= suboption.

You can modify the number of columns when you request BASIS=TPF by specifying the following `options`:

- **NOINT** excludes the intercept column.
- **NOPowers** excludes the intercept and polynomial columns.

By default, BASIS=BSPLINE.

- **DATABOUNDARY**
  uses the extremes of the data as boundary knots when building a B-spline basis.
DEGREE=$n$
specifies the degree of the spline transformation, where $n$ must be a nonnegative integer and is typically a small integer, such as 0, 1, 2, or 3. By default, DEGREE=3.

DETAILS
displays tables that show the knot locations and the knots associated with each spline basis function.

KNOTMAX=\textit{value} 
requests that, for each variable in the EFFECT statement, the right-side boundary knots be equally spaced starting at the maximum of the variable and ending at the specified value. This option is ignored for variables whose maximum value is greater than the specified value or if the DATABOUNDARY option is also specified.

KNOTMETHOD=\textit{knot-method\< (knot-options) >}
specifies how to construct the knots for spline effects. You can choose from the following \textit{knot-methods} and affect the knot construction further with the method-specific \textit{knot-options}:

\textbf{EQUAL\< (n) >}

specifies that \textit{n} equally spaced knots be positioned between the extremes of the data. By default, \textit{n}=3. For a B-spline basis, any needed boundary knots continue to be equally spaced unless the DATABOUNDARY option has also been specified. By default, KNOTMETHOD=EQUAL(3).

\textbf{LIST(number-list)}
specifies the list of internal knots to be used in forming the spline basis columns. For a B-spline basis, the data extremes are used as boundary knots.

\textbf{LISTWITHBOUNDARY(number-list)}
specifies the list of all knots that are used in forming the spline basis columns. When you use a truncated power function basis, this list is interpreted as the list of internal knots. When you use a B-spline basis of degree $d$, then the first $d$ entries are used as left-side boundary knots and the last $\max(d, 1)$ entries in the list are used as right-side boundary knots.

\textbf{MULTISCALE\< (multiscale-options) >}
generates multiple B-spline bases, which correspond to sets that have an increasing number of internal knots. As the number of internal knots increases, the spline basis that is generated can approximate features of the data at finer scales. So generating bases at multiple scales facilitates the modeling of both coarse- and fine-grained features of the data. For scale $i$, the spline basis corresponds to $2^i$ equally spaced internal knots. By default, the bases for scales 0–7 are generated. For each scale, a separate spline effect is generated. The name of the constructed spline effect at scale $i$ is formed by appending _Si to the effect name that you specify in the EFFECT statement. If you specify multiple variables in the EFFECT statement, then spline bases are generated separately for each variable at each scale and the name of the corresponding effect is obtained by appending the variable name followed by _Si to the name in the EFFECT statement. For example, the following statement generates effects named spl_x1_S0, spl_x1_S1, spl_x1_S2, ..., spl_x1_S7 and spl_x2_S1, spl_x2_S2, ..., spl_x2_S7:

\begin{verbatim}
EFFECT spl = spline(x1 x2 / knotmethod=multiscale);
\end{verbatim}

The MULTISCALE option is ignored if you specify the BASIS=TPF \textit{spline-option}. 

The following multiscale-options control which scales are included:

- **STARTSCALE=n**: specifies the start scale, where \( n \) is a positive integer. By default, \( \text{STARTSCALE}=0 \).
- **ENDSCALE=n**: specifies the end scale, where \( n \) is a positive integer. By default, \( \text{ENDSCALE}=7 \).

**PERCENTILES(\( n \))** requests that internal knots be placed at \( n \) equally spaced percentiles of the variable or variables named in the EFFECT statement. For example, the following statement positions internal knots at the deciles of the variable \( x \). For a B-spline basis, the extremes of the data are used as boundary knots:

```plaintext
EFFECT spl = spline(x / knotmethod=percentiles(9));
```

**RANGEFRACTIONS(\( \text{fraction-list} \))** places internal knots at each fraction of the ranges of the variables in the EFFECT statement. For example, if variable \( x_1 \) ranges between 1 and 3 and variable \( x_2 \) ranges between 0 and 20, then the following EFFECT statement uses internal knots 1.2, 2, and 2.5 for variable \( x_1 \) and internal knots 2, 10, and 15 for variable \( x_2 \):

```plaintext
EFFECT spl = spline(x1 x2 / knotmethod=rangefractions(.1 .5 .75));
```

For a B-spline basis, the data extremes are used as boundary knots.

**KNOTMIN=value** requests that, for each variable in the EFFECT statement, the left-side boundary knots be equally spaced starting at the specified value and ending at the minimum of the variable. This option is ignored for variables whose minimum value is less than the specified value or if the DATABOUNDARY option is also specified.

**NATURALCUBIC** uses a natural cubic spline basis for the spline expansion. Natural cubic splines, also known as restricted cubic splines, are cubic splines that are constrained to be linear beyond the extreme knots. The natural cubic spline basis that is produced by the EFFECT statement is obtained by starting from the unrestricted truncated power function cubic spline basis that is defined with \( n \) distinct knots and imposes the linearity constraints beyond the extreme knots. This basis consists of an intercept, the polynomial \( x \), and \( n - 2 \) functions that are all linear beyond the largest knot. The \( i \)th function, \( i = 1, 2, \ldots, n - 2 \), is 0 to the left of the \( i \)th knot, which is called the “break knot.” For more information about this basis, see the section “Splines and Spline Bases” on page 29. You can use the NOINT and NOPOWERS suboptions of the BASIS=TPF option to suppress the intercept and polynomial \( x \) when the columns of the natural cubic spline basis are formed. When you specify the NATURALCUBIC option, the options BASIS=BSPLINE, DATABOUNDARY, DEGREE=, and KNOTMETHOD=MULTISCALE are not applicable.

**SEPARATE** requests that, when multiple variables are specified in the EFFECT statement, the spline basis for each variable be treated as a separate effect. The names of these separated effects are formed by appending an underscore followed by the name of the variable to the name that you specify in the EFFECT statement. For example, the following statement generates the effect names spl_x1 and spl_x2:
EFFECT spl = spline(x1 x2 / separate);

In procedures that support variable selection, such as the REGSELECT procedure, these two effects can enter or leave the model independently during the selection process.

**SPLIT**

treats each individual column in the design matrix that corresponds to the spline effect as a separate effect that can enter or leave the model independently. Names for these split effects are generated by appending the variable name and an index for each column to the name that you specify in the EFFECT statement. For example, the effects generated for the spline effect in the following statement are spl_x1:1, spl_x1:2, ..., spl_x1:7 and spl_x2:1, spl_x2:2, ..., spl_x2:7:

EFFECT spl = spline(x1 x2 / split);

**Splines and Spline Bases**

This section provides details about how the EFFECT statement constructs spline bases. A spline function is a piecewise polynomial function in which the individual polynomials have the same degree and connect smoothly at join points whose abscissa values, called knots, are prespecified. You can use spline functions to fit curves to a wide variety of data.

A spline of degree 0 is a step function with steps located at the knots. A spline of degree 1 is a piecewise linear function where the lines connect at the knots. A spline of degree 2 is a piecewise quadratic curve whose values and slopes coincide at the knots. A spline of degree 3 is a piecewise cubic curve whose values, slopes, and curvature coincide at the knots. Visually, a cubic spline is a smooth curve, and it is the most commonly used spline when a smooth fit is desired. Note that when no knots are used, splines of degree \( d \) are simply polynomials of degree \( d \).

More formally, suppose you specify knots \( k_1 < k_2 < k_3 < \cdots < k_n \). Then a spline of degree \( d \geq 0 \) is a function \( S(x) \) with \( d-1 \) continuous derivatives such that

\[
S(x) = \begin{cases} 
  P_0(x) & x < k_1 \\
  P_i(x) & k_i \leq x < k_{i+1}; \ i = 1, 2, \ldots, n-1 \\
  P_n(x) & x \geq k_n 
\end{cases}
\]

where each \( P_i(x) \) is a polynomial of degree \( d \). The requirement that \( S(x) \) has \( d-1 \) continuous derivatives is satisfied by requiring that the function values and all derivatives up to order \( d-1 \) of the adjacent polynomials at each knot match.

A counting argument yields the number of parameters that define a spline with \( n \) knots. There are \( n + 1 \) polynomials of degree \( d \), producing \( (n + 1)(d + 1) \) coefficients. However, there are \( d \) restrictions at each of the \( n \) knots, so the number of free parameters is \( (n + 1)(d + 1) - nd = n + d + 1 \). In mathematical terminology this says that the dimension of the vector space of splines of degree \( d \) on \( n \) distinct knots is \( n + d + 1 \). If you have \( n + d + 1 \) basis vectors, then you can fit a curve to your data by regressing your dependent variable by using this basis for the corresponding design matrix columns. In this context, such a spline is known as a regression spline. The EFFECT statement provides a simple mechanism for obtaining such a basis.

If you remove the restriction that the knots of a spline must be distinct and allow repeated knots, then you can obtain functions that have less smoothness and even discontinuities at the repeated knot location. For a spline
of degree $d$ and a repeated knot that has multiplicity $m \leq d$, the piecewise polynomials that join such a knot are required to have only $d - m$ matching derivatives. Note that this increases the number of free parameters by $m - 1$ but also decreases the number of distinct knots by $m - 1$. Hence the dimension of the vector space of splines of degree $d$ with $n$ knots is still $n + d + 1$, provided that any repeated knot has a multiplicity less than or equal to $d$.

The EFFECT statement supports the commonly used truncated power function basis and $B$-spline basis. With exact arithmetic and by using the complete basis, you obtain the same fit with either of these bases. The following subsections provide details about constructing spline bases for the space of splines of degree $d$ with $n$ knots that satisfies $k_1 \leq k_2 \leq k_3 < \cdots \leq k_n$.

**Truncated Power Function Basis**

A truncated power function for a knot $k_i$ is a function defined by

$$t_i(x) = \begin{cases} 0 & x < k_i \\ (x - k_i)^d & x \geq k_i \end{cases}$$

Figure 2.1 shows such functions for $d = 1$ and $d = 3$ with a knot at $x = 1$.

![Figure 2.1 Truncated Power Functions with Knot at $x = 1$](image)

The name is derived from the fact that these functions are shifted power functions that are truncated to 0 to the left of the knot. These functions are piecewise polynomial functions that have two pieces whose function values and derivatives of all orders up to $d-1$ are 0 at the defining knot. Hence these functions are splines of degree $d$. It is easy to see that these $n$ functions are linearly independent. However, they do not form a basis, because such a basis requires $n+d-1$ functions. The usual way to add $d+1$ additional basis functions is to use the polynomials $1, x, x^2, \ldots, x^d$. These $d+1$ functions together with the $n$ truncated power functions $t_i(x), i = 1, 2, \ldots, n$ form the truncated power basis.

Note that each time a knot is repeated, the associated exponent used in the corresponding basis function is reduced by 1. For example, for splines of degree $d$ with three repeated knots $k_i = k_{i+1} = k_{i+2}$, the corresponding basis functions are $t_i(x) = (x - k_i)^d$, $t_{i+1}(x) = (x - k_i)^{d-1}$, and $t_{i+2}(x) = (x - k_i)^{d-2}$. Provided that the multiplicity of each repeated knot is less than or equal to the degree, this construction continues to yield a basis for the associated space of splines.

The main advantage of the truncated power function basis is the simplicity of its construction and the ease
of interpreting the parameters in a model that corresponds to these basis functions. However, there are two weaknesses when you use this basis for regression. These functions grow rapidly without bound as $x$ increases, resulting in numerical precision problems when the $x$ data span a wide range. Furthermore, many or even all of these basis functions can be nonzero when evaluated at some $x$ value, resulting in a design matrix that has few zeros and precludes the use of sparse matrix technology to speed up computation. This weakness can be addressed by using a B-spline basis.

**B-Spline Basis**
A B-spline basis can be built by starting with a set of Haar basis functions, which are functions that are 1 between adjacent knots and 0 elsewhere, and then applying a simple linear recursion relationship $d$ times, yielding the $n + d + 1$ needed basis functions. For the purpose of building the B-spline basis, the $n$ prespecified knots are called internal knots. This construction requires $d$ additional knots, known as boundary knots, to be positioned to the left of the internal knots, and $\max(d, 1)$ boundary knots to be positioned to the right of the internal knots. The actual values of these boundary knots can be arbitrary. The EFFECT statement provides several methods for placing the necessary boundary knots, including the common method of using repeated values of the data extremes as the boundary knots. The boundary knot placement affects the precise form of the basis functions that are generated, but it does not affect the following two desirable properties:

- The B-spline basis functions are nonzero over an interval that spans at most $d + 2$ knots. This yields design matrix columns each of whose rows contain at most $d + 2$ adjacent nonzero entries.
- The computation of the basis functions at any $x$ value is numerically stable and does not require evaluating powers of this value.

The following figures show the B-spline bases that are defined on $[0, 1]$ with four equally spaced internal knots at 0.2, 0.4, 0.6, and 0.8.

**Figure 2.2** shows a linear B-spline basis. This basis consists of six functions, each of which is nonzero over an interval that spans at most three knots.

**Figure 2.2** Linear B-Spline Basis with Four Equally Spaced Interior Knots

**Figure 2.3** shows a cubic B-spline basis where the necessary boundary knots are positioned at $x = 0$ and $x = 1$. This basis consists of eight functions, each of which is nonzero over an interval that spans at most five knots.
Figure 2.3 Cubic B-Spline Basis with Four Equally Spaced Interior Knots

Figure 2.4 shows a different cubic B-spline basis where the necessary left-side boundary knots are positioned at –0.6, –0.4, –0.2, and 0. The right-side boundary knots are positioned at 1, 1.2, 1.4, and 1.6. As in the basis shown in Figure 2.3, this basis consists of eight functions, each of which is nonzero over an interval that spans at most five knots. The different positioning of the boundary knots has merely changed the shape of the individual basis functions.

Figure 2.4 Cubic B-Spline Basis with Equally Spaced Boundary and Interior Knots

For more information about this construction, see Hastie, Tibshirani, and Friedman (2001).
**Natural Cubic Spline Basis**

Natural cubic splines are cubic splines with the additional restriction that the splines are required to be linear beyond the extreme knots. Some authors prefer the terminology “restricted cubic splines” to “natural cubic splines.” The space of unrestricted cubic splines on $n$ knots has the dimension $n + 4$. Imposing the restrictions that the cubic polynomials beyond the first and last knot reduce to linear polynomials reduces the number of degrees of freedom by 4, so a basis for the natural cubic splines consists of $n$ functions. Starting from the truncated power function basis for the unrestricted cubic splines, you can obtain a reduced basis by imposing linearity constraints. For more information about this construction, see Hastie, Tibshirani, and Friedman (2001). Figure 2.5 shows this natural cubic spline basis defined on $[0, 1]$ with four equally spaced internal knots at 0.2, 0.4, 0.6, and 0.8. This basis consists of four basis functions that are all linear beyond the extreme knots at 0.2 and 0.8.

![Figure 2.5 Natural Cubic Spline Basis with Four Equally Spaced Knots](image)

**ODS Table Names**

Each constructed effect produces one or more informative tables when the DETAILS option is also specified. Each table has a name associated with it. This name is used to refer to the table by procedures that support a DISPLAY or DISPLAYOUT statement. You also use this name to refer to the table in ODS statements. These names are listed in Table 2.7.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>BSplineDetails</td>
<td>B-spline basis details</td>
<td>BASIS=BSPLINE</td>
</tr>
<tr>
<td>CollectionLevelInfo</td>
<td>Levels of collection effects</td>
<td></td>
</tr>
<tr>
<td>MMLLevelInfo</td>
<td>Levels of multimember effects</td>
<td></td>
</tr>
<tr>
<td>PolyDetails</td>
<td>Number of variables and columns, polynomial</td>
<td></td>
</tr>
<tr>
<td></td>
<td>degree, and standardization method</td>
<td></td>
</tr>
<tr>
<td>PolyScaling</td>
<td>Centering and scaling details</td>
<td>STANDARDIZE</td>
</tr>
<tr>
<td>SplineKnots</td>
<td>knot and boundary knot values</td>
<td></td>
</tr>
<tr>
<td>TPFSplineDetails</td>
<td>Truncated power function spline basis details</td>
<td>BASIS=TPF or</td>
</tr>
<tr>
<td></td>
<td></td>
<td>NATURALCUBIC</td>
</tr>
</tbody>
</table>
PARTITION Statement

PARTITION partition-option ;

This section applies to the following procedures: ASSESS, BINNING, CARDINALITY, GENSELECT, KCLUS, LOGSELECT, NLMOD, PARTITION, PHSELECT, PLSMOD, QTRSELECT, REGSELECT, TREESPLIT, VARIMPUTE, and VARREDUCE.

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78. Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:

FRACTION(< TEST=frac > < VALIDATE=frac > < SEED=number >)
randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The SEED= option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify SEED=number or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

ROLE=variable (< TEST=value > < TRAIN=value > < VALIDATE=value >)
ROLEVAR=variable (< TEST=value > < TRAIN=value > < VALIDATE=value >)
names the variable in the input data table whose values are used to assign roles to each observation. This variable cannot also appear as an analysis variable in other statements or options. The TEST=, TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

SELECTION Statement

SELECTION < METHOD=method<(method-options)> >> <options> ;

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, and REGSELECT.

Procedures in this book that support model selection use the SELECTION statement to control details about the model selection process.
You can specify the following methods in the SELECTION statement:

METHOD=method < (method-options) >

specifies the method used to select the model. You can also specify method-options that apply to the specified method by enclosing them in parentheses after the method.

The following methods are available and are explained in detail in the section “Model Selection Methods” on page 60. By default, METHOD=STEPWISE.

NONE specifies no model selection.
BACKWARD specifies backward elimination. This method starts with all effects in the model and deletes effects.
FORWARD specifies forward selection. This method starts with no effects in the model and adds effects.
STEPWISE specifies stepwise regression. This method is similar to the FORWARD method except that effects already in the model do not necessarily stay there.
FORWARDSWAP specifies forward-swap selection, which is an extension of the forward selection method. Before any addition step, the procedure makes all pairwise swaps of one effect in the model and one effect out of the current model that improve the selection criterion. When the selection criterion is R square, this method is the same as the MAXR method in the REG procedure in SAS/STAT software. The only SAS Viya procedure that supports this method is the REGSELECT procedure.
LAR specifies least angle regression. Like forward selection, this method starts by adding effects to an empty model. The parameter estimates at any step are “shrunk” when they are compared to the corresponding least squares estimates. If the model contains classification variables, then these classification variables are split. For more information, see the SPLIT option in the CLASS statement. The only SAS Viya procedure that supports this method is the REGSELECT procedure.
LASSO adds and deletes parameters by using a version of ordinary least squares in which the sum of the absolute regression coefficients is constrained. If the model contains classification variables, then these classification variables are split. For more information, see the SPLIT option in the CLASS statement.

Table 2.8 lists the applicable method-options for each of these methods.
The syntax of the *method-options* that you can specify in parentheses after the SELECTION= option *method* follows. As described in Table 2.8, not all selection *method-options* are applicable to every *method*.

**ADAPTIVE < (GAMMA=nonnegative number) >**  
applies adaptive weights to each of the coefficients when METHOD=LASSO. Ordinary least squares estimates of the model parameters are used to form the adaptive weights. You use the GAMMA= option to specify the power transformation that is applied to the parameters in forming the adaptive weights. By default, GAMMA=1.

**CHOOSE=criterion**  
chooses from the list of models (at each step of the selection process) the model that yields the best value of the specified criterion. If the optimal value of the specified criterion occurs for models at more than one step, then the model that has the smallest number of parameters is chosen. If you do not specify the CHOOSE= option, then the selected model is the model at the final step in the selection process. The criteria that are supported depend on the type of model that is being fit. For the supported values of *criterion*, see the chapters for the relevant procedures.

**COMPETITIVE**  
is applicable as a *method-option* only when METHOD=STEPWISE and the SELECT= criterion is not SL. If you specify the COMPETITIVE option, then the SELECT= criterion is evaluated for all models in which an effect currently in the model is dropped or an effect not yet in the model is added. The effect whose removal from or addition to the model yields the maximum improvement to the SELECT= criterion is dropped or added.

**CRITERION=criterion**  
is an alias for the SELECT= option.
FAST
implements the computational algorithm of Lawless and Singhal (1978) to compute a first-order approximation to the remaining slope estimates for each subsequent elimination of a variable from the model. When applied in backward selection, this option essentially leads to approximating the selection process as the selection process of a linear regression model in which the crossproducts matrix equals the Hessian matrix in the full model under consideration. This option is available only when METHOD=BACKWARD is specified. It is computationally efficient because the model is not fit after removal of each effect.

LSCOEFFS
requests a hybrid version of the LAR and LASSO methods, in which the sequence of models is determined by the LAR or LASSO algorithm but the coefficients of the parameters for the model at any step are determined by using ordinary least squares.

MAXEFFECTS=n
specifies the maximum number of effects in any model that is considered during the selection process. This option is ignored when METHOD=BACKWARD is specified. If, at some step of the selection process, the model contains the specified maximum number of effects, then no candidates for addition are considered.

MAXSTEPS=n
specifies the maximum number of selection steps that are performed. The default value of n is the number of effects in the MODEL statement when METHOD=FORWARD, METHOD=BACKWARD, or METHOD=LAR. The default is three times the number of effects when METHOD=STEPWISE or METHOD=LASSO.

MINEFFECTS=n
specifies the minimum number of effects in any model that is considered during backward selection. This option is ignored unless METHOD=BACKWARD is specified. The backward selection process terminates if, at some step of the selection process, the model contains the specified minimum number of effects.

SELECT=SL | criterion
specifies the criterion that the procedure uses to determine the order in which effects enter or leave at each step of the selection method. For each step, the effect whose addition to or removal from the current model yields the maximum improvement in the specified criterion is selected. You can use the traditional significance-level approach by specifying the SL criterion; for other supported criteria, see the chapter for the relevant procedure. This option is not valid when METHOD=LAR or METHOD=LASSO.

SLENTRY=value
SLE=value
specifies the significance level for entry when STOP=SL or SELECT=SL. By default, SLENTRY=0.05.

SLSTAY=value
SLS=value
specifies the significance level for staying in the model when STOP=SL or SELECT=SL. By default, SLSTAY=0.05.
STOP=SL | NONE | criterion

specifies a criterion that is used to stop the selection process. The criteria that are supported depend on the type of model that is being fit. For information about the supported criteria, see the chapter for the relevant procedure.

If you do not specify the STOP= option but do specify the SELECT= option, then the criterion specified in the SELECT= option is also used as the STOP= criterion.

You can specify the following values:

NONE stops the selection process if no suitable add or drop candidates can be found or if a size-based limit is reached. For example, if you specify STOP=NONE MAXEFFECTS=5, then the selection process stops at the first step that produces a model that has five effects.

SL stops the selection process at the step where the significance level of the candidate for entry is greater than the SLENTRY= value for addition steps when METHOD=FORWARD or METHOD=STEPWISE and where the significance level of the candidate for removal is greater than the SLSTAY= value when METHOD=BACKWARD or METHOD=STEPWISE.

criterion stops the selection process if the selection process produces a local extremum of this criterion or if a size-based limit is reached. For example, if you specify STOP=AIC MAXSTEPS=5, then the selection process stops before step 5 if the sequence of models has a local minimum of the AIC criterion before step 5. The determination of whether a local minimum is reached is made on the basis of a stop horizon. The default stop horizon is 3, but you can change it by using the STOPHORIZON= option. If the stop horizon is $n$ and the STOP= criterion at any step is better than the stop criterion at the next $n$ steps, then the selection process terminates.

In addition, you can also specify the following options:

DETAILS=NONE | SUMMARY | ALL

DETAILS=STEPS<(CANDIDATES(ALL | $n$))>

specifies the level of detail to be produced about the selection process. The default is DETAILS=SUMMARY.

The DETAILS=ALL and DETAILS=STEPS options produce the following output:

- tables that provide information about the model that is selected at each step of the selection process.
- entry and removal statistics for inclusion or exclusion candidates at each step. By default, only the top 10 candidates at each step are shown. If you specify STEPS(CANDIDATES($n$)), then the best $n$ candidates are shown. If you specify STEPS(CANDIDATES(ALL)), then all candidates are shown.
- a selection summary table that shows by step the effect that is added to or removed from the model in addition to the values of the SELECT, STOP, and CHOOSE criteria for the resulting model.
- a stop reason table that describes why the selection process stopped.
a selection reason table that describes why the selected model was chosen.

- a selected effects table that lists the effects that are in the selected model.

The DETAILS=SUMMARY option produces only the selection summary, stop reason, selection reason, and selected effects tables.

HIERARCHY=NONE | SINGLE | SINGLECLASS

specifies whether and how the model hierarchy requirement is applied. You can specify that only classification effects, or both classification and continuous effects, be subject to the hierarchy requirement. This option is ignored unless you also specify one of the following options: METHOD=FORWARD, METHOD=BACKWARD, or METHOD=STEPWISE.

Model hierarchy refers to the requirement that, for any term to be in the model, all model effects that are contained in the term must be present in the model. For example, in order for the interaction A*B to enter the model, the main effects A and B must be in the model. Likewise, neither effect A nor effect B can leave the model while the interaction A*B is in the model.

You can specify the following values:

NONE

specifies that model hierarchy not be maintained. Any single effect can enter or leave the model at any step of the selection process.

SINGLE

specifies that only one effect enter or leave the model at one time, subject to the model hierarchy requirement. For example, suppose that the model contains the main effects A and B and the interaction A*B. In the first step of the selection process, either A or B can enter the model. In the second step, the other main effect can enter the model. The interaction effect can enter the model only when both main effects have already entered. Also, before A or B can be removed from the model, the A*B interaction must first be removed. All effects (CLASS and interval) are subject to the hierarchy requirement.

SINGLECLASS

is the same as HIERARCHY=SINGLE except that only CLASS effects are subject to the hierarchy requirement.

By default, HIERARCHY=NONE.

ORDERSELECT

specifies that effects in the selected model are displayed in the order in which they first entered the model. If you do not specify the ORDERSELECT option, then effects in the selected model are displayed in the order in which they appear in the MODEL statement.

PLOT < (global-plot-options) > <= plot-request < (options) >>

PLOTS < (global-plot-options) > <= (plot-request < (options) > <= ... plot-request < (options) >) >>

controls the selection process plots that are produced through ODS Graphics. When you specify only one plot request, you can omit the parentheses around it. Here are some examples:

plots=all
plots=coefficients(unpack)
plots(unpack)=(criteria fitByRole)

ODS Graphics must be enabled before you can request plots. For example:
ods graphics on;

proc regselect;
   model y = x1-x100;
   selection method=forward plots=all;
run;

ods graphics off;

Global Plot Options

Each global-plot-option applies to all plots that the SELECTION statement generates, unless you alter the option by using a specific plot option that follows a plot-request. You can specify the following global-plot-options:

ENDSTEP=n 
terminates the step ranges shown on the horizontal axes of plots at the specified step. By default, the step range that is shown terminates at the final step of the selection process.

LOGP | LOGPVALUE 
uses a logarithmic axis to display entry and removal significance levels.

MAXPARMLABEL=n 
specifies the maximum number of characters beyond which all parameter labels on the coefficient progression panel and the coefficient progression plot are suppressed. By default, MAXPARMLABEL=20.

MAXSTEPLABEL=n 
specifies the maximum number of characters of effect labels to display on the horizontal axes of the plots. By default, MAXSTEPLABEL=20. If the length of any effect label exceeds n, then step numbers are used on the horizontal axes of the plots.

STARTSTEP=n 
specifies that the step ranges shown on the horizontal axes of plots start at the specified step. By default, the step range that is shown starts at the initial step of the selection process.

STEPAXIS=EFFECT | NORMB | NUMBER 
specifies the horizontal axis to be used on the plots, where this axis represents the sequence of entering or departing effects. You can specify the following values:

EFFECT 
requests that each step be labeled by a prefix followed by the name of the effect that enters or leaves at that step. The prefix consists of the step number, followed by a “+” or a “−” sign, depending on whether the effect enters (+) or leaves (-) at that step.

NORMB 
requests that the horizontal axis value at step i be the L1 norm of the parameters at step i, normalized by the L1 norm of the parameters at the final step. STEPAXIS=NORMB is valid only with the LAR, LASSO, and elastic net selection methods.
NUMBER requests that each step be labeled by the step number.

UNPACK | UNPACKPANEL suppresses paneling. By default, multiple plots can appear in the coefficient progression panel and the criteria panel. Specify UNPACK to see each plot individually. You can also specify UNPACK as a suboption of the CRITERIA and COEFFICIENTS options.

Specific Plot Options

You can specify the following plot-requests and their options:

ALL produces all relevant plots.

COEFFICIENTS | COEFFICIENTPANEL < (UNPACK | UNPACKPANEL) > creates a panel of two plots. The upper plot shows the progression of the parameter values as the selection process proceeds. The lower plot shows the progression of the CHOOSE= criterion. If no CHOOSE= criterion is in effect, then only the coefficient progression is shown. If you specify the UNPACK option, then the coefficient progression and the CHOOSE= criterion progression are shown in separate plots.

CRITERIA | CRITERIONPANEL < (UNPACK | UNPACKPANEL) > creates a panel of model fit criteria. If you specify the UNPACK option, then each criterion progression is shown in a separate plot.

FITBYROLE plots the progression of a fit statistic on the training, test, and validation data. The fit statistic that is displayed depends on the type of model that is being fit. The fit by role plot is not produced if you do not specify a PARTITION statement.

NONE suppress all selection process plots, even if you specify other plot options.

SELECTION=NONE | BACKWARD | FORWARD | STEPWISE | LAR | LASSO is an alias for the METHOD= option.

STOPHORIZON=n specifies the number of consecutive steps at which the STOP= criterion must worsen in order for a local extremum to be detected. For example, suppose that STOP=AIC and the sequence of AIC values at steps 1 to 6 of a selection are 10, 7, 4, 6, 5, 2. If STOPHORIZON=2, then the AIC criterion is deemed to have a local minimum at step 3 because the AIC value at the next two steps are greater than the value 4 that occurs at step 3. However, if STOPHORIZON=3, then the value at step 3 is not deemed to be a local minimum because the AIC value at step 6 is lower than the AIC value at step 3. If you specify STOP=NONE then the stop horizon value is ignored. If you specify STOP=SL, METHOD=LAR, or METHOD=LASSO, then n is ignored and STOPHORIZON=1 is used. By default, STOPHORIZON=3.
Optimization Options

This section applies to the following procedures: GENSELECT, LOGSELECT, and NLMOD.

The following options are typically available in the PROC statement of the procedures in this book that perform optimizations:

**ABSCONV=r**

**ABSTOL=r**

specifies an absolute function convergence criterion. For minimization, termination requires \( f(\psi^{(k)}) \leq r \), where \( \psi \) is the vector of parameters in the optimization and \( f(\cdot) \) is the objective function. The default value of \( r \) is the negative square root of the largest double-precision value, which serves only as a protection against overflows.

**ABSFCONV=r < n>**

**ABSFSTOL=r < n>**

specifies an absolute function difference convergence criterion. For all techniques except NMSIMP, termination requires a small change of the function value in successive iterations:

\[
| f(\psi^{(k-1)}) - f(\psi^{(k)}) | \leq r
\]

Here, \( \psi \) denotes the vector of parameters that participate in the optimization, and \( f(\cdot) \) is the objective function. The same formula is used for the NMSIMP technique, but \( \psi^{(k)} \) is defined as the vertex that has the lowest function value and \( \psi^{(k-1)} \) is defined as the vertex that has the highest function value in the simplex. PROC NLMOD provides an optional integer value \( n \), which specifies the number of successive iterations for which the criterion must be satisfied before the process can be terminated. By default, ABSFCONV=0.

**ABSGCONV=r < n>**

**ABSGTOL=r < n>**

specifies an absolute gradient convergence criterion. Termination requires the maximum absolute gradient element to be small:

\[
\max_j | g_j(\psi^{(k)}) | \leq r
\]

Here, \( \psi \) denotes the vector of parameters that participate in the optimization, and \( g_j(\cdot) \) is the gradient of the objective function with respect to the \( j \)th parameter. This criterion is not used by the NMSIMP technique. PROC NLMOD provides an optional integer value \( n \), which specifies the number of successive iterations for which the criterion must be satisfied before the process can be terminated. By default, ABSGCONV=1E–5.

**ABSXCONV=r < n>**

**ABXTOL=r < n>**

specifies an absolute parameter convergence criterion: For all techniques except NMSIMP, termination requires a small Euclidean distance between successive parameter vectors,

\[
\| \psi^{(k)} - \psi^{(k-1)} \|_2 \leq r
\]
For the NMSIMP technique, termination requires either a small length $\alpha^{(k)}$ of the vertices of a restart simplex,

$$\alpha^{(k)} \leq r$$

or a small simplex size,

$$\delta^{(k)} \leq r$$

where the simplex size $\delta^{(k)}$ is defined as the L1 distance from the simplex vertex $\xi^{(k)}$ that has the smallest function value to the other $p$ simplex points $\psi_l^{(k)} \neq \xi^{(k)}$:

$$\delta^{(k)} = \sum_{l \neq y} \| \psi_l^{(k)} - \xi^{(k)} \|_1$$

PROC NLMOD provides an optional integer value $n$, which specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate. The default is $r = 1E^{-8}$ for the NMSIMP technique and $r = 0$ otherwise.

**FCONV=r<n>**

**FTOL=r<n>**

specifies a relative function difference convergence criterion. For all techniques except NMSIMP, termination requires a small relative change of the function value in successive iterations,

$$\frac{|f(\psi^{(k)}) - f(\psi^{(k-1)})|}{|f(\psi^{(k-1)})|} \leq r$$

Here, $\psi$ denotes the vector of parameters that participate in the optimization, and $f(\cdot)$ is the objective function. The same formula is used for the NMSIMP technique, but $\psi^{(k)}$ is defined as the vertex that has the lowest function value and $\psi^{(k-1)}$ is defined as the vertex that has the highest function value in the simplex.

PROC NLMOD provides an optional integer value $n$, which specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate. The default value is $r = 2 \times \epsilon$ where $\epsilon$ is the machine precision.

**FCONV2=r<n>**

**FTOL2=r<n>**

specifies a second function convergence criterion: For all techniques except NMSIMP, termination requires a small predicted reduction,

$$df^{(k)} \approx f(\psi^{(k)}) - f(\psi^{(k)} + s^{(k)})$$

of the objective function. The predicted reduction

$$df^{(k)} = -g^{(k)} s^{(k)} - \frac{1}{2} s^{(k)^t} \mathbf{H}^{(k)} s^{(k)}$$

is computed by approximating the objective function $f$ by the first two terms of the Taylor series and substituting the Newton step,

$$s^{(k)} = -\mathbf{H}^{(k)^{-1}} g^{(k)}$$
For the NMSIMP technique, termination requires a small standard deviation of the function values of the \( p + 1 \) simplex vertices \( \psi^{(k)}_l, \ l = 0, \ldots, p \),

\[
\sqrt{\frac{1}{n+1} \sum_l \left[ f(\psi^{(k)}_l) - \overline{f}(\psi^{(k)}) \right]^2} \leq r
\]

where \( \overline{f}(\psi^{(k)}) = \frac{1}{p+1} \sum_l f(\psi^{(k)}_l) \). If there are \( p_{\text{act}} \) boundary constraints active at \( \psi^{(k)} \), the mean and standard deviation are computed only for the \( n + 1 - p_{\text{act}} \) unconstrained vertices.

PROC NLMOD provides an optional integer value \( n \), which specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate. The default value is \( r = 1E-6 \) for the NMSIMP technique and \( r = 0 \) otherwise.

\[ \text{GCONV} = r < n > \]
\[ \text{GTOL} = r < n > \]

specifies a relative gradient convergence criterion. For all techniques except CONGRA and NMSIMP, termination requires that the normalized predicted function reduction be small:

\[
\frac{g(\psi^{(k)})[H^{(k)}]^{-1}g(\psi^{(k)})}{|f(\psi^{(k)})|} \leq r
\]

Here, \( \psi \) denotes the vector of parameters that participate in the optimization, \( f(\cdot) \) is the objective function, and \( g(\cdot) \) is the gradient. For the CONGRA technique (where a reliable Hessian estimate \( H \) is not available), the following criterion is used:

\[
\frac{\| g(\psi^{(k)}) \|_2^2 \| s(\psi^{(k)}) \|_2}{\| g(\psi^{(k)}) - g(\psi^{(k-1)}) \|_2 \| f(\psi^{(k)}) \|} \leq r
\]

This criterion is not used by the NMSIMP technique. PROC NLMOD provides an optional integer value \( n \), which specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate. By default, \( \text{GCONV}=1E-8 \).

\[ \text{GCONV}2 = r < n > \]
\[ \text{GTOL2} = r < n > \]

specifies another relative gradient convergence criterion. For the TRUREG, LEVMAR, NRRIDG, and NEWRAP techniques, the following criterion of Browne (1982) is used:

\[
\max_j \frac{|g_j(\psi^{(k)})|}{\sqrt{f(\psi^{(k)})H^{(k)}_{j,j}}} \leq r
\]

This criterion is not used by the other techniques.

PROC NLMOD provides an optional integer value \( n \), which specifies the number of successive iterations for which the criterion must be satisfied before the process can terminate. By default, \( \text{GCONV2}=0 \).
**MAXFUC=n**

**MAXFU=n**

specifies the maximum number \( n \) of function calls in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, and NEWRAP: 125
- QUANEW and DBLDOG: 500
- CONGRA: 1,000
- NMSIMP: 3,000

The optimization can terminate only after completing a full iteration. Therefore, the number of function calls that are actually performed can exceed the number that is specified by this option. You can specify the optimization technique in the **TECHNIQUE=** option.

**MAXITER=n**

**MAXIT=n**

specifies the maximum number \( n \) of iterations in the optimization process. The default values are as follows, depending on the optimization technique:

- TRUREG, NRRIDG, and NEWRAP: 50
- QUANEW and DBLDOG: 200
- CONGRA: 400
- NMSIMP: 1,000

These default values also apply when \( n \) is specified as a missing value. You can specify the optimization technique in the **TECHNIQUE=** option.

**MAXTIME=r**

specifies an upper limit of \( r \) seconds of CPU time for the optimization process. The time specified by \( r \) is checked only once at the end of each iteration. Therefore, the actual running time can be longer than \( r \). The default value is the largest floating-point double representation of your computer.

**MINITER=n**

**MINIT=n**

specifies the minimum number of iterations. If you request more iterations than are actually needed for convergence to a stationary point, the optimization algorithms can behave strangely. For example, the effect of rounding errors can prevent the algorithm from continuing for the required number of iterations. By default, MINITER=0.

**NORMALIZE=YES | NO**

specifies whether the objective function should be normalized during the optimization by the reciprocal of the used frequency count. This option affects the values reported in the “Iteration History” table. The results reported in the “Fit Statistics” are always displayed for the nonnormalized log-likelihood function. The default is to normalize the objective function.
**TECHNIQUE=technique**

**TECH=technique**

specifies the optimization technique for obtaining maximum likelihood estimates. You can specify one of the following techniques:

- **CONGRA** performs a conjugate-gradient optimization.
- **DBLDOG** performs a version of double-dogleg optimization.
- **LEVMAR** performs a Levenberg-Marquardt nonlinear least-squares minimization. This technique is available only with PROC NLMOD.
- **NEWRAP** performs a Newton-Raphson optimization with line search.
- **NMSIMP** performs a Nelder-Mead simplex optimization.
- **NONE** performs no optimization.
- **NRRIDG** performs a Newton-Raphson optimization with ridging.
- **QUANEW** performs a dual quasi-Newton optimization.
- **TRUREG** performs a trust-region optimization.

By default, TECHNIQUE=NRRIDG.

For more information, see the section “Choosing an Optimization Algorithm” on page 80.

**XCONV=r**

**XTOL=r**

specifies the relative parameter convergence criterion. Convergence requires a small relative parameter change in subsequent iterations,

\[
\max_{j} |\delta_{j}^{(i)}| < r
\]

where

\[
\delta_{j}^{(i)} = \begin{cases} 
\beta_{j}^{(i)} - \beta_{j}^{(i-1)} & |\beta_{j}^{(i-1)}| < 0.01 \\
\frac{\beta_{j}^{(i)} - \beta_{j}^{(i-1)}}{|\beta_{j}^{(i-1)}|} & \text{otherwise}
\end{cases}
\]

and \(\beta_{j}^{(i)}\) is the estimate of the \(j\)th parameter at iteration \(i\). The default value is \(r = 1E-8\) for the NMSIMP technique and \(r = 0\) otherwise.
A classification variable enters the statistical analysis or model not through its values but through its levels. The process of associating values of a variable with levels is called levelization.

During the process of levelization, observations that share the same value are assigned to the same level. The manner in which values are grouped can be affected by the inclusion of formats. The sort order of the levels can be determined by specifying the ORDER= option in the procedure statement. In procedures in this book, you can also control the sorting order separately for each variable in the CLASS statement.

Consider the data on nine observations in Table 2.9. The variable A is integer-valued, and the variable X is a continuous variable that has a missing value for the fourth observation. The fourth and fifth columns of Table 2.9 apply two different formats to the variable X.

### Table 2.9  Example Data for Levelization

<table>
<thead>
<tr>
<th>Obs</th>
<th>A</th>
<th>x</th>
<th>FORMAT x 3.0</th>
<th>FORMAT x 3.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>1.09</td>
<td>1</td>
<td>1.1</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1.13</td>
<td>1</td>
<td>1.1</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>1.27</td>
<td>1</td>
<td>1.3</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>5</td>
<td>3</td>
<td>2.26</td>
<td>2</td>
<td>2.3</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>2.48</td>
<td>2</td>
<td>2.5</td>
</tr>
<tr>
<td>7</td>
<td>4</td>
<td>3.34</td>
<td>3</td>
<td>3.3</td>
</tr>
<tr>
<td>8</td>
<td>4</td>
<td>3.34</td>
<td>3</td>
<td>3.3</td>
</tr>
<tr>
<td>9</td>
<td>4</td>
<td>3.14</td>
<td>3</td>
<td>3.1</td>
</tr>
</tbody>
</table>

By default, levelization of the variables groups the observations by the formatted value of the variable, except for numerical variables for which no explicit format is provided. Numerical variables for which no explicit format is provided are sorted by their internal value. The levelization of the four columns in Table 2.9 leads to the level assignment in Table 2.10.
Chapter 2: Shared Concepts

Table 2.10 Values and Levels

<table>
<thead>
<tr>
<th>Obs</th>
<th>Value</th>
<th>Level</th>
<th>Value</th>
<th>Level</th>
<th>FORMAT x 3.0</th>
<th>FORMAT x 3.1</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1.09</td>
<td>1</td>
<td>1</td>
<td>1.1</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1.13</td>
<td>2</td>
<td>1</td>
<td>1.1</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>1</td>
<td>1.27</td>
<td>3</td>
<td>1</td>
<td>1.3</td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>3</td>
<td>2</td>
<td>2.26</td>
<td>4</td>
<td>2</td>
<td>2.3</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>2</td>
<td>2.48</td>
<td>5</td>
<td>2</td>
<td>2.5</td>
</tr>
<tr>
<td>7</td>
<td>4</td>
<td>3</td>
<td>3.34</td>
<td>7</td>
<td>3</td>
<td>3.3</td>
</tr>
<tr>
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<td>4</td>
<td>3</td>
<td>3.34</td>
<td>7</td>
<td>3</td>
<td>3.3</td>
</tr>
<tr>
<td>9</td>
<td>4</td>
<td>3</td>
<td>3.14</td>
<td>6</td>
<td>3</td>
<td>3.1</td>
</tr>
</tbody>
</table>

The sort order for the levels of CLASS variables can be specified in the ORDER= option in the CLASS statement.

When ORDER=FORMATTED (which is the default) is in effect for numeric variables for which you have supplied no explicit format, the levels are ordered by their internal values. To order numeric classification levels that have no explicit format by their BEST12. formatted values, you can specify the BEST12. format explicitly for the CLASS variables.

Table 2.11 shows how values of the ORDER= option are interpreted.

Table 2.11 Interpretation of Values of ORDER= Option

<table>
<thead>
<tr>
<th>Value of ORDER=</th>
<th>Levels Sorted By</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMATTED</td>
<td>External formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. The sort order is machine-dependent.</td>
</tr>
<tr>
<td>FREQ</td>
<td>Descending frequency count (levels that have the most observations come first in the order)</td>
</tr>
<tr>
<td>INTERNAL</td>
<td>Unformatted value. The sort order is machine-dependent.</td>
</tr>
</tbody>
</table>

For more information about sort order, see the chapter about the SORT procedure in the SAS Visual Data Management and Utility Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts.

When the MISSING option is specified in the CLASS statement, the missing values (‘.’ for a numeric variable and blanks for a character variable) are included in the levelization and are assigned a level. Table 2.12 displays the results of levelizing the values in Table 2.9 when the MISSING option is in effect.
When the MISSING option is not specified, it is important to understand the implications of missing values for your statistical analysis. When a procedure in this book levelizes the CLASS variables, an observation for which any CLASS variable has a missing value is excluded from the analysis.

Procedures in this book print a “Number of Observations” table that shows the number of observations that are read from the data set and the number of observations that are used in the analysis. Pay careful attention to this table—especially when your data table contains missing values—to ensure that no observations are unintentionally excluded from the analysis.

### Table 2.12 Values and Levels When the MISSING Option Is Specified

<table>
<thead>
<tr>
<th>Obs</th>
<th>Value</th>
<th>Level</th>
<th>A Value</th>
<th>Level</th>
<th>X Value</th>
<th>Level</th>
<th>FORMAT x 3.0 Value</th>
<th>Level</th>
<th>FORMAT x 3.1 Value</th>
<th>Level</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1.09</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>1.1</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>1.13</td>
<td>3</td>
<td>1</td>
<td>2</td>
<td>1.1</td>
<td>2</td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>1</td>
<td>1.27</td>
<td>4</td>
<td>1</td>
<td>2</td>
<td>1.3</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>3</td>
<td>2</td>
<td>2.1</td>
<td>1</td>
<td>.</td>
<td>1</td>
<td>2.1</td>
<td>3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
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<td>5</td>
<td>2</td>
<td>3</td>
<td>2.3</td>
<td>4</td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>2</td>
<td>2.48</td>
<td>6</td>
<td>2</td>
<td>3</td>
<td>2.5</td>
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<td>3.34</td>
<td>8</td>
<td>3</td>
<td>4</td>
<td>3.3</td>
<td>7</td>
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<td></td>
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<tr>
<td>8</td>
<td>4</td>
<td>3</td>
<td>3.34</td>
<td>8</td>
<td>3</td>
<td>4</td>
<td>3.3</td>
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<td></td>
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<tr>
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<td>4</td>
<td>3</td>
<td>3.14</td>
<td>7</td>
<td>3</td>
<td>4</td>
<td>3.1</td>
<td>6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Specification and Parameterization of Model Effects

This section applies to the following procedures: GAMMOD, GENSELECT, LOGSELECT, NLMOD, PLSMOD, QTRSELECT, and REGSELECT.

Procedures in this book that have a MODEL statement support the formation of effects. An effect is an element in a linear model structure that is formed from one or more variables. At some point the statistical representations of these models involve linear structures such as

\[ X\beta \]

or

\[ X\beta + Z\gamma \]

The model matrices \( X \) and \( Z \) are formed according to effect-construction rules.

Procedures that also have a CLASS statement support the rich set of effects that is discussed in this section.

Procedures that also have an EFFECT statement enable you to construct special constructed effects that are discussed in “EFFECT Statement” on page 19.
In order to correctly interpret the results from a statistical analysis, you need to understand how construction (parameterization) rules apply to regression-type models, whether these are linear models as in the REGSELECT procedure or generalized linear models as in the LOGSELECT and GENSELECT procedures.

Effects are specified by a special notation that uses variable names and operators. There are two types of variables: classification (or CLASS) variables and continuous variables. Classification variables can be either numeric or character and are specified in a CLASS statement. For more information, see the section “Levelization of Classification Variables” on page 47. An independent variable that is not declared in the CLASS statement is assumed to be continuous. For example, the heights and weights of subjects are continuous variables.

Two primary operators (crossing and nesting) are used for combining the variables, and several additional operators are used to simplify effect specification. Operators are discussed in the section “Effect Operators” on page 50.

Procedures in this book that have a CLASS statement support a general linear model (GLM) parameterization and a reference parameterization for the classification variables. The GLM parameterization, commonly called dummy parameterization, is the default for all procedures in this book. For more information, see the sections “GLM Parameterization of Classification Variables and Effects” on page 52 and “Nonsingular Parameterization” on page 56.

**Effect Operators**

Table 2.13 summarizes the operators that are available for selecting and constructing effects. These operators are discussed in the following sections.

<table>
<thead>
<tr>
<th>Operator</th>
<th>Example</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Interaction</td>
<td>A*B</td>
<td>Crosses the levels of the effects</td>
</tr>
<tr>
<td>Nesting</td>
<td>A(B)</td>
<td>Nests A levels within B levels</td>
</tr>
<tr>
<td>Bar operator</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>At sign operator</td>
<td>A</td>
<td>B</td>
</tr>
<tr>
<td>Dash operator</td>
<td>A1-A10</td>
<td>Specifies sequentially numbered variables</td>
</tr>
<tr>
<td>Colon operator</td>
<td>A:</td>
<td>Specifies variables with common prefix</td>
</tr>
<tr>
<td>Double dash operator</td>
<td>A-C</td>
<td>Specifies sequential variables in data set order</td>
</tr>
</tbody>
</table>

**Bar and At Sign Operators**

You can shorten the specification of a large factorial model by using the bar operator. For example, two ways of writing the model for a full three-way factorial model follow:

\[
\text{model } Y = A \times B \times C \quad A \times B \quad A \times C \quad B \times C \quad A \times B \times C;
\]

\[
\text{model } Y = A | B | C;
\]

When the bar (|) is used, the right and left sides become effects, and the cross of them becomes an effect. Multiple bars are permitted. The expressions are expanded from left to right, using rules 2–4 in Searle (1971, p. 390).
• Multiple bars are evaluated from left to right. For example, \( A \bar{B} \bar{C} \) is evaluated as follows:

\[
A \bar{B} \bar{C} \rightarrow \{A \bar{B}\} \bar{C} \\
\rightarrow \{A \ B \ A^*B\} \bar{C} \\
\rightarrow A \ B \ A^*B \ C \ A^*C \ B^*C \ A^*B^*C
\]

• Crossed and nested groups of variables are combined. For example, \( A(B) \bar{C}(D) \) generates \( A^*C(B \ D) \), among other terms.

• Duplicate variables are removed. For example, \( A(C) \bar{B}(C) \) generates \( A^*B(C \ C) \), among other terms, and the extra \( C \) is removed.

• Effects are discarded if a variable occurs on both the crossed and nested parts of an effect. For example, \( A(B) \bar{B}(D \ E) \) generates \( A^*B(B \ D \ E) \), but this effect is eliminated immediately.

You can also specify the maximum number of variables involved in any effect that results from bar evaluation by specifying that maximum number, preceded by an at sign (@), at the end of the bar effect. For example, the following specification selects only those effects that contain two or fewer variables:

\[
\text{model } Y = A \bar{B} \bar{C} @2;
\]

The preceding example is equivalent to specifying the following MODEL statement:

\[
\text{model } Y = A \ B \ C \ A^*B \ A^*C \ B^*C;
\]

More examples of using the bar and at operators follow:

- \( A \bar{C}(B) \) is equivalent to \( A \ C(B) \ A^*C(B) \)
- \( A(B) \bar{C}(B) \) is equivalent to \( A(B) \ C(B) \ A^*C(B) \)
- \( A(B) \bar{B}(D \ E) \) is equivalent to \( A(B) \ B(D \ E) \)
- \( A \bar{B}(A) \bar{C} \) is equivalent to \( A \ B(A) \ C \ A^*C(B) \)
- \( A \bar{B}(A) \bar{C} @2 \) is equivalent to \( A \ B(A) \ C \ A^*C \)
- \( A \bar{B}(C \ D) \bar{D} @2 \) is equivalent to \( A \ B \ A^*B \ C \ A^*C \ B^*C \ D \ A^*D \ B^*D \ C^*D \)
- \( A^*B(C^*D) \) is equivalent to \( A^*B(C \ D) \)

**Colon, Dash, and Double Dash Operators**

You can simplify the specification of a large model when some of your variables have a common prefix by using the colon (:) operator and the dash (-) operator. The dash operator enables you to list variables that are numbered sequentially, and the colon operator selects all variables with a given prefix. For example, if your data set contains the variables \( X1 \) through \( X9 \), the following MODEL statements are equivalent:

\[
\text{model } Y = X1 \ X2 \ X3 \ X4 \ X5 \ X6 \ X7 \ X8 \ X9;
\]

\[
\text{model } Y = X1-X9;
\]

\[
\text{model } Y = X:\;
\]

If your data set contains only the three covariates \( X1 \), \( X2 \), and \( X9 \), then the colon operator selects all three variables:
model $Y = X$;

However, the following specification returns an error because $X_3$ through $X_8$ are not in the data set:

model $Y = X_1 - X_9$;

The double dash (--) operator enables you to select variables that are stored sequentially in the SAS data set, whether or not they have a common prefix. You can use the CONTENTS procedure (see SAS Visual Data Management and Utility Procedures Guide) to determine your variable ordering. For example, if you replace the dash in the preceding MODEL statement with a double dash, as follows, then all three variables are selected:

model $Y = X_1 -- X_9$;

If your data set contains the variables $A$, $B$, and $C$, then you can use the double dash operator to select these variables by specifying the following:

model $Y = A -- C$;

**GLM Parameterization of Classification Variables and Effects**

Table 2.14 shows the types of effects that are available in procedures in this book; they are discussed in more detail in the following subsections. Let $A$, $B$, and $C$ represent classification variables, and let $X$ and $Z$ represent continuous variables.

<table>
<thead>
<tr>
<th>Effect</th>
<th>Example</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>Default</td>
<td>Intercept (unless the NOINT option is specified)</td>
</tr>
<tr>
<td>Regression</td>
<td>$X Z$</td>
<td>Continuous variables</td>
</tr>
<tr>
<td>Polynomial</td>
<td>$X^Z$</td>
<td>Interaction of continuous variables</td>
</tr>
<tr>
<td>Main</td>
<td>$A B$</td>
<td>CLASS variables</td>
</tr>
<tr>
<td>Interaction</td>
<td>$A^B$</td>
<td>Crossing of CLASS variables</td>
</tr>
<tr>
<td>Nested</td>
<td>$A(B)$</td>
<td>Main effect $A$ nested within CLASS effect $B$</td>
</tr>
<tr>
<td>Continuous-by-class</td>
<td>$X^A$</td>
<td>Crossing of continuous and CLASS variables</td>
</tr>
<tr>
<td>Continuous-nesting-class</td>
<td>$X(A)$</td>
<td>Continuous variable $X_1$ nested within CLASS variable $A$</td>
</tr>
<tr>
<td>General</td>
<td>$X^Z^A(B)$</td>
<td>Combinations of different types of effects</td>
</tr>
</tbody>
</table>

Table 2.15 shows some examples of MODEL statements that use various types of effects.

<table>
<thead>
<tr>
<th>Specification</th>
<th>Type of Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>model $Y=X$;</td>
<td>Simple regression</td>
</tr>
<tr>
<td>model $Y=X Z$;</td>
<td>Multiple regression</td>
</tr>
<tr>
<td>model $Y=X^Z$;</td>
<td>Polynomial regression</td>
</tr>
<tr>
<td>model $Y=A$;</td>
<td>One-way analysis of variance (ANOVA)</td>
</tr>
<tr>
<td>model $Y=A B C$;</td>
<td>Main-effects ANOVA</td>
</tr>
<tr>
<td>model $Y=A B A^B$;</td>
<td>Factorial ANOVA with interaction</td>
</tr>
</tbody>
</table>
Specification and Parameterization of Model Effects

Table 2.15 continued

<table>
<thead>
<tr>
<th>Specification</th>
<th>Type of Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>model y=A B(A) C(B A);</td>
<td>Nested ANOVA</td>
</tr>
<tr>
<td>model Y=A X;</td>
<td>Analysis of covariance (ANCOVA)</td>
</tr>
<tr>
<td>model Y=A X(A);</td>
<td>Separate-slopes regression</td>
</tr>
<tr>
<td>model Y=A X X*A;</td>
<td>Homogeneity-of-slopes regression</td>
</tr>
</tbody>
</table>

**Intercept**
By default, linear models that are created by procedures in this book automatically include a column of 1s in X. This column corresponds to an intercept parameter. In many procedures, you can use the NOINT option in the MODEL statement to suppress this intercept. For example, the NOINT option is useful when the MODEL statement contains a classification effect and you want the parameter estimates to be in terms of the mean response for each level of that effect.

**Regression Effects**
Numeric variables or polynomial terms that involve them can be included in the model as regression effects (covariates). The actual values of such terms are included as columns of the relevant model matrices. You can use the bar operator along with a regression effect to generate polynomial effects. For example, X | X | X expands to X X*X X*X*X*X, which is a cubic model.

**Main Effects**
If a classification variable has m levels, the GLM parameterization generates m columns for its main effect in the model matrix. Each column is an indicator variable for a particular level. The order of the columns is the sort order of the values of their levels and can be controlled by the ORDER= option in the CLASS statement.

Table 2.16 is an example where $\beta_0$ denotes the intercept and A and B are classification variables that have two and three levels, respectively.

Table 2.16 Example of Main Effects

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
<td>$\beta_0$</td>
<td>A1</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

There are usually more columns for these effects than there are degrees of freedom to estimate them. In other words, the GLM parameterization of main effects is singular.
Interaction Effects

Often a model includes interaction (crossed) effects to account for how the effect of a variable changes along with the values of other variables. With an interaction, the terms are first reordered to correspond to the order of the variables in the CLASS statement. Thus, B*A becomes A*B if A precedes B in the CLASS statement. Then, the GLM parameterization generates columns for all combinations of levels that occur in the data. The order of the columns is such that the rightmost variables in the interaction change faster than the leftmost variables (Table 2.17).

Table 2.17  Example of Interaction Effects

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>B</th>
<th>A*B</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
<td>β₀</td>
<td>A₁</td>
<td>A₂</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

In the preceding matrix, main-effects columns are not linearly independent of crossed-effects columns. In fact, the column space for the crossed effects contains the space of the main effect.

When your model contains many interaction effects, you might be able to code them more parsimoniously by using the bar operator (|). The bar operator generates all possible interaction effects. For example, A | B | C expands to A B A*B C A*C B*C A*B*C. To eliminate higher-order interaction effects, use the at sign (@) in conjunction with the bar operator. For example, A | B | C | D@2 expands to A B A*B C A*C B*C D A*D B*D C*D.

Nested Effects

Nested effects are generated in the same manner as crossed effects. Hence, the design columns that are generated by the following two statements are the same (but the ordering of the columns is different):

```plaintext
model Y=A B(A);
model Y=A A*B;
```

The nesting operator in procedures in this book is more of a notational convenience than an operation that is distinct from crossing. Nested effects are typically characterized by the property that the nested variables do not appear as main effects. The order of the variables within nesting parentheses is made to correspond to the order of these variables in the CLASS statement. The order of the columns is such that variables outside the parentheses index faster than those inside the parentheses, and the rightmost nested variables index faster than the leftmost variables (Table 2.18).

Table 2.18  Example of Nested Effects

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>A</th>
<th>B(A)</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
<td>β₀</td>
<td>A₁</td>
<td>A₂</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
### Table 2.18 continued

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>B(A)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 2</td>
<td>1</td>
<td>0</td>
<td>1 0 0 0 0 0 0 0</td>
</tr>
<tr>
<td>1 3</td>
<td>1</td>
<td>0</td>
<td>0 0 1 0 0 0 0 0</td>
</tr>
<tr>
<td>2 1</td>
<td>1</td>
<td>0</td>
<td>0 0 0 1 0 0 0 0</td>
</tr>
<tr>
<td>2 2</td>
<td>1</td>
<td>0</td>
<td>0 0 0 0 1 0 0 0</td>
</tr>
<tr>
<td>2 3</td>
<td>1</td>
<td>0</td>
<td>0 0 0 0 0 0 0 1</td>
</tr>
</tbody>
</table>

#### Continuous-Nesting-Class Effects
When a continuous variable nests or crosses with a classification variable, the design columns are constructed by multiplying the continuous values into the design columns for the classification effect (Table 2.19).

### Table 2.19 Example of Continuous-Nesting-Class Effects

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>X</th>
<th>A</th>
<th>X(A)</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>A</td>
<td>β₀</td>
<td>A1</td>
<td>A2</td>
</tr>
<tr>
<td>21</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>21</td>
</tr>
<tr>
<td>24</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>24</td>
</tr>
<tr>
<td>22</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>22</td>
</tr>
<tr>
<td>28</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>19</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>23</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

This model estimates a separate intercept and a separate slope for X within each level of A.

#### Continuous-by-Class Effects
Continuous-by-class effects generate the same design columns as continuous-nesting-class effects. Table 2.20 shows the construction of the $X*A$ effect. The two columns for this effect are the same as the columns for the $X(A)$ effect in Table 2.19.

### Table 2.20 Example of Continuous-by-Class Effects

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>X</th>
<th>A</th>
<th>X*A</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>A</td>
<td>β₀</td>
<td>X</td>
<td>A1</td>
</tr>
<tr>
<td>21</td>
<td>1</td>
<td>1</td>
<td>21</td>
<td>1</td>
</tr>
<tr>
<td>24</td>
<td>1</td>
<td>1</td>
<td>24</td>
<td>1</td>
</tr>
<tr>
<td>22</td>
<td>1</td>
<td>1</td>
<td>22</td>
<td>1</td>
</tr>
<tr>
<td>28</td>
<td>2</td>
<td>1</td>
<td>28</td>
<td>0</td>
</tr>
<tr>
<td>19</td>
<td>2</td>
<td>1</td>
<td>19</td>
<td>0</td>
</tr>
<tr>
<td>23</td>
<td>2</td>
<td>1</td>
<td>23</td>
<td>0</td>
</tr>
</tbody>
</table>

You can use continuous-by-class effects together with pure continuous effects to test for homogeneity of slopes.
Chapter 2: Shared Concepts

General Effects
An example that combines all the effects is \(X_1 \times X_2 \times A \times B \times C(D, E)\). The continuous list comes first, followed by the crossed list, followed by the nested list in parentheses.

Effects might be renamed by the procedure to correspond to ordering rules. For example, \(B \times A(E, D)\) might be renamed \(A \times B(D, E)\) to satisfy the following:

- Classification variables that occur outside parentheses (crossed effects) are sorted in the order in which they appear in the CLASS statement.
- Variables within parentheses (nested effects) are sorted in the order in which they appear in the CLASS statement.

The sequencing of the parameters that are generated by an effect is determined by the variables whose levels are indexed faster:

- Variables in the crossed list index faster than variables in the nested list.
- Within a crossed or nested list, variables to the right index faster than variables to the left.

For example, suppose that a model includes four effects—\(A, B, C,\) and \(D\)—each having two levels, 1 and 2, and that the CLASS statement is as follows:

```plaintext
class A B C D;
```

Then the order of the parameters for the effect \(B \times A(C, D)\), which is renamed \(A \times B(C, D)\), is as follows:

\[
\begin{align*}
A_1B_1C_1D_1 & \rightarrow A_1B_2C_1D_1 \rightarrow A_2B_1C_1D_1 \rightarrow A_2B_2C_1D_1 \\
A_1B_1C_2D_1 & \rightarrow A_1B_2C_2D_1 \rightarrow A_2B_1C_2D_1 \rightarrow A_2B_2C_2D_1 \\
A_1B_1C_2D_2 & \rightarrow A_1B_2C_2D_2 \rightarrow A_2B_1C_2D_2 \rightarrow A_2B_2C_2D_2 \\
A_1B_2C_2D_2 & \rightarrow A_1B_2C_2D_2 \rightarrow A_2B_2C_2D_2 \rightarrow A_2B_2C_2D_2
\end{align*}
\]

Note that first the crossed effects \(B\) and \(A\) are sorted in the order in which they appear in the CLASS statement so that \(A\) precedes \(B\) in the parameter list. Then, for each combination of the nested effects in turn, combinations of \(A\) and \(B\) appear. The \(B\) effect changes fastest because it is rightmost in the cross list. Then \(A\) changes next fastest, and \(D\) changes next fastest. The \(C\) effect changes most slowly because it is leftmost in the nested list.

Nonsingular Parameterization
When a parameterization of main effects provides the same number of columns for the effects as there are degrees of freedom to estimate them, the parameterization is called nonsingular. A variety of nonsingular parameterizations for classification effects are available for many procedures in this book. In most of these procedures you use the PARAM= option in the CLASS statement to specify the parameterization.

Consider a model with one CLASS variable \(A\) that has four levels, 1, 2, 5, and 7. Details of the possible choices for the PARAM= option follow.
**REFERENCE**

Three columns are created to indicate group membership of the nonreference levels. For the reference level, all three dummy variables have a value of 0. For example, if the reference level is 7 (REF=7), the design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Effect Coding</th>
<th>Design Matrix</th>
<th>A</th>
<th>A1</th>
<th>A2</th>
<th>A5</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
</tbody>
</table>

Parameter estimates of CLASS main effects that use the reference coding scheme estimate the difference in the effect of each nonreference level compared to the effect of the reference level.

**EFFECT**

Three columns are created to indicate group membership of the nonreference levels. For the reference level, all three dummy variables have a value of –1. For example, if the reference level is 7 (REF=7), the design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Effect Coding</th>
<th>Design Matrix</th>
<th>A</th>
<th>A1</th>
<th>A2</th>
<th>A5</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>-1</td>
<td>-1</td>
<td>-1</td>
<td></td>
</tr>
</tbody>
</table>

Parameter estimates of CLASS main effects that use the effect coding scheme estimate the difference in the effect of each nonreference level compared to the average effect over all four levels.

**ORDINAL**

Three columns are created to indicate group membership of the higher levels of the effect. For the first level of the effect (which for A is 1), all three dummy variables have a value of 0. The design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Ordinal Coding</th>
<th>Design Matrix</th>
<th>A</th>
<th>A2</th>
<th>A5</th>
<th>A7</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>A</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td></td>
</tr>
</tbody>
</table>

The first level of the effect is a control or baseline level. Parameter estimates of CLASS main effects, using the ORDINAL coding scheme, estimate the differences
between effects of successive levels. When the parameters have the same sign, the effect is monotonic across the levels.

**POLYNOMIAL**  
Three columns are created. The first represents the linear term \(x\), the second represents the quadratic term \(x^2\), and the third represents the cubic term \(x^3\), where \(x\) is the level value. If the CLASS levels are not numeric, they are translated into 1, 2, 3, \ldots according to their sort order. The design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Polynomial Coding</th>
<th>Design Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>APOLY1</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>7</td>
<td>7</td>
</tr>
</tbody>
</table>

**ORTHEFFECT**  
The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=EFFECT. The design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Orthogonal Effect Coding</th>
<th>Design Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>AOEFF1</td>
</tr>
<tr>
<td>1</td>
<td>1.41421</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>−1.41421</td>
</tr>
</tbody>
</table>

**ORTHORDINAL**  
The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=ORDINAL. The design matrix columns for A are as follows.

<table>
<thead>
<tr>
<th>Orthogonal Ordinal Coding</th>
<th>Design Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>AOORD1</td>
</tr>
<tr>
<td>1</td>
<td>−1.73205</td>
</tr>
<tr>
<td>2</td>
<td>0.57735</td>
</tr>
<tr>
<td>5</td>
<td>0.57735</td>
</tr>
<tr>
<td>7</td>
<td>0.57735</td>
</tr>
</tbody>
</table>

**ORTHPOLY**  
The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=POLY. The design matrix columns for A are as follows.
Orthogonal Polynomial Coding

<table>
<thead>
<tr>
<th></th>
<th>AOPOLY1</th>
<th>AOPOLY2</th>
<th>AOPOLY5</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.15311</td>
<td>0.90712</td>
<td>-0.92058</td>
</tr>
<tr>
<td>2</td>
<td>-0.73380</td>
<td>-0.54041</td>
<td>1.47292</td>
</tr>
<tr>
<td>5</td>
<td>0.52414</td>
<td>-1.37034</td>
<td>-0.92058</td>
</tr>
<tr>
<td>7</td>
<td>1.36277</td>
<td>1.00363</td>
<td>0.36823</td>
</tr>
</tbody>
</table>

ORTHREF

The columns are obtained by applying the Gram-Schmidt orthogonalization to the columns for PARAM=REFERENCE. The design matrix columns for A are as follows.

Orthogonal Reference Coding

<table>
<thead>
<tr>
<th></th>
<th>AOREF1</th>
<th>AOREF2</th>
<th>AOREF3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1.73205</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>-0.57735</td>
<td>1.63299</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>-0.57735</td>
<td>-0.81650</td>
<td>1.41421</td>
</tr>
<tr>
<td>7</td>
<td>-0.57735</td>
<td>-0.81650</td>
<td>-1.41421</td>
</tr>
</tbody>
</table>

Class Variable Parameterization with Unbalanced Designs

Procedures in this book initially parameterize the CLASS variables by looking at the levels of the variables across the complete data set. If you have an unbalanced replication of levels across variables or BY groups, then the design matrix and the parameter interpretation might be different from what you expect. For example, suppose you have a model that has one CLASS variable A with three levels (1, 2, and 3), and another CLASS variable B with two levels (1 and 2). If the third level of A occurs only with the first level of B, if you use the EFFECT parameterization, and if your model contains the effect A(B) and an intercept, then the design for A within the second level of B is not a differential effect. In particular, the design looks like the following:

<table>
<thead>
<tr>
<th></th>
<th>A(B=1)</th>
<th>A(B=2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>B</td>
<td>A</td>
<td>A1</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>-1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0</td>
</tr>
</tbody>
</table>

Procedures in this book detect linear dependency among the last two design variables and set the parameter for A2(B=2) to 0, resulting in an interpretation of these parameters as if they were reference- or dummy-coded. The REFERENCE or GLM parameterization might be more appropriate for such problems.
Model Selection Methods

The model selection methods are specified in the METHOD= option in the SELECTION statement. The following methods are available, although specific procedures might support only a subset of these methods. Furthermore, the examples in this section refer to fit criteria that might not be supported by a specific procedure.

Full Model Fitted

When METHOD=NONE, the complete model that is specified in the MODEL statement is used to fit the model, and no effect selection is done.

Forward Selection

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, and REGSELECT.

METHOD=FORWARD specifies the forward selection technique, which begins with just the intercept and then sequentially adds the effect that most improves the fit. The process terminates when no significant improvement can be obtained by adding any effect.

In the traditional implementation of forward selection, the statistic that is used to determine whether to add an effect is the significance level of a hypothesis test that reflects an effect’s contribution to the model if it is included. At each step, the effect that is most significant is added. The process stops when the significance level for adding any effect is greater than some specified entry significance level.

An alternative approach to address the critical problem of when to stop the selection process is to assess the quality of the models that are produced by the forward selection method and choose the model from this sequence that “best” balances goodness of fit against model complexity. You can use several criteria for this purpose. These criteria fall into two groups—information criteria and criteria that are based on out-of-sample prediction performance.

You use the CHOOSE= option to specify the criterion for selecting one model from the sequence of models produced. If you do not specify a CHOOSE= criterion, then the model at the final step is the selected model.

For example, if you specify the following statement, then forward selection terminates at the step where no effect can be added at the 0.2 significance level:

```
selection method=forward(select=SL choose=AIC SLE=0.2);
```

However, the selected model is the first one that has the minimum value of Akaike’s information criterion. In some cases, this minimum value might occur at a step much earlier than the final step. In other cases, the AIC might start increasing only if more steps are performed—that is, a larger value is used for the significance level for entry. If you want to minimize AIC, then too many steps are performed in the former case and too few in the latter case. To address this issue, you can use the STOP= option to specify a stopping criterion. When you specify a stopping criterion, forward selection continues until a local extremum of the stopping criterion in the sequence of models generated is reached. To be deemed a local extremum, a criterion value at a particular step must be better than its value at the next \( n \) steps, where \( n \) is known as the “stop horizon.” By default, the stop horizon is three steps, but you can change this by specifying the STOPHORIZON= option.
For example, if you specify the following statement, then forward selection terminates at the step where the effect to be added at the next step would produce a model that has an AIC statistic larger than the AIC statistic of the current model:

```
selection method=forward(select=SL stop=AIC) stophorizon=1;
```

In most cases, provided that the entry significance level is large enough that the local extremum of the named criterion occurs before the final step, specifying either of the following statements selects the same model, but more steps are done in the first case:

```
selection method=forward(select=SL choose=CRITERION);
selection method=forward(select=SL stop=CRITERION);
```

In some cases, there might be a better local extremum that cannot be reached if you specify the STOP= option but can be found if you use the CHOOSE= option. Also, you can use the CHOOSE= option in preference to the STOP= option if you want to examine how the named criterion behaves as you move beyond the step where the first local minimum of this criterion occurs.

You can specify both the CHOOSE= and STOP= options. You can also use these options together with options that specify size-based limits on the selected model. You might want to consider models that are generated by forward selection and have at most some fixed number of effects, but select from within this set based on a criterion that you specify. For example, specifying the following statements requests that forward selection continue until there are 20 effects in the final model and chooses among the sequence of models the one that has the largest value of the adjusted R-square statistic:

```
selection method=forward(stop=none maxeffects=20 choose=ADJRSQ);
```

You can also combine these options to select a model where one of two conditions is met. For example, the following statement chooses whatever occurs first between a local minimum of the sum of squares on validation data and a local minimum of the corrected Akaike’s information criterion (AICC):

```
selection method=forward(stop=AICC choose=VALIDATE);
```

It is important to keep in mind that forward selection bases the decision about what effect to add at any step by considering models that differ by one effect from the current model. This search paradigm cannot guarantee reaching a “best” subset model. Furthermore, the add decision is greedy in the sense that the effect that is deemed most significant is the effect that is added. However, if your goal is to find a model that is best in terms of some selection criterion other than the significance level of the entering effect, then even this one step choice might not be optimal. For example, the effect that you would add to get a model that has the smallest value of the Mallows’ $C(p)$ statistic at the next step is not necessarily the same effect that is most significant based on a hypothesis test. You can specify the criterion to optimize at each step by using the SELECT= option. For example, the following statement requests that at each step the effect that is added be the one that produces a model that has the smallest value of the Mallows’ $C(p)$ statistic:

```
selection method=forward(select=CP);
```

When all effects are variables (that is, effects have one degree of freedom and no hierarchy), using ADJRSQ, AIC, AICC, BIC, CP, RSQUARE, or SBC as the selection criterion for forward selection produces the same sequence of additions. However, if the degrees of freedom contributed by different effects are not constant or if an out-of-sample prediction-based criterion is used, then different sequences of additions might be obtained.

You can use the SELECT= option together with the CHOOSE= and STOP= options. If you specify only the SELECT= criterion, then this criterion is also used as the stopping criterion. In the previous example, where
only the selection criterion is specified, not only do effects enter based on the Mallows’ $C(p)$ statistic, but the selection terminates when the $C(p)$ statistic has a local minimum.

You can find discussion and references to studies about criteria for variable selection in Burnham and Anderson (2002), along with some cautions and recommendations.

**Examples of Forward Selection Specifications**

The following statement adds effects that at each step produce the lowest value of the SBC statistic and stops at the step where adding any effect would increase the SBC statistic:

```
selection method=forward stophorizon=1;
```

The following statement adds effects based on significance level and stops when all candidate effects for entry at a step have a significance level greater than the default entry significance level of 0.05:

```
selection=forward(select=SL);
```

The following statement adds effects based on significance level and stops at a step where adding any effect increases the error sum of squares computed on the validation data:

```
selection=forward(select=SL stop=validation) stophorizon=1;
```

The following statement adds effects that at each step produce the lowest value of the AIC statistic and stops at the first step whose AIC value is smaller than the AIC value at the next three steps:

```
selection=forward(select=AIC);
```

The following statement adds effects that at each step produce the largest value of the adjusted R-square statistic and stops at the step where the significance level that corresponds to the addition of this effect is greater than 0.2:

```
selection=forward(select=ADJRSQ stop=SL SLE=0.2);
```

**Backward Elimination**

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, and REGSELECT.

METHOD=BACKWARD specifies the backward elimination technique. This technique starts from the full model, which includes all independent effects. Then effects are deleted one by one until a stopping condition is satisfied. At each step, the effect that shows the smallest contribution to the model is deleted.

In the traditional implementation of backward selection, the statistic that is used to determine whether to drop an effect is significance level. At any step, the least significant predictor is dropped and the process continues until all effects that remain in the model are significant at a specified stay significance level (SLS).

Just as with forward selection, you can use the SELECT= option to change the criterion that is used to assess effect contributions. You can also specify a stopping criterion in the STOP= option and use a CHOOSE= option to provide a criterion for selecting among the sequence of models produced. For more information, see the discussion in the section “Forward Selection” on page 60.
Examples of Backward Selection Specifications
The following statement removes effects that at each step produce the largest value of the Schwarz Bayesian information criterion (SBC) statistic and stops at the step where removing any effect increases the SBC statistic:

```
selection method=backward stophorizon=1;
```

The following statement bases removal of effects on significance level and stops when all candidate effects for removal at a step are significant at the default stay significance level of 0.05:

```
selection method=backward(select=SL);
```

The following statement bases removal of effects on significance level and stops when all effects in the model are significant at the 0.1 level. Finally, from the sequence of models generated, the chosen model is the one that produces the smallest average square error when scored on the validation data:

```
selection method=backward(select=SL choose=validate SLS=0.1);
```

The following statement applies in logistic regression models the fast backward technique of Lawless and Singhal (1978), a first-order approximation that has greater numerical efficiency than full backward selection:

```
selection method=backward(fast);
```

The fast technique fits an initial full logistic model and a reduced model after the candidate effects have been dropped. On the other hand, full backward selection fits a logistic regression model each time an effect is removed from the model.

Stepwise Selection

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, and REGSELECT.

METHOD=STEPWISE specifies the stepwise method, which modifies the forward selection technique by allowing effects already in the model to be removed.

In the traditional implementation of stepwise selection method, the same entry and removal significance levels for the forward selection and backward elimination methods are used to assess contributions of effects as they are added to or removed from a model. If, at a step of the stepwise method, any effect in the model is not significant at the SLSTAY= level, then the least significant of these effects is removed from the model and the algorithm proceeds to the next step. This ensures that no effect can be added to a model while some effect currently in the model is not deemed significant. Another effect can be added to the model only after all necessary deletions have been accomplished. In this case the effect whose addition is the most significant is added to the model and the algorithm proceeds to the next step. The stepwise process ends when none of the effects outside the model is significant at the SLENTRY= level and every effect in the model is significant at the SLSTAY= level. In some cases, neither of these two conditions for stopping is met and the sequence of models cycles. In this case, the stepwise method terminates at the end of the cycle.

Just as you can in forward selection and backward elimination, you can use the SELECT= option to change the criterion that is used to assess effect contributions. You can also use the STOP= option to specify a stopping criterion and use a CHOOSE= option to provide a criterion for selecting among the sequence of models produced. For more information, see the section “Forward Selection” on page 60.
For selection criteria other than the significance level, further modification to the stepwise method is supported. In the standard stepwise method, no effect can enter the model if removing any effect currently in the model would yield an improved value of the selection criterion. In the modification, you can use the COMPETITIVE option to specify that addition and deletion of effects should be treated competitively. The selection criterion is evaluated for all models that are produced by deleting an effect from the current model or by adding an effect to this model. The action that most improves the selection criterion is the action taken.

**Examples of Stepwise Selection Specifications**

The following statement requests stepwise selection based on the SBC criterion:

```plaintext
selection method=stepwise;
```

First, if removing any effect yields a model that has a lower SBC statistic than the current model, then the effect that produces the smallest SBC statistic is removed. If removing any effect increases the SBC statistic, then provided that adding some effect lowers the SBC statistic, the effect that produces the model that has the lowest SBC is added.

The following statement requests the traditional stepwise method:

```plaintext
selection=stepwise(select=SL)
```

First, if the removal of any effect in the model is not significant at the default stay level of 0.05, then the least significant effect is removed and the algorithm proceeds to the next step. Otherwise, the effect whose addition is the most significant is added, provided that it is significant at the default entry level of 0.05.

The following statement requests the traditional stepwise method, where effects enter and leave based on significance levels, but with the following extra check: if any effect to be added or removed yields a model whose SBC statistic is greater than the SBC statistic of the current model, then the stepwise method terminates at the current model.

```plaintext
selection method=stepwise(select=SL stop=SBC) stophorizon=1;
```

In this case, the entry and stay significance levels still play a role because they determine whether an effect is deleted from or added to the model. This extra check might result in the selection terminating before a local minimum of the SBC criterion is found.

The following statement selects effects to enter or drop as in the previous example except that the significance level for entry is now 0.1 and the significance level to stay is 0.08. From the sequence of models produced, the selected model is chosen to yield the minimum AIC statistic:

```plaintext
selection method=stepwise(select=SL SLE=0.1 SLS=0.08 choose=AIC);
```

The following statement requests stepwise selection that is based on the AICC criterion and treats additions and deletions competitively:

```plaintext
selection method=stepwise(select=AICC competitive);
```

Each step evaluates the AICC statistics that correspond to the removal of any effect in the current model or the addition of any effect to the current model and chooses the addition or removal that produced the minimum value, provided that this minimum is lower than the AICC statistic of the current model.

The following statement requests stepwise selection that is based on the SBC criterion, treats additions and deletions competitively, and stops based on the average square error over the validation data:
Model Selection Methods

\[ \text{selection=stepwise(select=SBC competitive stop=VALIDATE);} \]

At any step, SBC statistics that correspond to the removal of any effect from the current model or the addition of any effect to the current model are evaluated. The addition or removal that produces the minimum SBC value is made. The average square error on the validation data for the model with this addition or removal is evaluated. The selection stops when the average square error so produced increases for three consecutive steps.

**Forward-Swap Selection**

This section applies to the following procedures: REGSELECT.

METHOD=FORWARDSWAP specifies the forward-swap selection method, which is an extension of the forward selection method. The forward-swap selection method incorporates steps that improve a model by replacing an effect in the model with an effect that is not in the model. When the model selection criterion is R square, this method is the same as the maximum R-square improvement (MAXR) method that is implemented in the REG procedure in SAS/STAT software. You cannot use the effect significance level as the selection criterion for the forward-swap method.

The forward-swap selection method begins by finding the one-effect model that produces the best value of the selection criterion. Then another effect (the one that yields the greatest improvement in the selection criterion) is added. After the two-effect model is obtained, each of the effects in the model is compared to each effect that is not in the model. For each comparison, the forward-swap method determines whether removing one effect and replacing it with the other effect improves the selection criterion. After comparing all possible swaps, the forward-swap method makes the swap that produces the greatest improvement in the selection criterion. Comparisons begin again, and the process continues until the forward-swap method finds that no other swap could improve the selection criterion. Thus, the two-variable model that is produced is considered the “best” two-variable model that the technique can find. Another variable is then added to the model, and the comparing-and-swapping process is repeated to find the “best” three-variable model, and so on.

The difference between the stepwise selection method and the forward-swap selection method is that all swaps are evaluated before any addition is made in the forward-swap method. In the stepwise selection method, the “worst” effect might be removed without considering what adding the “best” remaining effects might accomplish. Because the forward-swap method needs to examine all possible pairwise effect swaps at each step of the selection process, the forward-swap method is much more computationally expensive than the stepwise selection method; it might not be appropriate for models that contain a large number of effects.

**Least Angle Regression**

This section applies to the following procedures: REGSELECT.

METHOD=LAR specifies least angle regression (LAR), which was introduced by Efron et al. (2004). Not only does this algorithm provide a selection method in its own right, but with one additional modification, it can be used to efficiently produce LASSO solutions. Just like the forward selection method, the LAR
algorithm produces a sequence of regression models in which one parameter is added at each step, terminating at the full least squares solution when all parameters have entered the model.

The algorithm starts by centering the covariates and response and scaling the covariates so that they all have the same corrected sum of squares. Initially all coefficients are 0, as is the predicted response. The predictor that is most correlated with the current residual is determined, and a step is taken in the direction of this predictor. The length of this step determines the coefficient of this predictor and is chosen so that some other predictor and the current predicted response have the same correlation with the current residual. At this point, the predicted response moves in the direction that is equiangular between these two predictors. Moving in this direction ensures that these two predictors continue to have a common correlation with the current residual. The predicted response moves in this direction until a third predictor has the same correlation with the current residual as the two predictors already in the model. A new direction is determined that is equiangular among these three predictors, and the predicted response moves in this direction until a fourth predictor, which has the same correlation with the current residual, joins the set. This process continues until all predictors are in the model.

As in other selection methods, the issue of when to stop the selection process is crucial. You can use the \texttt{CHOOSE=} option to specify a criterion for choosing among the models at each step. You can also use the \texttt{STOP=} option to specify a stopping criterion. These formulas use the approximation that at step \( k \) of the LAR algorithm, the model has \( k \) degrees of freedom. For a detailed discussion of this so-called simple approximation, see Efron et al. (2004).

A modification of LAR selection that is suggested in Efron et al. (2004) uses the LAR algorithm to select the set of covariates in the model at any step, but it uses ordinary least squares regression with just these covariates to obtain the regression coefficients. You can request this hybrid method by specifying the \texttt{LSCOEFFS} suboption of \texttt{METHOD=LAR}.

\section*{LASSO Selection}

This section applies to the following procedures: GENSELECT, LOGSELECT, and REGSELECT.

\texttt{METHOD=LASSO} specifies the least absolute shrinkage and selection operator (LASSO) method. LASSO arises from a constrained form of ordinary least squares regression where the sum of the absolute values of the regression coefficients is constrained to be smaller than a specified parameter. More precisely let \( X = (x_1, x_2, \ldots, x_m) \) denote the matrix of covariates and let \( y \) denote the response, where the \( x_i \) have been centered and scaled to have unit standard deviation and mean 0 and \( y \) has mean 0. Then for a particular parameter \( t \), the LASSO regression coefficients \( \beta = (\beta_1, \beta_2, \ldots, \beta_m) \) are the solution to the following constrained optimization problem:

\[
\text{minimize } \|y - X\beta\|^2 \quad \text{subject to } \sum_{j=1}^{m} |\beta_j| \leq t
\]

Provided that the LASSO parameter \( t \) is small enough, some of the regression coefficients are exactly 0. Hence, you can view the LASSO as selecting a subset of the regression coefficients for each LASSO parameter. By increasing the LASSO parameter in discrete steps, you obtain a sequence of regression coefficients in which the nonzero coefficients at each step correspond to selected parameters.
Early implementations (Tibshirani 1996) of LASSO selection used quadratic programming techniques to solve the constrained least squares problem for each LASSO parameter of interest. Later Osborne, Presnell, and Turlach (2000) developed a “homotopy method” that generates the LASSO solutions for all values of $t$. Efron et al. (2004) derived a variant of their algorithm for least angle regression that can be used to obtain a sequence of LASSO solutions from which all other LASSO solutions can be obtained by linear interpolation. This algorithm for METHOD=LASSO is used in PROC REGSELECT. It can be viewed as a stepwise procedure with a single addition to or deletion from the set of nonzero regression coefficients at any step.

As in the other selection methods, you can use the CHOOSE= option to specify a criterion to choose among the models at each step of the LASSO algorithm. You can also use the STOP= option to specify a stopping criterion. For more information, see the discussion in the section “Forward Selection” on page 60. The model degrees of freedom used at any step of the LASSO are simply the number of nonzero regression coefficients in the model at that step. Efron et al. (2004) cite empirical evidence for doing this but do not give any mathematical justification for this choice.

A modification of LASSO selection suggested in Efron et al. (2004) uses the LASSO algorithm to select the set of covariates in the model at any step, but it uses ordinary least squares regression and just these covariates to obtain the regression coefficients. You can request this hybrid method by specifying the LSCOEFFS suboption of SELECTION=LASSO.

### Adaptive LASSO Selection

This section applies to the following procedures: REGSELECT.

Adaptive LASSO selection is a modification of LASSO selection; in adaptive LASSO selection, weights are applied to each of the parameters in forming the LASSO constraint (Zou 2006). More precisely, suppose that the response $y$ has mean 0 and the regressors $x$ are scaled to have mean 0 and common standard deviation. Furthermore, suppose that you can find a suitable estimator $\hat{\beta}$ of the parameters in the true model and you define a weight vector by $w = 1/|\hat{\beta}|^\gamma$, where $\gamma \geq 0$. Then the adaptive LASSO regression coefficients $\hat{\beta} = (\beta_1, \beta_2, \ldots, \beta_m)$ are the solution to the following constrained optimization problem:

$$\text{minimize} \|y - X\beta\|^2 \quad \text{subject to} \quad \sum_{j=1}^{m} w_j |\beta_j| \leq t$$

The solution to the unconstrained least squares problem is used as the estimator $\hat{\beta}$. This is appropriate unless collinearity is a concern. If the regressors are collinear or nearly collinear, then Zou (2006) suggests using a ridge regression estimate to form the adaptive weights.

### Group LASSO Selection

This section applies to the following procedures: GENSELECT and LOGSELECT.

The group LASSO method, proposed by Yuan and Lin (2006), is a variant of LASSO that is specifically designed for models defined in terms of effects that have multiple degrees of freedom, such as the main effects
Chapter 2: Shared Concepts

of CLASS variables and interactions between CLASS variables. If all effects in the model are continuous, then the group LASSO method is the same as the LASSO method.

Recall that LASSO selection depends on solving a constrained optimization problem of the form

$$\min\{-L(\mu; y)\} \quad \text{subject to} \quad \sum_{j=1}^{m} |\beta_j| \leq t$$

where $L$ is the log-likelihood function. In this formulation, individual parameters can be included or excluded from the model independently, subject only to the overall constraint. In contrast, the group LASSO method uses a constraint that forces all parameters that correspond to the same effect to be included or excluded simultaneously. For a model that has $k$ effects, let $\beta_{G_j}$ be the group of linear coefficients that correspond to effect $j$ in the model. Then group LASSO depends on solving a constrained optimization problem of the form

$$\min\{-L(\mu; y)\} \quad \text{subject to} \quad \sum_{j=1}^{k} \sqrt{|G_j|||\beta_{G_j}||} \leq t$$

where $|G_j|$ is the number of parameters that correspond to effect $j$, and $||\beta_{G_j}||$ denotes the Euclidean norm of the parameters $\beta_{G_j}$,

$$||\beta_{G_j}|| = \sqrt{\sum_{i=1}^{G_j} \beta_i^2}$$

That is, instead of constraining the sum of the absolute value of individual parameters, group LASSO constrains the Euclidean norm of groups of parameters, where groups are defined by effects.

You can write the group LASSO method in the equivalent Lagrangian form, which is an example of a penalized log-likelihood function:

$$\min\{-L(\mu; y)\} + \lambda \sum_{j=1}^{k} \sqrt{|G_j|||\beta_{G_j}||}$$

The weight $\sqrt{|G_j|}$ was suggested by Yuan and Lin (2006) in order to take the size of the group into consideration in group LASSO.

Unlike LASSO for linear models, group LASSO does not allow a piecewise linear constant solution path as generated by a LAR algorithm. Instead, the method proposed by Nesterov (2013) is adopted to solve the Lagrangian form of the group LASSO problem that corresponds to a prespecified regularization parameter $\lambda$. Nesterov’s method is known to have an optimal convergence rate for first-order black-box optimization. Because the optimal $\lambda$ is usually unknown, a series of regularization parameters $\rho, \rho^2, \rho^3, \ldots$ is used, where $\rho$ is a positive value less than 1. You can specify $\rho$ by using the LASSORHO= option in the procedure; the default value is $\rho = 0.8$. In the $i$th step of group LASSO selection, the value that is used for $\lambda$ is $\rho^i$.

A unique feature of the group LASSO method is that it does not necessarily add or remove precisely one effect at each step of the process. This is different from the forward, stepwise, and backward selection methods.

As with the other selection methods, you can specify a criterion to choose among the models at each step of the group LASSO algorithm by using the CHOOSE= option in the SELECTION statement. You can also
specify a stopping criterion by using the \texttt{STOP=} option in the \texttt{SELECTION} statement. If you do not specify either the \texttt{CHOOSE=} or \texttt{STOP=} option, the model at the last LASSO step is chosen as the selected model and parameter estimates are reported for this model. These parameter estimates are used to compute predicted values for the output data tables.

For more information, see the discussion in the section “\texttt{SELECTION Statement}” on page 34.

The model degrees of freedom at any step of the LASSO are simply the number of nonzero regression coefficients in the model at that step. Efron et al. (2004) cite empirical evidence for doing this but do not give any mathematical justification for this choice.

Some distributions involve a dispersion parameter (the parameter $\phi$ in the expressions for the log likelihood). These parameters are not estimated by the LASSO optimization algorithm, and are set to either the default value or a value that you specify. You can use the \texttt{PHI=} option in the procedure to set the dispersion to a fixed value.

---

**Model Selection Plots**

This section describes the ODS graphical displays that you can request by using the \texttt{PLOTS=} option in the \texttt{SELECTION} statement.

This section applies to the following procedures: \texttt{GENSELECT}, \texttt{LOGSELECT}, \texttt{QTRSELECT}, and \texttt{REGSELECT}.

The example plots shown in this section are produced by using the \texttt{REGSELECT} procedure.

The following \texttt{DATA} step produces simulated example data that contain a variable that you can use to assign observations to the training, validation, and testing roles. In this case, each role has 5,000 observations. These statements assume that your CAS engine libref is named \texttt{mycas}, as in the section “Using CAS Sessions and CAS Engine Librefs” on page 8, but you can substitute any appropriately defined CAS engine libref.

```plaintext
data mycas.exampleData;
  drop i j;
  array x{20} x1-x20;
  array c{5} c1-c5;
  call streaminit(1);
  do i=1 to 15000;
    do j=1 to dim(x);
      x[j] = rand('NORMAL');
    end;
    do j=1 to dim(c);
      c[j] = 1+ int(rand('UNIFORM')*3);
    end;
    y = 1 + x1 + 2*x5 - 1.3*x10 + x20 + 5*(c1=1)+3*(c1=3) - 4*c4 + 25*rand('NORMAL');
    if mod(i,3)=1 then Role = 'TRAIN';
  end;
run;
```

---
else if mod(i,3)=2 then Role = 'VAL';
else
    Role = 'TEST';

    output;
end;
run;

The following statements perform forward selection to obtain a parsimonious linear regression model for the response:

   ods graphics on;
   proc regselect data=mycas.exampleData;
      partition rolevar=Role(train='TRAIN' validate='VAL' test='TEST');
      class c: ;
      model y = x: c: ;
      selection method=forward(stop=AICC CHOOSE=validate) plots=all;
   run;

Because you specified the PLOTS=ALL option in the SELECTION statement and have enabled ODS Graphics, the plots that are described in the following sections are produced.

**Coefficient Panel**

Figure 2.6 shows the coefficient panel, which contains two plots that show how the standardized coefficients and the criterion used to choose the final model evolve as the selection progresses.
Figure 2.6 Coefficient Panel

The upper plot in the panel displays the standardized coefficients as a function of the step number. To help trace the changes in a parameter, the standardized coefficients for each parameter are connected by lines. Coefficients that correspond to effects not in the selected model at a step are zero and hence not observable. Parameters that are nonzero at the final step of the selection are labeled if their magnitudes are greater than 1% of the range of the magnitudes of all the nonzero parameters at this step. To avoid collision, labels that correspond to parameters that have similar values at the final step might be suppressed.

The lower plot in the panel shows how the criterion used to choose among the examined models progresses. The selected step occurs at the optimal value of this criterion. In this example, this criterion is the average square error (ASE) on the validation data, and it achieves its minimal value at step 6 of the forward selection.

Criterion Panel

Figure 2.6 shows the criterion panel, which contains plots that show the progression of fit criteria.
The selected step is displayed as a vertical reference line on the plot of each criterion. The optimal value of each criterion is indicated with the “star” marker. Note that it is possible that a better value of a criterion might have been reached if more steps of the selection process had been done.

**Fit by Role Plot**

Figure 2.8 displays the fit by role plot, which shows the progression of a fit statistic evaluated separately on the training, validation, and test data. If you do not partition your data into roles by using a PARTITION statement, then the fit by role plot is not produced.
You use this plot to detect overfitting of the training data. For many types of regression (including the linear regression that is used in the examples in this section), the fit statistic shown in this plot is the average square error (ASE) evaluated separately for each data role. The ASE decreases monotonically on the training data as parameters are added to a model. However, the ASE on test and validation data usually starts increasing when overfitting occurs.

**Using Options to Customize Plots**

In some cases, particularly when the final step contains a large number of parameters, you might be interested in using the coefficient panel only to discern if and when the parameters in the model are essentially unchanged beyond a certain step. In such cases, you might want to suppress the labeling of the parameters and use a numeric axis on the horizontal axis of the plot. You can do this by using the STEPXAXIS= and MAXPARMLABEL= global plot options. The following statements provide an example:

```plaintext
proc regselect data=mycas.exampleData;
   partition rolevar=Role(train='TRAIN' validate='VAL' test='TEST');
   class c: ;
   model y = x: c: ;
```
The `selection` method=`forward`(`stop=none` `choose=validate`) `plots(maxparmlabel=1` `stepaxis=number)=(coefficients criteria(unpack))`; `run;`

The `STEPAXIS=NUMBER` option requests that a numeric horizontal axis showing step number be used on all plots. The `MAXPAMLABEL=1` option suppresses the labels for the parameters in the coefficient progression panel.

The “Coefficient Progression Panel” is shown in Figure 2.9. You can see that the standardized coefficients of the selected parameters do not vary greatly after the selected step (step 6).

![Coefficient Progression Panel](image)

The `UNPACK` option for the criterion panel specifies that the individual plots in this panel be shown as separate plots. Figure 2.10 shows the plot for the AIC criterion.
Examining Specific Step Ranges

The coefficient panel, criterion panel, and average square error plot display information for all the steps examined in the selection process. In some cases, you might want to focus attention on just a particular step range. For example, it is hard to discern the variation in the criteria displayed in Figure 2.7 near the selected step because the variation in these criteria in the steps close to the selected step is small relative to the variation across all steps. You can request a range of steps to display by using the STARTSTEP= and ENDF= suboptions of the PLOTS= option. The following statements provide an example:

```
proc regselect data=mycas.exampleData;
    partition rolevar=Role(train='TRAIN' validate='VAL' test='TEST');
    class c: ;
    model y = x: c: ;
    selection method=forward(stop=none choose=validate)
        plots(startstep=3 endstep=8)=criteria;
run;
ods graphics off;
```
Figure 2.11 shows the progression of the fit criteria between steps 3 and 8. Note that if the optimal value of a criterion does not occur in this specified step range, then no optimal marker appears for that criterion.

**Figure 2.11** Criterion Panel for Specified Step Range

---

**Informative Missingness**

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, and REGSELECT.

The concept of informative missingness is one way to account for missing values in statistical analyses and, in particular, statistical modeling. Missing values can be a problem because they reduce the amount of available data. When you work with classification variables (factors, which are levelized variables), you can treat a missing value as an actual level of the variable and allow it to participate in the analysis.

However, when continuous variables have missing values, the observation is removed from the analysis. In data that have many missing values, removing observations can reduce the amount of available data greatly,
and the sets of observations used in one model versus another model can vary based on which variables are
included in the model.

Of course, there are many reasons for missing values, and substituting values for missing values has to be
done with caution. For example, the famous Framingham Heart study data set contains 5,209 observations
on subjects in a longitudinal study that helped understand the relationship between smoking, cholesterol,
and coronary heart disease. One of the variables in the data set is \( \text{AgeCHDdiag} \). This variable represents the
age at which a patient was diagnosed with coronary heart disease (CHD). If you include this variable in a
statistical model, only 1,449 observations are available, because the value cannot be observed unless a patient
has experienced CHD. Including this variable acts as a filter that reduces the analysis set to the subjects who
have CHD. You cannot impute the value for subjects where the variable has a missing value, because you
cannot impute an age at which someone who has not had CHD would have contracted coronary heart disease.

With informative missingness, you are not so much substituting imputed values for the missing values as you
are modeling the missingness. Consider a simple linear regression model:

\[
y = \beta_0 + \beta_1 x + \epsilon
\]

Suppose that some of the values for the regressor variable \( x \) are missing. The fitted model uses only
observations for which \( y \) and \( x \) have been observed.

In order to predict the outcome \( y \) for an observation that has a missing \( x \), either you assume that \( y \) is missing or
you substitute a value (such as the average value, \( \bar{x} \)) for the missing \( x \). Because the estimate for the intercept
is in the simple linear regression model, the predicted value would be the average response of the nonmissing
values, \( \bar{y} \).

With informative missingness, you extend the model by adding extra effects for each effect that contains at
least one continuous variable. In the simple linear regression model, you add one column to the model and
slightly change the content of the \( x \) variable:

\[
y = \beta_0 + \beta_1 x^* + \beta_2 x_{\text{miss}} + \epsilon_1
\]

The variable \( x^* \) contains the original values of \( x \) if they are not missing, and the average of \( x \) otherwise:

\[
x^* = \begin{cases} 
  x & \text{if } x \text{ is not missing} \\
  \bar{x} & \text{otherwise}
\end{cases}
\]

The variable \( x_{\text{miss}} \) is a dummy variable whose value is 1 when \( x \) is missing, and 0 otherwise:

\[
x_{\text{miss}} = \begin{cases} 
  1 & \text{if } x \text{ is missing} \\
  0 & \text{otherwise}
\end{cases}
\]

The fitted model is not the same model that results from substituting \( \bar{x} \) for the missing values during training,
because the model that simply substitutes \( \bar{x} \) for the missing values is

\[
y = \beta_0 + \beta_1 x^* + \epsilon_2
\]

The informative missing model has an extra parameter, and unless all values of \( x_{\text{miss}} \) are 0 (in which case
there are no missing values), the informative missing model has a higher R-square value, because it picks up
more variation.

The parameter estimate for \( \beta_2 \) measures the amount by which the predicted value differs from a predicted
value at \( \bar{x} \).
Using Validation and Test Data

This section applies to the following procedures: GENSELECT, LOGSELECT, QTRSELECT, REGSELECT, and TREESPLIT.

When you have sufficient data, you can divide your data into three parts called the training, validation, and test data. During the selection process, models are fit on the training data, and the prediction errors for the models so obtained are found by using the validation data. This prediction error on the validation data can be used to decide when to terminate the selection process and to decide which model to select. Finally, after a model has been selected, the test set can be used to assess how the selected model generalizes on data that played no role in selecting the model.

In some cases, you might want to use only training and test data. For example, you might decide to use an information criterion to decide which effects to include and when to terminate the selection process. In this case, no validation data are required, but test data can still be useful in assessing the predictive performance of the selected model. In other cases, you might decide to use validation data during the selection process but forgo assessing the selected model on test data. Hastie, Tibshirani, and Friedman (2001) note that it is difficult to provide a general rule for how many observations you should assign to each role. They note that a typical split might be 50% for training and 25% each for validation and testing.

You use a PARTITION statement to logically subdivide the input data table into separate roles. You can specify the fractions of the data that you want to reserve as test data and validation data. For example, the following statements randomly divide the inData data table, reserving 50% for training and 25% each for validation and testing:

```plaintext
proc regselect data=mycas.inData;
   partition fraction(test=0.25 validate=0.25);
   ...
run;
```

You can specify the SEED= option in the PARTITION statement to create the same partition data tables for a particular number of compute nodes. However, changing the number of compute nodes changes the initial distribution of data, resulting in different partition data tables.

In some cases, you might need to exercise more control over the partitioning of the input data table. You can do this by naming both a variable in the input data table and a formatted value of that variable for each role. For example, the following statements assign roles to the observations in the inData data table that are based on the value of the variable Group in that data table. Observations whose value of Group is 'Group 1' are assigned for testing, and those whose value is 'Group 2' are assigned to training. All other observations are ignored.

```plaintext
proc regselect data=mycas.inData;
   partition roleVar=Group(test='Group 1' train='Group 2')
   ...
run;
```

When you have reserved observations for training, validation, and testing, a model that is fit on the training data is scored on the validation and test data, and statistics are computed separately for each of these subsets.
Using the Validation Statistic as the CHOOSE= Criterion

When you specify the CHOOSE=VALIDATE suboption of the METHOD= option in the SELECTION statement, the ASE is computed on the validation data for the models at each step of the selection process. The smallest model at any step that yields the smallest validation ASE is selected.

Using the Validation Statistic as the STOP= Criterion

When you specify the STOP=VALIDATE suboption of the METHOD= option in the SELECTION statement, the ASE is computed on the validation data for the models at each step of the selection process. At step \( k \) of the selection process, the best candidate effect to enter or leave the current model is determined and the validation ASE for this new model is computed. If this validation ASE is greater than the validation ASE for the model at step \( k \), then the selection process terminates at step \( k \).

Multithreading

This section applies to the following procedures: ASSESS, BINNING, CARDINALITY, CORRELATION, GAMMOD, GENSELECT, KCLUS, LOGSELECT, NLMOD, PARTITION, PCA, PHSELECT, PLSMOD, QTRSELECT, REGSELECT, TREESPLIT, VARIMPUTE, and VARREDUCE.

Threading refers to the organization of computational work into multiple tasks (processing units that can be scheduled by the operating system). A task is associated with a thread. Multithreading refers to the concurrent execution of threads. When multithreading is possible, substantial performance gains can be realized compared to sequential (single-threaded) execution. The number of threads spawned by a procedure in this book is determined by your installation.

The tasks that are multithreaded by procedures in this book are primarily defined by dividing the data that are processed on a single machine among the threads—that is, the procedures implement multithreading through a data-parallel model. For example, if the input data table has 1,000 observations and the procedure is running on four threads, then 250 observations are associated with each thread. All operations that require access to the data are then multithreaded. These operations include the following (not all operations are required for all procedures):

- variable levelization
- effect levelization
- formation of the initial crossproducts matrix
- formation of approximate Hessian matrices for candidate evaluation during model selection
- objective function calculation
- gradient calculation
- Hessian calculation
- scoring of observations

In addition, operations on matrices such as sweeps can be multithreaded provided that the matrices are of sufficient size to realize performance benefits from managing multiple threads for the particular matrix operation.
Choosing an Optimization Algorithm

This section applies to the following procedures: GAMMOD, GENSELECT, LOGSELECT, and NLMOD.

First- or Second-Order Algorithms

The factors that go into choosing a particular optimization technique for a particular problem are complex. Trial and error can be involved.

For many optimization problems, computing the gradient takes more computer time than computing the function value. Computing the Hessian sometimes takes much more computer time and memory than computing the gradient, especially when there are many decision variables. Unfortunately, optimization techniques that do not use some kind of Hessian approximation usually require many more iterations than techniques that do use a Hessian matrix, and as a result the total run time of these techniques is often longer. Techniques that do not use the Hessian also tend to be less reliable. For example, they can terminate more easily at stationary points than at global optima.

Table 2.21 shows which derivatives are required for each optimization technique.

<table>
<thead>
<tr>
<th>Algorithm</th>
<th>First-Order</th>
<th>Second-Order</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>x</td>
<td>x</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>x</td>
<td>x</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>x</td>
<td>x</td>
</tr>
<tr>
<td>QUANEW</td>
<td>x</td>
<td>-</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>x</td>
<td>-</td>
</tr>
<tr>
<td>CONGRA</td>
<td>x</td>
<td>-</td>
</tr>
<tr>
<td>LEVMAR</td>
<td>x</td>
<td>-</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>-</td>
<td>-</td>
</tr>
</tbody>
</table>

The second-derivative methods TRUREG, NEWRAP, and NRRIDG are best for small problems for which the Hessian matrix is not expensive to compute. Sometimes the NRRIDG algorithm can be faster than the TRUREG algorithm, but TRUREG can be more stable. The NRRIDG algorithm requires only one matrix with \( p(p + 1)/2 \) double words; TRUREG and NEWRAP require two such matrices. Here, \( p \) denotes the number of parameters in the optimization.

The first-derivative methods QUANEW and DBLDOG are best for medium-sized problems for which the objective function and the gradient can be evaluated much faster than the Hessian. In general, the QUANEW and DBLDOG algorithms require more iterations than TRUREG, NRRIDG, and NEWRAP, but each iteration can be much faster. The QUANEW and DBLDOG algorithms require only the gradient to update an approximate Hessian, and they require slightly less memory than TRUREG or NEWRAP.

The first-derivative method CONGRA is best for large problems for which the objective function and the gradient can be computed much faster than the Hessian and for which too much memory is required to store the (approximate) Hessian. In general, the CONGRA algorithm requires more iterations than QUANEW or
DBLDOG, but each iteration can be much faster. Because CONGRA requires only a factor of $p$ double-word memory, many large applications can be solved only by CONGRA.

The no-derivative method NMSIMP is best for small problems for which derivatives are not continuous or are very difficult to compute.

The LEVMAR method is appropriate only for least squares optimization problems.

Each optimization method uses one or more convergence criteria that determine when it has converged. An algorithm is considered to have converged when any one of the convergence criteria is satisfied. For example, under the default settings, the QUANEW algorithm converges if $\text{ABSGCONV} < 1E^{-5}$, $\text{FCONV} < 2 \times \epsilon$, or $\text{GCONV} < 1E^{-8}$.

By default, procedures in this book apply the NRRIDG algorithm because it can take advantage of multi-threading in Hessian computations and inversions. If the number of parameters becomes large, specifying the TECHNIQUE=QUANEW option, which is a first-order method with good overall properties, is recommended.

**Algorithm Descriptions**

The following subsections provide details about each optimization technique and follow the same order as Table 2.21.

**Trust Region Optimization (TRUREG)**

The trust region method uses the gradient $g(\psi^{(k)})$ and the Hessian matrix $H(\psi^{(k)})$; thus, it requires that the objective function $f(\psi)$ have continuous first- and second-order derivatives inside the feasible region.

The trust region method iteratively optimizes a quadratic approximation to the nonlinear objective function within a hyperelliptic trust region with radius $\Delta$ that constrains the step size that corresponds to the quality of the quadratic approximation. The trust region method is implemented based on Dennis, Gay, and Welsch (1981), Gay (1983), and Moré and Sorensen (1983).

The trust region method performs well for small- to medium-sized problems, and it does not need many function, gradient, and Hessian calls. However, if the computation of the Hessian matrix is computationally expensive, one of the dual quasi-Newton or conjugate gradient algorithms might be more efficient.

**Newton-Raphson Optimization with Line Search (NEWRAP)**

The NEWRAP technique uses the gradient $g(\psi^{(k)})$ and the Hessian matrix $H(\psi^{(k)})$; thus, it requires that the objective function have continuous first- and second-order derivatives inside the feasible region. If second-order derivatives are computed efficiently and precisely, the NEWRAP method can perform well for medium-sized to large problems, and it does not need many function, gradient, and Hessian calls.

This algorithm uses a pure Newton step when the Hessian is positive-definite and when the Newton step reduces the value of the objective function successfully. Otherwise, a combination of ridging and line search is performed to compute successful steps. If the Hessian is not positive-definite, a multiple of the identity matrix is added to the Hessian matrix to make it positive-definite (Eskow and Schnabel 1991).

In each iteration, a line search is performed along the search direction to find an approximate optimum of the objective function. The line-search method uses quadratic interpolation and cubic extrapolation.
**Newton-Raphson Ridge Optimization (NRRIDG)**
The NRRIDG technique uses the gradient $\mathbf{g}(\mathbf{p}^{(k)})$ and the Hessian matrix $\mathbf{H}(\mathbf{p}^{(k)})$; thus, it requires that the objective function have continuous first- and second-order derivatives inside the feasible region.

This algorithm uses a pure Newton step when the Hessian is positive-definite and when the Newton step reduces the value of the objective function successfully. If at least one of these two conditions is not satisfied, a multiple of the identity matrix is added to the Hessian matrix.

Because the NRRIDG technique uses an orthogonal decomposition of the approximate Hessian, each iteration of NRRIDG can be slower than that of the NEWRAP technique, which works with a Cholesky decomposition. However, NRRIDG usually requires fewer iterations than NEWRAP.

The NRRIDG method performs well for small- to medium-sized problems, and it does not require many function, gradient, and Hessian calls. However, if the computation of the Hessian matrix is computationally expensive, one of the dual quasi-Newton or conjugate gradient algorithms might be more efficient.

**Quasi-Newton Optimization (QUANEW)**
The dual quasi-Newton method uses the gradient $\mathbf{g}(\mathbf{p}^{(k)})$, and it does not need to compute second-order derivatives because they are approximated. It works well for medium-sized to moderately large optimization problems, where the objective function and the gradient can be computed much faster than the Hessian. However, in general the QUANEW technique requires more iterations than the TRUREG, NEWRAP, and NRRIDG techniques, which compute second-order derivatives. The QUANEW technique provides an appropriate balance between the speed and stability required for most nonlinear mixed model applications.

The QUANEW technique implemented by procedures in this book is the dual quasi-Newton algorithm, which updates the Cholesky factor of an approximate Hessian.

In each iteration, a line search is performed along the search direction to find an approximate optimum. The line-search method uses quadratic interpolation and cubic extrapolation to obtain a step size $\alpha$ that satisfies the Goldstein conditions (Fletcher 1987). One of the Goldstein conditions can be violated if the feasible region defines an upper limit of the step size. Violating the left-side Goldstein condition can affect the positive-definiteness of the quasi-Newton update. In that case, either the update is skipped or the iterations are restarted with an identity matrix, resulting in the steepest descent or ascent search direction.

**Double-Dogleg Optimization (DBLDOG)**
The double-dogleg optimization method combines the ideas of the quasi-Newton and trust region methods. In each iteration, the double-dogleg algorithm computes the step $s^{(k)}$ as the linear combination of the steepest descent or ascent search direction $s_1^{(k)}$ and a quasi-Newton search direction $s_2^{(k)}$:

$$s^{(k)} = \alpha_1 s_1^{(k)} + \alpha_2 s_2^{(k)}$$

The step is requested to remain within a prespecified trust region radius (Fletcher 1987, p. 107). Thus, the DBLDOG subroutine uses the dual quasi-Newton update but does not perform a line search.

The double-dogleg optimization technique works well for medium-sized to moderately large optimization problems, where the objective function and the gradient can be computed much faster than the Hessian. The implementation is based on Dennis and Mei (1979) and Gay (1983), but it is extended for dealing with boundary and linear constraints. The DBLDOG technique generally requires more iterations than the TRUREG, NEWRAP, and NRRIDG techniques, which require second-order derivatives; however, each of the DBLDOG iterations is computationally cheap. Furthermore, the DBLDOG technique requires only gradient calls for the update of the Cholesky factor of an approximate Hessian.
Conjugate Gradient Optimization (CONGRA)
Second-order derivatives are not required by the CONGRA algorithm and are not even approximated. The CONGRA algorithm can be expensive in function and gradient calls, but it requires only $O(p)$ memory for unconstrained optimization. In general, many iterations are required to obtain a precise solution, but each of the CONGRA iterations is computationally cheap.

The CONGRA subroutine should be used for optimization problems with large $p$. For the unconstrained or boundary-constrained case, CONGRA requires only $O(p)$ bytes of working memory, whereas all other optimization methods require order $O(p^2)$ bytes of working memory. During $p$ successive iterations, uninterrupted by restarts or changes in the working set, the conjugate gradient algorithm computes a cycle of $p$ conjugate search directions. In each iteration, a line search is performed along the search direction to find an approximate optimum of the objective function. The line-search method uses quadratic interpolation and cubic extrapolation to obtain a step size $\alpha$ that satisfies the Goldstein conditions. One of the Goldstein conditions can be violated if the feasible region defines an upper limit for the step size.

Levenberg-Marquardt Optimization (LEVMAR)
The LEVMAR algorithm performs a highly stable optimization; however, for large problems, it consumes more memory and takes longer than the other techniques. The Levenberg-Marquardt optimization technique is a slightly improved variant of the Moré (1978) implementation.

Nelder-Mead Simplex Optimization (NMSIMP)
The Nelder-Mead simplex method does not use any derivatives and does not assume that the objective function has continuous derivatives. The objective function itself needs to be continuous. This technique is quite expensive in the number of function calls, and it might be unable to generate precise results for $p \gg 40$.

The original Nelder-Mead simplex algorithm is implemented and extended to boundary constraints. This algorithm does not compute the objective for infeasible points, but it changes the shape of the simplex adapting to the nonlinearities of the objective function. This change contributes to an increased speed of convergence and uses a special termination criterion.

References


Chapter 2: Shared Concepts


Part II

Statistics
Overview: CORRELATION Procedure

The CORRELATION procedure computes Pearson correlation coefficients and the probabilities that are associated with these statistics in SAS Viya.

The Pearson product-moment correlation is a parametric measure of a linear relationship between two variables. When only one set of analysis variables is specified, the default correlation analysis includes
Chapter 3: The CORRELATION Procedure

Descriptive statistics for each analysis variable and pairwise Pearson correlation statistics for these variables. When two sets of analysis variables are specified, the default correlation analysis includes descriptive statistics for each analysis variable and pairwise Pearson correlation statistics between the two sets of variables. When the relationship between two variables is nonlinear or when outliers are present, the correlation coefficient might incorrectly estimate the strength of the relationship.

PROC CORRELATION Features

The CORRELATION procedure offers the following functionality:

- provides a WITH statement for analysis of pairwise Pearson correlation statistics between two sets of variables
- provides a FREQ statement for grouped analysis
- provides a WEIGHT statement for weighted analysis
- produces output data tables that contain descriptive statistics for analysis variables, Pearson correlation statistics, covariances, sums of squares, and corrected sums of squares
- computes Cronbach’s coefficient alpha for estimating reliability

Because the CORRELATION procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode
- exploits all the available cores and concurrent threads (for information about how PROC CORRELATION uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts”)

PROC CORRELATION Compared with Other SAS Procedures

The CORRELATION procedure provides functionality that is comparable to that of the HPCORR and CORR procedures in Base SAS software.

The functionality of the CORRELATION procedure closely resembles that of the HPCORR procedure, which is a high-performance procedure. The CORRELATION procedure is the next generation of the HPCORR procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations.

The CORRELATION procedure, the HPCORR procedure, and the CORR procedure have the similarities and differences shown in Table 3.1.
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

---

### Table 3.1 Comparison of PROC CORRELATION, PROC HPCORR, and PROC CORR

<table>
<thead>
<tr>
<th>Feature</th>
<th>CORRELATION</th>
<th>HPCORR</th>
<th>CORR</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supports the computation of Pearson correlation coefficients and the probabilities associated with these statistics</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports BY statement</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports DISPLAY and DISPLAYOUT statements</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Supports the computation of nonparametric measure of association</td>
<td>No</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports OUTP statements</td>
<td>Yes</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports Cronbach’s alpha coefficient alpha for estimating reliability</td>
<td>Yes</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Threading</td>
<td>Specifically designed for CAS; executes on multiple threads</td>
<td>Primarily designed for a distributed environment; executes on multiple threads</td>
<td>Executes on a single thread</td>
</tr>
</tbody>
</table>

---
cas mysess;
libname mycas cas sessref=mysess;

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

    cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

**Getting Started: CORRELATION Procedure**

This example creates a data table and then uses PROC CORRELATION to produce Pearson correlations.

The following statements create the Fitness data table in your CAS session. These data have been altered to contain some missing values:

```sas
*----------------- Data on Physical Fitness -----------------*
| These measurements were made on men involved in a physical |
| fitness course at N.C. State University.                  |
| The variables are Age (years), Weight (kg),               |
| Runtime (time to run 1.5 miles in minutes), and           |
| Oxygen (oxygen intake, ml per kg body weight per minute)  |
| Certain values were changed to missing for the analysis.  |
*---------------------------------------------------------------------*;

data mycas.Fitness;
    input Age Weight Oxygen RunTime @@;
datelines;
44 89.47 44.609 11.37 40 75.07 45.313 10.07
44 85.84 54.297 8.65 42 68.15 59.571 8.17
38 89.02 49.874 . 47 77.45 44.811 11.63
40 75.98 45.681 11.95 43 81.19 49.091 10.85
44 81.42 39.442 13.08 38 81.87 60.055 8.63
44 73.03 50.541 10.13 45 87.66 37.388 14.03
45 66.45 44.754 11.12 47 79.15 47.273 10.60
54 83.12 51.855 10.33 49 81.42 49.156 8.95
51 69.63 40.836 10.95 51 77.91 46.672 10.00
48 91.63 46.774 10.25 49 73.37 . 10.08
57 73.37 39.407 12.63 54 79.38 46.080 11.17
52 76.32 45.441 9.63 50 70.87 54.625 8.92
51 67.25 45.118 11.08 54 91.63 39.203 12.88
51 73.71 45.790 10.47 57 59.08 50.545 9.93
49 76.32 . . 48 61.24 47.920 11.50
52 82.78 47.467 10.50
; 
```
These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements invoke the CORRELATION procedure and request a correlation analysis:

```plaintext
proc correlation data=mycas.Fitness;
run;
```

The “Simple Statistics” table in Figure 3.1 displays univariate statistics for the analysis variables.

**Figure 3.1** Univariate Statistics

**The CORRELATION Procedure**

<table>
<thead>
<tr>
<th>Variable</th>
<th>N</th>
<th>Mean</th>
<th>Std Dev</th>
<th>Sum</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>31</td>
<td>47.67742</td>
<td>5.21144</td>
<td>1478</td>
<td>38.00000</td>
<td>57.00000</td>
</tr>
<tr>
<td>Weight</td>
<td>31</td>
<td>77.44452</td>
<td>8.32857</td>
<td>2401</td>
<td>59.08000</td>
<td>91.63000</td>
</tr>
<tr>
<td>Oxygen</td>
<td>29</td>
<td>47.22721</td>
<td>5.47718</td>
<td>1370</td>
<td>37.38800</td>
<td>60.05500</td>
</tr>
<tr>
<td>RunTime</td>
<td>29</td>
<td>10.67414</td>
<td>1.39194</td>
<td>309.55000</td>
<td>8.17000</td>
<td>14.03000</td>
</tr>
</tbody>
</table>

By default, all numeric variables not listed in other statements are used in the analysis. Observations that have nonmissing values for each variable are used to derive the univariate statistics for that variable.

The “Pearson Correlation Coefficients” table in Figure 3.2 displays the Pearson correlation, the \( p \)-value under the null hypothesis of zero correlation, and the number of nonmissing observations for each pair of variables.

**Figure 3.2** Pearson Correlation Coefficients

<table>
<thead>
<tr>
<th></th>
<th>Age</th>
<th>Weight</th>
<th>Oxygen</th>
<th>RunTime</th>
</tr>
</thead>
<tbody>
<tr>
<td>Prob &gt;</td>
<td>r</td>
<td>under H0: Rho=0</td>
<td>Number of Observations</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Age</td>
<td>Weight</td>
<td>Oxygen</td>
<td>RunTime</td>
</tr>
<tr>
<td>Age</td>
<td>1.0000</td>
<td>-0.2335</td>
<td>-0.3147</td>
<td>0.1448</td>
</tr>
<tr>
<td></td>
<td>0.2061</td>
<td>0.0963</td>
<td>0.4536</td>
<td></td>
</tr>
<tr>
<td></td>
<td>31</td>
<td>31</td>
<td>29</td>
<td>29</td>
</tr>
<tr>
<td>Weight</td>
<td>-0.2335</td>
<td>1.0000</td>
<td>-0.1536</td>
<td>0.2007</td>
</tr>
<tr>
<td></td>
<td>0.2061</td>
<td>0.4264</td>
<td>0.2965</td>
<td></td>
</tr>
<tr>
<td></td>
<td>31</td>
<td>31</td>
<td>29</td>
<td>29</td>
</tr>
<tr>
<td>Oxygen</td>
<td>-0.3147</td>
<td>-0.1536</td>
<td>1.0000</td>
<td>-0.8684</td>
</tr>
<tr>
<td></td>
<td>0.0963</td>
<td>0.4264</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td></td>
<td>29</td>
<td>29</td>
<td>29</td>
<td>29</td>
</tr>
<tr>
<td>RunTime</td>
<td>0.1448</td>
<td>0.2007</td>
<td>-0.8684</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>0.4536</td>
<td>0.2965</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td></td>
<td>29</td>
<td>29</td>
<td>28</td>
<td>29</td>
</tr>
</tbody>
</table>

By default, Pearson correlation statistics are computed from observations that have nonmissing values for each pair of analysis variables. Figure 3.2 displays a correlation of –0.86843 between RunTime and Oxygen, which is significant with a \( p \)-value less than 0.0001. That is, an inverse linear relationship exists between these two variables. As RunTime (time in minutes to run 1.5 miles) increases, Oxygen (oxygen intake in milliliters per kilogram body weight per minute) decreases.
Chapter 3: The CORRELATION Procedure

Syntax: CORRELATION Procedure

The following statements are available in PROC CORRELATION:

```plaintext
PROC CORRELATION <options> ;
    BY variables ;
    DISPLAY <table-list> </options> ;
    DISPLAYOUT table-spec-list </options> ;
    FREQ variable ;
    VAR variables ;
    WEIGHT variable ;
    WITH variables ;
```

The PROC CORRELATION statement is the only required statement for the CORRELATION procedure. The following sections describe the PROC CORRELATION statement and then describe the other statements in alphabetical order.

PROC CORRELATION Statement

```plaintext
PROC CORRELATION <options> ;
```

The PROC CORRELATION statement invokes the procedure. Table 3.2 summarizes the options available in the PROC CORRELATION statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Data Tables</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td>OUTP=</td>
<td>Specifies the CAS output data table to contain the Pearson correlation statistics</td>
</tr>
<tr>
<td><strong>Statistical Analysis</strong></td>
<td></td>
</tr>
<tr>
<td>EXCLNPWG'T</td>
<td>Excludes observations that have nonpositive weight values from the analysis</td>
</tr>
<tr>
<td>NOMISS</td>
<td>Excludes observations that have missing analysis values from the analysis</td>
</tr>
<tr>
<td><strong>Statistics</strong></td>
<td></td>
</tr>
<tr>
<td>ALPHA</td>
<td>Computes Cronbach’s coefficient alpha</td>
</tr>
<tr>
<td>COV</td>
<td>Computes covariances</td>
</tr>
<tr>
<td>CSSCP</td>
<td>Computes corrected sums of squares and crossproducts</td>
</tr>
<tr>
<td>SSCP</td>
<td>Computes sums of squares and crossproducts</td>
</tr>
<tr>
<td>VARDEF=</td>
<td>Specifies the divisor for variance calculations</td>
</tr>
<tr>
<td><strong>Printed Output</strong></td>
<td></td>
</tr>
<tr>
<td>BEST=</td>
<td>Displays the specified number of ordered correlation coefficients</td>
</tr>
<tr>
<td>NOCORR</td>
<td>Suppresses Pearson correlations</td>
</tr>
<tr>
<td>NOPROB</td>
<td>Suppresses p-values</td>
</tr>
<tr>
<td>NOSIMPLE</td>
<td>Suppresses descriptive statistics</td>
</tr>
<tr>
<td>RANK</td>
<td>Displays ordered correlation coefficients</td>
</tr>
</tbody>
</table>

Table 3.2  Summary of PROC CORRELATION Options
**ALPHA**
calculates and prints Cronbach’s coefficient alpha. PROC CORRELATION computes separate coefficients by using raw and standardized values (scaling the variables to a unit variance of 1). For each analysis variable, PROC CORRELATION computes the correlation between that variable and all the remaining variables. It also computes Cronbach’s coefficient alpha by using only the remaining variables.

When you specify this option, the Pearson correlations are also displayed. If you also specify the OUTP= option, the output data table also contains observations that have Cronbach’s coefficient alpha. For more information about Cronbach’s coefficient alpha, see the section “Cronbach’s Coefficient Alpha” on page 99.

This option is not valid if a WITH statement is specified.

**BEST=n**
prints the \( n \) highest correlation coefficients for each variable, where \( n \geq 1 \). Correlations are ordered from highest to lowest in absolute value. (If you do not specify this option, PROC CORRELATION prints correlations in a rectangular table, using the variable names as row and column labels.)

**COV**
displays the variance and covariance matrix. When you specify this option, the Pearson correlations are also displayed. If you also specify the OUTP= option, the output data table also contains the covariance matrix with the corresponding _TYPE_ variable value ‘COV.’

**CSSCP**
displays a table of the corrected sums of squares and crossproducts. When you specify this option, the Pearson correlations are also displayed. If you also specify the OUTP= option, the output data table also contains a CSSCP matrix with the corresponding _TYPE_ variable value ‘CSSCP.’

**DATA=**\( \text{CAS-libref.data-table} \)
names the input data table for PROC CORRELATION to use. The default is the most recently created data table. \( \text{CAS-libref.data-table} \) is a two-level name, where

\( \text{CAS-libref} \)
refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about \( \text{CAS-libref} \), see the section “Using CAS Sessions and CAS Engine Librefs” on page 89.

\( \text{data-table} \)
specifies the name of the input data table.

**EXCLNPWGT**
**EXCLNPWGTS**
excludes observations that have nonpositive weight values from the analysis. (By default, PROC CORRELATION treats observations that have negative weights like those observations that have zero weights and counts them in the total number of observations.)

**NOCORR**
suppresses display of Pearson correlations.
NOMISS
excludes observations that have missing values from the analysis. (If you do not specify this option, PROC CORRELATION computes correlation statistics by using all the nonmissing pairs of variables.)

NOPROB
suppresses display of the probabilities that are associated with each correlation coefficient.

NOSIMPLE
suppresses printing of simple descriptive statistics for each variable. However, if you request an output data table, the output data table still contains simple descriptive statistics for the variables.

OUTP=\texttt{CAS-libref.data-table}
creates an output data table that contains Pearson correlation statistics. \texttt{CAS-libref.data-table} is a two-level name, where

\texttt{CAS-libref}
refers to a collection of information that is defined in the LIBNAME statement and includes the \texttt{caslib}, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about \texttt{CAS-libref}, see the section “Using CAS Sessions and CAS Engine Librefs” on page 89.

\texttt{data-table}
specifies the name of the output data table.

This data table also includes means, standard deviations, and the number of observations. If you also specify the ALPHA option, the output data table also contains six observations that have Cronbach’s coefficient alpha.

RANK
displays the ordered correlation coefficients for each variable. Correlations are ordered from highest to lowest in absolute value.

SSCP
displays a table of the sums of squares and crossproducts. When you specify this option, the Pearson correlations are also displayed. If you also specify the OUTP= option, the output data table contains an SSCP matrix and the corresponding _TYPE_ variable value is ‘SSCP.’

\texttt{VARDEF=DF | N | WDF | WEIGHT | WGT}
specifies the variance divisor in the calculation of variances and covariances. The default is \texttt{VARDEF=DF}.

Table 3.3 displays available values and associated divisors for the \texttt{VARDEF=} option, where \( n \) is the number of nonmissing observations and \( w_j \) is the weight associated with the \( j \)th nonmissing observation.

<table>
<thead>
<tr>
<th>Value</th>
<th>Description</th>
<th>Divisor</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF</td>
<td>Degrees of freedom</td>
<td>( n - 1 )</td>
</tr>
<tr>
<td>N</td>
<td>Number of observations</td>
<td>( n )</td>
</tr>
<tr>
<td>WDF</td>
<td>Sum of weights minus one</td>
<td>( \sum_{j=1}^{n} w_j - 1 )</td>
</tr>
<tr>
<td>WEIGHT</td>
<td>Weight</td>
<td>( \sum_{j=1}^{n} w_j )</td>
</tr>
</tbody>
</table>
BY Statement

BY variables;

You can specify a BY statement in PROC CORRELATION to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in SAS Language Reference: Concepts.

DISPLAY Statement

DISPLAY < table-list > < / options > ;

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the table-list as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 102. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path Bygroup1.Summary.SelectionSummary. A partial pathname does not include all groups; for example, SelectionSummary and Summary.SelectionSummary are partial pathnames for Bygroup1.Summary.SelectionSummary.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both SelectionSummary and Summary.SelectionSummary select Bygroup1.Summary.SelectionSummary.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is not selected.

You can specify the following options after a slash (/):

CASESENSITIVE

performs a case-sensitive comparison of table names in the table-list to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the table-list in quotation marks.
EXCLUDE
displays all display tables except those that you specify in the table-list.

EXCLUDEALL
suppresses display of all tables. This option takes precedence over the other options.

TRACE
displays the display table names, labels, and paths.

DISPLAYOUT Statement

DISPLAYOUT table-spec-list < / options > ;

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The table-spec-list specifies a list of CAS output tables to create. Each entry in the list has either a key=value format or a key format:

key=value specifies key as the ODS table name, path, or partial pathname, and specifies value as the CAS output table name.

key specifies key as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

FREQ Statement

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC CORRELATION treats each observation as if it appears f times, where f is the value of the FREQ variable for the observation. If f is not an integer, it is truncated to an
integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

The effects of the FREQ and WEIGHT statements are similar except when \( n \) is not an integer and when degrees of freedom are calculated.

---

**VAR Statement**

```
VAR variables ;
```

The VAR statement lists `variables` for which to compute correlation coefficients. If the VAR statement is not specified, PROC CORRELATION computes correlations for all numeric variables that are not listed in other statements.

---

**WEIGHT Statement**

```
WEIGHT variable ;
```

The `variable` in the WEIGHT statement is used in the calculation of Pearson weighted product-moment correlations.

Observations that have missing weights are excluded from the analysis. By default, for observations that have nonpositive weights, weights are set to 0 and the observations are included in the analysis. You can use the EXCLNPWGT option to exclude observations that have negative or zero weights from the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

---

**WITH Statement**

```
WITH variables ;
```

The WITH statement lists `variables` for which to compute correlation coefficients. The WITH statement requests correlations of the form \( r(X_i, Y_j) \), where \( Y_1, \ldots, Y_n \) are the row analysis variables that are specified in the WITH statement and \( X_1, \ldots, X_m \) are the column analysis variables that are specified in the VAR statement; or, if there is no VAR statement, all numeric variables that are not specified in any other statement. The correlation matrix has a rectangular structure of the form

\[
\begin{bmatrix}
  r(Y_1, X_1) & \cdots & r(Y_1, X_m) \\
  \vdots & \ddots & \vdots \\
  r(Y_n, X_1) & \cdots & r(Y_n, X_m)
\end{bmatrix}
\]

For example, the statements

```
proc correlation data=mycas.data;
    var x1 x2;
    with y1 y2 y3;
run;
```
produce correlations for the following combinations:

\[
\begin{bmatrix}
  r(Y_1, X_1) & r(Y_1, X_2) \\
  r(Y_2, X_1) & r(Y_2, X_2) \\
  r(Y_3, X_1) & r(Y_3, X_2)
\end{bmatrix}
\]

**Details: CORRELATION Procedure**

**Pearson Product-Moment Correlation**

The Pearson product-moment correlation is a parametric measure of association for two variables. It measures both the strength and the direction of a linear relationship. If one variable \( X \) is an exact linear function of another variable \( Y \), a positive relationship exists if the correlation is 1, and a negative relationship exists if the correlation is –1. If there is no linear predictability between the two variables, the correlation is 0. If the two variables are normal with correlation 0, the two variables are independent. Correlation does not imply causality because an underlying causal relationship might not exist in some cases.

The formula for the population Pearson product-moment correlation, denoted \( \rho_{xy} \), is

\[
\rho_{xy} = \frac{\text{Cov}(x, y)}{\sqrt{\text{Var}(x)\text{Var}(y)}} = \frac{E((x - E(x))(y - E(y)))}{\sqrt{E(x - E(x))^2 E(y - E(y))^2}}
\]

The sample correlation, such as a Pearson product-moment correlation or weighted product-moment correlation, estimates the population correlation. The formula for the sample Pearson product-moment correlation is as follows, where \( \bar{x} \) is the sample mean of \( x \) and \( \bar{y} \) is the sample mean of \( y \):

\[
r_{xy} = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_i (y_i - \bar{y})^2}}
\]

The formula for a weighted Pearson product-moment correlation is as follows, where \( w_i \) is the weight, \( \bar{x}_w \) is the weighted mean of \( x \), and \( \bar{y}_w \) is the weighted mean of \( y \):

\[
r_{xy} = \frac{\sum_i w_i (x_i - \bar{x}_w)(y_i - \bar{y}_w)}{\sqrt{\sum_i w_i (x_i - \bar{x}_w)^2 \sum_i w_i (y_i - \bar{y}_w)^2}}
\]

**Probability Values**

Probability values for the Pearson correlation are computed by treating the following equation as if it came from a \( t \) distribution with \( (n - 2) \) degrees of freedom, where \( r \) is the sample correlation:

\[
t = (n - 2)^{1/2} \left( \frac{r^2}{1 - r^2} \right)^{1/2}
\]
Cronbach’s Coefficient Alpha

Analyzing latent constructs such as job satisfaction, motor ability, sensory recognition, or customer satisfaction requires instruments to accurately measure the constructs. Interrelated items can be summed to obtain an overall score for each participant. Cronbach’s coefficient alpha estimates the reliability of this type of scale by determining the internal consistency of the test or the average correlation of items within the test (Cronbach 1951).

When a value is recorded, the observed value contains some degree of measurement error. Two sets of measurements on the same variable for the same individual might not have identical values. However, repeated measurements for a series of individuals do show some consistency. Reliability measures internal consistency from one set of measurements to another. The observed value $Y$ is divided into two components, a true value $T$ and a measurement error $E$. The measurement error is assumed to be independent of the true value:

$$Y = T + E \quad \text{Cov}(T, E) = 0$$

The reliability coefficient of a measurement test is defined as the squared correlation between the observed value $Y$ and the true value $T$:

$$r^2(Y, T) = \frac{\text{Cov}(Y, T)^2}{\text{V}(Y)\text{V}(T)} = \frac{\text{V}(T)^2}{\text{V}(Y)\text{V}(T)} = \frac{\text{V}(T)}{\text{V}(Y)}$$

This coefficient is the proportion of the observed variance due to true differences among individuals in the sample. If $Y$ is the sum of several observed variables that measure the same feature, you can estimate $\text{V}(T)$. Cronbach’s coefficient alpha, which is based on a lower bound for $\text{V}(T)$, is an estimate of the reliability coefficient.

Suppose $p$ variables are used with $Y_j = T_j + E_j$ for $j = 1, 2, \ldots, p$, where $Y_j$ is the observed value, $T_j$ is the true value, and $E_j$ is the measurement error. The measurement errors ($E_j$) are independent of the true values ($T_j$) and are also independent of each other. Let $Y_0 = \sum_j Y_j$ be the total observed score, and let $T_0 = \sum_j T_j$ be the total true score. Because

$$(p - 1) \sum_j \text{V}(T_j) \geq \sum_{i \neq j} \text{Cov}(T_i, T_j)$$

a lower bound for $\text{V}(T_0)$ is given by

$$\frac{p}{p - 1} \sum_{i \neq j} \text{Cov}(T_i, T_j)$$

With $\text{Cov}(Y_i, Y_j) = \text{Cov}(T_i, T_j)$ for $i \neq j$, a lower bound for the reliability coefficient, $\text{V}(T_0)/\text{V}(Y_0)$, is then given by Cronbach’s coefficient alpha:

$$\alpha = \left( \frac{p}{p - 1} \right) \frac{\sum_{i \neq j} \text{Cov}(Y_i, Y_j)}{\text{V}(Y_0)} = \left( \frac{p}{p - 1} \right) \left( 1 - \frac{\sum_j \text{V}(Y_j)}{\text{V}(Y_0)} \right)$$

If the variances of the items vary widely, you can standardize the items to a standard deviation of 1 before computing the coefficient alpha. If the variables are dichotomous (0,1), the coefficient alpha is equivalent to the Kuder-Richardson 20 (KR-20) reliability measure.
When the correlation between each pair of variables is 1, the coefficient alpha has a maximum value of 1. With negative correlations between some variables, the coefficient alpha can have a value less than 0. The larger the overall alpha coefficient, the more likely that items contribute to a reliable scale. Nunnally and Bernstein (1994) suggest 0.70 as an acceptable reliability coefficient; smaller reliability coefficients are seen as inadequate. However, acceptability varies by discipline.

To determine how each item reflects the reliability of the scale, you calculate a coefficient alpha after deleting each variable independently from the scale. Cronbach’s coefficient alpha from all variables except the $k$th variable is given by

$$\alpha_k = \left( \frac{p - 1}{p - 2} \right) \left( 1 - \frac{\sum_{i \neq k} V(Y_i)}{V(\sum_{i \neq k} Y_i)} \right)$$

If the reliability coefficient increases after an item is deleted from the scale, you can assume that the item is not highly correlated with other items in the scale. Conversely, if the reliability coefficient decreases, you can assume that the item is highly correlated with other items in the scale. For more information about how to interpret Cronbach’s coefficient alpha, see Yu (2001).

Listwise deletion of observations that have missing values is necessary to correctly calculate Cronbach’s coefficient alpha. PROC CORRELATION does not automatically use listwise deletion if you specify the ALPHA option. Therefore, you should use the NOMISS option if the data table contains missing values. Otherwise, PROC CORRELATION prints a warning message that indicates that you need to use the NOMISS option with the ALPHA option.

**Missing Values**

Observations that have missing values for the variables in the FREQ or WEIGHT statement are omitted from the analysis.

By default, PROC CORRELATION uses pairwise deletion when observations contain missing values in the analysis variables for which correlation coefficients are computed. PROC CORRELATION includes all nonmissing pairs of values for each pair of variables in the statistical computations. Therefore, the correlation statistics might be based on different numbers of observations.

If you specify the NOMISS option, PROC CORRELATION uses listwise deletion and excludes all observations that have missing values from the analysis. Therefore, the number of observations for each pair of variables is identical.

**OUTP= Data Table**

If you specify the OUTP= option, PROC CORRELATION creates an output data table that contains statistics for Pearson correlation.

The new data table contains the following variables:

- BY variables, if any
- _TYPE_ variable, which identifies the type of observation
OUTP= Data Table

- _NAME_ variable, which identifies the variable that corresponds to a particular row of the correlation matrix
- INTERCEPT variable, which identifies variable sums when the SSCP option is specified
- the column analysis variables that are specified in the VAR statement or, if there is no VAR statement, all numeric variables that are not specified in any other statement

You can use a combination of the _TYPE_ and _NAME_ variables to identify the contents of an observation. The _NAME_ variable indicates which row of the correlation matrix the observation corresponds to. The values of the _TYPE_ variable are as follows:

- SSCP, uncorrected sums of squares and crossproducts
- CSSCP, corrected sums of squares and crossproducts
- COV, covariances
- MEAN, mean of each variable
- STD, standard deviation of each variable
- N, number of nonmissing observations for each variable
- SUMWGT, sum of the weights for each variable when a WEIGHT statement is specified
- CORR, correlation statistics for each variable

If you specify the SSCP option, the OUTP= data table includes an additional observation that contains intercept values. If you specify the ALPHA option, the OUTP= data table also includes observations that have the following _TYPE_ values:

- RAWALPHA, Cronbach’s coefficient alpha for raw variables
- STDALPHA, Cronbach’s coefficient alpha for standardized variables
- RAWALDEL, Cronbach’s coefficient alpha for raw variables after deleting one variable
- STDALDEL, Cronbach’s coefficient alpha for standardized variables after deleting one variable
- RAWCTDEL, the correlation between a raw variable and the total of the remaining raw variables
- STDCTDEL, the correlation between a standardized variable and the total of the remaining standardized variables

The output data table does not have a special type like the OUTP= data table that PROC CORR creates. Therefore, if the OUTP= output data table that PROC CORRELATION creates is provided as input to a SAS/STAT procedure that recognizes special data table types (such as the REG and FACTOR procedures), the input type must also be specified. For example, the following statements produce an output data table mycas.outdata:
Chapter 3: The CORRELATION Procedure

```sas
proc correlation data=mycas.data outp=mycas.outdata;
run;

proc factor data=mycas.outdata(Type=CORR);
run;
```

The mycas.outdata data table is then provided to PROC FACTOR as input with the `(Type=CORR)` option to indicate that the input data table contains a correlation matrix. This might save computational time when the initial data table mycas.data is large and the computation of the correlation matrix can be done in CAS using multiple threads.

### ODS Table Names

PROC CORRELATION assigns a name to each table it creates. You must use these names to refer to tables when you use the `DISPLAY` statement, the `DISPLAYOUT`, or the Output Delivery System (ODS). These names are listed in Table 3.4.

<table>
<thead>
<tr>
<th>ODS Table Name</th>
<th>Description</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cov</td>
<td>Covariances</td>
<td>COV</td>
</tr>
<tr>
<td>CronbachAlpha</td>
<td>Coefficient alpha</td>
<td>ALPHA</td>
</tr>
<tr>
<td>CronbachAlphaDel</td>
<td>Coefficient alpha with deleted variable</td>
<td>ALPHA</td>
</tr>
<tr>
<td>Csscp</td>
<td>Corrected sums of squares and crossproducts</td>
<td>CSSCP</td>
</tr>
<tr>
<td>PearsonCorr</td>
<td>Pearson correlations</td>
<td></td>
</tr>
<tr>
<td>SimpleStats</td>
<td>Simple descriptive statistics</td>
<td></td>
</tr>
<tr>
<td>Sscp</td>
<td>Sums of squares and crossproducts</td>
<td>SSCP</td>
</tr>
<tr>
<td>VarInformation</td>
<td>Variable information</td>
<td></td>
</tr>
</tbody>
</table>

### Examples: CORRELATION Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

**Example 3.1: Computing Correlations between Two Sets of Variables**

The following statements create the data table `Setosa`, which contains measurements for four iris parts from Fisher’s iris data (1936): sepal length, sepal width, petal length, and petal width. The data table has been altered to contain some missing values.
Example 3.1: Computing Correlations between Two Sets of Variables

*------------------- Data on Iris Setosa --------------------*
| The data table contains 50 iris specimens from the species  |
| Iris Setosa with the following four measurements:         |
| SepalLength (sepal length)                               |
| SepalWidth (sepal width)                                 |
| PetalLength (petal length)                               |
| PetalWidth (petal width)                                 |
| Certain values were changed to missing for the analysis.  |
*------------------------------------------------------------*;

data mycas.Setosa;
  input SepalLength SepalWidth PetalLength PetalWidth @@;
  label sepallength='Sepal Length in mm.'
    sepalwidth='Sepal Width in mm.'
    petallength='Petal Length in mm.'
    petalwidth='Petal Width in mm.';
  datalines;
  50 33 14 02 46 34 14 03 46 36 . 02
  51 33 17 05 55 35 13 02 48 31 16 02
  52 34 14 02 49 36 14 01 44 32 13 02
  50 35 16 06 44 30 13 02 47 32 16 02
  48 30 14 03 51 38 16 02 48 34 19 02
  50 30 16 02 50 32 12 02 43 30 11 .
  58 40 12 02 51 38 19 04 49 30 14 02
  51 35 14 02 50 34 16 04 46 32 14 02
  57 44 15 04 50 36 14 02 54 34 15 04
  52 41 15 . 55 42 14 02 49 31 15 02
  54 39 17 04 50 34 15 02 44 29 14 02
  47 32 13 02 46 31 15 02 51 34 15 02
  50 35 13 03 49 31 15 01 54 37 15 02
  54 39 13 04 51 35 14 03 48 34 16 02
  48 30 14 01 45 23 13 03 57 38 17 03
  51 38 15 03 54 34 17 02 51 37 15 04
  52 35 15 02 53 37 15 02
;  
The following statements request a correlation analysis between two sets of variables, the sepal measurements (length and width) and the petal measurements (length and width):

    title 'Fisher (1936) Iris Setosa Data';
    proc correlation data=mycas.Setosa sscp cov;
      var sepallength sepalwidth;
      with petallength petalwidth;
    run;

The “Simple Statistics” table in Output 3.1.1 displays univariate statistics for the analysis variables that are specified in the VAR and WITH statements.
Chapter 3: The CORRELATION Procedure

Output 3.1.1  Simple Statistics

Fisher (1936) Iris Setosa Data

The CORRELATION Procedure

<table>
<thead>
<tr>
<th>Simple Statistics</th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>N</td>
<td>Mean</td>
<td>Std Dev</td>
<td>Sum</td>
</tr>
<tr>
<td>PetalWidth</td>
<td>48</td>
<td>2.52083</td>
<td>1.03121</td>
<td>121.000000</td>
</tr>
<tr>
<td>SepalLength</td>
<td>50</td>
<td>50.06000</td>
<td>3.52490</td>
<td>2503</td>
</tr>
<tr>
<td>SepalWidth</td>
<td>50</td>
<td>34.28000</td>
<td>3.79064</td>
<td>1714</td>
</tr>
</tbody>
</table>

When the WITH statement is specified together with the VAR statement, the CORRELATION procedure produces rectangular matrices for statistics such as covariances and correlations. The matrix rows correspond to the variables specified in the WITH statement (PetalLength and PetalWidth), and the matrix columns correspond to the variables specified in the VAR statement (SepalLength and SepalWidth). The CORRELATION procedure uses the WITH variable labels to label the matrix rows.

The SSCP option requests a table of the uncorrected sum of squares and crossproducts matrix, and the COV option requests a table of the covariance matrix.

The sum of squares and crossproducts statistics for each pair of variables are computed by using observations that have nonmissing row and column variable values. The “Sums of Squares and Crossproducts” table in Output 3.1.2 displays the crossproduct, the sum of squares for the row variable, and the sum of squares for the column variable for each pair of variables.

Output 3.1.2  Sums of Squares and Crossproducts

<table>
<thead>
<tr>
<th>Sums of Squares and Crossproducts</th>
<th>SSCP / Row Var SS / Col Var SS</th>
</tr>
</thead>
<tbody>
<tr>
<td>SepalLength</td>
<td>Separ Length</td>
</tr>
<tr>
<td>PetalLength</td>
<td>36214.0000</td>
</tr>
<tr>
<td>Petal Length in mm.</td>
<td>24756.0000</td>
</tr>
<tr>
<td>10735.0000</td>
<td></td>
</tr>
<tr>
<td>10735.0000</td>
<td></td>
</tr>
<tr>
<td>123793.0000</td>
<td></td>
</tr>
<tr>
<td>58164.0000</td>
<td></td>
</tr>
<tr>
<td>PetalWidth</td>
<td>6113.0000</td>
</tr>
<tr>
<td>Petal Width in mm.</td>
<td>4191.0000</td>
</tr>
<tr>
<td>355.0000</td>
<td></td>
</tr>
<tr>
<td>355.0000</td>
<td></td>
</tr>
<tr>
<td>121356.0000</td>
<td></td>
</tr>
<tr>
<td>56879.0000</td>
<td></td>
</tr>
</tbody>
</table>

The variances are computed by using observations that have nonmissing values for the analysis variables. The “Variances and Covariances” table in Output 3.1.3 displays the covariance, variance for the row variable, variance for the column variable, and associated degrees of freedom for each pair of variables.
Example 3.2: Computing Cronbach's Coefficient Alpha

The following statements create the data table Fish1. The cubic root of the weight (Weight3) is computed as a one-dimensional measure of the size of a fish.

```
*------------------- Fish Measurement Data -----------------------*
| The data table contains 35 fish from the species Bream caught | |
| in Finland's Lake Laengelmavesi with the following measurements:| |
| Weight (in grams) | |
| Length3 (length from the nose to the end of the tail, in cm) | |
| HtPct (max height, as percentage of Length3) | |
| WidthPct (max width, as percentage of Length3) | |
*-----------------------------------------------------------------*

data mycas.Fish1 (drop=HtPct WidthPct);
  title 'Fish Measurement Data';
  input Weight Length3 HtPct WidthPct @@;
  Weight3= Weight**(1/3);
  Height=HtPct*Length3/100;
  Width=WidthPct*Length3/100;
datalines;
  242.0 30.0 38.4 13.4
  340.0 31.1 39.8 15.1
```

### Output 3.1.3  Variances and Covariances

<table>
<thead>
<tr>
<th>Variances and Covariances</th>
</tr>
</thead>
<tbody>
<tr>
<td>Covariance / Row Var</td>
</tr>
<tr>
<td>------------------------</td>
</tr>
<tr>
<td>SepalLength</td>
</tr>
<tr>
<td>PetalLength</td>
</tr>
<tr>
<td>Petal Length in mm.</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td>PetalWidth</td>
</tr>
<tr>
<td>Petal Width in mm.</td>
</tr>
<tr>
<td></td>
</tr>
<tr>
<td></td>
</tr>
</tbody>
</table>

When there are missing values in the analysis variables, the “Pearson Correlation Coefficients” table in Output 3.1.4 displays the correlation, the p-value under the null hypothesis of zero correlation, and the number of observations for each pair of variables.

### Output 3.1.4  Pearson Correlation Coefficients

| Pearson Correlation Coefficients |
| Prob > |r| under H0: Rho=0 |
| Number of Observations |
|------------------------|------------------|
| Sepal Length in mm.    | Sepal Width in mm. |

| PetalLength              | 0.2233 | 0.2201 |
| Petal Length in mm.      | 0.1229 | 0.1285 |
|                         | 49     | 49     |

| PetalWidth               | 0.2573 | 0.2754 |
| Petal Width in mm.       | 0.0775 | 0.0582 |
|                         | 48     | 48     |
Chapter 3: The CORRELATION Procedure

The following statements request a correlation analysis and compute Cronbach’s coefficient alpha for the variables `Weight3`, `Length3`, `Height`, and `Width`:

```
title 'Fish Measurement Data';
proc correlation data=mycas.fish1 nomiss alpha;
  var Weight3 Length3 Height Width;
run;
```

The ALPHA option computes Cronbach’s coefficient alpha for the analysis variables.

The “Simple Statistics” table in Output 3.2.1 displays univariate descriptive statistics for each analysis variable.

```
Output 3.2.1 Simple Statistics

Fish Measurement Data

The CORRELATION Procedure

<table>
<thead>
<tr>
<th>Simple Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>N Mean</td>
</tr>
<tr>
<td></td>
<td>Std Dev</td>
</tr>
<tr>
<td></td>
<td>Sum</td>
</tr>
<tr>
<td></td>
<td>Minimum</td>
</tr>
<tr>
<td></td>
<td>Maximum</td>
</tr>
<tr>
<td><strong>Weight3</strong></td>
<td>34 8.44751</td>
</tr>
<tr>
<td></td>
<td>287.21524</td>
</tr>
<tr>
<td><strong>Length3</strong></td>
<td>34 38.38529</td>
</tr>
<tr>
<td></td>
<td>1305 30.00000</td>
</tr>
<tr>
<td><strong>Height</strong></td>
<td>34 15.22057</td>
</tr>
<tr>
<td></td>
<td>517.49950</td>
</tr>
<tr>
<td><strong>Width</strong></td>
<td>34 5.43805</td>
</tr>
<tr>
<td></td>
<td>184.89370</td>
</tr>
</tbody>
</table>
```

The “Pearson Correlation Coefficients” table in Output 3.2.2 displays Pearson correlation statistics for pairs of analysis variables.
Example 3.2: Computing Cronbach’s Coefficient Alpha

Output 3.2.2  Pearson Correlation Coefficients

| Pearson Correlation Coefficients N = 34 | Prob > |r| under H0: Rho=0 |
|----------------------------------------|---------------------------------|
| Weight3                                | Length3 | Height | Width |
| Weight3                                | 1.0000 | 0.9652 | 0.9626 | 0.9279 |
| Length3                                | 0.9652 | 1.0000 | 0.9549 | 0.9217 |
| Height                                 | 0.9626 | 0.9549 | 1.0000 | 0.9263 |
| Width                                  | 0.9279 | 0.9217 | 0.9263 | 1.0000 |

Because the data table contains only one species of fish, all the variables are highly correlated. Using the ALPHA option, the CORRELATION procedure computes Cronbach’s coefficient alpha in Output 3.2.3. The Cronbach’s coefficient alpha is a lower bound for the reliability coefficient for the raw variables and the standardized variables. Positive correlation is needed for the alpha coefficient because variables measure a common entity.

Output 3.2.3  Cronbach’s Coefficient Alpha

<table>
<thead>
<tr>
<th>Cronbach Coefficient Alpha</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variables</td>
</tr>
<tr>
<td>Raw</td>
</tr>
<tr>
<td>Standardized</td>
</tr>
</tbody>
</table>

Because the variances of some variables vary widely, you should use the standardized score to estimate reliability. The overall standardized Cronbach’s coefficient alpha of 0.985145 provides an acceptable lower bound for the reliability coefficient. This is much greater than the suggested value of 0.70 given by Nunnally and Bernstein (1994).

The standardized alpha coefficient provides information about how each variable reflects the reliability of the scale with standardized variables. If the standardized alpha decreases after removing a variable from the construct, then this variable is strongly correlated with other variables in the scale. On the other hand, if the standardized alpha increases after removing a variable from the construct, then removing this variable from the scale makes the construct more reliable. The “Cronbach Coefficient Alpha with Deleted Variables” table in Output 3.2.4 does not show a significant increase or decrease in the standardized alpha coefficients. For more information about Cronbach’s alpha, see the section “Cronbach’s Coefficient Alpha” on page 99.

Output 3.2.4  Cronbach’s Coefficient Alpha with Deleted Variables

<table>
<thead>
<tr>
<th>Cronbach Coefficient Alpha with Deleted Variable</th>
</tr>
</thead>
<tbody>
<tr>
<td>Raw Variables</td>
</tr>
<tr>
<td>Correlation with Total</td>
</tr>
<tr>
<td>0.975379</td>
</tr>
<tr>
<td>0.967602</td>
</tr>
<tr>
<td>0.964715</td>
</tr>
<tr>
<td>0.934635</td>
</tr>
</tbody>
</table>
Example 3.3: Saving Correlations in an Output Data Table

The following statements compute Pearson correlations for the Fitness data table that is created in the section “Getting Started: CORRELATION Procedure” on page 90:

```plaintext
title 'Correlations for a Fitness and Exercise Study';
proc correlation data=mycas.Fitness nomiss outp=mycas.CorrOutp;
  var weight oxygen runtime;
run;
```

The NOMISS option excludes from the analysis observations that have missing values of the variables that are specified in the VAR statement—that is, the same set of 28 observations is used to compute the correlation for each pair of variables. The OUTP= option creates an output data table named CorrOutp to contain the Pearson correlation statistics.

The “Pearson Correlation Coefficients” table in Output 3.3.1 displays the correlation and the \( p \)-value under the null hypothesis of zero correlation.

**Output 3.3.1** Pearson Correlation Coefficients

**Correlations for a Fitness and Exercise Study**

**The CORRELATION Procedure**

<table>
<thead>
<tr>
<th></th>
<th>Weight</th>
<th>Oxygen</th>
<th>RunTime</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weight</td>
<td>1.0000</td>
<td>-0.1842</td>
<td>0.1950</td>
</tr>
<tr>
<td></td>
<td></td>
<td>0.3481</td>
<td>0.3199</td>
</tr>
<tr>
<td>Oxygen</td>
<td>-0.1842</td>
<td>1.0000</td>
<td>-0.8684</td>
</tr>
<tr>
<td></td>
<td>0.3481</td>
<td></td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>RunTime</td>
<td>0.1950</td>
<td>-0.8684</td>
<td>1.0000</td>
</tr>
<tr>
<td></td>
<td>0.3199</td>
<td></td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

The following statements display the output data table that is shown in Output 3.3.2:

```plaintext
title 'Output Data Table from PROC CORRELATION';
proc print data=mycas.CorrOutp noobs;
run;
```

**Output 3.3.2** OUTP= Data Table with Pearson Correlations

**Output Data Table from PROC CORRELATION**

<table>
<thead>
<tr>
<th><em>TYPE</em></th>
<th><em>NAME</em></th>
<th>Weight</th>
<th>Oxygen</th>
<th>RunTime</th>
</tr>
</thead>
<tbody>
<tr>
<td>MEAN</td>
<td></td>
<td>77.2168</td>
<td>47.1327</td>
<td>10.6954</td>
</tr>
<tr>
<td>STD</td>
<td></td>
<td>8.4495</td>
<td>5.5535</td>
<td>1.4127</td>
</tr>
<tr>
<td>N</td>
<td></td>
<td>28.0000</td>
<td>28.0000</td>
<td>28.0000</td>
</tr>
<tr>
<td>CORR</td>
<td>Weight</td>
<td>1.0000</td>
<td>-0.1842</td>
<td>0.1950</td>
</tr>
<tr>
<td>CORR</td>
<td>Oxygen</td>
<td>-0.1842</td>
<td>1.0000</td>
<td>-0.8684</td>
</tr>
<tr>
<td>CORR</td>
<td>RunTime</td>
<td>0.1950</td>
<td>-0.8684</td>
<td>1.0000</td>
</tr>
</tbody>
</table>
The output data table can be used as an input data table for regression or other statistical procedures. For example, the following statements request a regression analysis that uses CorrOutp instead of reading the original data in the REG procedure:

```sas
proc reg data=mycas.CorrOutp(type=CORR);
   model runtime= weight oxygen;
run;
```

The following statements read the original data and generate the same results as the preceding statements:

```sas
proc reg data=mycas.Fitness;
   model runtime= weight oxygen;
run;
```

### References


Chapter 4
The FREQTAB Procedure

Contents

Overview: FREQTAB Procedure .................................................. 112
PROC FREQTAB Features ....................................................... 113
PROC FREQTAB Compared with the FREQ Procedure ............... 113
Using CAS Sessions and CAS Engine Librefs ............................ 114
Getting Started: FREQTAB Procedure ..................................... 115
Syntax: FREQTAB Procedure .................................................. 121
PROC FREQTAB Statement ................................................... 121
BY Statement ................................................................. 124
EXACT Statement ............................................................ 124
Statistic Options ............................................................... 125
Computation Options ......................................................... 132
OUTPUT Statement ............................................................ 134
TABLES Statement ........................................................... 145
Without Options ............................................................... 146
Options ......................................................................... 147
TEST Statement ............................................................... 190
WEIGHT Statement ........................................................... 193
Details: FREQTAB Procedure ............................................... 194
Inputting Frequency Counts .................................................. 194
Missing Values ................................................................. 195
Statistical Computations ...................................................... 197
Definitions and Notation ...................................................... 197
Chi-Square Tests and Statistics ............................................. 199
Measures of Association ..................................................... 204
Binomial Proportion .......................................................... 214
Risks and Risk Differences .................................................. 222
Common Risk Difference .................................................... 232
Odds Ratio and Relative Risks for $2 \times 2$ Tables .................... 236
Cochran-Armitage Test for Trend ......................................... 246
Jonckheere-Terpstra Test ...................................................... 248
Tests and Measures of Agreement ........................................ 249
Cochran-Mantel-Haenszel Statistics ...................................... 256
Gail-Simon Test for Qualitative Interactions ........................... 265
Exact Statistics ................................................................. 265
Output Data Sets ............................................................... 270
Contents of the TABLES Statement Output Data Set ............... 270
Overview: FREQTAB Procedure

The FREQTAB procedure produces one-way to $n$-way frequency and crosstabulation (contingency) tables in SAS Viya. PROC FREQTAB also provides a variety of tests and measures to analyze frequency and crosstabulation tables.

For one-way frequency tables, PROC FREQTAB provides chi-square goodness-of-fit tests for equal proportions and for specified null proportions. It also provides several types of confidence limits for binomial proportions and binomial proportion tests (which include noninferiority and equivalence tests).

For two-way crosstabulation tables, PROC FREQTAB computes a variety of statistics to examine the relationships between the two classification variables. These statistics include the following:

- chi-square tests and measures
- measures and tests of association
- measures and tests of agreement
- tests for trend
- Cochran-Mantel-Haenszel statistics

For $2 \times 2$ tables, PROC FREQTAB provides several confidence limit types and tests for the following statistics:

- risk (proportion) differences
- odds ratios
- relative risks

For multiway ($n$-way) tables, PROC FREQTAB performs stratified analysis by computing statistics within strata (two-way tables) and across strata. These statistics include Cochran-Mantel-Haenszel statistics and measures of agreement. For multiway $2 \times 2$ tables, PROC FREQTAB provides confidence limits and tests for the common (stratified) risk difference, odds ratio, and relative risks.

By default, PROC FREQTAB computes asymptotic standard errors, confidence limits, and tests. Exact tests and confidence limits are also available for many statistics and measures.
PROC FREQTAB Features

The FREQTAB procedure offers the following functionality:

- provides TABLES statements to specify frequency and crosstabulation tables
- provides options for statistical analyses of frequency and crosstabulation tables
- provides an EXACT statement for exact tests and confidence limits
- provides a TEST statement for tests of measures of association and agreement
- provides a WEIGHT statement for weighted analyses
- produces ODS tables of tabulation and statistical analysis results
- uses ODS graphics to produce statistical plots as part of the output

Because the FREQTAB procedure constructs the frequency and crosstabulation tables on CAS, it also does the following:

- enables you to construct tables on a cluster of machines that distribute the data and the computations
- enables you to construct tables in single-machine mode on CAS
- exploits all the available cores and concurrent threads for table construction. For information about how PROC FREQTAB uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

PROC FREQTAB Compared with the FREQ Procedure

The FREQTAB procedure provides tabulation and statistical analysis capabilities that are very similar to the capabilities of the FREQ procedure in SAS/STAT software. Table 4.1 shows the major functional similarities and differences between these two procedures.
### Table 4.1  Comparison of PROC FREQTAB and PROC FREQ

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC FREQTAB</th>
<th>PROC FREQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accepts input data</td>
<td>Only CAS input data tables</td>
<td>Ordinary SAS data sets</td>
</tr>
<tr>
<td>Provides statistical analysis of frequency</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>and crosstabulation tables</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Provides OUT=, OUTPUT, and ODS output data</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>sets</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Threading</td>
<td>Tabulation designed for CAS; executes on multiple threads</td>
<td>Executes on a single thread</td>
</tr>
<tr>
<td>Supports MISSING option</td>
<td>In PROC FREQTAB statement</td>
<td>In TABLES statements</td>
</tr>
<tr>
<td>Supports SPARSE option</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports CHISQ(TESTP=SAS-data-set)</td>
<td>No</td>
<td>Yes</td>
</tr>
</tbody>
</table>

### Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
   libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
Getting Started: FREQTAB Procedure

This example shows you how to use the FREQTAB procedure to construct crosstabulation tables and produce chi-square statistics and measures of association.

The SAS data set School_Survey consists of hypothetical data that are based on a customer satisfaction survey for a school information system. This data set includes the following variables for the survey respondents: ID (respondent identification), Response, SchoolType, and State. Figure 4.1 displays the first 20 observations of the data set.

Figure 4.1 School_Survey Data Set (First 20 Observations)

<table>
<thead>
<tr>
<th>Obs</th>
<th>ID</th>
<th>Response</th>
<th>SchoolType (Public)</th>
<th>State</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>26629</td>
<td>Satisfied</td>
<td>Middle School</td>
<td>TN</td>
</tr>
<tr>
<td>2</td>
<td>25834</td>
<td>Neutral</td>
<td>High School (Public)</td>
<td>TN</td>
</tr>
<tr>
<td>3</td>
<td>14821</td>
<td>Very Satisfied</td>
<td>High School (Private)</td>
<td>NC</td>
</tr>
<tr>
<td>4</td>
<td>4153</td>
<td>Neutral</td>
<td>Middle School (Private)</td>
<td>GA</td>
</tr>
<tr>
<td>5</td>
<td>6185</td>
<td>Very Satisfied</td>
<td>High School (Private)</td>
<td>GA</td>
</tr>
<tr>
<td>6</td>
<td>6164</td>
<td>Unsatisfied</td>
<td>High School (Public)</td>
<td>GA</td>
</tr>
<tr>
<td>7</td>
<td>6386</td>
<td>Neutral</td>
<td>Middle School (Public)</td>
<td>GA</td>
</tr>
<tr>
<td>8</td>
<td>1011</td>
<td>Neutral</td>
<td>High School (Private)</td>
<td>GA</td>
</tr>
<tr>
<td>9</td>
<td>28916</td>
<td>Very Satisfied</td>
<td>High School (Private)</td>
<td>TN</td>
</tr>
<tr>
<td>10</td>
<td>10601</td>
<td>Neutral</td>
<td>High School (Public)</td>
<td>NC</td>
</tr>
<tr>
<td>11</td>
<td>17900</td>
<td>Satisfied</td>
<td>High School (Private)</td>
<td>NC</td>
</tr>
<tr>
<td>12</td>
<td>2935</td>
<td>Unsatisfied</td>
<td>High School (Private)</td>
<td>GA</td>
</tr>
<tr>
<td>13</td>
<td>9799</td>
<td>Unsatisfied</td>
<td>High School (Private)</td>
<td>NC</td>
</tr>
<tr>
<td>14</td>
<td>23754</td>
<td>Very Satisfied</td>
<td>Middle School (Public)</td>
<td>TN</td>
</tr>
<tr>
<td>15</td>
<td>9516</td>
<td>Neutral</td>
<td>Middle School (Public)</td>
<td>NC</td>
</tr>
<tr>
<td>16</td>
<td>4614</td>
<td>Very Unsatisfied</td>
<td>Middle School (Private)</td>
<td>GA</td>
</tr>
<tr>
<td>17</td>
<td>12443</td>
<td>Unsatisfied</td>
<td>Middle School (Public)</td>
<td>NC</td>
</tr>
<tr>
<td>18</td>
<td>5356</td>
<td>Very Satisfied</td>
<td>High School (Public)</td>
<td>GA</td>
</tr>
<tr>
<td>19</td>
<td>15189</td>
<td>Unsatisfied</td>
<td>High School (Private)</td>
<td>NC</td>
</tr>
<tr>
<td>20</td>
<td>3309</td>
<td>Satisfied</td>
<td>High School (Public)</td>
<td>GA</td>
</tr>
</tbody>
</table>

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following PROC FREQTAB statements request a two-way crosstabulation of SchoolType and Response. These statements assume that your CAS engine libref is named Mycas, but you can substitute any appropriately defined CAS engine libref.

```sas
proc freqtab data=Mycas.School_Survey;
  tables SchoolType * Response /
    crosslist chisq measures(cl);
run;
```

The PROC FREQTAB statement invokes the procedure and identifies the data set to be analyzed. The TABLES statement requests a two-way crosstabulation of SchoolType and Response. The table request syntax in PROC FREQTAB is identical to the table request syntax in the FREQ procedure. You can
specify one-way, two-way, and multiway table requests. You can specify more than one table request in the same TABLES statement, and you can specify multiple TABLES statements in the same invocation of the procedure.

The CROSSLIST option displays the crosstabulation table in column format; by default, PROC FREQTAB displays crosstabulation tables in table cell format. The CHISQ option requests chi-square tests, and the MEASURES option requests measures of association for this two-way crosstabulation table. The MEASURES(CL) option requests confidence limits for the measures of association.

Figure 4.2 shows the crosstabulation table of SchoolType by Response. You can customize the contents of this table by specifying options in the TABLES statement. For example, the NOCOL option suppresses the column percentages, the EXPECTED option displays the expected cell frequencies (under independence), and the STDRES option displays the standardized residuals.

**Figure 4.2** Crosstabulation Table

<table>
<thead>
<tr>
<th>SchoolType</th>
<th>Response</th>
<th>Frequency</th>
<th>Percent</th>
<th>Row Percent</th>
<th>Column Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Middle School (Private)</td>
<td>Very Satisfied</td>
<td>594</td>
<td>1.83</td>
<td>15.77</td>
<td>12.05</td>
</tr>
<tr>
<td></td>
<td>Satisfied</td>
<td>823</td>
<td>2.54</td>
<td>21.85</td>
<td>11.32</td>
</tr>
<tr>
<td></td>
<td>Neutral</td>
<td>1183</td>
<td>3.64</td>
<td>31.41</td>
<td>12.51</td>
</tr>
<tr>
<td></td>
<td>Unsatisfied</td>
<td>846</td>
<td>2.61</td>
<td>22.46</td>
<td>11.16</td>
</tr>
<tr>
<td></td>
<td>Very Unsatisfied</td>
<td>320</td>
<td>0.99</td>
<td>8.50</td>
<td>9.93</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td>3766</td>
<td>11.60</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td>Middle School (Public)</td>
<td>Very Satisfied</td>
<td>1261</td>
<td>3.88</td>
<td>13.94</td>
<td>25.58</td>
</tr>
<tr>
<td></td>
<td>Satisfied</td>
<td>1811</td>
<td>5.58</td>
<td>20.02</td>
<td>24.91</td>
</tr>
<tr>
<td></td>
<td>Neutral</td>
<td>2494</td>
<td>7.68</td>
<td>27.56</td>
<td>26.37</td>
</tr>
<tr>
<td></td>
<td>Unsatisfied</td>
<td>2364</td>
<td>7.28</td>
<td>26.13</td>
<td>31.18</td>
</tr>
<tr>
<td></td>
<td>Very Unsatisfied</td>
<td>1118</td>
<td>3.44</td>
<td>12.36</td>
<td>34.70</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td>9048</td>
<td>27.88</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td>High School (Private)</td>
<td>Very Satisfied</td>
<td>1459</td>
<td>4.49</td>
<td>18.23</td>
<td>29.60</td>
</tr>
<tr>
<td></td>
<td>Satisfied</td>
<td>2160</td>
<td>6.58</td>
<td>26.99</td>
<td>29.72</td>
</tr>
<tr>
<td></td>
<td>Neutral</td>
<td>2422</td>
<td>7.46</td>
<td>30.26</td>
<td>25.61</td>
</tr>
<tr>
<td></td>
<td>Unsatisfied</td>
<td>1363</td>
<td>4.20</td>
<td>17.03</td>
<td>17.98</td>
</tr>
<tr>
<td></td>
<td>Very Unsatisfied</td>
<td>599</td>
<td>1.85</td>
<td>7.48</td>
<td>18.59</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td>8003</td>
<td>24.66</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td>High School (Public)</td>
<td>Very Satisfied</td>
<td>1615</td>
<td>4.98</td>
<td>13.87</td>
<td>32.77</td>
</tr>
<tr>
<td></td>
<td>Satisfied</td>
<td>2475</td>
<td>7.63</td>
<td>21.26</td>
<td>34.05</td>
</tr>
<tr>
<td></td>
<td>Neutral</td>
<td>3359</td>
<td>10.35</td>
<td>28.85</td>
<td>35.51</td>
</tr>
<tr>
<td></td>
<td>Unsatisfied</td>
<td>3008</td>
<td>9.27</td>
<td>25.84</td>
<td>39.68</td>
</tr>
<tr>
<td></td>
<td>Very Unsatisfied</td>
<td>1185</td>
<td>3.65</td>
<td>10.18</td>
<td>36.78</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td>11642</td>
<td>35.87</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td>Very Satisfied</td>
<td>4929</td>
<td>15.19</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Satisfied</td>
<td>7269</td>
<td>22.39</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Neutral</td>
<td>9458</td>
<td>29.14</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Unsatisfied</td>
<td>7581</td>
<td>23.36</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Very Unsatisfied</td>
<td>3222</td>
<td>9.93</td>
<td>100.00</td>
<td></td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td>32459</td>
<td>100.00</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Figure 4.3 shows the chi-square statistics, and Figure 4.4 shows the measures of association for the table of SchoolType and Response.

Figure 4.3 Chi-Square Statistics

Statistics for Table of SchoolType by Response

<table>
<thead>
<tr>
<th>Statistic</th>
<th>DF</th>
<th>Value</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chi-Square</td>
<td>12</td>
<td>505.1446</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Likelihood Ratio Chi-Square</td>
<td>12</td>
<td>512.2769</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Mantel-Haenszel Chi-Square</td>
<td>1</td>
<td>0.0050</td>
<td>0.9438</td>
</tr>
<tr>
<td>Phi Coefficient</td>
<td></td>
<td>0.1247</td>
<td></td>
</tr>
<tr>
<td>Contingency Coefficient</td>
<td></td>
<td>0.1238</td>
<td></td>
</tr>
<tr>
<td>Cramer's V</td>
<td></td>
<td>0.0720</td>
<td></td>
</tr>
</tbody>
</table>

Figure 4.4 Measures of Association

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Value</th>
<th>ASE</th>
<th>95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gamma</td>
<td>0.0024</td>
<td>0.0061</td>
<td>-0.0097</td>
</tr>
<tr>
<td>Kendall's Tau-b</td>
<td>0.0018</td>
<td>0.0046</td>
<td>-0.0073</td>
</tr>
<tr>
<td>Stuart's Tau-c</td>
<td>0.0018</td>
<td>0.0046</td>
<td>-0.0072</td>
</tr>
<tr>
<td>Somers' D CJR</td>
<td>0.0018</td>
<td>0.0048</td>
<td>-0.0075</td>
</tr>
<tr>
<td>Somers' D RC</td>
<td>0.0017</td>
<td>0.0044</td>
<td>-0.0070</td>
</tr>
<tr>
<td>Pearson Correlation</td>
<td>-0.0004</td>
<td>0.0055</td>
<td>-0.0112</td>
</tr>
<tr>
<td>Spearman Correlation</td>
<td>0.0018</td>
<td>0.0056</td>
<td>-0.0090</td>
</tr>
<tr>
<td>Lambda Asymmetric CJR</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Lambda Asymmetric RJC</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Lambda Symmetric</td>
<td>0.0000</td>
<td>0.0000</td>
<td>0.0000</td>
</tr>
<tr>
<td>Uncertainty Coefficient CJR</td>
<td>0.0051</td>
<td>0.0004</td>
<td>0.0042</td>
</tr>
<tr>
<td>Uncertainty Coefficient RJC</td>
<td>0.0060</td>
<td>0.0005</td>
<td>0.0050</td>
</tr>
<tr>
<td>Uncertainty Coefficient Symmetric</td>
<td>0.0055</td>
<td>0.0005</td>
<td>0.0046</td>
</tr>
</tbody>
</table>

Sample Size = 32459
PROC FREQTAB can produce plots as part of its output by using ODS Graphics. The following statements show how to produce a frequency plot and a mosaic plot for a two-way crosstabulation table. The ODS GRAPHICS ON statement enables ODS Graphics, which is required in order to produce plots.

The PLOTS=FREQPLOT option in the TABLES statement requests a frequency plot of the two-way table of Response by SchoolType. The TWOWAY=CLUSTER plot-option requests a cluster grouped bar chart. The ORIENT=H plot-option specifies horizontal orientation, which places the variable levels on the Y-axis and the percentages on the X-axis. The SCALE=GROUPPERCENT plot-option requests a plot of group (column) percentages (instead of frequencies).

The PLOTS=MOSAICPLOT option requests a mosaic plot of Response by SchoolType. The COLORSTAT=STDRES plot-option colors the mosaic plot tiles according to the standardized residuals of the corresponding table cells.

```
ods graphics on;
proc freqtab data=Mycas.School_Survey;
   tables Response * SchoolType /
         plots=(freqplot(twoway=cluster orient=h scale=grouppercent)
                 mosaicplot(colorstat=stdres));
run;
ods graphics off;
```

Figure 4.5 displays the two-way frequency plot of SchoolType and Response. Figure 4.6 displays the mosaic plot of this crosstabulation.

**Figure 4.5** Frequency Plot (Grouped Bar Chart)

![Distribution of Response by SchoolType](image)
The following PROC FREQTAB statements produce a multiway table of State by SchoolType by Response. The TABLES statement requests the multiway table in which SchoolType is the row variable, Response is the column variable, and State is the stratum variable. This request produces a separate two-way table of SchoolType by Response for each level (stratum) of the variable State. The CMH option in the TABLES statement requests stratified analysis, which adjusts for the effect of State.

```plaintext
proc freqtab data=Mycas.School_Survey;
   tables State * SchoolType * Response / cmh;
run;
```

Figure 4.7 displays the two-way table of SchoolType and Response for State = ‘GA’. PROC FREQTAB also produces two-way tables for the other states, but these results are not displayed here. Figure 4.8 displays the CMH summary statistics.
Figure 4.7  Two-Way Table for State=GA

The FREQTAB Procedure

Table 1 of SchoolType by Response

<table>
<thead>
<tr>
<th>SchoolType</th>
<th>Very Satisfied</th>
<th>Satisfied</th>
<th>Neutral</th>
<th>Unsatisfied</th>
<th>Very Unsatisfied</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Middle School (Private)</td>
<td>146</td>
<td>193</td>
<td>293</td>
<td>243</td>
<td>82</td>
<td>957</td>
</tr>
<tr>
<td></td>
<td>1.77</td>
<td>2.34</td>
<td>3.56</td>
<td>2.95</td>
<td>1.00</td>
<td>11.63</td>
</tr>
<tr>
<td>Middle School (Public)</td>
<td>281</td>
<td>406</td>
<td>625</td>
<td>631</td>
<td>295</td>
<td>2238</td>
</tr>
<tr>
<td></td>
<td>3.41</td>
<td>4.93</td>
<td>7.59</td>
<td>7.67</td>
<td>3.58</td>
<td>27.19</td>
</tr>
<tr>
<td>High School (Private)</td>
<td>369</td>
<td>537</td>
<td>651</td>
<td>357</td>
<td>174</td>
<td>2088</td>
</tr>
<tr>
<td></td>
<td>4.48</td>
<td>6.52</td>
<td>7.91</td>
<td>4.34</td>
<td>2.11</td>
<td>25.37</td>
</tr>
<tr>
<td>High School (Public)</td>
<td>404</td>
<td>611</td>
<td>866</td>
<td>762</td>
<td>305</td>
<td>2948</td>
</tr>
<tr>
<td></td>
<td>4.91</td>
<td>7.42</td>
<td>10.52</td>
<td>9.26</td>
<td>3.71</td>
<td>35.82</td>
</tr>
<tr>
<td></td>
<td>13.70</td>
<td>20.73</td>
<td>29.38</td>
<td>25.85</td>
<td>10.35</td>
<td></td>
</tr>
<tr>
<td></td>
<td>33.67</td>
<td>34.97</td>
<td>35.56</td>
<td>38.23</td>
<td>35.63</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>1200</td>
<td>1747</td>
<td>2435</td>
<td>1993</td>
<td>856</td>
<td>8231</td>
</tr>
<tr>
<td></td>
<td>14.58</td>
<td>21.22</td>
<td>29.58</td>
<td>24.21</td>
<td>10.40</td>
<td>100.00</td>
</tr>
</tbody>
</table>

Figure 4.8  CMH Test of No Association

The FREQTAB Procedure

Summary Statistics for SchoolType by Response

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Alternative Hypothesis</th>
<th>DF</th>
<th>Value</th>
<th>Prob</th>
</tr>
</thead>
<tbody>
<tr>
<td>1  Nonzero Correlation</td>
<td>1</td>
<td></td>
<td>0.0086</td>
<td>0.9262</td>
</tr>
<tr>
<td>2  Row Mean Scores Differ</td>
<td>3</td>
<td></td>
<td>406.7786</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>3  General Association</td>
<td>12</td>
<td></td>
<td>508.7656</td>
<td>&lt;.0001</td>
</tr>
</tbody>
</table>

Total Sample Size = 32459
Syntax: FREQTAB Procedure

The following statements are available in the FREQTAB procedure:

```
PROC FREQTAB <options> ;
   BY variables ;
   EXACT statistic-options </ computation-options> ;
   OUTPUT <OUT=SAS-data-set> output-options ;
   TABLES requests </ options> ;
   TEST options ;
   WEIGHT variable </ option> ;
```

The PROC FREQTAB statement is the only required statement for the FREQTAB procedure. If you specify the following statements, PROC FREQTAB produces a one-way frequency table for each variable in the most recently created data set.

```
proc freqtab;
   run;
```

Table 4.2 summarizes the basic functions of the procedure statements. The following sections provide detailed syntax information for the BY, EXACT, OUTPUT, TABLES, TEST, and WEIGHT statements in alphabetical order after the description of the PROC FREQTAB statement.

<table>
<thead>
<tr>
<th>Statement</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>BY</td>
<td>Provides separate analyses for each BY group</td>
</tr>
<tr>
<td>EXACT</td>
<td>Requests exact tests</td>
</tr>
<tr>
<td>OUTPUT</td>
<td>Requests an output data set of statistics</td>
</tr>
<tr>
<td>TABLES</td>
<td>Specifies tables and requests analyses</td>
</tr>
<tr>
<td>TEST</td>
<td>Requests tests for measures of association and agreement</td>
</tr>
<tr>
<td>WEIGHT</td>
<td>Identifies a weight variable</td>
</tr>
</tbody>
</table>

PROC FREQTAB Statement

```
PROC FREQTAB <options> ;
```

The PROC FREQTAB statement invokes the FREQTAB procedure. Optionally, it also identifies the input data set. By default, the procedure uses the most recently created SAS data set.

Table 4.3 lists the options available in the PROC FREQTAB statement. Descriptions of the options follow in alphabetical order.
### Table 4.3 PROC FREQTAB Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMPRESS</td>
<td>Begins the next one-way table on the current page</td>
</tr>
<tr>
<td>DATA=</td>
<td>Names the CAS input data table</td>
</tr>
<tr>
<td>FORMCHAR=</td>
<td>Specifies outline and cell-divider characters for cell-format crosstabulation tables</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as a valid level</td>
</tr>
<tr>
<td>MISSPRINT</td>
<td>Displays missing levels</td>
</tr>
<tr>
<td>NLEVELS</td>
<td>Displays the number of levels for each TABLES statement variable</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses all displayed output</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the order for reporting variable values</td>
</tr>
<tr>
<td>PAGE</td>
<td>Displays one table per page</td>
</tr>
</tbody>
</table>

You can specify the following *options* in the PROC FREQTAB statement.

**COMPRESS**

begins display of the next one-way frequency table on the same page as the preceding one-way table if there is enough space to begin the table. By default, the next one-way table begins on the current page only if the entire table fits on that page. The COMPRESS option is not valid with the PAGE option.

**DATA=** *CAS-libref.data-table*

names the input data table for PROC FREQTAB to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where

*CAS-libref* refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 114.

*data-table* specifies the name of the input data table.

**FORMCHAR(1,2,7)=** *formchar-string*

defines the characters to use for constructing the outlines and dividers for the cells in crosstabulation tables that are displayed in the default, table-cell format. The *formchar-string* should be three characters long. The characters are used to draw the vertical separators (1), the horizontal separators (2), and the vertical-horizontal intersections (7). If you do not specify the FORMCHAR= option, PROC FREQTAB uses FORMCHAR(1,2,7)=’l+-’ by default. Table 4.4 summarizes the formatting characters used by PROC FREQTAB.

### Table 4.4 Formatting Characters Used by PROC FREQTAB

<table>
<thead>
<tr>
<th>Position</th>
<th>Default</th>
<th>Used to Draw</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td></td>
<td>Vertical separators</td>
</tr>
<tr>
<td>2</td>
<td>-</td>
<td>Horizontal separators</td>
</tr>
<tr>
<td>7</td>
<td>+</td>
<td>Intersections of vertical and horizontal separators</td>
</tr>
</tbody>
</table>
The FORMCHAR= option can specify 20 different SAS formatting characters used to display output; however, PROC FREQTAB uses only the first, second, and seventh formatting characters. Therefore, the proper specification for PROC FREQTAB is FORMCHAR(1,2,7)= ‘formchar-string’.

Specifying all blanks for formchar-string produces crosstabulation tables with no outlines or dividers—for example, FORMCHAR(1,2,7)=’ ’. You can use any character in formchar-string, including hexadecimal characters. If you use hexadecimal characters, you must put an x after the closing quote. For information about which hexadecimal codes to use for which characters, see the documentation for your hardware.

See the CALENDAR, PLOT, and TABULATE procedures in the SAS Visual Data Management and Utility Procedures Guide for more information about form characters.

MISSING
treats missing values as a valid nonmissing level for all classification variables that you specify in the TABLES statements. This option displays missing levels in frequency and crosstabulation tables and includes the frequencies (of missing levels) in the computation of the frequency total, percentages, and statistics.

By default (if you do not specify the MISSING or MISSPRINT option), PROC FREQTAB excludes an observation from a table if the observation contains a missing value for any variable in the table request. For more information, see the section “Missing Values” on page 195.

MISSPRINT
displays missing levels in frequency tables but does not include the corresponding frequencies in the computation of totals, percentages, or statistics. This option is available for one-way frequency tables and for tables in list format (which you can request by specifying the LIST option in the TABLES statement).

By default (if you do not specify the MISSING or MISSPRINT option), PROC FREQTAB excludes an observation from a table if the observation contains a missing value for any variable in the table request. For more information, see the section “Missing Values” on page 195.

NLEVELS
displays the “Number of Variable Levels” table, which provides the number of levels for each variable that you name in a TABLES statement. PROC FREQTAB determines the variable levels by using the formatted variable values.

NOPRINT
suppresses the display of all output. You can use the NOPRINT option when you only want to create an output data set. For more information about the output data sets that PROC FREQTAB produces, see the section “Output Data Sets” on page 270. The NOPRINT option temporarily disables the Output Delivery System (ODS). For more information, see the SAS Output Delivery System: User’s Guide.

NOTE: A NOPRINT option is also available in the TABLES statement. This option suppresses display of the crosstabulation tables but allows display of the statistics tables.

ORDER=FORMATTED | FREQ | INTERNAL
specifies the order of the variable levels in the frequency and crosstabulation tables, which you request in the TABLES statement.

The ORDER= option can take the following values:
Chapter 4: The FREQTAB Procedure

<table>
<thead>
<tr>
<th>Value of ORDER=</th>
<th>Levels Ordered By</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMATTED</td>
<td>External formatted value (in ascending order)</td>
</tr>
<tr>
<td>FREQ</td>
<td>Descending frequency count</td>
</tr>
<tr>
<td>INTERNAL</td>
<td>Unformatted value</td>
</tr>
</tbody>
</table>

By default, ORDER=INTERNAL. The FORMATTED and INTERNAL orders are machine-dependent. When you specify ORDER=FORMATTED, numeric variables that have no explicit format are sorted by their unformatted (internal) value.

When you specify ORDER=FREQ, levels that have larger frequencies (more observations) appear first in the order. ORDER=FREQ is not available when you specify a WEIGHT statement.

The ORDER= option does not apply to missing values, which are always ordered first.

For more information about sort order, see the chapter on the SORT procedure in the SAS Visual Data Management and Utility Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts.

PAGE

displays only one table per page. Otherwise, PROC FREQTAB displays multiple tables per page as space permits. The PAGE option is not valid with the COMPRESS option.

BY Statement

BY variables ;

You can specify a BY statement in PROC FREQTAB to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in SAS Language Reference: Concepts.

EXACT Statement

EXACT statistic-options </ computation-options> ;

The EXACT statement requests exact tests and confidence limits for selected statistics. The statistic-options identify which statistics to compute, and the computation-options specify options for computing exact statistics. For more information, see the section “Exact Statistics” on page 265.

NOTE: PROC FREQTAB computes exact tests by using fast and efficient algorithms that are superior to direct enumeration. Exact tests are appropriate when a data set is small, sparse, skewed, or heavily tied. For some large problems, computation of exact tests might require a considerable amount of time and memory. Consider using asymptotic tests for such problems. Alternatively, when asymptotic methods might not be sufficient for such large problems, consider using Monte Carlo estimation of exact $p$-values. You can request Monte Carlo estimation by specifying the MC computation-option in the EXACT statement. See the section “Computational Resources” on page 268 for more information.
Statistic Options

The statistic-options specify which exact tests and confidence limits to compute. Table 4.5 lists the available statistic-options and the exact statistics that are computed. Descriptions of the statistic-options follow the table in alphabetical order.

For one-way tables, exact \( p \)-values are available for binomial proportion tests, the chi-square goodness-of-fit test, and the likelihood ratio chi-square test. Exact (Clopper-Pearson) confidence limits are available for the binomial proportion.

For two-way tables, exact \( p \)-values are available for the following tests: Pearson chi-square test, likelihood ratio chi-square test, Mantel-Haenszel chi-square test, Fisher’s exact test, Jonckheere-Terpstra test, Cochran-Armitage test for trend, and Bowker’s symmetry test. Exact \( p \)-values are also available for tests of the following statistics: Pearson correlation coefficient, Spearman correlation coefficient, Kendall’s tau-\( b \), Stuart’s tau-\( c \), Somers’ \( D(C|R) \), Somers’ \( D(R|C) \), simple kappa coefficient, and weighted kappa coefficient.

For \( 2 \times 2 \) tables, PROC FREQTAB provides the exact McNemar’s test, exact confidence limits for the odds ratio, and Barnard’s unconditional exact test for the risk (proportion) difference. PROC FREQTAB also provides exact unconditional confidence limits for the risk difference and for the relative risk (ratio of proportions). For stratified \( 2 \times 2 \) tables, PROC FREQTAB provides Zelen’s exact test for equal odds ratios, exact confidence limits for the common odds ratio, and an exact test for the common odds ratio.

Most of the statistic-option names listed in Table 4.5 are identical to the corresponding option names in the TABLES and OUTPUT statements. You can request exact computations for groups of statistics by using statistic-options that are identical to the TABLES statement options CHISQ, MEASURES, and AGREE. For example, when you specify the CHISQ statistic-option in the EXACT statement, PROC FREQTAB computes exact \( p \)-values for the Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square tests for two-way tables. You can request an exact test for an individual statistic by specifying the corresponding statistic-option from the list in Table 4.5.

Using the EXACT Statement with the TABLES Statement

You must use a TABLES statement with the EXACT statement. If you use only one TABLES statement, you do not need to specify the same options in both the TABLES and EXACT statements; when you specify a statistic-option in the EXACT statement, PROC FREQTAB automatically invokes the corresponding TABLES statement option. However, when you use an EXACT statement with multiple TABLES statements, you must specify options in the TABLES statements to request statistics. PROC FREQTAB then provides exact tests or confidence limits for those statistics that you also specify in the EXACT statement.

Table 4.5 EXACT Statement Statistic Options

<table>
<thead>
<tr>
<th>Statistic Option</th>
<th>Exact Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGREE</td>
<td>McNemar’s test (for ( 2 \times 2 ) tables), simple kappa test, weighted kappa test</td>
</tr>
<tr>
<td>BARNARD</td>
<td>Barnard’s test (for ( 2 \times 2 ) tables)</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Binomial proportion tests for one-way tables</td>
</tr>
<tr>
<td>CHISQ</td>
<td>Chi-square goodness-of-fit test for one-way tables; Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square tests for two-way tables</td>
</tr>
<tr>
<td>COMOR</td>
<td>Confidence limits for the common odds ratio, common odds ratio test (for ( h \times 2 \times 2 ) tables)</td>
</tr>
</tbody>
</table>
## Table 4.5  continued

<table>
<thead>
<tr>
<th>Statistic Option</th>
<th>Exact Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>EQOR</td>
<td>ZELEN</td>
</tr>
<tr>
<td>FISHER</td>
<td>Fisher’s exact test</td>
</tr>
<tr>
<td>JT</td>
<td>Jonckheere-Terpstra test</td>
</tr>
<tr>
<td>KAPPA</td>
<td>Test for the simple kappa coefficient</td>
</tr>
<tr>
<td>KENTB</td>
<td>TAUB</td>
</tr>
<tr>
<td>LRCHI</td>
<td>Likelihood ratio chi-square test (one-way and two-way tables)</td>
</tr>
<tr>
<td>MCNEM</td>
<td>McNemar’s test (for $2 \times 2$ tables)</td>
</tr>
<tr>
<td>MEASURES</td>
<td>Tests for the Pearson correlation and Spearman correlation, confidence limits for the odds ratio (for $2 \times 2$ tables)</td>
</tr>
<tr>
<td>MHCHI</td>
<td>Mantel-Haenszel chi-square test</td>
</tr>
<tr>
<td>OR</td>
<td>ODDSRATIO</td>
</tr>
<tr>
<td>PCHI</td>
<td>Pearson chi-square test (one-way and two-way tables)</td>
</tr>
<tr>
<td>PCORR</td>
<td>Test for the Pearson correlation coefficient</td>
</tr>
<tr>
<td>RELRISK</td>
<td>Confidence limits for the relative risk (for $2 \times 2$ tables)</td>
</tr>
<tr>
<td>RISKDIFF</td>
<td>Confidence limits for the risk difference (for $2 \times 2$ tables)</td>
</tr>
<tr>
<td>SCORR</td>
<td>Test for the Spearman correlation coefficient</td>
</tr>
<tr>
<td>SMDCR</td>
<td>Test for Somers’ $D(C</td>
</tr>
<tr>
<td>SMDCR</td>
<td>Test for Somers’ $D(R</td>
</tr>
<tr>
<td>STUTC</td>
<td>TAUC</td>
</tr>
<tr>
<td>SYMMETRY</td>
<td>BOWKER</td>
</tr>
<tr>
<td>TREND</td>
<td>Cochran-Armitage test for trend</td>
</tr>
<tr>
<td>WTKAPPA</td>
<td>WTKAP</td>
</tr>
</tbody>
</table>

You can specify the following **statistic-options**:

**AGREE**

requests McNemar’s exact test, an exact test for the simple kappa coefficient, and an exact test for the weighted kappa coefficient. For more information, see the sections “Tests and Measures of Agreement” on page 249 and “Exact Statistics” on page 265.

For McNemar’s test, you can specify the null hypothesis ratio of discordant proportions by using the **AGREE(MNULLRATIO=)** option in the TABLES statement; by default, MNULLRATIO=1. For the weighted kappa coefficient, you can request Fleiss-Cohen weights by specifying the **AGREE(WT=FC)** option in the TABLES statement; by default, PROC FREQTAB computes the weighted kappa coefficient by using Cicchetti-Allison agreement weights.

McNemar’s test is available for $2 \times 2$ tables. Kappa coefficients are defined only for square two-way tables, where the number of rows equals the number of columns. If your table is not square because some observations have weights of 0, you can specify the **ZEROS** option in the WEIGHT statement to include these observations in the analysis. For more information, see the section “Tables with Zero-Weight Rows or Columns” on page 256.

For $2 \times 2$ tables, the weighted kappa coefficient is equivalent to the simple kappa coefficient, and PROC FREQTAB displays only analyses for the simple kappa coefficient.
BARNARD
requests Barnard’s exact unconditional test for the risk (proportion) difference for $2 \times 2$ tables. For more information, see the section “Barnard’s Unconditional Exact Test” on page 232.

To request exact unconditional confidence limits for the risk difference, you can specify the RISKDIFF option in the EXACT statement. The RISKDIFF option in the TABLES statement provides asymptotic tests and several types of confidence limits for the risk difference. For more information, see the section “Risks and Risk Differences” on page 222.

BINOMIAL
BIN
requests an exact test for the binomial proportion (for one-way tables). For more information, see the section “Binomial Tests” on page 217. You can specify the null hypothesis proportion by using the BINOMIAL(P=) option in the TABLES statement; by default, P=0.5.

The BINOMIAL option in the TABLES statement provides exact (Clopper-Pearson) confidence limits for the binomial proportion by default. You can specify the BINOMIAL(CL=MIDP) option in the TABLES statement to request exact mid-$p$ confidence limits for the binomial proportion. The BINOMIAL option in the TABLES statement also provides asymptotic (Wald) tests and several other confidence limit types for the binomial proportion. For more information, see the section “Binomial Proportion” on page 214.

CHISQ
requests the following exact chi-square tests for two-way tables: Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square. For more information, see the section “Chi-Square Tests and Statistics” on page 199. The CHISQ option in the TABLES statement provides asymptotic tests for these statistics.

For one-way tables, the CHISQ option requests an exact chi-square goodness-of-fit test. You can specify null hypothesis proportions for this test by using the CHISQ(TESTP=) option in the TABLES statement. By default, the one-way chi-square test is based on the null hypothesis of equal proportions. For more information, see the section “Chi-Square Test for One-Way Tables” on page 199.

COMOR
requests an exact test and exact confidence limits for the common odds ratio for multiway $2 \times 2$ tables. For more information, see the section “Exact Confidence Limits for the Common Odds Ratio” on page 263. The CMH option in the TABLES statement provides Mantel-Haenszel and logit estimates of the common odds ratio along with their asymptotic confidence limits.

EQOR
ZELEN
requests Zelen’s exact test for equal odds ratios for multiway $2 \times 2$ tables. For more information, see the section “Zelen’s Exact Test for Equal Odds Ratios” on page 262. The CMH option in the TABLES statement provides an (asymptotic) Breslow-Day test for homogeneity of odds ratios.

FISHER
requests Fisher’s exact test. For more information, see the sections “Fisher’s Exact Test” on page 203 and “Exact Statistics” on page 265. For $2 \times 2$ tables, the CHISQ option in the TABLES statement provides Fisher’s exact test. For general $R \times C$ tables, Fisher’s exact test is also known as the Freeman-Halton test.
Chapter 4: The FREQTAB Procedure

JT
requests an exact Jonckheere-Terpstra test. For more information, see the sections “Jonckheere-Terpstra Test” on page 248 and “Exact Statistics” on page 265. The JT option in the TABLES statement provides an asymptotic Jonckheere-Terpstra test.

KAPPA
requests an exact test for the simple kappa coefficient. For more information, see the sections “Simple Kappa Coefficient” on page 251 and “Exact Statistics” on page 265. The AGREE option in the TABLES statement provides the simple kappa estimate, standard error, and confidence limits. The KAPPA option in the TEST statement provides an asymptotic test for the simple kappa coefficient.

Kappa coefficients are defined only for square two-way tables, where the number of rows equals the number of columns. If your table is not square because some observations have weights of 0, you can specify the ZEROS option in the WEIGHT statement to include these observations in the analysis. For more information, see the section “Tables with Zero-Weight Rows or Columns” on page 256.

KENTB
requests an exact test for Kendall’s tau-\(b\). For more information, see the sections “Kendall’s Tau-\(b\)” on page 206 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides an estimate and standard error of Kendall’s tau-\(b\). The KENTB option in the TEST statement provides an asymptotic test for Kendall’s tau-\(b\).

LRCHI
requests an exact test for the likelihood ratio chi-square for two-way tables. For more information, see the sections “Likelihood Ratio Chi-Square Test” on page 202 and “Exact Statistics” on page 265. The CHISQ option in the TABLES statement provides an asymptotic likelihood ratio chi-square test for two-way tables.

For one-way tables, the LRCHI option requests an exact likelihood ratio goodness-of-fit test. You can specify null hypothesis proportions by using the CHISQ(TESTP=) option in the TABLES statement. By default, the one-way test is based on the null hypothesis of equal proportions. For more information, see the section “Likelihood Ratio Chi-Square Test for One-Way Tables” on page 201.

MCNEM
requests an exact McNemar’s test. For more information, see the sections “McNemar’s Test” on page 249 and “Exact Statistics” on page 265. You can specify the null hypothesis ratio of discordant proportions by using the AGREE(MNULLRATIO=) option in the TABLES statement; by default, MNULLRATIO=1. The AGREE option in the TABLES statement provides an asymptotic McNemar’s test.

MEASURES
requests exact tests for the Pearson and Spearman correlations. For more information, see the sections “Pearson Correlation Coefficient” on page 208, “Spearman Rank Correlation Coefficient” on page 209, and “Exact Statistics” on page 265. The PCORR and SCORR options in the TEST statement provide asymptotic tests for the Pearson and Spearman correlations, respectively.

The MEASURES option also requests exact confidence limits for the odds ratio for 2 × 2 tables. For more information, see the subsection Exact Confidence Limits in the section “Confidence Limits for the Odds Ratio” on page 237. You can also request exact confidence limits for the odds ratio by specifying the OR option in the EXACT statement.
MHCHI
requests an exact test for the Mantel-Haenszel chi-square. For more information, see the sections “Mantel-Haenszel Chi-Square Test” on page 202 and “Exact Statistics” on page 265. The CHISQ option in the TABLES statement provides an asymptotic Mantel-Haenszel chi-square test.

OR
ODDSRATIO
requests exact confidence limits for the odds ratio for $2 \times 2$ tables. For more information, see the subsection “Exact Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237.

You can request exact mid-$p$ confidence limits for the odds ratio by specifying the OR(CL=MIDP) option in the TABLES statement. The OR(CL=) option in the TABLES statement also provides other types of confidence limits for the odds ratio. For more information, see the section “Confidence Limits for the Odds Ratio” on page 237.

The ALPHA= option in the TABLES statement determines the confidence level of the exact confidence limits; by default, ALPHA=0.05, which produces 95% confidence limits for the odds ratio.

PCHI
requests an exact test for the Pearson chi-square for two-way tables. For more information, see the sections “Pearson Chi-Square Test for Two-Way Tables” on page 200 and “Exact Statistics” on page 265. The CHISQ option in the TABLES statement provides an asymptotic Pearson chi-square test.

For one-way tables, the PCHI option requests an exact chi-square goodness-of-fit test. You can specify null hypothesis proportions by using the CHISQ(TESTP=) option in the TABLES statement. By default, the goodness-of-fit test is based on the null hypothesis of equal proportions. For more information, see the section “Chi-Square Test for One-Way Tables” on page 199.

PCORR
requests an exact test for the Pearson correlation coefficient. For more information, see the sections “Pearson Correlation Coefficient” on page 208 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides the estimate and standard error of the Pearson correlation. The PCORR option in the TEST statement provides an asymptotic test for the Pearson correlation.

RELRISK (options)
requests exact unconditional confidence limits for the relative risk for $2 \times 2$ tables. By default (beginning in SAS/STAT 14.3), the exact confidence limits are computed by inverting two separate one-sided exact tests that are based on the score statistic (Chan and Zhang 1999). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

The RELRISK(CL=) option in the TABLES statement provides additional types of confidence limits for the relative risk. For more information, see the section “Confidence Limits for the Risk Difference” on page 224.

The ALPHA= option in the TABLES statement determines the confidence level; by default, ALPHA=0.05, which produces 95% confidence limits for the relative risk.

You can specify the following options:
COLUMN=1 | 2 | BOTH
specifies the table column of the relative risk. By default, COLUMN=1, which provides exact confidence limits for the column 1 relative risk. COLUMN=BOTH provides exact confidence limits for both column 1 and column 2 relative risks.

METHOD=NOSCORE | SCORE | SCORE2
specifies the computation method for the exact confidence limits. By default, METHOD=SCORE. You can specify one of the following methods:

NOSCORE
computes the exact confidence limits by inverting two separate one-sided exact tests that are based on the unstandardized relative risk (Santner and Snell 1980). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240. This method is the default in releases before SAS/STAT 14.3.

SCORE
computes the exact confidence limits by inverting two separate one-sided exact tests that are based on the score statistic (Chan and Zhang 1999). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240. This method is the default beginning in SAS/STAT 14.3.

SCORE2
computes the exact confidence limits by inverting a single two-sided exact test that is based on the score statistic (Agresti and Min 2001). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

RISKDIFF < (options)>
requests exact unconditional confidence limits for the risk difference for $2 \times 2$ tables. By default (beginning in SAS/STAT 14.3), the exact confidence limits are computed by inverting two separate one-sided exact tests that are based on the score statistic (Chan and Zhang 1999). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

The RISKDIFF(CL=) option in the TABLES statement provides additional types of confidence limits for the risk difference. For more information, see the section “Confidence Limits for the Risk Difference” on page 224.

The ALPHA= option in the TABLES statement determines the confidence level; by default, ALPHA=0.05, which produces 95% confidence limits for the risk difference.

You can specify the following options:

COLUMN=1 | 2 | BOTH
specifies the table column of the risk difference. By default, COLUMN=BOTH and the exact confidence limits are displayed in the ‘Risk Estimates’ tables. If you specify the RISKDIFF(NORISKS) option in the TABLES statement to suppress the ‘Risk Estimates’ tables, COLUMN=1 by default and the exact confidence limits are displayed in the ‘Risk Difference Confidence Limits’ table.
METHOD=NOSCORE | SCORE | SCORE2
specifies the computation method for the exact confidence limits. By default, METHOD=SCORE.

You can specify one of the following methods:

**NOSCORE**
computes the exact confidence limits by inverting two separate one-sided exact tests that are based on the unstandardized risk difference (Santner and Snell 1980). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224. This method is the default in releases before SAS/STAT 14.3.

**SCORE**
computes the exact confidence limits by inverting two separate one-sided exact tests that are based on the score statistic (Chan and Zhang 1999). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224. This method is the default beginning in SAS/STAT 14.3.

**SCORE2**
computes the exact confidence limits by inverting a single two-sided exact test that is based on the score statistic (Agresti and Min 2001). For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

**SCORR**
requests an exact test for the Spearman correlation coefficient. For more information, see the sections “Spearman Rank Correlation Coefficient” on page 209 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides the estimate and standard error of the Spearman correlation. The SCORR option in the TEST statement provides an asymptotic test for the Spearman correlation.

**SMDCR**
requests an exact test for Somers’ $D(C | R)$. For more information, see the sections “Somers’ $D$” on page 208 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides the estimate and standard error of Somers’ $D(C | R)$. The SMDCR option in the TEST statement provides an asymptotic test for Somers’ $D(C | R)$.

**SMDRC**
requests an exact test for Somers’ $D(R|C)$. For more information, see the sections “Somers’ $D$” on page 208 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides the estimate and standard error of Somers’ $D(R|C)$. The SMDRC option in the TEST statement provides an asymptotic test for Somers’ $D(C | R)$.

**STUTC**
requests an exact test for Stuart’s tau-$.c$. For more information, see the sections “Stuart’s Tau-c” on page 207 and “Exact Statistics” on page 265. The MEASURES option in the TABLES statement provides the estimate and standard error of Stuart’s tau-$.c$. The STUTC option in the TEST statement provides an asymptotic test for Stuart’s tau-$.c$. 

**TAUC**
**SYMMETRY**

**BOWKER**
requests an exact symmetry test. This test is available for square \( R \times R \) two-way tables where the table dimension \( R \) is greater than 2. For more information, see the section “Exact Symmetry Test” on page 250. The AGREE option in the TABLES statement provides an asymptotic symmetry test.

**TREND**

requests the exact Cochran-Armitage test for trend. For more information, see the sections “Cochran-Armitage Test for Trend” on page 246 and “Exact Statistics” on page 265. The TREND option in the TABLES statement provides an asymptotic Cochran-Armitage test for trend. This test is available for tables of dimensions \( 2 \times C \) or \( R \times 2 \).

**WTKAPPA**

**WTKAP**
requests an exact test for the weighted kappa coefficient. For more information, see the sections “Weighted Kappa Coefficient” on page 252 and “Exact Statistics” on page 265. By default, PROC FREQTAB computes the weighted kappa coefficient by using Cicchetti-Allison agreement weights. You can request Fleiss-Cohen agreement weights by specifying the AGREE(WT=FC) option in the TABLES statement.

Kappa coefficients are defined only for square two-way tables, where the number of rows equals the number of columns. If your table is not square because some observations have weights of 0, you can specify the ZEROS option in the WEIGHT statement to include these observations in the analysis. For more information, see the section “Tables with Zero-Weight Rows or Columns” on page 256.

For \( 2 \times 2 \) tables, the weighted kappa coefficient is equivalent to the simple kappa coefficient, and PROC FREQTAB displays only analyses for the simple kappa coefficient.

**Computation Options**

The *computation-options* specify options for computing exact statistics. You can specify the following *computation-options* in the EXACT statement after a slash (/).

**ALPHA=\( \alpha \)**

specifies the level of the confidence limits for Monte Carlo \( p \)-value estimates. The value of \( \alpha \) must be between 0 and 1; a confidence level of \( \alpha \) produces \( 100(1 - \alpha)\% \) confidence limits. By default ALPHA=0.01, which produces 99\% confidence limits for the Monte Carlo estimates.

The ALPHA= option invokes the MC option.

**MAXTIME=\( \text{value} \)**

specifies the maximum clock time (in seconds) that PROC FREQTAB can use to compute an exact \( p \)-value. If the procedure does not complete the computation within the specified time, the computation terminates. The MAXTIME= \( \text{value} \) must be a positive number. This option is available for Monte Carlo estimation of exact \( p \)-values, in addition to direct exact \( p \)-value computation. For more information, see the section “Computational Resources” on page 268.

**MC**

requests Monte Carlo estimation of exact \( p \)-values instead of direct exact \( p \)-value computation. Monte Carlo estimation can be useful for large problems that require a considerable amount of time and
memory for exact computations but for which asymptotic approximations might not be sufficient. For more information, see the section “Monte Carlo Estimation” on page 269.

This option is available for all EXACT statistic-options except the BINOMIAL option and the following options that apply only to $2 \times 2$ or $h \times 2 \times 2$ tables: BARNARD, COMOR, EQOR, MCNEM, OR, RELRISK, and RISKDIFF. PROC FREQTAB always computes exact tests or confidence limits (not Monte Carlo estimates) for these statistics.

The ALPHA=, N=, and SEED= options invoke the MC option.

**MIDP**
requests exact mid $p$-values for the exact tests. The exact mid $p$-value is defined as the exact $p$-value minus half the exact point probability. For more information, see the section “Definition of $p$-Values” on page 267.

The MIDP option is available for all EXACT statement statistic-options except the following: BARNARD, EQOR, OR, RELRISK, and RISKDIFF. You cannot specify both the MIDP option and the MC option.

**N=n**
specifies the number of samples for Monte Carlo estimation. The value of $n$ must be a positive integer, and the default is 10,000. Larger values of $n$ produce more precise estimates of exact $p$-values. Because larger values of $n$ generate more samples, the computation time increases.

The N= option invokes the MC option.

**PFORMAT=**

specifies the display format for exact $p$-values. PROC FREQTAB applies this format to one- and two-sided exact $p$-values, exact point probabilities, and exact mid $p$-values. By default, PROC FREQTAB displays exact $p$-values in the PVALUE6.4 format.

You can provide a format-name or you can specify PFORMAT=EXACT to control the format of exact $p$-values. The value of format-name can be any standard SAS numeric format or a user-defined format. The format length must not exceed 24. For information about formats, see the FORMAT procedure in the SAS Visual Data Management and Utility Procedures Guide and the FORMAT statement and SAS format in SAS Formats and Informats: Reference.

If you specify PFORMAT=EXACT, PROC FREQTAB uses the 6.4 format to display exact $p$-values that are greater than or equal to 0.001; the procedure uses the E10.3 format to display values that are between 0.000 and 0.001. This is the format that PROC FREQTAB uses to display exact $p$-values in releases before SAS/STAT 12.3. Beginning in SAS/STAT 12.3, by default PROC FREQTAB uses the PVALUE6.4 format to display exact $p$-values.

**POINT**

requests exact point probabilities for the exact tests. The exact point probability is the exact probability that the test statistic equals the observed value. For more information, see the section “Definition of $p$-Values” on page 267.

The POINT option is available for all EXACT statement statistic-options except the following: BARNARD, EQOR, OR, RELRISK, and RISKDIFF. You cannot specify both the POINT option and the MC option.
SEED=number
specifies the initial seed for random number generation for Monte Carlo estimation. The value of the
SEED= option must be an integer. If you do not specify the SEED= option or if the SEED= value is
negative or 0, PROC FREQTAB uses the time of day from the computer’s clock to obtain the initial
seed.

The SEED= option invokes the MC option.

OUTPUT Statement

OUTPUT <OUT=SAS-data-set> output-options ;

The OUTPUT statement creates a SAS data set that contains statistics that are computed by PROC FREQTAB.
Table 4.6 lists the statistics that can be stored in the output data set. You identify which statistics to include
by specifying output-options.

You must use a TABLES statement with the OUTPUT statement. The OUTPUT statement stores statistics for
only one table request. If you use multiple TABLES statements, the contents of the output data set correspond
to the last TABLES statement. If you use multiple table requests in a single TABLES statement, the contents
of the output data set correspond to the last table request. Only one OUTPUT statement is allowed in a single
invocation of the procedure.

For a one-way or two-way table, the output data set contains one observation that stores the requested
statistics for the table. For a multiway table, the output data set contains an observation for each two-way
table (stratum) of the multiway crosstabulation. If you request summary statistics for the multiway table, the
output data set also contains an observation that stores the across-strata summary statistics. If you use a BY
statement, the output data set contains an observation or set of observations for each BY group. For more
information about the contents of the output data set, see the section “Contents of the OUTPUT Statement
Output Data Set” on page 271.

The output data set that is created by the OUTPUT statement is not the same as the output data set that
is created by the OUT= option in the TABLES statement. The OUTPUT statement creates a data set that
contains statistics (such as the Pearson chi-square and its $p$-value), and the OUT= option in the TABLES
statement creates a data set that contains frequency table counts and percentages. See the section “Output
Data Sets” on page 270 for more information.

As an alternative to the OUTPUT statement, you can use the Output Delivery System (ODS) to store statistics
that PROC FREQTAB computes. ODS can create a SAS data set from any table that PROC FREQTAB
produces. See the section “ODS Table Names” on page 282 for more information.

You can specify the following options in the OUTPUT statement:

OUT=SAS-data-set
specifies the name of the output data set. When you use an OUTPUT statement but do not use the
OUT= option, PROC FREQTAB creates a data set and names it by using the DATA$n$ convention.

output-options
specify the statistics to include in the output data set. Table 4.6 lists the output-options that are available
in the OUTPUT statement, together with the TABLES statement options that are required to produce
the statistics. Descriptions of the output-options follow the table in alphabetical order.
You can specify output-options to request individual statistics, or you can request groups of statistics by using output-options that are identical to the group options in the TABLES statement (for example, the CHISQ, MEASURES, CMH, AGREE, and ALL options).

When you specify an output-option, the output data set includes statistics from the corresponding analysis. In addition to the estimate or test statistic, the output data set includes associated values such as standard errors, confidence limits, p-values, and degrees of freedom. For more information, see the section “Contents of the OUTPUT Statement Output Data Set” on page 271.

To store a statistic in the output data set, you must also request computation of that statistic with the appropriate TABLES, EXACT, or TEST statement option. For example, the PCHI output-option includes the Pearson chi-square in the output data set. You must also request computation of the Pearson chi-square by specifying the CHISQ option in the TABLES statement. Or, if you use only one TABLES statement, you can request computation of the Pearson chi-square by specifying the PCHI or CHISQ option in the EXACT statement. Table 4.6 lists the TABLES statement options that are required to produce the OUTPUT data set statistics.

### Table 4.6 OUTPUT Statement Output Options

<table>
<thead>
<tr>
<th>Output Option</th>
<th>Output Data Set Statistics</th>
<th>Required TABLES Statement Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGREE</td>
<td>McNemar’s test (2 × 2 tables), Bowker’s test, simple and weighted kappas; for multiple strata, overall simple and weighted kappas, tests for equal kappas, and Cochran’s Q (h × 2 × 2 tables)</td>
<td>AGREE</td>
</tr>
<tr>
<td>AJCHI</td>
<td>Continuity-adjusted chi-square (2 × 2 tables)</td>
<td>CHISQ</td>
</tr>
<tr>
<td>ALL</td>
<td>CHISQ, MEASURES, and CMH statistics; N (number of nonmissing observations)</td>
<td>ALL</td>
</tr>
<tr>
<td>BDCHI</td>
<td>Breslow-Day test (h × 2 × 2 tables)</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Binomial statistics (one-way tables)</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>CHISQ</td>
<td>For one-way tables, goodness-of-fit test; for two-way tables, Pearson, likelihood ratio, continuity-adjusted, and Mantel-Haenszel chi-squares, Fisher’s exact test (2 × 2 tables), phi and contingency coefficients, Cramér’s V</td>
<td>BHISQ</td>
</tr>
<tr>
<td>CMH</td>
<td>Cochran-Mantel-Haenszel (CMH) correlation, row mean scores (ANOVA), and general association statistics; for 2 × 2 tables, logit and Mantel-Haenszel common odds ratios and relative risks, Breslow-Day test</td>
<td>CMH</td>
</tr>
<tr>
<td>CMH1</td>
<td>CMH statistics, except row mean scores (ANOVA) and general association statistics</td>
<td>CMH or CMH1</td>
</tr>
<tr>
<td>CMH2</td>
<td>CMH statistics, except general association statistic</td>
<td>CMH or CMH2</td>
</tr>
<tr>
<td>CMHCOR</td>
<td>CMH correlation statistic</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>CMHGA</td>
<td>CMH general association statistic</td>
<td>CMH</td>
</tr>
<tr>
<td>CMHRMS</td>
<td>CMH row mean scores (ANOVA) statistic</td>
<td>CMH or CMH2</td>
</tr>
<tr>
<td>COCHQ</td>
<td>Cochran’s Q (h × 2 × 2 tables)</td>
<td>AGREE</td>
</tr>
<tr>
<td>CONTGY</td>
<td>Contingency coefficient</td>
<td>CHISQ</td>
</tr>
</tbody>
</table>
Table 4.6  continued

<table>
<thead>
<tr>
<th>Output Option</th>
<th>Output Data Set Statistics</th>
<th>Required TABLES Statement Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CRAMV</td>
<td>Cramér’s $V$</td>
<td>CHISQ</td>
</tr>
<tr>
<td>EQKAP</td>
<td>Test for equal simple kappas</td>
<td>AGREE</td>
</tr>
<tr>
<td>EQOR</td>
<td>Zelen’s test for equal odds ratios ($h \times 2 \times 2$ tables)</td>
<td>CHISQ and EXACT EQOR</td>
</tr>
<tr>
<td>EQWKP</td>
<td>Test for equal weighted kappas</td>
<td>AGREE</td>
</tr>
<tr>
<td>FISHER</td>
<td>Fisher’s exact test</td>
<td>CHISQ or FISHER $^1$</td>
</tr>
<tr>
<td>GAMMA</td>
<td>Gamma</td>
<td>MEASURES</td>
</tr>
<tr>
<td>GS</td>
<td>Gail-Simon test</td>
<td>CMH(GAILSIMON)</td>
</tr>
<tr>
<td>JT</td>
<td>Jonckheere-Terpstra test</td>
<td>JT</td>
</tr>
<tr>
<td>KAPPA</td>
<td>Simple kappa coefficient</td>
<td>AGREE</td>
</tr>
<tr>
<td>KENTB</td>
<td>Kendall’s tau-$b$</td>
<td>MEASURES</td>
</tr>
<tr>
<td>LAMCR</td>
<td>Lambda asymmetric ($C</td>
<td>R$)</td>
</tr>
<tr>
<td>LAMDAS</td>
<td>Lambda symmetric</td>
<td>MEASURES</td>
</tr>
<tr>
<td>LAMRC</td>
<td>Lambda asymmetric ($R</td>
<td>C$)</td>
</tr>
<tr>
<td>LGOR</td>
<td>Logit common odds ratio</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>LGRRC1</td>
<td>Logit common relative risk, column 1</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>LGRRC2</td>
<td>Logit common relative risk, column 2</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>LRCHI</td>
<td>Likelihood ratio chi-square</td>
<td>CHISQ</td>
</tr>
<tr>
<td>MCNEM</td>
<td>McNemar’s test ($2 \times 2$ tables)</td>
<td>AGREE</td>
</tr>
<tr>
<td>MEASURES</td>
<td>Gamma, Kendall’s tau-$b$, Stuart’s tau-$c$, Somers’ $D(C</td>
<td>R)$ and $D(R</td>
</tr>
<tr>
<td>MHCHI</td>
<td>Mantel-Haenszel chi-square</td>
<td>CHISQ</td>
</tr>
<tr>
<td>MHOR</td>
<td>Mantel-Haenszel common odds ratio</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>MHRRC1</td>
<td>Mantel-Haenszel common relative risk, column 1</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>MHRRC2</td>
<td>Mantel-Haenszel common relative risk, column 2</td>
<td>CMH, CMH1, or CMH2</td>
</tr>
<tr>
<td>N</td>
<td>Number of nonmissing observations</td>
<td></td>
</tr>
<tr>
<td>NMISS</td>
<td>Number of missing observations</td>
<td></td>
</tr>
<tr>
<td>OR</td>
<td>Odds ratio ($2 \times 2$ tables)</td>
<td>MEASURES, OR, or RELRISK</td>
</tr>
<tr>
<td>PCHI</td>
<td>Chi-square goodness-of-fit test (one-way tables), Pearson chi-square (two-way tables)</td>
<td>CHISQ</td>
</tr>
<tr>
<td>PCORR</td>
<td>Pearson correlation coefficient</td>
<td>MEASURES</td>
</tr>
<tr>
<td>PHI</td>
<td>Phi coefficient</td>
<td>CHISQ</td>
</tr>
<tr>
<td>PLCORR</td>
<td>Polychoric correlation coefficient</td>
<td>PLCORR</td>
</tr>
<tr>
<td>RDIF1</td>
<td>Column 1 risk difference (row 1 – row 2)</td>
<td>RISKDIFF</td>
</tr>
<tr>
<td>RDIF2</td>
<td>Column 2 risk difference (row 1 – row 2)</td>
<td>RISKDIFF</td>
</tr>
<tr>
<td>RELRISK</td>
<td>Odds ratio and relative risks ($2 \times 2$ tables)</td>
<td>MEASURES or RELRISK</td>
</tr>
</tbody>
</table>

$^1$CHISQ computes Fisher’s exact test for $2 \times 2$ tables. Use the FISHER option to compute Fisher’s exact test for general $r \times c$ tables.
Table 4.6  continued

<table>
<thead>
<tr>
<th>Output Option</th>
<th>Output Data Set Statistics</th>
<th>Required TABLES Statement Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>RISKDIFF</td>
<td>Risks and risk differences (2 × 2 tables)</td>
<td>RISKDIFF</td>
</tr>
<tr>
<td>RISKDIFF1</td>
<td>Risks and risk difference, column 1</td>
<td>RISKDIFF</td>
</tr>
<tr>
<td>RISKDIFF2</td>
<td>Risks and risk difference, column 2</td>
<td>RISKDIFF</td>
</tr>
<tr>
<td>RRC1</td>
<td>RELRISK1</td>
<td>Relative risk, column 1</td>
</tr>
<tr>
<td>RRC2</td>
<td>RELRISK2</td>
<td>Relative risk, column 2</td>
</tr>
<tr>
<td>RSK1</td>
<td>RELRISK1</td>
<td>Column 1 overall risk</td>
</tr>
<tr>
<td>RSK11</td>
<td>RISK11</td>
<td>Column 1 risk for row 1</td>
</tr>
<tr>
<td>RSK12</td>
<td>RISK12</td>
<td>Column 2 risk for row 1</td>
</tr>
<tr>
<td>RSK2</td>
<td>RELRISK2</td>
<td>Column 2 overall risk</td>
</tr>
<tr>
<td>RSK21</td>
<td>RISK21</td>
<td>Column 1 risk for row 2</td>
</tr>
<tr>
<td>RSK22</td>
<td>RISK22</td>
<td>Column 2 risk for row 2</td>
</tr>
<tr>
<td>SCORR</td>
<td>Spearman correlation coefficient</td>
<td>MEASURES</td>
</tr>
<tr>
<td>SMDCR</td>
<td>Somers’ $D(C</td>
<td>R)$</td>
</tr>
<tr>
<td>SMDRC</td>
<td>Somers’ $D(R</td>
<td>C)$</td>
</tr>
<tr>
<td>STUTC</td>
<td>TAUC</td>
<td>Stuart’s tau-c</td>
</tr>
<tr>
<td>TREND</td>
<td>Cochran-Armitage test for trend</td>
<td>TREND</td>
</tr>
<tr>
<td>TSYM</td>
<td>BOWKER</td>
<td>Bowker’s symmetry test</td>
</tr>
<tr>
<td>U</td>
<td>Symmetric uncertainty coefficient</td>
<td>MEASURES</td>
</tr>
<tr>
<td>UCR</td>
<td>Uncertainty coefficient $(C</td>
<td>R)$</td>
</tr>
<tr>
<td>URC</td>
<td>Uncertainty coefficient $(R</td>
<td>C)$</td>
</tr>
<tr>
<td>WTKAPPA</td>
<td>WTKAP</td>
<td>Weighted kappa coefficient</td>
</tr>
</tbody>
</table>

You can specify the following **output-options** in the OUTPUT statement.

**AGREE**

 includes the following tests and measures of agreement in the output data set: McNemar’s test (for $2 \times 2$ tables), Bowker’s symmetry test, the simple kappa coefficient, and the weighted kappa coefficient. For multiway tables, the **AGREE** option also includes the following statistics in the output data set: overall simple and weighted kappa coefficients, tests for equal simple and weighted kappa coefficients, and Cochran’s $Q$ test.

The **AGREE** option in the **TABLES** statement requests computation of tests and measures of agreement. For more information, see the section “Tests and Measures of Agreement” on page 249.

**AGREE** statistics are computed only for square tables, where the number of rows equals the number of columns. **PROC FREQTAB** provides Bowker’s symmetry test and weighted kappa coefficients only for tables larger than $2 \times 2$. (For $2 \times 2$ tables, Bowker’s test is identical to McNemar’s test, and the weighted kappa coefficient equals the simple kappa coefficient.) Cochran’s $Q$ is available for multiway $2 \times 2$ tables.

**AJCHI**

 includes the continuity-adjusted chi-square in the output data set. The continuity-adjusted chi-square is available for $2 \times 2$ tables and is provided by the **CHISQ** option in the **TABLES** statement. For more information, see the section “Continuity-Adjusted Chi-Square Test” on page 202.
Chapter 4: The FREQTAB Procedure

**ALL**
includes all statistics that are requested by the CHISQ, MEASURES, and CMH output-options in the output data set. ALL also includes the number of nonmissing observations, which you can request individually by specifying the N output-option.

**BDCHI**
includes the Breslow-Day test in the output data set. The Breslow-Day test for homogeneity of odds ratios is computed for multiway $2 \times 2$ tables and is provided by the CMH, CMH1, and CMH2 options in the TABLES statement. For more information, see the section “Breslow-Day Test for Homogeneity of the Odds Ratios” on page 262.

**BINOMIAL**
includes the binomial proportion estimate, confidence limits, and tests in the output data set. The BINOMIAL option in the TABLES statement requests computation of binomial statistics, which are available for one-way tables. For more information, see the section “Binomial Proportion” on page 214.

**CHISQ**
includes the following chi-square tests and measures in the output data set for two-way tables: Pearson chi-square, likelihood ratio chi-square, Mantel-Haenszel chi-square, phi coefficient, contingency coefficient, and Cramér’s $V$. For $2 \times 2$ tables, CHISQ also includes Fisher’s exact test and the continuity-adjusted chi-square in the output data set. For more information, see the section “Chi-Square Tests and Statistics” on page 199. For one-way tables, CHISQ includes the chi-square goodness-of-fit test in the output data set. For more information, see the section “Chi-Square Test for One-Way Tables” on page 199. The CHISQ option in the TABLES statement requests computation of these statistics.

If you specify the CHISQ(WARN=OUTPUT) option in the TABLES statement, the CHISQ option also includes the variable WARN_PCHI in the output data set. This variable indicates the validity warning for the asymptotic Pearson chi-square test.

**CMH**
includes the following Cochran-Mantel-Haenszel statistics in the output data set: correlation, row mean scores (ANOVA), and general association. For $2 \times 2$ tables, the CMH option also includes the Mantel-Haenszel and logit estimates of the common odds ratio and relative risks. For multiway (stratified) $2 \times 2$ tables, the CMH option includes the Breslow-Day test for homogeneity of odds ratios. The CMH option in the TABLES statement requests computation of these statistics. For more information, see the section “Cochran-Mantel-Haenszel Statistics” on page 256.

If you specify the CMH(MANTELFLEISS) option in the TABLES statement, the CMH option includes the Mantel-Fleiss analysis in the output data set. The variables MF_CMH and WARN_CMH contain the Mantel-Fleiss criterion and the warning indicator, respectively.

**CMH1**
includes the CMH statistics in the output data set, with the exception of the row mean scores (ANOVA) statistic and the general association statistic. The CMH1 option in the TABLES statement requests computation of these statistics. For more information, see the section “Cochran-Mantel-Haenszel Statistics” on page 256.
CMH2
includes the CMH statistics in the output data set, with the exception of the general association statistic. The CMH2 option in the TABLES statement requests computation of these statistics. For more information, see the section “Cochran-Mantel-Haenszel Statistics” on page 256.

CMHCOR
includes the Cochran-Mantel-Haenszel correlation statistic in the output data set. The CMH option in the TABLES statement requests computation of this statistic. For more information, see the section “Correlation Statistic” on page 258.

CMHGA
includes the Cochran-Mantel-Haenszel general association statistic in the output data set. The CMH option in the TABLES statement requests computation of this statistic. For more information, see the section “General Association Statistic” on page 259.

CMHRMS
includes the Cochran-Mantel-Haenszel row mean scores (ANOVA) statistic in the output data set. The CMH option in the TABLES statement requests computation of this statistic. For more information, see the section “ANOVA (Row Mean Scores) Statistic” on page 258.

COCHQ
includes Cochran’s $Q$ test in the output data set. The AGREE option in the TABLES statement requests computation of this test, which is available for multiway $2 \times 2$ tables. For more information, see the section “Cochran’s $Q$ Test” on page 256.

CONTGY
includes the contingency coefficient in the output data set. The CHISQ option in the TABLES statement requests computation of the contingency coefficient. For more information, see the section “Contingency Coefficient” on page 204.

CRAMV
includes Cramér’s $V$ in the output data set. The CHISQ option in the TABLES statement requests computation of Cramér’s $V$. For more information, see the section “Cramér’s $V$” on page 204.

EQKAP
includes the test for equal simple kappa coefficients in the output data set. The AGREE option in the TABLES statement requests computation of this test, which is available for multiway square ($h \times r \times r$) tables. For more information, see the section “Tests for Equal Kappa Coefficients” on page 255.

EQOR
includes Zelen’s exact test for equal odds ratios in the output data set. The EQOR option in the EXACT statement requests computation of this test, which is available for multiway $2 \times 2$ tables. For more information, see the section “Zelen’s Exact Test for Equal Odds Ratios” on page 262.

EQWKP
includes the test for equal weighted kappa coefficients in the output data set. The AGREE option in the TABLES statement requests computation of this test. The test for equal weighted kappas is available for multiway, square ($h \times r \times r$) tables where $r > 2$. For more information, see the section “Tests for Equal Kappa Coefficients” on page 255.
FISHER
includes Fisher’s exact test in the output data set. For a $2 \times 2$ table, the CHISQ option in the TABLES statement provides Fisher’s exact test. For tables larger than $2 \times 2$, the FISHER option in the EXACT statement provides Fisher’s exact test. For more information, see the section “Fisher’s Exact Test” on page 203.

GAMMA
includes the gamma statistic in the output data set. The MEASURES option in the TABLES statement requests computation of the gamma statistic. For more information, see the section “Gamma” on page 206.

GS
includes the Gail-Simon test for qualitative interaction in the output data set. The CMH(GAILSIMON) option in the TABLES statement requests computation of this test. For more information, see the section “Gail-Simon Test for Qualitative Interactions” on page 265.

JT
includes the Jonckheere-Terpstra test in the output data set. The JT option in the TABLES statement requests the Jonckheere-Terpstra test. For more information, see the section “Jonckheere-Terpstra Test” on page 248.

KAPPA
includes the simple kappa coefficient in the output data set. The AGREE option in the TABLES statement requests computation of kappa, which is available for square tables (where the number of rows equals the number of columns). For multiway square tables, the KAPPA option also includes the overall kappa coefficient in the output data set. For more information, see the sections “Simple Kappa Coefficient” on page 251 and “Overall Kappa Coefficient” on page 255.

KENTB
includes Kendall’s tau-$b$ in the output data set. The MEASURES option in the TABLES statement requests computation of Kendall’s tau-$b$. For more information, see the section “Kendall’s Tau-$b$” on page 206.

LAMCR
includes the asymmetric lambda $\lambda(C|R)$ in the output data set. The MEASURES option in the TABLES statement requests computation of lambda. For more information, see the section “Lambda (Asymmetric)” on page 212.

LAMDAS
includes the symmetric lambda in the output data set. The MEASURES option in the TABLES statement requests computation of lambda. For more information, see the section “Lambda (Symmetric)” on page 212.

LAMRC
includes the asymmetric lambda $\lambda(R|C)$ in the output data set. The MEASURES option in the TABLES statement requests computation of lambda. For more information, see the section “Lambda (Asymmetric)” on page 212.
LGOR

includes the logit estimate of the common odds ratio in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.

LGRRC1

includes the logit estimate of the common relative risk (column 1) in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.

LGRRC2

includes the logit estimate of the common relative risk (column 2) in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.

LRCHI

includes the likelihood ratio chi-square in the output data set. The CHISQ option in the TABLES statement requests computation of the likelihood ratio chi-square. For more information, see the section “Likelihood Ratio Chi-Square Test” on page 202.

MCNEM

includes McNemar’s test (for $2 \times 2$ tables) in the output data set. The AGREE option in the TABLES statement requests computation of McNemar’s test. For more information, see the section “McNemar’s Test” on page 249.

MEASURES

includes the following measures of association in the output data set: gamma, Kendall’s tau-$b$, Stuart’s tau-$c$, Somers’ $D(C \mid R)$, Somers’ $D(R \mid C)$, Pearson and Spearman correlation coefficients, lambda (symmetric and asymmetric), and uncertainty coefficients (symmetric and asymmetric). For $2 \times 2$ tables, the MEASURES option also includes the odds ratio, column 1 relative risk, and column 2 relative risk. The MEASURES option in the TABLES statement requests computation of these statistics. For more information, see the section “Measures of Association” on page 204.

MHCHI

includes the Mantel-Haenszel chi-square in the output data set. The CHISQ option in the TABLES statement requests computation of the Mantel-Haenszel chi-square. For more information, see the section “Mantel-Haenszel Chi-Square Test” on page 202.

MHOR

COMOR

includes the Mantel-Haenszel estimate of the common odds ratio in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.
MHRRC1
includes the Mantel-Haenszel estimate of the common relative risk (column 1) in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.

MHRRC2
includes the Mantel-Haenszel estimate of the common relative risk (column 2) in the output data set. The CMH option in the TABLES statement requests computation of this statistic, which is available for $2 \times 2$ tables. For more information, see the section “Adjusted Odds Ratio and Relative Risk Estimates” on page 260.

N
includes the number of nonmissing observations in the output data set.

NMISS
includes the number of missing observations in the output data set. For more information, see the section “Missing Values” on page 195.

OR
ODDSRATIO
RROR
includes the odds ratio (for $2 \times 2$ tables) in the output data set. The MEASURES, OR, and RELRISK options in the TABLES statement request this statistic. For more information, see the section “Odds Ratio” on page 236.

PCHI
includes the Pearson chi-square in the output data set for two-way tables. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. For one-way tables, the PCHI option includes the chi-square goodness-of-fit test in the output data set. For more information, see the section “Chi-Square Test for One-Way Tables” on page 199. The CHISQ option in the TABLES statement requests computation of these statistics.

If you specify the CHISQ(WARN=OUTPUT) option in the TABLES statement, the PCHI option also includes the variable WARN_PCHI in the output data set. This variable indicates the validity warning for the asymptotic Pearson chi-square test.

PCORR
includes the Pearson correlation coefficient in the output data set. The MEASURES option in the TABLES statement requests computation of the Pearson correlation. For more information, see the section “Pearson Correlation Coefficient” on page 208.

PHI
includes the phi coefficient in the output data set. The CHISQ option in the TABLES statement requests computation of the phi coefficient. For more information, see the section “Phi Coefficient” on page 204.

PLCORR
includes the polychoric correlation coefficient in the output data set. For $2 \times 2$ tables, this statistic is known as the tetrachoric correlation coefficient. The PLCORR option in the TABLES statement requests computation of the polychoric correlation. For more information, see the section “Polychoric Correlation” on page 211.
RDIF1 includes the column 1 risk difference (row 1 – row 2) in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

RDIF2 includes the column 2 risk difference (row 1 – row 2) in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

RELRISK includes the column 1 and column 2 relative risks (for $2 \times 2$ tables) in the output data set. The MEASURES and RELRISK options in the TABLES statement request these statistics. For more information, see the section “Relative Risks” on page 240.

RISKDIFF includes risks (binomial proportions) and risk differences for $2 \times 2$ tables in the output data set. These statistics include the row 1 risk, row 2 risk, total (overall) risk, and risk difference (row 1 – row 2) for column 1 and column 2. The RISKDIFF option in the TABLES statement requests computation of these statistics. For more information, see the section “Risks and Risk Differences” on page 222.

RISKDIFF1 includes column 1 risks (binomial proportions) and risk differences for $2 \times 2$ tables in the output data set. These statistics include the row 1 risk, row 2 risk, total (overall) risk, and risk difference (row 1 – row 2). The RISKDIFF option in the TABLES statement requests computation of these statistics. For more information, see the section “Risks and Risk Differences” on page 222.

RISKDIFF2 includes column 2 risks (binomial proportions) and risk differences for $2 \times 2$ tables in the output data set. These statistics include the row 1 risk, row 2 risk, total (overall) risk, and risk difference (row 1 – row 2). The RISKDIFF option in the TABLES statement requests computation of these statistics. For more information, see the section “Risks and Risk Differences” on page 222.

RRC1

RRC2

RELRISK1 includes the column 1 relative risk in the output data set. The MEASURES and RELRISK options in the TABLES statement request relative risks, which are available for $2 \times 2$ tables. For more information, see the section “Odds Ratio and Relative Risks for $2 \times 2$ Tables” on page 236.

RELRISK2 includes the column 2 relative risk in the output data set. The MEASURES and RELRISK options in the TABLES statement request relative risks, which are available for $2 \times 2$ tables. For more information, see the section “Odds Ratio and Relative Risks for $2 \times 2$ Tables” on page 236.

RSK1

RISK1 includes the overall column 1 risk in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.
RSK1

includes the column 1 risk for row 1 in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

RSK12

includes the column 2 risk for row 1 in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

RSK2

includes the overall column 2 risk in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences. For more information, see the section “Risks and Risk Differences” on page 222.

RSK21

includes the column 1 risk for row 2 in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

RSK22

includes the column 2 risk for row 2 in the output data set. The RISKDIFF option in the TABLES statement requests computation of risks and risk differences, which are available for $2 \times 2$ tables. For more information, see the section “Risks and Risk Differences” on page 222.

SCORR

includes the Spearman correlation coefficient in the output data set. The MEASURES option in the TABLES statement requests computation of the Spearman correlation. For more information, see the section “Spearman Rank Correlation Coefficient” on page 209.

SMDCR

includes Somers’ $D(C|R)$ in the output data set. The MEASURES option in the TABLES statement requests computation of Somers’ $D$. For more information, see the section “Somers’ $D$” on page 208.

SMDRC

includes Somers’ $D(R|C)$ in the output data set. The MEASURES option in the TABLES statement requests computation of Somers’ $D$. For more information, see the section “Somers’ $D$” on page 208.

STUTC

includes Stuart’s tau-c in the output data set. The MEASURES option in the TABLES statement requests computation of tau-c. For more information, see the section “Stuart’s Tau-c” on page 207.
The TABLES Statement requests one-way to n-way frequency and crosstabulation tables and statistics for those tables.

If you omit the TABLES statement, PROC FREQTAB generates one-way frequency tables for all data set variables that are not listed in the other statements.

The following argument is required in the TABLES statement.

requests specify the frequency and crosstabulation tables to produce. A request is composed of one variable name or several variable names separated by asterisks. To request a one-way frequency table, use a
single variable. To request a two-way crosstabulation table, use an asterisk between two variables. To request a multiway table (an \( n \)-way table, where \( n > 2 \)), separate the variables with asterisks. The unique values of these variables form the rows, columns, and strata of the table. You can include up to 50 variables in a single multiway table request.

For two-way to multiway tables, the values of the last variable form the crosstabulation table columns, and the values of the next-to-last variable form the rows. Each level (or combination of levels) of the other variables forms one stratum. PROC FREQTAB produces a separate crosstabulation table for each stratum. For example, a specification of A*B*C*D in a TABLES statement produces \( k \) tables, where \( k \) is the number of different combinations of values for A and B. Each table lists the values for C down the side and the values for D across the top.

You can use multiple TABLES statements in the PROC FREQTAB step. PROC FREQTAB builds all the table requests in one pass of the data, so that there is essentially no loss of efficiency. You can also specify any number of table requests in a single TABLES statement. To specify multiple table requests quickly, use a grouping syntax by placing parentheses around several variables and joining other variables or variable combinations. For example, the statements shown in Table 4.7 illustrate grouping syntax.

<table>
<thead>
<tr>
<th>TABLES Request</th>
<th>Equivalent to</th>
</tr>
</thead>
<tbody>
<tr>
<td>A*(B C)</td>
<td>A<em>B A</em>C</td>
</tr>
<tr>
<td>(A B)*(C D)</td>
<td>A<em>C B</em>C A<em>D B</em>D</td>
</tr>
<tr>
<td>(A B C)*D</td>
<td>A<em>D B</em>D C*D</td>
</tr>
<tr>
<td>A – C</td>
<td>A B C</td>
</tr>
<tr>
<td>(A – C)*D</td>
<td>A<em>D B</em>D C*D</td>
</tr>
</tbody>
</table>

The TABLES statement variables are one or more variables from the DATA= input data set. These variables can be either character or numeric, but the procedure treats them as categorical variables. PROC FREQTAB uses the formatted values of the TABLES variable to determine the categorical variable levels. For more information, see the discussion of the FORMAT procedure in the SAS Visual Data Management and Utility Procedures Guide and the discussion of SAS formats in SAS Formats and Informats: Reference.

By default, the frequency or crosstabulation table lists the values of both character and numeric variables in ascending order based on internal (unformatted) variable values. You can change the order of the values in the table by specifying the ORDER= option in the PROC FREQTAB statement. To list the values in ascending order by formatted value, use ORDER=FORMATTED.

### Without Options

If you request a one-way frequency table without specifying any options, PROC FREQTAB provides the following for each table level or cell: frequency, cumulative frequency, percentage of the total frequency, and cumulative percentage. If you request a two-way or multiway (\( n \)-way) crosstabulation table without specifying any options, PROC FREQTAB provides the following for each table cell: frequency, percentage of the total frequency, percentage of the row frequency, and percentages of the column frequency. PROC FREQTAB also displays the frequency of missing values after the table. For more information, see the section “Displayed Output” on page 273.
Options

Table 4.8 lists the options available in the TABLES statement. Descriptions of the options follow in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Control Statistical Analysis</strong></td>
<td></td>
</tr>
<tr>
<td>AGREE</td>
<td>Requests tests and measures of classification agreement</td>
</tr>
<tr>
<td>ALL</td>
<td>Requests tests and measures of association produced by the CHISQ, MEASURES, and CMH options</td>
</tr>
<tr>
<td>ALPHA=</td>
<td>Sets confidence level for confidence limits</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>BIN</td>
</tr>
<tr>
<td>CHISQ</td>
<td>Requests chi-square tests and measures based on chi-square</td>
</tr>
<tr>
<td>CL</td>
<td>Requests confidence limits for MEASURES statistics</td>
</tr>
<tr>
<td>CMH</td>
<td>Requests all Cochran-Mantel-Haenszel statistics</td>
</tr>
<tr>
<td>CMH1</td>
<td>Requests CMH correlation statistic, adjusted odds ratios, and adjusted relative risks</td>
</tr>
<tr>
<td>CMH2</td>
<td>Requests CMH correlation and row mean scores (ANOCV) statistics, adjusted odds ratios, and adjusted relative risks</td>
</tr>
<tr>
<td>COMMONRISKDIFF</td>
<td>Requests common risk difference for $h \times 2 \times 2$ tables</td>
</tr>
<tr>
<td>FISHER</td>
<td>Requests Fisher’s exact test for tables larger than $2 \times 2$</td>
</tr>
<tr>
<td>GAILSIMON</td>
<td>Requests Gail-Simon test for qualitative interactions</td>
</tr>
<tr>
<td>JT</td>
<td>Requests Jonckheere-Terpstra test</td>
</tr>
<tr>
<td>MEASURES</td>
<td>Requests measures of association</td>
</tr>
<tr>
<td>OR</td>
<td>Requests the odds ratio for $2 \times 2$ tables</td>
</tr>
<tr>
<td>PLCORR</td>
<td>Requests polychoric correlation</td>
</tr>
<tr>
<td>RELRISK</td>
<td>Requests relative risks for $2 \times 2$ tables</td>
</tr>
<tr>
<td>RISKDIFF</td>
<td>Requests risks and risk differences for $2 \times 2$ tables</td>
</tr>
<tr>
<td>SCORES=</td>
<td>Specifies type of row and column scores</td>
</tr>
<tr>
<td>TREND</td>
<td>Requests Cochran-Armitage test for trend</td>
</tr>
<tr>
<td><strong>Control Additional Table Information</strong></td>
<td></td>
</tr>
<tr>
<td>CELLCHI2</td>
<td>Displays cell contributions to the Pearson chi-square statistic</td>
</tr>
<tr>
<td>CUMCOL</td>
<td>Displays cumulative column percentages</td>
</tr>
<tr>
<td>DEVIATION</td>
<td>Displays deviations of cell frequencies from expected values</td>
</tr>
<tr>
<td>EXPECTED</td>
<td>Displays expected cell frequencies</td>
</tr>
<tr>
<td>PEARSONRES</td>
<td>Displays Pearson residuals in the CROSSLIST table</td>
</tr>
<tr>
<td>PRINTKWTS</td>
<td>Displays kappa coefficient weights</td>
</tr>
<tr>
<td>SCOROUT</td>
<td>Displays row and column scores</td>
</tr>
<tr>
<td>STDRES</td>
<td>Displays standardized residuals in the CROSSLIST table</td>
</tr>
<tr>
<td>TOTPCT</td>
<td>Displays percentages of total frequency for $n$-way tables ($n &gt; 2$)</td>
</tr>
<tr>
<td><strong>Control Displayed Output</strong></td>
<td></td>
</tr>
<tr>
<td>CONTENTS=</td>
<td>Specifies contents label for crosstabulation tables</td>
</tr>
<tr>
<td>CROSSLIST</td>
<td>Displays crosstabulation tables in ODS column format</td>
</tr>
<tr>
<td>FORMAT=</td>
<td>Formats frequencies in crosstabulation tables</td>
</tr>
</tbody>
</table>
Table 4.8  

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LIST</td>
<td>Displays two-way to n-way tables in list format</td>
</tr>
<tr>
<td>MAXLEVELS=</td>
<td>Specifies maximum number of levels to display in one-way tables</td>
</tr>
<tr>
<td>NOCOL</td>
<td>Suppresses display of column percentages</td>
</tr>
<tr>
<td>NOCUM</td>
<td>Suppresses display of cumulative frequencies and percentages</td>
</tr>
<tr>
<td>NOFREQ</td>
<td>Suppresses display of frequencies</td>
</tr>
<tr>
<td>NOPERCENT</td>
<td>Suppresses display of percentages</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses display of crosstabulation tables but displays statistics</td>
</tr>
<tr>
<td>NOROW</td>
<td>Suppresses display of row percentages</td>
</tr>
<tr>
<td>NOSPARSE</td>
<td>Suppresses zero-frequency levels in the CROSSLIST table, LIST table, and OUT= data set</td>
</tr>
<tr>
<td>NOWARN</td>
<td>Suppresses log warning message for the chi-square test</td>
</tr>
</tbody>
</table>

**Produce Statistical Graphics**

PLOTS= Requests plots from ODS Graphics

**Create an Output Data Set**

OUT= Names an output data set to contain frequency counts

OUTCUM Includes cumulative frequencies and percentages in the output data set

OUTEXPECT Includes expected frequencies in the output data set

OUTPCT Includes row, column, and two-way table percentages in the output data set

You can specify the following *options* in a TABLES statement.

**AGREE < (agree-options) >**

requests tests and measures of classification agreement for square tables. This option provides the simple and weighted kappa coefficients along with their standard errors and confidence limits. For multiway tables, this option also produces the overall simple and weighted kappa coefficients (along with their standard errors and confidence limits) and tests for equal kappas among strata. For $2 \times 2$ tables, this option provides McNemar’s test; for square tables that have more than two response categories (levels), this option provides Bowker’s symmetry test. For multiway tables that have two response categories, this option also produces Cochran’s $Q$ test. For more information, see the section “Tests and Measures of Agreement” on page 249.

Measures of agreement can be computed only for square tables, where the number of rows equals the number of columns. If your table is not square because some observations have weights of 0, you can specify the ZEROS option in the WEIGHT statement to include these observations in the analysis. For more information, see the section “Tables with Zero-Weight Rows or Columns” on page 256.

For $2 \times 2$ tables, the weighted kappa coefficient is equivalent to the simple kappa coefficient, and PROC FREQTAB displays only analyses for the simple kappa coefficient.

You can specify the confidence level in the ALPHA= option. By default, ALPHA=0.05, which produces 95% confidence limits.
You can specify the **EXACT** statement to request McNemar’s exact test (for $2 \times 2$ tables), an exact symmetry test, and exact tests for the simple and weighted kappa coefficients. For more information, see the section “Exact Statistics” on page 265.

You can specify the following *agree-options*:

**AC1**
requests the AC1 agreement coefficient. For more information, see the section “AC1 Agreement Coefficient” on page 255.

**DFSYM=df | ADJUST**
controls the degrees of freedom for Bowker’s symmetry test. You can specify the value of the degrees of freedom ($df$), or you can specify DFSYM=ADJUST to adjust the degrees of freedom for empty table cells. The value of $df$ must be a positive number. By default, $df = R(R - 1)/2$, where $R$ is the dimension of the two-way table.

When you specify DFSYM=ADJUST, the degrees of freedom are reduced by the number of off-diagonal table-cell pairs that have a total frequency of 0. By default, the degrees of freedom count all off-diagonal table-cell pairs. For more information, see the section “Bowker’s Symmetry Test” on page 250.

**KAPPADETAILS**
**DETAILS**
displays the “Kappa Details” table, which includes the following statistics for the simple kappa coefficient: observed agreement, chance-expected agreement, maximum kappa, and the $B_n$ measure. If the two-way table is $2 \times 2$, the “Kappa Details” table also includes the prevalence index and the bias index. For more information, see the section “Simple Kappa Coefficient” on page 251.

If the two-way table is larger than $2 \times 2$, this option also displays the “Weighted Kappa Details” table, which includes the observed agreement and chance-expected agreement components of the weighted kappa coefficient. For more information, see the section “Weighted Kappa Coefficient” on page 252.

**MNULAR_RATIO=value**
specifies the null value of the ratio of discordant proportions for McNemar’s test. By default, MNULAR_RATIO=1. For more information, see the section “McNemar’s Test” on page 249.

**NULLKAPPA=value**
requests the simple kappa coefficient test and specifies the null value for the test. The null value must be between –1 and 1. By default, NULLKAPPA=0. For more information, see the section “Simple Kappa Coefficient” on page 251.

This option is not available when you specify the KAPPA option in the EXACT statement, which requests an exact test for the kappa coefficient.

**NULLWTKAPPA=value**
requests the weighted kappa coefficient test and specifies the null value for the test. The null value must be between –1 and 1. By default, NULLWTKAPPA=0. For more information, see the section “Weighted Kappa Coefficient” on page 252.

This option is not available when you specify the WTKAPPA option in the EXACT statement, which requests an exact test for the weighted kappa coefficient.
Chapter 4: The FREQTAB Procedure

PABAK
requests the prevalence-adjusted bias-adjusted kappa coefficient. For more information, see the section “Prevalence-Adjusted Bias-Adjusted Kappa” on page 254.

PRINTKWTS
displays the agreement weights that PROC FREQTAB uses to compute the weighted kappa coefficient. Agreement weights reflect the relative agreement between pairs of variable levels. By default, PROC FREQTAB uses Cicchetti-Allison agreement weights. If you specify the WT=FC option, the procedure uses Fleiss-Cohen agreement weights. For more information, see the section “Weighted Kappa Coefficient” on page 252.

TABLES=RESTORE
displays agreement tables (which are produced by the AGREE option) in factoid (label-value) format, which is the format of these tables in releases before SAS/STAT 14.2. Beginning in SAS/STAT 14.3, PROC FREQTAB displays all agreement tables in tabular format (instead of factoid format) by default.

In SAS/STAT 14.2, PROC FREQTAB displays agreement tables in tabular format (instead of factoid format) by default when you specify any of the following agree-options: AC1, KAPPADETAILS, NULLKAPPA=, NULLWTKAPPA=, PABAK, or WTKAPPADETAILS.

WT=FC
specifies Fleiss-Cohen agreement weights in the computation of the weighted kappa coefficient. Agreement weights reflect the relative agreement between pairs of variable levels. By default, PROC FREQTAB uses Cicchetti-Allison agreement weights to compute the weighted kappa coefficient. For more information, see the section “Weighted Kappa Coefficient” on page 252.

WTKAPPADETAILS
displays the “Weighted Kappa Details” table, which includes the observed agreement and chance-expected agreement components of the weighted kappa coefficient. This information is available for two-way tables that are larger than $2 \times 2$. For more information, see the section “Weighted Kappa Coefficient” on page 252.

ALL
requests all tests and measures that are produced by the CHISQ, MEASURES, and CMH options. You can control the number of CMH statistics to compute by specifying the CMH1 or CMH2 option.

ALPHA=\alpha
specifies the level of confidence limits. The value of \alpha must be between 0 and 1; a confidence level of \alpha produces $100(1 - \alpha)\%$ confidence limits. By default ALPHA=0.05, which produces 95% confidence limits.

This option applies to confidence limits that you request in the TABLES statement. The ALPHA= option in the EXACT statement applies to confidence limits for Monte Carlo estimates of exact $p$-values, which you request by specifying the MC option in the EXACT statement.
BINOMIAL <(binomial-options)>  
BIN <(binomial-options)>

requests the binomial proportion for one-way tables. When you specify this option, by default PROC FREQTAB provides the asymptotic standard error, asymptotic Wald and exact (Clopper-Pearson) confidence limits, and the asymptotic equality test for the binomial proportion.

You can specify binomial-options in parentheses after the BINOMIAL option. The LEVEL= binomial-option identifies the variable level for which to compute the proportion. If you do not specify this option, PROC FREQTAB computes the proportion for the first level that appears in the one-way frequency table. The P= binomial-option specifies the null proportion for the binomial tests. If you do not specify this option, PROC FREQTAB uses 0.5 as the null proportion for the binomial tests.

You can also specify binomial-options to request additional tests and confidence limits for the binomial proportion. The EQUIV, NONINF, and SUP binomial-options request tests of equivalence, noninferiority, and superiority, respectively. The CL= binomial-option requests confidence limits for the binomial proportion.

You can specify the level for the binomial confidence limits in the ALPHA= option. By default, ALPHA=0.05, which produces 95% confidence limits. As part of the noninferiority, superiority, and equivalence analyses, PROC FREQTAB provides null-based equivalence limits that have a confidence coefficient of 100(1 - 2α)% (Schuirmann 1999). In these analyses, the default of ALPHA=0.05 produces 90% equivalence limits. For more information, see the sections “Noninferiority Test” on page 219 and “Equivalence Test” on page 220.

To request exact tests for the binomial proportion, you can specify the BINOMIAL option in the EXACT statement. PROC FREQTAB computes exact p-values for all binomial tests that you request, which can include noninferiority, superiority, and equivalence tests, in addition to the equality test that the BINOMIAL option produces by default.

For more information, see the section “Binomial Proportion” on page 214.

Table 4.9 summarizes the binomial-options.
### Table 4.9 BINOMIAL Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CORRECT</td>
<td>Requests continuity correction</td>
</tr>
<tr>
<td>LEVEL=</td>
<td>Specifies the variable level</td>
</tr>
<tr>
<td>OUTLEVEL</td>
<td>Includes the level in the output data sets</td>
</tr>
<tr>
<td>P=</td>
<td>Specifies the null proportion</td>
</tr>
</tbody>
</table>

#### Request Confidence Limits

- **CL=AGRESTICOULL | AC** Requests Agresti-Coull confidence limits
- **CL=BLAKER** Requests Blaker confidence limits
- **CL=EXACT | CLOPPERPEARSON** Requests exact (Clopper-Pearson) confidence limits
- **CL=JEFFREYS** Requests Jeffreys confidence limits
- **CL=LIKELIHOODRATIO | LR** Requests likelihood ratio confidence limits
- **CL=LOGIT** Requests logit confidence limits
- **CL=MIDP** Requests exact mid-$p$ confidence limits
- **CL=WALD** Requests Wald confidence limits
- **CL=WILSON | SCORE** Requests Wilson (score) confidence limits

#### Request Tests

- **EQUIV | EQUIVALENCE** Requests an equivalence test
- **MARGIN=** Specifies the test margin
- **NONINF | NONINFERIORITY** Requests a noninferiority test
- **SUP | SUPERIORITY** Requests a superiority test
- **VAR=NULL | SAMPLE** Specifies the test variance

You can specify the following *binomial-options*:

**CL=type | (types)** requests confidence limits for the binomial proportion. You can specify one or more *types* of confidence limits. When you specify only one *type*, you can omit the parentheses around the request. PROC FREQTAB displays the confidence limits in the “Binomial Confidence Limits” table.

The **ALPHA=** option determines the level of the confidence limits that the **CL= binomial-option** provides. By default, **ALPHA=0.05**, which produces 95% confidence limits for the binomial proportion.

You can specify the **CL= binomial-option** with or without requests for binomial tests. The confidence limits that **CL=** produces do not depend on the tests that you request and do not use the value of the test margin (which you can specify in the **MARGIN= binomial-option**).

If you do not specify the **CL= binomial-option**, the BINOMIAL option displays Wald and exact (Clopper-Pearson) confidence limits in the “Binomial Proportion” table.

You can specify the following *types*:
AGRESTICOULL
AC requests Agresti-Coull confidence limits for the binomial proportion. For more information, see the section “Agresti-Coull Confidence Limits” on page 215.

BLAKER
requests Blaker confidence limits for the binomial proportion. For more information, see the section “Blaker Confidence Limits” on page 216.

EXACT
CLOPPERPEARSON requests exact (Clopper-Pearson) confidence limits for the binomial proportion. For more information, see the section “Exact (Clopper-Pearson) Confidence Limits” on page 215.

If you do not specify the CL= binomial-option, PROC FREQTAB displays Wald and exact (Clopper-Pearson) confidence limits in the “Binomial Proportion” table. To request exact tests for the binomial proportion, you can specify the BINOMIAL option in the EXACT statement.

JEFFREYS
requests Jeffreys confidence limits for the binomial proportion. For more information, see the section “Jeffreys Confidence Limits” on page 216.

LIKELIHOODRATIO
LR requests likelihood ratio confidence limits for the binomial proportion. For more information, see the section “Likelihood Ratio Confidence Limits” on page 216.

LOGIT
requests logit confidence limits for the binomial proportion. For more information, see the section “Logit Confidence Limits” on page 216.

MIDP
requests exact mid-p confidence limits for the binomial proportion. For more information, see the section “Mid-p Confidence Limits” on page 217.

WALD < (CORRECT) >
requests Wald confidence limits for the binomial proportion. For more information, see the section “Wald Confidence Limits” on page 214.

If you specify CL=WALD(CORRECT), the Wald confidence limits include a continuity correction. If you specify the CORRECT binomial-option, both the Wald confidence limits and the Wald tests include continuity corrections.

If you do not specify the CL= binomial-option, PROC FREQTAB displays Wald and exact (Clopper-Pearson) confidence limits in the “Binomial Proportion” table.

WILSON < (CORRECT) >
SCORE < (CORRECT) > requests Wilson confidence limits for the binomial proportion. These are also known as score confidence limits. For more information, see the section “Wilson (Score) Confidence Limits” on page 217.
If you specify CL=WILSON(CORRECT) or the **CORRECT** **binomial-option**, the Wilson confidence limits include a continuity correction.

**CORRECT** includes a continuity correction in the Wald confidence limits, Wald tests, and Wilson confidence limits.

You can request continuity corrections individually for Wald or Wilson confidence limits by specifying the **CL=WALD(CORRECT)** or **CL=WILSON(CORRECT)** **binomial-option**, respectively.

**EQUIV EQUIVALENCE** requests a test of equivalence for the binomial proportion. For more information, see the section “Equivalence Test” on page 220. You can specify the equivalence test margins, the null proportion, and the variance type in the **MARGIN=**, **P=**, and **VAR= binomial-options**, respectively. To request an exact equivalence test, you can specify the **BINOMIAL** option in the **EXACT** statement.

**LEVEL=level-number | ‘level-value’** specifies the variable level for the binomial proportion. You can specify the **level-number**, which is the order in which the level appears in the one-way frequency table. Or you can specify the **level-value**, which is the formatted value of the variable level. The **level-number** must be a positive integer. You must enclose the **level-value** in single quotes.

By default, PROC FREQTAB computes the binomial proportion for the first variable level that appears in the one-way frequency table.

**MARGIN=value | (lower, upper)** specifies the margin for the noninferiority, superiority, and equivalence tests, which you can request by specifying the **NONINF**, **SUP**, and **EQUIV** **binomial-options**, respectively. By default, **MARGIN=0.2**.

For noninferiority and superiority tests, specify a single **value** in the **MARGIN=** option. The **MARGIN= value** must be a positive number. You can specify **value** as a number between 0 and 1. Or you can specify **value** in percentage form as a number between 1 and 100, and PROC FREQTAB converts that number to a proportion. PROC FREQTAB treats the value 1 as 1%.

For noninferiority and superiority tests, the test limits must be between 0 and 1. The limits are determined by the null proportion value (which you can specify in the **P= binomial-option**) and by the margin value. The noninferiority limit is the null proportion minus the margin. By default, the null proportion is 0.5 and the margin is 0.2, which produces a noninferiority limit of 0.3. The superiority limit is the null proportion plus the margin, which is 0.7 by default.

For an equivalence test, you can specify a single **MARGIN= value**, or you can specify both **lower** and **upper** values. If you specify a single **MARGIN= value**, it must be a positive number, as described previously. If you specify a single **MARGIN= value** for an equivalence test, PROC FREQTAB uses **−value** as the lower margin and **value** as the upper margin for the test. If you specify both **lower** and **upper** values for an equivalence test, you can specify them in proportion form as numbers between −1 and 1. Or you can specify them in percentage form as numbers between −100 and 100, and PROC FREQTAB converts the numbers to proportions. The value of **lower** must be less than the value of **upper**.
The equivalence limits must be between 0 and 1. The equivalence limits are determined by the null proportion value (which you can specify in the \texttt{P= binomial-option}) and by the margin values. The lower equivalence limit is the null proportion plus the lower margin. By default, the null proportion is 0.5 and the lower margin is –0.2, which produces a lower equivalence limit of 0.3. The upper equivalence limit is the null proportion plus the upper margin, which is 0.7 by default.

For more information, see the sections “Noninferiority Test” on page 219 and “Equivalence Test” on page 220.

\textbf{NONINF}
\textbf{NONINFERIORITY}
requests a test of noninferiority for the binomial proportion. For more information, see the section “Noninferiority Test” on page 219. You can specify the noninferiority test margin, the null proportion, and the variance type in the \texttt{MARGIN=}, \texttt{P=} and \texttt{VAR=} binomial-options, respectively. To request an exact noninferiority test, you can specify the \texttt{BINOMIAL} option in the \texttt{EXACT} statement.

\textbf{OUTLEVEL}
includes the variables \texttt{LevelNumber} and \texttt{LevelValue} in all ODS output data sets that PROC \texttt{FREQTAB} produces when you specify the \texttt{BINOMIAL} option in the \texttt{TABLES} statement. The \texttt{OUTLEVEL} option also includes the variables \texttt{LevelNumber} and \texttt{LevelValue} in the statistics output data set that PROC \texttt{FREQTAB} produces when you specify the \texttt{BINOMIAL} option in the \texttt{OUTPUT} statement.

The \texttt{LevelNumber} and \texttt{LevelValue} variables identify the analysis variable level for which PROC \texttt{FREQTAB} computes the binomial proportion. The value of \texttt{LevelNumber} is the order of the level in the one-way frequency table. The value of \texttt{LevelValue} is the formatted value of the level. You can specify the \texttt{OUTLEVEL binomial-option} with or without the \texttt{LEVEL= binomial-option}.

\textbf{P=\texttt{value}}
specifies the null hypothesis proportion for the binomial tests. The null proportion \texttt{value} must be a positive number. You can specify \texttt{value} as a number between 0 and 1. Or you can specify \texttt{value} in percentage form (as a number between 1 and 100), and PROC \texttt{FREQTAB} converts that number to a proportion. PROC \texttt{FREQTAB} treats the value 1 as 1%. By default, \texttt{P=0.5}.

\textbf{SUP}
\textbf{SUPERIORITY}
requests a test of superiority for the binomial proportion. For more information, see the section “Superiority Test” on page 220. You can specify the superiority test margin, the null proportion, and the variance type in the \texttt{MARGIN=}, \texttt{P=} and \texttt{VAR=} binomial-options, respectively. To request an exact superiority test, you can specify the \texttt{BINOMIAL} option in the \texttt{EXACT} statement.

\textbf{VAR=NULL | SAMPLE}
specifies the type of variance to use in the Wald tests of noninferiority, superiority, and equivalence. If you specify \texttt{VAR=SAMPLE}, PROC \texttt{FREQTAB} computes the variance estimate by using the sample proportion. If you specify \texttt{VAR=NULL}, PROC \texttt{FREQTAB} computes a test-based variance by using the null hypothesis proportion (which you can specify in the \texttt{P= binomial-option}). For more information, see the sections “Noninferiority Test” on page 219 and “Equivalence Test” on page 220. The default is \texttt{VAR=SAMPLE}.
**CELLCHI2**

displays each table cell’s contribution to the Pearson chi-square statistic in the crosstabulation table. The cell chi-square is computed as \((\text{frequency} - \text{expected})^2 / \text{expected}\), where \(\text{frequency}\) is the table cell frequency (count) and \(\text{expected}\) is the expected cell frequency, which is computed under the null hypothesis that the row and column variables are independent. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. This option has no effect for one-way tables or for tables that are displayed in list format (which you can request by specifying the LIST option).

**CHISQ < (chisq-options) >**

requests chi-square tests of homogeneity or independence and measures of association that are based on the chi-square statistic. For two-way tables, the chi-square tests include the Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square tests. The chi-square measures include the phi coefficient, contingency coefficient, and Cramér’s \(V\). For \(2 \times 2\) tables, the CHISQ option also provides Fisher’s exact test and the continuity-adjusted chi-square test. For more information, see the section “Chi-Square Tests and Statistics” on page 199.

For one-way tables, the CHISQ option provides the Pearson chi-square goodness-of-fit test. You can also request the likelihood ratio goodness-of-fit test for one-way tables by specifying the LRCHI chisq-option in parentheses after the CHISQ option. By default, the one-way chi-square tests are based on the null hypothesis of equal proportions. Alternatively, you can provide null hypothesis proportions or frequencies by specifying the TESTP= or TESTF= chisq-option, respectively. See the section “Chi-Square Test for One-Way Tables” on page 199 for more information.

To request Fisher’s exact test for tables larger than \(2 \times 2\), specify the FISHER option in the EXACT statement. Exact \(p\)-values are also available for the Pearson, likelihood ratio, and Mantel-Haenszel chi-square tests. See the description of the EXACT statement for more information.

You can specify the following chisq-options:

**DF=\(df\)**

specifies the degrees of freedom for the chi-square tests. The value of \(df\) must not be 0. If the value of \(df\) is positive, PROC FREQTAB uses \(df\) as the degrees of freedom for the chi-square tests. If the value of \(df\) is negative, PROC FREQTAB uses \(df\) to adjust the default degrees of freedom for the chi-square tests.

By default for one-way tables, the value of \(df\) is \((n - 1)\), where \(n\) is the number of variable levels in the table. By default for two-way tables, the value of \(df\) is \((r - 1) (c - 1)\), where \(r\) is the number of rows in the table and \(c\) is the number of columns. See the sections “Chi-Square Test for One-Way Tables” on page 199 and “Chi-Square Tests and Statistics” on page 199 for more information.

If you specify a negative value of \(df\), PROC FREQTAB adjusts the default degrees of freedom by adding the (negative) value of \(df\) to the default value to produce the adjusted degrees of freedom. The adjusted degrees of freedom must be positive.

The DF= chisq-option specifies or adjusts the degrees of freedom for the following chi-square tests: the Pearson and likelihood ratio goodness-of-fit tests for one-way tables; and the Pearson, likelihood ratio, and Mantel-Haenszel chi-square tests for two-way tables.
LRCHI
requests the likelihood ratio goodness-of-fit test for one-way tables. See the section “Likelihood Ratio Chi-Square Test for One-Way Tables” on page 201 for more information.

By default, this test is based on the null hypothesis of equal proportions. You can provide null hypothesis proportions or frequencies by specifying the TESTP= or TESTF= chisq-option, respectively. You can request an exact likelihood ratio goodness-of-fit test by specifying the LRCHI option in the EXACT statement.

TESTF=(values)
specifies null hypothesis frequencies for chi-square tests for one-way tables (goodness-of-fit tests). For more information, see the section “Chi-Square Test for One-Way Tables” on page 199.

You can separate the values by using blanks or commas, and you must enclose the list of values in parentheses. The values must be positive numbers. The number of values must equal the number of variable levels in the one-way table. The sum of the values must equal the total frequency in the one-way table. List the values in the same order in which the corresponding variable levels appear in the output.

TESTP=(values)
specifies null hypothesis proportions for chi-square tests for one-way tables (goodness-of-fit tests). For more information, see the section “Chi-Square Test for One-Way Tables” on page 199.

You can separate the values by using blanks or commas, and you must enclose the list of values in parentheses. The values must be positive numbers. The number of values must equal the number of variable levels in the one-way table. List the values in the same order in which the corresponding variable levels appear in the output.

You can specify values in probability form as numbers between 0 and 1, where the proportions sum to 1. Or you can specify values in percentage form as numbers between 0 and 100, where the percentages sum to 100. PROC FREQTAB treats the value 1 as the percentage form 1%.

WARN=type | (types)
controls the warning message for the validity of the asymptotic Pearson chi-square test. By default, PROC FREQTAB displays a warning message when more than 20% of the table cells have expected frequencies that are less than 5. If you specify the NOPRINT option in the PROC FREQTAB statement, the procedure displays the warning in the log; otherwise, the procedure displays the warning as a footnote in the chi-square table. You can use the WARN= option to suppress the warning and to include a warning indicator in the output data set.

You can specify one or more of the following types in the WARN= option. If you specify more than one type value, enclose the values in parentheses after WARN=. For example, warn = (output noprint).

<table>
<thead>
<tr>
<th>Value of WARN=</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>OUTPUT</td>
<td>Adds a warning indicator variable to the output data set</td>
</tr>
<tr>
<td>NOLOG</td>
<td>Suppresses the chi-square warning message in the log</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses the chi-square warning message in the display</td>
</tr>
<tr>
<td>NONE</td>
<td>Suppresses the chi-square warning message entirely</td>
</tr>
</tbody>
</table>

If you specify the WARN=OUTPUT option, the ODS output data set ChiSq contains a variable named Warning that equals 1 for the Pearson chi-square observation when more than 20% of the...
table cells have expected frequencies that are less than 5 and equals 0 otherwise. If you specify
WARN=OUTPUT and also specify the CHISQ option in the OUTPUT statement, the statistics
output data set contains a variable named WARN_PCHI that indicates the warning.

The WARN=NOLOG option has the same effect as the NOWARN option in the TABLES
statement.

**CL**

requests confidence limits for the measures of association, which you can request by specifying the
MEASURES option. For more information, see the sections “Measures of Association” on page 204
and “Confidence Limits” on page 205. You can set the level of the confidence limits by using the
ALPHA= option; by default, ALPHA=0.05, which produces 95% confidence limits.

If you omit the MEASURES option, the CL option invokes MEASURES. The CL option is equivalent
to the MEASURES(CL) option.

**CMH < (cmh-options) >**

requests Cochran-Mantel-Haenszel statistics, which test for association between the row and column
variables after adjusting for the remaining variables in a multiway table. The Cochran-Mantel-Haenszel
statistics include the nonzero correlation statistic, the row mean scores (ANOVA) statistic, and the
general association statistic. In addition, for 2 × 2 tables, the CMH option provides the adjusted
Mantel-Haenszel and logit estimates of the odds ratio and relative risks, together with their confidence
limits. For stratified 2 × 2 tables, the CMH option provides the Breslow-Day test for homogeneity of
odds ratios. (To request Tarone’s adjustment for the Breslow-Day test, specify the BDT cmh-option.)
For more information, see the section “Cochran-Mantel-Haenszel Statistics” on page 256.

You can use the CMH1 or CMH2 option to control the number of CMH statistics that PROC FREQTAB
computes.

For stratified 2 × 2 tables, you can request Zelen’s exact test for equal odds ratios by specifying the
EQOR option in the EXACT statement. For more information, see the section “Zelen’s Exact Test
for Equal Odds Ratios” on page 262. You can request exact confidence limits for the common odds
ratio by specifying the COMOR option in the EXACT statement. This option also provides a common
odds ratio test. For more information, see the section “Exact Confidence Limits for the Common Odds
Ratio” on page 263.

You can specify the following cmh-options in parentheses after the CMH option. These cmh-options,
which apply to stratified 2 × 2 tables, are also available with the CMH1 or CMH2 option.

**BDT**

requests Tarone’s adjustment in the Breslow-Day test for homogeneity of odds ratios. For
more information, see the section “Breslow-Day Test for Homogeneity of the Odds Ratios” on
page 262.

**GAILSIMON < (COLUMN=1 | 2) >**

**GS < (COLUMN=1 | 2) >**

requests the Gail-Simon test for qualitative interaction, which applies to stratified 2 × 2 tables.
For more information, see the section “Gail-Simon Test for Qualitative Interactions” on page 265.

The COLUMN= option specifies the column of the risk differences to use to compute the
Gail-Simon test. By default, PROC FREQTAB uses column 1 risk differences. If you specify
COLUMN=2, PROC FREQTAB uses column 2 risk differences.
The GAILSIMON cmh-option has the same effect as the GAILSIMON option in the TABLES statement.

**MANTELFLEISS**

**MF**

requests the Mantel-Fleiss criterion for the Mantel-Haenszel statistic for stratified $2 \times 2$ tables. For more information, see the section “Mantel-Fleiss Criterion” on page 259.

**CMH1** <$\text{cmh-options}$>

requests the Cochran-Mantel-Haenszel correlation statistic. This option does not provide the CMH row mean scores (ANOVA) statistic or the general association statistic, which are provided by the CMH option. For tables larger than $2 \times 2$, the CMH1 option requires less memory than the CMH option, which can require an enormous amount of memory for large tables.

For $2 \times 2$ tables, the CMH1 option also provides the adjusted Mantel-Haenszel and logit estimates of the odds ratio and relative risks, together with their confidence limits. For stratified $2 \times 2$ tables, the CMH1 option provides the Breslow-Day test for homogeneity of odds ratios.

The **cmh-options** for CMH1 are the same as the **cmh-options** that are available with the CMH option. For more information, see the description of the CMH option.

**CMH2** <$\text{cmh-options}$>

requests the Cochran-Mantel-Haenszel correlation statistic and the row mean scores (ANOVA) statistic. This option does not provide the CMH general association statistic, which is provided by the CMH option. For tables larger than $2 \times 2$, the CMH2 option requires less memory than the CMH option, which can require an enormous amount of memory for large tables.

For $2 \times 2$ tables, the CMH1 option also provides the adjusted Mantel-Haenszel and logit estimates of the odds ratio and relative risks, together with their confidence limits. For stratified $2 \times 2$ tables, the CMH1 option provides the Breslow-Day test for homogeneity of odds ratios.

The **cmh-options** for CMH2 are the same as the **cmh-options** that are available with the CMH option. For more information, see the description of the CMH option.

**COMMONRISKDIFF** <$\text{options}$>

requests the common (stratified) risk difference for multiway $2 \times 2$ tables, where the risk difference is the difference between the row 1 proportion and the row 2 proportion in a $2 \times 2$ table. By default, this option provides Mantel-Haenszel and summary score estimates of the common risk difference, together with their confidence limits. For more information, see the section “Common Risk Difference” on page 232.

You can specify the following **options** to request confidence limit types and tests for the common risk difference:

**CL=** *type* | *(types)*

requests confidence limits for the common risk difference. You can specify one or more **types** of confidence limits. When you specify only one **type**, you can omit the parentheses. You can specify CL=NONE to suppress the “Confidence Limits for the Common Risk Difference” table.

You can specify the confidence level in the **ALPHA=** option. By default, ALPHA=0.05, which produces 95% confidence limits for the common risk difference.

You can specify one or more of the following **types**: 

---

TABLES Statement ♦ 159
MH
requests Mantel-Haenszel confidence limits, which are computed by using Mantel-Haenszel stratum weights and the Sato variance estimator (Sato 1989). For more information, see the section “Mantel-Haenszel Confidence Limits and Test” on page 232.

MR
MINRISK
requests minimum risk confidence limits, which are computed by using minimum risk weights. For more information, see the section “Minimum Risk Confidence Limits and Test” on page 233.

NEWCOMBE
requests stratified Newcombe confidence limits that use Mantel-Haenszel weights to combine the stratum components. For more information, see the section “Stratified Newcombe Confidence Limits” on page 235.

NEWCOMBEMR
requests stratified Newcombe confidence limits that use minimum risk weights to combine the stratum components. For more information, see the section “Stratified Newcombe Confidence Limits” on page 235.

NONE
suppresses the “Confidence Limits for the Common Risk Difference” table.

SCORE
requests summary score confidence limits. For more information, see the section “Summary Score Confidence Limits” on page 235.

COLUMN=1 | 2
specifies the table column for which to compute the common risk difference statistics. If you do not specify this option but you do specify the RISKDIFF(COLUMN=) option, PROC FREQTAB provides the common risk difference statistics for the column that you specify in the RISKDIFF(COLUMN=) option. If you do not specify either of these options, COLUMN=1 by default.

CORRECT=NO
removes the continuity correction in the minimum risk confidence limits and in the minimum risk test, which you can request by specifying the CL=MR and TEST=MR options, respectively. For more information, see the section “Minimum Risk Confidence Limits and Test” on page 233.

PRINTWTS <=(MH | MR)>
displays the stratum weights together with the stratum risk differences and frequencies. By default, this option displays the weight type or types for the confidence limits and tests that you request. Optionally, you can specify the weight type to display; the PRINTWTS=MH option displays Mantel-Haenszel weights and the PRINTWTS=MR option displays minimum risk weights. You can display both weight types by specifying PRINTWTS=(MH MR).
**TEST < =type | (types) >**

requests common risk difference tests. You can specify one or more types. When you specify only one type, you can omit the parentheses. If you do not specify types, this option provides tests that correspond to the confidence limit types that you specify in the CL= option.

You can specify one or more of the following types:

**MH**

requests a Mantel-Haenszel test, which is computed by using Mantel-Haenszel stratum weights and the Sato variance estimator (Sato 1989). For more information, see the section “Mantel-Haenszel Confidence Limits and Test” on page 232.

**MR < (VAR=SAMPLE) >**

**MINRISK < (VAR=SAMPLE) >**

requests the minimum risk test, which is computed by using minimum risk weights. If you specify VAR=SAMPLE, PROC FREQTAB uses the sample (observed) variance estimate instead of a null variance estimate to compute the minimum risk test statistic. For more information, see the section “Minimum Risk Confidence Limits and Test” on page 233.

**SCORE**

requests the summary score test. For more information, see the section “Summary Score Confidence Limits” on page 235.

**CONTENTS=’string’**

specifies the label to use for crosstabulation tables in the contents file, the Results window, and the trace record. For information about output presentation, see the *SAS Output Delivery System: User’s Guide*.

If you omit the CONTENTS= option, the contents label for crosstabulation tables is “Cross-Tabular Freq Table” by default.

Note that contents labels for all crosstabulation tables that are produced by a single TABLES statement use the same text. To specify different contents labels for different crosstabulation tables, request the tables in separate TABLES statements and use the CONTENTS= option in each TABLES statement.

To remove the crosstabulation table entry from the contents file, you can specify a null label with CONTENTS=’’.

The CONTENTS= option affects only contents labels for crosstabulation tables. It does not affect contents labels for other PROC FREQTAB tables.

To specify the contents label for any PROC FREQTAB table, you can use PROC TEMPLATE to create a customized table template. The CONTENTS_LABEL attribute in the DEFINE TABLE statement of PROC TEMPLATE specifies the contents label for the table. See the chapter “The TEMPLATE Procedure” in the *SAS Output Delivery System: User’s Guide* for more information.

**CROSSLIST < (options) >**

displays crosstabulation tables by using an ODS column format instead of the default crosstabulation cell format. In the CROSSLIST table display, the rows correspond to the crosstabulation table cells, and the columns correspond to descriptive statistics such as frequencies and percentages. The CROSSLIST table displays the same information as the default crosstabulation table (but it uses an ODS column
format). For more information about the contents of the CROSSLIST table, see the section “Two-Way and Multiway Tables” on page 274.

You can control the contents of a CROSSLIST table by specifying the same options available for the default crosstabulation table. These include the NOFREQ, NOPERCENT, NOROW, and NOCOL options. You can request additional information in a CROSSLIST table by specifying the CELLCHI2, DEVIATION, EXPECTED, MISSPRINT, and TOTPCT options. You can also display standardized residuals or Pearson residuals in a CROSSLIST table by specifying the CROSSLIST(STDRES) or CROSSLIST(PEARSONRES) option, respectively; these options are not available for the default crosstabulation table. The FORMAT= and CUMCOL options have no effect on CROSSLIST tables. You cannot specify both the LIST option and the CROSSLIST option in the same TABLES statement.

You can specify the NOSPARSE option along with the CROSSLIST option to suppress variable levels that have frequencies of 0. By default for CROSSLIST tables, PROC FREQTAB displays all levels of the column variable within each level of the row variable, including any levels that have frequencies of 0. By default for multiway CROSSLIST tables, PROC FREQTAB displays all levels of the row variable within each stratum of the table, including any row levels that have frequencies of 0 in the stratum.

You can specify the following options:

**STDRES**

- displays the standardized residuals of the table cells in the CROSSLIST table. The standardized residual is the ratio of \((frequency – expected)\) to its standard error, where \(frequency\) is the table cell frequency (count) and \(expected\) is the expected table cell frequency, which is computed under the null hypothesis that the row and column variables are independent. For more information, see the section “Standardized Residuals” on page 200. You can display the expected values and deviations by specifying the EXPECTED and DEVIATION options, respectively.

**PEARSONRES**

- displays the Pearson residuals of the table cells in the CROSSLIST table. The Pearson residual is the square root of the table cell’s contribution to the Pearson chi-square statistic. The Pearson residual is computed as \((frequency – expected)/\sqrt{expected}\), where \(frequency\) is the table cell frequency (count) and \(expected\) is the expected table cell frequency, which is computed under the null hypothesis that the row and column variables are independent. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. You can display the expected values, deviations, and cell chi-squares by specifying the EXPECTED, DEVIATION, and CELLCHI2 options, respectively.

**CUMCOL**

- displays the cumulative column percentages in the cells of the crosstabulation table. The CUMCOL option does not apply to crosstabulation tables produced with the LIST or CROSSLIST option.

**DEVIATION**

- displays the deviations of the frequencies from the expected frequencies \((frequency – expected)\) in the crosstabulation table. The expected frequencies are computed under the null hypothesis that the row and column variables are independent. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. You can display the expected values by specifying the EXPECTED option. This option has no effect for one-way tables or for tables that are displayed in list format (which you can request by specifying the LIST option).
EXPECTED

displays the expected cell frequencies in the crosstabulation table. The expected frequencies are computed under the null hypothesis that the row and column variables are independent. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. This option has no effect for one-way tables or for tables that are displayed in list format (which you can request by specifying the LIST option).

FISHER

requests Fisher’s exact test for tables that are larger than $2 \times 2$. (For $2 \times 2$ tables, the CHISQ option provides Fisher’s exact test.) This test is also known as the Freeman-Halton test. See the sections “Fisher’s Exact Test” on page 203 and “Exact Statistics” on page 265 for more information.

If you omit the CHISQ option in the TABLES statement, the FISHER option invokes CHISQ. You can also request Fisher’s exact test by specifying the FISHER option in the EXACT statement.

NOTE: PROC FREQTAB computes exact tests by using fast and efficient algorithms that are superior to direct enumeration. Exact tests are appropriate when a data set is small, sparse, skewed, or heavily tied. For some large problems, computation of exact tests might require a substantial amount of time and memory. Consider using asymptotic tests for such problems. Alternatively, when asymptotic methods might not be sufficient for such large problems, consider using Monte Carlo estimation of exact $p$-values. You can request Monte Carlo estimation by specifying the MC computation-option in the EXACT statement. See the section “Computational Resources” on page 268 for more information.

FORMAT= format-name

specifies a format for the following crosstabulation table cell values: frequency, expected frequency, and deviation. PROC FREQTAB also uses the specified format to display the row and column total frequencies and the overall total frequency in crosstabulation tables.

You can specify any standard SAS numeric format or a numeric format defined with the FORMAT procedure. The format length must not exceed 24. If you omit the FORMAT= option, by default PROC FREQTAB uses the BEST6. format to display frequencies less than $1E6$, and the BEST7. format otherwise.

The FORMAT= option applies only to crosstabulation tables displayed in the default format. It does not apply to crosstabulation tables produced with the LIST or CROSSLIST option.

To change display formats in any table that PROC FREQTAB produces, you can use PROC TEMPLATE. For more information, see the chapter “The TEMPLATE Procedure” in the SAS Output Delivery System: User’s Guide.

GAILSIMON < (COLUMN=1 | 2) >

GS < (COLUMN=1 | 2) >

requests the Gail-Simon test for qualitative interaction, which applies to stratified $2 \times 2$ tables. For more information, see the section “Gail-Simon Test for Qualitative Interactions” on page 265.

The COLUMN= option specifies the column of the risk differences to use to compute the Gail-Simon test. By default, PROC FREQTAB uses column 1 risk differences. If you specify COLUMN=2, PROC FREQTAB uses column 2 risk differences.
requests the Jonckheere-Terpstra test. For more information, see the section “Jonckheere-Terpstra Test” on page 248. To request exact p-values for the Jonckheere-Terpstra test, specify the JT option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

LIST displays two-way and multiway tables by using a list format instead of the default crosstabulation cell format. This option displays an entire multiway table in a single table instead of separate two-way (stratum) tables. Each row of a table in list format corresponds to a single crosstabulation table cell. For more information, see the section “Two-Way and Multiway Tables” on page 274.

A table in list format does not display table cells for which the total frequency is 0 unless you specify the ZEROS option in the WEIGHT statement.

The LIST option is not available together with statistic options in the same TABLES statement. When you specify statistic options in a TABLES statement, you must display the crosstabulation tables by using the default table cell format or the CROSSLIST format. You can specify the LIST option and statistic options in different TABLES statements in the same invocation of PROC FREQTAB.

specifies the maximum number of variable levels to display in one-way frequency tables. The value of \( n \) must be a positive integer. PROC FREQTAB displays the first \( n \) variable levels, matching the order in which the levels appear in the one-way frequency table. (The ORDER= option controls the order of the variable levels. By default, ORDER=INTERNAL, which orders the variable levels by unformatted value.)

The MAXLEVELS= option also applies to one-way frequency plots, which you can request by specifying the PLOTS=FREQPLOT option when ODS Graphics is enabled.

If you specify the MISSPRINT option to display missing levels in the frequency table, the MAXLEVELS= option displays the first \( n \) nonmissing levels.

The MAXLEVELS= option does not apply to the OUT= output data set, which includes all variable levels. The MAXLEVELS= option does not affect the computation of percentages, statistics, or tests for the one-way table; these values are based on the complete table.

requests measures of association and their asymptotic standard errors. This option provides the following measures: gamma, Kendall’s tau-b, Stuart’s tau-c, Somers’ D(C|R), Somers’ D(R|C), Pearson and Spearman correlation coefficients, lambda (symmetric and asymmetric), and uncertainty coefficients (symmetric and asymmetric). If you specify the CL option in parentheses after the MEASURES option, PROC FREQTAB provides confidence limits for the measures of association. For more information, see the section “Measures of Association” on page 204.

For 2 \( \times \) 2 tables, the MEASURES option also provides the odds ratio, column 1 relative risk, column 2 relative risk, and their asymptotic Wald confidence limits. You can request the odds ratio and relative risks separately (without the other measures of association) by specifying the RELRISK option. You can request confidence limits for the odds ratio by specifying the OR(CL=) option.

You can use the TEST statement to request asymptotic tests for the following measures of association: gamma, Kendall’s tau-b, Stuart’s tau-c, Somers’ D(C|R), Somers’ D(R|C), and Pearson and Spearman correlation coefficients. You can use the EXACT statement to request exact confidence limits
for the odds ratio, exact unconditional confidence limits for the relative risks, and exact tests for the following measures of association: Kendall’s tau-\(b\), Stuart’s tau-\(c\), Somers’ D(\(C|R\)) and D(\(R|C\)), and Pearson and Spearman correlation coefficients. For more information, see the descriptions of the TEST and EXACT statements and the section “Exact Statistics” on page 265.

**NOCOL**
suppresses the display of column percentages in crosstabulation table cells.

**NOCUM**
suppresses the display of cumulative frequencies and percentages in one-way frequency tables and in list-format crosstabulation tables (which you can request by specifying the LIST option).

**NOFREQ**
suppresses the display of table cell frequencies in crosstabulation tables. The NOFREQ option also suppresses row total frequencies. This option has no effect for one-way tables or for list-format crosstabulation tables (which you can request by specifying the LIST option).

**NOPERCENT**
suppresses the display of overall percentages in crosstabulation tables. These percentages include the tables cell percentages, row percentages, and column percentages of the total two-way table frequency. To suppress display of cell percentages of row or column totals, you can specify the NOROW or NOCOL option, respectively.

For one-way frequency tables and crosstabulation tables in list format, the NOPERCENT option suppresses the display of percentages and cumulative percentages.

**NOPRINT**
suppresses the display of frequency and crosstabulation tables but displays all requested tests and statistics. To suppress the display of all output, including tests and statistics, use the NOPRINT option in the PROC FREQTAB statement.

**NOROW**
suppresses the display of row percentages in crosstabulation table cells.

**NOSPARSE**
suppresses zero-frequency cells in the LIST table, CROSSLIST table, and OUT= data set.

The NOSPARSE option is available when you specify the ZEROS option in the WEIGHT statement, which includes observations that have weights of 0. By default, the ZEROS option displays zero-frequency cells in the LIST table and includes them in the OUT= data set; the NOSPARSE option suppresses the zero-frequency cells. For more information, see the description of the ZEROS option.

The NOSPARSE option is also available when you specify the CROSSLIST option. By default for CROSSLIST tables, PROC FREQTAB displays all levels of the column variable within each level of the row variable, which includes any levels that have frequencies of 0. By default for multiway CROSSLIST tables, PROC FREQTAB displays all levels of the row variable within each stratum of the table, which includes any row levels that have 0 frequencies in the stratum. The NOSPARSE option suppresses the zero-frequency levels in the CROSSLIST table.
NOWARN

suppresses the log warning message for the validity of the asymptotic Pearson chi-square test. By
default, PROC FREQTAB provides a validity warning for the asymptotic Pearson chi-square test when
more than 20 cells have expected frequencies that are less than 5. This warning message appears in the
log if you specify the NOPRINT option in the PROC FREQTAB statement.

The NOWARN option is equivalent to the CHISQ(WARN=NOLOG) option. You can also use the
CHISQ(WARN=) option to suppress the warning message in the display and to request a warning
variable in the chi-square ODS output data set or in the OUTPUT data set.

OR < (CL=type | (types ) >

ODDSRATIO < (CL=type | (types ) >

requests the odds ratio and confidence limits for $2 \times 2$ tables. For more information, see the section
“Odds Ratio” on page 236.

You can specify one or more types of confidence limits. When you specify only one confidence limit
type, you can omit the parentheses around the request. PROC FREQTAB displays the confidence
limits in the “Confidence Limits for the Odds Ratio” table.

Specifying the OR option without the CL= option is equivalent to specifying the RELRISK option,
which produces the “Odds Ratio and Relative Risks” table. For more information, see the description
of the RELRISK option. When you specify the OR(CL=) option, PROC FREQTAB does not produce
the “Odds Ratio and Relative Risks” table unless you also specify the RELRISK or MEASURES
option.

The ALPHA= option determines the confidence level; by default, ALPHA=0.05, which produces 95%
confidence limits for the odds ratio.

You can specify the following types:

EXACT
displays exact confidence limits for the odds ratio in the “Confidence Limits for the Odds Ratio”
table. (By default, PROC FREQTAB displays the exact confidence limits in a separate table.)
You must also request computation of the exact confidence limits by specifying the OR option in
the EXACT statement. For more information, see the subsection “Exact Confidence Limits” in
the section “Confidence Limits for the Odds Ratio” on page 237.

LR

LIKELIHOODRATIO
requests likelihood ratio confidence limits for the odds ratio. For more information, see the
subsection “Likelihood Ratio Confidence Limits” in the section “Confidence Limits for the Odds
Ratio” on page 237.

MIDP
requests exact mid-p confidence limits for the odds ratio. For more information, see the subsection
“Exact Mid-p Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237.

SCORE < (CORRECT=NO) >
requests score confidence limits for the odds ratio. For more information, see the subsection
“Score Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237.
If you specify CORRECT=NO, PROC FREQTAB provides the uncorrected form of the score
confidence limits.
WALD
requests asymptotic Wald confidence limits, which are based on a log transformation of the odds ratio. For more information, see the subsection “Wald Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237.

WALDMODIFIED
requests Wald modified confidence limits for the odds ratio. For more information, see the subsection “Wald Modified Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237.

OUT=SAS-data-set
names an output data set that contains frequency or crosstabulation table counts and percentages. If more than one table request appears in the TABLES statement, the contents of the OUT= data set correspond to the last table request in the TABLES statement. The OUT= data set variable COUNT contains the frequencies and the variable PERCENT contains the percentages. For more information, see the section “Contents of the TABLES Statement Output Data Set” on page 270. You can specify the following options to include additional information in the OUT= data set: OUTCUM, OUTEXPECT, and OUTPCT.

OUTCUM
includes cumulative frequencies and cumulative percentages in the OUT= data set. The variable CUM_FREQ contains the cumulative frequencies, and the variable CUM_PCT contains the cumulative percentages. For more information, see the section “Contents of the TABLES Statement Output Data Set” on page 270. This option is available for one-way frequency tables and for tables that you display in list format (which you can request by specifying the LIST option).

OUTEXPECT
includes expected cell frequencies in the OUT= data set for crosstabulation tables. The variable EXPECTED contains the expected cell frequencies. For more information, see the section “Contents of the TABLES Statement Output Data Set” on page 270. This option has no effect for one-way tables or for tables that you display in list format (which you can request by specifying the LIST option).

OUTPCT
includes the following additional variables in the OUT= data set for crosstabulation tables:

- PCT_COL percentage of column frequency
- PCT_ROW percentage of row frequency
- PCT_TABL percentage of stratum (two-way table) frequency, for \( n \)-way tables where \( n > 2 \)

For more information, see the section “Contents of the TABLES Statement Output Data Set” on page 270. This option has no effect for one-way tables or for tables that you display in list format (which you can request by specifying the LIST option).

PLCORR < (options)>
POLYCHORIC < (options)>
requests the polychoric correlation coefficient and its asymptotic standard error. For \( 2 \times 2 \) tables, this statistic is more commonly known as the tetrachoric correlation coefficient and is labeled as such in the displayed output. For more information, see the section “Polychoric Correlation” on page 211.
If you also specify the CL or MEASURES(CL) option, PROC FREQTAB provides confidence limits for the polychoric correlation. If you specify the PLCORR option in the TEST statement, the procedure provides Wald and likelihood ratio tests for the polychoric correlation. The PLCORR option invokes the MEASURES option.

You can specify the following options:

**ADJUST**

replaces a $2 \times 2$ table cell frequency of 0 by 0.5 before computing the tetrachoric correlation (Brown and Benedetti 1977a, p. 353). To maintain the row and column marginal frequencies, adjacent cell frequencies are decreased by 0.5 and the opposite cell frequency is increased by 0.5.

This option is available for $2 \times 2$ tables and is applied only when a single cell frequency is 0. It has no effect when both off-diagonal cell frequencies are 0 (and therefore the correlation is 1) or when both diagonal cell frequencies are 1 (and therefore the correlation is −1).

**CONVERGE=value**

specifies the convergence criterion. The value must be a positive number. By default, CONVERGE=0.0001. Iterative computation of the polychoric correlation stops when the convergence measure falls below value or when the number of iterations exceeds the MAXITER= number, whichever happens first. For parameter values that are less than 0.01, PROC FREQTAB evaluates convergence by using the absolute difference instead of the relative difference. For more information, see the section “Polychoric Correlation” on page 211.

**MAXITER=number**

specifies the maximum number of iterations. The value of number must be a positive integer. By default, MAXITER=50. Iterative computation of the polychoric correlation stops when the number of iterations exceeds the maximum number or when the convergence measure falls below the CONVERGE= value, whichever happens first. For more information, see the section “Polychoric Correlation” on page 211.

**PLOTS < (global-plot-options) > < =plot-request < (plot-options) >>**

controls the plots that are produced through ODS Graphics. *Plot-requests* identify the plots, and *plot-options* control the appearance and content of the plots. You can specify *plot-options* in parentheses after a *plot-request*. A *global-plot-option* applies to all plots for which it is available unless it is altered by a specific *plot-option*. You can specify *global-plot-options* in parentheses after the PLOTS option.

When you specify only one *plot-request*, you can omit the parentheses around the request. For example:

```
plots=all
plots=freqplot
plots=(freqplot oddsratioplot)
plots(only)=(cumfreqplot deviationplot)
```

ODS Graphics must be enabled before plots can be requested. For example:
ods graphics on;
proc freqtab;
   tables treatment*response / chisq plots=freqplot;
   weight wt;
run;
ods graphics off;

If ODS Graphics is enabled but you do not specify the PLOTS= option, PROC FREQTAB produces all plots that are associated with the analyses that you request, with the exception of the frequency, cumulative frequency, and mosaic plots. To produce a frequency plot or cumulative frequency plot when ODS Graphics is enabled, you must specify the FREQPLOT or CUMFREQPLOT plot-request, respectively, in the PLOTS= option, or you must specify the PLOTS=ALL option. To produce a mosaic plot when ODS Graphics is enabled, you must specify the MOSAICPLOT plot-request in the PLOTS= option, or you must specify the PLOTS=ALL option.

PROC FREQTAB produces the remaining plots (listed in Table 4.10) by default when you request the corresponding TABLES statement options. You can suppress default plots and request specific plots by using the PLOTS(ONLY)= option; PLOTS(ONLY)=(plot-requests) produces only the plots that are specified as plot-requests. You can suppress all plots by specifying the PLOTS=NONE option. The PLOTS option has no effect when you specify the NOPRINT option in the PROC FREQTAB statement.

Plot Requests

Table 4.10 lists the available plot-requests together with their required TABLES statement options. Descriptions of the plot-requests follow the table in alphabetical order.

<table>
<thead>
<tr>
<th>Plot Request</th>
<th>Description</th>
<th>Required TABLES Statement Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>AGREEPLOT</td>
<td>Agreement plot</td>
<td>AGREE (r x r table)</td>
</tr>
<tr>
<td>ALL</td>
<td>All plots</td>
<td>None</td>
</tr>
<tr>
<td>CUMFREQPLOT</td>
<td>Cumulative frequency plot</td>
<td>One-way table request</td>
</tr>
<tr>
<td>DEVIATIONPLOT</td>
<td>Deviation plot</td>
<td>CHISQ (one-way table)</td>
</tr>
<tr>
<td>FREQPLOT</td>
<td>Frequency plot</td>
<td>Any table request</td>
</tr>
<tr>
<td>KAPPAPLOT</td>
<td>Kappa plot</td>
<td>AGREE (h x r x r table)</td>
</tr>
<tr>
<td>MOSAICPLOT</td>
<td>Mosaic plot</td>
<td>Two-way or multiway table request</td>
</tr>
<tr>
<td>NONE</td>
<td>No plots</td>
<td>None</td>
</tr>
<tr>
<td>ODDSRATIOPLOT</td>
<td>Odds ratio plot</td>
<td>MEASURES, OR, or RELRISK (h x 2 x 2 table)</td>
</tr>
<tr>
<td>RELRISKPLOT</td>
<td>Relative risk plot</td>
<td>MEASURES or RELRISK (h x 2 x 2 table)</td>
</tr>
<tr>
<td>RISKDIFFPLOT</td>
<td>Risk difference plot</td>
<td>RISKDIFF (h x 2 x 2 table)</td>
</tr>
<tr>
<td>WTKAPPAPLOT</td>
<td>Weighted kappa plot</td>
<td>AGREE (h x r x r table, r &gt; 2)</td>
</tr>
</tbody>
</table>
You can specify the following plot-requests:

**AGREEPLOT < (plot-options) >**
requests an agreement plot (Bangdiwala and Bryan 1987). An agreement plot displays the strength of agreement in a two-way table, where the row and column variables represent two independent ratings of $n$ subjects. For information about agreement plots, see Bangdiwala (1988), Bangdiwala et al. (2008), and Friendly (2000, Section 3.7.2).

To produce an agreement plot, you must also specify the AGREE option in the TABLES statement. Agreement statistics and plots are available for two-way square tables, where the number of rows equals the number of columns.

Table 4.11 lists the plot-options that are available for agreement plots. For descriptions of the plot-options, see the subsection “Plot Options” in this section.

![Table 4.11 Plot Options for AGREEPLOT](image)

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>LEGEND=</td>
<td>Legend</td>
<td>NO or YES*</td>
</tr>
<tr>
<td>PARTIAL=</td>
<td>Partial agreement</td>
<td>NO or YES*</td>
</tr>
<tr>
<td>SHOWSCALE=</td>
<td>Frequency scale</td>
<td>NO or YES*</td>
</tr>
<tr>
<td>STATS</td>
<td>Statistics</td>
<td>None</td>
</tr>
</tbody>
</table>

*Default

If you specify the STATS plot-option, the agreement plot displays the values of the kappa coefficient, the weighted kappa coefficient, the $B_n$ measure (Bangdiwala and Bryan 1987), and the sample size. PROC FREQTAB stores these statistics in an ODS table named BnMeasure, which is not displayed. For more information, see the section “ODS Table Names” on page 282.

**ALL**
requests all plots that are associated with the specified analyses. Table 4.10 lists the available plot-requests and the corresponding analysis options. If you specify the PLOTS=ALL option, PROC FREQTAB produces the frequency, cumulative frequency, and mosaic plots that are associated with the tables that you request. (These plots are not produced by default when ODS Graphics is enabled.)

**CUMFREQPLOT < (plot-options) >**
requests a plot of cumulative frequencies. Cumulative frequency plots are available for one-way frequency tables.

To produce a cumulative frequency plot, you must specify the CUMFREQPLOT plot-request in the PLOTS= option, or you must specify the PLOTS=ALL option. PROC FREQTAB does not produce cumulative frequency plots by default when ODS Graphics is enabled.

Table 4.12 lists the plot-options that are available for cumulative frequency plots. For descriptions of the plot-options, see the subsection “Plot Options” in this section.
Table 4.12  Plot Options for CUMFREQPLOT

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORIENT=</td>
<td>Orientation</td>
<td>HORIZONTAL or VERTICAL*</td>
</tr>
<tr>
<td>SCALE=</td>
<td>Scale</td>
<td>FREQ* or PERCENT</td>
</tr>
<tr>
<td>TYPE=</td>
<td>Type</td>
<td>BARCHART* or DOTPLOT</td>
</tr>
</tbody>
</table>

*Default

DEVIATIONPLOT <(plot-options)> requests a plot of relative deviations from expected frequencies. Deviation plots are available for chi-square analysis of one-way frequency tables. To produce a deviation plot, you must also specify the CHISQ option in the TABLES statement for a one-way frequency table.

Table 4.13 lists the plot-options that are available for deviation plots. For descriptions of the plot-options, see the subsection “Plot Options” in this section.

Table 4.13  Plot Options for DEVIATIONPLOT

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>NOSTAT</td>
<td>No statistic</td>
<td>None</td>
</tr>
<tr>
<td>ORIENT=</td>
<td>Orientation</td>
<td>HORIZONTAL or VERTICAL*</td>
</tr>
<tr>
<td>TYPE=</td>
<td>Type</td>
<td>BARCHART* or DOTPLOT</td>
</tr>
</tbody>
</table>

*Default

FREQPLOT <(plot-options)> requests a frequency plot. Frequency plots are available for frequency and crosstabulation tables. For multiway crosstabulation tables, PROC FREQTAB provides a two-way frequency plot for each stratum (two-way table).

To produce a frequency plot, you must specify the FREQPLOT plot-request in the PLOTS= option, or you must specify the PLOTS=ALL option. PROC FREQTAB does not produce frequency plots by default when ODS Graphics is enabled.

Table 4.14 lists the plot-options that are available for frequency plots. For descriptions of the plot-options, see the subsection “Plot Options” in this section.
### Table 4.14  Plot Options for FREQPLOT

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>GROUPBY=**</td>
<td>Primary group</td>
<td>COLUMN* or ROW</td>
</tr>
<tr>
<td>NPANELPOS=**</td>
<td>Sections per panel</td>
<td>Number (4*)</td>
</tr>
<tr>
<td>ORIENT=</td>
<td>Orientation</td>
<td>HORIZONTAL or VERTICAL*</td>
</tr>
<tr>
<td>SCALE=</td>
<td>Scale</td>
<td>FREQ*, GROUPTPERCENT**, LOG, PERCENT, SQRT</td>
</tr>
<tr>
<td>TWOWAY=**</td>
<td>Two-way layout</td>
<td>CLUSTER, GROUPTHORIZONTAL, GROUPTVERTICAL*, or STACKED</td>
</tr>
<tr>
<td>TYPE=</td>
<td>Type</td>
<td>BARCHART* or DOTPLOT</td>
</tr>
</tbody>
</table>

*Default
**For two-way tables

You can specify the following *plot-options* for all frequency plots: ORIENT=, SCALE=, and TYPE=. You can specify the following *plot-options* for frequency plots of two-way (and multiway) tables: GROUPBY=, NPANELPOS=, and TWOWAY=. The NPANELPOS= *plot-option* is not available with the TWOWAY=CLUSTER or TWOWAY=STACKED layout, which is always displayed in a single panel.

By default, PROC FREQTAB displays frequency plots as bar charts. To display frequency plots as dot plots, specify **TYPE=DOTPLOT**. To plot percentages instead of frequencies, specify **SCALE=PERCENT**. For two-way tables, there are four frequency plot layouts available, which you can request by specifying the TWOWAY= *plot-option*. For more information, see the subsection “Plot Options” in this section.

By default, graph cells in a two-way layout are first grouped by column variable levels; row variable levels are then displayed within the column variable levels. To group first by row variable levels, specify **GROUPBY=ROW**.

**KAPPA PLOT <(plot-options)>**

requests a plot of kappa statistics along with confidence limits. Kappa plots are available for multiway square tables and display the kappa statistic (with confidence limits) for each two-way table (stratum). Kappa plots also display the overall kappa statistic unless you specify the **COMMON=NO** *plot-option*. To produce a kappa plot, you must specify the **AGREE** option in the TABLES statement to compute kappa statistics.

Table 4.15 lists the *plot-options* that are available for kappa plots. For descriptions of the *plot-options*, see the subsection “Plot Options” in this section.
**Table 4.15** Plot Options for KAPPAPLOT and WTKAPPAPLOT

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLDISPLAY=</td>
<td>Error bar type</td>
<td>BAR, LINE, LINEARROW, SERIF*, or SERIFARROW</td>
</tr>
<tr>
<td>COMMON=</td>
<td>Overall kappa</td>
<td>NO or YES*</td>
</tr>
<tr>
<td>NPANELPOS=</td>
<td>Statistics per graphic</td>
<td>Number (all*)</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Order of two-way levels</td>
<td>ASCENDING or DESCENDING</td>
</tr>
<tr>
<td>RANGE=</td>
<td>Range to display</td>
<td>Values or CLIP</td>
</tr>
<tr>
<td>STATS</td>
<td>Statistic values</td>
<td>None</td>
</tr>
</tbody>
</table>

*M: Default

**MOSAICPLOT < (plot-options) >**

requests a mosaic plot. Mosaic plots are available for two-way and multiway crosstabulation tables; for multiway tables, PROC FREQTAB provides a mosaic plot for each two-way table (stratum).

To produce a mosaic plot, you must specify the MOSAICPLOT *plot-request* in the PLOTS= option, or you must specify the PLOTS=ALL option. PROC FREQTAB does not produce mosaic plots by default when ODS Graphics is enabled.

Mosaic plots display tiles that correspond to the crosstabulation table cells. The areas of the tiles are proportional to the frequencies of the table cells. The column variable is displayed on the X axis, and the tile widths are proportional to the relative frequencies of the column variable levels. The row variable is displayed on the Y axis, and the tile heights are proportional to the relative frequencies of the row levels within column levels. For more information, see Friendly (2000).

By default, the colors of the tiles correspond to the row variable levels. If you specify the COLORSTAT= *plot-option*, the tiles are colored according to the values of the Pearson or standardized residuals.

You can specify the following *plot-options*:

**COLORSTAT < =PEARSONRES | STDRES >**

colors the mosaic plot tiles according to the values of residuals. If you specify COLORSTAT=PEARSONRES, the tiles are colored according to the Pearson residuals of the corresponding table cells. For more information, see the section “Pearson Chi-Square Test for Two-Way Tables” on page 200. If you specify COLORSTAT=STDRES, the tiles are colored according to the standardized residuals of the corresponding table cells. For more information, see the section “Standardized Residuals” on page 200. You can display the Pearson or standardized residuals in the CROSSLIST table by specifying the CROSSLIST(PEARSONRES) or CROSSLIST(STDRES) option, respectively.

**SQUARE**

produces a square mosaic plot, where the height of the Y axis equals the width of the X axis. In a square mosaic plot, the scale of the relative frequencies is the same on both axes. By default, PROC FREQTAB produces a rectangular mosaic plot.
NONE
suppresses all plots.

ODDSRATIOPLOT <(plot-options)>
requests a plot of odds ratios along with confidence limits. Odds ratio plots are available for multiway 2 × 2 tables and display the odds ratio (with confidence limits) for each 2 × 2 table (stratum). To produce an odds ratio plot, you must also specify the MEASURES, OR, or RELRISK option in the TABLES statement to compute the odds ratios.

Table 4.16 lists the plot-options that are available for odds ratio plots. For descriptions of the plot-options, see the subsection “Plot Options” in this section.

<table>
<thead>
<tr>
<th>Plot Option</th>
<th>Description</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>CL=</td>
<td>Confidence limit type</td>
<td>Type</td>
</tr>
<tr>
<td>CLDISPLAY=</td>
<td>Error bar type</td>
<td>BAR, LINE, LINEARROW, SERIF*, or SERIFARROW</td>
</tr>
<tr>
<td>COLUMN=**</td>
<td>Risk column</td>
<td>1* or 2</td>
</tr>
<tr>
<td>COMMON=</td>
<td>Common value</td>
<td>NO or YES*</td>
</tr>
<tr>
<td>LOGBASE=***</td>
<td>Axis scale</td>
<td>2, E, or 10</td>
</tr>
<tr>
<td>NPANELPOS=</td>
<td>Statistics per graphic</td>
<td>Number (all*)</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Order of two-way levels</td>
<td>ASCENDING or DESCENDING</td>
</tr>
<tr>
<td>RANGE=</td>
<td>Range to display</td>
<td>Values or CLIP</td>
</tr>
<tr>
<td>STATS</td>
<td>Statistic values</td>
<td>None</td>
</tr>
</tbody>
</table>

*Default
**Available for RELRISKPLOT and RISKDIFFPLOT
***Available for ODDSRATIOPLOT and RELRISKPLOT

You can specify one of the following confidence limit types for the odds ratio plot: exact (CL=EXACT), likelihood ratio (CL=LR), exact mid-p (CL=MIDP), score (CL=SCORE), Wald (CL=WALD), or Wald modified (CL=WALDMODIFIED). By default, the odds ratio plot displays Wald confidence limits. For more information, see the descriptions of the CL= plot-option and the OR(CL=) option.

To display exact confidence limits in the odds ratio plot, you must also request their computation by specifying the OR option in the EXACT statement.

When CL=WALD or CL=EXACT, the odds ratio plot displays the common odds ratio by default when it is available. To compute the common odds ratio along with Wald confidence limits, specify the CMH option in the TABLES statement. To compute the common odds ratio along with exact confidence limits, specify the COMOR option in the EXACT statement. To suppress display of the common odds ratio, specify COMMON=NO.

RELRISKPLOT <(plot-options)>
requests a plot of relative risks along with confidence limits. Relative risk plots are available for multiway 2 × 2 tables and display the relative risk (with confidence limits) for each 2 × 2 table (stratum). To produce a relative risk plot, you must also specify the MEASURES or RELRISK option in the TABLES statement to compute relative risks.
Table 4.16 lists the *plot-options* that are available for relative risk plots. For descriptions of the *plot-options*, see the subsection “Plot Options” in this section.

You can specify one of the following confidence limit types for the relative risk plot: exact (CL=EXACT), likelihood ratio (CL=LR), score (CL=SCORE), Wald (CL=WALD), or Wald modified (CL=WALDMODIFIED). By default, the relative risk plot displays Wald confidence limits. For more information, see the descriptions of the CL= *plot-option* and the RELRISK(CL=) option.

To display exact confidence limits in the relative risk plot, you must also request their computation by specifying the RELRISK option in the EXACT statement. The risk column that you specify for the confidence limits must match the risk column that you specify for the plot.

The relative risk plot displays the common relative risk by default when you specify CL=WALD and the CMH option in the TABLES statement. To suppress display of the common relative risk, specify COMMON=NO.

**RISKDIFFPLOT < (plot-options) >**

requests a plot of risk (proportion) differences along with confidence limits. Risk difference plots are available for multiway 2 x 2 tables and display the risk difference (with confidence limits) for each 2 x 2 table (stratum). To produce a risk difference plot, you must also specify the RISKDIFF option in the TABLES statement to compute risk differences.

Table 4.16 lists the *plot-options* that are available for risk difference plots. For descriptions of the *plot-options*, see the subsection “Plot Options” in this section.

You can specify one of the following confidence limit types for the risk difference plot: Agresti-Caffo (CL=AC), exact (CL=EXACT), Hauck-Anderson (CL=HA), Miettinen-Nurminen (score) (CL=MN), Newcombe (CL=NEWCOMBE), and Wald (CL=WALD). By default, the plot displays Wald confidence limits for the risk difference. For more information, see the descriptions of the CL= *plot-option* and the RISKDIFF(CL=) option.

To display exact confidence limits in the risk difference plot, you must also request their computation by specifying the RISKDIFF option in the EXACT statement. The risk column that you specify for the confidence limits must match the risk column that you specify for the plot.

By default, the risk difference plot displays the common risk difference when you specify the RISKDIFF(COMMON) option and one of the following confidence limit types in the CL= *plot-option*: Miettinen-Nurminen (score) (CL=MN), Newcombe (CL=NEWCOMBE), or Wald (CL=WALD). To suppress display of the common risk difference, specify COMMON=NO.

**WTKAPPAPLOT < (plot-options) >**

requests a plot of weighted kappa coefficients along with confidence limits. Weighted kappa plots are available for multiway square tables and display the weighted kappa coefficient (with confidence limits) for each two-way table (stratum). Weighted kappa plots also display the overall weighted kappa coefficient unless you specify the COMMON=NO *plot-option*.

To produce a weighted kappa plot, you must specify the AGREE option in the TABLES statement to compute weighted kappa coefficients, and the table dimension must be greater than 1.

Table 4.15 lists the *plot-options* that are available for weighted kappa plots. For descriptions of the *plot-options*, see the subsection “Plot Options” in this section.
Chapter 4: The FREQTAB Procedure

Global Plot Options

A global-plot-option applies to all plots for which the option is available unless it is altered by an individual plot-option. You can specify global-plot-options in parentheses after the PLOTS option. For example:

```
plots(order=ascending stats)=(riskdiffplot oddsratioplot)
plots(only)=freqplot
```

The following plot-options are available as global-plot-options: CLDISPLAY=, COLUMN=, COMMON=, EXACT, LOGBASE=, NPANELPOS=, ORDER=, ORIENT=, RANGE=, SCALE=, STATS, and TYPE=. For descriptions of these plot-options, see the subsection “Plot Options” in this section.

In addition to these plot-options, you can specify the following global-plot-option:

ONLY

suppresses the default plots and requests only the plots that are specified as plot-requests.

Plot Options

You can specify the following plot-options in parentheses after a plot-request:

CL=type

specifies the type of confidence limits to display. You can specify the CL= plot-option when you specify any of the following plot-requests: ODDSRATIO PLOT, RELRISK PLOT, and RISKDIFF PLOT.

For odds ratio plots (ODDSRATIO PLOT), the available confidence limit types include the following: exact (CL=EXACT), likelihood ratio (CL=LR), exact mid-

$\phi$

(CL=MIDP), score (CL=SCORE), Wald (CL=WALD), and Wald modified (CL=WALDMODIFIED). For more information, see the description of the OR(CL=) option and the section “Confidence Limits for the Odds Ratio” on page 237. By default, CL=WALD. When you specify CL=EXACT to display exact confidence limits, you must also request computation of exact confidence limits by specifying the OR option in the EXACT statement.

For relative risk plots (RELRISK PLOT), the available confidence limit types include the following: exact (CL=EXACT), likelihood ratio (CL=LR), score (CL=SCORE), Wald (CL=WALD), and Wald modified (CL=WALDMODIFIED). For more information, see the description of the RELRISK(CL=) option and the section “Confidence Limits for the Relative Risk” on page 240. By default, CL=WALD. When you specify CL=EXACT to display exact confidence limits, you must also request computation of exact confidence limits by specifying the RELRISK option in the EXACT statement.

For risk difference plots (RISKDIFF PLOT), the available confidence limit types include the following: Agresti-Caffo (CL=AC), exact (CL=EXACT), Hauck-Anderson (CL=HA), Miettinen-Nurminen (score) (CL=MN), Newcombe (CL=NEWCOMBE), and Wald (CL=WALD). For more information, see the description of the RISKDIFF(CL=) option and the section “Confidence Limits for the Risk Difference” on page 224. By default, CL=WALD. When you specify CL=EXACT to display exact confidence limits in the plot, you must also request computation of exact confidence limits by specifying the RISKDIFF option in the EXACT statement.
CLDISPLAY=BAR < width > | LINE | LINEARROW | SERIF | SERIFARROW
controls the appearance of the confidence limit error bars. You can specify the CLDISPLAY=
plot-option when you specify the following plot-requests: KAPPAPLOT, ODDSRATIO PLOT,
RELRISK PLOT, RISKDIFFPLOT, and WTKAPPAPLOT.

The default is CLDISPLAY=SERIF, which displays the confidence limits as lines with serifs.
CLDISPLAY=LINE displays the confidence limits as plain lines without serifs. The CLDIS-
PLAY=SERIFARROW and CLDISPLAY=LINEARROW plot-options display arrowheads on
any error bars that are clipped by the RANGE= plot-option; if an entire error bar is cut from the
plot, the plot displays an arrowhead that points toward the statistic.

CLDISPLAY=BAR displays the confidence limits as bars. By default, the width of the bars
equals the size of the marker for the estimate. You can control the width of the bars and the
size of the marker by specifying the value of width as a percentage of the distance between bars,
0 < width <= 1. The bar might disappear when the value of width is very small.

COLUMN=1 | 2
specifies the table column to use to compute the risks (proportion) for the relative risk plot
(RELRISK PLOT) and the risk difference plot (RISKDIFFPLOT). If you specify COLUMN=1,
the plot displays the column 1 relative risks or the column 1 risk differences. Similarly, if you
specify COLUMN=2, the plot displays the column 2 relative risks or risk differences.

For relative risk plots, the default is COLUMN=1. For risk difference plots, the default is
COLUMN=1 if you request computation of both column 1 and column 2 risk differences by
specifying the RISKDIFF option. If you request computation of only the column 1 (or column
2) risk differences by specifying the RISKDIFF(COLUMN=1) (or RISKDIFF(COLUMN=2))
option, by default the risk difference plot displays the risk differences for the column that you
specify.

COMMON=NO | YES
controls the display of the common (overall) statistic in plots that display stratum (two-way table)
statistics for multiway tables. You can specify the COMMON= plot-option when you specify the
following plot-requests: KAPPAPLOT, ODDSRATIO PLOT, RELRISK PLOT, RISKDIFFPLOT,
and WTKAPPAPLOT.

COMMON=NO suppresses display of the common statistic and its confidence limits. By default,
COMMON=YES, which displays the common statistic and its confidence limits when these
values are available. For more information, see the descriptions of the plot-requests.

EXACT
requests display of exact confidence limits instead of asymptotic confidence limits. You can spec-
ify the EXACT plot-option when you specify the following plot-requests: ODDSRATIO PLOT,
RELRISK PLOT, and RISKDIFFPLOT. The EXACT plot-option is equivalent to the CL=EXACT
plot-option.

When you specify the EXACT plot-option, you must also request computation of exact confidence
limits by specifying the appropriate statistic-option in the EXACT statement.

GROUPBY=COLUMN | ROW
specifies the primary grouping for two-way frequency plots, which you can request by specifying
the FREQPLOT plot-request. The default is GROUPBY=COLUMN, which groups graph cells
first by column variable and displays row variable levels within column variable levels. You can
specify GROUPBY=ROW to group first by row variable. In two-way and multiway table requests, the column variable is the last variable specified and forms the columns of the crosstabulation table. The row variable is the next-to-last variable specified and forms the rows of the table.

By default for a bar chart that is displayed in the TWOWAY=STACKED layout, bars correspond to the column variable levels, and row levels are displayed (stacked) within each column bar. By default for a bar chart that is displayed in the TWOWAY=CLUSTER layout, bars are first grouped by column variable levels, and row levels are displayed as adjacent bars within each column-level group. You can reverse the default row and column variable grouping by specifying GROUPBY=ROW.

LOGBASE=2 | E | 10
applies to the odds ratio plot (ODDSRATIO PLOT) and the relative risk plot (RELRISK PLOT). This plot-option displays the odds ratio or relative risk axis on the log scale that you specify.

LEGEND=NO | YES
applies to the agreement plot (AGREE PLOT). LEGEND=NO suppresses the legend that identifies the areas of exact and partial agreement. The default is LEGEND=YES.

NOSTAT
applies to the deviation plot (DEVIATION PLOT). NOSTAT suppresses the chi-square p-value that deviation plot displays by default.

NPANELPOS=n
divides the plot into multiple panels that display at most |n| statistics or sections.

If n is positive, the number of statistics or sections per panel is balanced; if n is negative, the number of statistics per panel is not balanced. For example, suppose you want to display 21 odds ratios. NPANELPOS=20 displays two panels, the first with 11 odds ratios and the second with 10 odds ratios; NPANELPOS=−20 displays 20 odds ratios in the first panel but only 1 odds ratio in the second panel. This plot-option is available for all plots except mosaic plots and one-way weighted frequency plots.

For two-way frequency plots (FREQ PLOT), NPANELPOS=n requests that panels display at most |n| sections, where sections correspond to row or column variable levels, depending on the type of plot and the grouping. By default, n=4 and each panel includes at most four sections. This plot-option applies to two-way plots that are displayed in the TWOWAY=GROUPVERTICAL or TWOWAY=GROUPHORIZONTAL layout. The NPANELPOS= plot-option does not apply to the TWOWAY=CLUSTER and TWOWAY=STACKED layouts, which are always displayed in a single panel.

For plots that display statistics along with confidence limits, NPANELPOS=n requests that panels display at most |n| statistics. By default, n=0 and all statistics are displayed in a single panel. This plot-option applies to the following plots: KAPPAPLOT, ODDS RATIO PLOT, RELRISK PLOT, RISKDIFF PLOT, and WTKAPPAPLOT.

ORDER=ASCENDING | DESCENDING
displays the two-way table (strata) statistics in order of the statistic value. You can specify the ORDER= plot-option when you specify the following plot-requests: KAPPAPLOT, ODDS RATIO PLOT, RELRISK PLOT, RISKDIFF PLOT, and WTKAPPAPLOT.
If you specify ORDER=ASCENDING or ORDER=DESCENDING, the plot displays the statistics in ascending or descending order, respectively. By default, the order of the statistics in the plot matches the order that the two-way table strata appear in the multiway table display.

**ORIENT=HORIZONTAL | VERTICAL**

controls the orientation of the plot. You can specify the ORIENT= plot-option when you specify the following plot-requests: CUMFREQPLOT, DEVIATIONPLOT, and FREQPLOT.

ORIENT=HORIZONTAL places the variable levels on the Y axis and the frequencies, percentages, or statistic values on the X axis. ORIENT=VERTICAL places the variable levels on the X axis. The default orientation is ORIENT=VERTICAL for bar charts (TYPE=BARCHART) and ORIENT=HORIZONTAL for dot plots (TYPE=DOTPLOT).

**PARTIAL=NO | YES**

controls the display of partial agreement in the agreement plot (AGREEPLOT). PARTIAL=NO suppresses the display of partial agreement. When you specify PARTIAL=NO, the agreement plot displays only exact agreement. Exact agreement includes the diagonal cells of the square table, where the row and column variable levels are the same. Partial agreement includes the adjacent off-diagonal table cells, where the row and column values are within one level of exact agreement. The default is PARTIAL=YES.

**RANGE=(<min>, <max>) | CLIP**

specifies the range of values to display. You can specify the RANGE= plot-option when you specify the following plot-requests: KAPPAPLOT, ODDSRATIOPLOT, RELRISKPLOT, RISKDIFFPLOT, and WTKAPPAPLOT.

If you specify RANGE=CLIP, the confidence limits are clipped and the display range is determined by the minimum and maximum values of the statistics. By default, the display range includes all confidence limits.

**SCALE=FREQ | GROUPPERCENT | LOG | PERCENT | SQRT**

specifies the scale of the frequencies to display. This plot-option is available for frequency plots (FREQPLOT) and cumulative frequency plots (CUMFREQPLOT).

The default is SCALE=FREQ, which displays unscaled frequencies. SCALE=PERCENT displays percentages (relative frequencies) of the total frequency. SCALE=LOG displays log (base 10) frequencies. SCALE=SQRT displays square roots of the frequencies, producing a plot known as a rootogram.

SCALE=GROUPPERCENT is available for two-way frequency plots. This option displays the row or column percentages instead of the overall percentages (of the table frequency). By default (or when you specify the GROUPBY=COLUMN plot-option), SCALE=GROUPPERCENT displays the column percentages. If you specify the GROUPBY=ROW plot-option, the primary grouping of graph cells is by row variable level and the plot displays row percentages. For more information, see the description of the GROUPBY= plot-option.

**SHOWSCALE=NO | YES**

controls the display of the cumulative frequency scale on the right side of the agreement plot (AGREEPLOT). SHOWSCALE=NO suppresses the display of the scale. The default is SHOWSCALE=YES.
STATS

displays statistic values in the plot. For the following plot-requests, the STATS plot-option displays the statistics and their confidence limits on the right side of the plot: KAPPAPLOT, ODDSRATIO PLOT, RELRISK PLOT, RISKDIFF PLOT, and WTKAPPAPLOT.

For the agreement plot (AGREEPLOT), the STATS plot-option displays the values of the kappa statistic, the weighted kappa statistic, the $B_n$ measure (Bangdiwala and Bryan 1987), and the sample size. PROC FREQTAB stores these statistics in an ODS table named BNMeasure, which is not displayed. For more information, see the section “ODS Table Names” on page 282.

If you do not request the STATS plot-option, these plots do not display the statistic values.

TWOWAY=CLUSTER | GROUPHORIZONTAL | GROUPVERTICAL | STACKED

specifies the layout for two-way frequency plots.

All TWOWAY= layouts are available for bar charts (TYPE=BARCHART). All TWOWAY= layouts except TWOWAY=CLUSTER are available for dot plots (TYPE=DOTPLOT). The ORIENT= and GROUPBY= plot-options are available for all TWOWAY= layouts.

The default two-way layout is TWOWAY=GROUPVERTICAL, which produces a grouped plot that has a vertical common baseline. By default for bar charts (TYPE=BARCHART, ORIENT=VERTICAL), the X axis displays column variable levels, and the Y axis displays frequencies. The plot includes a vertical (Y-axis) block for each row variable level. The relative positions of the graph cells in this plot layout are the same as the relative positions of the table cells in the crosstabulation table. You can reverse the default row and column grouping by specifying the GROUPBY=ROW plot-option.

The TWOWAY=GROUPHORIZONTAL layout produces a grouped plot that has a horizontal common baseline. By default (GROUPBY=COLUMN), the plot displays a block on the X axis for each column variable level. Within each column-level block, the plot displays row variable levels.

The TWOWAY=STACKED layout produces stacked displays of frequencies. By default (GROUPBY=COLUMN) in a stacked bar chart, the bars correspond to column variable levels, and row levels are stacked within each column level. By default in a stacked dot plot, the dotted lines correspond to column levels, and cell frequencies are plotted as data dots on the corresponding column line. The dot color identifies the row level.

The TWOWAY=CLUSTER layout, which is available only for bar charts, displays groups of adjacent bars. By default, the primary grouping is by column variable level, and row levels are displayed within each column level.

You can reverse the default row and column grouping in any layout by specifying the GROUPBY=ROW plot-option. The default is GROUPBY=COLUMN, which groups first by column variable.

TYPE=BARCHART | DOTPLOT

specifies the plot type (format) of the frequency (FREQPLOT), cumulative frequency (CUMFREQPLOT), and deviation plots (DEVIATIONPLOT). TYPE=BARCHART produces a bar chart and TYPE=DOTPLOT produces a dot plot. The default is TYPE=BARCHART.
PRINTKWTS displays the agreement weights that PROC FREQTAB uses to compute the weighted kappa coefficient. Agreement weights reflect the relative agreement between pairs of variable levels. By default, PROC FREQTAB uses the Cicchetti-Allison form of agreement weights. If you specify the AGREE(WT=FC) option, the procedure uses the Fleiss-Cohen form of agreement weights. For more information, see the section “Weighted Kappa Coefficient” on page 252.

This option has no effect unless you also specify the AGREE option to compute the weighted kappa coefficient. The PRINTKWTS option is equivalent to the AGREE(PRINTKWTS) option.

RELRISK <(relrisk-options)>
requests relative risk measures and their confidence limits for $2 \times 2$ tables. These measures include the odds ratio, the column 1 relative risk, and the column 2 relative risk. For more information, see the section “Odds Ratio and Relative Risks for $2 \times 2$ Tables” on page 236. By default, PROC FREQTAB displays the relative risk measures and their asymptotic Wald confidence limits in the “Odds Ratio and Relative Risks” table. You can also obtain this table by specifying the MEASURES option, which produces other measures of association in addition to the relative risks.

You can specify relrisk-options in parentheses after the RELRISK option to request tests and additional confidence limits for the column 1 or column 2 relative risk. Table 4.17 summarizes the relrisk-options.

When you request tests or additional confidence limit types for the relative risk, PROC FREQTAB does not display the “Odds Ratio and Relative Risks” table unless you also specify the PRINTALL relrisk-option.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COLUMN=1</td>
<td>2</td>
</tr>
<tr>
<td>PRINTALL</td>
<td>Displays “Odds Ratio and Relative Risks” table</td>
</tr>
<tr>
<td>Request Confidence Limits</td>
<td></td>
</tr>
<tr>
<td>CL=EXACT</td>
<td>Displays exact confidence limits</td>
</tr>
<tr>
<td>CL=LR</td>
<td>Requests likelihood ratio confidence limits</td>
</tr>
<tr>
<td>CL=SCORE</td>
<td>Requests score confidence limits</td>
</tr>
<tr>
<td>CL=WALD</td>
<td>Requests Wald confidence limits</td>
</tr>
<tr>
<td>CL=WALDMODIFIED</td>
<td>Requests Wald modified confidence limits</td>
</tr>
<tr>
<td>Request Tests</td>
<td></td>
</tr>
<tr>
<td>EQUAL(NULL=)</td>
<td>Requests an equality test</td>
</tr>
<tr>
<td>EQUIV</td>
<td>EQUIVALENCE</td>
</tr>
<tr>
<td>MARGIN=</td>
<td>Specifies the test margin</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the test method</td>
</tr>
<tr>
<td>NONINF</td>
<td>NONINFERIORITY</td>
</tr>
<tr>
<td>SUP</td>
<td>SUPERIORITY</td>
</tr>
</tbody>
</table>
You can specify the following `relrisk-options`:

```plaintext
CL=type | (types)
```
specifies confidence limit types for the relative risk. You can specify one or more types of confidence limits. When you specify only one type, you can omit the parentheses around the request. When you specify the `CL= relrisk-option`, PROC FREQTAB displays the confidence limits in the “Confidence Limits for the Relative Risk” table.

The `ALPHA=` option determines the level of the confidence limits that the `CL= relrisk-option` provides. By default, `ALPHA=0.05`, which produces 95% confidence limits for the relative risk.

You can specify the following types:

- **EXACT**
  displays exact unconditional confidence limits for the relative risk in the “Confidence Limits for the Relative Risk” table. (By default, PROC FREQTAB displays the exact confidence limits in a separate table.) You must also request computation of the exact confidence limits by specifying the `RELRISK` option in the EXACT statement. For more information, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

- **LR**
  **LIKELIHOOD RATIO**
  requests likelihood ratio confidence limits for the relative risk. For more information, see the subsection “Likelihood Ratio Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

- **SCORE <(CORRECT=NO)>**
  requests score confidence limits for the relative risk. For more information, see the subsection “Score Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240. If you specify `CORRECT=NO`, PROC FREQTAB provides the uncorrected form of the confidence limits.

- **WALD**
  requests asymptotic Wald confidence limits, which are based on a log transformation of the relative risk. For more information, see the subsection “Wald Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

- **WALDMODIFIED**
  requests Wald modified confidence limits for the odds ratio. For more information, see the subsection “Wald Modified Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240.

- **COLUMN=1 | 2**
  specifies the table column for which to compute the relative risk confidence limits (which you request by specifying the `CL= relrisk-option`) and the relative risk tests (EQUAL, EQUIV, NONINF, and SUP). By default, `COLUMN=1`.

  This option has no effect on the “Odds Ratio and Relative Risks” table, which displays both column 1 and column 2 relative risks.
EQUAL < (NULL=value)>
requests an equality test for the relative risk. For more information, see the subsection “Equality Test” in the section “Relative Risk Tests” on page 243. You can specify the test in the METHOD=relrisk-option, and you can specify the null hypothesis value of the relative risk in the NULL=option. The null value must be a positive number. By default, METHOD=WALD and NULL=1.

EQUIV
EQUIVALENCE
requests an equivalence test for the relative risk. For more information, see the subsection “Equivalence Test” in the section “Relative Risk Tests” on page 243. You can specify the test method in the METHOD=relrisk-option, and you can specify the test margins in the MARGIN=relrisk-option. By default, METHOD=WALD and MARGIN=(0.8,1.25).

MARGIN=value | (lower, upper)
specifies the margin for the noninferiority, superiority, and equivalence tests, which you request by specifying the NONINF, SUP, and EQUIV relrisk-options, respectively. By default, MARGIN=0.8 for noninferiority tests, MARGIN=1.25 for superiority tests, and MARGIN=(0.8,1.25) for equivalence tests.

For noninferiority and superiority tests, specify a single value in the MARGIN= option. The value must be a positive number. For a noninferiority test, the value should be less than 1; for a superiority test, the value should be greater than 1.

For an equivalence test, you can specify a single MARGIN= value, or you can specify both lower and upper values. All values must be positive numbers. If you specify a single value, PROC FREQTAB uses value as the lower margin and the inverse of value as the upper margin. If you specify both lower and upper values, the value of lower must be less than the value of upper.

METHOD=method
specifies the method to be used for the equality, equivalence, noninferiority, and superiority tests, which you request by specifying the EQUAL, EQUIV, NONINF, and SUP relrisk-options, respectively. By default, METHOD=WALD.

You can specify one of the following methods:

FM
SCORE
requests Farrington-Manning (score) tests for the equality, equivalence, noninferiority, and superiority analyses of the relative risk. For more information, see the subsection “Farrington-Manning (Score) Test” in the section “Relative Risk Tests” on page 243.

LR
LIKELIHOODRATIO
requests likelihood ratio tests for the equality, equivalence, noninferiority, and superiority analyses of the relative risk. For more information, see the subsection “Likelihood Ratio Test” in the section “Relative Risk Tests” on page 243.

WALD
requests Wald tests for the equality, equivalence, noninferiority, and superiority analyses of the relative risk. For more information, see the subsection “Wald Test” in the section “Relative Risk Tests” on page 243.
Chapter 4: The FREQTAB Procedure

WALDMODIFIED
requests Wald modified tests for the equality, equivalence, noninferiority, and superiority analyses of the relative risk. For more information, see the subsection “Wald Modified Test” in the section “Relative Risk Tests” on page 243.

NONINF
NONINFERIORITY
requests a noninferiority test for the relative risk. For more information, see the subsection “Noninferiority Test” in the section “Relative Risk Tests” on page 243. You can specify the test method in the METHOD= RELRISK-OPTION, and you can specify the margin in the MARGIN= RELRISK-OPTION. By default, METHOD=WALD and MARGIN=0.8.

PRINTALL
displays the “Odds Ratio and Relative Risks” table when you request tests or additional confidence limits by specifying RELRISK-OPTIONS. By default, PROC FREQTAB does not display this table when you request tests or additional confidence limits for the relative risk.

SUP
SUPERIORITY
requests a superiority test for the relative risk. For more information, see the subsection “Superiority Test” in the section “Relative Risk Tests” on page 243. You can specify the test method in the METHOD= RELRISK-OPTION, and you can specify the margin in the MARGIN= RELRISK-OPTION. By default, METHOD=WALD and MARGIN=1.25.

RISKDIFF < (riskdiff-options) >
requests risks (binomial proportions) and risk differences for 2 × 2 tables. By default, this option provides the row 1 risk, row 2 risk, total (overall) risk, and risk difference (row 1 – row 2), together with their asymptotic standard errors and Wald confidence limits; by default, this option also provides exact (Clopper-Pearson) confidence limits for the row 1, row 2, and total risks. You can request exact unconditional confidence limits for the risk difference by specifying the RISKDIFF option in the EXACT statement. PROC FREQTAB displays these results in the column 1 and column 2 “Risk Estimates” tables (which you can suppress by specifying the NORISKS riskdiff-option).

You can specify riskdiff-options in parentheses after the RISKDIFF option to request tests and additional confidence limits for the risk difference, in addition to estimates of the common risk difference for multiway 2 × 2 tables. Table 4.18 summarizes the riskdiff-options.

The CL= riskdiff-option requests confidence limits for the risk difference. Available confidence limit types include Agresti-Caffo, exact unconditional, Hauck-Anderson, Miettinen-Nurminen (score), Newcombe, and Wald. Continuity-corrected Newcombe and Wald confidence limits are also available. You can request more than one type of confidence limits in the same analysis. PROC FREQTAB displays the confidence limits in the “Confidence Limits for the Risk Difference” table.

The CL=EXACT riskdiff-option displays exact unconditional confidence limits in the “Confidence Limits for the Risk Difference” table. When you specify CL=EXACT, you must also request computation of the exact confidence limits by specifying the RISKDIFF option in the EXACT statement.

The EQUAL, EQUIV, NONINF, and SUP riskdiff-options request tests of equality, equivalence, noninferiority, and superiority, respectively, for the risk difference. Available test methods include Farrington-Manning (score), Hauck-Anderson, and Wald. Newcombe (hybrid-score) confidence limits are available for the equivalence, noninferiority, and superiority analyses.
As part of the noninferiority, superiority, and equivalence analyses, PROC FREQTAB provides null-based equivalence limits that have a confidence coefficient of $100(1 - 2\alpha)\%$ (Schuirmann 1999). The ALPHA= option determines the confidence level; by default, ALPHA=0.05, which produces 90% equivalence limits for these analyses. For more information, see the sections “Noninferiority Tests” on page 228 and “Equivalence Test” on page 231.

### Table 4.18  RISKDIFF (Proportion Difference) Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COLUMN=1</td>
<td>2</td>
</tr>
<tr>
<td>COMMON</td>
<td>Requests common risk difference</td>
</tr>
<tr>
<td>CORRECT</td>
<td>Requests continuity correction</td>
</tr>
<tr>
<td>NORISKS</td>
<td>Suppresses default risk tables</td>
</tr>
<tr>
<td><strong>Request Confidence Limits</strong></td>
<td></td>
</tr>
<tr>
<td>CL=AC</td>
<td>Requests Agresti-Caffo confidence limits</td>
</tr>
<tr>
<td>CL=EXACT</td>
<td>Displays exact confidence limits</td>
</tr>
<tr>
<td>CL=HA</td>
<td>Requests Hauck-Anderson confidence limits</td>
</tr>
<tr>
<td>CL=MN</td>
<td>SCORE</td>
</tr>
<tr>
<td>CL=NEWCOMBE</td>
<td>Requests Newcombe confidence limits</td>
</tr>
<tr>
<td>CL=WALD</td>
<td>Requests Wald confidence limits</td>
</tr>
<tr>
<td><strong>Request Tests</strong></td>
<td></td>
</tr>
<tr>
<td>EQUAL(NULL=)</td>
<td>Requests an equality test</td>
</tr>
<tr>
<td>EQUIV</td>
<td>EQUIVALENCE</td>
</tr>
<tr>
<td>MARGIN=</td>
<td>Specifies the test margin</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the test method</td>
</tr>
<tr>
<td>NONINF</td>
<td>NONINFERIORITY</td>
</tr>
<tr>
<td>SUP</td>
<td>SUPERIORITY</td>
</tr>
<tr>
<td>VAR=SAMPLE</td>
<td>NULL</td>
</tr>
</tbody>
</table>

You can specify the following riskdiff-options:

**CL=type | (types)**
requests confidence limits for the risk difference. You can specify one or more types of confidence limits. When you specify only one type, you can omit the parentheses around the request. PROC FREQTAB displays the confidence limits in the “Confidence Limits for the Risk Difference” table.

The ALPHA= option determines the level of the confidence limits. By default, ALPHA=0.05, which produces 95% confidence limits for the risk difference.

You can specify the CL= riskdiff-option with or without requests for risk difference tests. The confidence limits that CL= produces do not depend on the tests that you request and do not use the value of the test margin (which you can specify in the MARGIN= riskdiff-option).

You can specify the following types:
AC
AGRESTICAFFO
requests Agresti-Caffo confidence limits for the risk difference. For more information, see the subsection “Agresti-Caffo Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

EXACT
displays exact unconditional confidence limits for the risk difference in the “Confidence Limits for the Risk Difference” table. You must also request computation of the exact confidence limits by specifying the RISKDIFF option in the EXACT statement.

By default, PROC FREQTAB computes the exact confidence limits by inverting two separate one-sided exact tests that are based on the score statistic. For more information, see the RISKDIFF option in the EXACT statement and the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

By default, PROC FREQTAB also displays these exact confidence limits in the “Risk Estimates” table. You can suppress this table by specifying the NORISKS riskdiff-option.

HA
requests Hauck-Anderson confidence limits for the risk difference. For more information, see the subsection “Hauck-Anderson Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

MN < (CORRECT=NO | MEE) >
SCORE < (CORRECT=NO | MEE) >
requests Miettinen-Nurminen (score) confidence limits for the risk difference. For more information, see the subsection “Miettinen-Nurminen (Score) Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224. By default, the Miettinen-Nurminen confidence limits include a bias correction factor (Miettinen and Nurminen 1985; Newcombe and Nurminen 2011). If you specify CL=MN(CORRECT=NO), PROC FREQTAB provides the uncorrected form of the confidence limits (Mee 1984).

NEWCOMBE < (CORRECT) >
requests Newcombe hybrid-score confidence limits for the risk difference. If you specify CL=NEWCOMBE(CORRECT) or the CORRECT riskdiff-option, the Newcombe confidence limits include a continuity correction. For more information, see the subsection “Newcombe Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

WALD < (CORRECT) >
requests Wald confidence limits for the risk difference. If you specify CL=WALD(CORRECT) or the CORRECT riskdiff-option, the Wald confidence limits include a continuity correction. For more information, see the subsection “Wald Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

COLUMN=1 | 2 | BOTH
specifies the table column for which to compute the risk difference tests (EQUAL, EQUIV, NONINF, and SUP) and the risk difference confidence limits (which you request by specifying the CL= riskdiff-option). By default, COLUMN=1.
This option has no effect on the “Risk Estimates” table, which is produced for both column 1 and column 2. You can suppress the “Risk Estimates” table by specifying the **NORISKS** riskdiff-option.

**COMMON**
requests estimates of the common (overall) risk difference for multiway 2 × 2 tables. This option provides Mantel-Haenszel and summary score estimates for the common risk difference, together with their confidence limits. If you specify the **RISKDIFF(CL=NEWCOMBE)** option, the **RISKDIFF(COMMON)** option also provides Newcombe confidence limits for the common risk difference. For more information, see the section “Common Risk Difference” on page 232.

You can use the **COMMONRISKDIFF** option to request additional confidence limits and tests for the common risk difference.

If you do not specify the COLUMN= riskdiff-option, PROC FREQTAB provides the common risk difference for column 1 by default. If you specify COLUMN=2, PROC FREQTAB provides the common risk difference for column 2. COLUMN=BOTH does not apply to the common risk difference.

**CORRECT**
includes a continuity correction in the Wald confidence limits, Wald tests, and Newcombe confidence limits. For more information, see the section “Risks and Risk Differences” on page 222.

**EQUAL < (NULL=value)>**
requests an equality test for the risk difference. For more information, see the section “Equality Tests” on page 228. You can specify the test method in the METHOD= riskdiff-option, and you can specify the null hypothesis value of the risk difference in the NULL= option. By default, METHOD=WALD and NULL=0. You can specify the null value in proportion form as a number between −1 and 1, or you can specify the null value in percentage form as a number between −100 and 100. When the value is between −100 and −1 or between 1 and 100, PROC FREQTAB converts the number to a proportion. PROC FREQTAB treats the values −1 and 1 as percentages.

**EQUIV**
requests an equivalence test for the risk difference. For more information, see the section “Equivalence Test” on page 231. You can specify the test method in the METHOD= riskdiff-option, and you can specify the margins in the MARGIN= riskdiff-option. By default, METHOD=WALD and MARGIN=0.2.

**MARGIN=value | (lower, upper)**
specifies the margin for the noninferiority, superiority, and equivalence tests, which you request by specifying the **NONINF**, **SUP**, and **EQUIV** riskdiff-options, respectively. By default, MARGIN=0.2.

For noninferiority and superiority tests, specify a single value in the MARGIN= option. The value must be a positive number. You can specify value as a number between 0 and 1. Or you can specify value in percentage form as a number between 1 and 100, and PROC FREQTAB converts that number to a proportion. PROC FREQTAB treats the value 1 as 1%.

For an equivalence test, you can specify a single MARGIN= value, or you can specify both lower and upper values. If you specify a single value, it must be a positive number, as described
If you specify a single value for an equivalence test, PROC FREQTAB uses \(-value\) as the lower margin and \(value\) as the upper margin for the test. If you specify both lower and upper values for an equivalence test, you can specify them in proportion form as numbers between \(-1\) and \(1\). Or you can specify them in percentage form as numbers between \(-100\) and \(100\), and PROC FREQTAB converts the numbers to proportions. The value of lower must be less than the value of upper.

**METHOD=method**
specifies the method to be used for the equality, equivalence, noninferiority, and superiority tests, which you request by specifying the EQUAL, EQUIV, NONINF, and SUP riskdiff-options, respectively. By default, METHOD=WALD.

You can specify the following methods:

**FM**
requests Farrington-Manning (score) tests for the equality, equivalence, noninferiority, and superiority analyses. For more information, see the subsection “Farrington-Manning (Score) Test” in the section “Noninferiority Tests” on page 228.

**HA**
requests Hauck-Anderson tests for the equality, equivalence, noninferiority, and superiority analyses. For more information, see the subsection “Hauck-Anderson Test” in the section “Noninferiority Tests” on page 228.

**NEWCOMBE**
requests Newcombe (hybrid-score) confidence limits for the equivalence, noninferiority, and superiority analyses. If you specify the CORRECT riskdiff-option, the Newcombe confidence limits include a continuity correction. For more information, see the subsection “Newcombe Noninferiority Analysis” in the section “Noninferiority Tests” on page 228.

**WALD**
requests Wald tests for the equality, equivalence, noninferiority, and superiority analyses. If you specify the CORRECT riskdiff-option, the Wald tests and confidence limits include a continuity correction. If you specify the VAR=NULL riskdiff-option, the tests use the null (test-based) variance instead of the sample variance. For more information, see the subsection “Wald Test” in the section “Noninferiority Tests” on page 228.

**NONINF**
requests a noninferiority test for the risk difference. For more information, see the section “Noninferiority Tests” on page 228. You can specify the test method in the METHOD= riskdiff-option, and you can specify the margin in the MARGIN= riskdiff-option. By default, METHOD=WALD and MARGIN=0.2.

**NORISKS**
suppresses display of the “Risk Estimates” tables, which the RISKDIFF option produces by default for column 1 and column 2. The “Risk Estimates” tables contain the risks and risk differences, together with their asymptotic standard errors, Wald confidence limits, and exact confidence limits.
SUP

SUPERIORITY
requests a superiority test for the risk difference. For more information, see the section “Superiority Test” on page 230. You can specify the test method in the METHOD= riskdiff-option, and you can specify the margin in the MARGIN= riskdiff-option. By default, METHOD=WALD and MARGIN=0.2.

VAR=NULL | SAMPLE
specifies the type of variance to use in the Wald tests of equality, equivalence, noninferiority, and superiority. If you specify VAR=SAMPLE, PROC FREQTAB uses the sample variance. If you specify VAR=NULL, PROC FREQTAB uses a test-based variance that is computed by using the null hypothesis value of the risk difference. For more information, see the sections “Equality Tests” on page 228 and “Noninferiority Tests” on page 228. The default is VAR=SAMPLE.

SCORES=type
specifies the type of row and column scores that PROC FREQTAB uses to compute the following statistics: Mantel-Haenszel chi-square, Pearson correlation, Cochran-Armitage test for trend, weighted kappa coefficient, and Cochran-Mantel-Haenszel statistics. The value of type can be one of the following:

- MODRIDIT
- RANK
- RIDIT
- TABLE

See the section “Scores” on page 198 for descriptions of these score types.

If you do not specify the SCORES= option, PROC FREQTAB uses SCORES=TABLE by default. For character variables, the row and column TABLE scores are the row and column numbers. That is, the TABLE score is 1 for row 1, 2 for row 2, and so on. For numeric variables, the row and column TABLE scores equal the variable values. For more information, see the section “Scores” on page 198. Using MODRIDIT, RANK, or RIDIT scores yields nonparametric analyses.

You can use the SCOROUT option to display the row and column scores.

SCOROUT
displays the row and column scores that PROC FREQTAB uses to compute score-based tests and statistics. You can specify the score type by using the SCORES= option. For more information, see the section “Scores” on page 198.

The scores are computed and displayed only when PROC FREQTAB computes statistics for two-way tables. You can use ODS to store the scores in an output data set. See the section “ODS Table Names” on page 282 for more information.

TOTPCT
displays the percentage of the total multiway table frequency in multiway crosstabulation tables (n-way tables where n > 2). By default, PROC FREQTAB displays the percentage of the individual two-way table (stratum) frequency but does not display the percentage of the overall total frequency. For more information, see the section “Two-Way and Multiway Tables” on page 274.
By default, tables in list format (which you can request by specifying the LIST option) display the percentage of the total multiway table frequency. The variable PERCENT in the OUT= output data set also provides the percentage of the total multiway table frequency.

**TREND**
requests the Cochran-Armitage test for trend. The table must be $2 \times C$ or $R \times 2$ to compute the trend test. For more information, see the section “Cochran-Armitage Test for Trend” on page 246. To request exact $p$-values for the trend test, specify the TREND option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

**TEST Statement**

```
TEST test-options;
```

The TEST statement requests asymptotic tests for measures of association and measures of agreement. The test-options identify which tests to compute. Table 4.19 lists the available test-options, together with their corresponding TABLES statement options. Descriptions of the test-options follow the table in alphabetical order.

For each measure of association or agreement that you request in the TEST statement, PROC FREQTAB provides an asymptotic test that the measure is 0. The procedure displays the asymptotic standard error under the null hypothesis, the test statistic, and the one-sided and two-sided $p$-values. PROC FREQTAB also provides confidence limits for the measure. The ALPHA= option in the TABLES statement determines the confidence level; by default, ALPHA=0.05, which provides 95% confidence limits. For more information, see the sections “Asymptotic Tests” on page 205 and “Confidence Limits” on page 205. For information about the individual measures, see the sections “Measures of Association” on page 204 and “Tests and Measures of Agreement” on page 249.

You can also request exact tests for selected measures of association and agreement by using the EXACT statement. For more information, see the section “Exact Statistics” on page 265.

**Using the TEST Statement with the TABLES Statement**

You must use a TABLES statement with the TEST statement. If you use only one TABLES statement, you do not need to specify the same options in both the TABLES and TEST statements; when you specify an option in the TEST statement, PROC FREQTAB automatically invokes the corresponding TABLES statement option. However, when you use the TEST statement with multiple TABLES statements, you must specify options in the TABLES statements to request statistics; PROC FREQTAB then provides asymptotic tests for those statistics that you specify in the TEST statement.
You can specify the following test-options in the TEST statement.

AGREE
requests asymptotic tests for the simple kappa coefficient and the weighted kappa coefficient. For more information, see the sections “Simple Kappa Coefficient” on page 251 and “Weighted Kappa Coefficient” on page 252.

By default, these tests are based on null values of 0; you can specify nonzero null values for the simple kappa and weighted kappa tests by using the AGREE(NULLKAPPA=) and AGREE(NULLWTKAPPA=) options, respectively, in the TABLES statement.

The AGREE option in the TABLES statement provides estimates, standard errors, and confidence limits for kappa coefficients. You can request exact tests for kappa coefficients by using the EXACT statement.

Kappa coefficients are defined only for square tables, where the number of rows equals the number of columns. Kappa coefficients are not computed for tables that are not square. For $2 \times 2$ tables, the weighted kappa coefficient is identical to the simple kappa coefficient, and PROC FREQTAB presents only the simple kappa coefficient.

GAMMA
requests an asymptotic test for the gamma statistic. For more information, see the section “Gamma” on page 206. The MEASURES option in the TABLES statement provides the gamma statistic and its asymptotic standard error.

KAPPA
requests an asymptotic test for the simple kappa coefficient. For more information, see the section “Simple Kappa Coefficient” on page 251.

By default, the null value of kappa for this test is 0; you can specify a nonzero null value by using the AGREE(NULLKAPPA=) option in the TABLES statement.
Chapter 4: The FREQTAB Procedure

The AGREE option in the TABLES statement provides the kappa statistic, its standard error, and its confidence limits. You can request an exact test for the simple kappa coefficient by specifying the KAPPA option in the EXACT statement.

Kappa coefficients are defined only for square tables, where the number of rows equals the number of columns. PROC FREQTAB does not compute kappa coefficients for tables that are not square.

KENTB requests an asymptotic test for Kendall’s tau-b. For more information, see the section “Kendall’s Tau-b” on page 206.

The MEASURES option in the TABLES statement provides Kendall’s tau-b and its standard error. You can request an exact test for Kendall’s tau-b by specifying the KENTB option in the EXACT statement.

MEASURES requests asymptotic tests for the following measures of association: gamma, Kendall’s tau-b, Pearson correlation coefficient, Somers’ \text{D(C|R)}, Somers’ \text{D(R|C)}, Spearman correlation coefficient, and Stuart’s tau-c. For more information, see the section “Measures of Association” on page 204.

The MEASURES option in the TABLES statement provides measures of association and their asymptotic standard errors. You can request exact tests for selected measures by using the EXACT statement.

PCORR requests an asymptotic test for the Pearson correlation coefficient. For more information, see the section “Pearson Correlation Coefficient” on page 208.

The MEASURES option in the TABLES statement provides the Pearson correlation and its standard error. You can request an exact test for the Pearson correlation by specifying the PCORR option in the EXACT statement.

PLCORR requests Wald and likelihood ratio tests for the polychoric correlation coefficient. For more information, see the section “Polychoric Correlation” on page 211.

The PLCORR option in the TABLES statement provides the polychoric correlation and its standard error.

SCORR requests an asymptotic test for the Spearman correlation coefficient. For more information, see the section “Spearman Rank Correlation Coefficient” on page 209.

The MEASURES option in the TABLES statement provides the Spearman correlation and its standard error. You can request an exact test for the Spearman correlation by specifying the SCORR option in the EXACT statement.

SMDCR requests an asymptotic test for Somers’ \text{D(C|R)}. For more information, see the section “Somers’ \text{D}” on page 208.

The MEASURES option in the TABLES statement provides Somers’ \text{D(C|R)} and its standard error. You can request an exact test for Somers’ \text{D(C|R)} by specifying the SMDCR option in the EXACT statement.
SMDRC
requests an asymptotic test for Somers’ \( D(R|C) \). For more information, see the section “Somers’ \( D \)” on page 208.

The MEASURES option in the TABLES statement provides Somers’ \( D(R|C) \) and its standard error. You can request an exact test for Somers’ \( D(R|C) \) by specifying the SMDRC option in the EXACT statement.

STUTC
TAUC
requests an asymptotic test for Stuart’s \( \tau_c \). For more information, see the section “Stuart’s \( \tau_c \)” on page 207.

The MEASURES option in the TABLES statement provides Stuart’s \( \tau_c \) and its standard error. You can request an exact test for Stuart’s \( \tau_c \) by specifying the STUTC option in the EXACT statement.

WTKAPPA
WTKAP
requests an asymptotic test for the weighted kappa coefficient. For more information, see the section “Weighted Kappa Coefficient” on page 252.

By default, the null value of weighted kappa for this test is 0; you can specify a nonzero null value by using the AGREE(NULLWTKAPPA=) option in the TABLES statement.

The AGREE option in the TABLES statement provides the weighted kappa coefficient, its standard error, and confidence limits. You can request an exact test for the weighted kappa by specifying the WTKAPPA option in the EXACT statement.

Kappa coefficients are defined only for square tables, where the number of rows equals the number of columns. PROC FREQTAB does not compute kappa coefficients for tables that are not square. For \( 2 \times 2 \) tables, the weighted kappa coefficient is identical to the simple kappa coefficient, and PROC FREQTAB presents only the simple kappa coefficient.

WEIGHT Statement

WEIGHT variable < / option > ;

The WEIGHT statement names a numeric variable that provides a weight for each observation in the input data set. The WEIGHT statement is most commonly used to input cell count data. See the section “Inputting Frequency Counts” on page 194 for more information. If you use a WEIGHT statement, PROC FREQTAB assumes that an observation represents \( n \) observations, where \( n \) is the value of variable. The value of the WEIGHT variable is not required to be an integer.

If the value of the WEIGHT variable is missing, PROC FREQTAB does not use that observation in the analysis. If the value of the WEIGHT variable is 0, PROC FREQTAB ignores the observation unless you specify the ZEROS option, which includes observations that have weights of 0. If you do not specify a WEIGHT statement, PROC FREQTAB assigns a weight of 1 to each observation. The sum of the WEIGHT variable values represents the total number of observations.

If any value of the WEIGHT variable is negative, PROC FREQTAB displays the frequencies computed from the weighted values but does not compute percentages and statistics. If you create an output data set by using
the `OUT=` option in the TABLES statement, PROC FREQTAB assigns missing values to the PERCENT variable. PROC FREQTAB also assigns missing values to the variables that the OUTEXPECT and OUTPCT options provide. If any value of the WEIGHT variable is negative, you cannot create an output data set by using the `OUTPUT` statement because statistics are not computed when there are negative weights.

You can specify the following option in the WEIGHT statement:

**ZEROS**

includes observations that have weights of 0. By default, PROC FREQTAB ignores observations that have weights of 0.

If you specify the ZEROS option, frequency and crosstabulation tables display levels that contain only zero-weight observations. If you do not specify the ZEROS option, PROC FREQTAB does not process observations that have weights of 0 and therefore does not display levels that contain only zero-weight observations.

When you specify the ZEROS option, PROC FREQTAB includes zero-weight levels in chi-square tests and binomial computations for one-way tables. This makes it possible to compute binomial tests and estimates for a reference level that contains no observations with positive weights.

For two-way tables, the ZEROS option enables computation of kappa statistics when there are levels that contain no observations with positive weights. For more information, see the section “Tables with Zero-Weight Rows or Columns” on page 256.

Even when you specify the ZEROS option, PROC FREQTAB does not compute CHISQ or MEASURES statistics for two-way tables that contain a zero-weight row or column because most of these statistics are undefined in this case.

By default, the ZEROS option includes zero-weight table cells in the LIST table and the `OUT=` data set. To suppress zero-weight cells, you can specify the NOSPARSE option in the TABLES statement.

---

**Details: FREQTAB Procedure**

**Inputting Frequency Counts**

PROC FREQTAB can use either raw data or cell count data to produce frequency and crosstabulation tables. *Raw data*, also known as case-record data, report the data as one record for each subject or sample member. *Cell count data* report the data as a table, listing all possible combinations of data values along with the frequency counts. This way of presenting data often appears in published results.

The following DATA step statements store raw data in a SAS data set:

```sas
   data Raw;
      input Subject $ R C @@;
   datalines;
   01 1 1 02 1 1 03 1 1 04 1 1 05 1 1
   06 1 2 07 1 2 08 1 2 09 2 1 10 2 1
   11 2 1 12 2 1 13 2 2 14 2 2
   ;
```
You can store the same data as cell counts by using the following DATA step statements:

```plaintext
data CellCounts;
  input R C Count @@;
datalines;
  1 1 5 1 2 3
  2 1 4 2 2 3
;
```

The variable `R` contains the values for the rows, and the variable `C` contains the values for the columns. The variable `Count` contains the cell count for each row and column combination.

Both the Raw data set and the CellCounts data set produce identical frequency counts, two-way tables, and statistics. When using the CellCounts data set, you must include a WEIGHT statement to specify that the variable `Count` contains cell counts. For example, the following PROC FREQTAB statements create a two-way crosstabulation table by using the CellCounts data set:

```plaintext
proc freqtab data=CellCounts;
  tables R*C;
  weight Count;
run;
```

### Missing Values

If an observation has a missing value for the `WEIGHT` variable, PROC FREQTAB excludes that observation from the analysis.

If an observation has a missing value for a TABLES statement variable, by default PROC FREQTAB does not include that observation in the frequency or crosstabulation table (or in the frequency total, percentages, and statistics). PROC FREQTAB displays the frequency of missing values after the frequency or crosstabulation table.

PROC FREQTAB includes the frequency of missing values in the output data sets. The OUT= data set that you specify in the TABLES statement includes an observation that contains the frequency of missing values. The OUT= data set that you specify in the OUTPUT statement includes the frequency of missing values in the variable `NMISS` when you specify the NMISS option in the OUTPUT statement.

The following options change the way that PROC FREQTAB handles missing values of TABLES statement variables:

- **MISSPRINT** displays missing value frequencies in frequency tables but does not include them in computing percentages or statistics. This option is available for one-way frequency tables and for tables in list format (which you can request by specifying the `LIST` option in the TABLES statement).
- **MISSING** treats missing values as a valid nonmissing level for all TABLES statement variables. This option displays missing levels in frequency and crosstabulation tables and includes them in computing percentages and statistics.

This example shows the three ways that PROC FREQTAB can handle missing values of TABLES statement variables. The following DATA step statements create a data set that contains a missing value for the variable `A`:
The following PROC FREQTAB statements request a one-way frequency table for the variable A. The first request does not specify a missing value option. The second request specifies the MISSPRINT option in the PROC FREQTAB statement. The third request specifies the MISSING option in the PROC FREQTAB statement.

```sas
proc freqtab data=mycas.One;
   tables A;
   weight Freq;
   title 'Default';
run;
proc freqtab data=mycas.One missprint;
   tables A;
   weight Freq;
   title 'MISSPRINT Option';
run;
proc freqtab data=mycas.One missing;
   tables A;
   weight Freq;
   title 'MISSING Option';
run;
```

Figure 4.9 displays the frequency tables produced by this example. The first table shows PROC FREQTAB’s default behavior for handling missing values. The frequency table does not include the missing level of the TABLES statement variable A. PROC FREQTAB displays the frequency of missing values after the table.

The second table, for which the MISSPRINT option is specified, displays the missing level of A but does not include its frequency in computing the total frequency and percentages.

The third table, for which the MISSING option is specified, treats the missing level as a valid nonmissing level. The frequency table displays the missing level of A and includes its frequency in computing the total frequency and percentages.

**Figure 4.9** Missing Values in Frequency Tables

**Default**

<table>
<thead>
<tr>
<th>A</th>
<th>Frequency</th>
<th>Percent</th>
<th>Cumulative Frequency</th>
<th>Cumulative Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>50.00</td>
<td>2</td>
<td>50.00</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>50.00</td>
<td>4</td>
<td>100.00</td>
</tr>
</tbody>
</table>

Frequency Missing = 2
When a combination of variable levels in a two-way table is missing, PROC FREQTB assigns 0 to the frequency count of the corresponding table cell. The default crosstabulation table and the CROSSLIST crosstabulation table display table cells that have frequencies of 0.

By default, the LIST crosstabulation table and the OUT= output data set do not include table cells that have frequencies of 0. If you specify the ZEROS option in the WEIGHT statement to include observations that have weights of 0, the LIST table and the OUT= output data set include zero-frequency table cells by default unless you specify the NOSPARSE option in the TABLES statement.

Statistical Computations
Definitions and Notation

A two-way table represents the crosstabulation of row variable X and column variable Y. Let the table row values or levels be denoted by \( X_i, i = 1, 2, \ldots, R \), and the column values by \( Y_j, j = 1, 2, \ldots, C \). Let \( n_{ij} \) denote the frequency of the table cell in the \( i \)th row and \( j \)th column and define the following notation:

\[
\begin{align*}
\quad n_i &= \sum_j n_{ij} \quad \text{(row totals)} \\
\quad n_j &= \sum_i n_{ij} \quad \text{(column totals)} \\
\quad n &= \sum_i \sum_j n_{ij} \quad \text{(overall total)} \\
\quad p_{ij} &= \frac{n_{ij}}{n} \quad \text{(cell percentages)} \\
\quad p_i &= \frac{n_i}{n} \quad \text{(row percentages of total)} \\
\quad p_j &= \frac{n_j}{n} \quad \text{(column percentages of total)}
\end{align*}
\]
$R_i = \text{score for row } i$
$C_j = \text{score for column } j$

$\bar{R} = \sum_i n_i R_i / n$ (average row score)

$\bar{C} = \sum_j n_j C_j / n$ (average column score)

$A_{ij} = \sum_{k<i} \sum_{l>j} n_{kl} + \sum_{k<i} \sum_{l<j} n_{kl}$

$D_{ij} = \sum_{k>i} \sum_{l<j} n_{kl} + \sum_{k<i} \sum_{l>j} n_{kl}$

$P = \sum_i \sum_j n_{ij} A_{ij}$ (twice the number of concordances)

$Q = \sum_i \sum_j n_{ij} D_{ij}$ (twice the number of discordances)

**Scores**

PROC FREQTAB uses scores of the variable values to compute the Mantel-Haenszel chi-square, Pearson correlation, Cochran-Armitage test for trend, weighted kappa coefficient, and Cochran-Mantel-Haenszel statistics. The SCORES= option in the TABLES statement specifies the score type that PROC FREQTAB uses. The available score types are TABLE, RANK, RIDIT, and MODRIDIT scores. The default score type is TABLE. Using MODRIDIT, RANK, or RIDIT scores yields nonparametric analyses.

For numeric variables, table scores are the values of the row and column levels. If the row or column variable is formatted, then the table score is the internal numeric value corresponding to that level. If two or more numeric values are classified into the same formatted level, then the internal numeric value for that level is the smallest of these values. For character variables, table scores are defined as the row numbers and column numbers (that is, 1 for the first row, 2 for the second row, and so on).

Rank scores, which you request with the SCORES=RANK option, are defined as

$$R_i^1 = \sum_{k<i} n_k + (n_i + 1)/2 \quad i = 1, 2, \ldots, R$$

$$C_j^1 = \sum_{l<j} n_l + (n_j + 1)/2 \quad j = 1, 2, \ldots, C$$

where $R_i^1$ is the rank score of row $i$, and $C_j^1$ is the rank score of column $j$. Note that rank scores yield midranks for tied values.

Ridit scores, which you request with the SCORES=RIDIT option, are defined as rank scores standardized by the sample size (Bross 1958; Mack and Skillings 1980). Ridit scores are derived from the rank scores as

$$R_i^2 = R_i^1 / n \quad i = 1, 2, \ldots, R$$

$$C_j^2 = C_j^1 / n \quad j = 1, 2, \ldots, C$$

Modified ridit scores (SCORES=MODRIDIT) represent the expected values of the order statistics of the uniform distribution on (0,1) (Van Elteren 1960; Lehmann and D’Abrera 2006). Modified ridit scores are
derived from rank scores as

\[ R_i^3 = R_i^1/(n + 1) \quad i = 1, 2, \ldots, R \]

\[ C_j^3 = C_j^1/(n + 1) \quad j = 1, 2, \ldots, C \]

### Chi-Square Tests and Statistics

The CHISQ option provides chi-square tests of homogeneity or independence and measures of association that are based on the chi-square statistic. When you specify the CHISQ option in the TABLES statement, PROC FREQTAB computes the following chi-square tests for each two-way table: Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square tests. PROC FREQTAB provides the following measures of association that are based on the Pearson chi-square statistic: phi coefficient, contingency coefficient, and Cramér’s V. For 2 × 2 tables, the CHISQ option also provides Fisher’s exact test and the continuity-adjusted chi-square statistic. You can request Fisher’s exact test for general \( R \times C \) tables by specifying the FISHER option in the TABLES or EXACT statement.

If you specify the CHISQ option for one-way tables, PROC FREQTAB provides a one-way Pearson chi-square goodness-of-fit test. If you specify the CHISQ(LRCHI) option for one-way tables, PROC FREQTAB also provides a one-way likelihood ratio chi-square test. The other tests and statistics that the CHISQ option produces are available only for two-way tables.

For two-way tables, the null hypothesis for the chi-square tests is no association between the row variable and the column variable. When the sample size \( n \) is large, the test statistics have asymptotic chi-square distributions under the null hypothesis. When the sample size is not large, or when the data set is sparse or heavily tied, exact tests might be more appropriate than asymptotic tests. PROC FREQTAB provides exact \( p \)-values for the Pearson chi-square, likelihood ratio chi-square, and Mantel-Haenszel chi-square tests, in addition to Fisher’s exact test. For one-way tables, PROC FREQTAB provides exact \( p \)-values for the Pearson and likelihood ratio chi-square goodness-of-fit tests. You can request these exact tests by specifying the corresponding options in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

The Mantel-Haenszel chi-square statistic is appropriate only when both variables lie on an ordinal scale. The other chi-square tests and statistics in this section are appropriate for either nominal or ordinal variables. The following sections give the formulas that PROC FREQTAB uses to compute the chi-square tests and statistics. For more information about these statistics, see Agresti (2007) and Stokes, Davis, and Koch (2012), and the other references cited.

### Chi-Square Test for One-Way Tables

For one-way frequency tables, the CHISQ option in the TABLES statement provides a chi-square goodness-of-fit test. Let \( C \) denote the number of classes, or levels, in the one-way table. Let \( f_i \) denote the frequency of class \( i \) (or the number of observations in class \( i \)) for \( i = 1, 2, \ldots, C \). Then PROC FREQTAB computes the one-way chi-square statistic as

\[ Q_P = \sum_{i=1}^{C} (f_i - e_i)^2 / e_i \]

where \( e_i \) is the expected frequency for class \( i \) under the null hypothesis.

In the test for equal proportions, which is the default for the CHISQ option, the null hypothesis specifies equal proportions of the total sample size for each class. Under this null hypothesis, the expected frequency
for each class equals the total sample size divided by the number of classes,

\[ e_i = \frac{n}{C} \quad \text{for } i = 1, 2, \ldots, C \]

In the test for specified frequencies, which PROC FREQTAB computes when you input null hypothesis frequencies by using the TESTF= option, the expected frequencies are the TESTF= values that you specify. In the test for specified proportions, which PROC FREQTAB computes when you input null hypothesis proportions by using the TESTP= option, the expected frequencies are determined from the specified TESTP= proportions \( p_i \) as

\[ e_i = p_i \times n \quad \text{for } i = 1, 2, \ldots, C \]

Under the null hypothesis (of equal proportions, specified frequencies, or specified proportions), \( Q_P \) has an asymptotic chi-square distribution with \( C-1 \) degrees of freedom.

In addition to the asymptotic test, you can request an exact one-way chi-square test by specifying the CHISQ option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

**Pearson Chi-Square Test for Two-Way Tables**

The Pearson chi-square for two-way tables involves the differences between the observed and expected frequencies, where the expected frequencies are computed under the null hypothesis of independence. The Pearson chi-square statistic is computed as

\[ Q_P = \sum_i \sum_j \frac{(n_{ij} - e_{ij})^2}{e_{ij}} \]

where \( n_{ij} \) is the observed frequency in table cell \((i, j)\) and \( e_{ij} \) is the expected frequency for table cell \((i, j)\). The expected frequency is computed under the null hypothesis that the row and column variables are independent,

\[ e_{ij} = \frac{(n_i, n_j)}{n} \]

When the row and column variables are independent, \( Q_P \) has an asymptotic chi-square distribution with \((R-1)(C-1)\) degrees of freedom. For large values of \( Q_P \), this test rejects the null hypothesis in favor of the alternative hypothesis of general association.

In addition to the asymptotic test, you can request an exact Pearson chi-square test by specifying the PCHI or CHISQ option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

For \(2 \times 2\) tables, the Pearson chi-square is also appropriate for testing the equality of two binomial proportions. For \(R \times 2\) and \(2 \times C\) tables, the Pearson chi-square tests the homogeneity of proportions. For more information, see Fienberg (1980).

**Standardized Residuals**

When you specify the CROSSLIST(STDRES) option in the TABLES statement for two-way or multiway tables, PROC FREQTAB displays the standardized residuals in the CROSSLIST table.

The standardized residual of a crosstabulation table cell is the ratio of \((\text{frequency} - \text{expected})\) to its standard error, where \text{frequency} is the table cell frequency and \text{expected} is the estimated expected cell frequency. The expected frequency is computed under the null hypothesis that the row and column variables are independent. See the section “Pearson Chi-Square Test for Two-Way Tables” on page 200 for more information.
PROC FREQTAB computes the standardized residual of table cell \((i, j)\) as

\[
\frac{(n_{ij} - e_{ij})}{\sqrt{e_{ij}(1 - p_i)(1 - p_j)}},
\]

where \(n_{ij}\) is the observed frequency of table cell \((i, j)\), \(e_{ij}\) is the expected frequency of the table cell, \(p_i\) is the proportion in row \(i (n_i/n)\), and \(p_j\) is the proportion in column \(j (n_j/n)\). The expected frequency of table cell \((i, j)\) is computed as

\[
e_{ij} = \frac{(n_i, n_j)}{n}
\]

Under the null hypothesis of independence, each standardized residual has an asymptotic standard normal distribution. See section 2.4.5 of Agresti (2007) for more information.

**Likelihood Ratio Chi-Square Test for One-Way Tables**

For one-way frequency tables, the CHISQ(LRCHI) option in the TABLES statement provides a likelihood ratio chi-square goodness-of-fit test. By default, the likelihood ratio test is based on the null hypothesis of equal proportions in the \(C\) classes (levels) of the one-way table. If you specify null hypothesis proportions or frequencies by using the CHISQ(TESTP=) or CHISQ(TESTF=) option, respectively, the likelihood ratio test is based on the null hypothesis values that you specify.

PROC FREQTAB computes the one-way likelihood ratio test as

\[
G^2 = 2 \sum_{i=1}^{C} f_i \ln\left(\frac{f_i}{e_i}\right)
\]

where \(f_i\) is the observed frequency of class \(i\), and \(e_i\) is the expected frequency of class \(i\) under the null hypothesis.

For the null hypothesis of equal proportions, the expected frequency of each class equals the total sample size divided by the number of classes,

\[
e_i = \frac{n}{C} \quad \text{for} \quad i = 1, 2, \ldots, C
\]

If you provide null hypothesis frequencies by specifying the CHISQ(TESTF=) option in the TABLES statement, the expected frequencies are the TESTF= values that you specify. If you provide null hypothesis proportions by specifying the CHISQ(TESTP=) option in the TABLES statement, PROC FREQTAB computes the expected frequencies as

\[
e_i = p_i \times n \quad \text{for} \quad i = 1, 2, \ldots, C
\]

where the proportions \(p_i\) are the TESTP= values that you specify.

Under the null hypothesis (of equal proportions, specified frequencies, or specified proportions), the likelihood ratio statistic \(G^2\) has an asymptotic chi-square distribution with \(C-1\) degrees of freedom.

In addition to the asymptotic test, you can request an exact one-way likelihood ratio chi-square test by specifying the LRCHI option in the EXACT statement. See the section “**Exact Statistics**” on page 265 for more information.
Likelihood Ratio Chi-Square Test

The likelihood ratio chi-square involves the ratios between the observed and expected frequencies. The likelihood ratio chi-square statistic is computed as

$$G^2 = 2 \sum_i \sum_j n_{ij} \ln \left( \frac{n_{ij}}{e_{ij}} \right)$$

where $n_{ij}$ is the observed frequency in table cell $(i, j)$ and $e_{ij}$ is the expected frequency for table cell $(i, j)$.

When the row and column variables are independent, $G^2$ has an asymptotic chi-square distribution with $(R-1)(C-1)$ degrees of freedom.

In addition to the asymptotic test, you can request an exact likelihood ratio chi-square test by specifying the LRCHI or CHISQ option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

Continuity-Adjusted Chi-Square Test

The continuity-adjusted chi-square for $2 \times 2$ tables is similar to the Pearson chi-square, but it is adjusted for the continuity of the chi-square distribution. The continuity-adjusted chi-square is most useful for small sample sizes. The use of the continuity adjustment is somewhat controversial; this chi-square test is more conservative (and more like Fisher’s exact test) when the sample size is small. As the sample size increases, the continuity-adjusted chi-square becomes more like the Pearson chi-square.

The continuity-adjusted chi-square statistic is computed as

$$Q_C = \sum_i \sum_j \left( \max(0, |n_{ij} - e_{ij}| - 0.5) \right)^2 / e_{ij}$$

Under the null hypothesis of independence, $Q_C$ has an asymptotic chi-square distribution with $(R-1)(C-1)$ degrees of freedom.

Mantel-Haenszel Chi-Square Test

The Mantel-Haenszel chi-square statistic tests the alternative hypothesis that there is a linear association between the row variable and the column variable. Both variables must lie on an ordinal scale. The Mantel-Haenszel chi-square statistic is computed as

$$Q_{MH} = (n - 1)r^2$$

where $r$ is the Pearson correlation between the row variable and the column variable. For a description of the Pearson correlation, see the “Pearson Correlation Coefficient” on page 208. The Pearson correlation and thus the Mantel-Haenszel chi-square statistic use the scores that you specify in the SCORES= option in the TABLES statement. See Mantel and Haenszel (1959) and Landis, Heyman, and Koch (1978) for more information.

Under the null hypothesis of no association, $Q_{MH}$ has an asymptotic chi-square distribution with 1 degree of freedom.

In addition to the asymptotic test, you can request an exact Mantel-Haenszel chi-square test by specifying the MHCHI or CHISQ option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.
**Fisher’s Exact Test**

Fisher’s exact test is another test of association between the row and column variables. This test assumes that the row and column totals are fixed and uses the hypergeometric distribution to compute probabilities of possible tables conditional on the observed row and column totals. Fisher’s exact test does not depend on any large-sample distribution assumptions, and so it is appropriate even for small sample sizes and for sparse tables.

### 2×2 Tables

For 2×2 tables, PROC FREQTAB gives the following information for Fisher’s exact test: table probability, two-sided p-value, left-sided p-value, and right-sided p-value. The table probability equals the hypergeometric probability of the observed table, and is in fact the value of the test statistic for Fisher’s exact test.

Where \( p \) is the hypergeometric probability of a specific table with the observed row and column totals, Fisher’s exact p-values are computed by summing probabilities \( p \) over defined sets of tables,

\[
\text{Prob} = \sum_A p
\]

The two-sided p-value is the sum of all possible table probabilities (conditional on the observed row and column totals) that are less than or equal to the observed table probability. For the two-sided p-value, the set \( A \) includes all possible tables with hypergeometric probabilities less than or equal to the probability of the observed table. A small two-sided p-value supports the alternative hypothesis of association between the row and column variables.

For 2×2 tables, one-sided p-values for Fisher’s exact test are defined in terms of the frequency of the cell in the first row and first column of the table, the (1,1) cell. Denoting the observed (1,1) cell frequency by \( n_{11} \), the left-sided p-value for Fisher’s exact test is the probability that the (1,1) cell frequency is less than or equal to \( n_{11} \). For the left-sided p-value, the set \( A \) includes those tables with a (1,1) cell frequency less than or equal to \( n_{11} \). A small left-sided p-value supports the alternative hypothesis that the probability of an observation being in the first cell is actually less than expected under the null hypothesis of independent row and column variables.

Similarly, for a right-sided alternative hypothesis, \( A \) is the set of tables where the frequency of the (1,1) cell is greater than or equal to that in the observed table. A small right-sided p-value supports the alternative that the probability of the first cell is actually greater than that expected under the null hypothesis.

Because the (1,1) cell frequency completely determines the 2×2 table when the marginal row and column sums are fixed, these one-sided alternatives can be stated equivalently in terms of other cell probabilities or ratios of cell probabilities. The left-sided alternative is equivalent to an odds ratio less than 1, where the odds ratio equals \( \frac{n_{11}n_{22}}{n_{12}n_{21}} \). The left-sided alternative is also equivalent to the column 1 risk for row 1 being less than the column 1 risk for row 2, \( p_{1|1} \times p_{1|2} \). Similarly, the right-sided alternative is equivalent to the column 1 risk for row 1 being greater than the column 1 risk for row 2, \( p_{1|1} > p_{1|2} \). For more information, see Agresti (2007).

### R×C Tables

Fisher’s exact test was extended to general \( R \times C \) tables by Freeman and Halton (1951), and this test is also known as the Freeman-Halton test. For \( R \times C \) tables, the two-sided p-value definition is the same as for 2×2 tables. The set \( A \) contains all tables with p less than or equal to the probability of the observed table. A small p-value supports the alternative hypothesis of association between the row and column variables. For \( R \times C \) tables, Fisher’s exact test is inherently two-sided. The alternative hypothesis is defined only in terms of general, and not linear, association. Therefore, Fisher’s exact test does not have right-sided or left-sided p-values for general \( R \times C \) tables.
For $R \times C$ tables, PROC FREQTAB computes Fisher’s exact test by using the network algorithm of Mehta and Patel (1983), which provides a faster and more efficient solution than direct enumeration. See the section “Exact Statistics” on page 265 for more details.

**Phi Coefficient**
The phi coefficient is a measure of association derived from the Pearson chi-square. The range of the phi coefficient is $-1 \leq \phi \leq 1$ for $2 \times 2$ tables. For tables larger than $2 \times 2$, the range is $0 \leq \phi \leq \min(\sqrt{R - 1}, \sqrt{C - 1})$ (Liebetrau 1983). The phi coefficient is computed as

$$
\phi = \frac{(n_{11}n_{22} - n_{12}n_{21})}{\sqrt{n_{11}n_{22}n_{12}n_{21}}} \quad \text{for } 2 \times 2 \text{ tables}
$$

$$
\phi = \sqrt{\frac{Q_P}{n}} \quad \text{otherwise}
$$

See Fleiss, Levin, and Paik (2003, pp. 98–99) for more information.

**Contingency Coefficient**
The contingency coefficient is a measure of association derived from the Pearson chi-square. The range of the contingency coefficient is $0 \leq P \leq \sqrt{(m - 1)/m}$, where $m = \min(R, C)$ (Liebetrau 1983). The contingency coefficient is computed as

$$
P = \frac{\sqrt{Q_P}}{(Q_P + n)}
$$

See Kendall and Stuart (1979, pp. 587–588) for more information.

**Cramér’s $V$**
Cramér’s $V$ is a measure of association derived from the Pearson chi-square. It is designed so that the attainable upper bound is always 1. The range of Cramér’s $V$ is $-1 \leq V \leq 1$ for $2 \times 2$ tables; for tables larger than $2 \times 2$, the range is $0 \leq V \leq 1$. Cramér’s $V$ is computed as

$$
V = \phi \quad \text{for } 2 \times 2 \text{ tables}
$$

$$
V = \sqrt{\frac{Q_P}{\min(R - 1, C - 1)}} \quad \text{otherwise}
$$

See Kendall and Stuart (1979, p. 588) for more information.

**Measures of Association**

When you specify the MEASURES option in the TABLES statement, PROC FREQTAB computes several statistics that describe the association between the row and column variables of the contingency table. The following are measures of ordinal association that consider whether the column variable $Y$ tends to increase as the row variable $X$ increases: gamma, Kendall’s tau-$b$, Stuart’s tau-$c$, and Somers’ $D$. These measures are appropriate for ordinal variables, and they classify pairs of observations as concordant or discordant. A pair is concordant if the observation with the larger value of $X$ also has the larger value of $Y$. A pair is discordant if the observation with the larger value of $X$ has the smaller value of $Y$. See Agresti (2007) and the other references cited for the individual measures of association.

The Pearson correlation coefficient and the Spearman rank correlation coefficient are also appropriate for ordinal variables. The Pearson correlation describes the strength of the linear association between the row and column variables, and it is computed by using the row and column scores specified by the SCORES= option.
option in the TABLES statement. The Spearman correlation is computed with rank scores. The polychoric correlation (requested by the PLCORR option) also requires ordinal variables and assumes that the variables have an underlying bivariate normal distribution. The following measures of association do not require ordinal variables and are appropriate for nominal variables: lambda asymmetric, lambda symmetric, and the uncertainty coefficients.

PROC FREQTAB computes estimates of the measures according to the formulas given in the following sections. For each measure, PROC FREQTAB computes an asymptotic standard error (ASE), which is the square root of the asymptotic variance denoted by Var in the following sections.

**Confidence Limits**

If you specify the CL option in the TABLES statement, PROC FREQTAB computes asymptotic confidence limits for all MEASURES statistics. The confidence coefficient is determined according to the value of the ALPHA= option, which, by default, is 0.05 and produces 95% confidence limits.

The confidence limits are computed as

\[ \text{Est} \pm (z_{\alpha/2} \times \text{ASE}) \]

where Est is the estimate of the measure, \( z_{\alpha/2} \) is the 100(1 - \( \alpha \))/2th percentile of the standard normal distribution, and ASE is the asymptotic standard error of the estimate.

**Asymptotic Tests**

For each measure that you specify in the TEST statement, PROC FREQTAB computes an asymptotic test of the null hypothesis that the measure is 0. Asymptotic tests are available for the following measures of association: gamma, Kendall’s tau-\( b \), Stuart’s tau-\( c \), Somers’ \( D(C|R) \), Somers’ \( D(R|C) \), the Pearson correlation coefficient, and the Spearman rank correlation coefficient. To compute an asymptotic test, PROC FREQTAB uses a standardized test statistic \( z \), which has an asymptotic standard normal distribution under the null hypothesis. The test statistic is computed as

\[ z = \frac{\text{Est}}{\sqrt{\text{Var}_0(\text{Est})}} \]

where Est is the estimate of the measure and \( \text{Var}_0(\text{Est}) \) is the variance of the estimate under the null hypothesis. Formulas for \( \text{Var}_0(\text{Est}) \) for the individual measures of association are given in the following sections.

Note that the ratio of Est to \( \sqrt{\text{Var}_0(\text{Est})} \) is the same for the following measures: gamma, Kendall’s tau-\( b \), Stuart’s tau-\( c \), Somers’ \( D(C|R) \), and Somers’ \( D(R|C) \). Therefore, the tests for these measures are identical. For example, the \( p \)-values for the test of \( H_0: \gamma = 0 \) equal the \( p \)-values for the test of \( H_0: \tau - b = 0 \).

PROC FREQTAB computes one-sided and two-sided \( p \)-values for each of these tests. When the test statistic \( z \) is greater than its null hypothesis expected value of 0, PROC FREQTAB displays the right-sided \( p \)-value, which is the probability of a larger value of the statistic occurring under the null hypothesis. A small right-sided \( p \)-value supports the alternative hypothesis that the true value of the measure is greater than 0. When the test statistic is less than or equal to 0, PROC FREQTAB displays the left-sided \( p \)-value, which is the probability of a smaller value of the statistic occurring under the null hypothesis. A small left-sided \( p \)-value supports the alternative hypothesis that the true value of the measure is less than 0. The one-sided \( p \)-value \( P_1 \) can be expressed as

\[
P_1 = \begin{cases} \text{Prob}(Z > z) & \text{if } z > 0 \\ \text{Prob}(Z < z) & \text{if } z \leq 0 \end{cases}
\]
where \( Z \) has a standard normal distribution. The two-sided \( p \)-value \( P_2 \) is computed as

\[
P_2 = \text{Prob}( |Z| > |z| )
\]

**Exact Tests**

Exact tests are available for the following measures of association: Kendall’s tau-\( b \), Stuart’s tau-\( c \), Somers’ \( D(C|R) \) and \( (R|C) \), the Pearson correlation coefficient, and the Spearman rank correlation coefficient. If you request an exact test for a measure of association in the EXACT statement, PROC FREQTAB computes the exact test of the hypothesis that the measure is 0. For more information, see the section “Exact Statistics” on page 265.

**Gamma**

The gamma (\( \Gamma \)) statistic is based only on the number of concordant and discordant pairs of observations. It ignores tied pairs (that is, pairs of observations that have equal values of \( X \) or equal values of \( Y \)). Gamma is appropriate only when both variables lie on an ordinal scale. The range of gamma is \(-1 \leq \Gamma \leq 1\). If the row and column variables are independent, gamma tends to be close to 0. Gamma is computed as

\[
G = \frac{(P - Q)}{(P + Q)}
\]

and the asymptotic variance is

\[
\text{Var}(G) = \frac{16}{(P + Q)^4} \sum_i \sum_j n_{ij} (Q A_{ij} - P D_{ij})^2
\]

For \( 2 \times 2 \) tables, gamma is equivalent to Yule’s \( Q \). See Goodman and Kruskal (1979) and Agresti (2002) for more information.

The variance under the null hypothesis that gamma equals 0 is computed as

\[
\text{Var}_0(G) = \frac{4}{(P + Q)^2} \left( \sum_i \sum_j n_{ij} (A_{ij} - D_{ij})^2 - (P - Q)^2 / n \right)
\]

For more information, see Brown and Benedetti (1977b).

**Kendall’s Tau-\( b \)**

Kendall’s tau-\( b \) (\( \tau_b \)) is similar to gamma except that tau-\( b \) uses a correction for ties. Tau-\( b \) is appropriate only when both variables lie on an ordinal scale. The range of tau-\( b \) is \(-1 \leq \tau_b \leq 1\). Kendall’s tau-\( b \) is computed as

\[
\tau_b = \frac{(P - Q)}{\sqrt{w_r w_c}}
\]

and the asymptotic variance is

\[
\text{Var}(\tau_b) = \frac{1}{w^4} \left( \sum_i \sum_j n_{ij} (2 w d_{ij} + t_b v_{ij})^2 - n^3 t_b^2 (w_r + w_c)^2 \right)
\]
where

\[
\begin{align*}
  w &= \sqrt{w_r w_c} \\
  w_r &= n^2 - \sum_i n_i^2 \\
  w_c &= n^2 - \sum_j n_j^2 \\
  d_{ij} &= A_{ij} - D_{ij} \\
  v_{ij} &= n_i w_c + n_j w_r
\end{align*}
\]

See Kendall (1955) for more information.

The variance under the null hypothesis that tau-\( b \) equals 0 is computed as

\[
\text{Var}_0(\tau_b) = \frac{4}{w_r w_c} \left( \sum_i \sum_j n_{ij} (A_{ij} - D_{ij})^2 - (P - Q)^2/n \right)
\]

For more information, see Brown and Benedetti (1977b).

PROC FREQTAB also provides an exact test for the Kendall’s tau-\( b \). You can request this test by specifying the KENTB option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

**Stuart’s Tau-c**

Stuart’s tau-\( c \) (\( \tau_c \)) makes an adjustment for table size in addition to a correction for ties. Tau-\( c \) is appropriate only when both variables lie on an ordinal scale. The range of tau-\( c \) is \(-1 \leq \tau_c \leq 1\). Stuart’s tau-\( c \) is computed as

\[
\tau_c = \frac{m(P - Q)}{n^2(m - 1)}
\]

and the asymptotic variance is

\[
\text{Var}(\tau_c) = \frac{4m^2}{(m - 1)^2 n^4} \left( \sum_i \sum_j n_{ij} d_{ij}^2 - (P - Q)^2/n \right)
\]

where \( m = \min(R, C) \) and \( d_{ij} = A_{ij} - D_{ij} \). The variance under the null hypothesis that tau-\( c \) equals 0 is the same as the asymptotic variance

\[
\text{Var}_0(\tau_c) = \text{Var}(\tau_c)
\]

For more information, see Brown and Benedetti (1977b).

PROC FREQTAB also provides an exact test for the Stuart’s tau-\( c \). You can request this test by specifying the STUTC option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.
**Somers’ D**

Somers’ $D(C|R)$ and Somers’ $D(R|C)$ are asymmetric modifications of tau-$b$. $C|R$ indicates that the row variable $X$ is regarded as the independent variable and the column variable $Y$ is regarded as dependent. Similarly, $R|C$ indicates that the column variable $Y$ is regarded as the independent variable and the row variable $X$ is regarded as dependent. Somers’ $D$ differs from tau-$b$ in that it uses a correction only for pairs that are tied on the independent variable. Somers’ $D$ is appropriate only when both variables lie on an ordinal scale. The range of Somers’ $D$ is $-1 \leq D \leq 1$. Somers’ $D(C|R)$ is computed as

$$D(C|R) = (P - Q) / w_r$$

and its asymptotic variance is

$$\text{Var}(D(C|R)) = \frac{4}{w_r^4} \sum_i \sum_j n_{ij} (w_r d_{ij} - (P - Q)(n - n_i))^2$$

where $d_{ij} = A_{ij} - D_{ij}$ and

$$w_r = n^2 - \sum_i n_i^2.$$  

For more information, see Somers (1962); Goodman and Kruskal (1979); Liebetrau (1983).

The variance under the null hypothesis that $D(C|R)$ equals 0 is computed as

$$\text{Var}_0(D(C|R)) = \frac{4}{w_r^2} \left( \sum_i \sum_j n_{ij} (A_{ij} - D_{ij})^2 - (P - Q)^2 / n \right)$$

For more information, see Brown and Benedetti (1977b).

Formulas for Somers’ $D(R|C)$ are obtained by interchanging the indices.

PROC FREQTAB also provides exact tests for Somers’ $D(C|R)$ and $(R|C)$. You can request these tests by specifying the SMDCR and SMDCR options in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

**Pearson Correlation Coefficient**

The Pearson correlation coefficient ($\rho$) is computed by using the scores specified in the SCORES= option. This measure is appropriate only when both variables lie on an ordinal scale. The range of the Pearson correlation is $-1 \leq \rho \leq 1$. The Pearson correlation coefficient is computed as

$$r = v/w = \overline{s_{rc}} / \sqrt{\overline{s_{rr}} \overline{s_{cc}}}$$

and its asymptotic variance is

$$\text{Var}(r) = \frac{1}{w_r^4} \sum_i \sum_j n_{ij} \left( w(R_i - \bar{R})(C_j - \bar{C}) - \frac{b_{ij}v}{2w} \right)^2$$
where $R_i$ and $C_j$ are the row and column scores and

$$ss_r = \sum_i \sum_j n_{ij}(R_i - \bar{R})^2$$

$$ss_c = \sum_i \sum_j n_{ij}(C_j - \bar{C})^2$$

$$ss_{rc} = \sum_i \sum_j n_{ij}(R_i - \bar{R})(C_j - \bar{C})$$

$$b_{ij} = (R_i - \bar{R})^2 ss_c + (C_j - \bar{C})^2 ss_r$$

$$u = ss_{rc}$$

$$w = \sqrt{ss_r ss_c}$$

See Snedecor and Cochran (1989) for more information.

The SCORES= option in the TABLES statement determines the type of row and column scores used to compute the Pearson correlation (and other score-based statistics). The default is SCORES=TABLE. See the section “Scores” on page 198 for details about the available score types and how they are computed.

The variance under the null hypothesis that the correlation equals 0 is computed as

$$\text{Var}_0(r) = \left( \frac{\sum_i \sum_j n_{ij}(R_i - \bar{R})^2(C_j - \bar{C})^2 - ss_{rc}^2 / n}{ss_r ss_c} \right) / ss_r ss_c$$

This expression for the variance is derived for multinomial sampling in a contingency table framework, and it differs from the form obtained under the assumption that both variables are continuous and normally distributed. For more information, see Brown and Benedetti (1977b).

PROC FREQTAB also provides an exact test for the Pearson correlation coefficient. You can request this test by specifying the PCORR option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

**Spearman Rank Correlation Coefficient**

The Spearman correlation coefficient ($\rho_s$) is computed by using rank scores, which are defined in the section “Scores” on page 198. This measure is appropriate only when both variables lie on an ordinal scale. The range of the Spearman correlation is $-1 \leq \rho_s \leq 1$. The Spearman correlation coefficient is computed as

$$r_s = u / w$$

and its asymptotic variance is

$$\text{Var}(r_s) = \frac{1}{n^2 w^4} \sum_i \sum_j n_{ij}(z_{ij} - \bar{z})^2$$
where \( R_1^i \) and \( C_1^j \) are the row and column rank scores and

\[
\begin{align*}
v &= \sum_i \sum_j n_{ij} R(i) C(j) \\
w &= \frac{1}{12} \sqrt{FG} \\
F &= n^3 - \sum_i n_i^3 \\
G &= n^3 - \sum_j n_j^3 \\
R(i) &= R_1^i - n/2 \\
C(j) &= C_1^j - n/2 \\
\bar{z} &= \frac{1}{n} \sum_i \sum_j n_{ij} z_{ij} \\
z_{ij} &= w_{ij} - v w_{ij}
\end{align*}
\]

\[
\begin{align*}
v_{ij} &= n \left( R(i) C(j) + \frac{1}{2} \sum_l n_{il} C(l) + \frac{1}{2} \sum_k n_{kj} R(k) + \sum_{l, k > i} n_{kl} C(l) + \sum_{k, l > j} n_{kl} R(k) \right) \\
w_{ij} &= \frac{-n}{96w} \left( F n_{ij}^2 + G n_i^2 \right)
\end{align*}
\]

See Snedecor and Cochran (1989) for more information.

The variance under the null hypothesis that the correlation equals 0 is computed as

\[
\text{Var}_0(r_s) = \frac{1}{n^2 w^2} \sum_i \sum_j n_{ij} (v_{ij} - \bar{v})^2
\]

where

\[
\bar{v} = \frac{\sum_i \sum_j n_{ij} v_{ij}}{n}
\]

This expression for the variance is derived for multinomial sampling in a contingency table framework, and it differs from the form obtained under the assumption that both variables are continuous and normally distributed. For more information, see Brown and Benedetti (1977b).

PROC FREQTAB also provides an exact test for the Spearman correlation coefficient. You can request this test by specifying the SCORR option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.
Polychoric Correlation

When you specify the PLCORR option in the TABLES statement, PROC FREQTAB computes the polychoric correlation and its standard error. The polychoric correlation is based on the assumption that the two ordinal, categorical variables of the frequency table have an underlying bivariate normal distribution. The polychoric correlation coefficient is the maximum likelihood estimate of the product-moment correlation between the underlying normal variables. The range of the polychoric correlation is from –1 to 1. For $2 \times 2$ tables, the polychoric correlation is also known as the tetrachoric correlation (and it is labeled as such in the displayed output). See Drasgow (1986) for an overview of polychoric correlation coefficient.

Olsson (1979) gives the likelihood equations and the asymptotic standard errors for estimating the polychoric correlation. The underlying continuous variables relate to the observed crosstabulation table through thresholds, which define a range of numeric values that correspond to each categorical (table) level. PROC FREQTAB uses Olsson’s maximum likelihood method for simultaneous estimation of the polychoric correlation and the thresholds. (Olsson also presents a two-step method that estimates the thresholds first.)

PROC FREQTAB iteratively solves the likelihood equations by using a Newton-Raphson algorithm. The initial estimates of the thresholds are computed from the inverse of the normal distribution function at the cumulative marginal proportions of the table. Iterative computation of the polychoric correlation stops when the convergence measure falls below the convergence criterion or when the maximum number of iterations is reached, whichever occurs first. For parameter values that are less than 0.01, the procedure evaluates convergence by using the absolute difference instead of the relative difference. The PLCORR(CONVERGE=) option specifies the convergence criterion, which is 0.0001 by default. The PLCORR(MAXITER=) option specifies the maximum number of iterations, which is 20 by default.

If you specify the CL option in the TABLES statement, PROC FREQTAB provides confidence limits for the polychoric correlation. The confidence limits are computed as

$$
\hat{\rho} \pm (z_{a/2} \times SE(\hat{\rho}))
$$

where $\hat{\rho}$ is the estimate of the polychoric correlation, $z_{a/2}$ is the $100(1 - \alpha/2)$th percentile of the standard normal distribution, and $SE(\hat{\rho})$ is the standard error of the polychoric correlation estimate.

If you specify the PLCORR option in the TEST statement, PROC FREQTAB provides Wald and likelihood ratio tests of the null hypothesis that the polychoric correlation is 0. The Wald test statistic is computed as

$$
z = \frac{\hat{\rho}}{SE(\hat{\rho})}
$$

which has a standard normal distribution under the null hypothesis. PROC FREQTAB computes one-sided and two-sided $p$-values for the Wald test. When the test statistic $z$ is greater than its null expected value of 0, PROC FREQTAB displays the right-sided $p$-value. When the test statistic is less than or equal to 0, PROC FREQTAB displays the left-sided $p$-value.

The likelihood ratio statistic for the polychoric correlation is computed as

$$
G^2 = -2 \ln(L_0/L_1)
$$

where $L_0$ is the value of the likelihood function (Olsson 1979) when the polychoric correlation is 0, and $L_1$ is the value of the likelihood function at the maximum (where all parameters are replaced by their maximum likelihood estimates). Under the null hypothesis, the likelihood ratio statistic has an asymptotic chi-square distribution with 1 degree of freedom.
**Lambda (Asymmetric)**

Asymmetric lambda, \( \lambda(C | R) \), is interpreted as the probable improvement in predicting the column variable \( Y \) given knowledge of the row variable \( X \). The range of asymmetric lambda is \( 0 \leq \lambda(C | R) \leq 1 \). Asymmetric lambda \( (C | R) \) is computed as

\[
\lambda(C | R) = \frac{\sum_i r_i - r}{n - r}
\]

and its asymptotic variance is

\[
\text{Var}(\lambda(C | R)) = \frac{n - \sum_i r_i}{(n - r)^3} \left( \sum_i r_i + r - 2 \sum_i (r_i | l_i = l) \right)
\]

where

\[
\begin{align*}
    r_i &= \max_j (n_{ij}) \\
    r &= \max_j (n_{.j}) \\
    c_j &= \max_i (n_{ij}) \\
    c &= \max_i (n_{i.})
\end{align*}
\]

The values of \( l_i \) and \( l \) are determined as follows. Denote by \( l_i \) the unique value of \( j \) such that \( r_i = n_{ij} \), and let \( l \) be the unique value of \( j \) such that \( r = n_{.j} \). Because of the uniqueness assumptions, ties in the frequencies or in the marginal totals must be broken in an arbitrary but consistent manner. In case of ties, \( l \) is defined as the smallest value of \( j \) such that \( r = n_{.j} \).

For those columns containing a cell \((i, j)\) for which \( n_{ij} = r_i = c_j \), \( cs_j \) records the row in which \( c_j \) is assumed to occur. Initially \( cs_j \) is set equal to \(-1\) for all \( j \). Beginning with \( i=1 \), if there is at least one value \( j \) such that \( n_{ij} = r_i = c_j \), and if \( cs_j = -1 \), \( l_i \) is defined to be the smallest such value of \( j \), and \( cs_j \) is set equal to \( i \). Otherwise, if \( n_{i\cdot} = r_i \), \( l_i \) is defined to be equal to \( l \). If neither condition is true, \( l_i \) is taken to be the smallest value of \( j \) such that \( n_{ij} = r_i \).

The formulas for lambda asymmetric \((R|C)\) can be obtained by interchanging the indices.

See Goodman and Kruskal (1979) for more information.

**Lambda (Symmetric)**

The nondirectional lambda is the average of the two asymmetric lambdas, \( \lambda(C | R) \) and \( \lambda(R | C) \). Its range is \( 0 \leq \lambda \leq 1 \). Lambda symmetric is computed as

\[
\lambda = \frac{\sum_i r_i + \sum_j c_j - r - c}{2n - r - c} = \frac{w - v}{w}
\]

and its asymptotic variance is computed as

\[
\text{Var}(\lambda) = \frac{1}{w^4} \left( wvy - 2w^2(n - \sum_i \sum_j (n_{ij} | j = l_i, i = k_j)) - 2v^2(n - n_{kl}) \right)
\]
where
\[
\begin{align*}
  r_i &= \max_j (n_{ij}) \\
  r &= \max_j (n_{ij}) \\
  c_j &= \max_i (n_{ij}) \\
  c &= \max_i (n_{i.}) \\
  w &= 2n - r - c \\
  v &= 2n - \sum_i r_i - \sum_j c_j \\
  x &= \sum_i (r_i | l_i = l) + \sum_j (c_j | k_j = k) + r_k + c_l \\
  y &= 8n - w - v - 2x
\end{align*}
\]

The definitions of \(l_i\) and \(l\) are given in the previous section. The values \(k_j\) and \(k\) are defined in a similar way for lambda asymmetric (\(R|C\)).

See Goodman and Kruskal (1979) for more information.

**Uncertainty Coefficients (Asymmetric)**

The uncertainty coefficient \(U(C|R)\) measures the proportion of uncertainty (entropy) in the column variable \(Y\) that is explained by the row variable \(X\). Its range is \(0 \leq U(C|R) \leq 1\). The uncertainty coefficient is computed as
\[
U(C|R) = \frac{(H(X) + H(Y) - H(XY))}{H(Y)} = \frac{v}{w}
\]
and its asymptotic variance is
\[
\text{Var}(U(C|R)) = \frac{1}{n^2w^4} \sum_i \sum_j n_{ij}(H(Y) \ln \left(\frac{n_{ij}}{n_{i.}}\right) + (H(X) - H(XY)) \ln \left(\frac{n_{i.}}{n}\right))^2
\]
where
\[
\begin{align*}
  v &= H(X) + H(Y) - H(XY) \\
  w &= H(Y) \\
  H(X) &= -\sum_i \left(\frac{n_{ij}}{n}\right) \ln \left(\frac{n_{ij}}{n}\right) \\
  H(Y) &= -\sum_j \left(\frac{n_{.j}}{n}\right) \ln \left(\frac{n_{.j}}{n}\right) \\
  H(XY) &= -\sum_i \sum_j \left(\frac{n_{ij}}{n}\right) \ln \left(\frac{n_{ij}}{n}\right)
\end{align*}
\]
Chapter 4: The FREQTAB Procedure

The formulas for the uncertainty coefficient $U(R|C)$ can be obtained by interchanging the indices. See Theil (1972, pp. 115–120) and Goodman and Kruskal (1979) for more information.

**Uncertainty Coefficient (Symmetric)**

The uncertainty coefficient $U$ is the symmetric version of the two asymmetric uncertainty coefficients. Its range is $0 \leq U \leq 1$. The uncertainty coefficient is computed as

$$U = 2 \left( H(X) + H(Y) - H(XY) \right) / \left( H(X) + H(Y) \right)$$

and its asymptotic variance is

$$\text{Var}(U) = 4 \sum_{i} \sum_{j} n_{ij} \left( H(XY) \ln \left( \frac{n_{i,j}}{n^2} \right) - (H(X) + H(Y)) \ln \left( \frac{n_{ij}}{n} \right) \right)^2$$

where $H(X)$, $H(Y)$, and $H(XY)$ are defined in the previous section. See Goodman and Kruskal (1979) for more information.

**Binomial Proportion**

If you specify the BINOMIAL option in the TABLES statement, PROC FREQTAB computes the binomial proportion for one-way tables. By default, this is the proportion of observations in the first variable level that appears in the output. (You can use the LEVEL= option to specify a different level for the proportion.) The binomial proportion is computed as

$$\hat{p} = \frac{n_1}{n}$$

where $n_1$ is the frequency of the first (or designated) level and $n$ is the total frequency of the one-way table. The standard error of the binomial proportion is computed as

$$\text{se}(\hat{p}) = \sqrt{\frac{\hat{p} (1 - \hat{p})}{n}}$$

**Binomial Confidence Limits**

PROC FREQTAB provides Wald and exact (Clopper-Pearson) confidence limits for the binomial proportion. You can also request the following binomial confidence limit types by specifying the BINOMIAL(CL=) option: Agresti-Coull, Blaker, Jeffrey's, exact mid-$p$, likelihood ratio, logit, and Wilson (score). For more information, see Brown, Cai, and DasGupta (2001), Agresti and Coull (1998), and Newcombe (1998b), in addition to the references cited for each confidence limit type.

**Wald Confidence Limits**

Wald asymptotic confidence limits are based on the normal approximation to the binomial distribution. PROC FREQTAB computes the Wald confidence limits for the binomial proportion as

$$\hat{p} \pm \left( z_{\alpha/2} \times \text{se}(\hat{p}) \right)$$

where $z_{\alpha/2}$ is the 100$(1 - \alpha/2)$th percentile of the standard normal distribution. The confidence level $\alpha$ is determined by the ALPHA= option; by default, ALPHA=0.05, which produces 95% confidence limits.

If you specify CL=WALD(CORRECT) or the CORRECT binomial-option, PROC FREQTAB includes a continuity correction of $1/2n$ in the Wald asymptotic confidence limits. The purpose of this correction is to adjust for the difference between the normal approximation and the discrete binomial distribution. See Fleiss, Levin, and Paik (2003) for more information. The continuity-corrected Wald confidence limits for the binomial proportion are computed as

$$\hat{p} \pm \left( z_{\alpha/2} \times \text{se}(\hat{p}) + (1/2n) \right)$$
**Exact (Clopper-Pearson) Confidence Limits**  
Exact (Clopper-Pearson) confidence limits for the binomial proportion are constructed by inverting the equal-tailed test based on the binomial distribution. This method is attributed to Clopper and Pearson (1934). The exact confidence limits $P_L$ and $P_U$ satisfy the following equations, for $n_1 = 1, 2, \ldots, n - 1$:

$$\sum_{x=n_1}^{n} \binom{n}{x} P_L^x (1 - P_L)^{n-x} = \alpha/2$$

$$\sum_{x=0}^{n_1} \binom{n}{x} P_U^x (1 - P_U)^{n-x} = \alpha/2$$

The lower confidence limit is 0 when $n_1 = 0$, and the upper confidence limit is 1 when $n_1 = n$.

PROC FREQTAB computes the exact (Clopper-Pearson) confidence limits by using the $F$ distribution as

$$P_L = \left(1 + \frac{n - n_1 + 1}{P_L \cdot F(\alpha/2, 2n_1, 2(n-n_1+1))}\right)^{-1}$$

$$P_U = \left(1 + \frac{n - n_1}{(n_1 + 1) \cdot P_U \cdot F(\alpha/2, 2n_1, 2(n-n_1+1))}\right)^{-1}$$

where $F(\alpha/2, b, c)$ is the $(\alpha/2)$th percentile of the $F$ distribution with $b$ and $c$ degrees of freedom. See Leemis and Trivedi (1996) for a derivation of this expression. Also see Collett (1991) for more information about exact binomial confidence limits.

Because this is a discrete problem, the confidence coefficient (coverage probability) of the exact (Clopper-Pearson) interval is not exactly $1 - \alpha$, but is at least $(1 - \alpha)$. Thus, this confidence interval is conservative. Unless the sample size is large, the actual coverage probability can be much larger than the target value. For more information about the performance of these confidence limits, see Agresti and Coull (1998), Brown, Cai, and DasGupta (2001), and Leemis and Trivedi (1996).

**Agresti-Coull Confidence Limits**  
If you specify the CL=AGRESTICOULL binomial-option, PROC FREQTAB computes Agresti-Coull confidence limits for the binomial proportion as

$$\tilde{p} \pm (z_{\alpha/2} \times \sqrt{\tilde{p} (1 - \tilde{p}) / \tilde{n}})$$

where

$$\tilde{n}_1 = n_1 + z_{\alpha/2}^2 / 2$$

$$\tilde{n} = n + z_{\alpha/2}^2$$

$$\tilde{p} = \frac{\tilde{n}_1}{\tilde{n}}$$

The Agresti-Coull confidence interval has the same general form as the standard Wald interval but uses $\tilde{p}$ in place of $\hat{p}$. For $\alpha = 0.05$, the value of $z_{\alpha/2}$ is close to 2, and this interval is the “add 2 successes and 2 failures” adjusted Wald interval of Agresti and Coull (1998).
Chapter 4: The FREQTAB Procedure

**Blaker Confidence Limits** If you specify the CL=BLAKER binomial-option, PROC FREQTAB computes Blaker confidence limits for the binomial proportion, which are constructed by inverting the two-sided exact Blaker test (Blaker 2000). The 100(1 − \(\alpha\))% Blaker confidence interval consists of all values of the proportion \(p_0\) for which the test statistic \(B(p_0, n_1)\) falls in the acceptance region,

\[
\{p_0 : B(p_0, n_1) > \alpha\}
\]

where

\[
B(p_0, n_1) = \text{Prob}(\gamma(p_0, X) \leq \gamma(p_0, n_1) | p_0)
\]

\[
\gamma(p_0, n_1) = \min(\text{Prob}(X \geq n_1 | p_0), \text{Prob}(X \leq n_1 | p_0))
\]

and \(X\) is a binomial random variable. For more information, see Blaker (2000).

**Jeffreys Confidence Limits** If you specify the CL=JEFFREYS binomial-option, PROC FREQTAB computes Jeffreys confidence limits for the binomial proportion as

\[
\beta(\alpha/2, n_1 + 1/2, n - n_1 + 1/2), \beta(1 - \alpha/2, n_1 + 1/2, n - n_1 + 1/2)
\]

where \(\beta(\alpha, b, c)\) is the \(\alpha\)th percentile of the beta distribution with shape parameters \(b\) and \(c\). The lower confidence limit is set to 0 when \(n_1 = 0\), and the upper confidence limit is set to 1 when \(n_1 = n\). This is an equal-tailed interval based on the noninformative Jeffreys prior for a binomial proportion. For more information, see Brown, Cai, and DasGupta (2001). For information about using beta priors for inference on the binomial proportion, see Berger (1985).

**Likelihood Ratio Confidence Limits** If you specify the CL=LIKELIHOODRATIO binomial-option, PROC FREQTAB computes likelihood ratio confidence limits for the binomial proportion by inverting the likelihood ratio test. The likelihood ratio test statistic for the null hypothesis that the proportion equals \(p_0\) can be expressed as

\[
L(p_0) = -2(n_1 \log(\hat{p}/p_0) + (n - n_1) \log((1 - \hat{p})/(1 - p_0)))
\]

The 100(1 − \(\alpha\))% likelihood ratio confidence interval consists of all values of \(p_0\) for which the test statistic \(L(p_0)\) falls in the acceptance region,

\[
\{p_0 : L(p_0) < \chi^2_{1, \alpha}\}
\]

where \(\chi^2_{1, \alpha}\) is the 100(1 − \(\alpha\))th percentile of the chi-square distribution with 1 degree of freedom. PROC FREQTAB finds the confidence limits by iterative computation. For more information, see Fleiss, Levin, and Paik (2003), Brown, Cai, and DasGupta (2001), Agresti (2013), and Newcombe (1998b).

**Logit Confidence Limits** If you specify the CL=LOGIT binomial-option, PROC FREQTAB computes logit confidence limits for the binomial proportion, which are based on the logit transformation \(Y = \log(\hat{p}/(1 - \hat{p}))\). Approximate confidence limits for \(Y\) are computed as

\[
Y_L = \log(\hat{p}/(1 - \hat{p})) - z_{\alpha/2} \sqrt{n/(n_1(n - n_1))}
\]

\[
Y_U = \log(\hat{p}/(1 - \hat{p})) + z_{\alpha/2} \sqrt{n/(n_1(n - n_1))}
\]

The confidence limits for \(Y\) are inverted to produce 100(1 − \(\alpha\))% logit confidence limits \(P_L\) and \(P_U\) for the binomial proportion \(p\) as

\[
P_L = \exp(Y_L)/(1 + \exp(Y_L))
\]

\[
P_U = \exp(Y_U)/(1 + \exp(Y_U))
\]

For more information, see Brown, Cai, and DasGupta (2001) and Korn and Graubard (1998).
Mid-p Confidence Limits  If you specify the CL=MIDP binomial-option, PROC FREQTAB computes exact mid-p confidence limits for the binomial proportion by inverting two one-sided binomial tests that include mid-p tail areas. The mid-p approach replaces the probability of the observed frequency by half of that probability in the Clopper-Pearson sum, which is described in the section “Exact (Clopper-Pearson) Confidence Limits” on page 215. The exact mid-p confidence limits $P_L$ and $P_U$ are the solutions to the equations

$$\sum_{x=n_1+1}^{n} \binom{n}{x} P_L^x (1 - P_L)^{n-x} + \frac{1}{2} \binom{n}{n_1} P_L^{n_1} (1 - P_L)^{n-n_1} = \alpha/2$$

$$\sum_{x=0}^{n_1-1} \binom{n}{x} P_U^x (1 - P_U)^{n-x} + \frac{1}{2} \binom{n}{n_1} P_U^{n_1} (1 - P_U)^{n-n_1} = \alpha/2$$

For more information, see Agresti and Gottard (2007), Agresti (2013), Newcombe (1998b), and Brown, Cai, and DasGupta (2001).

Wilson (Score) Confidence Limits  If you specify the CL=WILSON binomial-option, PROC FREQTAB computes Wilson confidence limits for the binomial proportion. These are also known as score confidence limits (Wilson 1927). The confidence limits are based on inverting the normal test that uses the null proportion in the variance (the score test). Wilson confidence limits are the roots of

$$|p - \hat{p}| = z_{\alpha/2} \sqrt{p(1-p)/n}$$

and are computed as

$$\left( \hat{p} + z_{\alpha/2}^2 / 2n \pm z_{\alpha/2} \sqrt{\left( \hat{p}(1-\hat{p}) + z_{\alpha/2}^2 / 4n \right) / n} \right) / \left( 1 + z_{\alpha/2}^2 / n \right)$$

If you specify CL=WILSON(CORRECT) or the CORRECT binomial-option, PROC FREQTAB provides continuity-corrected Wilson confidence limits, which are computed as the roots of

$$|p - \hat{p}| - 1/2n = \alpha/2 \sqrt{p(1-p)/n}$$

The Wilson interval has been shown to have better performance than the Wald interval and the exact (Clopper-Pearson) interval. For more information, see Agresti and Coull (1998), Brown, Cai, and DasGupta (2001), and Newcombe (1998b).

Binomial Tests
The BINOMIAL option provides an asymptotic equality test for the binomial proportion by default. You can also specify binomial-options to request tests of noninferiority, superiority, and equivalence for the binomial proportion. If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB also computes exact $p$-values for the tests that you request with the binomial-options.
**Equality Test**  
PROC FREQTAB computes an asymptotic test of the hypothesis that the binomial proportion equals \( p_0 \), where you can specify the value of \( p_0 \) with the **P=** **binomial-option**. If you do not specify a null value with **P=**, PROC FREQTAB uses \( p_0 = 0.5 \) by default. The binomial test statistic is computed as

\[
z = (\hat{p} - p_0) / se
\]

By default, the standard error is based on the null hypothesis proportion as

\[
se = \sqrt{p_0(1 - p_0) / n}
\]

If you specify the **VAR=SAMPLE** **binomial-option**, the standard error is computed from the sample proportion as

\[
se = \sqrt{\hat{p}(1 - \hat{p}) / n}
\]

If you specify the **CORRECT** **binomial-option**, PROC FREQTAB includes a continuity correction in the asymptotic test statistic, towards adjusting for the difference between the normal approximation and the discrete binomial distribution. For more information, see Fleiss, Levin, and Paik (2003). The continuity correction of \((1/2n)\) is subtracted from the numerator of the test statistic if \((\hat{p} - p_0)\) is positive; otherwise, the continuity correction is added to the numerator.

PROC FREQTAB computes one-sided and two-sided \( p \)-values for this test. When the test statistic \( z \) is greater than 0 (its expected value under the null hypothesis), PROC FREQTAB computes the right-sided \( p \)-value, which is the probability of a larger value of the statistic occurring under the null hypothesis. A small right-sided \( p \)-value supports the alternative hypothesis that the true value of the proportion is greater than \( p_0 \). When the test statistic is less than or equal to 0, PROC FREQTAB computes the left-sided \( p \)-value, which is the probability of a smaller value of the statistic occurring under the null hypothesis. A small left-sided \( p \)-value supports the alternative hypothesis that the true value of the proportion is less than \( p_0 \). The one-sided \( p \)-value \( P_1 \) can be expressed as

\[
P_1 = \begin{cases} 
\text{Prob}(Z > z) & \text{if } z > 0 \\
\text{Prob}(Z < z) & \text{if } z \leq 0 
\end{cases}
\]

where \( Z \) has a standard normal distribution. The two-sided \( p \)-value is computed as \( P_2 = 2 \times P_1 \).

If you specify the **BINOMIAL** option in the **EXACT** statement, PROC FREQTAB also computes an exact test of the null hypothesis \( H_0: p = p_0 \). To compute the exact test, PROC FREQTAB uses the binomial probability function,

\[
\text{Prob}(X = x \mid p_0) = \binom{n}{x} p_0^x (1 - p_0)^{(n-x)} \quad \text{for } x = 0, 1, 2, \ldots, n
\]

where the variable \( X \) has a binomial distribution with parameters \( n \) and \( p_0 \). To compute the left-sided \( p \)-value, \( \text{Prob}(X \leq n_1) \), PROC FREQTAB sums the binomial probabilities over \( x \) from 0 to \( n_1 \). To compute the right-sided \( p \)-value, \( \text{Prob}(X \geq n_1) \), PROC FREQTAB sums the binomial probabilities over \( x \) from \( n_1 \) to \( n \). The exact one-sided \( p \)-value is the minimum of the left-sided and right-sided \( p \)-values,

\[
P_1 = \min ( \text{Prob}(X \leq n_1 \mid p_0), \text{Prob}(X \geq n_1 \mid p_0) )
\]

and the exact two-sided \( p \)-value is computed as \( P_2 = 2 \times P_1 \).
Noninferiority Test  If you specify the NONINF binomial-option, PROC FREQTAB provides a noninferiority test for the binomial proportion. The null hypothesis for the noninferiority test is

\[ H_0: p - p_0 \leq -\delta \]

versus the alternative

\[ H_a: p - p_0 > -\delta \]

where \( \delta \) is the noninferiority margin and \( p_0 \) is the null proportion. Rejection of the null hypothesis indicates that the binomial proportion is not inferior to the null value. See Chow, Shao, and Wang (2003) for more information.

You can specify the value of \( \delta \) with the MARGIN= binomial-option, and you can specify \( p_0 \) with the P= binomial-option. By default, \( \delta = 0.2 \) and \( p_0 = 0.5 \).

PROC FREQTAB provides an asymptotic Wald test for noninferiority. The test statistic is computed as

\[ z = \frac{\hat{p} - p^*_0}{se} \]

where \( p^*_0 \) is the noninferiority limit,

\[ p^*_0 = p_0 - \delta \]

By default, the standard error is computed from the sample proportion as

\[ se = \sqrt{\hat{p}(1 - \hat{p})/n} \]

If you specify the VAR=NULL binomial-option, the standard error is based on the noninferiority limit (determined by the null proportion and the margin) as

\[ se = \sqrt{p^*_0(1 - p^*_0)/n} \]

If you specify the CORRECT binomial-option, PROC FREQTAB includes a continuity correction in the asymptotic test statistic \( z \). The continuity correction of \( (1/2n) \) is subtracted from the numerator of the test statistic if \( \hat{p} - p^*_0 \) is positive; otherwise, the continuity correction is added to the numerator.

The \( p \)-value for the noninferiority test is

\[ P_z = \text{Prob}(Z > z) \]

where \( Z \) has a standard normal distribution.

As part of the noninferiority analysis, PROC FREQTAB provides asymptotic Wald confidence limits for the binomial proportion. These confidence limits are computed as described in the section “Wald Confidence Limits” on page 214 but use the same standard error (VAR=NULL or VAR=SAMPLE) as the noninferiority test statistic \( z \). The confidence coefficient is \( 100(1 - 2\alpha)\% \) (Schuirmann 1999). By default, if you do not specify the ALPHA= option, the noninferiority confidence limits are 90% confidence limits. You can compare the confidence limits to the noninferiority limit, \( p^*_0 = p_0 - \delta \).

If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB provides an exact noninferiority test for the binomial proportion. The exact \( p \)-value is computed by using the binomial probability function with parameters \( p^*_0 \) and \( n \),

\[ P_x = \sum_{k=n_1}^{k=n} \binom{n}{k} (p^*_0)^k (1 - p^*_0)^{(n-k)} \]
For more information, see Chow, Shao, and Wang (2003, p. 116). If you request exact binomial statistics, PROC FREQTAB also includes exact (Clopper-Pearson) confidence limits for the binomial proportion in the equivalence analysis display. For more information, see the section “Exact (Clopper-Pearson) Confidence Limits” on page 215.

**Superiority Test**  If you specify the SUP binomial-option, PROC FREQTAB provides a superiority test for the binomial proportion. The null hypothesis for the superiority test is

\[ H_0: p - p_0 \leq \delta \]

versus the alternative

\[ H_a: p - p_0 > \delta \]

where \( \delta \) is the superiority margin and \( p_0 \) is the null proportion. Rejection of the null hypothesis indicates that the binomial proportion is superior to the null value. You can specify the value of \( \delta \) with the MARGIN= binomial-option, and you can specify the value of \( p_0 \) with the P= binomial-option. By default, \( \delta = 0.2 \) and \( p_0 = 0.5 \).

The superiority analysis is identical to the noninferiority analysis but uses a positive value of the margin \( \delta \) in the null hypothesis. The superiority limit equals \( p_0 + \delta \). The superiority computations follow those in the section “Noninferiority Test” on page 219 but replace \(-\delta \) with \( \delta \). See Chow, Shao, and Wang (2003) for more information.

**Equivalence Test**  If you specify the EQUIV binomial-option, PROC FREQTAB provides an equivalence test for the binomial proportion. The null hypothesis for the equivalence test is

\[ H_0: p - p_0 \leq \delta_L \text{ or } p - p_0 \geq \delta_U \]

versus the alternative

\[ H_a: \delta_L < p - p_0 < \delta_U \]

where \( \delta_L \) is the lower margin, \( \delta_U \) is the upper margin, and \( p_0 \) is the null proportion. Rejection of the null hypothesis indicates that the binomial proportion is equivalent to the null value. See Chow, Shao, and Wang (2003) for more information.

You can specify the value of the margins \( \delta_L \) and \( \delta_U \) with the MARGIN= binomial-option. If you do not specify MARGIN=, PROC FREQTAB uses lower and upper margins of \(-0.2 \) and \( 0.2 \) by default. If you specify a single margin value \( \delta \), PROC FREQTAB uses lower and upper margins of \(-\delta \) and \( \delta \). You can specify the null proportion \( p_0 \) with the P= binomial-option. By default, \( p_0 = 0.5 \).

PROC FREQTAB computes two one-sided tests (TOST) for equivalence analysis (Schuirmann 1987). The TOST approach includes a right-sided test for the lower margin and a left-sided test for the upper margin. The overall \( p \)-value is taken to be the larger of the two \( p \)-values from the lower and upper tests.

For the lower margin, the asymptotic Wald test statistic is computed as

\[ z_L = (\hat{p} - p^*_L) / se \]

where the lower equivalence limit is

\[ p^*_L = p_0 + \delta_L \]
By default, the standard error is computed from the sample proportion as

$$se = \sqrt{\hat{p}(1 - \hat{p})/n}$$

If you specify the VAR=NULL binomial-option, the standard error is based on the lower equivalence limit (determined by the null proportion and the lower margin) as

$$se = \sqrt{p^*_L(1 - p^*_L)/n}$$

If you specify the CORRECT binomial-option, PROC FREQTAB includes a continuity correction in the asymptotic test statistic $z_L$. The continuity correction of $(1/2n)$ is subtracted from the numerator of the test statistic $(\hat{p} - p^*_L)$ if the numerator is positive; otherwise, the continuity correction is added to the numerator.

The $p$-value for the lower margin test is

$$P_{z,L} = \text{Prob}(Z > z_L)$$

The asymptotic test for the upper margin is computed similarly. The Wald test statistic is

$$z_U = (\hat{p} - p^*_U) / se$$

where the upper equivalence limit is

$$p^*_U = p_0 + \delta_U$$

By default, the standard error is computed from the sample proportion. If you specify the VAR=NULL binomial-option, the standard error is based on the upper equivalence limit as

$$se = \sqrt{p^*_U(1 - p^*_U)/n}$$

If you specify the CORRECT binomial-option, PROC FREQTAB includes a continuity correction of $(1/2n)$ in the asymptotic test statistic $z_U$.

The $p$-value for the upper margin test is

$$P_{z,U} = \text{Prob}(Z < z_U)$$

Based on the two one-sided tests (TOST), the overall $p$-value for the test of equivalence equals the larger $p$-value from the lower and upper margin tests, which can be expressed as

$$P_z = \max(P_{z,L}, P_{z,U})$$

As part of the equivalence analysis, PROC FREQTAB provides asymptotic Wald confidence limits for the binomial proportion. These confidence limits are computed as described in the section “Wald Confidence Limits” on page 214, but use the same standard error (VAR=NULL or VAR=SAMPLE) as the equivalence test statistics and have a confidence coefficient of $100(1 - 2\alpha)\%$ (Schuirmann 1999). By default, if you do not specify the ALPHA= option, the equivalence confidence limits are 90% limits. If you specify VAR=NULL, separate standard errors are computed for the lower and upper margin tests, each based on the null proportion and the corresponding (lower or upper) margin. The confidence limits are computed by using
the maximum of these two standard errors. You can compare the confidence limits to the equivalence limits, 
\((p_0 + \delta_L, p_0 + \delta_U)\).

If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB also provides an exact equivalence test by using two one-sided exact tests (TOST). The procedure computes lower and upper margin exact tests by using the binomial probability function as described in the section “Noninferiority Test” on page 219. The overall exact \(p\)-value for the equivalence test is taken to be the larger \(p\)-value from the lower and upper margin exact tests. If you request exact statistics, PROC FREQTAB also includes exact (Clopper-Pearson) confidence limits in the equivalence analysis display. The confidence coefficient is 100\((1 - 2\alpha)\%\) (Schuirmann 1999). For more information, see the section “Exact (Clopper-Pearson) Confidence Limits” on page 215.

### Risks and Risk Differences

The RISKDIFF option in the TABLES statement provides estimates of risks (binomial proportions) and risk differences for 2 \(\times\) 2 tables. This analysis might be appropriate when comparing the proportion of some characteristic for two groups, where row 1 and row 2 correspond to the two groups, and the columns correspond to two possible characteristics or outcomes. For example, the row variable might be a treatment or dose, and the column variable might be the response. For more information, see Collett (1991); Fleiss, Levin, and Paik (2003); Stokes, Davis, and Koch (2012).

Let the frequencies of the 2 \(\times\) 2 table be represented as follows.

<table>
<thead>
<tr>
<th></th>
<th>Column 1</th>
<th>Column 2</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Row 1</td>
<td>(n_{11})</td>
<td>(n_{12})</td>
<td>(n_1)</td>
</tr>
<tr>
<td>Row 2</td>
<td>(n_{21})</td>
<td>(n_{22})</td>
<td>(n_2)</td>
</tr>
<tr>
<td>Total</td>
<td>(n_{1})</td>
<td>(n_{2})</td>
<td>(n)</td>
</tr>
</tbody>
</table>

By default when you specify the RISKDIFF option, PROC FREQTAB provides estimates of the row 1 risk (proportion), the row 2 risk, the overall risk, and the risk difference for column 1 and for column 2 of the 2 \(\times\) 2 table. The risk difference is defined as the row 1 risk minus the row 2 risk. The risks are binomial proportions of their rows (row 1, row 2, or overall), and the computation of their standard errors and Wald confidence limits follow the binomial proportion computations, which are described in the section “Binomial Proportion” on page 214.

The column 1 risk for row 1 is the proportion of row 1 observations classified in column 1,

\[
\hat{p}_1 = \frac{n_{11}}{n_1},
\]

which estimates the conditional probability of the column 1 response, given the first level of the row variable. The column 1 risk for row 2 is the proportion of row 2 observations classified in column 1,

\[
\hat{p}_2 = \frac{n_{21}}{n_2}.
\]

The overall column 1 risk is the proportion of all observations classified in column 1,

\[
\hat{p} = \frac{n_{1}}{n}
\]

The column 1 risk difference compares the risks for the two rows, and it is computed as the column 1 risk for row 1 minus the column 1 risk for row 2,

\[
\hat{d} = \hat{p}_1 - \hat{p}_2
\]
The standard error of the column 1 risk for row $i$ is computed as

$$se(\hat{p}_i) = \sqrt{\hat{p}_i (1 - \hat{p}_i) / n_i}.$$ 

The standard error of the overall column 1 risk is computed as

$$se(\hat{p}) = \sqrt{\hat{p} (1 - \hat{p}) / n}.$$ 

Where the two rows represent independent binomial samples, the standard error of the column 1 risk difference is computed as

$$se(\hat{d}) = \sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}.$$ 

The computations are similar for the column 2 risks and risk difference.

**Confidence Limits**

By default, the RISKDIFF option provides Wald asymptotic confidence limits for the risks (row 1, row 2, and overall) and the risk difference. By default, the RISKDIFF option also provides exact (Clopper-Pearson) confidence limits for the risks. You can suppress the display of this information by specifying the NORISKS riskdiff-option. You can specify riskdiff-options to request tests and other types of confidence limits for the risk difference. For more information, see the sections “Confidence Limits for the Risk Difference” on page 224 and “Risk Difference Tests” on page 228.

The risks are equivalent to the binomial proportions of their corresponding rows. This section describes the Wald confidence limits that are provided by default when you specify the RISKDIFF option. The BINOMIAL option provides additional confidence limit types and tests for risks (binomial proportions). For more information, see the sections “Binomial Confidence Limits” on page 214 and “Binomial Tests” on page 217.

The Wald confidence limits are based on the normal approximation to the binomial distribution. PROC FREQTAB computes the Wald confidence limits for the risks and risk differences as

$$\text{Est} \pm (z_{\alpha/2} \times se(\text{Est}))$$

where Est is the estimate, $z_{\alpha/2}$ is the 100(1 - $\alpha$/2)th percentile of the standard normal distribution, and se(\text{Est}) is the standard error of the estimate. The confidence level $\alpha$ is determined by the value of the ALPHA= option; by default, ALPHA=0.05, which produces 95% confidence limits.

If you specify the CORRECT riskdiff-option, PROC FREQTAB includes continuity corrections in the Wald confidence limits for the risks and risk differences. The purpose of a continuity correction is to adjust for the difference between the normal approximation and the binomial distribution, which is discrete. See Fleiss, Levin, and Paik (2003) for more information. The continuity-corrected Wald confidence limits are computed as

$$\text{Est} \pm (z_{\alpha/2} \times se(\text{Est}) + cc)$$

where $cc$ is the continuity correction. For the row 1 risk, $cc = (1/2n_1)$; for the row 2 risk, $cc = (1/2n_2)$; for the overall risk, $cc = (1/2n)$; and for the risk difference, $cc = ((1/n_1 + 1/n_2)/2)$. The column 1 and column 2 risks use the same continuity corrections.

By default when you specify the RISKDIFF option, PROC FREQTAB also provides exact (Clopper-Pearson) confidence limits for the column 1, column 2, and overall risks. These confidence limits are constructed by inverting the equal-tailed test that is based on the binomial distribution. For more information, see the section “Exact (Clopper-Pearson) Confidence Limits” on page 215.
Confidence Limits for the Risk Difference  PROC FREQTAB provides the following confidence limit types for the risk difference: Agresti-Caffo, exact unconditional, Hauck-Anderson, Miettinen-Nurminen (score), Newcombe (hybrid-score), and Wald confidence limits. Continuity-corrected forms of Newcombe and Wald confidence limits are also available.

The confidence coefficient for the confidence limits produced by the CL= riskdiff-option is $100(1 - \alpha)\%$, where the value of $\alpha$ is determined by the ALPHA= option. By default, ALPHA=0.05, which produces 95% confidence limits. This differs from the test-based confidence limits that are provided with the equivalence, noninferiority, and superiority tests, which have a confidence coefficient of $100(1 - 2\alpha)\%$ (Schuirmann 1999). For more information, see the section “Risk Difference Tests” on page 228.

**Agresti-Caffo Confidence Limits**
Agresti-Caffo confidence limits for the risk difference are computed as

$$\tilde{d} \pm (z_{\alpha/2} \times se(\tilde{d}))$$

where $\tilde{d} = \tilde{p}_1 - \tilde{p}_2$, $\tilde{p}_i = (n_{i1} + 1)/(n_i + 2)$,

$$se(\tilde{d}) = \sqrt{\tilde{p}_1(1 - \tilde{p}_2)/(n_1 + 2) + \tilde{p}_2(1 - \tilde{p}_2)/(n_2 + 2)}$$

and $z_{\alpha/2}$ is the 100$(1 - \alpha/2)$th percentile of the standard normal distribution.

The Agresti-Caffo interval adjusts the Wald interval for the risk difference by adding a pseudo-observation of each type (success and failure) to each sample. See Agresti and Caffo (2000) and Agresti and Coull (1998) for more information.

**Hauck-Anderson Confidence Limits**
Hauck-Anderson confidence limits for the risk difference are computed as

$$\hat{d} \pm (cc + z_{\alpha/2} \times se(\hat{d}))$$

where $\hat{d} = \hat{p}_1 - \hat{p}_2$ and $z_{\alpha/2}$ is the 100$(1 - \alpha/2)$th percentile of the standard normal distribution. The standard error is computed from the sample proportions as

$$se(\hat{d}) = \sqrt{\hat{p}_1(1 - \hat{p}_1)/(n_1 - 1) + \hat{p}_2(1 - \hat{p}_2)/(n_2 - 1)}$$

The Hauck-Anderson continuity correction $cc$ is computed as

$$cc = 1 / (2 \ min(n_1, n_2))$$

See Hauck and Anderson (1986) for more information. The subsection “Hauck-Anderson Test” in the section “Noninferiority Tests” on page 228 describes the corresponding noninferiority test.

**Miettinen-Nurminen (Score) Confidence Limits**
Miettinen-Nurminen (score) confidence limits for the risk difference (Miettinen and Nurminen 1985) are computed by inverting score tests for the risk difference. A score-based test statistic for the null hypothesis that the risk difference equals $\delta$ can be expressed as

$$T(\delta) = (\hat{d} - \delta)/\sqrt{\text{Var}(\delta)}$$
where \( \hat{d} \) is the observed value of the risk difference \( (\hat{p}_1 - \hat{p}_2) \),

\[
\sqrt{\text{Var}(\delta)} = \frac{n}{(n-1)} \left( \frac{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}{\hat{p}_1(\hat{p}_1)(1 - \hat{p}_1) + \hat{p}_2(\hat{p}_2)(1 - \hat{p}_2)} \right)
\]

and \( \hat{p}_1(\delta) \) and \( \hat{p}_2(\delta) \) are the maximum likelihood estimates of the row 1 and row 2 risks (proportions) under the restriction that the risk difference is \( \delta \). For more information, see Miettinen and Nurminen (1985, pp. 215–216) and Miettinen (1985, chapter 12).

The 100(1 - \( \alpha \))% confidence interval for the risk difference consists of all values of \( \delta \) for which the score test statistic \( T(\delta) \) falls in the acceptance region,

\[
\{ \delta : T(\delta) < z_{\alpha/2} \}
\]

where \( z_{\alpha/2} \) is the 100(1 - \( \alpha \))/2th percentile of the standard normal distribution. PROC FREQTAB finds the confidence limits by iterative computation, which stops when the iteration increment falls below the convergence criterion or when the maximum number of iterations is reached, whichever occurs first. By default, the convergence criterion is 0.0000001 and the maximum number of iterations is 100.

By default, the Miettinen-Nurminen confidence limits include the bias correction factor \( n/(n-1) \) in the computation of \( \sqrt{\text{Var}(\delta)} \) (Miettinen and Nurminen 1985, p. 216). For more information, see Newcombe and Nurminen (2011). If you specify the \texttt{CL=MN(CORRECT=NO)} \texttt{riskdiff-option}, PROC FREQTAB does not include the bias correction factor in this computation (Mee 1984). See also Agresti (2002, p. 77). The uncorrected confidence limits are labeled as “Miettinen-Nurminen-Mee” confidence limits in the displayed output.

The maximum likelihood estimates of \( p_1 \) and \( p_2 \), subject to the constraint that the risk difference is \( \delta \), are computed as

\[
\hat{p}_1 = 2u \cos(w) - b/3a \quad \text{and} \quad \hat{p}_2 = \hat{p}_1 - \delta
\]

where

\[
\begin{align*}
    w &= (\pi + \cos^{-1}(v/u^3))/3 \\
    v &= b^3/(3a)^3 - bc/6a^2 + d/2a \\
    u &= \text{sign}(v) \sqrt{b^2/(3a)^2 - c/3a} \\
    a &= 1 + \theta \\
    b &= -(1 + \theta + \hat{p}_1 + \theta \hat{p}_2 + \delta(\theta + 2)) \\
    c &= \delta^2 + \delta(2\hat{p}_1 + \theta + 1) + \hat{p}_1 + \theta \hat{p}_2 \\
    d &= -\hat{p}_1 \delta(1 + \delta) \\
    \theta &= n_2/n_1.
\end{align*}
\]

For more information, see Farrington and Manning (1990, p. 1453).

**Newcombe Confidence Limits**

Newcombe (hybrid-score) confidence limits for the risk difference are constructed from the Wilson score confidence limits for each of the two individual proportions. The confidence limits for the individual proportions are used in the standard error terms of the Wald confidence limits for the proportion difference. See Newcombe (1998a) and Barker et al. (2001) for more information.
Wilson score confidence limits for \( p_1 \) and \( p_2 \) are the roots of
\[
|p_i - \hat{p}_i| = z_{\alpha/2} \sqrt{p_i(1-p_i)/n_i},
\]
for \( i = 1, 2 \). The confidence limits are computed as
\[
\left( \hat{p}_i + z_{\alpha/2}/2n_i, \hat{p}_i + z_{\alpha/2}/2 \sqrt{\left( \hat{p}_i(1-\hat{p}_i) + z_{\alpha/2}^2/4n_i \right)/n_i} \right) / \left( 1 + z_{\alpha/2}^2/n_i \right)
\]
For more information, see the section “Wilson (Score) Confidence Limits” on page 217.

Denote the lower and upper Wilson score confidence limits for \( p_1 \) as \( L_1 \) and \( U_1 \), and denote the lower and upper confidence limits for \( p_2 \) as \( L_2 \) and \( U_2 \). The Newcombe confidence limits for the proportion difference \((d = p_1 - p_2)\) are computed as
\[
d_L = (\hat{p}_1 - \hat{p}_2) - \sqrt{(\hat{p}_1 - L_1)^2 + (U_2 - \hat{p}_2)^2}
\]
\[
d_U = (\hat{p}_1 - \hat{p}_2) + \sqrt{(U_1 - \hat{p}_1)^2 + (\hat{p}_2 - L_2)^2}
\]
If you specify the CORRECT riskdiff-option, PROC FREQTAB provides continuity-corrected Newcombe confidence limits. By including a continuity correction of \( 1/2n_i \), the Wilson score confidence limits for the individual proportions are computed as the roots of
\[
|p_i - \hat{p}_i| - 1/2n_i = z_{\alpha/2} \sqrt{p_i(1-p_i)/n_i}.
\]
The continuity-corrected confidence limits for the individual proportions are then used to compute the proportion difference confidence limits \( d_L \) and \( d_U \).

**Wald Confidence Limits**

Wald confidence limits for the risk difference are computed as
\[
\hat{d} \pm \left( z_{\alpha/2} \times se(\hat{d}) \right)
\]
where \( \hat{d} = \hat{p}_1 - \hat{p}_2 \), \( z_{\alpha/2} \) is the 100(1 - \( \alpha/2 \))th percentile of the standard normal distribution, and the standard error is computed from the sample proportions as
\[
se(\hat{d}) = \sqrt{\hat{p}_1(1-\hat{p}_1)/n_1 + \hat{p}_2(1-\hat{p}_2)/n_2}.
\]
If you specify the CORRECT riskdiff-option, the Wald confidence limits include a continuity correction \( cc \),
\[
\hat{d} \pm \left( cc \times se(\hat{d}) \right)
\]
where \( cc = (1/n_1 + 1/n_2)/2 \).
The subsection “Wald Test” in the section “Noninferiority Tests” on page 228 describes the corresponding noninferiority test.

**Exact Unconditional Confidence Limits**

If you specify the RISKDIFF option in the EXACT statement, PROC FREQTAB provides exact unconditional
confidence limits for the risk difference \( (d = p_1 - p_2) \). The exact unconditional approach fixes the row margins of the 2 \times 2 table and eliminates the nuisance parameter \( p_2 \) by using the maximum \( p \)-value (worst-case scenario) over all possible values of \( p_2 \) (Santner and Snell 1980). The conditional approach, which is described in the section “Exact Statistics” on page 265, does not apply to the risk difference because of the nuisance parameter (Agresti 1992).

By default, PROC FREQTAB computes the confidence limits by the tail method, which inverts two separate one-sided exact tests of the risk difference, where the tests are based on the score statistic (Chan and Zhang 1999). The size of each one-sided exact test is at most \( \alpha/2 \). If you specify the RISKDIFF(METHOD=NOSCORE) option in the EXACT statement, PROC FREQTAB computes the confidence limits by inverting two separate one-sided exact tests that are based on the unstandardized risk difference. If you specify the RISKDIFF(METHOD=SCORE2) option in the EXACT statement, PROC FREQTAB computes the confidence limits by inverting a single two-sided exact test that is based on the score statistic (Agresti and Min 2001).

The score statistic is a less discrete static than the unstandardized risk difference and produces less information, see Agresti and Min (2001) and Santner et al. (2007). The two-sided score method evaluates the \( p \)-values \( P_U(d_*) \) and \( P_L(d_*) \) by comparing \( |T(a)| \) to \( |t_0| \). To compute the confidence limits \( d_L \) and \( d_U \), the two-sided method compares the \( p \)-values to \( \alpha \). For more information, see Agresti and Min (2001) and Santner et al. (2007).
**Risk Difference Tests**

PROC FREQTAB provides tests of equality, noninferiority, superiority, and equivalence for the risk (proportion) difference. The following analysis methods are available: Wald (with and without continuity correction), Hauck-Anderson, Farrington-Manning (score), and Newcombe (with and without continuity correction). You can specify the method by using the METHOD= riskdiff-option; by default, PROC FREQTAB provides Wald tests.

**Equality Tests**  The equality test for the risk difference tests the null hypothesis that the risk difference equals the null value. You can specify a null value by using the EQUAL(NULL=) riskdiff-option; by default, the null value is 0. This test can be expressed as $H_0: d = d_0$ versus the alternative $H_a: d \neq d_0$, where $d = p_1 - p_2$ denotes the risk difference (for column 1 or column 2) and $d_0$ denotes the null value.

The test statistic is computed as

$$z = (\hat{d} - d_0)/se(\hat{d})$$

where the standard error $se(\hat{d})$ is computed by using the method that you specify. Available methods for the equality test include Wald (with and without continuity correction), Hauck-Anderson, and Farrington-Manning (score). For a description of the standard error computation, see the subsections “Wald Test,” “Hauck-Anderson Test,” and “Farrington-Manning (Score) Test,” respectively, in the section “Noninferiority Tests” on page 228.

PROC FREQTAB computes one-sided and two-sided $p$-values for equality tests. When the test statistic $z$ is greater than 0, PROC FREQTAB displays the right-sided $p$-value, which is the probability of a larger value occurring under the null hypothesis. The one-sided $p$-value can be expressed as

$$P_1 = \begin{cases} \text{Prob}(Z > z) & \text{if } z > 0 \\ \text{Prob}(Z < z) & \text{if } z \leq 0 \end{cases}$$

where $Z$ has a standard normal distribution. The two-sided $p$-value is computed as $P_2 = 2 \times P_1$.

**Noninferiority Tests**  If you specify the NONINF riskdiff-option, PROC FREQTAB provides a noninferiority test for the risk difference, or the difference between two proportions. The null hypothesis for the noninferiority test is

$$H_0: p_1 - p_2 \leq -\delta$$

versus the alternative

$$H_a: p_1 - p_2 > -\delta$$

where $\delta$ is the noninferiority margin. Rejection of the null hypothesis indicates that the row 1 risk is not inferior to the row 2 risk. See Chow, Shao, and Wang (2003) for more information.

You can specify the value of $\delta$ with the MARGIN= riskdiff-option. By default, $\delta = 0.2$. You can specify the test method with the METHOD= riskdiff-option. The following methods are available for the risk difference noninferiority analysis: Wald (with and without continuity correction), Hauck-Anderson, Farrington-Manning (score), and Newcombe (with and without continuity correction). The Wald, Hauck-Anderson, and Farrington-Manning methods provide tests and corresponding test-based confidence limits; the Newcombe method provides only confidence limits. If you do not specify METHOD=, PROC FREQTAB uses the Wald test by default.
The confidence coefficient for the test-based confidence limits is $100(1 - 2\alpha)\%$ (Schuirmann 1999). By default, if you do not specify the ALPHA= option, these are 90% confidence limits. You can compare the confidence limits to the noninferiority limit, $-\delta$.

The following sections describe the noninferiority analysis methods for the risk difference.

**Wald Test**

If you specify the METHOD=WALD riskdiff-option, PROC FREQTAB provides an asymptotic Wald test of noninferiority for the risk difference. This is also the default method. The Wald test statistic is computed as

$$z = (\hat{d} + \delta) / se(\hat{d})$$

where $(\hat{d} = \hat{p}_1 - \hat{p}_2)$ estimates the risk difference and $\delta$ is the noninferiority margin.

By default, the standard error for the Wald test is computed from the sample proportions as

$$se(\hat{d}) = \sqrt{\hat{p}_1(1 - \hat{p}_1)/n_1 + \hat{p}_2(1 - \hat{p}_2)/n_2}.$$ 

If you specify the VAR=NULL riskdiff-option, the standard error is based on the null hypothesis that the risk difference equals $-\delta$ (Dunnett and Gent 1977). The standard error is computed as

$$se(\hat{d}) = \sqrt{\hat{p}(1 - \hat{p})/n_2 + (\hat{p} - \delta)(1 - \hat{p} + \delta)/n_1}.$$ 

where

$$\hat{p} = (n_{11} + n_{21} + \delta n_{1.})/n$$

If you specify the CORRECT riskdiff-option, the test statistic includes a continuity correction. The continuity correction is subtracted from the numerator of the test statistic if the numerator is greater than 0; otherwise, the continuity correction is added to the numerator. The value of the continuity correction is $(1/n_1 + 1/n_2)/2$.

The $p$-value for the Wald noninferiority test is $P_z = \text{Prob}(Z > z)$, where $Z$ has a standard normal distribution.

**Hauck-Anderson Test**

If you specify the METHOD=HA riskdiff-option, PROC FREQTAB provides the Hauck-Anderson test for noninferiority. The Hauck-Anderson test statistic is computed as

$$z = (\hat{d} + \delta \pm cc) / se(\hat{d})$$

where $\hat{d} = \hat{p}_1 - \hat{p}_2$ and the standard error is computed from the sample proportions as

$$se(\hat{d}) = \sqrt{\hat{p}_1(1 - \hat{p}_1)/(n_1 - 1) + \hat{p}_2(1 - \hat{p}_2)/(n_2 - 1)}.$$ 

The Hauck-Anderson continuity correction $cc$ is computed as

$$cc = 1 / (2 \cdot \min(n_1, n_2))$$

The $p$-value for the Hauck-Anderson noninferiority test is $P_z = \text{Prob}(Z > z)$, where $Z$ has a standard normal distribution. See Hauck and Anderson (1986) and Schuirmann (1999) for more information.
**Farrington-Manning (Score) Test**

If you specify the METHOD=FM `riskdiff-option`, PROC FREQTAB provides the Farrington-Manning (score) test of noninferiority for the risk difference. A score test statistic for the null hypothesis that the risk difference equals $-\delta$ can be expressed as

$$z = \frac{\hat{d} + \delta}{se(\hat{d})}$$

where $\hat{d}$ is the observed value of the risk difference ($\hat{p}_1 - \hat{p}_2$),

$$se(\hat{d}) = \sqrt{\frac{\hat{p}_1(1 - \hat{p}_1)}{n_1} + \frac{\hat{p}_2(1 - \hat{p}_2)}{n_2}}.$$

and $\hat{p}_1$ and $\hat{p}_2$ are the maximum likelihood estimates of the row 1 and row 2 risks (proportions) under the restriction that the risk difference is $-\delta$. The $p$-value for the noninferiority test is $P_z = \text{Prob}(Z > z)$, where $Z$ has a standard normal distribution. For more information, see Miettinen and Nurminen (1985); Miettinen (1985); Farrington and Manning (1990); Dann and Koch (2005).

The maximum likelihood estimates of $p_1$ and $p_1$, subject to the constraint that the risk difference is $-\delta$, are computed as

$$\hat{p}_1 = 2u \cos(w) - b/3a \quad \text{and} \quad \hat{p}_2 = \hat{p}_1 + \delta$$

where

\[
\begin{align*}
  w &= (\pi + \cos^{-1}(v/u^3))/3 \\
  v &= b^3/(3a)^3 - bc/6a^2 + d/2a \\
  u &= \text{sign}(v)\sqrt{b^2/(3a)^2 - c/3a} \\
  a &= 1 + \theta \\
  b &= -(1 + \theta + \hat{p}_1 + \theta \hat{p}_2 - \delta(\theta + 2)) \\
  c &= \delta^2 - \delta(2\hat{p}_1 + \theta + 1) + \hat{p}_1 + \theta \hat{p}_2 \\
  d &= \hat{p}_1\delta(1 - \delta) \\
  \theta &= n_2/n_1.
\end{align*}
\]

For more information, see Farrington and Manning (1990, p. 1453).

**Newcombe Noninferiority Analysis**

If you specify the METHOD=NEWCOMBE `riskdiff-option`, PROC FREQTAB provides a noninferiority analysis that is based on Newcombe hybrid-score confidence limits for the risk difference. The confidence coefficient for the confidence limits is $100(1 - 2\alpha)%$ (Schuirmann 1999). By default, if you do not specify the ALPHA= option, these are 90% confidence limits. You can compare the confidence limits with the noninferiority limit, $-\delta$. If you specify the CORRECT `riskdiff-option`, the confidence limits includes a continuity correction. See the subsection “Newcombe Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224 for more information.

**Superiority Test**  If you specify the SUP `riskdiff-option`, PROC FREQTAB provides a superiority test for the risk difference. The null hypothesis is

$$H_0: p_1 - p_2 \leq \delta$$
versus the alternative

\[ H_a: p_1 - p_2 > \delta \]

where \( \delta \) is the superiority margin. Rejection of the null hypothesis indicates that the row 1 proportion is superior to the row 2 proportion. You can specify the value of \( \delta \) with the MARGIN= riskdiff-option. By default, \( \delta = 0.2 \).

The superiority analysis is identical to the noninferiority analysis but uses a positive value of the margin \( \delta \) in the null hypothesis. The superiority computations follow those in the section “Noninferiority Tests” on page 228 by replacing \(-\delta\) by \(\delta\). See Chow, Shao, and Wang (2003) for more information.

**Equivalence Test** If you specify the EQUIV riskdiff-option, PROC FREQTAB provides an equivalence test for the risk difference, or the difference between two proportions. The null hypothesis for the equivalence test is

\[ H_0: p_1 - p_2 \leq -\delta_L \quad \text{or} \quad p_1 - p_2 \geq \delta_U \]

versus the alternative

\[ H_a: \delta_L < p_1 - p_2 < \delta_U \]

where \( \delta_L \) is the lower margin and \( \delta_U \) is the upper margin. Rejection of the null hypothesis indicates that the two binomial proportions are equivalent. See Chow, Shao, and Wang (2003) for more information.

You can specify the value of the margins \( \delta_L \) and \( \delta_U \) with the MARGIN= riskdiff-option. If you do not specify MARGIN=, PROC FREQTAB uses lower and upper margins of \(-0.2\) and 0.2 by default. If you specify a single margin value \( \delta \), PROC FREQTAB uses lower and upper margins of \(-\delta\) and \(\delta\). You can specify the test method with the METHOD= riskdiff-option. The following methods are available for the risk difference equivalence analysis: Wald (with and without continuity correction), Hauck-Anderson, Farrington-Manning (score), and Newcombe (with and without continuity correction). The Wald, Hauck-Anderson, and Farrington-Manning methods provide tests and corresponding test-based confidence limits; the Newcombe method provides only confidence limits. If you do not specify METHOD=, PROC FREQTAB uses the Wald test by default.

PROC FREQTAB computes two one-sided tests (TOST) for equivalence analysis (Schuirmann 1987). The TOST approach includes a right-sided test for the lower margin \( \delta_L \) and a left-sided test for the upper margin \( \delta_U \). The overall \( p \)-value is taken to be the larger of the two \( p \)-values from the lower and upper tests.

The section “Noninferiority Tests” on page 228 gives details about the Wald, Hauck-Anderson, Farrington-Manning (score), and Newcombe methods for the risk difference. The lower margin equivalence test statistic takes the same form as the noninferiority test statistic but uses the lower margin value \( \delta_L \) in place of \(-\delta\). The upper margin equivalence test statistic take the same form as the noninferiority test statistic but uses the upper margin value \( \delta_U \) in place of \(-\delta\).

The test-based confidence limits for the risk difference are computed according to the equivalence test method that you select. If you specify METHOD=WALD with VAR=NULL, or METHOD=FM, separate standard errors are computed for the lower and upper margin tests. In this case, the test-based confidence limits are computed by using the maximum of these two standard errors. These confidence limits have a confidence coefficient of \( 100(1 - 2\alpha)\% \) (Schuirmann 1999). By default, if you do not specify the ALPHA= option, these are 90% confidence limits. You can compare the test-based confidence limits to the equivalence limits, \((\delta_L, \delta_U)\).
**Barnard’s Unconditional Exact Test**

The BARNARD option in the EXACT statement provides an unconditional exact test for the risk (proportion) difference for $2 \times 2$ tables. The reference set for the unconditional exact test consists of all $2 \times 2$ tables that have the same row sums as the observed table (Barnard 1945, 1947, 1949). This differs from the reference set for exact conditional inference, which is restricted to the set of tables that have the same row sums and the same column sums as the observed table. See the sections “Fisher’s Exact Test” on page 203 and “Exact Statistics” on page 265 for more information.

The test statistic is the standardized risk difference, which is computed as

$$T = d / \sqrt{p_1 (1 - p_1) (1/n_1 + 1/n_2)}$$

where the risk difference $d$ is defined as the difference between the row 1 and row 2 risks (proportions), $d = (n_{11}/n_1 - n_{21}/n_2)$; $n_1$ and $n_2$ are the row 1 and row 2 totals, respectively; and $p_1$ is the overall proportion in column 1, $(n_{11} + n_{21})/n$.

Under the null hypothesis that the risk difference is 0, the joint probability function for a table can be expressed in terms of the table cell frequencies, the row totals, and the unknown parameter $\pi$ as

$$f(n_{11}, n_{21}; n_1, n_2, \pi) = \binom{n_1}{n_{11}} \binom{n_2}{n_{21}} \pi^{n_{11} + n_{21}} (1 - \pi)^{n - n_{11} - n_{21}}$$

where $\pi$ is the common value of the risk (proportion).

PROC FREQTAB sums the table probabilities over the reference set for those tables where the test statistic is greater than or equal to the observed value of the test statistic. This sum can be expressed as

$$\text{Prob}(\pi) = \sum_{A, T(a) \geq t_0} f(n_{11}, n_{21}; n_1, n_2, \pi)$$

where the set $A$ contains all $2 \times 2$ tables with row sums equal to $n_1$ and $n_2$, and $T(a)$ denotes the value of the test statistic for table $a$ in $A$. The sum includes probabilities of those tables for which $(T(a) \geq t_0)$, where $t_0$ is the value of the test statistic for the observed table.

The sum Prob($\pi$) depends on the unknown value of $\pi$. To compute the exact $p$-value, PROC FREQTAB eliminates the nuisance parameter $\pi$ by taking the maximum value of Prob($\pi$) over all possible values of $\pi$,

$$\text{Prob} = \sup_{0 \leq \pi \leq 1} (\text{Prob}(\pi))$$


**Common Risk Difference**

If you specify the COMMONRISKDIFF option in the TABLES statement, PROC FREQTAB provides estimates, confidence limits, and tests for the common (overall) risk difference for multiway $2 \times 2$ tables.

**Mantel-Haenszel Confidence Limits and Test**

PROC FREQTAB computes the Mantel-Haenszel estimate, confidence limits, and test for the common risk difference by using Mantel-Haenszel stratum weights (Mantel and Haenszel 1959) and the Sato variance estimator (Sato 1989). The Mantel-Haenszel estimate of the common risk difference is

$$\hat{d}_{MH} = \sum_h \hat{d}_h w_h$$
where $\hat{d}_h$ is the risk difference in stratum $h$ and

$$w_h = \frac{n_{h1} n_{h2}}{n_h} / \sum_i \frac{n_{i1} n_{i2}}{n_i}$$

is the Mantel-Haenszel weight of stratum $h$. The column 1 risk difference in stratum ($2 \times 2$ table) $h$ is computed as

$$\hat{d}_h = \hat{p}_{h1} - \hat{p}_{h2} = (n_{h1}/n_h) - (n_{h21}/n_{h2})$$

where $\hat{p}_{h1}$ is the proportion of row 1 observations that are classified in column 1 and $\hat{p}_{h2}$ is the proportion or row 2 observations that are classified in column 1. The column 2 risk is computed in the same way. For more information, see Agresti (2013, p. 231).

PROC FREQTAB computes the variance of $\hat{d}_{MH}$ (Sato 1989) as

$$\hat{\sigma}^2(\hat{d}_{MH}) = \left( \hat{d}_{MH} \sum_h P_h + \sum_h Q_h \right) / \left( \sum_h n_{h1} n_{h2} / n_h \right)^2$$

where

$$P_h = (n_{h1}^2 n_{h21} - n_{h2}^2 n_{h11} + n_{h1} n_{h2} (n_{h21} - n_{h11}) / 2) / n_h^2$$

$$Q_h = (n_{h11} (n_{h21} - n_{h2}) + n_{h21} (n_{h11} - n_{h1})) / 2 n_h$$

The 100$(1 - \alpha)$% confidence limits for the common risk difference are

$$\hat{d}_{MH} \pm z_{\alpha/2} \times \hat{\sigma}(\hat{d}_{MH})$$

If you specify the COMMONRISKDIFF(TEST=MH) option, PROC FREQTAB provides a Mantel-Haenszel test of the null hypothesis that the common risk difference is 0, which is computed as $z_{MH} = \hat{d}_{MH} / \hat{\sigma}(\hat{d}_{MH})$. The two-sided $p$-value is $\text{Prob}(|Z| > |z_{MH}|)$, where $Z$ has a standard normal distribution.

**Minimum Risk Confidence Limits and Test**

PROC FREQTAB computes the minimum risk estimate, confidence limits, and test for the common risk difference by using the method of Mehrotra and Railkar (2000). The stratum estimates are weighted by minimum risk weights, which minimize the mean square error of the estimate of the common risk difference. Minimum risk weights are designed to improve precision and reduce bias (compared to other weighting strategies) and can minimize the power loss that can occur when underlying assumptions are not met. For more information, see Mehrotra (2001) and Dmitrienko et al. (2005, section 1.3.3).

The minimum risk estimate of the common risk difference is

$$\hat{d}_{MR} = \sum_h \hat{d}_h w_h^*$$

where $\hat{d}_h$ is the risk difference in stratum $h$ and $w_h^*$ is the minimum risk weight of stratum $h$ (which is described in the section “Minimum Risk Weights” on page 234). The variance of $\hat{d}_{MR}$ is estimated by

$$\hat{V}(\hat{d}_{MR}) = \sum_h w_h^{*2} \hat{V}_h$$
where $\hat{V}_h$ (the variance estimate of the stratum $h$ risk difference) is computed as:

$$\hat{V}_h = \hat{p}_{h1}(1 - \hat{p}_{h1})/n_{h1} + \hat{p}_{h2}(1 - \hat{p}_{h2})/n_{h2}.$$ 

The $100(1 - \alpha)$% minimum risk confidence limits for the common risk difference are

$$\hat{d}_{MR} \pm \left( cc + z_{\alpha/2} \sqrt{\hat{V}(\hat{d}_{MR})} \right)$$

where the continuity correction is

$$cc = 0.1875 / \sum_h (n_{h1} n_{h2}/n_h)$$

The continuity correction is applied only when $cc < |\hat{d}_{MR}|$ (Fleiss, Levin, and Paik 2003). You can remove the continuity correction by specifying the COMMONRISKDIFF(CORRECT=NO) option.

By default, the minimum risk test is computed as

$$z_{MR} = \left( \hat{d}_{MR} \pm cc \right) / \sqrt{\hat{V}_0(\hat{d}_{MR})}$$

The continuity correction $cc$ is subtracted from $\hat{d}_{MR}$ if $\hat{d}_{MR} > 0$ and added to $\hat{d}_{MR}$ if $\hat{d}_{MR} < 0$. The null variance of the common risk difference is estimated by

$$\hat{V}_0(\hat{d}_{MR}) = \sum_h w_h^2 \hat{V}_0(\hat{d}_h)$$

where $\hat{V}_0(\hat{d}_h)$ (an estimate of the variance of the stratum $h$ risk difference under the null hypothesis) is

$$\hat{V}_0(\hat{d}_h) = \hat{p}_h(1 - \hat{p}_h) (1/n_{h1} + 1/n_{h2})$$

and

$$\hat{p}_h = (n_{h1} \hat{p}_{h1} + n_{h2} \hat{p}_{h2}) / (n_{h1} + n_{h2})$$

The two-sided $p$-value is $\text{Prob}(|Z| > |z_{MR}|)$, where $Z$ has a standard normal distribution.

If you specify the VAR=SAMPLE option for COMMONRISKDIFF(TEST=MR), PROC FREQTAB uses the sample variance estimate $\hat{V}(\hat{d}_{MR})$ instead of the null variance estimate $\hat{V}_0(\hat{d}_{MR})$ in the denominator of the test statistic $z_{MR}$. If you specify the COMMONRISKDIFF(CORRECT=NO) option, the continuity correction is not included in the test statistic.

**Minimum Risk Weights**  The estimate of the minimum risk weight for stratum $h$ is defined by Mehrotra and Railkar (2000), as

$$w_h^* = \frac{\beta_h}{\sum_i \hat{V}_i^{-1}} - \left( \frac{\alpha_h \hat{V}_h^{-1}}{\sum_i \hat{V}_i^{-1} + \sum_k \alpha_k \hat{d}_i \hat{V}_i^{-1}} \right) \left( \frac{\sum_i \hat{d}_i \beta_i}{\sum_i \hat{V}_i^{-1}} \right)$$

where

$$\alpha_h = \sum_i \hat{V}_i^{-1} - \sum_i \hat{d}_i \hat{V}_i^{-1}$$
Statistical Computations

\[ \beta_h = \hat{V}_h \left( 1 + \alpha_h \sum_i f_i \hat{d}_i \right) \]

and \( f_h \) is the fraction in stratum \( h \)

\[ f_h = n_h / \sum_i n_h \]

All sums are over the \( s \) strata (2 \( \times \) 2 tables) in the multiway table request, \( \hat{d}_i \) denotes the risk difference estimate in stratum \( i \), and \( \hat{V}_i \) denotes the sample variance estimate of the risk difference in stratum \( i \).

**Summary Score Confidence Limits**

PROC FREQTAB computes the summary score estimate of the common risk difference (Agresti 2013, p. 231) by using inverse-variance stratum weights and Miettinen-Nurminen (score) confidence limits for the stratum risk differences. For more information, see the section “Miettinen-Nurminen (Score) Confidence Limits.”

The score confidence interval for the risk difference in stratum \( h \) can be expressed as \( \hat{d}_h \pm z_{\alpha/2} s_h' \), where \( \hat{d}_h' \) is the midpoint of the score confidence interval and \( s_h' \) is the width of the confidence interval divided by \( 2z_{\alpha/2} \). The summary score estimate of the common risk difference is computed as

\[ \hat{d}_S = \sum_h \hat{d}_h' w_h' \]

where

\[ w_h' = (1/s_h'^2) / \sum_i (1/s_i'^2) \]

The variance of \( \hat{d}_S \) is computed as

\[ \hat{\sigma}^2(\hat{d}_S) = 1 / \sum_h (1/s_h'^2) \]

The 100(1 - \( \alpha \))% summary score confidence limits for the common risk difference are

\[ \hat{d}_S \pm \left( z_{\alpha/2} \times \hat{\sigma}(\hat{d}_S) \right) \]

If you specify the **COMMONRISKDIFF(TEST=SCORE)** option, PROC FREQTAB provides a summary score test of the null hypothesis that the common risk difference is 0. The test statistic is \( z_S = \hat{d}_S / \hat{\sigma}(\hat{d}_S) \). The two-sided \( p \)-value is \( \text{Prob}(|Z| > |z_S|) \) where \( Z \) has a standard normal distribution.

**Stratified Newcombe Confidence Limits**

PROC FREQTAB computes stratified Newcombe confidence limits for the common risk (proportion) difference by using the method of Yan and Su (2010). The stratified Newcombe confidence limits are constructed from stratified Wilson confidence limits for the common (overall) row proportions. By default, the strata are weighted by Mantel-Haenszel weights; if you specify the **COMMONRISKDIFF(CL=NEWCOMBEMR)** option, the strata are weighted by minimum risk weights.

PROC FREQTAB first computes individual Wilson confidence limits for the row proportions in each 2 \( \times \) 2 table (stratum), as described in the section “Wilson (Score) Confidence Limits” on page 217. These stratum
Wilson confidence limits are then combined to form stratified Wilson confidence limits for the overall row proportions by using stratum weights (either Mantel-Haenszel or minimum risk). The confidence levels of the stratum Wilson confidence limits are chosen so that the overall confidence coefficient (for the stratified Wilson confidence limits) is $100(1 - \alpha)\%$ (Yan and Su 2010).

Denote the lower and upper stratified Wilson score confidence limits for the common row 1 proportion as $L_1$ and $U_1$, respectively, and denote the lower and upper stratified Wilson confidence limits for the common row 2 proportion as $L_2$ and $U_2$, respectively. The $100(1 - \alpha)\%$ stratified Newcombe confidence limits for the common risk (proportion) difference are

$$
L = \hat{d} - z_{\alpha/2} \sqrt{\lambda_1 L_1(1 - L_1) + \lambda_2 U_2(1 - U_2)}
$$

$$
U = \hat{d} + z_{\alpha/2} \sqrt{\lambda_2 L_2(1 - L_2) + \lambda_1 U_1(1 - U_1)}
$$

where $\hat{d}$ is the weighted estimate of the common risk difference and

$$
\lambda_1 = \sum_h w_h^2 / n_{h1},
$$

$$
\lambda_2 = \sum_h w_h^2 / n_{h2}.
$$

By default, the strata are weighted by Mantel-Haenszel weights, which are defined as

$$
w_h = \frac{n_{h1} n_{h2}}{n_h} / \sum_i \frac{n_{i1} n_{i2}}{n_i}
$$

and the weighted estimate of the common risk difference is $\hat{d}_{MH}$. For more information, see the section “Mantel-Haenszel Confidence Limits and Test” on page 232. Optionally, the strata are weighted by minimum risk weights, and the weighted estimate of the common risk difference is $\hat{d}_{MR}$. For more information, see the section “Minimum Risk Confidence Limits and Test” on page 233.

When there is a single stratum, the stratified Newcombe confidence interval is equivalent to the (unstratified) Newcombe confidence interval. For more information, see the subsection “Newcombe Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224. See also Kim and Won (2013).

**Odds Ratio and Relative Risks for $2 \times 2$ Tables**

**Odds Ratio**

The odds ratio is a useful measure of association for a variety of study designs. For a retrospective design called a *case-control study*, the odds ratio can be used to estimate the relative risk when the probability of positive response is small (Agresti 2002). In a case-control study, two independent samples are identified based on a binary (yes-no) response variable, and the conditional distribution of a binary explanatory variable is examined within fixed levels of the response variable. For more information, see Stokes, Davis, and Koch (2012), Agresti (2013), and Agresti (2007).

The odds of a positive response (column 1) in row 1 is $n_{11}/n_{12}$. Similarly, the odds of a positive response in row 2 is $n_{21}/n_{22}$. The odds ratio is formed as the ratio of the row 1 odds to the row 2 odds. The odds ratio for a $2 \times 2$ table is defined as

$$
OR = \frac{n_{11}/n_{12}}{n_{21}/n_{22}} = \frac{n_{11} n_{22}}{n_{12} n_{21}}
$$
The odds ratio can be any nonnegative number. When the row and column variables are independent, the true value of the odds ratio is 1. An odds ratio greater than 1 indicates that the odds of a positive response are higher in row 1 than in row 2. An odds ratio less than 1 indicates that the odds of a positive response are higher in row 2. The strength of association increases as the deviation from 1 increases.

The transformation $G = (OR - 1)/(OR + 1)$ transforms the odds ratio to the range $(-1,1)$, where $G = 0$ when $OR = 1$; $G = -1$ when $OR = 0$; and $G$ approaches 1 as $OR$ approaches infinity. $G$ is the gamma statistic, which PROC FREQTAB computes when you specify the MEASURES option.

**Confidence Limits for the Odds Ratio** The following types of confidence limits are available for the odds ratio: exact, exact mid-$p$, likelihood ratio, score, Wald, and Wald modified.

**Wald Confidence Limits**
The asymptotic Wald confidence limits are based on a log transformation of the odds ratio (Woolf 1955; Haldane 1955). PROC FREQTAB computes the Wald confidence limits as

$$( OR \times \exp(-z \sqrt{v}), \ OR \times \exp(z \sqrt{v}) )$$

where

$$v = \text{Var}(\ln OR) = 1/n_{11} + 1/n_{12} + 1/n_{21} + 1/n_{22}$$

and $z$ is the $100(1 - \alpha/2)$th percentile of the standard normal distribution. The confidence level $\alpha$ is determined by the ALPHA= option in the TABLES statement; by default, ALPHA=0.05, which produces 95% confidence limits for the odds ratio. If any of the four cell frequencies are 0, $v$ is undefined and the Wald confidence limits cannot be computed. For more information, see Agresti (2013, p. 70).

**Wald Modified Confidence Limits**
PROC FREQTAB computes Wald modified confidence limits (Haldane 1955) for the odds ratio by replacing the $n_{ij}$ by $(n_{ij} + 0.5)$ in the estimator $OR$ and the variance $v$ as follows:

$$OR = \frac{(n_{11} + 0.5) (n_{22} + 0.5)}{(n_{12} + 0.5) (n_{21} + 0.5)}$$

$$v = \text{Var}(\ln OR) = 1/(n_{11} + 0.5) + 1/(n_{12} + 0.5) + 1/(n_{21} + 0.5) + 1/(n_{22} + 0.5)$$

The modified confidence limits are then computed as

$$( OR \times \exp(-z \sqrt{v}), \ OR \times \exp(z \sqrt{v}) )$$

where $z$ is the $100(1 - \alpha/2)$th percentile of the standard normal distribution. For more information, see Fleiss, Levin, and Paik (2003) and Agresti (2013).

**Score Confidence Limits**
Score confidence limits for the odds ratio (Miettinen and Nurminen 1985) are computed by inverting score tests for the odds ratio. A score-based chi-square test statistic for the null hypothesis that the odds ratio equals $\theta$ can be expressed as

$$Q(\theta) = \{n_1 (\hat{p}_1 - \bar{p}_1))^2 / \{n/(n-1)} \{1/ (n_1 \hat{p}_1 (1 - \bar{p}_1)) + 1/(n_2 \hat{p}_2 (1 - \bar{p}_2))\}^{-1}$$
where $\hat{p}_1$ is the observed row 1 risk ($n_{11}/n_1$), and $\tilde{p}_1$ and $\tilde{p}_2$ are the maximum likelihood estimates of the row 1 and row 2 risks under the restriction that the odds ratio ($n_{11}n_{22}/n_{12}n_{21}$) is $\theta$. For more information, see Miettinen and Nurminen (1985) and Miettinen (1985, chapter 14).

The 100(1 − $\alpha$)% score confidence interval for the odds ratio consists of all values of $\theta$ for which the test statistic $Q(\theta)$ falls in the acceptance region,

$$\{\theta : Q(\theta) < x^2_{1,\alpha}\}$$

where $x^2_{1,\alpha}$ is the 100(1 − $\alpha$)th percentile of the chi-square distribution with 1 degree of freedom. For more information about score confidence limits, see Agresti (2013).

By default, the score confidence limits include the bias correction factor $n/(n - 1)$ in the denominator of $Q(\theta)$ (Miettinen and Nurminen 1985, p. 217). If you specify the CL=SCORE(CORRECT=NO) option, PROC FREQTAB does not include this factor in the computation.

The maximum likelihood estimates of $p_1$ and $p_2$, subject to the constraint that the odds ratio is $\theta$, are computed as

$$\tilde{p}_2 = \left(-b + \sqrt{b^2 - 4ac}\right)/2a \quad \text{and} \quad \tilde{p}_1 = \tilde{p}_2 \theta / (1 + \tilde{p}_2(\theta - 1))$$

where

$$a = n_2(\theta - 1)$$
$$b = n_1 \theta + n_2 - \tilde{p}_1(\theta - 1)$$
$$c = -\tilde{p}_1$$

For more information, see Miettinen and Nurminen (1985, pp. 217–218) and Miettinen (1985, chapter 14).

**Likelihood Ratio Confidence Limits**

Likelihood ratio (profile likelihood) confidence limits for the odds ratio are computed by inverting likelihood ratio tests. The likelihood ratio test statistic for the null hypothesis that the odds ratio equals $\theta$ can be expressed as

$$G^2(\theta) = 2 \left(n_{11} \ln(\hat{p}_1/\tilde{p}_1) + n_{12} \ln((1 - \hat{p}_1)/(1 - \tilde{p}_1)) + n_{21} \ln(\hat{p}_2/\tilde{p}_2) + n_{22} \ln((1 - \hat{p}_2)/(1 - \tilde{p}_2))\right)$$

where $\hat{p}_i$ is the observed row $i$ risk ($n_{ii}/n_i$) and $\tilde{p}_i$ is the maximum likelihood estimate of the row $i$ risk under the restriction that the odds ratio is $\theta$. The computation of the maximum likelihood estimates is described in the subsection “Score Confidence Limits” in this section. For more information, see Agresti (2013), Miettinen and Nurminen (1985), and Miettinen (1985, chapter 14).

The 100(1 − $\alpha$)% likelihood ratio confidence interval for the odds ratio consists of all values of $\theta$ for which the test statistic $G^2(\theta)$ falls in the acceptance region,

$$\{\theta : G^2(\theta) < x^2_{1,\alpha}\}$$

where $x^2_{1,\alpha}$ is the 100(1 − $\alpha$)th percentile of the chi-square distribution with 1 degree of freedom.

**Exact Confidence Limits**

PROC FREQTAB computes exact confidence limits for the odds ratio by inverting two one-sided (equal-tail)
exact tests that are based on the noncentral hypergeometric distribution, where the distribution is conditional on the observed marginal totals of the $2 \times 2$ table. The exact confidence limits $\phi_1$ and $\phi_2$ are the solutions to the equations

$$\sum_{i=n_{11}}^{n_{11}} f(i : n_1, n_{11}, n_{22}, \phi_1) = \alpha/2$$
$$\sum_{i=0}^{n_{11}} f(i : n_1, n_{11}, n_{22}, \phi_2) = \alpha/2$$

where

$$f(i : n_1, n_{11}, n_{22}, \phi) = \left(\begin{array}{c} n_1 \\ i \end{array}\right) \left(\begin{array}{c} n_{22} \\ n_{11} - i \end{array}\right) \phi^i / \sum_{i=0}^{n_{11}} \left(\begin{array}{c} n_1 \\ i \end{array}\right) \left(\begin{array}{c} n_{22} \\ n_{11} - i \end{array}\right) \phi^i$$

For more information, see Fleiss, Levin, and Paik (2003), Thomas (1971), and Gart (1971).

Because this is a discrete problem, the confidence coefficient for the exact confidence interval is not exactly $(1 - \alpha)$ but is at least $(1 - \alpha)$; thus, these confidence limits are conservative. For more information, see Agresti (1992).

When the odds ratio is 0, which occurs when either $n_{11} = 0$ or $n_{22} = 0$, PROC FREQTAB sets the lower exact confidence limit to 0 and determines the upper limit by using the level $\alpha$ (instead of $\alpha/2$). Similarly, when the odds ratio is infinity, which occurs when either $n_{12} = 0$ or $n_{21} = 0$, PROC FREQTAB sets the upper exact confidence limit to infinity and determines the lower limit by using level $\alpha$.

**Exact Mid-p Confidence Limits**

PROC FREQTAB computes exact mid-p confidence limits for the odds ratio by inverting two one-sided hypergeometric tests that include mid-p tail areas. The mid-p approach replaces the probability of the observed table by half of that probability in the hypergeometric probability sums, which are described in the subsection “Exact Confidence Limits” in this section. The exact mid-p confidence limits $\phi_1$ and $\phi_2$ are the solutions to the equations

$$\sum_{i=n_{11}+1}^{n_{11}} f(i : n_1, n_{11}, n_{22}, \phi_1) + (1/2) f(n_{11} : n_1, n_{11}, n_{22}, \phi_1) = \alpha/2$$
$$\sum_{i=0}^{n_{11}-1} f(i : n_1, n_{11}, n_{22}, \phi_2) + (1/2) f(n_{11} : n_1, n_{11}, n_{22}, \phi_2) = \alpha/2$$

where

$$f(i : n_1, n_{11}, n_{22}, \phi) = \left(\begin{array}{c} n_1 \\ i \end{array}\right) \left(\begin{array}{c} n_{22} \\ n_{11} - i \end{array}\right) \phi^i / \sum_{i=0}^{n_{11}} \left(\begin{array}{c} n_1 \\ i \end{array}\right) \left(\begin{array}{c} n_{22} \\ n_{11} - i \end{array}\right) \phi^i$$

For more information, see Agresti (2013).

When the odds ratio is 0, which occurs when either $n_{11} = 0$ or $n_{22} = 0$, PROC FREQTAB sets the lower exact confidence limit to 0 and determines the upper limit by using the level $\alpha$ (instead of $\alpha/2$). Similarly, when the odds ratio is infinity, which occurs when either $n_{12} = 0$ or $n_{21} = 0$, PROC FREQTAB sets the upper exact confidence limit to infinity and determines the lower limit by using level $\alpha$. 
**Relative Risks**

Relative risks are useful measures in cohort (prospective) study designs, where two samples are identified based on the presence or absence of an explanatory factor. The two samples are observed in future time for the binary (yes-no) response variable under study. Relative risks are also useful in cross-sectional studies, where two variables are observed simultaneously. For more information, see Stokes, Davis, and Koch (2012) and Agresti (2007).

The relative risk is the ratio of the row 1 risk to the row 2 risk in a $2 \times 2$ table. The column 1 risk in row 1 is the proportion of row 1 observations that are classified in column 1, which can be expressed as

$$p_1 = \frac{n_{11}}{n_1}.$$  

Similarly, the column 1 risk in row 2 is

$$p_2 = \frac{n_{21}}{n_2}.$$  

The column 1 relative risk is computed as

$$R = \frac{p_1}{p_2}.$$  

A relative risk greater than 1 indicates that the probability of positive response is greater in row 1 than in row 2. Similarly, a relative risk less than 1 indicates that the probability of positive response is less in row 1 than in row 2. The strength of association increases as the deviation from 1 increases.

**Confidence Limits for the Relative Risk**  
PROC FREQTAB provides the following types of confidence limits for the relative risk: exact unconditional, likelihood ratio, score, Wald, and Wald modified.

**Wald Confidence Limits**  
The asymptotic Wald confidence limits are based on a log transformation of the relative risk. PROC FREQTAB computes the Wald confidence limits for the column 1 relative risk as

$$\left( \hat{r} \times \exp(-z\sqrt{v}), \hat{r} \times \exp(z\sqrt{v}) \right)$$  

where $\hat{r}$ is the observed value of the relative risk, $\hat{p}_1/\hat{p}_2$, and

$$v = \text{Var}(\ln(\hat{r})) = \left( \frac{(1 - \hat{p}_1/n_{11})}{n_1} + \frac{(1 - \hat{p}_2/n_{21})}{n_2} \right)$$

and $z$ is the 100(1 - $\alpha$/2)th percentile of the standard normal distribution. The confidence level $\alpha$ is determined by the ALPHA= option in the TABLES statement; by default, ALPHA=0.05, which produces 95% confidence limits. If either cell frequency $n_{11}$ or $n_{21}$ is 0, then $v$ is undefined and the Wald confidence limits cannot be computed.

PROC FREQTAB computes the confidence limits for the column 2 relative risk in the same way.

**Wald Modified Confidence Limits**  
PROC FREQTAB computes Wald modified confidence limits (Haldane 1955) for the relative risk by replacing the $n_{ij}$ with $(n_{ij} + 0.5)$ and the $n_i$, with $(n_i + 0.5)$ in the estimator $R$ and the variance $v$ as follows:

$$\hat{r}_m = \frac{\hat{p}_1}{\hat{p}_2} = \frac{(n_{11} + 0.5)/(n_1 + 0.5)}{(n_{21} + 0.5)/(n_2 + 0.5)}$$
\[ v = \text{Var}(\ln(\hat{r}_m)) = 1/(n_{11} + 0.5) + 1/(n_{21} + 0.5) - 1/(n_1 + 0.5) - 1/(n_2 + 0.5) \]

The confidence limits are computed as
\[
\left( \hat{r}_m \times \exp(-z\sqrt{v}), \hat{r}_m \times \exp(z\sqrt{v}) \right)
\]
where \( z \) is the 100\((1 - \alpha/2)\)th percentile of the standard normal distribution. For more information, see Fleiss, Levin, and Paik (2003) and Agresti (2013).

**Score Confidence Limits**

Score confidence limits (Miettinen and Nurminen 1985; Farrington and Manning 1990) are computed by inverting score tests for the relative risk. A score-based chi-square test statistic for the null hypothesis that the relative risk is \( r_0 \) can be expressed as
\[ Q(r_0) = (\hat{p}_1 - r_0 \hat{p}_2)^2 / \text{Var}(r_0) \]
where \( \hat{p}_1 \) and \( \hat{p}_2 \) are the observed row 1 and row 2 risks (proportions), respectively,
\[ \text{Var}(r_0) = (n/(n - 1)) \left( \frac{\hat{p}_1(1 - \hat{p}_1)/n_1 + r_0^2 \hat{p}_2(1 - \hat{p}_2)/n_2}{\hat{p}_1(1 - \hat{p}_1)/n_1 + r_0^2 \hat{p}_2(1 - \hat{p}_2)/n_2} \right) \]
where \( \hat{p}_1 \) and \( \hat{p}_2 \) are the maximum likelihood estimates of \( p_1 \) and \( p_2 \), respectively, under the null hypothesis that the relative risk is \( r_0 \). For more information, see Miettinen and Nurminen (1985) and Miettinen (1985, chapter 13).

The 100\((1 - \alpha)\)% score confidence interval for the relative risk consists of all values of \( r_0 \) for which the test statistic \( Q(r_0) \) falls in the acceptance region,
\[ \{ r_0 : Q(r_0) < \chi^2_{1, \alpha} \} \]
where \( \chi^2_{1, \alpha} \) is the 100\((1 - \alpha)\)th percentile of the chi-square distribution with 1 degree of freedom. For more information, see Agresti (2013).

By default, the score confidence limits include the bias correction factor \( n/(n - 1) \) in the denominator of \( Q(r_0) \) (Miettinen and Nurminen 1985, p. 217). If you specify the CL=SCORE(CORRECT=NO) option, PROC FREQTAB does not include this factor in the computation.

The maximum likelihood estimates of \( p_1 \) and \( p_2 \), subject to the constraint that the relative risk is \( r_0 \), are computed as
\[ \hat{p}_1 = \left( -b - \sqrt{b^2 - 4ac} \right) / 2a \quad \text{and} \quad \hat{p}_2 = \hat{p}_1 / r_0 \]
where
\[
\begin{align*}
a &= 1 + \theta \\
b &= - (r_0 (1 + \theta \hat{p}_2) + \theta + \hat{p}_1) \\
c &= r_0 (\hat{p}_1 + \theta \hat{p}_2) \\
\theta &= n_2/n_1.
\end{align*}
\]
For more information, see Farrington and Manning (1990, p. 1454) and Miettinen and Nurminen (1985, p. 217).
**Likelihood Ratio Confidence Limits**

Likelihood ratio (profile likelihood) confidence limits for the relative risk are computed by inverting likelihood ratio tests. The likelihood ratio test statistic for the null hypothesis that the relative risk ratio is $r_0$ can be expressed as

$$G^2(r_0) = 2 \left( n_{11} \ln(\hat{p}_1/\hat{p}_1) + n_{12} \ln((1-\hat{p}_1)/(1-\hat{p}_1)) + n_{21} \ln(\hat{p}_2/\hat{p}_2) + n_{22} \ln((1-\hat{p}_2/(1-\hat{p}_2)) \right)$$

where $\hat{p}_i$ is the observed row $i$ risk ($n_{ii}/n_i$) and $\hat{p}_i$ is the maximum likelihood estimate of the row $i$ risk under the restriction that the relative risk is $r_0$. Expressions for the maximum likelihood estimates $\hat{p}_1$ and $\hat{p}_2$ are given in the subsection “Score Confidence Limits” in this section. For more information, see Miettinen and Nurminen (1985) and Miettinen (1985, chapter 13).

The $100(1 - \alpha)\%$ likelihood ratio confidence interval for the relative risk consists of all values of $r_0$ for which the test statistic $G^2(r_0)$ falls in the acceptance region,

$$\{ \theta : G^2(r_0) < \chi^2_{1,\alpha} \}$$

where $\chi^2_{1,\alpha}$ is the $100(1 - \alpha)$th percentile of the chi-square distribution with 1 degree of freedom.

**Exact Unconditional Confidence Limits**

If you specify the RELRISK option in the EXACT statement, PROC FREQTAB provides exact unconditional confidence limits for the relative risk. The exact unconditional approach fixes the row margins of the $2 \times 2$ table and eliminates the nuisance parameter $p_2$ by using the maximum $p$-value (worst-case scenario) over all possible values of $p_2$ (Santner and Snell 1980). The conditional approach, which is described in the section “Exact Statistics” on page 265, does not apply to the relative risk because of the nuisance parameter (Agresti 1992).

By default, PROC FREQTAB computes the confidence limits by the tail method, which inverts two separate one-sided exact tests of the relative risk, where the tests are based on the score statistic (Chan and Zhang 1999). The size of each one-sided exact test is at most $\alpha/2$, and the confidence coefficient is at least $(1 - \alpha)$. If you specify the RELRISK(METHOD=NOSCORE) option in the EXACT statement, PROC FREQTAB computes the confidence limits by inverting two separate one-sided exact tests that are based on the unstandardized relative risk. If you specify the RELRISK(METHOD=SCORE2) option in the EXACT statement, PROC FREQTAB computes the confidence limits by inverting a single two-sided exact test that is based on the score statistic (Agresti and Min 2001).

PROC FREQTAB uses the relative risk score statistic (or the modified form of the unstandardized relative risk) to compute the exact confidence limits as described in the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Risk Difference” on page 224.

The score statistic is a less discrete statistic than the unstandardized risk difference and produces less conservative confidence limits (Agresti and Min 2001). For more information, see Santner et al. (2007). The relative risk score statistic (Miettinen and Nurminen 1985; Farrington and Manning 1990) is computed as

$$z(r_0) = (\hat{p}_1 - r_0 \hat{p}_2) / \text{se}(r_0)$$

where

$$\text{se}(r_0) = \sqrt{\hat{p}_1(1-\hat{p}_1)/n_1 + r_0^2 \hat{p}_2(1-\hat{p}_2)/n_2}.$$
where $\hat{p}_1$ and $\hat{p}_2$ are the maximum likelihood estimates of $p_1$ and $p_2$ under the restriction that the relative risk is $r_0$. Expressions for the maximum likelihood estimates $\hat{p}_1$ and $\hat{p}_2$ are given in the subsection “Score Confidence Limits” in this section. For more information, see Farrington and Manning (1990, p. 1454) and Miettinen and Nurminen (1985, p. 217).

When the confidence limits are computed by using the unstandardized relative risk as the test statistic (METHOD=NOSCORE), PROC FREQTAB uses a modified form of the relative risk to ensure that the statistic is defined when there are zero-frequency table cells. The modified form adds 0.5 to the table cell and row frequencies (Gart and Nam 1988) and is computed as:

$$\hat{\tau} = \frac{(n_{11} + 0.5) / (n_1 + 0.5)}{(n_{21} + 0.5) / (n_2 + 0.5)}$$

For more information, see the subsection “Wald Modified Confidence Limits” in this section.

**Relative Risk Tests**

PROC FREQTAB provides tests of equality, noninferiority, superiority, and equivalence for the relative risk. The following analysis methods are available: Wald (which is based on a log transformation), Wald modified, score, and likelihood ratio. You can specify the method by using the METHOD= relrisk-option; by default, PROC FREQTAB provides Wald tests.

**Equality Test**

An equality test for the relative risk can be expressed as

$$H_0: R = r_0$$

versus the alternative

$$H_a: R \neq r_0$$

where $R = p_1 / p_2$ denotes the relative risk (for column 1 or column 2) and $r_0$ denotes the null value. You can specify a null value by using the EQUAL(NULL=) relrisk-option; by default, the null value is 1.

The test statistic is computed by the method that you specify; by default, PROC FREQTAB uses the Wald test. For information about test statistic computation, see the subsections “Wald Test,” “Wald Modified Test,” “Farrington-Manning (Score) Test,” and “Likelihood Ratio Test” in this section.

For the Wald and score methods, the test statistics $z$ have standard normal distributions under the null hypothesis. For the likelihood ratio test, the test statistic $G^2$ has a chi-square distribution with 1 degree of freedom under the null hypothesis.

When the test statistic $z$ is greater than 0, PROC FREQTAB displays the right-sided $p$-value, which is the probability of a larger value occurring under the null hypothesis. The one-sided $p$-value can be expressed as

$$P_1 = \begin{cases} \text{Prob}(Z > z) & \text{if } z > 0 \\ \text{Prob}(Z < z) & \text{if } z \leq 0 \end{cases}$$

where $Z$ has a standard normal distribution. The two-sided $p$-value is computed as $P_2 = 2 \times P_1$.

**Noninferiority Test**

A noninferiority test for the relative risk can be expressed as

$$H_0: R \leq \delta$$
versus the alternative

\[ H_a: R > \delta \]

where \( R = \frac{p_1}{p_2} \) denotes the relative risk (for column 1 or column 2) and \( \delta \) denotes the noninferiority margin (limit). You can specify the margin by using the MARGIN= relrisk-option; by default, the noninferiority margin is 0.8. The noninferiority margin for a relative risk test should be less than 1. Rejection of the null hypothesis indicates that the row 1 risk is not inferior to the row 2 risk. For more information, see Chow, Shao, and Wang (2008).

The test statistic \( z \) is computed by the method that you specify. For information about test statistic computation, see the subsections “Wald Test,” “Wald Modified Test,” “Farrington-Manning (Score) Test,” and “Likelihood Ratio Test” in this section. The test statistic \( z \) is computed by using the noninferiority margin (limit) as the null value of the relative risk. Under the null hypothesis, the test statistic has a standard normal distribution. The \( p \)-value for the noninferiority test is the right-sided \( p \)-value (the probability that \( Z > z \)).

As part of the noninferiority analysis, PROC FREQTAB also provides confidence limits for the relative risk. The confidence coefficient is \( 100(1 - 2\alpha)\% \) (Schuirmann 1999). The confidence level \( \alpha \) is determined by the ALPHA= option in the TABLES statement; by default, ALPHA=0.05, which produces 90% confidence limits for the noninferiority analysis. You can compare the confidence limits to the value of the noninferiority limit \( \delta \).

**Superiority Test**

A superiority test for the relative risk can be expressed as

\[ H_0: R \leq \delta \]

versus the alternative

\[ H_a: R > \delta \]

where \( R = \frac{p_1}{p_2} \) denotes the relative risk (for column 1 or column 2) and \( \delta \) denotes the superiority margin (limit). You can specify the margin by using the MARGIN= relrisk-option; by default, the superiority margin is 1.25. The superiority margin for a relative risk test should be greater than 1. Rejection of the null hypothesis indicates that the row 1 risk is superior to the row 2 risk. For more information, see Chow, Shao, and Wang (2008).

The test statistic \( z \) is computed by using the superiority margin (limit) as the null value of the relative risk. Under the null hypothesis, the test statistic has a standard normal distribution. The \( p \)-value for the superiority test is the right-sided \( p \)-value (the probability that \( Z > z \)).

The computations for the superiority analysis are the same as the computations for the noninferiority analysis, which are described in the subsection “Noninferiority Test” in this section.

**Equivalence Test**

An equivalence test for the relative risk can be expressed as

\[ H_0: R \leq \delta_L \quad \text{or} \quad R \geq \delta_U \]

versus the alternative

\[ H_a: \delta_L < R < \delta_U \]
where $\delta_L$ is the lower margin and $\delta_U$ is the upper margin. Rejection of the null hypothesis indicates that the two risks are equivalent. For more information, see Chow, Shao, and Wang (2008).

You can specify the margins by using the `MARGIN= relrisk-option`; by default, the lower margin is 0.8 and the upper margin is 1.25. If you specify a single margin value, PROC FREQTAB uses this value as the lower margin for the equivalence test and computes the upper margin as the inverse of the lower margin.

PROC FREQTAB computes two one-sided tests (TOST) for equivalence analysis (Schuirmann 1987), which include a right-sided test for the lower margin $\delta_L$ and a left-sided test for the upper margin $\delta_U$. The lower test statistic uses the lower margin as the null relative risk value, and the $p$-value is the right-sided probability ($Z > z_L$). The upper test statistic uses the upper margin as the null value, and the $p$-value is the left-sided probability ($Z < z_U$). The overall $p$-value is taken to be the larger of the two $p$-values for the lower and upper tests.

The test statistics are computed by the method that you specify. For more information about the test statistic computation, see the subsections “Wald Test,” “Wald Modified Test,” “Farrington-Manning (Score) Test,” and “Likelihood Ratio Test” in this section.

As part of the equivalence analysis, PROC FREQTAB also provides confidence limits for the relative risk. The confidence coefficient is $100(1 - 2\alpha)\%$ (Schuirmann 1999). The confidence level $\alpha$ is determined by the `ALPHA=` option in the TABLES statement; by default, `ALPHA=0.05`, which produces 90% confidence limits for the equivalence analysis. You can compare the confidence limits to the equivalence limits, which are $\delta_L$ and $\delta_U$.

### Wald Test

The Wald test statistic (which is based on a log transformation of the relative risk) is computed as $z(r_0) = (\ln(\hat{r}) - \ln(r_0))/\sqrt{v}$, where $\hat{r}$ is the relative risk estimate ($\hat{p}_1 / \hat{p}_2$), $r_0$ is the null value of the relative risk, and

$$v = \text{Var}(\ln(\hat{r})) = 1/n_{11} + 1/(n_{21} - 1/n_1 - 1/n_2).$$

The null value is determined by the type of test (equality, noninferiority, superiority, or equivalence) and the null or margin values that you specify. The side of the $p$-value and the interpretation of the test are also determined by the type of test; for more information, see the subsections “Equality Test,” “Noninferiority Test,” “Superiority Test,” and “Equivalence Test” in this section.

### Wald Modified Test

The Wald modified test statistic is computed by replacing the $n_{ij}$ with $(n_{ij} + 0.5)$ and the $n_i$ with $(n_i + 0.5)$ in the relative risk estimator $R$ and the variance $v$. The test statistic is computed as $z(r_0) = (\ln(\hat{r}) - \ln(r_0))/\sqrt{v}$, where $r_0$ is the null value of the relative risk,

$$\hat{r} = \hat{p}_1 / \hat{p}_2 = \frac{(n_{11} + 0.5)/(n_1 + 0.5)}{(n_{21} + 0.5)/(n_2 + 0.5)}$$

$$v = \text{Var}(\ln(\hat{r})) = 1/(n_{11} + 0.5) + 1/(n_{21} + 0.5) - 1/(n_1 + 0.5) - 1/(n_2 + 0.5)$$

The null value is determined by the type of test (equality, noninferiority, superiority, or equivalence) and the null or margin values that you specify. The side of the $p$-value and the interpretation of the test are also determined by the type of test; for more information, see the subsections “Equality Test,” “Noninferiority Test,” “Superiority Test,” and “Equivalence Test” in this section.
**Farrington-Manning (Score) Test**

The relative risk score test statistic (Miettinen and Nurminen 1985; Farrington and Manning 1990) for the null value \( r_0 \) is computed as

\[
    z(r_0) = \frac{\hat{p}_1 - r_0 \hat{p}_2}{\text{se}(r_0)}
\]

where

\[
    \text{se}(r_0) = \sqrt{\frac{\hat{p}_1 (1 - \hat{p}_1)}{n_1} + \frac{r_0^2 \hat{p}_2 (1 - \hat{p}_2)}{n_2}}.
\]

where \( \hat{p}_1 \) and \( \hat{p}_2 \) are the maximum likelihood estimates of \( p_1 \) and \( p_2 \) under the null value \( r_0 \). Expressions for the maximum likelihood estimates \( \hat{p}_1 \) and \( \hat{p}_2 \) are given in the subsection “Score Confidence Limits” in this section.

The null value is determined by the type of test (equality, noninferiority, superiority, or equivalence) and the null or margin values that you specify. The side of the \( p \)-value and the interpretation of the test are also determined by the type of test; for more information, see the subsections “Equality Test,” “Noninferiority Test,” “Superiority Test,” and “Equivalence Test” in this section.

**Likelihood Ratio Test**

The likelihood ratio statistic for the null relative risk value \( r_0 \) is computed as

\[
    G^2(r_0) = 2 \left( n_{11} \ln(\hat{p}_1/\hat{p}_1) + n_{12} \ln((1 - \hat{p}_1)/(1 - \hat{p}_1)) + n_{21} \ln(\hat{p}_2/\hat{p}_2) + n_{22} \ln((1 - \hat{p}_2)/(1 - \hat{p}_2)) \right)
\]

where \( \hat{p}_1 \) and \( \hat{p}_2 \) are the maximum likelihood estimates of \( p_1 \) and \( p_2 \) under the null value \( r_0 \). Expressions for the maximum likelihood estimates \( \hat{p}_1 \) and \( \hat{p}_2 \) are given in the subsection “Score Confidence Limits” in this section. For more information, see Miettinen and Nurminen (1985) and Miettinen (1985, chapter 13).

PROC FREQTAB computes the likelihood ratio test statistic \( z(r_0) \) for the noninferiority, superiority, and equivalence tests as \( \sqrt{G^2(r_0)} \), where the sign is positive if the estimate is greater than the null value \( (\hat{r} \geq r_0) \) and negative otherwise \( (\hat{r} < r_0) \).

The null value is determined by the type of test (equality, noninferiority, superiority, or equivalence) and the null or margin values that you specify. The side of the \( p \)-value and the interpretation of the test are also determined by the type of test; for more information, see the subsections “Equality Test,” “Noninferiority Test,” “Superiority Test,” and “Equivalence Test” in this section.

**Cochran-Armitage Test for Trend**

The TREND option in the TABLES statement provides the Cochran-Armitage test for trend, which tests for trend in binomial proportions across levels of a single factor or covariate. This test is appropriate for a two-way table where one variable has two levels and the other variable is ordinal. The two-level variable represents the response, and the other variable represents an explanatory variable with ordered levels. When the two-way has two columns and \( R \) rows, PROC FREQTAB tests for trend across the \( R \) levels of the row variable, and the binomial proportion is computed as the proportion of observations in the first column. When the table has two rows and \( C \) columns, PROC FREQTAB tests for trend across the \( C \) levels of the column variable, and the binomial proportion is computed as the proportion of observations in the first row.

The trend test is based on the regression coefficient for the weighted linear regression of the binomial proportions on the scores of the explanatory variable levels. For more information, see Margolin (1988) and
Agresti (2002). If the table has two columns and \( R \) rows, the trend test statistic is computed as

\[
T = \sum_{i=1}^{R} n_{i1}(R_i - \bar{R}) / \sqrt{p_1 (1 - p_1) s^2}
\]

where \( R_i \) is the score of row \( i \), \( \bar{R} \) is the average row score, and

\[
s^2 = \sum_{i=1}^{R} n_{i1}(R_i - \bar{R})^2
\]

The SCORES= option in the TABLES statement determines the type of row scores used in computing the trend test (and other score-based statistics). The default is SCORES=TABLE. For more information, see the section “Scores” on page 198. For character variables, the table scores for the row variable are the row numbers (for example, 1 for the first row, 2 for the second row, and so on). For numeric variables, the table score for each row is the numeric value of the row level. When you perform the trend test, the explanatory variable might be numeric (for example, dose of a test substance), and the variable values might be appropriate scores. If the explanatory variable has ordinal levels that are not numeric, you can assign meaningful scores to the variable levels. Sometimes equidistant scores, such as the table scores for a character variable, might be appropriate. For more information on choosing scores for the trend test, see Margolin (1988).

The null hypothesis for the Cochran-Armitage test is no trend, which means that the binomial proportion \( p_{i1} = n_{i1}/n_i \) is the same for all levels of the explanatory variable. Under the null hypothesis, the trend statistic has an asymptotic standard normal distribution.

PROC FREQTAB computes one-sided and two-sided \( p \)-values for the trend test. When the test statistic is greater than its null hypothesis expected value of 0, PROC FREQTAB displays the right-sided \( p \)-value, which is the probability of a larger value of the statistic occurring under the null hypothesis. A small right-sided \( p \)-value supports the alternative hypothesis of increasing trend in proportions from row 1 to row \( R \). When the test statistic is less than or equal to 0, PROC FREQTAB displays the left-sided \( p \)-value. A small left-sided \( p \)-value supports the alternative of decreasing trend.

The one-sided \( p \)-value for the trend test is computed as

\[
P_1 = \begin{cases} 
\text{Prob}(Z > T) & \text{if } T > 0 \\
\text{Prob}(Z < T) & \text{if } T \leq 0
\end{cases}
\]

where \( Z \) has a standard normal distribution. The two-sided \( p \)-value is computed as

\[
P_2 = \text{Prob}(|Z| > |T|)
\]

PROC FREQTAB also provides exact \( p \)-values for the Cochran-Armitage trend test. You can request the exact test by specifying the TREND option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.
Jonckheere-Terpstra Test

The JT option in the TABLES statement provides the Jonckheere-Terpstra test, which is a nonparametric test for ordered differences among classes. It tests the null hypothesis that the distribution of the response variable does not differ among classes. It is designed to detect alternatives of ordered class differences, which can be expressed as \( \tau_1 \leq \tau_2 \leq \cdots \leq \tau_R \) (or \( \tau_1 \geq \tau_2 \geq \cdots \geq \tau_R \)), with at least one of the inequalities being strict, where \( \tau_i \) denotes the effect of class \( i \). For such ordered alternatives, the Jonckheere-Terpstra test can be preferable to tests of more general class difference alternatives, such as the Kruskal–Wallis test (produced by the WILCOXON option in the NPAR1WAY procedure). See Pirie (1983) and Hollander and Wolfe (1999) for more information about the Jonckheere-Terpstra test.

The Jonckheere-Terpstra test is appropriate for a two-way table in which an ordinal column variable represents the response. The row variable, which can be nominal or ordinal, represents the classification variable. The levels of the row variable should be ordered according to the ordering you want the test to detect. The order of variable levels is determined by the ORDER= option in the PROC FREQTAB statement. The default is ORDER=INTERNAL, which orders by unformatted values. If you specify ORDER=DATA, PROC FREQTAB orders values according to their order in the input data set. For more information about how to order variable levels, see the ORDER= option.

The Jonckheere-Terpstra test statistic is computed by first forming \( R(R-1)/2 \) Mann-Whitney counts \( M_{i,j'} \), where \( i < i' \), for pairs of rows in the contingency table,

\[
M_{i,j'} = \begin{cases} 
\text{number of times } X_{i,j} < X_{i',j'}, & j = 1, \ldots, n_i; \ j' = 1, \ldots, n_{i'}; \\
+ \frac{1}{2} \text{ number of times } X_{i,j} = X_{i',j'}, & j = 1, \ldots, n_i; \ j' = 1, \ldots, n_{i'}; 
\end{cases}
\]

where \( X_{i,j} \) is response \( j \) in row \( i \). The Jonckheere-Terpstra test statistic is computed as

\[
J = \sum_{1 \leq i < i' \leq R} M_{i,i'}
\]

This test rejects the null hypothesis of no difference among classes for large values of \( J \). Asymptotic \( p \)-values for the Jonckheere-Terpstra test are obtained by using the normal approximation for the distribution of the standardized test statistic. The standardized test statistic is computed as

\[
J^* = \frac{(J - E_0(J))}{\sqrt{\text{Var}_0(J)}}
\]

where \( E_0(J) \) and \( \text{Var}_0(J) \) are the expected value and variance of the test statistic under the null hypothesis,

\[
E_0(J) = \left( n^2 - \sum_i n_i^2 \right) / 4
\]

\[
\text{Var}_0(J) = A/72 + B / (36n(n-1)(n-2)) + C / (8n(n-1))
\]

where

\[
A = n(n-1)(2n + 5) - \sum_i n_i(n_i - 1)(2n_i + 5) - \sum_j n_j(n_j - 1)(2n_j + 5)
\]

\[
B = \left( \sum_i n_i(n_i - 1)(n_i - 2) \right) \left( \sum_j n_j(n_j - 1)(n_j - 2) \right)
\]
PROC FREQTAB computes one-sided and two-sided $p$-values for the Jonckheere-Terpstra test. When the standardized test statistic is greater than its null hypothesis expected value of 0, PROC FREQTAB displays the right-sided $p$-value, which is the probability of a larger value of the statistic occurring under the null hypothesis. A small right-sided $p$-value supports the alternative hypothesis of increasing order from row 1 to row $R$. When the standardized test statistic is less than or equal to 0, PROC FREQTAB displays the left-sided $p$-value. A small left-sided $p$-value supports the alternative of decreasing order from row 1 to row $R$.

The one-sided $p$-value for the Jonckheere-Terpstra test, $P_1$, is computed as

$$P_1 = \begin{cases} \text{Prob}(Z > J^*) & \text{if } J^* > 0 \\ \text{Prob}(Z < J^*) & \text{if } J^* \leq 0 \end{cases}$$

where $Z$ has a standard normal distribution. The two-sided $p$-value, $P_2$, is computed as

$$P_2 = \text{Prob}(|Z| > |J^*|)$$

PROC FREQTAB also provides exact $p$-values for the Jonckheere-Terpstra test. You can request the exact test by specifying the JT option in the EXACT statement. See the section “Exact Statistics” on page 265 for more information.

Tests and Measures of Agreement

When you specify the AGREE option in the TABLES statement, PROC FREQTAB computes tests and measures of agreement for square tables (for which the number of rows equals the number of columns). By default, these statistics include McNemar’s test for $2 \times 2$ tables, Bowker’s symmetry test, the simple kappa coefficient, and the weighted kappa coefficient. For multiple strata ($n$-way tables, where $n > 2$), the AGREE option provides the overall simple and weighted kappa coefficients, in addition to tests for equal kappas (simple and weighted) among strata. For multiple strata of $2 \times 2$ tables, the AGREE option provides Cochran’s $Q$ test.

Optionally, PROC FREQTAB provides kappa tests and other agreement statistics. In addition to the asymptotic tests described in this section, PROC FREQTAB provides exact $p$-values for McNemar’s test, the simple kappa coefficient test, and the weighted kappa coefficient test. You can request these exact tests by specifying the corresponding options in the EXACT statement. For more information, see the section “Exact Statistics” on page 265.

The following sections provide the formulas that PROC FREQTAB uses to compute agreement statistics. For information about the use and interpretation of these statistics, see Agresti (2002, 2007); Fleiss, Levin, and Paik (2003), and the other references cited for each statistic.

McNemar’s Test

PROC FREQTAB computes McNemar’s test (McNemar 1947) for $2 \times 2$ tables when you specify the AGREE option. This test is appropriate when you are analyzing data from matched pairs of subjects with a dichotomous (yes-no) response. By default, the null hypothesis for McNemar’s test is marginal homogeneity, which can be expressed as $p_{11} = p_{1}$. This is equivalent to a discordant proportion ratio ($p_{12}/p_{21}$) of 1. The corresponding test statistic is computed as

$$Q_M = \frac{(n_{12} - n_{21})^2}{(n_{12} + n_{21})}$$
Under the null hypothesis, \( Q_M \) has an asymptotic chi-square distribution with 1 degree of freedom.

Optionally, you can specify the null ratio of discordant proportions (\( p_{12}/p_{21} \)) by using the \texttt{AGREE(MNULLRATIO=)} option. When the null ratio is \( r \), McNemar’s test is computed as

\[
Q_M (r) = \frac{(n_{12} - e_{12})^2}{e_{12}} + \frac{(n_{21} - e_{21})^2}{e_{21}}
\]

where \( e_{12} = D/(1 + 1/r) \), \( e_{21} = D/(1 + r) \), and \( D \) is the number of discordant pairs, \( (n_{12} + n_{21}) \). Under the null hypothesis, \( Q_M (r) \) has an asymptotic chi-square distribution with 1 degree of freedom.

PROC FREQTAB also computes an exact \( p \)-value for McNemar’s test when you specify the \texttt{MCNEM} option in the EXACT statement.

**Bowker’s Symmetry Test**

The null hypothesis for Bowker’s symmetry test (Bowker 1948) is symmetric table-cell proportions, which can be expressed as \( p_{ij} = p_{ji} \) for all off-diagonal pairs of table cells. For \( 2 \times 2 \) tables, Bowker’s test is identical to McNemar’s test; therefore, PROC FREQTAB provides Bowker’s test only for square tables that are larger than \( 2 \times 2 \).

Bowker’s symmetry test is computed as

\[
Q_B = \sum_{i<j} \sum (n_{ij} - n_{ji})^2 / (n_{ij} + n_{ji})
\]

For large samples, \( Q_B \) has an asymptotic chi-square distribution with \( R(R-1)/2 \) degrees of freedom under the null hypothesis of symmetry, where \( R \) is the dimension of the square, two-way table.

By default, the number of degrees of freedom for this test \( (R(R-1)/2) \) is the number of off-diagonal table-cell comparisons. You can specify the number of degrees of freedom in the \texttt{AGREE(DFSYM=)} option. Alternatively, you can specify the \texttt{AGREE(DFSYM=ADJUST)} option, which reduces the degrees of freedom by the number of off-diagonal table-cell pairs that have a total frequency of 0. For more information, see Hoenig, Morgan, and Brown (1995).

**Exact Symmetry Test**

When you specify the \texttt{SYMMETRY} option in the EXACT statement, PROC FREQTAB provides an exact symmetry test by using the method of Krauth (1973). This exact test is computed by conditioning on the observed frequency sums of the complementary off-diagonal table-cell pairs \( (n_{ij} + n_{ji}) \). PROC FREQTAB evaluates the symmetry test statistic for all tables in the reference set, which includes all possible tables in which the frequency sums of the off-diagonal table-cell pairs match the corresponding frequency sums in the observed table. The exact \( p \)-value is then computed as the sum of the table probabilities for those tables for which the symmetry test statistic is greater than or equal to the observed test statistic. The table probabilities are computed as products of \( R(R-1)/2 \) binomial probabilities (which correspond to the off-diagonal table-cell pairs in tables of dimension \( R \)) by using the binomial proportion 0.5 under the null hypothesis of symmetry. For more information, see the section “Exact Statistics” on page 265.

Alternatively, you can request a Monte Carlo estimate of the exact \( p \)-value by specifying the \texttt{SYMMETRY} option together with the \texttt{MC computation-option} in the EXACT statement. The Monte Carlo computation for the exact symmetry test is conditional on the same reference set that the exact test uses (tables in which the frequency sums of the off-diagonal table-cell pairs match the corresponding sums in the observed table). For more information, see the section “Monte Carlo Estimation” on page 269.
Simple Kappa Coefficient

The simple kappa coefficient (Cohen 1960) is a measure of interrater agreement. PROC FREQTAB computes the simple kappa coefficient as

\[ \hat{k} = \frac{P_o - P_e}{1 - P_e} \]

where \( P_o = \sum_i p_{ii} \) and \( P_e = \sum_i p_{i}.p_{.i} \). The component \( P_o \) is the proportion of observed agreement, and the component \( P_e \) represents the proportion of chance-expected agreement.

If the two response variables are viewed as two independent ratings of the \( n \) subjects, the kappa coefficient is +1 when there is complete agreement of the raters. When the observed agreement exceeds the chance-expected agreement, the kappa coefficient is positive, and its magnitude reflects the strength of agreement. When the observed agreement is less than the chance-expected agreement, the kappa coefficient is negative. The minimum value of kappa is between –1 and 0, depending on the marginal proportions of the table.

PROC FREQTAB computes the asymptotic variance of the simple kappa coefficient as

\[ \text{Var}(\hat{k}) = \frac{A + B - C}{(1 - P_e)^2 n} \]

where

\[ A = \sum_i p_{ii} (1 - (p_{i.} + p_{.i})(1 - \hat{k}))^2 \]
\[ B = (1 - \hat{k})^2 \sum_{i \neq j} p_{ij}(p_{i.} + p_{.j})^2 \]
\[ C = (\hat{k} - P_e(1 - \hat{k}))^2 \]

For more information, see Fleiss, Cohen, and Everitt (1969).

Confidence limits for the simple kappa coefficient are computed as

\[ \hat{k} \pm \left( z_{\alpha/2} \times \sqrt{\text{Var}(\hat{k})} \right) \]

where \( z_{\alpha/2} \) is the 100\( (1 - \alpha/2) \)th percentile of the standard normal distribution. The value of \( \alpha \) is determined by the \texttt{ALPHA=} option; by default \texttt{ALPHA=0.05}, which produces 95% confidence limits.

PROC FREQTAB provides an asymptotic test for the simple kappa coefficient. By default, the null hypothesis value of kappa is 0; alternatively, you can specify a nonzero null value of kappa (by using the \texttt{AGREE(NULLKAPPA=} option in the \texttt{TABLES} statement). When the null value of kappa is nonzero, PROC FREQTAB computes the test statistic as

\[ z = \frac{(\hat{k} - \kappa_0)}{\sqrt{\text{Var}(\hat{k})}} \]

where \( \kappa_0 \) is the null value that you specify and \( \text{Var}(\hat{k}) \) is the variance of the kappa coefficient.

When the null value of kappa is 0, PROC FREQTAB computes the test statistic as

\[ z = \hat{k} / \sqrt{\text{Var}_0(\hat{k})} \]

where \( \text{Var}_0(\hat{k}) \) is the variance of the kappa coefficient under the null hypothesis (that kappa is 0) and is computed as

\[ \text{Var}_0(\hat{k}) = \left( P_e + P_e^2 - \sum_i p_{i.}p_{.i}(p_{i.} + p_{.i}) \right) / (1 - P_e)^2 n \]
This test statistic has an asymptotic standard normal distribution under the null hypothesis. For more information, see Fleiss, Levin, and Paik (2003).

PROC FREQTAB also provides an exact test for the simple kappa coefficient. You can request the exact test by specifying the KAPPA or AGREE option in the EXACT statement. For more information, see the section “Exact Statistics” on page 265.

Kappa Details When you specify the AGREE(KAPPADETAILS) option, PROC FREQTAB displays the “Kappa Details” table, which includes the observed agreement $P_o$, chance-expected agreement $P_e$, maximum kappa, and $B_n$ measure.

The maximum kappa, which is the maximum possible value of the kappa coefficient given the marginal proportions of the two-way table, is computed as

$$\max(\kappa) = \frac{\max(P_o) - P_e}{1 - P_e}$$

where

$$\max(P_o) = \frac{\left(\sum_i \min(n_{i1}, n_{i2})\right)}{n}$$

The $B_n$ measure (Bangdiwala 1988; Bangdiwala et al. 2008) is computed as

$$B_n = \frac{\left(\sum_i n_{i}^2\right)}{\left(\sum_i \sum_j n_{i1} n_{i2}\right)}$$

For $2 \times 2$ tables, the “Kappa Details” table also includes the prevalence index and the bias index. The prevalence index is the absolute difference between the agreement proportions, $|p_{11} - p_{22}|$. The bias index is the absolute difference between the disagreement proportions, $|p_{12} - p_{21}|$. For more information, see Sim and Wright (2005) and Byrt, Bishop, and Carlin (1993).

Weighted Kappa Coefficient

The weighted kappa coefficient is a generalization of the simple kappa coefficient that uses weights to quantify the relative differences between categories. For $2 \times 2$ tables, the weighted kappa coefficient is equivalent to the simple kappa coefficient; therefore, PROC FREQTAB displays the weighted kappa coefficient only for tables larger than $2 \times 2$. PROC FREQTAB computes the kappa weights from the column scores, by using either Cicchetti-Allison weights or Fleiss-Cohen weights, both of which are described in the section “Kappa Weights” on page 254. The kappa weights $w_{ij}$ are constructed so that $0 \leq w_{ij} < 1$ for all $i \neq j$, $w_{ii} = 1$ for all $i$, and $w_{ij} = w_{ji}$. The weighted kappa coefficient is computed as

$$\hat{\kappa}_w = \frac{P_o(w) - P_e(w)}{1 - P_e(w)}$$

where

$$P_o(w) = \sum_i \sum_j w_{ij} p_{ij}$$

$$P_e(w) = \sum_i \sum_j w_{ij} p_{i1} p_{i2}$$
The component $P_{o(w)}$ is the proportion of observed (weighted) agreement, and the component $P_{e(w)}$ represents the proportion of chance-expected (weighted) agreement. When you specify the AGREE(WTKAPDETAILS) option, PROC FREQTAB displays these components in the “Weighted Kappa Details” table.

PROC FREQTAB computes the asymptotic variance of the weighted kappa coefficient as

$$\text{Var}(\hat{k}_w) = \left( \sum_i \sum_j p_{ij} \left( w_{ij} - (\overline{w}_{i.} + \overline{w}_{.j})(1 - \hat{k}_w) \right)^2 - (\hat{k}_w - P_{e(w)}(1 - \hat{k}_w))^2 \right) / (1 - P_{e(w)})^2 n$$

where

$$\overline{w}_{i.} = \sum_j p_{i.} w_{ij}$$

$$\overline{w}_{.j} = \sum_i p_{i.} w_{ij}$$

For more information, see Fleiss, Cohen, and Everitt (1969).

Confidence limits for the weighted kappa coefficient are computed as

$$\hat{k}_w \pm \left( z_{\alpha/2} \times \sqrt{\text{Var}(\hat{k}_w)} \right)$$

where $z_{\alpha/2}$ is the $100(1 - \alpha/2)$th percentile of the standard normal distribution. The value of $\alpha$ is determined by the ALPHA= option; by default ALPHA=0.05, which produces 95% confidence limits.

PROC FREQTAB provides an asymptotic test for the weighted kappa coefficient. By default, the null hypothesis value of weighted kappa is 0; alternatively, you can specify a nonzero null value of weighted kappa (by using the AGREE(NULLWTKAPPA=) option in the TABLES statement). When the null value of weighted kappa is nonzero, PROC FREQTAB computes the test statistic as

$$z = (\hat{k}_w - \kappa_{w(0)}) / \sqrt{\text{Var}(\hat{k}_w)}$$

where $\kappa_{w(0)}$ is the null value that you specify and $\text{Var}(\hat{k}_w)$ is the variance of the weighted kappa coefficient.

When the null value of weighted kappa is 0, PROC FREQTAB computes the test statistic as

$$z = \hat{k}_w / \sqrt{\text{Var}_0(\hat{k}_w)}$$

where $\text{Var}_0(\hat{k}_w)$ is the variance of the weighted kappa coefficient under the null hypothesis (that weighted kappa is 0) and is computed as

$$\text{Var}_0(\hat{k}_w) = \left( \sum_i \sum_j p_{ij} p_{.j} \left( w_{ij} - (\overline{w}_{i.} + \overline{w}_{.j}) \right)^2 - P_{e(w)}^2 \right) / (1 - P_{e(w)})^2 n$$

This test statistic has an asymptotic standard normal distribution under the null hypothesis. For more information, see Fleiss, Levin, and Paik (2003).

PROC FREQTAB also provides an exact test for the weighted kappa coefficient. You can request the exact test by specifying the KAPPA or AGREE option in the EXACT statement. For more information, see the section “Exact Statistics” on page 265.
**Kappa Weights**  PROC FREQTAB computes kappa coefficient weights by using the column scores and one of the two available weight types. The column scores are determined by the SCORES= option in the TABLES statement. The two available types of kappa weights are Cicchetti-Allison and Fleiss-Cohen weights. By default, PROC FREQTAB uses Cicchetti-Allison weights. If you specify the AGREE(WT=FC) option, PROC FREQTAB uses Fleiss-Cohen weights to compute the weighted kappa coefficient.

PROC FREQTAB computes Cicchetti-Allison kappa coefficient weights as

$$w_{ij} = 1 - \frac{|C_i - C_j|}{C - C_1}$$

where $C_i$ is the score for column $i$ and $C$ is the number of categories or columns. For more information, see Cicchetti and Allison (1971).

The SCORES= option in the TABLES statement determines the type of column scores used to compute the kappa weights (and other score-based statistics). The default is SCORES=TABLE. For more information, see the section “Scores” on page 198. For numeric variables, table scores are the values of the variable levels. You can assign numeric values to the levels in a way that reflects their level of similarity. For example, suppose you have four levels and order them according to similarity. If you assign them values of 0, 2, 4, and 10, the Cicchetti-Allison kappa weights take the following values: $w_{12} = 0.8$, $w_{13} = 0.6$, $w_{14} = 0$, $w_{23} = 0.8$, $w_{24} = 0.2$, and $w_{34} = 0.4$. Note that when there are only two categories (that is, $C = 2$), the weighted kappa coefficient is identical to the simple kappa coefficient.

If you specify the AGREE(WT=FC) option in the TABLES statement, PROC FREQTAB computes Fleiss-Cohen kappa coefficient weights as

$$w_{ij} = 1 - \frac{(C_i - C_j)^2}{(C - C_1)^2}$$

For more information, see Fleiss and Cohen (1973).

For the preceding example, the Fleiss-Cohen kappa weights are $w_{12} = 0.96$, $w_{13} = 0.84$, $w_{14} = 0$, $w_{23} = 0.96$, $w_{24} = 0.36$, and $w_{34} = 0.64$.

**Prevalence-Adjusted Bias-Adjusted Kappa**

When you specify the AGREE(PABAK) option, PROC FREQTAB provides the prevalence-adjusted bias-adjusted kappa coefficient (PABAK) (Byrt, Bishop, and Carlin 1993). This coefficient is computed as

$$\hat{\kappa}_a = \left( P_o - \frac{1}{R} \right) / \left( 1 - \frac{1}{R} \right)$$

where $P_o = \sum_i p_{ii}$ and $R$ is the dimension of the square, two-way table. The component $P_o$ is the proportion of observed agreement, and the component $1/R$ represents the chance-expected agreement. When the table is $2 \times 2$, $\hat{\kappa}_a = 2P_o - 1$. For more information, see Sim and Wright (2005), Xie (2013), and Holley and Guilford (1964).

PROC FREQTAB computes the variance of the prevalence-adjusted bias-adjusted kappa as

$$\text{Var}(\hat{\kappa}_a) = \left( \frac{R}{(R - 1)} \right)^2 \left( P_o(1 - P_o)/n \right)$$

Confidence limits are computed as

$$\hat{\kappa}_a \pm \left( z_{\alpha/2} \times \sqrt{\text{Var}(\hat{\kappa}_a)} \right)$$

where $z_{\alpha/2}$ is the 100(1-$\alpha/2$)th percentile of the standard normal distribution. The value of $\alpha$ is determined by the ALPHA= option; by default ALPHA=0.05, which produces 95% confidence limits.
**AC1 Agreement Coefficient**

When you specify the `AGREE(AC1)` option, PROC FREQTAB provides Gwet’s first-order agreement coefficient, AC1 (Gwet 2008). This coefficient is computed as

\[ \hat{\gamma} = \frac{(P_o - P_e)}{(1 - P_e)} \]

where \( P_o = \sum_i p_{ii}, \ P_e = \sum_i e_i(1 - e_i)/(R - 1), \) and \( e_i = (p_{i.} + p_{.i})/2 \) The component \( P_o \) is the proportion of observed agreement, and the component \( P_e \) represents the proportion of chance-expected agreement. For more information, see Xie (2013) and Blood and Spratt (2007).

PROC FREQTAB computes the variance of AC1 as

\[ \text{Var}(\hat{\gamma}) = \frac{(P_o(1 - P_o) - 4(1 - \hat{\gamma})A + 4(1 - \hat{\gamma}^2)B)}{n(1 - P_e)^2} \]

where

\[ A = \sum_i p_{ii}(1 - e_i)/(R - 1) - P_o P_e \]
\[ B = \sum_i \sum_j p_{ij} (1 - (e_i + e_j)/2)^2 / (R - 1)^2 - P_e^2 \]

Confidence limits for AC1 are computed as

\[ \hat{\gamma} \pm \left( z_{\alpha/2} \times \sqrt{\text{Var}(\hat{\gamma})} \right) \]

where \( z_{\alpha/2} \) is the \( (100 - \alpha/2)\)th percentile of the standard normal distribution. The value of \( \alpha \) is determined by the `ALPHA=` option; by default `ALPHA=0.05`, which produces 95% confidence limits.

**Overall Kappa Coefficient**

When there are multiple strata, PROC FREQTAB combines the stratum-level estimates of kappa into an overall estimate of the supposed common value of kappa. Assume there are \( q \) strata, indexed by \( h = 1, 2, \ldots, q \), and let \( \text{Var}(\hat{\kappa}_h) \) denote the variance of \( \hat{\kappa}_h \). The estimate of the overall kappa coefficient is computed as

\[ \hat{\kappa}_T = \frac{\sum_{h=1}^q \hat{\kappa}_h / \text{Var}(\hat{\kappa}_h)}{\sum_{h=1}^q 1 / \text{Var}(\hat{\kappa}_h)} \]

For more information, see Fleiss, Levin, and Paik (2003).

PROC FREQTAB computes an estimate of the overall weighted kappa in the same way.

**Tests for Equal Kappa Coefficients**

When there are multiple strata, the following chi-square statistic tests whether the stratum-level values of kappa are equal:

\[ Q_K = \sum_{h=1}^q (\hat{\kappa}_h - \hat{\kappa}_T)^2 / \text{Var}(\hat{\kappa}_h) \]

Under the null hypothesis of equal kappas for the \( q \) strata, \( Q_K \) has an asymptotic chi-square distribution with \( q - 1 \) degrees of freedom. See Fleiss, Levin, and Paik (2003) for more information. PROC FREQTAB computes a test for equal weighted kappa coefficients in the same way.
Cochran’s $Q$ Test

Cochran’s $Q$ is computed for multiway tables when each variable has two levels, that is, for $2 \times 2 \cdots \times 2$ tables. Cochran’s $Q$ statistic is used to test the homogeneity of the one-dimensional margins. Let $m$ denote the number of variables and $N$ denote the total number of subjects. Cochran’s $Q$ statistic is computed as

$$Q_C = m(m-1) \left( \sum_{j=1}^{m} T_j^2 - T^2 \right) / \left( mT - \sum_{k=1}^{N} S_k^2 \right)$$

where $T_j$ is the number of positive responses for variable $j$, $T$ is the total number of positive responses over all variables, and $S_k$ is the number of positive responses for subject $k$. Under the null hypothesis, Cochran’s $Q$ has an asymptotic chi-square distribution with $m-1$ degrees of freedom. For more information, see Cochran (1950). When there are only two binary response variables ($m=2$), Cochran’s $Q$ simplifies to McNemar’s test. When there are more than two response categories, you can test for marginal homogeneity by using the repeated measures capabilities of the CATMOD procedure.

Tables with Zero-Weight Rows or Columns

The AGREE statistics are defined only for square tables, where the number of rows equals the number of columns; if a table is not square, PROC FREQTAB does not compute AGREE statistics for the table. In the kappa statistic framework, where two independent raters assign ratings to each of $n$ subjects, suppose one of the raters does not use all possible $r$ rating levels. If the corresponding table contains $r$ rows but only $r-1$ columns, the table is not square and PROC FREQTAB does not compute AGREE statistics. To create a square table in this situation, you can use the ZEROS option in the WEIGHT statement, which includes zero-weight observations in the analysis. You can include zero-weight observations in the input data set to represent any rating levels that are not used by a rater, so that the input data set has at least one observation for each possible rater and rating combination. When you use this input data set and specify the ZEROS option, the analysis includes all rating levels (even when all levels are not actually assigned by both raters). The resulting table (of rater 1 by rater 2) is a square table, and AGREE statistics can be computed.

For more information, see the description of the ZEROS option in the WEIGHT statement. By default, PROC FREQTAB does not process observations that have weights of 0 because these observations do not contribute to the total frequency count, and because many of the tests and measures of association are undefined for tables that contain zero-weight rows or columns. However, kappa statistics are defined for tables that contain zero-weight rows or columns, and the ZEROS option enables you to input zero-weight observations and construct the tables needed to compute kappa statistics.

Cochran-Mantel-Haenszel Statistics

The CMH option in the TABLES statement gives a stratified statistical analysis of the relationship between the row and column variables after controlling for the strata variables in a multiway table. For example, for the table request A*B*C*D, the CMH option provides an analysis of the relationship between C and D, after controlling for A and B. The stratified analysis provides a way to adjust for the possible confounding effects of A and B without being forced to estimate parameters for them.

The CMH analysis produces Cochran-Mantel-Haenszel statistics, which include the correlation statistic, the ANOVA (row mean scores) statistic, and the general association statistic. For $2 \times 2$ tables, the CMH option also provides Mantel-Haenszel and logit estimates of the common odds ratio and the common relative risks, in addition to the Breslow-Day test for homogeneity of the odds ratios.

Exact statistics are also available for stratified $2 \times 2$ tables. If you specify the EQOR option in the EXACT statement, PROC FREQTAB provides Zelen’s exact test for equal odds ratios. If you specify the COMOR
option in the EXACT statement, PROC FREQTAB provides exact confidence limits for the common odds ratio and an exact test that the common odds ratio equals one.

Let the number of strata be denoted by $q$, indexing the strata by $h = 1, 2, \ldots, q$. Each stratum contains a contingency table with $X$ representing the row variable and $Y$ representing the column variable. For table $h$, denote the cell frequency in row $i$ and column $j$ by $n_{hij}$, with corresponding row and column marginal totals denoted by $n_{hi}$ and $n_{hj}$, and the overall stratum total by $n_h$.

Because the formulas for the Cochran-Mantel-Haenszel statistics are more easily defined in terms of matrices, the following notation is used. Vectors are presumed to be column vectors unless they are transposed ($'$).

\[ n'_{hi} = (n_{h11}, n_{h21}, \ldots, n_{h1C}) \quad (1 \times C) \]
\[ n'_h = (n'_{h1}, n'_{h2}, \ldots, n'_{hR}) \quad (1 \times RC) \]
\[ p_{hi} = n_{hi} / n_h \quad (1 \times 1) \]
\[ p_{hj} = n_{hj} / n_h \quad (1 \times 1) \]
\[ P'_{h*} = (p_{h1}, p_{h2}, \ldots, p_{hR}) \quad (1 \times R) \]
\[ P'_{h*} = (p'_{h1}, p'_{h2}, \ldots, p'_{hC}) \quad (1 \times C) \]

Assume that the strata are independent and that the marginal totals of each stratum are fixed. The null hypothesis, $H_0$, is that there is no association between $X$ and $Y$ in any of the strata. The corresponding model is the multiple hypergeometric; this implies that, under $H_0$, the expected value and covariance matrix of the frequencies are, respectively,

\[ \mathbf{m}_h = E[n_h | H_0] = n_h (P'_{h*} \otimes P'_{h*}) \]
\[ \text{Var}[n_h | H_0] = c \left( (D_{P'_{h*}} - P'_{h*} P'_{h*}) \otimes (D_{P'_{h*}} - P'_{h*} P'_{h*}) \right) \]

where

\[ c = n_h^2 / (n_h - 1) \]

and where $\otimes$ denotes Kronecker product multiplication and $D_a$ is a diagonal matrix with the elements of $a$ on the main diagonal.

The generalized CMH statistic (Landis, Heyman, and Koch 1978) is defined as

\[ Q_{CMH} = \mathbf{G}' \mathbf{V}_G^{-1} \mathbf{G} \]

where

\[ \mathbf{G} = \sum_h \mathbf{B}_h (n_h - \mathbf{m}_h) \]
\[ \mathbf{V}_G = \sum_h \mathbf{B}_h \left( \text{Var}[n_h | H_0] \right) \mathbf{B}_h' \]

and where

\[ \mathbf{B}_h = C_h \otimes R_h \]
Chapter 4: The FREQTAB Procedure

is a matrix of fixed constants based on column scores \( C_h \) and row scores \( R_h \). When the null hypothesis is true, the CMH statistic has an asymptotic chi-square distribution with degrees of freedom equal to the rank of \( B_h \). If \( V_G \) is found to be singular, PROC FREQTAB prints a message and sets the value of the CMH statistic to missing.

PROC FREQTAB computes three CMH statistics by using this formula for the generalized CMH statistic, with different row and column score definitions for each statistic. The CMH statistics that PROC FREQTAB computes are the correlation statistic, the ANOVA (row mean scores) statistic, and the general association statistic. These statistics test the null hypothesis of no association against different alternative hypotheses. The following sections describe the computation of these CMH statistics.

**CAUTION:** The CMH statistics have low power for detecting an association in which the patterns of association for some of the strata are in the opposite direction of the patterns displayed by other strata. Thus, a nonsignificant CMH statistic suggests either that there is no association or that no pattern of association has enough strength or consistency to dominate any other pattern.

**Correlation Statistic**
The correlation statistic, popularized by Mantel and Haenszel, has 1 degree of freedom and is known as the Mantel-Haenszel statistic (Mantel and Haenszel 1959; Mantel 1963).

The alternative hypothesis for the correlation statistic is that there is a linear association between \( X \) and \( Y \) in at least one stratum. If either \( X \) or \( Y \) does not lie on an ordinal (or interval) scale, this statistic is not meaningful.

To compute the correlation statistic, PROC FREQTAB uses the formula for the generalized CMH statistic with the row and column scores determined by the SCORES= option in the TABLES statement. See the section “Scores” on page 198 for more information about the available score types. The matrix of row scores \( R_h \) has dimension \( 1 \times R \), and the matrix of column scores \( C_h \) has dimension \( 1 \times C \).

When there is only one stratum, this CMH statistic reduces to \((n - 1)r^2\), where \( r \) is the Pearson correlation coefficient between \( X \) and \( Y \). When nonparametric (RANK or RIDIT) scores are specified, the statistic reduces to \((n - 1)r_s^2\), where \( r_s \) is the Spearman rank correlation coefficient between \( X \) and \( Y \). When there is more than one stratum, this CMH statistic becomes a stratum-adjusted correlation statistic.

**ANOVA (Row Mean Scores) Statistic**
The ANOVA statistic can be used only when the column variable \( Y \) lies on an ordinal (or interval) scale so that the mean score of \( Y \) is meaningful. For the ANOVA statistic, the mean score is computed for each row of the table, and the alternative hypothesis is that, for at least one stratum, the mean scores of the \( R \) rows are unequal. In other words, the statistic is sensitive to location differences among the \( R \) distributions of \( Y \).

The matrix of column scores \( C_h \) has dimension \( 1 \times C \), and the column scores are determined by the SCORES= option.

The matrix of row scores \( R_h \) has dimension \((R - 1) \times R \) and is created internally by PROC FREQTAB as

\[
R_h = [I_{R-1}, -J_{R-1}]
\]

where \( I_{R-1} \) is an identity matrix of rank \( R - 1 \) and \( J_{R-1} \) is an \((R - 1) \times 1\) vector of ones. This matrix has the effect of forming \( R - 1 \) independent contrasts of the \( R \) mean scores.

When there is only one stratum, this CMH statistic is essentially an analysis of variance (ANOVA) statistic in the sense that it is a function of the variance ratio \( F \) statistic that would be obtained from a one-way ANOVA on the dependent variable \( Y \). If nonparametric scores are specified in this case, the ANOVA statistic is a Kruskal-Wallis test.
When there is more than one stratum, this CMH statistic corresponds to a stratum-adjusted ANOVA or Kruskal-Wallis test. In the special case where there is one subject per row and one subject per column in the contingency table of each stratum, this CMH statistic is identical to Friedman’s chi-square.

**General Association Statistic**

The alternative hypothesis for the general association statistic is that, for at least one stratum, there is some kind of association between \( X \) and \( Y \). This statistic is always interpretable because it does not require an ordinal scale for either \( X \) or \( Y \).

For the general association statistic, the matrix \( R_h \) is the same as the one used for the ANOVA statistic. The matrix \( C_h \) is defined similarly as

\[
C_h = [I_{C-1}, -J_{C-1}]
\]

PROC FREQTAB generates both score matrices internally. When there is only one stratum, the general association CMH statistic reduces to \( Q_P(n - 1)/n \), where \( Q_P \) is the Pearson chi-square statistic. When there is more than one stratum, the CMH statistic becomes a stratum-adjusted Pearson chi-square statistic. Note that a similar adjustment can be made by summing the Pearson chi-squares across the strata. However, the latter statistic requires a large sample size in each stratum to support the resulting chi-square distribution with \( q(R-1)(C-1) \) degrees of freedom. The CMH statistic requires only a large overall sample size because it has only \( (R-1)(C-1) \) degrees of freedom.

See Cochran (1954); Mantel and Haenszel (1959); Mantel (1963); Birch (1965); Landis, Heyman, and Koch (1978).

**Mantel-Fleiss Criterion**

If you specify the CMH(MANTELFLEISS) option in the TABLES statement, PROC FREQTAB computes the Mantel-Fleiss criterion for stratified \( 2 \times 2 \) tables. The Mantel-Fleiss criterion can be used to assess the validity of the chi-square approximation for the distribution of the Mantel-Haenszel statistic for \( 2 \times 2 \) tables. For more information, see Mantel and Fleiss (1980); Mantel and Haenszel (1959); Stokes, Davis, and Koch (2012); Dmitrienko et al. (2005).

The Mantel-Fleiss criterion is computed as

\[
MF = \min \left( \frac{\sum h m_{h11} - \sum h (n_{h11})_L}{\sum h (n_{h11})_U - \sum h m_{h11}} \right)
\]

where \( m_{h11} \) is the expected value of \( n_{h11} \) under the hypothesis of no association between the row and column variables in table \( h \), \( (n_{h11})_L \) is the minimum possible value of the table cell frequency, and \( (n_{h11})_U \) is the maximum possible value,

\[
m_{h11} = \frac{n_{h1} \cdot n_{h1} / n_h}{n_{h1} \cdot n_{h1} / n_h}
\]

\[
(n_{h11})_L = \max (0, n_{h1} - n_{h2})
\]

\[
(n_{h11})_U = \min (n_{h1}, n_{h1})
\]

The Mantel-Fleiss guideline accepts the validity of the Mantel-Haenszel approximation when the value of the criterion is at least 5. When the criterion is less than 5, PROC FREQTAB displays a warning.
Adjusted Odds Ratio and Relative Risk Estimates

The CMH option provides adjusted odds ratio and relative risk estimates for stratified $2 \times 2$ tables. For each of these measures, PROC FREQTAB computes a Mantel-Haenszel estimate and a logit estimate. These estimates apply to $n$-way table requests in the TABLES statement, when the row and column variables both have two levels.

For example, for the table request $A*B*C*D$, if the row and column variables $C$ and $D$ both have two levels, PROC FREQTAB provides odds ratio and relative risk estimates, adjusting for the confounding variables $A$ and $B$.

The choice of an appropriate measure depends on the study design. For case-control (retrospective) studies, the odds ratio is appropriate. For cohort (prospective) or cross-sectional studies, the relative risk is appropriate. See the section “Odds Ratio and Relative Risks for $2 \times 2$ Tables” on page 236 for more information on these measures.

Throughout this section, $z$ denotes the $100(1 - \alpha/2)$th percentile of the standard normal distribution.

Odds Ratio, Case-Control Studies

PROC FREQTAB provides Mantel-Haenszel and logit estimates for the common odds ratio for stratified $2 \times 2$ tables.

Mantel-Haenszel Estimator

The Mantel-Haenszel estimate of the common odds ratio is computed as

$$OR_{MH} = \left( \sum_h n_{h11} n_{h22} / n_h \right) / \left( \sum_h n_{h12} n_{h21} / n_h \right)$$

It is always computed unless the denominator is 0. For more information, see Mantel and Haenszel (1959) and Agresti (2002).

To compute confidence limits for the common odds ratio, PROC FREQTAB uses the Robins, Breslow, and Greenland (1986) variance estimate for $\ln(OR_{MH})$. The $100(1 - \alpha/2)$% confidence limits for the common odds ratio are

$$\left( OR_{MH} \times \exp(-z\hat{\sigma}), \ OR_{MH} \times \exp(z\hat{\sigma}) \right)$$

where

$$\hat{\sigma}^2 = \frac{\text{Var}(\ln(OR_{MH}))}{\sum_h (n_{h11} + n_{h22})(n_{h11} n_{h22}) / n_h^2}$$

$$= \frac{2 \left( \sum_h n_{h11} n_{h22} / n_h \right)^2}{\sum_h (n_{h11} + n_{h22})(n_{h12} n_{h21}) + (n_{h12} + n_{h21})(n_{h11} n_{h22}) / n_h^2}$$

$$+ \frac{\sum_h (n_{h11} + n_{h22})(n_{h12} n_{h21}) / n_h^2}{\sum_h n_{h11} n_{h22} / n_h \left( \sum_h n_{h12} n_{h21} / n_h \right)}$$

$$+ \frac{\sum_h (n_{h12} + n_{h21})(n_{h12} n_{h21}) / n_h^2}{2 \left( \sum_h n_{h12} n_{h21} / n_h \right)^2}$$
Note that the Mantel-Haenszel odds ratio estimator is less sensitive to small $n_h$ than the logit estimator.

**Logit Estimator**
The adjusted logit estimate of the common odds ratio (Woolf 1955) is computed as

\[
OR_L = \exp \left( \sum_h w_h \ln(OR_h) / \sum_h w_h \right)
\]

and the corresponding 100(1 − $\alpha$)% confidence limits are

\[
\left( OR_L \times \exp \left( -z / \sqrt{\sum_h w_h} \right), \ OR_L \times \exp \left( z / \sqrt{\sum_h w_h} \right) \right)
\]

where $OR_h$ is the odds ratio for stratum $h$, and

\[
w_h = 1 / \text{Var} (\ln(OR_h))
\]

If any table cell frequency in a stratum $h$ is 0, PROC FREQTAB adds 0.5 to each cell of the stratum before computing $OR_h$ and $w_h$ (Haldane 1955) for the logit estimate. The procedure provides a warning when this occurs.

**Relative Risks, Cohort Studies** PROC FREQTAB provides Mantel-Haenszel and logit estimates of the common relative risks for stratified $2 \times 2$ tables.

**Mantel-Haenszel Estimator**
The Mantel-Haenszel estimate of the common relative risk for column 1 is computed as

\[
RR_{MH} = \left( \sum_h n_{h11} n_{h2.} / n_h \right) / \left( \sum_h n_{h21} n_{h1.} / n_h \right)
\]

It is always computed unless the denominator is 0. See Mantel and Haenszel (1959) and Agresti (2002) for more information.

To compute confidence limits for the common relative risk, PROC FREQTAB uses the Greenland and Robins (1985) variance estimate for $\log(\text{RR}_{MH})$. The 100(1 − $\alpha/2$)% confidence limits for the common relative risk are

\[
\left( RR_{MH} \times \exp(-z\hat{\sigma}), \ RR_{MH} \times \exp(z\hat{\sigma}) \right)
\]

where

\[
\hat{\sigma}^2 = \text{Var}(\ln(\text{RR}_{MH})) = \frac{\sum_h (n_{h1.} n_{h2.} n_{h1} - n_{h11} n_{h21} n_h) / n_h^2}{(\sum_h n_{h11} n_{h2.} / n_h) (\sum_h n_{h21} n_{h1.} / n_h)}
\]

**Logit Estimator**
The adjusted logit estimate of the common relative risk for column 1 is computed as

\[
RR_L = \exp \left( \sum_h w_h \ln(OR_h) / \sum_h w_h \right)
\]
and the corresponding 100\((1 - \alpha)\)% confidence limits are

\[
\left( RR_L \times \exp \left( -z / \sqrt{\sum_h w_h} \right), \quad RR_L \times \exp \left( z / \sqrt{\sum_h w_h} \right) \right)
\]

where \(RR_h\) is the column 1 relative risk estimate for stratum \(h\) and

\[
w_h = 1 / \text{Var}(\ln(RR_h))
\]

If \(n_{h11}\) or \(n_{h21}\) is 0, PROC FREQTAB adds 0.5 to each cell of the stratum before computing \(RR_h\) and \(w_h\) for the logit estimate. The procedure prints a warning when this occurs. For more information, see Kleinbaum, Kupper, and Morgenstern (1982, Sections 17.4 and 17.5).

**Breslow-Day Test for Homogeneity of the Odds Ratios**

When you specify the CMH option, PROC FREQTAB computes the Breslow-Day test for stratified \(2 \times 2\) tables. It tests the null hypothesis that the odds ratios for the \(q\) strata are equal. When the null hypothesis is true, the statistic has approximately a chi-square distribution with \(q-1\) degrees of freedom. See Breslow and Day (1980) and Agresti (2007) for more information.

The Breslow-Day statistic is computed as

\[
Q_{BD} = \sum_h (n_{h11} - E(n_{h11} | OR_{MH}))^2 / \text{Var}(n_{h11} | OR_{MH})
\]

where \(E\) and \(\text{Var}\) denote expected value and variance, respectively. The summation does not include any table that contains a row or column that has a total frequency of 0. If \(OR_{MH}\) equals 0 or if it is undefined, PROC FREQTAB does not compute the statistic and prints a warning message.

For the Breslow-Day test to be valid, the sample size should be relatively large in each stratum, and at least 80% of the expected cell counts should be greater than 5. Note that this is a stricter sample size requirement than the requirement for the Cochran-Mantel-Haenszel test for \(q \times 2 \times 2\) tables, in that each stratum sample size (not just the overall sample size) must be relatively large. Even when the Breslow-Day test is valid, it might not be very powerful against certain alternatives, as discussed in Breslow and Day (1980).

If you specify the BDT option, PROC FREQTAB computes the Breslow-Day test with Tarone’s adjustment, which subtracts an adjustment factor from \(Q_{BD}\) to make the resulting statistic asymptotically chi-square. The Breslow-Day-Tarone statistic is computed as

\[
Q_{BDT} = Q_{BD} - \left( \sum_h (n_{h11} - E(n_{h11} | OR_{MH})) \right)^2 / \sum_h \text{Var}(n_{h11} | OR_{MH})
\]

See Tarone (1985); Jones et al. (1989); Breslow (1996) for more information.

**Zelen’s Exact Test for Equal Odds Ratios**

If you specify the EQOR option in the EXACT statement, PROC FREQTAB computes Zelen’s exact test for equal odds ratios for stratified \(2 \times 2\) tables. Zelen’s test is an exact counterpart to the Breslow-Day asymptotic test for equal odds ratios. The reference set for Zelen’s test includes all possible \(q \times 2 \times 2\) tables with the same row, column, and stratum totals as the observed multiway table and with the same sum of cell \((1,1)\) frequencies as the observed table. The test statistic is the probability of the observed \(q \times 2 \times 2\) table conditional on the fixed margins, which is a product of hypergeometric probabilities.
The \( p \)-value for Zelen’s test is the sum of all table probabilities that are less than or equal to the observed table probability, where the sum is computed over all tables in the reference set determined by the fixed margins and the observed sum of cell (1,1) frequencies. This test is similar to Fisher’s exact test for two-way tables. For more information, see Zelen (1971); Hirji (2006); Agresti (1992). PROC FREQTAB computes Zelen’s exact test by using the polynomial multiplication algorithm of Hirji et al. (1996).

**Exact Confidence Limits for the Common Odds Ratio**

If you specify the COMOR option in the EXACT statement, PROC FREQTAB computes exact confidence limits for the common odds ratio for stratified \( 2 \times 2 \) tables. This computation assumes that the odds ratio is constant over all the \( 2 \times 2 \) tables. Exact confidence limits are constructed from the distribution of \( S = \sum_h n_{h11} \), conditional on the marginal totals of the \( 2 \times 2 \) tables.

Because this is a discrete problem, the confidence coefficient for these exact confidence limits is not exactly \( 1 - \alpha \) but is at least \( 1 - \alpha \). Thus, these confidence limits are conservative. See Agresti (1992) for more information.


Conditional on the marginal totals of \( 2 \times 2 \) table \( h \), let the random variable \( S_h \) denote the frequency of table cell (1,1). Given the row totals \( n_{h1} \) and \( n_{h2} \) and column totals \( n_{h1} \) and \( n_{h2} \), the lower and upper bounds for \( S_h \) are \( l_h \) and \( u_h \),

\[
l_h = \max ( 0, \; n_{h1} - n_{h2} ) \\
u_h = \min ( n_{h1}, \; n_{h2} )
\]

Let \( C_{s_h} \) denote the hypergeometric coefficient,

\[
C_{s_h} = \binom{n_{h1}}{s_h} \binom{n_{h2}}{n_{h1} - s_h}
\]

and let \( \phi \) denote the common odds ratio. Then the conditional distribution of \( S_h \) is

\[
P( S_h = s_h \mid n_{11}, n_{1}, n_{2} ) = C_{s_h} \phi^{s_h} / \sum_{x = l_h}^{u_h} C_x \phi^x
\]

Summing over all the \( 2 \times 2 \) tables, \( S = \sum_h S_h \), and the lower and upper bounds of \( S \) are \( l \) and \( u \),

\[
l = \sum_h l_h \quad \text{and} \quad u = \sum_h u_h
\]

The conditional distribution of the sum \( S \) is

\[
P( S = s \mid n_{h1}, n_{h1}, n_{h2}; h = 1, \ldots, q ) = C_s \phi^s / \sum_{x = l}^{u} C_x \phi^x
\]

where

\[
C_s = \sum_{s_1 + \cdots + s_q = s} \left( \prod_h C_{s_h} \right)
\]
Let $s_0$ denote the observed sum of cell (1,1) frequencies over the $q$ tables. The following two equations are solved iteratively for lower and upper confidence limits for the common odds ratio, $\phi_1$ and $\phi_2$:

$$\sum_{x = s_0}^{x = u} C_x \phi_1^x / \sum_{x = l}^{x = u} C_x \phi_1^x = \alpha/2$$

$$\sum_{x = l}^{x = s_0} C_x \phi_2^x / \sum_{x = l}^{x = u} C_x \phi_2^x = \alpha/2$$

When the observed sum $s_0$ equals the lower bound $l$, PROC FREQTAB sets the lower confidence limit to 0 and determines the upper limit with level $\alpha$. Similarly, when the observed sum $s_0$ equals the upper bound $u$, PROC FREQTAB sets the upper confidence limit to infinity and determines the lower limit with level $\alpha$.

When you specify the COMOR option in the EXACT statement, PROC FREQTAB also computes the exact test that the common odds ratio equals one. Setting $\phi = 1$, the conditional distribution of the sum $S$ under the null hypothesis becomes

$$P_0( S = s \mid n_{h1}, n_{h1}, n_{h2}; h = 1, \ldots, q ) = C_s / \sum_{x = l}^{x = u} C_x$$

The point probability for this exact test is the probability of the observed sum $s_0$ under the null hypothesis, conditional on the marginals of the stratified $2 \times 2$ tables, and is denoted by $P_0(s_0)$. The expected value of $S$ under the null hypothesis is

$$E_0(S) = \sum_{x = l}^{x = u} C_x / \sum_{x = l}^{x = u} C_x$$

The one-sided exact $p$-value is computed from the conditional distribution as $P_0(S >= s_0)$ or $P_0(S <= s_0)$, depending on whether the observed sum $s_0$ is greater or less than $E_0(S)$,

$$P_1 = P_0( S >= s_0 ) = \sum_{x = s_0}^{x = u} C_x / \sum_{x = l}^{x = u} C_x \quad \text{if } s_0 > E_0(S)$$

$$P_1 = P_0( S <= s_0 ) = \sum_{x = l}^{x = s_0} C_x / \sum_{x = l}^{x = u} C_x \quad \text{if } s_0 \leq E_0(S)$$

PROC FREQTAB computes two-sided $p$-values for this test according to three different definitions. A two-sided $p$-value is computed as twice the one-sided $p$-value, setting the result equal to one if it exceeds one,

$$P_2^a = 2 \times P_1$$

In addition, a two-sided $p$-value is computed as the sum of all probabilities less than or equal to the point probability of the observed sum $s_0$, summing over all possible values of $s$, $l \leq s \leq u$,

$$P_2^b = \sum_{l \leq s \leq u; P_0(s) \leq P_0(s_0)} P_0(s)$$

Also, a two-sided $p$-value is computed as the sum of the one-sided $p$-value and the corresponding area in the opposite tail of the distribution, equidistant from the expected value,

$$P_2^c = P_0( |S - E_0(S)| \geq |s_0 - E_0(S)| )$$
Gail-Simon Test for Qualitative Interactions

The GAILSIMON option in the TABLES statement provides the Gail-Simon test for qualitative interaction for stratified $2 \times 2$ tables. For more information, see Gail and Simon (1985); Silvapulle (2001); Dmitrienko et al. (2005).

The Gail-Simon test is based on the risk differences in stratified $2 \times 2$ tables, where the risk difference is defined as the row 1 risk (proportion in column 1) minus the row 2 risk. For more information, see the section “Risks and Risk Differences” on page 222. By default, PROC FREQTAB uses column 1 risks to compute the Gail-Simon test. If you specify the GAILSIMON(COLUMN=2) option, PROC FREQTAB uses column 2 risks.

PROC FREQTAB computes the Gail-Simon test statistics as described in Gail and Simon (1985),

$$Q^- = \sum_{h} (d_h/s_h)^2 I(d_h > 0)$$

$$Q^+ = \sum_{h} (d_h/s_h)^2 I(d_h < 0)$$

$$Q = \min (Q^-, Q^+)$$

where $d_h$ is the risk difference in table $h$, $s_h$ is the standard error of the risk difference, and $I(d_h > 0)$ equals 1 if $d_h > 0$ and 0 otherwise. Similarly, $I(d_h < 0)$ equals 1 if $d_h < 0$ and 0 otherwise. The $q$ $2 \times 2$ tables (strata) are indexed by $h = 1, 2, \ldots, q$.

The $p$-values for the Gail-Simon statistics are computed as

$$p(Q^-) = \sum_{h} (1 - F_h(Q^-)) B(h; n = q, p = 0.5)$$

$$p(Q^+) = \sum_{h} (1 - F_h(Q^+)) B(h; n = q, p = 0.5)$$

$$p(Q) = \sum_{h=1}^{q-1} (1 - F_h(Q)) B(h; n = (q - 1), p = 0.5)$$

where $F_h(\cdot)$ is the cumulative chi-square distribution function with $h$ degrees of freedom and $B(h; n, p)$ is the binomial probability function with parameters $n$ and $p$. The statistic $Q$ tests the null hypothesis of no qualitative interaction. The statistic $Q^-$ tests the null hypothesis of positive risk differences. A small $p$-value for $Q^-$ indicates negative differences; similarly, a small $p$-value for $Q^+$ indicates positive risk differences.

Exact Statistics

Exact statistics can be useful in situations where the asymptotic assumptions are not met, and so the asymptotic $p$-values are not close approximations for the true $p$-values. Standard asymptotic methods involve the assumption that the test statistic follows a particular distribution when the sample size is sufficiently large. When the sample size is not large, asymptotic results might not be valid, with the asymptotic $p$-values
differing perhaps substantially from the exact $p$-values. Asymptotic results might also be unreliable when 
the distribution of the data is sparse, skewed, or heavily tied. See Agresti (2007) and Bishop, Fienberg, 
and Holland (1975) for more information. Exact computations are based on the statistical theory of exact 

In addition to computation of exact $p$-values, PROC FREQTAB provides the option of estimating exact 
$p$-values by Monte Carlo simulation. This can be useful for problems that are so large that exact computations 
require a great amount of time and memory, but for which asymptotic approximations might not be sufficient.

Exact statistics are available for many PROC FREQTAB tests. For one-way tables, PROC FREQTAB 
provides exact $p$-values for the binomial proportion tests and the chi-square goodness-of-fit test. Exact 
(Clopper-Pearson) confidence limits are available for the binomial proportion. For two-way tables, PROC 
FREQTAB provides exact $p$-values for the following tests: Pearson chi-square test, likelihood ratio chi-square 
test, Mantel-Haenszel chi-square test, Fisher’s exact test, Jonckheere-Terpstra test, Cochran-Armitage test 
for trend, and the symmetry test. PROC FREQTAB also computes exact $p$-values for tests of the following 
statistics: Kendall’s tau-$b$, Stuart’s tau-$c$, Somers’ $D(C|R)$, Somers’ $D(R|C)$, Pearson correlation coefficient, 
Spearman correlation coefficient, simple kappa coefficient, and weighted kappa coefficient. For $2 \times 2$ tables, 
PROC FREQTAB provides McNemar’s exact test and exact confidence limits for the odds ratio. PROC 
FREQTAB also provides exact unconditional confidence limits for the proportion (risk) difference and for the 
relative risk. For stratified $2 \times 2$ tables, PROC FREQTAB provides Zelen’s exact test for equal odds ratios, 
effectively limits for the common odds ratio, and an exact test for the common odds ratio.

The following sections summarize the exact computational algorithms, define the exact $p$-values that PROC 
FREQTAB computes, discuss the computational resource requirements, and describe the Monte Carlo 
estimation option.

**Computational Algorithms**

PROC FREQTAB computes exact $p$-values for general $R \times C$ tables by using the network algorithm developed 
by Mehta and Patel (1983). This algorithm provides a substantial advantage over direct enumeration, which 
can be very time-consuming and feasible only for small problems. See Agresti (1992) for a review of 
algorithms for computation of exact $p$-values, and see Mehta, Patel, and Tsai (1984) and Mehta, Patel, and 

The reference set for a given contingency table is the set of all contingency tables with the observed marginal 
row and column sums. Corresponding to this reference set, the network algorithm forms a directed acyclic 
network consisting of nodes in a number of stages. A path through the network corresponds to a distinct 
table in the reference set. The distances between nodes are defined so that the total distance of a path through 
the network is the corresponding value of the test statistic. At each node, the algorithm computes the shortest 
and longest path distances for all the paths that pass through that node. For statistics that can be expressed as 
a linear combination of cell frequencies multiplied by increasing row and column scores, PROC FREQTAB 
computes shortest and longest path distances by using the algorithm of Agresti, Mehta, and Patel (1990). For 
statistics of other forms, PROC FREQTAB computes an upper bound for the longest path and a lower bound 
for the shortest path by following the approach of Valz and Thompson (1994).

The longest and shortest path distances or bounds for a node are compared to the value of the test statistic 
to determine whether all paths through the node contribute to the $p$-value, none of the paths through the 
node contribute to the $p$-value, or neither of these situations occurs. If all paths through the node contribute, 
the $p$-value is incremented accordingly, and these paths are eliminated from further analysis. If no paths 
contribute, these paths are eliminated from the analysis. Otherwise, the algorithm continues, still processing 
this node and the associated paths. The algorithm finishes when all nodes have been accounted for.
In applying the network algorithm, PROC FREQTAB uses full numerical precision to represent all statistics, row and column scores, and other quantities involved in the computations. Although it is possible to use rounding to improve the speed and memory requirements of the algorithm, PROC FREQTAB does not do this because it can result in reduced accuracy of the \( p \)-values.

For one-way tables, PROC FREQTAB computes the exact chi-square goodness-of-fit test by the method of Radlow and Alf (1975). PROC FREQTAB generates all possible one-way tables with the observed total sample size and number of categories. For each possible table, PROC FREQTAB compares its chi-square value with the value for the observed table. If the table’s chi-square value is greater than or equal to the observed chi-square, PROC FREQTAB increments the exact \( p \)-value by the probability of that table, which is calculated under the null hypothesis by using the multinomial frequency distribution. By default, the null hypothesis states that all categories have equal proportions. If you specify null hypothesis proportions or frequencies by using the TESTP= or TESTF= option in the TABLES statement, PROC FREQTAB calculates the exact chi-square test based on that null hypothesis.

Other exact computations are described in sections about the individual statistics. For information about the computation of exact confidence limits and tests for the binomial proportion, see the section “Binomial Proportion” on page 214. For information about computation of exact confidence limits for the odds ratio, see the subsection “Exact Confidence Limits” in the section “Confidence Limits for the Odds Ratio” on page 237. For information about other exact computations, see the subsection “Exact Unconditional Confidence Limits” in the section “Confidence Limits for the Relative Risk” on page 240, and the sections “Exact Symmetry Test” on page 250, “Exact Confidence Limits for the Common Odds Ratio” on page 263 and “Zelen’s Exact Test for Equal Odds Ratios” on page 262.

**Definition of \( p \)-Values**

For several tests in PROC FREQTAB, the test statistic is nonnegative, and large values of the test statistic indicate a departure from the null hypothesis. Such nondirectional tests include the Pearson chi-square, the likelihood ratio chi-square, the Mantel-Haenszel chi-square, Fisher’s exact test for tables larger than \( 2 \times 2 \), McNemar’s test, the symmetry test, and the one-way chi-square goodness-of-fit test. The exact \( p \)-value for a nondirectional test is the sum of probabilities for those tables having a test statistic greater than or equal to the value of the observed test statistic.

There are other tests where it might be appropriate to test against either a one-sided or a two-sided alternative hypothesis. For example, when you test the null hypothesis that the true parameter value equals 0 (\( T = 0 \)), the alternative of interest might be one-sided (\( T \leq 0 \), or \( T \geq 0 \)) or two-sided (\( T \neq 0 \)). Such tests include the Pearson correlation coefficient, Spearman correlation coefficient, Jonckheere-Terpstra test, Cochran-Armitage test for trend, simple kappa coefficient, and weighted kappa coefficient. For these tests, PROC FREQTAB displays the right-sided \( p \)-value when the observed value of the test statistic is greater than its expected value. The right-sided \( p \)-value is the sum of probabilities for those tables for which the test statistic is greater than or equal to the observed test statistic. Otherwise, when the observed test statistic is less than or equal to the expected value, PROC FREQTAB displays the left-sided \( p \)-value. The left-sided \( p \)-value is the sum of probabilities for those tables for which the test statistic is less than or equal to the one observed. The one-sided \( p \)-value \( P_1 \) can be expressed as

\[
P_1 = \begin{cases} 
\text{Prob( Test Statistic } \geq t) & \text{if } t > E_0(T) \\
\text{Prob( Test Statistic } \leq t) & \text{if } t \leq E_0(T)
\end{cases}
\]

where \( t \) is the observed value of the test statistic and \( E_0(T) \) is the expected value of the test statistic under the null hypothesis. PROC FREQTAB computes the two-sided \( p \)-value as the sum of the one-sided \( p \)-value and
the corresponding area in the opposite tail of the distribution of the statistic, equidistant from the expected value. The two-sided $p$-value $P_2$ can be expressed as

$$P_2 = \Pr (|\text{Test Statistic} - E_0(T)| \geq |t - E_0(T)|)$$

If you specify the POINT option in the EXACT statement, PROC FREQTAB provides exact point probabilities for the exact tests. The exact point probability is the exact probability that the test statistic equals the observed value.

If you specify the MIDP option in the EXACT statement, PROC FREQTAB provides exact mid-$p$-values. The exact mid $p$-value is defined as the exact $p$-value minus half the exact point probability, which equals the average of $\Pr(\text{Test Statistic} \geq t)$ and $\Pr(\text{Test Statistic} > t)$ for a right-sided test. The exact mid $p$-value is smaller and less conservative than the non-adjusted exact $p$-value. For more information, see Agresti (2013, section 1.1.4) and Hirji (2006, sections 2.5 and 2.11.1).

**Computational Resources**

PROC FREQTAB uses relatively fast and efficient algorithms for exact computations. These recently developed algorithms, together with improvements in computer power, now make it feasible to perform exact computations for data sets where previously only asymptotic methods could be applied. Nevertheless, there are still large problems that might require a prohibitive amount of time and memory for exact computations, depending on the speed and memory available on your computer. For large problems, consider whether exact methods are really needed or whether asymptotic methods might give results quite close to the exact results and require much less computer time and memory. When asymptotic methods might not be sufficient for such large problems, consider using Monte Carlo estimation of exact $p$-values, as described in the section “Monte Carlo Estimation” on page 269.

A formula does not exist that can predict in advance how much time and memory are needed to compute an exact $p$-value for a certain problem. The time and memory required depend on several factors, including which test is being performed, the total sample size, the number of rows and columns, and the specific arrangement of the observations into table cells. Generally, larger problems (in terms of total sample size, number of rows, and number of columns) tend to require more time and memory. For a fixed total sample size, time and memory requirements tend to increase as the number of rows and number of columns increase because the number of tables in the reference set increases. Also for a fixed sample size, time and memory requirements tend to increase as the marginal row and column totals become more homogeneous. For more information, see Agresti, Mehta, and Patel (1990) and Gail and Mantel (1977).

When PROC FREQTABLE is computing exact $p$-values, you can terminate the computations by pressing the system interrupt key sequence (see the *SAS Companion* for your system) and choosing to stop computations. After you terminate exact computations, PROC FREQTAB completes all other remaining tasks. The procedure produces the requested output and reports missing values for any exact $p$-values that were not computed by the time of termination.

You can also use the MAXTIME= option in the EXACT statement to limit the amount of time PROC FREQTAB uses for exact computations. You specify a MAXTIME= value that is the maximum amount of clock time (in seconds) that PROC FREQTAB can use to compute an exact $p$-value. If PROC FREQTAB does not finish computing an exact $p$-value within that time, it terminates the computation and completes all other remaining tasks.
Monte Carlo Estimation

If you specify the option MC in the EXACT statement, PROC FREQTAB computes Monte Carlo estimates of the exact $p$-values instead of directly computing the exact $p$-values. Monte Carlo estimation can be useful for large problems that require a great amount of time and memory for exact computations but for which asymptotic approximations might not be sufficient. To describe the precision of each Monte Carlo estimate, PROC FREQTAB provides the asymptotic standard error and $100(1 - \alpha)\%$ confidence limits. The ALPHA= option in the EXACT statement determines the confidence level $\alpha$; by default, ALPHA=0.01, which produces 99% confidence limits. The N=n option in the EXACT statement specifies the number of samples that PROC FREQTAB uses for Monte Carlo estimation; the default is 10000 samples. You can specify a larger value for $n$ to improve the precision of the Monte Carlo estimates. Because larger values of $n$ generate more samples, the computation time increases. Alternatively, you can specify a smaller value of $n$ to reduce the computation time.

To compute a Monte Carlo estimate of an exact $p$-value, PROC FREQTAB generates a random sample of tables with the same total sample size, row totals, and column totals as the observed table. PROC FREQTAB uses the algorithm of Agresti, Wackerly, and Boyett (1979), which generates tables in proportion to their hypergeometric probabilities conditional on the marginal frequencies. For each sample table, PROC FREQTAB computes the value of the test statistic and compares it to the value for the observed table. When estimating a right-sided $p$-value, PROC FREQTAB counts all sample tables for which the test statistic is greater than or equal to the observed test statistic. Then the $p$-value estimate equals the number of these tables divided by the total number of tables sampled.

$$
\hat{P}_{MC} = \frac{M}{N}
$$

\begin{align*}
M &= \text{number of samples with } (\text{Test Statistic } \geq t) \\
N &= \text{total number of samples} \\
t &= \text{observed Test Statistic}
\end{align*}

PROC FREQTAB computes left-sided and two-sided $p$-value estimates in a similar manner. For left-sided $p$-values, PROC FREQTAB evaluates whether the test statistic for each sampled table is less than or equal to the observed test statistic. For two-sided $p$-values, PROC FREQTAB examines the sample test statistics according to the expression for $P_2$ given in the section “Definition of $p$-Values” on page 267.

The variable $M$ is a binomially distributed variable with $N$ trials and success probability $p$. It follows that the asymptotic standard error of the Monte Carlo estimate is

$$
se(\hat{P}_{MC}) = \sqrt{\frac{\hat{P}_{MC} (1 - \hat{P}_{MC})}{(N - 1)}}
$$

PROC FREQTAB constructs asymptotic confidence limits for the $p$-values according to

$$
\hat{P}_{MC} \pm \left( z_{\alpha/2} \times se(\hat{P}_{MC}) \right)
$$

where $z_{\alpha/2}$ is the $100(1 - \alpha/2)\text{th}$ percentile of the standard normal distribution and the confidence level $\alpha$ is determined by the ALPHA= option in the EXACT statement.

When the Monte Carlo estimate $\hat{P}_{MC}$ is 0, PROC FREQTAB computes the confidence limits for the $p$-value as

$$
(0, \ 1 - \alpha^{(1/N)})
$$
When the Monte Carlo estimate $\hat{P}_{MC}$ is 1, PROC FREQTAB computes the confidence limits as

$$\left( \alpha^{(1/N)}, 1 \right)$$

**Output Data Sets**

PROC FREQTAB produces two types of output data sets that you can use with other statistical and reporting procedures. You can request these data sets as follows:

- Specify the OUT= option in a TABLES statement. This creates an output data set that contains frequency or crosstabulation table counts and percentages.
- Specify an OUTPUT statement. This creates an output data set that contains statistics.

PROC FREQTAB does not display the output data sets. Use PROC PRINT, PROC REPORT, or any other SAS reporting tool to display an output data set.

In addition to these two output data sets, you can create a SAS data set from any piece of PROC FREQTAB output by using the Output Delivery System. See the section “ODS Table Names” on page 282 for more information.

**Contents of the TABLES Statement Output Data Set**

The OUT= option in the TABLES statement creates an output data set that contains one observation for each combination of variable values (or table cell) in the last table request. By default, each observation contains the frequency and percentage for the table cell. The output data set includes the following variables:

- BY variables
- table request variables, such as A, B, C, and D in the table request A*B*C*D
- COUNT, which contains the table cell frequency
- PERCENT, which contains the table cell percentage

If you specify the OUTEXPECT option in the TABLES statement for a two-way or multiway table, the output data set also includes expected cell frequencies. If you specify the OUTPCT option for a two-way or multiway table, the output data set also includes row, column, and table percentages. The additional variables are as follows:

- EXPECTED, which contains the expected frequency
- PCT_TABL, which contains the percentage of two-way table frequency, for $n$-way tables where $n > 2$
- PCT_ROW, which contains the percentage of row frequency
- PCT_COL, which contains the percentage of column frequency
The OUTEXPECT and OUTPCT options have no effect for one-way tables or for tables that you display in list format (which you can request by specifying the LIST option).

If you specify the OUTCUM option in the TABLES statement for a one-way table or for a table in list format, the output data set also includes cumulative frequencies and cumulative percentages. The additional variables are as follows:

- **CUM_FREQ**, which contains the cumulative frequency
- **CUM_PCT**, which contains the cumulative percentage

The following PROC FREQTAB statements create an output data set of frequencies and percentages:

```sas
proc freqtab;
   tables A A*B / out=D;
run;
```

The output data set D contains frequencies and percentages for the table of A by B, which is the last table request listed in the TABLES statement. If A has two levels (1 and 2), B has three levels (1,2, and 3), and no table cell count is 0 or missing, the output data set D includes six observations, one for each combination of A and B levels. The first observation corresponds to A=1 and B=1; the second observation corresponds to A=1 and B=2; and so on. The data set includes the variables COUNT and PERCENT. The value of COUNT is the number of observations with the given combination of A and B levels. The value of PERCENT is the percentage of the total number of observations with that A and B combination.

When PROC FREQTAB combines different variable values into the same formatted level, the output data set contains the smallest internal value for the formatted level. For example, suppose a variable X has the values 1.1., 1.4, 1.7, 2.1, and 2.3. When you submit the statement

```sas
format X 1.;
```

in a PROC FREQTAB step, the formatted levels listed in the frequency table for X are 1 and 2. If you create an output data set with the frequency counts, the internal values of the levels of X are 1.1 and 1.7. To report the internal values of X when you display the output data set, use a format of 3.1 for X.

### Contents of the OUTPUT Statement Output Data Set

The OUTPUT statement creates a SAS data set that contains statistics computed by PROC FREQTAB. Table 4.6 lists the statistics that can be stored in the output data set. You identify which statistics to include by specifying **output-options**. For more information, see the description of the OUTPUT statement.

If you specify multiple TABLES statements or multiple table requests in a single TABLES statement, the contents of the output data set correspond to the last table request.

For a one-way table or a two-way table, the output data set contains one observation that stores the requested statistics for the table. For a multiway table, the output data set contains an observation for each two-way table (stratum) of the multiway crosstabulation. If you request summary statistics for the multiway table, the output data set also contains an observation that stores the across-strata summary statistics. If you use a BY statement, the output data set contains an observation (for one-way or two-way tables) or set of observations (for multiway tables) for each BY group.

The OUTPUT data set can include the following variables:
BY variables

- Variables that identify the stratum for multiway tables, such as A and B in the table request A*B*C*D
- Variables that contain the specified statistics

In addition to the specified estimate or test statistic, the output data set includes associated values such as standard errors, confidence limits, $p$-values, and degrees of freedom.

PROC FREQTAB constructs variable names for the statistics in the output data set by enclosing the *output-option* names in underscores. Variable names for the corresponding standard errors, confidence limits, $p$-values, and degrees of freedom are formed by combining the *output-option* names with prefixes that identify the associated values. Table 4.20 lists the prefixes and their descriptions.

<table>
<thead>
<tr>
<th>Prefix</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>E_</td>
<td>Asymptotic standard error (ASE)</td>
</tr>
<tr>
<td>L_</td>
<td>Lower confidence limit</td>
</tr>
<tr>
<td>U_</td>
<td>Upper confidence limit</td>
</tr>
<tr>
<td>E0_</td>
<td>Null hypothesis ASE</td>
</tr>
<tr>
<td>Z_</td>
<td>Standardized value</td>
</tr>
<tr>
<td>DF_</td>
<td>Degrees of freedom</td>
</tr>
<tr>
<td>P_</td>
<td>$p$-value</td>
</tr>
<tr>
<td>P2_</td>
<td>Two-sided $p$-value</td>
</tr>
<tr>
<td>PL_</td>
<td>Left-sided $p$-value</td>
</tr>
<tr>
<td>PR_</td>
<td>Right-sided $p$-value</td>
</tr>
<tr>
<td>XP_</td>
<td>Exact $p$-value</td>
</tr>
<tr>
<td>XP2_</td>
<td>Exact two-sided $p$-value</td>
</tr>
<tr>
<td>XPL_</td>
<td>Exact left-sided $p$-value</td>
</tr>
<tr>
<td>XPR_</td>
<td>Exact right-sided $p$-value</td>
</tr>
<tr>
<td>XPT_</td>
<td>Exact point probability</td>
</tr>
<tr>
<td>XMP_</td>
<td>Exact mid $p$-value</td>
</tr>
<tr>
<td>XL_</td>
<td>Exact lower confidence limit</td>
</tr>
<tr>
<td>XU_</td>
<td>Exact upper confidence limit</td>
</tr>
</tbody>
</table>

For example, the PCHI *output-option* in the OUTPUT statement includes the Pearson chi-square test in the output data set. The variable names for the Pearson chi-square statistic, its degrees of freedom, and the corresponding $p$-value are _PCHI_, DF_PCHI, and P_PCHI, respectively. For variables that were added to the output data set before SAS/STAT 8.2, PROC FREQTAB truncates the variable name to eight characters when the length of the prefix plus the *output-option* name exceeds eight characters.
Number of Variable Levels Table

If you specify the NLEVELS option in the PROC FREQTAB statement, PROC FREQTAB displays the “Number of Variable Levels” table. This table provides the number of levels for all variables named in the TABLES statements. PROC FREQTAB determines the variable levels by using the formatted variable values. The “Number of Variable Levels” table contains the following information:

- Variable name
- Levels, which is the total number of levels of the variable

One-Way Frequency Tables

PROC FREQTAB displays one-way frequency tables for all one-way table requests in the TABLES statements, unless you specify the NOPRINT option in the PROC FREQTAB statement or the NOPRINT option in the TABLES statement. For a one-way table showing the frequency distribution of a single variable, PROC FREQTAB displays the name of the variable and its values. For each variable value or level, PROC FREQTAB displays the following information:

- Frequency count, which is the number of observations in the level
- Test Frequency count, if you specify the CHISQ and TESTF= options to request a chi-square goodness-of-fit test for specified frequencies
- Percent, which is the percentage of the total number of observations. (The NOPERCENT option suppresses this information.)
- Test Percent, if you specify the CHISQ and TESTP= options to request a chi-square goodness-of-fit test for specified percents. (The NOPERCENT option suppresses this information.)
- Cumulative Frequency count, which is the sum of the frequency counts for that level and all other levels listed above it in the table. The last cumulative frequency is the total number of nonmissing observations. (The NOCUM option suppresses this information.)
- Cumulative Percent, which is the percentage of the total number of observations in that level and in all other levels listed above it in the table. (The NOCUM or the NOPERCENT option suppresses this information.)

The one-way table also displays the Frequency Missing, which is total frequency of missing values.

Statistics for One-Way Frequency Tables

For one-way tables, two statistical options are available in the TABLES statement. The CHISQ option provides a chi-square goodness-of-fit test, and the BINOMIAL option provides binomial proportion statistics and tests. PROC FREQTAB displays the following information, unless you specify the NOPRINT option in the PROC FREQTAB statement:
If you specify the CHISQ option for a one-way table, PROC FREQTAB provides a chi-square goodness-of-fit test, displaying the Chi-Square statistic, the degrees of freedom (DF), and the probability value (Pr > ChiSq). If you specify the CHISQ option in the EXACT statement, PROC FREQTAB also displays the exact probability value for this test. If you specify the POINT option with the CHISQ option in the EXACT statement, PROC FREQTAB displays the exact point probability for the test statistic. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the exact mid-p-value for the chi-square test.

If you specify the BINOMIAL option for a one-way table, PROC FREQTAB displays the estimate of the binomial Proportion, which is the proportion of observations in the first class listed in the one-way table. PROC FREQTAB also displays the asymptotic standard error (ASE) and the asymptotic (Wald) and exact (Clopper-Pearson) confidence limits by default. For the binomial proportion test, PROC FREQTAB displays the asymptotic standard error under the null hypothesis (ASE Under H0), the standardized test statistic (Z), and the one-sided and two-sided probability values.

If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB also displays the exact one-sided and two-sided probability values for this test. If you specify the POINT option with the BINOMIAL option in the EXACT statement, PROC FREQTAB displays the exact point probability for the test. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the exact mid-p-value for the binomial proportion test.

If you request binomial confidence limits by specifying the BINOMIAL(CL=) option, PROC FREQTAB displays the “Binomial Confidence Limits” table, which includes the Lower and Upper Confidence Limits for each confidence limit Type that you request. In addition to Wald and Clopper-Pearson (Exact) confidence limits, you can request the following confidence limit types for the binomial proportion: Agresti-Coull, Blaker, Jeffreys, Likelihood Ratio, Logit, Mid-p, and Wilson (score).

If you request a binomial noninferiority or superiority test by specifying the NONINF or SUP binomial-option, PROC FREQTAB displays a Noninferiority Analysis or Superiority Analysis table that contains the following information: the binomial Proportion, the test ASE (under H0 or Sample), the test statistic Z, the probability value, the noninferiority or superiority limit, and the test confidence limits. If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB also provides the exact probability value for the test, and exact test confidence limits.

If you request a binomial equivalence test by specifying the EQUIV binomial-option, PROC FREQTAB displays an Equivalence Analysis table that contains the following information: binomial Proportion and the test ASE (under H0 or Sample). PROC FREQTAB displays two one-sided tests (TOST) for equivalence, which include test statistics (Z) and probability values for the Lower and Upper tests, together with the Overall probability value. PROC FREQTAB also displays the equivalence limits and the test-based confidence limits. If you specify the BINOMIAL option in the EXACT statement, PROC FREQTAB provides exact probability values for the TOST and exact test-based confidence limits.

Two-Way and Multiway Tables

PROC FREQTAB displays all multiway table requests in the TABLES statements, unless you specify the NOPRINT option in the PROC FREQTAB statement or the NOPRINT option in the TABLES statement.

For two-way to multiway crosstabulation tables, the values of the last variable in the table request form the table columns. The values of the next-to-last variable form the rows. Each level (or combination of levels) of the other variables forms one stratum.
There are three ways to display multiway tables in PROC FREQTAB. By default, PROC FREQTAB displays multiway tables as separate two-way crosstabulation tables for each stratum of the multiway table. Also by default, PROC FREQTAB displays these two-way crosstabulation tables in table cell format. Alternatively, if you specify the CROSSLIST option, PROC FREQTAB displays the two-way crosstabulation tables in ODS column format. If you specify the LIST option, PROC FREQTAB displays multiway tables in list format, which presents the entire multiway crosstabulation in a single table.

**Crosstabulation Tables**

By default, PROC FREQTAB displays two-way crosstabulation tables in table cell format. The row variable values are listed down the side of the table, the column variable values are listed across the top of the table, and each row and column variable level combination forms a table cell.

Each cell of a crosstabulation table can contain the following information:

- Frequency, which is the number of observations in the table cell. (The NOFREQ option suppresses this information.)
- Expected frequency under the hypothesis of independence, if you specify the EXPECTED option
- Deviation of the cell frequency from the expected value, if you specify the DEVIATION option
- Cell Chi-Square, which is the cell’s contribution to the total chi-square statistic, if you specify the CELLCHI2 option
- Tot Pct, which is the cell’s percentage of the total multiway table frequency, for n-way tables when n > 2, if you specify the TOTPCT option
- Percent, which is the cell’s percentage of the total (two-way table) frequency. (The NOPERCENT option suppresses this information.)
- Row Pct, or the row percentage, which is the cell’s percentage of the total frequency for its row. (The NOROW option suppresses this information.)
- Col Pct, or column percentage, which is the cell’s percentage of the total frequency for its column. (The NOCOL option suppresses this information.)
- Cumulative Col%, or cumulative column percentage, if you specify the CUMCOL option

The table also displays the Frequency Missing, which is the total frequency of missing values.

**CROSSLIST Tables**

If you specify the CROSSLIST option, PROC FREQTAB displays two-way crosstabulation tables in ODS column format. The CROSSLIST column format is different from the default crosstabulation table cell format, but the CROSSLIST table provides the same information (frequencies, percentages, and other statistics) as the default crosstabulation table.

In the CROSSLIST table format, the rows of the display correspond to the crosstabulation table cells, and the columns of the display correspond to descriptive statistics such as frequencies and percentages. Each table cell is identified by the values of its TABLES row and column variable levels, with all column variable levels listed within each row variable level. The CROSSLIST table also provides row totals, column totals, and overall table totals.

For a crosstabulation table in CROSSLIST format, PROC FREQTAB displays the following information:
Chapter 4: The FREQTAB Procedure

- the row variable name and values
- the column variable name and values
- Frequency, which is the number of observations in the table cell. (The NOFREQ option suppresses this information.)
- Expected cell frequency under the hypothesis of independence, if you specify the EXPECTED option
- Deviation of the cell frequency from the expected value, if you specify the DEVIATION option
- Standardized Residual, if you specify the CROSSLIST(STDRES) option
- Pearson Residual, if you specify the CROSSLIST(PEARSONRES) option
- Cell Chi-Square, which is the cell’s contribution to the total chi-square statistic, if you specify the CELLCHI2 option
- Total Percent, which is the cell’s percentage of the total multiway table frequency, for \( n \)-way tables when \( n > 2 \), if you specify the TOTPCT option
- Percent, which is the cell’s percentage of the total (two-way table) frequency. (The NOPERCENT option suppresses this information.)
- Row Percent, which is the cell’s percentage of the total frequency for its row. (The NOROW option suppresses this information.)
- Column Percent, the cell’s percentage of the total frequency for its column. (The NOCOL option suppresses this information.)

The table also displays the Frequency Missing, which is the total frequency of missing values.

LIST Tables

If you specify the LIST option in the TABLES statement, PROC FREQTAB displays two-way and multiway tables by using a list format instead of the default crosstabulation cell format. The list format displays an entire multiway table in a single table instead of separate two-way (stratum) tables. Each row of a table in list format corresponds to a single crosstabulation cell. Tables that are displayed in list format do not include row percentages, column percentages, or optional two-way table information such as expected frequencies and cell chi-squares.

PROC FREQTAB displays the following information in a list table:

- the variable names and values
- Frequency, which is the number of observations in the level (with the indicated variable values)
- Percent, which is the level’s percentage of the total number of observations. (The NOPERCENT option suppresses this information.)
- Cumulative Frequency, which is the accumulated frequency of the level and all other levels listed above it in the table. The last cumulative frequency in the table is the total number of nonmissing observations. (The NOCUM option suppresses this information.)
• Cumulative Percent, which is the accumulated percentage of the level and all other levels listed above it in the table. (The NOCUM or the NOPERCENT option suppresses this information.)

The table also displays the Frequency Missing, which is the total frequency of missing values.

Statistics for Two-Way and Multiway Tables

PROC FREQTAB computes statistical tests and measures for crosstabulation tables, depending on which statements and options you specify. You can suppress the display of these results by specifying the NOPRINT option in the PROC FREQTAB statement. With any of the following information, PROC FREQTAB also displays the Sample Size and the Frequency Missing.

• If you specify the SCOROUT option in the TABLES statement, PROC FREQTAB displays the Row Scores and Column Scores that it uses for statistical computations. The Row Scores table displays the row variable values and the Score corresponding to each value. The Column Scores table displays the column variable values and the corresponding Scores. PROC FREQTAB also identifies the score type used to compute the row and column scores. You can specify the score type with the SCORES= option in the TABLES statement.

• If you specify the CHISQ option, PROC FREQTAB displays the following statistics for each two-way table: Pearson Chi-Square, Likelihood Ratio Chi-Square, Continuity-Adjusted Chi-Square (for $2 \times 2$ tables), Mantel-Haenszel Chi-Square, the Phi Coefficient, the Contingency Coefficient, and Cramér’s V. For each test statistic, PROC FREQTAB also displays the degrees of freedom (DF) and the probability value (Prob).

• If you specify the FISHER option in the TABLES statement (or, equivalently, the FISHER option in the EXACT statement), PROC FREQTAB displays Fisher’s exact test for tables larger than $2 \times 2$. The test output includes the table probability (P) and the probability value. If you specify the POINT option in the EXACT statement, PROC FREQTAB displays the exact point probability for Fisher’s exact test. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the Mid $p$-Value for the test.

• If you specify the PCHI, LRCHI, or MHCHI option in the EXACT statement, PROC FREQTAB displays the corresponding exact test: Pearson Chi-Square, Likelihood Ratio Chi-Square, or Mantel-Haenszel Chi-Square, respectively. The test output includes the test statistic, the degrees of freedom (DF), and the asymptotic and exact probability values. If you also specify the POINT option in the EXACT statement, PROC FREQTAB displays the point probability for each exact test requested. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the exact mid $p$-value for each test. If you specify the CHISQ option in the EXACT statement, PROC FREQTAB displays exact probability values for all three of these chi-square tests.

• If you specify the MC option in the EXACT statement, PROC FREQTAB displays Monte Carlo estimates for all exact $p$-values that you request in the EXACT statement. The Monte Carlo output
includes the \( p \)-value Estimate, its Confidence Limits, the Number of Samples used to compute the Monte Carlo estimate, and the Initial Seed for random number generation.

- If you specify the `MEASURES` option, PROC FREQTAB displays the following statistics and their asymptotic standard errors (ASE) for each two-way table: Gamma, Kendall’s Tau-\(b\), Stuart’s Tau-\(c\), Somers’ \(D(C|R)\), Somers’ \(D(R|C)\), Pearson Correlation, Spearman Correlation, Lambda Asymmetric \((C|R)\), Lambda Asymmetric \((R|C)\), Lambda Symmetric, Uncertainty Coefficient \((C|R)\), Uncertainty Coefficient \((R|C)\), and Uncertainty Coefficient Symmetric. If you specify the `CL` option, PROC FREQTAB also displays confidence limits for these measures.

- If you specify the `PLCORR` option, PROC FREQTAB displays the polychoric correlation and its asymptotic standard error (ASE). For \(2 \times 2\) tables, this statistic is known as the tetrachoric correlation (and is labeled as such in the displayed output). If you specify the `CL` option, PROC FREQTAB also displays confidence limits for the polychoric correlation. If you specify the `PLCORR` option in the `TEST` statement, PROC FREQTAB displays the polychoric correlation, asymptotic standard error (ASE), confidence limits, and the following: the standardized test statistic (\(Z\)), the corresponding one-sided and two-sided probability values, the likelihood ratio (LR) chi-square, and the probability value (Pr > ChiSq).

- If you specify the `GAMMA`, `KENTB`, `STUTC`, `SMDCR`, `SMDRC`, `PCORR`, or `SCORR` option in the `TEST` statement, PROC FREQTAB displays asymptotic tests for Gamma, Kendall’s Tau-\(b\), Stuart’s Tau-\(c\), Somers’ \(D(C|R)\), Somers’ \(D(R|C)\), the Pearson Correlation, or the Spearman Correlation, respectively. If you specify the `MEASURES` option in the `TEST` statement, PROC FREQTAB displays all these asymptotic tests. The test output includes the statistic, its asymptotic standard error (ASE), Confidence Limits, the ASE under the null hypothesis \(H_0\), the standardized test statistic (\(Z\)), and the one-sided and two-sided probability values.

- If you specify the `KENTB`, `STUTC`, `SMDCR`, `SMDRC`, `PCORR`, or `SCORR` option in the `EXACT` statement, PROC FREQTAB displays asymptotic and exact tests for the corresponding measure of association: Kendall’s Tau-\(b\), Stuart’s Tau-\(c\), Somers’ \(D(C|R)\), Somers’ \(D(R|C)\), the Pearson Correlation, or the Spearman Correlation, respectively. If you also specify the `POINT` option in the `EXACT` statement, PROC FREQTAB displays the point probability for each exact test requested. If you specify the `MIDP` option in the `EXACT` statement, PROC FREQTAB displays the exact Mid \(p\)-Value for each test.

- If you specify the `RISKDIFF` option for \(2 \times 2\) tables, PROC FREQTAB displays the Column 1 and Column 2 Risk Estimates. For each column, PROC FREQTAB displays the Row 1 Risk, Row 2 Risk, Total Risk, and Risk Difference, together with their asymptotic standard errors (ASE) and Asymptotic Confidence Limits. PROC FREQTAB also displays Exact Confidence Limits for the Row 1 Risk, Row 2 Risk, and Total Risk. If you specify the `RISKDIFF` option in the `EXACT` statement, PROC FREQTAB provides unconditional Exact Confidence Limits for the Risk Difference. You can suppress this table by specifying the `RISKDIFF(NORISKS)` option.

- If you specify the `RISKDIFF(CL=)` option for \(2 \times 2\) tables, PROC FREQTAB displays the “Confidence Limits for the Proportion (Risk) Difference” table, which includes the Lower and Upper Confidence Limits for each confidence limit Type that you request (Agresti-Caffo, Exact, Hauck-Anderson, Miettinen-Nurminen, Newcombe, or Wald).
- If you specify the **RISKDIFF(NONINF)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Noninferiority Analysis for the Risk Difference" table, which includes the Risk Difference, test ASE, standardized test statistic Z, probability value (Pr > Z), Noninferiority Limit, and (test-based) Confidence Limits.

- If you specify the **RISKDIFF(SUP)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Superiority Analysis for the Risk Difference" table, which includes the Risk Difference, test ASE, standardized test statistic Z, probability value (Pr > Z), Superiority Limit, and (test-based) Confidence Limits.

- If you specify the **RISKDIFF(EQUIV)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Equivalence Analysis for the Risk Difference" table, which includes the Risk Difference, test ASE, Equivalence Limits, and (test-based) Confidence Limits. PROC FREQTAB also displays the "Two One-Sided Tests (TOST)" table, which includes test statistics (Z) and P-Values for the Lower Margin and Upper Margin tests, along with the Overall P-Value.

- If you specify the **RISKDIFF(EQUAL)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Risk Difference Test" table, which includes the Risk Difference, test ASE, standardized test statistic Z, One-sided probability value (Pr > Z or Pr < Z), and Two-sided probability value (Pr > |Z|).

- If you specify the **MEASURES** option or the **RELRISK** option for $2 \times 2$ tables, PROC FREQTAB displays the "Odds Ratio and Relative Risks" table, which includes the following statistics with their confidence limits: Odds Ratio, Relative Risk (Column 1), and Relative Risk (Column 2). If you specify the OR option in the EXACT statement, PROC FREQTAB also displays the "Exact Confidence Limits for the Odds Ratio" table. If you specify the RELRISK option in the EXACT statement, PROC FREQTAB displays the "Exact Confidence Limits for the Relative Risk" table.

- If you specify the **OR(CL=)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Confidence Limits for the Odds Ratio" table, which includes the Lower and Upper Confidence Limits for each confidence limit Type that you request (Exact, Mid-p, Likelihood Ratio, Score, Wald, or Wald Modified).

- If you specify the **RELRISK(CL=)** option for $2 \times 2$ tables, PROC FREQTAB displays the "Confidence Limits for the Relative Risk" table, which includes the Lower and Upper Confidence Limits for each confidence limit Type that you request (Exact, Likelihood Ratio, Score, Wald, or Wald Modified).

- If you specify the **RELRISK(NONINF)** option, PROC FREQTAB displays the "Noninferiority Analysis for the Relative Risk" table, which includes the Relative Risk, standardized test statistic Z, probability value (Pr > Z), Noninferiority Limit, and Confidence Limits.

- If you specify the **RELRISK(SUP)** option, PROC FREQTAB displays the "Superiority Analysis for the Relative Risk" table, which includes the Relative Risk, standardized test statistic Z, probability value (Pr > Z), Superiority Limit, and Confidence Limits.

- If you specify the **RELRISK(EQUIV)** option, PROC FREQTAB displays the "Equivalence Analysis for the Relative Risk" table, which includes the Relative Risk, Equivalence Limits, and Confidence Limits. PROC FREQTAB also displays the "Two One-Sided Tests(TOST)" table, which includes test statistics (Z) and P-Values for the Lower Margin and Upper Margin tests, along with the Overall P-Value.

- If you specify the **RELRISK(EQUAL)** option, PROC FREQTAB displays the "Relative Risk Test" table, which includes the Relative Risk, standardized test statistic Z, One-sided probability value (Pr > Z or Pr < Z), and Two-sided probability value (Pr > |Z|).
If you specify the TREND option, PROC FREQTAB displays the Cochran-Armitage Trend Test for tables that are $2 \times C$ or $R \times 2$. For this test, PROC FREQTAB gives the Statistic ($Z$) and the one-sided and two-sided probability values. If you specify the TREND option in the EXACT statement, PROC FREQTAB also displays the exact one-sided and two-sided probability values for this test. If you specify the POINT option with the TREND option in the EXACT statement, PROC FREQTAB displays the exact point probability for the trend statistic. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the exact Mid $p$-Value for the trend test.

If you specify the JT option, PROC FREQTAB displays the Jonckheere-Terpstra Test, showing the Statistic (JT), the standardized test statistic ($Z$), and the one-sided and two-sided probability values. If you specify the JT option in the EXACT statement, PROC FREQTAB also displays the exact one-sided and two-sided probability values for this test. If you specify the POINT option with the JT option in the EXACT statement, PROC FREQTAB displays the exact point probability for the test statistic. If you specify the MIDP option in the EXACT statement, PROC FREQTAB displays the exact Mid $p$-Value for the Jonckheere-Terpstra test.

If you specify the AGREE option for a $2 \times 2$ table, PROC FREQTAB displays the “McNemar’s Test” table. This table includes the McNemar test statistic (chi-square), the degrees of freedom, and the $p$-value. If you specify the MCNEM option in the EXACT statement, this table also includes the exact $p$-value. If you specify the POINT option or the MIDP option in the EXACT statement, the “McNemar’s Test” table includes the exact point probability or the exact mid $p$-value, respectively.

If you specify the AGREE option for a square table of dimension greater than 2, PROC FREQTAB displays the “Symmetry Test” table. This table displays Bowker’s symmetry test statistic (chi-square), the degrees of freedom, and the $p$-value. If you specify the SYMMETRY option in the EXACT statement, this table also includes the exact $p$-value. If you specify the POINT option or the MIDP option in the EXACT statement, the “Symmetry Test” table includes the exact point probability or the exact mid $p$-value, respectively.

The AGREE option also produces the “Kappa Statistics” table, which displays the simple kappa coefficient. If the dimension of the two-way table is greater than 2, the “Kappa Statistics” table includes the weighted kappa coefficient. If you specify the AGREE(AC1) option or the AGREE(PABAK) option, this table includes the AC1 agreement coefficient or the prevalence-adjusted bias-adjusted kappa (PABAK), respectively. The “Kappa Statistics” table displays the standard error and confidence limits for each agreement statistic.

If you specify the AGREE(KAPPADetails) option, PROC FREQTAB displays the “Kappa Details” table, which includes the observed agreement, the chance-expected agreement, the maximum kappa, and the B_N measure. For $2 \times 2$ tables, the “Kappa Details” table also includes the prevalence index and the bias index.

If you specify the AGREE(WTKAPPADetails) or AGREE(KAPPADetails) option for a square table of dimension greater than 2, PROC FREQTAB produces the “Weighted Kappa Details” table, which displays the observed agreement and the chance-expected agreement components of the weighted kappa coefficient.

If you specify the AGREE(PRINTKWTS) option for a square table of dimension greater than 2, PROC FREQTAB displays the matrix of agreement weights in the “Kappa Coefficient Weights” table.

If you request a simple kappa coefficient test, PROC FREQTAB produces the “Kappa Test” table. You can request this test by specifying the KAPPA option in the TEST statement, the KAPPA option in the
EXACT statement, or the AGREE(NULLKAPPA=) option in the TABLES statement. The “Kappa Test” table displays the kappa coefficient, null test value, standard error (when the null value is 0), standardized test statistic (Z), and one-sided and two-sided p-values.

If you request an exact test (by specifying the KAPPA option in the EXACT statement), the “Kappa Test” table also includes the exact one-sided and two-sided p-values. If you specify the POINT option or the MIDP option in the EXACT statement, the “Kappa Test” table includes the point probability or the exact mid p-value, respectively.

- If you request a weighted kappa coefficient test for a square table of dimension greater than 2, PROC FREQTAB produces the “Weighted Kappa Test” table. You can request this test by specifying the WTKAPPA option in the TEST statement, the WTKAPPA option in the EXACT statement, or the AGREE(NULLWTKAPPA=) option in the TABLES statement. The “Weighted Kappa Test” table displays the weighted kappa coefficient, null test value, standard error (when the null value is 0), standardized test statistic (Z), and one-sided and two-sided p-values.

If you request an exact test (by specifying the WTKAPPA option in the EXACT statement), the “Weighted Kappa Test” table also includes the exact one-sided and two-sided p-values. If you specify the POINT option or the MIDP option in the EXACT statement, the “Weighted Kappa Test” table includes the point probability or the exact mid p-value, respectively.

- If you specify the AGREE option for a multiway square table, PROC FREQTAB displays the “Overall Kappa Coefficients” table, which includes the overall simple kappa coefficient together with its standard error and confidence limits. This table also includes the overall weighted kappa coefficient if the two-way table dimension is greater than 2.

- For multiway square tables, the AGREE option also produces the “Tests for Equal Kappa Coefficients” table. This table includes the chi-square statistic, degrees of freedom, and p-value for the test of equal simple kappa coefficients (over all strata). If the two-way table dimension is greater than 2, this table also includes the test for equal weighted kappa coefficients.

- For multiway 2 × 2 tables, the AGREE option displays the “Cochran’s Q” table, which includes Cochran’s Q statistic (to test for marginal homogeneity), the degrees of freedom, and the p-value.

- If you specify the COMMONRISKDIFF option for a multiway 2 × 2 table, PROC FREQTAB displays the “Confidence Limits for the Common Risk Difference” table, which includes the Method, Value of the common risk difference, Standard Error, and Confidence Limits for each confidence limit type that you request (Mantel-Haenszel, Minimum Risk, Newcombe, Newcombe MR, or Summary Score).

- If you specify the COMMONRISKDIFF(TEST) option for a multiway 2 × 2 table, PROC FREQTAB displays the “Common Risk Difference Tests” table, which includes Method, Risk Difference, Z, and Pr > |Z| for each test that you request (Mantel-Haenszel, Minimum Risk, or Summary Score).

- If you specify the COMMONRISKDIFF(PRINTWTS) option for a multiway 2 × 2 table, PROC FREQTAB displays the “Stratum Weights” table, which includes the following information for each stratum (2 × 2 table): Stratum index, variable levels, Risk Difference, Frequency, Fraction, Mantel-Haenszel Weight, and Minimum Risk Weight.

- If you specify the CMH option, PROC FREQTAB displays Cochran-Mantel-Haenszel Statistics for the following three alternative hypotheses: Nonzero Correlation, Row Mean Scores Differ (ANOVA Statistic), and General Association. For each of these statistics, PROC FREQTAB gives the degrees of freedom (DF) and the probability value (Prob). If you specify the MANTELFLEISS option, PROC
FREQTAB displays the Mantel-Fleiss Criterion for $2 \times 2$ tables. For $2 \times 2$ tables, PROC FREQTAB also displays Estimates of the Common Relative Risk for Case-Control and Cohort studies, together with their confidence limits. These include both Mantel-Haenszel and Logit stratum-adjusted estimates of the common Odds Ratio, Column 1 Relative Risk, and Column 2 Relative Risk. Also for $2 \times 2$ tables, PROC FREQTAB displays the Breslow-Day Test for Homogeneity of the Odds Ratios. For this test, PROC FREQTAB gives the Chi-Square, the degrees of freedom (DF), and the probability value (Pr > ChiSq).

- If you specify the CMH option in the TABLES statement and also specify the COMOR option in the EXACT statement for a multiway $2 \times 2$ table, PROC FREQTAB displays exact confidence limits for the Common Odds Ratio. PROC FREQTAB also displays the Exact Test of H0: Common Odds Ratio = 1. The test output includes the Cell (1,1) Sum (S), Mean of S Under H0, One-sided Pr <= S, and Point Pr = S. PROC FREQTAB also provides exact two-sided probability values for the test, computed according to the following three methods: 2 * One-sided, Sum of probabilities <= Point probability, and Pr >= |S - Mean|. If you specify the MIDP option in the EXACT statement, PROC FREQTAB provides the exact Mid p-Value for the common odds ratio test.

- If you specify the CMH option in the TABLES statement and also specify the EQOR option in the EXACT statement for a multiway $2 \times 2$ table, PROC FREQTAB computes Zelen’s exact test for equal odds ratios. PROC FREQTAB displays Zelen’s test along with the asymptotic Breslow-Day test produced by the CMH option. PROC FREQTAB displays the test statistic, Zelen’s Exact Test (P), and the probability value, Exact Pr <= P.

- If you specify the GAILSIMON option in the TABLES statement for a multiway $2 \times 2$ tables, PROC FREQTAB displays the Gail-Simon test for qualitative interactions. The display include the following statistics and their p-values: Q+ (Positive Risk Differences), Q- (Negative Risk Differences), and Q (Two-Sided).

### ODS Table Names

PROC FREQTAB assigns a name to each table that it creates. You can use these names to refer to tables when you use the Output Delivery System (ODS) to select tables and create output data sets. For more information about ODS, see the *SAS Output Delivery System: User’s Guide*.

Table 4.21 lists the ODS table names together with their descriptions and the options required to produce the tables. Note that the ALL option in the TABLES statement invokes the CHISQ, MEASURES, and CMH options.

<table>
<thead>
<tr>
<th>ODS Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>BarnardsTest</td>
<td>Barnard’s exact test</td>
<td>EXACT</td>
<td>BARNARD</td>
</tr>
<tr>
<td>BinomialCLs</td>
<td>Binomial confidence limits</td>
<td>TABLES</td>
<td>BINOMIAL(CL=)</td>
</tr>
<tr>
<td>BinomialEquiv</td>
<td>Binomial equivalence analysis</td>
<td>TABLES</td>
<td>BINOMIAL(EQUIV)</td>
</tr>
<tr>
<td>BinomialEquivLimits</td>
<td>Binomial equivalence limits</td>
<td>TABLES</td>
<td>BINOMIAL(EQUIV)</td>
</tr>
<tr>
<td>BinomialEquivTest</td>
<td>Binomial equivalence test</td>
<td>TABLES</td>
<td>BINOMIAL(EQUIV)</td>
</tr>
<tr>
<td>BinomialNoninf</td>
<td>Binomial noninferiority test</td>
<td>TABLES</td>
<td>BINOMIAL(NONINF)</td>
</tr>
</tbody>
</table>
## Table 4.21  continued

<table>
<thead>
<tr>
<th>ODS Table Name</th>
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<th>Option</th>
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</thead>
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<td>TABLES</td>
<td>BINOMIAL</td>
</tr>
<tr>
<td>BinomialTest</td>
<td>Binomial proportion test</td>
<td>TABLES</td>
<td>BINOMIAL</td>
</tr>
<tr>
<td>BinomialSup</td>
<td>Binomial superiority test</td>
<td>TABLES</td>
<td>BINOMIAL(SUP)</td>
</tr>
<tr>
<td>BnMeasure</td>
<td>Agreement measures</td>
<td>TABLES</td>
<td>PLOTS=AGREEPLOT(STATS)</td>
</tr>
<tr>
<td>BreslowDayTest</td>
<td>Breslow-Day test</td>
<td>TABLES</td>
<td>CMH (h x 2 x 2 table)</td>
</tr>
<tr>
<td>CMH</td>
<td>Cochran-Mantel-Haenszel statistics</td>
<td>TABLES</td>
<td>CMH</td>
</tr>
<tr>
<td>ChiSq</td>
<td>Chi-square tests</td>
<td>TABLES</td>
<td>CHISQ</td>
</tr>
<tr>
<td>CochransQ</td>
<td>Cochran's $Q$</td>
<td>TABLES</td>
<td>AGREE (h x 2 x 2 table)</td>
</tr>
<tr>
<td>ColScores</td>
<td>Column scores</td>
<td>TABLES</td>
<td>SCOROUT</td>
</tr>
<tr>
<td>CommonOdds-RatioCI</td>
<td>Exact confidence limits for the common odds ratio ($h x 2 x 2$ table)</td>
<td>EXACT</td>
<td>COMOR</td>
</tr>
<tr>
<td>CommonOdds-RatioTest</td>
<td>Common odds ratio exact test ($h x 2 x 2$ table)</td>
<td>EXACT</td>
<td>COMOR</td>
</tr>
<tr>
<td>CommonPdiff</td>
<td>Common risk difference confidence limits ($h x 2 x 2$ table)</td>
<td>TABLES</td>
<td>COMMONRISKDIFF(TESTS)</td>
</tr>
<tr>
<td>CommonRelRisks</td>
<td>Common relative risks</td>
<td>TABLES</td>
<td>CMH (h x 2 x 2 table)</td>
</tr>
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<td>CrossList</td>
<td>Crosstabulation table in column format ($n$-way table, $n &gt; 1$)</td>
<td>TABLES</td>
<td>CROSSLIST</td>
</tr>
<tr>
<td>CrossTabFreqs</td>
<td>Crosstabulation table</td>
<td>TABLES</td>
<td>AGREE</td>
</tr>
<tr>
<td>EqualKappaTest</td>
<td>Test for equal simple kappas ($h x 2 x 2$ table)</td>
<td>TABLES</td>
<td>AGREE</td>
</tr>
<tr>
<td>EqualKappaTests</td>
<td>Tests for equal kappas</td>
<td>TABLES</td>
<td>(h x r x r table, r &gt; 2)</td>
</tr>
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<td>Tests for equal odds ratios ($h x 2 x 2$ table)</td>
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<td>EQOR</td>
</tr>
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<td>Gail-Simon test</td>
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<td>Fisher’s exact test</td>
<td>EXACT</td>
<td>FISHER</td>
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<td>FishersExactMC</td>
<td>Monte Carlo estimates for Fisher’s exact test</td>
<td>EXACT</td>
<td>FISHER / MC</td>
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<td>Gamma</td>
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<td>Jonckheere-Terpstra test</td>
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<td>Monte Carlo estimates for Jonckheere-Terpstra exact test ($h x 2 x 2$ table)</td>
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<td>JT / MC</td>
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<td>AGREE(KAPPADETAILS)</td>
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<td>Monte Carlo exact test for simple kappa coefficient</td>
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<td>KAPPA / MC</td>
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Table 4.21  continued

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<td>or TABLES</td>
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<td>AGREE(PRINTKWTS)</td>
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<td>LRCHI / MC</td>
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<td>OR (2 × 2 table)</td>
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<td>CHISQ / MC</td>
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<td>(h × 2 × 2 table)</td>
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<td></td>
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<td>(h × r × r table, r &gt; 2)</td>
</tr>
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<td>PdiffCLs</td>
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<td>TABLES</td>
<td>RISKDIFF(NONINF)</td>
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<tr>
<td>ODS Table Name</td>
<td>Description</td>
<td>Statement</td>
<td>Option</td>
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</tr>
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<td>Superiority test for the risk difference</td>
<td>TABLES</td>
<td>RISKDIFF(SUP) (2 × 2 table)</td>
</tr>
<tr>
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<td>Risk difference test</td>
<td>TABLES</td>
<td>RISKDIFF(EQUAL) (2 × 2 table)</td>
</tr>
<tr>
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<td>Pearson chi-square exact test</td>
<td>EXACT</td>
<td>PCHI</td>
</tr>
<tr>
<td>PearsonChiSqMC</td>
<td>Monte Carlo exact test for Pearson chi-square</td>
<td>EXACT</td>
<td>PCHI / MC</td>
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<td>PCORR / MC</td>
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<td>PCORR</td>
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<td>Polychoric correlation test</td>
<td>TEST</td>
<td>PLCORR</td>
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<td>RelativeRiskCLs</td>
<td>Relative risk confidence limits</td>
<td>TABLES</td>
<td>RELRISK(CL=) (2 × 2 table)</td>
</tr>
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<td>Relative risk estimates</td>
<td>TABLES</td>
<td>RELRISK or MEASURES (2 × 2 table)</td>
</tr>
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<td>Exact confidence limits for column 1 relative risk</td>
<td>EXACT</td>
<td>RELRISK (2 × 2 table)</td>
</tr>
<tr>
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<td>Exact confidence limits for column 2 relative risk</td>
<td>EXACT</td>
<td>RELRISK (2 × 2 table)</td>
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<td>RELRISK(EQUIV) (2 × 2 table)</td>
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<td>TABLES</td>
<td>RELRISK(SUP) (2 × 2 table)</td>
</tr>
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<td>Relative risk test</td>
<td>TABLES</td>
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<td>Column 1 risk estimates</td>
<td>TABLES</td>
<td>RISKDIFF (2 × 2 table)</td>
</tr>
<tr>
<td>RiskDiffCol2</td>
<td>Column 2 risk estimates</td>
<td>TABLES</td>
<td>RISKDIFF (2 × 2 table)</td>
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<td>Row scores</td>
<td>TABLES</td>
<td>SCOROUT</td>
</tr>
<tr>
<td>SomersDCR</td>
<td>Somers’ $D(C \mid R)$</td>
<td>TEST</td>
<td>SMDCR</td>
</tr>
<tr>
<td>SomersDCRMC</td>
<td>Monte Carlo exact test for Somers’ $D(C \mid R)$</td>
<td>EXACT</td>
<td>SMDCR / MC</td>
</tr>
<tr>
<td>SomersDCRTest</td>
<td>Somers’ $D(C \mid R)$ test</td>
<td>TEST</td>
<td>SMDCR</td>
</tr>
<tr>
<td>SomersDRC</td>
<td>Somers’ $D(R \mid C)$</td>
<td>TEST</td>
<td>SMDRC</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>SMDRC</td>
</tr>
</tbody>
</table>
### Table 4.21 continued

<table>
<thead>
<tr>
<th>ODS Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SomersDRCMC</td>
<td>Monte Carlo exact test for Somers’ $D(R</td>
<td>C)$</td>
<td>EXACT</td>
</tr>
<tr>
<td>SomersDRCCTest</td>
<td>Somers’ $D(R</td>
<td>C)$ test</td>
<td>TEST</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>SMDRC</td>
</tr>
<tr>
<td>SpearmanCorr</td>
<td>Spearman correlation</td>
<td>TEST</td>
<td>SCORR</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>SCORR</td>
</tr>
<tr>
<td>SpearmanCorrMC</td>
<td>Monte Carlo exact test for Spearman correlation</td>
<td>EXACT</td>
<td>SCORR / MC</td>
</tr>
<tr>
<td>SpearmanCorrTest</td>
<td>Spearman correlation test</td>
<td>TEST</td>
<td>SCORR</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>SCORR</td>
</tr>
<tr>
<td>StratumWeights</td>
<td>Stratum weights and risk differences</td>
<td>TABLES</td>
<td>COMMONRISKDIFF</td>
</tr>
<tr>
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<td></td>
<td></td>
<td>($h \times 2 \times 2$ table)</td>
</tr>
<tr>
<td>SymmetryTest</td>
<td>Symmetry test</td>
<td>TABLES</td>
<td>AGREE</td>
</tr>
<tr>
<td>SymmetryMC</td>
<td>Monte Carlo exact symmetry test</td>
<td>EXACT</td>
<td>SYMMETRY / MC</td>
</tr>
<tr>
<td>TauB</td>
<td>Kendall’s tau-$b$</td>
<td>TEST</td>
<td>KENTB</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>KENTB</td>
</tr>
<tr>
<td>TauBMC</td>
<td>Monte Carlo exact test for Kendall’s tau-$b$</td>
<td>EXACT</td>
<td>KENTB / MC</td>
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<tr>
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<td>KENTB</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>KENTB</td>
</tr>
<tr>
<td>TauC</td>
<td>Stuart’s tau-$c$</td>
<td>TEST</td>
<td>STUTC</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>STUTC</td>
</tr>
<tr>
<td>TauCMC</td>
<td>Monte Carlo exact test for Stuart’s tau-$c$</td>
<td>EXACT</td>
<td>STUTC / MC</td>
</tr>
<tr>
<td>TauCTest</td>
<td>Stuart’s tau-$c$ test</td>
<td>TEST</td>
<td>STUTC</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>STUTC</td>
</tr>
<tr>
<td>TrendTest</td>
<td>Cochran-Armitage trend test</td>
<td>TABLES</td>
<td>TREND</td>
</tr>
<tr>
<td>TrendTestMC</td>
<td>Monte Carlo exact test for trend</td>
<td>EXACT</td>
<td>TREND / MC</td>
</tr>
<tr>
<td>WtKappaDetails</td>
<td>Weighted kappa details</td>
<td>TABLES</td>
<td>AGREE(WTKAPPADETAILS)</td>
</tr>
<tr>
<td>WtKappaMC</td>
<td>Monte Carlo exact test for weighted kappa coefficient</td>
<td>EXACT</td>
<td>WTKAPPA / MC</td>
</tr>
<tr>
<td>WtKappaTest</td>
<td>Weighted kappa test</td>
<td>TEST</td>
<td>WTKAPPA</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or EXACT</td>
<td>WTKAPPA</td>
</tr>
<tr>
<td></td>
<td></td>
<td>or TABLES</td>
<td>AGREE(NULLWTKAPPA=)</td>
</tr>
</tbody>
</table>

**ODS Graphics**

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in *SAS/STAT User's Guide*. 
Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.

When ODS Graphics is enabled, you can request specific plots with the PLOTS= option in the TABLES statement. To produce a frequency plot or cumulative frequency plot, you must specify the FREQPLOT or CUMFREQPLOT plot-request, respectively, in the PLOTS= option. To produce a mosaic plot, you must specify the MOSAICPLOT plot-request in the PLOTS= option. You can also produce frequency, cumulative frequency, and mosaic plots by specifying the PLOTS=ALL option. By default, PROC FREQTAB produces all other plots that are associated with the analyses that you request in the TABLES statement. You can suppress the default plots and request specific plots by using the PLOTS(ONLY)= option. For more information, see the description of the PLOTS= option.

PROC FREQTAB assigns a name to each graph that it creates with ODS Graphics. You can use these names to refer to the graphs. Table 4.22 lists the names of the graphs that PROC FREQTAB generates together with their descriptions, their PLOTS= options (plot-requests), and the TABLES statement options that are required to produce the graphs.

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Description</th>
<th>PLOTS= Option</th>
<th>TABLES Statement Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>AgreePlot</td>
<td>Agreement plot</td>
<td>AGREEPLOT</td>
<td>AGREE (r × r table)</td>
</tr>
<tr>
<td>CumFreqPlot</td>
<td>Cumulative frequency plot</td>
<td>CUMFREQPLOT</td>
<td>One-way table request</td>
</tr>
<tr>
<td>DeviationPlot</td>
<td>Deviation plot</td>
<td>DEVIATIONPLOT</td>
<td>CHISQ (one-way table)</td>
</tr>
<tr>
<td>FreqPlot</td>
<td>Frequency plot</td>
<td>FREQPLOT</td>
<td>Any table request</td>
</tr>
<tr>
<td>KappaPlot</td>
<td>Kappa plot</td>
<td>KAPPAPLOT</td>
<td>AGREE (h × r × r table)</td>
</tr>
<tr>
<td>MosaicPlot</td>
<td>Mosaic plot</td>
<td>MOSAICPLOT</td>
<td>Two-way or multiway table request</td>
</tr>
<tr>
<td>ORPlot</td>
<td>Odds ratio plot</td>
<td>ODDSRATIOPLOT</td>
<td>MEASURES, OR, RELRISK (h × 2 × 2 table)</td>
</tr>
<tr>
<td>RelRiskPlot</td>
<td>Relative risk plot</td>
<td>RELRISKPLOT</td>
<td>MEASURES or RELRISK (h × 2 × 2 table)</td>
</tr>
<tr>
<td>RiskDiffPlot</td>
<td>Risk difference plot</td>
<td>RISKDIFFPLOT</td>
<td>RISKDIFF (h × 2 × 2 table)</td>
</tr>
<tr>
<td>WtKappaPlot</td>
<td>Weighted kappa plot</td>
<td>WTKAPPAPLOT</td>
<td>AGREE (h × r × r table, r &gt; 2)</td>
</tr>
</tbody>
</table>

References


## Chapter 5
### The GAMMOD Procedure

**Contents**

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: GAMMOD Procedure</td>
<td>296</td>
</tr>
<tr>
<td>PROC GAMMOD Features</td>
<td>296</td>
</tr>
<tr>
<td>PROC GAMMOD Contrasted with Other SAS Procedures</td>
<td>297</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>299</td>
</tr>
<tr>
<td>Getting Started: GAMMOD Procedure</td>
<td>299</td>
</tr>
<tr>
<td>Syntax: GAMMOD Procedure</td>
<td>306</td>
</tr>
<tr>
<td><strong>PROC GAMMOD Statement</strong></td>
<td>306</td>
</tr>
<tr>
<td><strong>BY Statement</strong></td>
<td>309</td>
</tr>
<tr>
<td><strong>CLASS Statement</strong></td>
<td>310</td>
</tr>
<tr>
<td><strong>DISPLAY Statement</strong></td>
<td>310</td>
</tr>
<tr>
<td><strong>DISPLAYOUT Statement</strong></td>
<td>311</td>
</tr>
<tr>
<td><strong>FREQ Statement</strong></td>
<td>312</td>
</tr>
<tr>
<td><strong>MODEL Statement</strong></td>
<td>312</td>
</tr>
<tr>
<td><strong>OUTPUT Statement</strong></td>
<td>320</td>
</tr>
<tr>
<td><strong>WEIGHT Statement</strong></td>
<td>322</td>
</tr>
<tr>
<td>Details: GAMMOD Procedure</td>
<td>322</td>
</tr>
<tr>
<td><strong>Missing Values</strong></td>
<td>322</td>
</tr>
<tr>
<td><strong>Thin-Plate Regression Splines</strong></td>
<td>322</td>
</tr>
<tr>
<td><strong>Generalized Additive Models</strong></td>
<td>325</td>
</tr>
<tr>
<td><strong>Model Evaluation Criteria</strong></td>
<td>327</td>
</tr>
<tr>
<td><strong>Fitting Algorithms</strong></td>
<td>327</td>
</tr>
<tr>
<td><strong>Degrees of Freedom</strong></td>
<td>329</td>
</tr>
<tr>
<td><strong>Model Inference</strong></td>
<td>330</td>
</tr>
<tr>
<td><strong>Dispersion Parameter</strong></td>
<td>330</td>
</tr>
<tr>
<td><strong>Tests for Smoothing Components</strong></td>
<td>331</td>
</tr>
<tr>
<td><strong>Multithreading</strong></td>
<td>332</td>
</tr>
<tr>
<td><strong>Optimization Algorithms</strong></td>
<td>332</td>
</tr>
<tr>
<td><strong>Displayed Output</strong></td>
<td>332</td>
</tr>
<tr>
<td><strong>ODS Table Names</strong></td>
<td>335</td>
</tr>
<tr>
<td><strong>ODS Graphics</strong></td>
<td>336</td>
</tr>
<tr>
<td>Examples: GAMMOD Procedure</td>
<td>337</td>
</tr>
<tr>
<td>Example 5.1: Scatter Plot Smoothing</td>
<td>337</td>
</tr>
<tr>
<td>Example 5.2: Nonparametric Logistic Regression</td>
<td>342</td>
</tr>
<tr>
<td>Example 5.3: Nonparametric Tweedie Regression</td>
<td>348</td>
</tr>
<tr>
<td>References</td>
<td>353</td>
</tr>
</tbody>
</table>
Overview: GAMMOD Procedure

The GAMMOD procedure fits generalized additive models that are based on low-rank regression splines (Wood 2006) in SAS Viya.

Generalized additive models are extensions of generalized linear models. They relax the generalized linear models’ assumption of linearity by allowing spline terms that characterize nonlinear dependency structures. Each spline term is constructed by the thin-plate regression spline technique (Wood 2003). A roughness penalty is applied to each spline term by a smoothing parameter that controls the balance between goodness of fit and the roughness of the spline curve. PROC GAMMOD fits models for standard distributions in the exponential family, such as the normal, Poisson, gamma, and Tweedie distributions.

PROC GAMMOD Features

PROC GAMMOD offers the following basic features:

- estimates the regression parameters of a generalized additive model that has fixed smoothing parameters by using penalized likelihood estimation
- estimates the smoothing parameters of a generalized additive model by using either the performance iteration method or the outer iteration method
- estimates the regression parameters of a generalized linear model by using maximum likelihood techniques
- tests the total contribution of each spline term based on the Wald statistic
- provides model-building syntax in the CLASS statement and effect-based parametric effects in the MODEL statement, which are used in other SAS/STAT analytic procedures (in particular, the GLM, LOGISTIC, GLIMMIX, and MIXED procedures)
- provides response-variable options
- enables you to construct a spline term by using multiple variables
- provides control options for constructing a spline term, such as fixed degrees of freedom, initial smoothing parameter, fixed smoothing parameter, smoothing parameter search range, user-supplied knot values, and so on
- provides multiple link functions for any distribution
- provides a WEIGHT statement for weighted analysis
- provides a FREQ statement for grouped analysis
- provides an OUTPUT statement to produce a data table that has predicted values and other observationwise statistics
- produces graphs via ODS Graphics
Because the GAMMOD procedure runs on SAS Cloud Analytic Services (CAS), it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode
- exploits all the available cores and concurrent threads (for information about how PROC GAMMOD uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts”)

---

PROC GAMMOD Contrasted with Other SAS Procedures

The GAMMOD procedure provides generalized additive modeling functionality that is comparable to that of GAMPL and GAM procedures in SAS/STAT software.

PROC GAMMOD Compared with the GAMPL Procedure

The functionality of the GAMMOD procedure closely resembles that of the GAMPL procedure, which is a high-performance SAS/STAT procedure. The GAMMOD procedure is the next generation of the GAMPL procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations. Both procedures perform computations in multiple threads.

PROC GAMMOD provides all the features and options that PROC GAMPL supports; in addition, it supports BY processing. The default link functions for two distributions differ between the two procedures, as shown in Table 5.1.

<table>
<thead>
<tr>
<th>Distribution</th>
<th>GAMMOD</th>
<th>GAMPL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gamma</td>
<td>Log</td>
<td>Reciprocal</td>
</tr>
<tr>
<td>Inverse Gaussian</td>
<td>Log</td>
<td>Reciprocal square</td>
</tr>
</tbody>
</table>

You should expect close results between these two procedures, although exactly equivalent models are not guaranteed because their implementations are different.

PROC GAMMOD Compared with the GAM Procedure

Both the GAMMOD procedure and the GAM procedure in SAS/STAT software fit generalized additive models. However, the GAMMOD procedure uses different approaches for constructing spline basis expansions, fitting generalized additive models, and testing smoothing components. The GAMMOD procedure focuses on automatic smoothing parameter selection by using global model-evaluation criteria to find optimal models. The GAM procedure focuses on constructing models by fitting partial residuals against each smoothing term with fixed degrees of freedom. In general, you should not expect similar results from these two procedures. Table 5.2 summarizes the main differences.
## Table 5.2  PROC GAMMOD Compared with PROC GAM

<table>
<thead>
<tr>
<th>Functionality</th>
<th>GAMMOD</th>
<th>GAM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Constructing spline basis expansions</td>
<td>Uses thin-plate regression splines to construct basis expansions for each spline term, and each term allows multiple variables.</td>
<td>Uses univariate or bivariate smoothing splines to construct basis expansions, and each term allows only one or two variables. Also allows loess smoothers.</td>
</tr>
<tr>
<td>Fitting generalized additive models</td>
<td>Fits models that have fixed smoothness terms by optimizing penalized likelihood. For models that have varying smoothness terms, PROC GAMMOD estimates smoothing parameters simultaneously by optimizing global model fit criteria such as generalized cross validation (GCV).</td>
<td>Fits models that have fixed smoothness terms by fitting partial residuals against each smoothness term. For models that have varying smoothness terms, PROC GAM estimates each smoothing parameter by optimizing the local GCV criterion for one spline term at a time.</td>
</tr>
<tr>
<td>Distribution families and link functions</td>
<td>Supports more distributions, including the negative binomial and the Tweedie families. Also supports any applicable link functions for each distribution.</td>
<td>Supports major distribution families and the canonical link function for each distribution.</td>
</tr>
<tr>
<td>Testing smoothing components</td>
<td>Tests the total contribution for a spline term.</td>
<td>Tests the existence of nonlinearity for a spline term beyond the linear trend.</td>
</tr>
<tr>
<td>Model inference</td>
<td>A global Bayesian posterior covariance matrix is available. The confidence limits for each observation’s prediction is available, in addition to componentwise confidence limits.</td>
<td>A local Bayesian posterior covariance matrix is available for each spline term. Only the componentwise confidence limits are available.</td>
</tr>
<tr>
<td>Model degrees of freedom</td>
<td>Uses the trace of the global degrees-of-freedom matrix.</td>
<td>Uses the summation of the traces of individual smoothing matrix for each smoothing term.</td>
</tr>
<tr>
<td>Multithreading scheme</td>
<td>Specifically designed to operate in SAS Viya and performs computations in multiple threads.</td>
<td>Executes in a single thread on a single machine.</td>
</tr>
</tbody>
</table>
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: GAMMOD Procedure

This example concerns the proportions and demographic and geographic characteristics of votes that were cast in 3,107 counties in the United States in the 1980 presidential election. You can use the data set `sashelp.Vote1980` directly from the `Sashelp` library or download it from the StatLib data sets archive (Vlachos 1998). For more information about the data set, see Pace and Barry (1997).

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
You can load the sashelp.Vote1980 data set into your CAS session by using your CAS engine libref with the following DATA step:

```plaintext
data mycas.Vote1980;
  set sashelp.Vote1980;
run;
```

These statements assume that your CAS engine libref is named `mycas`, as in the section “Using CAS Sessions and CAS Engine Librefs” on page 299, but you can substitute any appropriately defined CAS engine libref.

The data table contains 3,107 observations and seven variables. The dependent variable `LogVoteRate` is the logarithm transformation of the proportion of the county population who voted for any candidate. The six explanatory variables are the number of people in the county 18 years of age or older (`Pop`), the number of people in the county who have a 12th-grade or higher education (`Edu`), the number of owned housing units (`Houses`), the aggregate income (`Income`), and the scaled longitude and latitude of geographic centroids (`Longitude` and `Latitude`).

The following statements produce a plot of `LogVoteRate` with respect to the geographic locations `Longitude` and `Latitude`:

```plaintext
%let off0 = offsetmin=0 offsetmax=0
  linearopts=(thresholdmin=0 thresholdmax=0);
proc template;
  define statgraph surface;
    dynamic _title _z;
    begingraph / designwidth=defaultDesignHeight;
      entrytitle _title;
      layout overlay / xaxisopts=(&off0) yaxisopts=(&off0);
        contourplotparm z=_z y=Latitude x=Longitude / gridded=FALSE;
      endlayout;
    endgraph;
  end;
end;
run;

proc sgrender data=mycas.Vote1980 template=surface;
  dynamic _title = 'US County Vote Proportion in the 1980 Election'
    _z = 'LogVoteRate';
run;
```

Figure 5.1 shows the map of the logarithm transformation of the proportion of the county population who voted for any candidate in the 1980 US presidential election.
The objective is to explore the nonlinear dependency structure between the dependent variable and the demographic variables (Pop, Edu, Houses, and Income), in addition to the nonlinear dependency structure between the response and the Longitude and Latitude variables. The following statements use thin-plate regression splines to fit a generalized additive model:

```
ods graphics on;
proc gammod data=mycas.Vote1980 plots seed=12345;
  model LogVoteRate = spline(Pop) spline(Edu) spline(Houses)
                   spline(Income) spline(Longitude Latitude);
  output out=mycas.VotePred copyvars=(Longitude Latitude);
run;
```

With ODS Graphics enabled by the first statement, the PLOTS option in the PROC GAMMOD statement requests a smoothing component panel of fitted spline terms. The SEED option specifies the random seed so that you can reproduce the analysis.

The default output from this analysis is presented in Figure 5.2 through Figure 5.9.

Figure 5.2 displays the “Model Information” table. The response variable LogVoteRate is modeled by using a normal distribution whose mean is modeled by an identity link function. The GAMMOD procedure uses
the performance iteration method and the generalized cross validation (GCV) criterion as the fitting criterion. PROC GAMMOD searches for the optimum smoothing parameters by using the Newton-Raphson algorithm to optimize the fitting criterion. The random number seed is set to 12,345. Random number generation is used for sampling from observations to form spline knots and truncated eigendecomposition. Changing the random number seed might yield slightly different model fits.

**Figure 5.2** Model Information

<table>
<thead>
<tr>
<th>The GAMMOD Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Model Information</strong></td>
</tr>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Fitting Method</td>
</tr>
<tr>
<td>Fitting Criterion</td>
</tr>
<tr>
<td>Optimization Technique for Smoothing</td>
</tr>
<tr>
<td>Random Number Seed</td>
</tr>
</tbody>
</table>

Figure 5.3 displays the “Number of Observations” table. All 3,107 observations in the data table are used in the analysis. For data tables that have missing or invalid values, the number of used observations might be less than the number of observations read.

**Figure 5.3** Number of Observations

| Number of Observations Read | 3107 |
| Number of Observations Used | 3107 |

Figure 5.4 displays the convergence status of the performance iteration method.

**Figure 5.4** Convergence Status

The performance iteration converged after 2 steps.

Figure 5.5 shows the “Fit Statistics” table. The penalized log likelihood and the roughness penalty are displayed. You can use effective degrees of freedom to compare generalized additive models with generalized linear models that do not have spline transformations. Information criteria such as Akaike’s information criterion (AIC), Akaike’s bias-corrected information criterion (AICC), and Schwarz Bayesian information criterion (BIC) can also be used for comparisons. These criteria penalize the –2 log likelihood for effective degrees of freedom. The GCV criterion is used to compare against other generalized additive models or models that are penalized.
The “Parameter Estimates” table in Figure 5.6 shows the regression parameter and dispersion parameter estimates. In this model, the intercept is the only regression parameter because (1) all variables are characterized by spline terms and no parametric effects are present and (2) the intercept absorbs the constant effect that is extracted from each spline term to make fitted splines identifiable. The dispersion parameter is estimated by maximizing the likelihood, given other model parameters.

The “Estimates for Smoothing Components” table is shown in Figure 5.7. For each spline term, the effective degrees of freedom, the estimated smoothing parameter, and the corresponding roughness penalty are displayed. The table also displays additional information about spline terms, such as the number of parameters, penalty matrix rank, and number of spline knots.

Figure 5.8 displays the hypothesis testing results for each smoothing component. The null hypothesis for each spline term is whether the total dependency on each variable is 0. The effective degrees of freedom for fit and the effective degrees of freedom for test are displayed.
Figure 5.9 displays the “Smoothing Component Panel” for all the spline terms used in the model. It displays predicted spline curves and 95% Bayesian posterior confidence bands for each univariate spline term.

The preceding program requests the prediction for each observation by default, and the OUTPUT statement saves the results in the data table mycas.VotePred. The COPYVARS= option in the OUTPUT statement copies the specified variables (Longitude and Latitude) from the input data table, mycas.Vote1980, to the output data table, mycas.VotePred. The following run of the SGRENDER procedure produces the fitted surface of the log vote proportion in the 1980 presidential election:
proc sgrender data=mycas.VotePred template=surface;
   dynamic _title='Predicted US County Vote Proportion in the 1980 Election'
                _z = 'Pred';
run;

Figure 5.10 shows the map of predictions of the logarithm transformation of the proportion of county population who voted for any candidates in the 1980 US presidential election from the fitted generalized additive model.

Figure 5.10  Predicted US County Vote Proportion in the 1980 Election

Compared to the map of the logarithm transformations of the proportion of votes cast shown in Figure 5.1, the map of the predictions of the logarithm transformations of the proportion of votes cast has a smoother surface.
Syntax: GAMMOD Procedure

The following statements are available in the GAMMOD procedure:

```
PROC GAMMOD <options>;  
   BY variables;  
   CLASS variable <(options)> . . . <variable <(options)>> </global-options>;  
   DISPLAY <table-list> </options>;  
   DISPLAYOUT table-spec-list </options>;  
   FREQ variable;  
   MODEL response <(response-options)> = <PARAM(effects)>  
      <spline-effects> </model-options>;  
   MODEL events / trials = <PARAM(effects)> <spline-effects> </model-options>;  
   OUTPUT OUT=CAS-libref.data-table <keyword <name>> . . . <keyword <name>> </options>  
      ;  
   WEIGHT variable;  
```

The PROC GAMMOD statement and at least one MODEL statement are required. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statements. The following sections describe the PROC GAMMOD statement and then describe the other statements in alphabetical order.

PROC GAMMOD Statement

```
PROC GAMMOD <options>;  
```

The PROC GAMMOD statement invokes the procedure. Table 5.3 summarizes the available options in the PROC GAMMOD statement by function. The options are then described fully in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>ALPHA=</td>
<td>Specifies a global significance level</td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td>SEED=</td>
<td>Sets the seed for pseudorandom number generation</td>
</tr>
<tr>
<td><strong>Display Options</strong></td>
<td></td>
</tr>
<tr>
<td>ITDETAILS</td>
<td>Displays the “Iteration History” table</td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Limits or suppresses the display of classification variable levels</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>PLOTS=</td>
<td>Controls plots that are produced through ODS Graphics</td>
</tr>
<tr>
<td><strong>Optimization Subject Options</strong></td>
<td></td>
</tr>
<tr>
<td>PLIKEOPTIONS</td>
<td>Sets optimization parameters for likelihood estimation</td>
</tr>
<tr>
<td>SMOOTHOPTIONS</td>
<td>Sets optimization parameters for smoothing parameter estimation</td>
</tr>
</tbody>
</table>

Table 5.3   PROC GAMMOD Statement Options
Table 5.3  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Tolerance Options</strong></td>
<td></td>
</tr>
<tr>
<td>SINGCHOL=</td>
<td>Tunes the singularity criterion for Cholesky decompositions</td>
</tr>
<tr>
<td>SINGULAR=</td>
<td>Tunes the general singularity criterion</td>
</tr>
</tbody>
</table>

You can specify the following *options* in the PROC GAMMOD statement.

**ALPHA=number**
specifies a global significance level for the hypothesis testing of smoothing components and the construction of Bayesian confidence bands of predictions. The confidence level is $1 - number$. The value of *number* must be between 0 and 1; the default is 0.05. You can override this global significance level for Bayesian confidence bands of predictions by specifying the **ALPHA=** option in the **OUTPUT** statement.

**DATA=**CAS-libref.data-table
names the input data table for PROC GAMMOD to use. The default is the most recently created data table. **CAS-libref.data-table** is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the *caslib*, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about **CAS-libref**, see the section “Using CAS Sessions and CAS Engine Librefs” on page 299.
- **data-table** specifies the name of the input data table.

**ITDETAILS**
adds to the “Iteration History” table the current values of the parameter estimates and their gradients. If the optimization algorithm is used to determine at least one smoothing parameter, the table lists values for smoothing parameters. If all smoothing parameters are fixed or a parametric generalized linear model is specified, the table lists values for regression parameters. These quantities are reported only for parameters that participate in the optimization.

**NOCLPRINT<=number>**
suppresses the display of the “Class Level Information” table if you do not specify *number*. If you specify *number*, the values of the classification variables are displayed for only those variables whose number of levels is less than *number*. Specifying a *number* helps reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

**NOPRINT**
suppresses the generation of ODS output.

**PLIKEOPTIONS**(optimization-parameters)
specifies optimization parameters for either maximum or penalized likelihood estimation. For more information about which **optimization-parameters** you can specify, see the section “Optimization Parameters” on page 309. For the performance iteration method, only the **ABSFCONV=**, **FCONV=**, **
and MAXITER= options are effective for determining when the performance iteration should have converged. If the distribution family involves a dispersion parameter that needs to be estimated by the maximum likelihood method, all the optimization parameters in this option are applicable.

**PLOTS<(global-plot-option)> <= plot-requests<(option)>**

controls the plots that are produced through ODS Graphics. When ODS Graphics is enabled, PROC GAMMOD produces by default a panel of plots of partial prediction curves or surfaces of smoothing components.

```plaintext
ods graphics on;
proc gammod plots;
   model y=spline(x1) spline(x2);
run;
ods graphics off;
```

You can specify the following *global-plot-option*, which applies to the smoothing component plots that the GAMMOD procedure generates:

**UNPACK | UNPACKPANEL**

suppresses paneling. By default, multiple smoothing component plots can appear in some output panels. Specify UNPACK to get each plot individually.

You can specify the following *plot-requests*:

**ALL**

requests that all default plots be produced.

**COMPONENTS<(component-option)>**

plots a panel of smoothing components of the fitted model. You can specify the following *component-option*:

**COMMONAXES**

requests that the smoothing component plots use a common vertical axis except for bivariate contour plots. This option enables you to visually judge the relative effect size.

**NONE**

suppresses all plots.

**SEED=number**

specifies an integer that is used to start the pseudorandom number generator for truncated eigendecomposition and for subset sampling from observations to form knots if necessary. If you do not specify this option or if *number* ≤ 0, the seed is generated from the time of day, which is read from the computer’s clock.

**SINGCHOL=number**

tunes the singularity criterion in Cholesky decomposition and matrix inversion operations. The default is 1E4 times the machine epsilon; this product is approximately 1E–12 on most computers.
SINGULAR=number

tunes the singularity criterion in truncated eigendecomposition to determine its convergence. The
default is 1E4 times the machine epsilon; this product is approximately 1E–12 on most computers.

SMOOTHOPTIONS(optimization-parameters)

specifies optimization parameters for smoothing parameter estimation. For more information about
which optimization-parameters you can specify, see the next section. For parametric generalized
linear models or generalized additive models that have fixed smoothing parameters, any optimization
parameters that you specify for this option are ignored.

Optimization Parameters

You can specify optimization-parameters for both the PLIKEOPTIONS and SMOOTHOPTIONS options.
Depending on the modeling context, some optimization parameters might have no effect. The optimization
algorithm is considered to have converged when any one of the convergence criteria that are specified
in optimization-parameters is satisfied. Table 5.4 lists the available optimization parameters for both the
PLIKEOPTIONS and SMOOTHOPTIONS options.

Table 5.4  Optimization Parameters

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABSCONV=</td>
<td>Tunes the absolute function convergence criterion</td>
</tr>
<tr>
<td>ABSFCONV=</td>
<td>Tunes the absolute function difference convergence criterion</td>
</tr>
<tr>
<td>ABSGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>FCONV=</td>
<td>Tunes the relative function difference convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Chooses the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit of CPU time (in seconds) for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
</tbody>
</table>

The optimization-parameters are fully described in the section “Optimization Options” on page 42 in
Chapter 2, “Shared Concepts.”

NOTE: By default, TECHNIQUE=NEWRAP for the performance iteration (METHOD=PERFORMANCE),
and TECHNIQUE=QUANEW for the outer iteration (METHOD=OUTER).

BY Statement

    BY variables;

You can specify a BY statement in PROC GAMMOD to obtain separate analyses of observations in groups
that are defined by the values of the BY variables. If you specify more than one BY statement, only the last
one specified is used. For more information, see the discussion of BY-group processing in SAS Language
Reference: Concepts.
### CLASS Statement

```bash
CLASS variable < (options) > . . . < variable < (options) > > < / global-options > ;
```

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required. Table 5.5 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
</tbody>
</table>

### DISPLAY Statement

```bash
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 335. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`. 
A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following options after a slash (/):

**CASESENSITIVE**

performs a case-sensitive comparison of table names in the table-list to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the table-list in quotation marks.

**EXCLUDE**

displays all display tables except those that you specify in the table-list.

**EXCLUDEALL**

suppresses display of all tables. This option takes precedence over the other options.

**TRACE**

displays the display table names, labels, and paths.

---

**DISPLAYOUT Statement**

`DISPLAYOUT table-spec-list < /options > ;`

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.
- `key` specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

**INCLUDEALL**

creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the `table-spec-list` specification is ignored.

**NOREPLACE**

does not replace any existing CAS output table of the same name.
The REPEATED statement replicates all CAS output tables on all nodes.

---

**FREQ Statement**

```plaintext
FREQ variable;
```

The `variable` in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC GAMMOD treats each observation as if it appears `f` times, where `f` is the value of the FREQ `variable` for the observation. If `f` is not an integer, it is truncated to an integer. If `f` is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

---

**MODEL Statement**

```plaintext
MODEL response < (response-options) > = < PARAM(effects) > < spline-effects > </ model-options > ;
MODEL events / trials = < PARAM(effects) > < spline-effects > </ model-options > ;
```

The MODEL statement specifies the response (dependent or target) variable and the predictor (independent or explanatory) effects of the model. You can specify the response in the form of a single variable or in the form of a ratio of two variables, which are denoted `events/trials`. The first form applies to all distribution families; the second form applies only to summarized binomial response data. When you have binomial data, the `events` variable contains the number of positive responses (or events) and the `trials` variable contains the number of trials. The values of both `events` and `(trials – events)` must be nonnegative, and the value of `trials` must be positive. If you specify a single `response` variable that is in a CLASS statement, then the response is assumed to be binary.

You can specify parametric effects that are constructed from variables in the input data and include the effects in the parentheses of a PARAM( ) option, which can appear multiple times. For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

You can specify `spline-effects` by including independent variables inside the parentheses of the SPLINE( ) option. Only continuous variables (not classification variables) can be specified in `spline-effects`. Each `spline-effect` can have at least one variable and optionally some `spline-options`. You can specify any number of `spline-effects`. The following table shows some examples.

<table>
<thead>
<tr>
<th>Spline Effect Specification</th>
<th>Meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>spline(x)</code></td>
<td>Constructs a univariate spline by using <code>x</code> and uses the observed data points as knots. The maximum degrees of freedom is 10. PROC GAMMOD uses an optimization algorithm to determine the optimal smoothing parameter.</td>
</tr>
<tr>
<td><code>spline(x1/knots=list(1 to 10))</code></td>
<td>Constructs a univariate spline by using <code>x1</code> and a supplied list of knots from 1 to 10. PROC GAMMOD uses an optimization algorithm to determine the optimal smoothing parameter.</td>
</tr>
</tbody>
</table>
Both parametric effects and spline effects are optional. If none are specified, a model that contains only an intercept is fitted. If only parametric effects are present, PROC GAMMOD fits a parametric generalized linear model by using the terms inside the parentheses of all PARAM( ) terms. If only spline effects are present, PROC GAMMOD fits a nonparametric additive model. If both types of effects are present, PROC GAMMOD fits a semiparametric model by using the parametric effects as the linear part of the model.

There are three sets of options in the MODEL statement. The response-options determine how the GAMMOD procedure models probabilities for binary data. The spline-options controls how each spline term forms basis expansions. The model-options control other aspects of model formation and inference. Table 5.7 summarizes these options, and subsequent sections describe them in detail.

### Table 5.7  MODEL Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Response Variable Options</strong></td>
<td></td>
</tr>
<tr>
<td>DESCENDING</td>
<td>Reverses the response categories</td>
</tr>
<tr>
<td>EVENT=</td>
<td>Specifies the event category</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference category</td>
</tr>
<tr>
<td><strong>Spline Effect Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Requests detailed spline information</td>
</tr>
<tr>
<td>DF=</td>
<td>Specifies the fixed degrees of freedom</td>
</tr>
<tr>
<td>INITSMOOTH=</td>
<td>Specifies the starting value for the smoothing parameter</td>
</tr>
<tr>
<td>KNOTS=</td>
<td>Specifies the knots to use for constructing the spline</td>
</tr>
<tr>
<td>M=</td>
<td>Specifies polynomial orders for constructing the spline</td>
</tr>
<tr>
<td>MAXDF=</td>
<td>Specifies the maximum degrees of freedom</td>
</tr>
<tr>
<td>MAXKNOTS=</td>
<td>Specifies the maximum number of knots to use for constructing the spline</td>
</tr>
<tr>
<td>MAXSMOOTH=</td>
<td>Specifies the upper bound for the smoothing parameter</td>
</tr>
<tr>
<td>MINSMOOCH=</td>
<td>Specifies the lower bound for the smoothing parameter</td>
</tr>
<tr>
<td>SMOOTH=</td>
<td>Specifies a fixed smoothing parameter</td>
</tr>
<tr>
<td><strong>Model Options</strong></td>
<td></td>
</tr>
<tr>
<td>ALLOBS</td>
<td>Requests all nonmissing values of spline variables for constructing spline basis functions regardless of other model variables</td>
</tr>
<tr>
<td>CRITERION=</td>
<td>Specifies the model evaluation criterion</td>
</tr>
<tr>
<td>DISPERSION</td>
<td>PHI= Specifies the fixed dispersion parameter</td>
</tr>
</tbody>
</table>
### Table 5.7  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DISTRIBUTION</td>
<td>Specifies the response distribution</td>
</tr>
<tr>
<td>FDHESSIAN</td>
<td>Requests a finite-difference Hessian for smoothing parameter selection</td>
</tr>
<tr>
<td>INITIALPHI=</td>
<td>Specifies the starting value of the dispersion parameter</td>
</tr>
<tr>
<td>LINK=</td>
<td>Specifies the link function</td>
</tr>
<tr>
<td>NORMALIZE</td>
<td>Requests normalized spline basis functions for model fitting</td>
</tr>
<tr>
<td>MAXPHI=</td>
<td>Specifies the upper bound for searching the dispersion parameter</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the algorithm for selecting smoothing parameters</td>
</tr>
<tr>
<td>MINPHI=</td>
<td>Specifies the lower bound for searching the dispersion parameter</td>
</tr>
<tr>
<td>OFFSET=</td>
<td>Specifies the offset variable</td>
</tr>
<tr>
<td>RIDGE=</td>
<td>Specifies the ridge parameter</td>
</tr>
<tr>
<td>SCALE=</td>
<td>Specifies the method for estimating the dispersion parameter</td>
</tr>
</tbody>
</table>

### Response Variable Options

Response variable options determine how the GAMMOD procedure models probabilities for binary data.

You can specify the following *response-options* by enclosing them in parentheses after the *response* variable.

**DESCENDING**

**DESC**

reverses the order of the response categories. If you specify both the DESCENDING and ORDER= options, PROC GAMMOD orders the response categories according to the ORDER= option and then reverses that order.

**EVENT=’category’ | FIRST | LAST**

specifies the event category for the binary response model. PROC GAMMOD models the probability of the event category. This option has no effect when there are more than two response categories.

You can specify any of the following:

*’category’* specifies that observations whose value matches *category* (formatted, if a format is applied) in quotation marks represent events in the data. For example, the following statements specify that observations that have a formatted value of ‘1’ represent events in the data. The probability that is modeled by the GAMMOD procedure is thus the probability that the variable def takes on the (formatted) value ‘1’.

```plaintext
proc gammod data=mycas.MyData;
   class A B C;
   model def(event =’1’) = param(A B C) spline(x1 x2 x3);
run;
```

**FIRST** designates the first ordered category as the event.

**LAST** designates the last ordered category as the event.

By default, EVENT=FIRST.
ORDER=FORMATTED | FREQ | INTERNAL

specifies the sort order for the levels of the response variable. You can specify the following values:

FORMATTED sorts the levels by external formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. For numeric variables for which you have supplied no explicit format (that is, for which there is no corresponding FORMAT statement in the current PROC GAMMOD run or in the DATA step that created the data table), the levels are ordered by their internal (numeric) value. The sort order is machine-dependent.

FREQ sorts the levels by descending frequency count (levels that have the most observations come first in the order).

INTERNAL sorts the levels by unformatted value. The sort order is machine-dependent.

By default, ORDER=FORMATTED.

For more information about sort order, see the chapter about the SORT procedure in Base SAS Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts.

REF='category' | FIRST | LAST

specifies the reference category for the binary response model. Specifying one response category as the reference is the same as specifying the other response category as the event category. You can specify any of the following:

‘category’ specifies that observations whose value matches category (formatted, if a format is applied) are designated as the reference.

FIRST designates the first ordered category as the reference

LAST designates the last ordered category as the reference.

By default, REF=LAST.

Spline Effect Options

Spline effect options control how each spline term forms basis expansions.

You can specify the following spline-effects inside the parentheses of a SPLINE( ) term:

DETAILS requests a detailed spline specification information table.

DF=number specifies a fixed degrees of freedom. When you specify this option, no smoothing parameter selection is performed on the spline term. If number is not an integer, then number is truncated to an integer.

IGINSMOOTH=number specifies the starting value for a smoothing parameter. The number must be nonnegative.

KNOTS=method specifies the method for supplying user-defined knot values instead of using data values for constructing basis expansions. You can use the following methods for supplying the knots:
**LIST(list-of-values)**

specifies a list of values as knots for the spline construction. For a multivariate spline term, the listed values are taken as multiple row vectors, where each vector has values that are ordered by specified variables. If the last row vector of knots contains fewer values than the number of variables, then the last row vector is ignored. For example, the following specification of a spline term produces two actual knot vectors \((k_1\) and \(k_2\)) and the value 5 is ignored.

\[
spline(x1\ x2/\text{knots=list}(1\ 2\ 3\ 4\ 5))
\]

<table>
<thead>
<tr>
<th>Table 5.8</th>
<th>Knot Values for a Bivariate Spline with a Supplied List</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>x1</td>
</tr>
<tr>
<td>(k_1)</td>
<td>1</td>
</tr>
<tr>
<td>(k_2)</td>
<td>3</td>
</tr>
</tbody>
</table>

**EQUAL(n)**

specifies the number of equally spaced interior knots for every variable in a spline term. Two boundary knots are automatically added to the knot list for each variable such that the total number of knots is \((n + 2)^d\), where \(d\) is the number of variables in the spline term. For a multivariate spline term, knot values for each variable are determined independently from the corresponding boundary values. For example, if the boundary points for \(x1\) are 1 and 5 and the boundary points for \(x2\) are 2 and 6, then the following specification of a spline term produces nine actual knots \((k_1\) through \(k_9\)), which consist of two boundary knots and one interior knot for each variable.

\[
spline(x1\ x2/\text{knots=equal}(1))
\]

<table>
<thead>
<tr>
<th>Table 5.9</th>
<th>Knot Values for a Bivariate Spline with One Interior Knot</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>x1</td>
</tr>
<tr>
<td>(k_1)</td>
<td>1</td>
</tr>
<tr>
<td>(k_2)</td>
<td>1</td>
</tr>
<tr>
<td>(k_3)</td>
<td>1</td>
</tr>
<tr>
<td>(k_4)</td>
<td>3</td>
</tr>
<tr>
<td>(k_5)</td>
<td>3</td>
</tr>
<tr>
<td>(k_6)</td>
<td>3</td>
</tr>
<tr>
<td>(k_7)</td>
<td>5</td>
</tr>
<tr>
<td>(k_8)</td>
<td>5</td>
</tr>
<tr>
<td>(k_9)</td>
<td>5</td>
</tr>
</tbody>
</table>

**M=number**

specifies the order of the derivative in the penalty term. The \(number\) must be a positive integer. The default is \(\max(2, \lceil d/2 \rceil + 1)\), where \(d\) is the number of variables in the spline term.

**MAXDF=number**

specifies the maximum \(number\) of degrees of freedom. When a thin-plate regression spline is formed, the specified \(number\) is used for constructing a low-rank penalty matrix to approximate the penalty
matrix via the truncated eigendecomposition. The number must be greater than \((\frac{m+d-1}{d})\), where \(m\) is the derivative order that is specified in the \(M=\) option, and \(d\) is the number of variables in the spline term. The default is \(10 \times d\). For more information, see the section “Thin-Plate Regression Splines” on page 322.

**MAXKNOTS=** *number*

specifies the maximum number of knots if data points are used to form knots. If \(KNOTS=\)LIST(*list-of-values*) is not specified, PROC GAMMOD forms knots from unique data points. If the number of unique data points is greater than number, a subset of size number is formed by random sampling from all unique data points. The number cannot exceed the largest integer that can be stored on the CAS server. By default, MAXKNOTS=2000.

**MAXSMOOTH=** *number*

specifies the upper bound for the smoothing parameter. The default is the largest double-precision value.

**MINSMOOTH=** *number*

specifies the lower bound for the smoothing parameter. By default, MINSMOOTH=0.

**SMOOTH=** *number*

specifies a fixed smoothing parameter. When you specify this option, no smoothing parameter selection is performed on the spline term.

**Model Options**

You can specify the following *model-options* in the MODEL statement after a slash (/):

**ALLOBS**

requests that all nonmissing values of the variables be used in a spline term for constructing the spline basis functions, regardless of whether other model variables are missing.

**CRITERION=** *criterion*

specifies the model evaluation criterion for selecting smoothing parameters for *spline-effects*. You can specify the following values:

- **GACV**< *(FACTOR=number | GAMMA=number)* >
  
  uses the generalized approximate cross validation (GACV) criterion to evaluate models.

- **GCV**< *(FACTOR=number | GAMMA=number)* >
  
  uses the generalized cross validation (GCV) criterion to evaluate models.

- **UBRE**< *(FACTOR=number | GAMMA=number)* >
  
  uses the unbiased risk estimator (UBRE) criterion to evaluate models.

The default criterion depends on the value of the DISTRIBUTION= option. For distributions that involve dispersion parameters, GCV is the default. For distributions without dispersion parameters, UBRE is the default. For all three criteria, you can optionally use the FACTOR= option to specify an extra tuning parameter in order to penalize more for model roughness. The value of number must be greater than or equal to 1. For more information about the model evaluation criteria, see the section “Model Evaluation Criteria” on page 327.
**DISPERSION=** number

**PHI=** number

specifies a fixed dispersion parameter for distributions that have a dispersion parameter. The dispersion parameter that is used in all computations is fixed at number; it is not estimated.

**DISTRIBUTION=** keyword

specifies the response distribution for the model. The keywords and their associated distributions are shown in Table 5.10.

<table>
<thead>
<tr>
<th>DISTRIBUTION=</th>
<th>Distribution Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>BINARY</td>
<td>Binary</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Binary or binomial</td>
</tr>
<tr>
<td>GAMMA</td>
<td>Gamma</td>
</tr>
<tr>
<td>INVERSEGAUSSIAN</td>
<td>IG</td>
</tr>
<tr>
<td>NEGATIVEBINOMIAL</td>
<td>NB</td>
</tr>
<tr>
<td>NORMAL</td>
<td>GAUSSIAN</td>
</tr>
<tr>
<td>POISSON</td>
<td>Poisson</td>
</tr>
<tr>
<td>TWEEDIE&lt; <em>(Tweedie-options)</em></td>
<td>Tweedie</td>
</tr>
</tbody>
</table>

When DISTRIBUTION=TWEEDIE, you can specify the following Tweedie-options:

**INITIALP=**

specifies a starting value for iterative estimation of the Tweedie power parameter.

**P=**

requests a fixed Tweedie power parameter.

If you do not specify a link function in the **LINK=** option, a default link function is used. The default link function for each distribution is shown in Table 5.11. You can use any link function shown in Table 5.12 by specifying the **LINK=** option. Other commonly used link functions for each distribution are shown in Table 5.11.

<table>
<thead>
<tr>
<th>DISTRIBUTION=</th>
<th>Default Link Function</th>
<th>Other Commonly Used Link Functions</th>
</tr>
</thead>
<tbody>
<tr>
<td>BINARY</td>
<td>Logit</td>
<td>Probit, complementary log-log, log-log</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Logit</td>
<td>Probit, complementary log-log, log-log</td>
</tr>
<tr>
<td>GAMMA</td>
<td>Log</td>
<td>Reciprocal</td>
</tr>
<tr>
<td>INVERSEGAUSSIAN</td>
<td>IG</td>
<td>Log</td>
</tr>
<tr>
<td>NEGATIVEBINOMIAL</td>
<td>NB</td>
<td>Log</td>
</tr>
<tr>
<td>NORMAL</td>
<td>GAUSSIAN</td>
<td>Identity</td>
</tr>
<tr>
<td>POISSON</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>TWEEDIE</td>
<td>Log</td>
<td></td>
</tr>
</tbody>
</table>
FDHESSIAN
requests that the second-order derivatives (Hessian) be computed using finite-difference approximations based on evaluation of the first-order derivatives (gradient). This option might be useful if the analytical Hessian takes a long time to compute.

INITIALPHI=number
specifies a starting value for iterative maximum likelihood estimation of the dispersion parameter for distributions that have a dispersion parameter.

LINK=keyword
specifies the link function for the model. The keywords and the associated link functions are shown in Table 5.12. Default and commonly used link functions for the available distributions are shown in Table 5.11.

Table 5.12 Built-In Link Functions

<table>
<thead>
<tr>
<th>LINK=</th>
<th>Link Function</th>
<th>( g(\mu) = \eta = )</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLOGLOG</td>
<td>Complementary log-log \log(-\log(1-\mu))</td>
<td></td>
</tr>
<tr>
<td>IDENTITY</td>
<td>Identity ( \mu )</td>
<td></td>
</tr>
<tr>
<td>INV</td>
<td>Reciprocal ( 1/\mu )</td>
<td></td>
</tr>
<tr>
<td>INV2</td>
<td>Reciprocal square ( 1/\mu^2 )</td>
<td></td>
</tr>
<tr>
<td>LOG</td>
<td>Logarithm ( \log(\mu) )</td>
<td></td>
</tr>
<tr>
<td>LOGIT</td>
<td>Logit \log(\mu/(1-\mu))</td>
<td></td>
</tr>
<tr>
<td>LOGLOG</td>
<td>Log-log ( -\log(-\log(\mu)) )</td>
<td></td>
</tr>
<tr>
<td>PROBIT</td>
<td>Probit ( \Phi^{-1}(\mu) )</td>
<td></td>
</tr>
</tbody>
</table>

\( \Phi^{-1}(\cdot) \) denotes the quantile function of the standard normal distribution.

MAXPHI=number
specifies an upper bound for maximum likelihood estimation of the dispersion parameter for distributions that have a dispersion parameter.

METHOD=OUTER | PERFORMANCE
specifies the algorithm for selecting smoothing parameters for spline-effects. You can specify the following values:

OUTER specifies the outer iteration method for selecting smoothing parameters. For more information about this method, see the section “Outer Iteration” on page 328.

PERFORMANCE specifies the performance iteration method for selecting smoothing parameters. For more information about this method, see the section “Performance Iteration” on page 329.

By default, METHOD=PERFORMANCE.
**MINPHI=number**
specifies a lower bound for maximum likelihood estimation of the dispersion parameter for distributions that have a dispersion parameter.

**NORMALIZE**
requests normalized spline basis functions for model fitting. After the regression spline basis functions are computed, each column is standardized to have a unit standard error. The corresponding penalty matrix is also scaled accordingly. This option might be helpful when you have badly scaled data.

**OFFSET=variable**
specifies a variable to be used as an offset to the linear predictor. An offset plays the role of an effect whose coefficient is known to be 1. The offset variable cannot appear in the CLASS statement or elsewhere in the MODEL statement. Observations that have missing values for the offset variable are excluded from the analysis.

**RIDGE=number**
allows a ridge parameter such that a diagonal matrix $H_i = number$ is added to the optimization problem with respect to regression parameters:

\[
\min (y - X\beta)'(y - X\beta) + \beta'S\beta + \beta'H\beta
\]

with respect to $\beta$

By default, RIDGE=0. Specifying a small ridge parameter might be helpful if the model matrix $X'X + S_\lambda$ is close to singular.

**SCALE=DEVIANCE | MLE | PEARSON**
specifies the method for estimating the scale and dispersion parameters. You can specify the following values:

- **DEVIANCE**
estimates the dispersion parameter by using the deviance statistic.

- **MLE**
computes the dispersion parameter by maximizing the likelihood or penalized likelihood.

- **PEARSON**
estimates the dispersion parameter by using Pearson’s statistic.

By default, SCALE=MLE.

---

**OUTPUT Statement**

```
OUTPUT OUT=CAS-libref.data-table
   < ALPHA=number> < COMPONENT > < COPYVARS=(variables) >
   < keyword <=name>> . . . < keyword <=name>> ;
```

The OUTPUT statement creates a data table that contains observationwise statistics that PROC GAMMOD computes after fitting the model. In order to avoid data duplication for large data tables, the variables in the input data table are not included in the output data table unless you specify them in the COPYVARS= option.

The computation of the output statistics is based on the final parameter estimates. If the model fit does not converge, missing values are produced for the quantities that depend on the estimates.

You must specify the following option:
OUT=\texttt{CAS-libref.data-table} names the output data table for PROC GAMMOD to use. You must specify this option before any other options. \texttt{CAS-libref.data-table} is a two-level name, where

\begin{itemize}
  \item \texttt{CAS-libref} refers to a collection of information that is defined in the LIBNAME statement and includes the \texttt{caslib}, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about \texttt{CAS-libref}, see the section \enquote{Using CAS Sessions and CAS Engine Librefs} on page 299.
  \item \texttt{data-table} specifies the name of the output data table.
\end{itemize}

You can also specify the following syntax elements:

\begin{description}
  \item[\texttt{ALPHA=}\texttt{number}] specifies the significance level for the construction of confidence intervals in the output data table. The confidence level is \(1 - \texttt{number}\). The value of \texttt{number} must be between 0 and 1. By default, \texttt{number} is equal to the value of the \texttt{ALPHA=} option in the \texttt{PROC GAMMOD} statement, or 0.05 if that option is not specified.
  \item[\texttt{COMPONENT}] requests componentwise statistics for all spline terms if \texttt{LINP}, \texttt{LOWER}, \texttt{STD}, or \texttt{UPPER} is specified as a \texttt{keyword}.
  \item[\texttt{COPYVAR=}\texttt{variable}] \texttt{COPYVARS=}\texttt{(variables)} transfers one or more \texttt{variables} from the input data table to the output data table.
  \item[\texttt{keyword} \texttt{<=} \texttt{name}>] specifies a statistic to include in the output data table and optionally assigns a \texttt{name} to the variable. If you do not provide a \texttt{name}, the GAMMOD procedure assigns a default name based on the \texttt{keyword}.
\end{description}

You can specify the following \texttt{keywords} for adding statistics to the OUTPUT data table:

\begin{description}
  \item[\texttt{LINP | XBETA}] requests the linear predictor \(\eta = x^T \beta\). For observations in which only the response variable is missing, values of the linear predictor are computed even though these observations do not affect the model fit. The default \texttt{name} is \texttt{Xbeta}.
  \item[\texttt{LOWER}] requests a lower Bayesian confidence band value for the predicted value. The default \texttt{name} is \texttt{Lower}.
  \item[\texttt{PEARSON | PEAR | RESCHI}] requests the Pearson residual, \(\frac{y - \mu}{\sqrt{V(\mu)}}\), where \(\mu\) is the estimate of the predicted response mean and \(V(\mu)\) is the response distribution variance function. The default \texttt{name} is \texttt{Pearson}.
  \item[\texttt{PREDICTED | PRED | P}] requests predicted values for the response variable. For observations in which only the response variable is missing, the predicted values are computed even though these observations do not affect the model fit. The default \texttt{name} is \texttt{Pred}.
\end{description}
RESIDUAL | RESID | R
requests the raw residual, \( y - \mu \), where \( \mu \) is the estimate of the predicted mean. The default name is Residual.

STD
requests a standard error for the linear predictor. The default name is Std.

UPPER
requests an upper Bayesian confidence band value for the predicted value. The default name is Upper.

**WEIGHT Statement**

```plaintext
WEIGHT variable ;
```

The *variable* in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, then all observations that are used in the analysis are assigned a weight of 1.

**Details: GAMMOD Procedure**

**Missing Values**

Any observation that has missing values for the response, frequency, weight, offset, or explanatory variables is excluded from the analysis; however, missing values are valid for response and explanatory variables if you specify the MISSING option in the CLASS statement. Observations that have a nonpositive weight or a frequency less than 1 are also excluded. For Poisson, negative binomial, and Tweedie distributions, observations that have a negative response value are excluded. For gamma and inverse Gaussian distributions, observations that have a nonpositive response value are excluded.

The estimated linear predictor and the fitted means are not computed for any observation that has missing offset or explanatory variables. However, if only the response value is missing, the linear predictor and the fitted means can be computed and output to a data table by using the OUTPUT statement.

**Thin-Plate Regression Splines**

The GAMMOD procedure uses thin-plate regression splines (Wood 2003) to construct spline basis expansions. The thin-plate regression splines are based on thin-plate smoothing splines (Duchon 1976, 1977). Compared to thin-plate smoothing splines, thin-plate regression splines produce fewer basis expansions and thus make direct fitting of generalized additive models possible.
Thin-Plate Smoothing Splines

Consider the problem of estimating a smoothing function \( f \) of \( x \) with \( d \) covariates from \( n \) observations. The model assumes

\[
y_i = f(x_i) + \epsilon_i, i = 1, \ldots, n
\]

Then the thin-plate smoothing splines estimate the smoothing function \( f \) by minimizing the penalized least squares function:

\[
\sum_{i=1}^{n} (y_i - f(x_i))^2 + \lambda J_{m,d}(f)
\]

The penalty term \( \lambda J_{m,d}(f) \) includes the function that measures roughness on the \( f \) estimate:

\[
J_{m,d}(f) = \int \cdots \int \sum_{\alpha_1 + \cdots + \alpha_d = m} \frac{m!}{\alpha_1! \cdots \alpha_d!} \left( \frac{\partial^m f}{\partial x_1^{\alpha_1} \cdots \partial x_d^{\alpha_d}} \right)^2 \, dx_1 \cdots dx_d
\]

The parameter \( m \) (which corresponds to the \( \text{M=} \) option for a spline effect) specifies how the penalty is applied to the function roughness. Function derivatives whose order is less than \( m \) are not penalized. The relation \( 2m > d \) must be satisfied.

The penalty term also includes the smoothing parameter \( \lambda \in [0, \infty) \), which controls the trade-off between the model’s fidelity to the data and the function smoothness of \( f \). When \( \lambda = 0 \), the function estimate corresponds to an interpolation. When \( \lambda \to \infty \), the function estimate becomes the least squares fit. By using the defined penalized least squares criterion and a fixed \( \lambda \) value, you can explicitly express the estimate of the smooth function \( f \) in the following form:

\[
f_\lambda(x) = \sum_{j=1}^{M} \theta_j \phi_j(x) + \sum_{i} \delta_i \eta_{m,d}(\|x - x_i\|)
\]

In the expression of \( f_\lambda(x) \), \( \delta_i \) and \( \theta_j \) are coefficients to be estimated. The functions \( \phi_j(x) \) correspond to unpenalized polynomials of \( x \) with degrees up to \( m - 1 \). The total number of these polynomials is \( M = \binom{m+d-1}{d} \). The function \( \eta_{m,d} \) models the extra nonlinearity besides the polynomials and is a function of the Euclidean distance \( r \) between any \( x \) value and an observed \( x_i \) value:

\[
\eta_{m,d}(r) = \begin{cases} 
\frac{(-1)^{m+1+d/2}}{2^{m-1} \pi^{d/2} (m-1)! (m-d/2)!} r^{2m-d} \log(r) & \text{if } d \text{ is even} \\
\frac{\Gamma(d/2-m)}{2^{m+1} \pi^{d/2} (m-1)!} r^{2m-d} & \text{if } d \text{ is odd}
\end{cases}
\]

Define the penalty matrix \( E \) such that each entry \( E_{ij} = \eta_{m,d}(\|x_i - x_j\|) \), let \( y \) be the vector of the response, let \( T \) be the matrix where each row is formed by \( \phi_j(x) \), and let \( \theta \) and \( \delta \) be vectors of coefficients \( \theta_j \) and \( \delta_i \). Then you can obtain the function estimate \( f_\lambda \) from the following minimization problem:

\[
\min \|y - T\theta - E\delta\|^2 + \lambda \delta' E \delta \quad \text{subject to} \quad T' \delta = 0
\]
Low-Rank Approximation

Given the representation of the thin-plate smoothing spline, the estimate of \( f \) involves as many parameters as the number of unique data points. Solving \( (\theta, \delta) \) with an optimum \( \lambda \) becomes difficult for large problems.

Because the matrix \( E \) is symmetric and nonnegative definite, the eigendecomposition can be taken as \( E = UDU' \), where \( D \) is the diagonal matrix of eigenvalues \( d_i \) of \( E \), and \( U \) is the matrix of eigenvectors that corresponds to \( d_i \). The truncated eigendecomposition forms \( \tilde{E}_k \), which is an approximation to \( E \) such that

\[
\tilde{E}_k = U_k D_k U_k'
\]

where \( D_k \) is a diagonal matrix that contains the \( k \) most extreme eigenvalues in descending order of absolute values: \( |\tilde{d}_1| > \cdots > |\tilde{d}_k| \). \( U_k \) is the matrix that is formed by columns of eigenvectors that correspond to the eigenvalues in \( D_k \).

The approximation \( \tilde{E}_k \) not only reduces the dimension from \( n \times n \) of \( E \) to \( n \times k \) but also is optimal in two senses. First, \( \tilde{E}_k \) minimizes the spectral norm \( \| E - F_k \|_2 \) between \( E \) and all rank \( k \) matrices \( F_k \). Second, \( \tilde{E}_k \) also minimizes the worst possible change that is introduced by the eigenspace truncation as defined by

\[
\max_{\delta \neq 0} \frac{\delta'(E - G_k)\delta}{\|\delta\|^2}
\]

where \( G_k \) is formed by any \( k \) eigenvalues and corresponding eigenvectors. For more information, see Wood (2003).

Now given \( E \approx \tilde{E}_k \) and \( \tilde{E}_k = U_k D_k U_k' \), and letting \( \delta_k = U_k' \delta \), the minimization problem becomes

\[
\min \| y - T\theta - U_k D_k \delta_k \|^2 + \lambda \delta_k'D_k \delta_k \quad \text{subject to} \quad T'U_k \delta_k = 0
\]

You can turn the constrained optimization problem into an unconstrained one by using any orthogonal column basis \( Z \). One way to form \( Z \) is via the QR decomposition of \( U_k' T \):

\[
U_k' T = [Q_1 Q_2] \begin{bmatrix} R \\ 0 \end{bmatrix}
\]

Let \( Z = Q_2 \). Then it is verified that

\[
T'U_k Z = R'Q_1 Q_2 = 0
\]

So for \( \delta_k \) such that \( T'U_k \delta_k = 0 \), it is true that \( \delta_k = Z \tilde{\delta} \). Now the problem becomes the unconstrained optimization,

\[
\min \| y - T\theta - U_k D_k Z \tilde{\delta} \|^2 + \lambda \tilde{\delta}'Z'D_k Z \tilde{\delta}
\]

Let

\[
\beta = \begin{bmatrix} \theta \\ \tilde{\delta} \end{bmatrix}, \quad X = [T : U_k D_k Z], \quad \text{and} \quad S = \begin{bmatrix} 0 & 0 \\ 0 & Z'D_k Z \end{bmatrix}
\]

The optimization is simplified as

\[
\min \| y - X\beta \|^2 + \lambda \beta'S\beta \quad \text{with respect to} \quad \beta
\]
Generalized Additive Models

Generalized Linear Models

All probability distributions that the GAMMOD procedure fits are members of an exponential family of distributions. For the specification of an exponential family, see the section “Exponential Family Distributions” in Chapter 6, “The GENSELECT Procedure” (SAS Visual Statistics: Procedures Guide).

Table 5.13 lists and defines some common notation that is used in the context of generalized linear models and generalized additive models.

<table>
<thead>
<tr>
<th>Notation</th>
<th>Meaning</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\ell$</td>
<td>Log-likelihood</td>
</tr>
<tr>
<td>$\ell_p$</td>
<td>Penalized log-likelihood</td>
</tr>
<tr>
<td>$D$</td>
<td>Deviance</td>
</tr>
<tr>
<td>$D_p$</td>
<td>Penalized deviance</td>
</tr>
<tr>
<td>$g$</td>
<td>Link function</td>
</tr>
<tr>
<td>$g^{-1}$</td>
<td>Inverse link function</td>
</tr>
<tr>
<td>$\mu$</td>
<td>Response mean $\mu = g^{-1}(\eta)$</td>
</tr>
<tr>
<td>$\eta$</td>
<td>Linear predictor $\eta = X\beta$</td>
</tr>
<tr>
<td>$\phi$</td>
<td>Dispersion parameter</td>
</tr>
<tr>
<td>$z$</td>
<td>Column of adjusted response variable</td>
</tr>
<tr>
<td>$v$</td>
<td>Column of response variance</td>
</tr>
<tr>
<td>$\omega_i$</td>
<td>Prior weight for each observation</td>
</tr>
<tr>
<td>$w_i$</td>
<td>Adjusted weight for each observation</td>
</tr>
<tr>
<td>$W$</td>
<td>Diagonal matrix of adjusted weights</td>
</tr>
</tbody>
</table>

The GAMMOD procedure supports the following distributions: binary, binomial, gamma, inverse Gaussian, negative binomial, normal (Gaussian), Poisson, and Tweedie.


Generalized Additive Models

Generalized additive models are extensions of generalized linear models (Nelder and Wedderburn 1972). For each observation that has a response $Y_i$ and a row vector of the model matrix $x_i$, both generalized additive models and generalized linear models assume the model additivity,

$$ g(\mu_i) = f_1(x_{i1}) + \cdots + f_p(x_{ip}) $$

where $\mu_i = E(Y_i)$ and $Y_i$ is independently distributed in some exponential family. Generalized linear models further assume model linearity by $f_j(x_{ij}) = x_{ij}\beta_j$ for $j = 1, \ldots, p$. Generalized additive models relax the linearity assumption by allowing some smoothing functions $f_j$ to characterize the dependency. The GAMMOD procedure constructs the smoothing functions by using thin-plate regression splines.

Consider a generalized additive model that has some linear terms $X_L$ with coefficients $\beta_L$ and $p$ smoothing functions $f_j$. Each smoothing function can be constructed by thin-plate regression splines with a smoothing
Chapter 5: The GAMMOD Procedure

parameter \( \lambda_j \). Using the notations described in the section “Low-Rank Approximation” on page 324, you can characterize each smoothing function by

\[
\beta_j = \begin{bmatrix} \theta_j \\ \delta_j \end{bmatrix}, \quad X_j = [T_j : U_{kj} D_{kj} Z_j], \quad \text{and} \quad S_j = \begin{bmatrix} 0 & 0 \\ 0 & Z'_j D_{kj} Z_j \end{bmatrix}
\]

Notice that each smoothing function representation contains a zero-degree polynomial that corresponds to a constant. Having multiple constant terms makes the smoothing functions unidentifiable. The solution is to include a global constant term (that is, the intercept) in the model and enforce the centering constraint to each smoothing function. You can write the constraint as

\[ 1'X_j \beta_j = 0 \]

By using a similar approach as the linear constraint for thin-plate regression splines, you obtain the orthogonal column basis \( V_j \) via the QR decomposition of \( X_j'1 \) such that \( 1'X_j V_j = 0 \). Each smoothing function can be reparameterized as \( X_j' = X_j V_j \).

Let \( X = [X_L : \bar{X}_1 : \ldots : \bar{X}_p] \) and \( \beta' = [\beta'_L : \beta'_1 : \ldots : \beta'_p] \). Then the generalized additive model can be represented as \( g(\mu) = X \beta \). The roughness penalty matrix is represented as a block diagonal matrix:

\[
S_\lambda = \begin{bmatrix}
0 & 0 & \cdots & 0 \\
0 & \lambda_1 S_1 & \cdots & 0 \\
\vdots & \vdots & \ddots & \vdots \\
0 & 0 & \cdots & \lambda_p S_p
\end{bmatrix}
\]

Then the roughness penalty is measured in the quadratic form \( \beta' S_\lambda \beta \).

Penalized Likelihood Estimation

Given a fixed vector of smoothing parameters, \( \lambda = [\lambda_1, \ldots, \lambda_p]' \), you can fit the generalized additive models by the penalized likelihood estimation. In contrast to the maximum likelihood estimation, penalized likelihood estimation obtains an estimate for \( \beta \) by maximizing the penalized log likelihood,

\[
\ell_p(\beta) = \ell(\beta) - \frac{1}{2} \beta' S_\lambda \beta
\]

Any optimization technique that you can use for maximum likelihood estimation can also be used for penalized likelihood estimation. If first-order derivatives are required for the optimization technique, you can compute the gradient as

\[
\frac{\partial \ell_p}{\partial \beta} = \frac{\partial \ell}{\partial \beta} - S_\lambda \beta
\]

If second-order derivatives are required for the optimization technique, you can compute the Hessian as

\[
\frac{\partial^2 \ell_p}{\partial \beta \partial \beta'} = \frac{\partial^2 \ell}{\partial \beta \partial \beta'} - S_\lambda
\]

In the gradient and Hessian forms, \( \partial \ell / \partial \beta \) and \( \partial^2 \ell / (\partial \beta \partial \beta') \) are the corresponding gradient and Hessian, respectively, for the log likelihood for generalized linear models. For more information about optimization techniques, see the section “Optimization Options” on page 42 in Chapter 2, “Shared Concepts.”
Model Evaluation Criteria

Given a fixed set of smoothing parameters $\lambda$ in which each $\lambda_i$ controls the smoothness of each spline term, you can fit a generalized additive model by penalized likelihood estimation. There are infinitely many sets of smoothing parameters. In order to search optimum models, some model evaluation criteria need to be defined to quantify the model’s goodness of fit. The GAMMOD procedure uses the following model evaluation criteria:

- generalized cross validation (GCV), $V_g$ (Craven and Wahba 1979)
- unbiased risk estimator (UBRE), $V_u$ (Craven and Wahba 1979)
- generalized approximate cross validation (GACV), $V_a$ (Xiang and Wahba 1996)

Consider the optimization problem

$$\min (y - X\beta)'(y - X\beta) + \beta'S_\lambda\beta$$

with respect to $\beta$

The parameter estimate for $\beta$ can be represented as

$$\hat{\beta} = (X'X + S_\lambda)^{-1}X'y$$

And the smoothing matrix (also called the influence matrix or hat matrix) is thus represented as

$$H_\lambda = X(X'X + S_\lambda)^{-1}X'$$

With the defined smoothing matrix, you can form the model evaluation criteria as follows:

$$V_g(\lambda) = \frac{n\|y - H_\lambda y\|^2}{(\text{tr}(I - \gamma H_\lambda))^2}$$

$$V_u(\lambda) = \frac{1}{n}\|y - H_\lambda y\|^2 - \frac{2}{n}\sigma^2\text{tr}(I - \gamma H_\lambda) + \sigma^2$$

$$V_a(\lambda) = \frac{1}{n}\|y - H_\lambda y\|^2 \left( 1 + 2\gamma \frac{\text{tr}(H_\lambda)}{\text{tr}(I - H_\lambda)} \right)$$

In the equations, $\gamma \geq 1$ (which corresponds to the GAMMA= suboption of the CRITERION= option) is the tuning parameter that is sometimes used to enforce smoother models.

The GAMMOD procedure uses fitting algorithms that involve minimizing the model evaluation criterion with respect to unknown smoothing parameters $\lambda$.

Fitting Algorithms

For models that assume a normally distributed response variable, you can minimize the model evaluation criteria directly by searching for optimal smoothing parameters. For models that have nonnormal distributions, you cannot use the model evaluation criteria directly because the involved statistics keep changing between iterations. The GAMMOD procedure enables you to use either of two fitting approaches to search for
optimum models: the outer iteration method and the performance iteration method. The outer iteration method modifies the model evaluation criteria so that a global objective function can be minimized in order to find the best smoothing parameters. The performance iteration method minimizes a series of objective functions in an iterative fashion and then obtains the optimum smoothing parameters at convergence. For large data tables, the performance iteration method usually converges faster than the outer iteration method.

**Outer Iteration**

The outer iteration method is outlined in Wood (2006). The method uses modified model evaluation criteria, which are defined as follows:

\[
\begin{align*}
\mathcal{V}_g^o(\lambda) &= \frac{nD_\lambda(\mu)}{(n - \gamma \text{tr}(H_\lambda))^2} \\
\mathcal{V}_u^o(\lambda) &= \frac{D_\lambda(\mu)}{n} - 2\frac{\sigma^2 \text{tr}((I - \gamma H_\lambda)) + \sigma^2}{n} \\
\mathcal{V}_a^o(\lambda) &= \frac{D_\lambda(\mu)}{n} + \frac{2\gamma \text{tr}(H_\lambda) P_\lambda}{n\text{tr}(I - H_\lambda)}
\end{align*}
\]

By replacing \(\|y - H_\lambda y\|^2\) with model deviance \(D_\lambda(\mu)\), the modified model evaluation criteria relate to the smoothing parameter \(\lambda\) in a direct way such that the analytic gradient and Hessian are available in explicit forms. Pearson’s statistic \(P_\lambda\) is used in the GACV criterion \(\mathcal{V}_u^o(\lambda)\) (Wood 2008). The algorithm for the outer iteration is thus as follows:

1. Initialize smoothing parameters by taking one step of performance iteration based on adjusted response and adjusted weight except for spline terms whose initial values are specified in the INITSMOOTH= option.

2. Search for the best smoothing parameters by minimizing the modified model evaluation criteria. The optimization process stops when any of the convergence criteria that are specified in the SMOOTHOPTIONS option is met. At each optimization step:
   a) Initialize by setting initial regression parameters \(\beta = \{g(\hat{y}), 0, \ldots, 0\}'\). Set the initial dispersion parameter if necessary.
   b) Search for the best regression parameters \(\beta\) by minimizing the penalized deviance \(D_p\) (or maximizing the penalized likelihood \(\ell_p\) for negative binomial distribution). The optimization process stops when any of the convergence criteria that are specified in the PLIKEOPTIONS option is met.
   c) At convergence, evaluate derivatives of the model evaluation criteria with respect to \(\lambda\) by using \(\partial D_p / \partial \beta, \partial^2 D_p / (\partial \beta \partial \beta)'\), \(\partial \beta / \partial \lambda_j\), and \(\partial^2 \beta / (\partial \lambda_j \partial \lambda_k)\).

Step 2b usually converges quickly because it is essentially penalized likelihood estimation given that \(D_p = 2\phi(\ell_{\text{max}} - \ell) + \beta S_\lambda \beta\). Step 2c contains involved computation by using the chain rule of derivatives. For more information about computing derivatives of \(\mathcal{V}_g^o\) and \(\mathcal{V}_u^o\), see Wood (2008, 2011).
Performance Iteration

The performance iteration method is proposed by Gu and Wahba (1991). Wood (2004) modifies and stabilizes the algorithm for fitting generalized additive models. The algorithm for the performance iteration method is as follows:

1. Initialize smoothing parameters $\lambda = \{1, \ldots, 1\}$, except for spline terms whose initial values are specified in the INITSMOOTH= option. Set the initial regression parameters $\beta = \{g(\bar{y}), 0, \ldots, 0\}'$. Set the initial dispersion parameter if necessary.

2. Repeat the following steps until any of these three conditions is met: (1) the absolute function change in penalized likelihood is sufficiently small; (2) the absolute relative function change in penalized likelihood is sufficiently small; (3) the number of iterations exceeds the maximum iteration limit.

   a) Form the adjusted response and adjusted weight from $\mu = g^{-1}(\eta)$. For each observation,
      $$z_i = \eta_i + (y_i - \mu_i)/\mu'_i, \quad w_i = \omega_i \mu'_i^2/\nu_i$$

   b) Search for the best smoothing parameters for the current iteration based on valid adjusted response values and adjusted weight values.

   c) Use the smoothing parameters to construct the linear predictor and the predicted means.

   d) Obtain an estimate for the dispersion parameter if necessary.

In step 2b, you can use different optimization techniques to search for the best smoothing parameters. The Newton-Raphson optimization is efficient in finding the optimum $\lambda$ where the first- and second-order derivatives are available. For more information about computing derivatives of $\nu_g$ and $\nu_u$ with respect to $\lambda$, see Wood (2004). 

Degrees of Freedom

Let $W$ be the adjusted weight matrix at convergence, and let $S_\lambda$ be the roughness penalty matrix with selected smoothing parameters. The degrees of freedom matrix is defined as in Wood (2006):

$$F = (X'WX + S_\lambda)^{-1}X'WX$$

Given the adjusted response $z$, the parameter estimate is shown to be $\hat{\beta} = (X'WX)^{-1}X'Wz$ for the model without penalization, and the parameter estimate is $\hat{\beta} = (X'WX + S_\lambda)^{-1}X'Wz = F\hat{\beta}$ with penalization. $F$ is thus the matrix that projects or maps the unpenalized parameter estimates to the penalized ones.

The model degrees of freedom is given as

$$df = \text{tr}(F)$$

And the degrees of freedom for error is given as

$$df_r = n - 2df + \text{tr}(FF)$$
For the \( j \)th spline term, the degrees of freedom for the component is defined to be the trace of the submatrix of \( F \) that corresponds to parameter estimates \( \beta_j \):

\[
\text{df}_j = \text{tr}(F_j)
\]

The degrees of freedom for the smoothing component test of the \( j \)th term is defined similarly as

\[
\text{df}'_j = 2\text{df}_j - \text{tr}((FF)_j)
\]

---

### Model Inference

Wahba (1983) proposes a Bayesian covariance matrix for parameter estimates \( \beta \) by interpreting a smoothing spline as a posterior mean. Nychka (1988) shows that the derived Bayesian posterior confidence limits work well from frequentist viewpoints. The Bayesian posterior covariance matrix for the parameters is

\[
V_\beta = (X'WX + S_\lambda)^{-1} \sigma^2
\]

The posterior distribution for \( \beta \) is thus

\[
\beta | y \sim N(\hat{\beta}, V_\beta)
\]

For a particular point whose design row is vector \( x \), the prediction is \( x\hat{\beta} \) and the standard error is \( \sqrt{xV_\beta x'} \). The Bayesian posterior confidence limits are thus

\[
(x\hat{\beta} \pm z_{\alpha/2} \sqrt{xV_\beta x'})
\]

where \( z_{\alpha/2} \) is the \( 1 - \alpha/2 \) quantile of the standard normal distribution.

For the \( j \)th spline term, the prediction for the component is formed by \( x_j \hat{\beta} \), where \( x_j \) is a row vector of zeros except for columns that correspond to basis expansions of the \( j \)th spline term. And the standard error for the component is \( \sqrt{x_jV_\beta x_j'} \).

---

### Dispersion Parameter

Some distribution families (Gaussian, gamma, inverse Gaussian, negative binomial, and Tweedie) have a dispersion parameter that you can specify in the \texttt{DISPERSION=} option in the \texttt{MODEL} statement or that you can estimate from the data. The following three suboptions for the \texttt{SCALE=} option in the \texttt{MODEL} statement correspond to three ways to estimate the dispersion parameter:

- **DEViance** estimates the dispersion parameter by the deviance, given the regression parameter estimates:

\[
\hat{\phi} = \frac{\sum_i D_i(y_i, \mu_i)}{n - \text{df}}
\]
MLE estimates the dispersion parameter by maximizing the penalized likelihood, given the regression parameter estimates:

$$\hat{\phi} = \arg\max_{\phi} \ell_p(\hat{\beta}, \phi)$$

The MLE option is the only option that you can use to estimate the dispersion parameter for the negative binomial and Tweedie distributions.

PEARSON estimates the dispersion parameter by Pearson’s statistic, given the regression parameter estimates:

$$\hat{\phi} = \frac{\sum_i \omega_i (y_i - \mu_i)^2 / v_i}{n - df}$$

If the dispersion parameter is estimated, it contributes one additional degree of freedom to the fitted model.

---

Tests for Smoothing Components

The GAMMOD procedure performs a smoothing component test on the null hypothesis $f_j = 0$ for the $j$th component. In contrast to the analysis of deviance that is used in the GAM procedure (which tests existence of nonlinearity for each smoothing component), the smoothing component test used in PROC GAMMOD tests for the existence of a contribution for each smoothing component.

The hypothesis test is based on the Wald statistic. Define $X_j$ as the matrix of all zeros except for columns that correspond to basis expansions of the $j$th spline term. Then the column vector of predictions is $\hat{f}_j = X_j \hat{\beta}$, and the covariance matrix for the predictions is $V_j = X_j V \beta X_j'$. The Wald statistic for testing is

$$T_r = \hat{f}_j' V_j^{-1} \hat{f}_j = \hat{\beta}' X_j' (X_j V \beta X_j')^{-1} X_j \hat{\beta}$$

where $V_j^{-1}$ is the rank-$r$ pseudo-inverse of $V_j$. If $R_j$ is the Cholesky root for $X_j' X_j$ such that $R_j' R_j = X_j' X_j$, then the test statistic can be written as

$$T_r = \hat{\beta}' R_j' (R_j V \beta R_j')^{-1} R_j \hat{\beta}$$

Wood (2012) proposes using the $\text{df}_j$ degrees of freedom for test (which is defined in the section “Degrees of Freedom” on page 329) as the rank $r$. Because spline terms in fitted models often have noninteger degrees of freedom, the GAMMOD procedure uses a rounded value of $\text{df}_j$ as the rank:

$$r = \begin{cases} \lfloor \text{df}_j \rfloor & \text{if } \text{df}_j - \lfloor \text{df}_j \rfloor \leq 0.05 \text{ or } \text{df}_j < 1 \\ \lfloor \text{df}_j \rfloor & \text{otherwise} \end{cases}$$

Let $K$ be a symmetric and nonnegative definite matrix, and let its eigenvalues be sorted as $d_1 > d_2 > \cdots$; then the rank-$r$ pseudo-inverse of $K$ is formed by

$$K^{-1} = U_k \left[ \begin{array}{cccc} d_1^{-1} & & \\ & \ddots & \\ & & d_r^{-1} \end{array} \right] U_k'$$

where $U_k$ are formed by columns of eigenvectors that correspond to the $r$ eigenvalues.
Under the null hypothesis, the Wald statistic $T_r$ approximately follows the chi-square distribution $T_r \sim \chi^2_r$. For an observed test statistic $t_r$, the $p$-value for rejecting the null hypothesis is computed as $P(\chi^2_r > t_r)$ if the dispersion parameter is constant, or $P(F_{r,dfr} > t_r)$ with $dfr$ error degrees of freedom if the dispersion parameter is estimated.

Be cautious when you interpret the results of the smoothing component test because $p$-values are computed by approximation and the test does not take the smoothing parameter selection process into account.

**Multithreading**

The GAMMOD procedure allocates data to different threads and calculates the likelihood function, gradient, and Hessian by accumulating the values from all threads. For more information about how PROC GAMMOD uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

**Optimization Algorithms**

Several optimization techniques are available in PROC GAMMOD. You can choose a particular optimizer by using the TECHNIQUE= option in the PROC GAMMOD statement. Table 5.14 summarizes the optimization techniques available in PROC GAMMOD.

<table>
<thead>
<tr>
<th>TECHNIQUE=</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>Trust region method</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>Newton-Raphson method with line search</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>Newton-Raphson method with ridging</td>
</tr>
<tr>
<td>QUANEW</td>
<td>Quasi-Newton methods</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>Double-dogleg method</td>
</tr>
<tr>
<td>CONGRA</td>
<td>Conjugate gradient methods</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>Nelder-Mead simplex method</td>
</tr>
</tbody>
</table>

There is no algorithm for optimizing general nonlinear functions that always finds the global optimum for a general nonlinear optimization problem in a reasonable amount of time. Because no single optimization technique is always superior to others, PROC GAMMOD provides a variety of optimization techniques that work well in various circumstances. However, you can devise problems for which none of the techniques in PROC GAMMOD can find the correct solution. Moreover, nonlinear optimization can be computationally expensive in terms of time and memory, so you must be careful when matching an algorithm to a problem. The section “Choosing an Optimization Algorithm” on page 80 in Chapter 2, “Shared Concepts,” is helpful in choosing a suitable optimization algorithm.

**Displayed Output**

The following sections describe the output that the GAMMOD procedure produces by default. The output is organized into various tables, which are discussed in the order of their appearance.
Model Information

The “Model Information” table displays basic information about the model, such as the response variable, frequency variable, link function, and model category that the GAMMOD procedure determines based on your input and options. The “Model Information” table also displays the distribution of the data that PROC GAMMOD assumes. For information about the supported response distributions, see the section “DISTRIBUTION=keyword” on page 318.

Number of Observations

The “Number of Observations” table displays the number of observations that are read from the input data table and the number of observations that are used in the analysis. If a FREQ statement is present, the sum of the frequencies read and used is displayed. If the events/trials syntax is used, the number of events and trials is also displayed.

Response Profile

The “Response Profile” table displays the ordered values from which the GAMMOD procedure determines the probability that is modeled as an event in binary models. For each response category level, the frequency that is used in the analysis is reported. You can affect the ordering of the response values by specifying response-options in the MODEL statement. For binary models, the note that follows the “Response Profile” table indicates which outcome is modeled as the event in binary models and which value serves as the reference category.

The “Response Profile” table is not produced for binomial (events/trials) data. You can find information about the number of events and trials in the “Number of Observations” table.

Class Level Information

The “Class Level Information” table lists the levels of every variable that is specified in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by specifying the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by specifying the NOCLPRINT= option in the PROC GAMMOD statement.

If the classification variables use reference parameterization, the “Class Level Information” table also displays the reference value for each variable.

Specifications for Spline(spline-variables)

The “Specifications for Spline(spline-variables)” table displays basic information (such as the number of variables, specified degrees of freedom, search range for the smoothing parameter, and so on) about how to construct a spline term that the GAMMOD procedure uses to construct basis expansions and search for the smoothing parameter. PROC GAMMOD generates the “Specifications for Spline(spline-variables)” table only when you specify the DETAILS option for a spline term.

Optimization Iteration History

For each iteration of the optimization, the “Iteration History” table displays the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element.
The objective function that PROC GAMMOD uses in the optimization is normalized by default to enable comparisons across data tables that have different sampling intensity.

If you specify the ITDETAILS option in the PROC GAMMOD statement, information about the parameter estimates and gradients in the course of the optimization is added to the “Iteration History” table.

For a parametric generalized linear model or for a generalized additive model that has fixed smoothing parameters, the “Iteration History” table displays information about regression parameter estimates and gradients. For a generalized additive model that has unknown smoothing parameters, the “Iteration History” table displays information about smoothing parameter estimates and gradients. If the performance iteration method is used, a column of performance iteration steps is added to the table.

**Convergence Status**

The convergence status table is a small ODS table that follows the “Iteration History” table in the default output. In the listing, this table appears as a message that indicates whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message indicates the reason for the failure. If you save the convergence status table to an output data table, a numeric Status variable is added that enables you to programmatically assess convergence. The values of the Status variable encode the following:

0  Convergence was achieved, or an optimization was not performed because TECHNIQUE=NONE was specified.
1  The objective function could not be improved.
2  Convergence was not achieved because of a user interrupt or because a limit (such as the maximum number of iterations or the maximum number of function evaluations) was reached. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC GAMMOD statement.
3  Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

**Fit Statistics**

The “Fit Statistics” table displays a variety of likelihood-based measures of fit in addition to the model roughness measurement. All information criteria are presented in “smaller is better” form.

The calculation of the information criteria uses the following formulas, where df denotes the model degrees of freedom, \( f \) denotes the number of frequencies used, and \( \ell \) is the log likelihood that is evaluated at the converged estimates:

\[
\text{AIC} = -2\ell + 2df \\
\text{AICC} = \begin{cases} 
-2\ell + 2df f/(f - df - 1) & \text{when } f > df + 2 \\
-2\ell + 2df(df + 2) & \text{otherwise}
\end{cases} \\
\text{BIC} = -2\ell + df \log(f)
\]

If no FREQ statement is specified, then \( f \) equals \( n \), the number of observations that are used.
Parameter Estimates

The “Parameter Estimates” table displays the regression parameter estimates, their estimated (asymptotic) standard errors, chi-square statistics, and p-values for the hypothesis that the parameter is 0.

Estimates for Smoothing Components

The “Estimates for Smoothing Components” table displays a summary of the fitted spline terms, including effective degrees of freedom, smoothing parameters, roughness penalty values, number of parameters, rank of penalty matrix, and number of knots.

Tests for Smoothing Components

The “Tests for Smoothing Components” table displays effective degrees of freedom, effective degrees of freedom for test, $F/\chi^2$ statistics, and p-values for rejecting the hypothesis that the smoothing component has zero contribution.

Timing

The “Timing” table displays the amount of time (in seconds) that PROC GAMMOD required to perform different tasks in the analysis.

Output CAS Tables

When you specify the OUTPUT statement, the GAMMOD procedure produces the output data table along with a table that lists the CAS library, the data table name, and the number of rows and columns in that data table.

---

**ODS Table Names**

Each table that the GAMMOD procedure creates has a name that is associated with it, and you must use this name to refer to the table when you use ODS statements. These names are listed in Table 5.15.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
<td></td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Status of optimization at conclusion of optimization</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default output</td>
<td>PROC GAM-</td>
</tr>
<tr>
<td>LikelihoodHist</td>
<td>Iteration history for maximum likelihood estimation or penalized likelihood estimation</td>
<td>PROC GAM- MOD</td>
<td>ITDETAILS</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Information about the modeling environment</td>
<td>Default output</td>
<td></td>
</tr>
</tbody>
</table>
Table 5.15  

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>NObs</td>
<td>Number of observations read and used, and number of events and trials, if applicable</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>OutputCASTables</td>
<td>Library and name of the output data table, and number of rows and columns in the table</td>
<td>OUTPUT</td>
<td>OUT=</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates that are associated with effects in MODEL statements</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>ResponseProfile</td>
<td>Response categories and the category that is modeled in models for binary and multinomial data</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>SmoothingEstimates</td>
<td>Information for spline terms after model fitting</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>SmoothingHist</td>
<td>Iteration history for smoothing parameter estimation</td>
<td>PROC GAMMOD</td>
<td>ITDETAILS</td>
</tr>
<tr>
<td>SmoothingTests</td>
<td>Smoothing components test result</td>
<td>Default output</td>
<td></td>
</tr>
<tr>
<td>SplineDetails</td>
<td>Information about spline construction and smoothing parameter search</td>
<td>MODEL</td>
<td>SPLINE(variables / DETAILS)</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times for tasks performed by the procedure</td>
<td>Default output</td>
<td></td>
</tr>
</tbody>
</table>

ODS Graphics

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in SAS/STAT User’s Guide.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.

When ODS Graphics is enabled, the GAMMOD procedure by default produces plots of the partial predictions for each spline term in the model. Use the PLOTS option in the PROC GAMMOD statement to control aspects of these plots.

PROC GAMMOD assigns a name to each graph that it creates by using ODS. You can use these names to refer to the graphs when using ODS. The names are listed in Table 5.16.
By default, prediction plots for each spline component are displayed in panels that contain at most six plots. If you specify more than six smoothing components, multiple panels are used. Use the PLOTS(UNPACK) option in the PROC GAMMOD statement to display these plots individually.

### Examples: GAMMOD Procedure

#### Example 5.1: Scatter Plot Smoothing

This example shows how you can use PROC GAMMOD to perform scatter plot smoothing.

The example uses the LIDAR data set (Ruppert, Wand, and Carroll 2003). This data set is used in many books and journals to illustrate different smoothing techniques. Scientists use a technique known as LIDAR (light detection and ranging), which uses laser reflections to detect chemical compounds in the atmosphere. The following DATA step creates the data table `Lidar`. This DATA step assumes that your CAS engine libref is named `mycas`, but you can substitute any appropriately defined CAS engine libref.

```sas
   title 'Scatter Plot Smoothing';
   data mycas.Lidar;
      input Range LogRatio @@;
datalines;
   390  -0.05035573  391  -0.06009706  393  -0.04190091  394  -0.0509847
   396  -0.05991345  397  -0.02842392  399  -0.05958421  400  -0.03988881
   402  -0.02939582  403  -0.03949445  405  -0.04764749  406  -0.06038
   408  -0.03123034  409  -0.03816584  411  -0.07562269  412  -0.05001751
   414  -0.0457295  415  -0.07766966  417  -0.02460641  418  -0.07133184
   ... more lines ...
   702  -0.4716702  703  -0.7801088  705  -0.6668431  706  -0.5783479
   708  -0.7874522  709  -0.6156956  711  -0.8967602  712  -0.7077379
   714  -0.672567  715  -0.6218413  717  -0.8657611  718  -0.557754
   720  -0.8026684 ;
```

In this data table, `Range` records the distance that light travels before it is reflected back to the source. `LogRatio` is the logarithm of the ratio of light that is received from two laser sources. The objective is to use scatter plot smoothing to discover the nonlinear pattern in the data. SAS provides different methods (for

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS= Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SmoothingComponentPanel</td>
<td>Panel of multiple prediction curves</td>
<td>Default</td>
</tr>
<tr>
<td>SmoothingComponentPlot</td>
<td>Unpacked prediction curves</td>
<td>PLOTS(UNPACK)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PLOTS=COMPONENTS(UNPACK)</td>
</tr>
</tbody>
</table>

---

Examples: GAMMOD Procedure

#### Table 5.16 Graphs Produced by PROC GAMMOD

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS= Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SmoothingComponentPanel</td>
<td>Panel of multiple prediction curves</td>
<td>Default</td>
</tr>
<tr>
<td>SmoothingComponentPlot</td>
<td>Unpacked prediction curves</td>
<td>PLOTS(UNPACK)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>PLOTS=COMPONENTS(UNPACK)</td>
</tr>
</tbody>
</table>

---

Examples: GAMMOD Procedure

#### Example 5.1: Scatter Plot Smoothing

This example shows how you can use PROC GAMMOD to perform scatter plot smoothing.

The example uses the LIDAR data set (Ruppert, Wand, and Carroll 2003). This data set is used in many books and journals to illustrate different smoothing techniques. Scientists use a technique known as LIDAR (light detection and ranging), which uses laser reflections to detect chemical compounds in the atmosphere. The following DATA step creates the data table `Lidar`. This DATA step assumes that your CAS engine libref is named `mycas`, but you can substitute any appropriately defined CAS engine libref.

```sas
   title 'Scatter Plot Smoothing';
   data mycas.Lidar;
      input Range LogRatio @@;
datalines;
   390  -0.05035573  391  -0.06009706  393  -0.04190091  394  -0.0509847
   396  -0.05991345  397  -0.02842392  399  -0.05958421  400  -0.03988881
   402  -0.02939582  403  -0.03949445  405  -0.04764749  406  -0.06038
   408  -0.03123034  409  -0.03816584  411  -0.07562269  412  -0.05001751
   414  -0.0457295  415  -0.07766966  417  -0.02460641  418  -0.07133184
   ... more lines ...
   702  -0.4716702  703  -0.7801088  705  -0.6668431  706  -0.5783479
   708  -0.7874522  709  -0.6156956  711  -0.8967602  712  -0.7077379
   714  -0.672567  715  -0.6218413  717  -0.8657611  718  -0.557754
   720  -0.8026684 ;
```

In this data table, `Range` records the distance that light travels before it is reflected back to the source. `LogRatio` is the logarithm of the ratio of light that is received from two laser sources. The objective is to use scatter plot smoothing to discover the nonlinear pattern in the data. SAS provides different methods (for
example, local regression) for scatter plot smoothing. You can perform scatter plot smoothing by using the SGPLOT procedure, as shown in the following statements:

```sas
proc sgplot data=mycas.Lidar;
   scatter x=Range y=LogRatio;
   loess x=Range y=LogRatio / nomarkers;
   pbspline x=Range y=LogRatio / nomarkers;
run;
```

Output 5.1.1 shows the scatter plot of Range and LogRatio and the smoothing curves that are fitted by the local regression and penalized B-splines smoothing techniques.

**Output 5.1.1 Scatter Plot Smoothing**

![Scatter Plot Smoothing](image)

Both scatter plot smoothing techniques show a significant nonlinear structure between Range and LogRatio that cannot be easily modeled by ordinary polynomials. You can also use the GAMMOD procedure to perform scatter plot smoothing on these data, as in the following statements:

```sas
proc gammod data=mycas.Lidar seed=12345;
   model LogRatio = spline(Range/details);
   output out=mycas.LidarOut pred=p;
run;
```
The “Specifications for Spline(Range)” table in Output 5.1.2 displays the specifications for constructing the spline term for Range. The maximum degrees of freedom is 10, which sets the upper limit of effective degrees of freedom for the spline term to be 9 after one degree of freedom is absorbed in the intercept. The order of the derivative in the penalty is 2, which means that the unpenalized portion of the spline term involves polynomials with degrees up to 2.

Output 5.1.2  Spline Specification

### Scatter Plot Smoothing

#### The GAMMOD Procedure

<table>
<thead>
<tr>
<th>Specifications for Spline(Range)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Variables</td>
</tr>
<tr>
<td>Rank of Penalty Approximation</td>
</tr>
<tr>
<td>Order of Derivative in the Penalty</td>
</tr>
<tr>
<td>Maximum Number of Knots</td>
</tr>
</tbody>
</table>

The “Fit Statistics” table in Output 5.1.3 shows the summary statistics for the fitted model.

Output 5.1.3  Fit Statistics

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
</tr>
<tr>
<td>Roughness Penalty</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
</tr>
<tr>
<td>GCV (smaller is better)</td>
</tr>
</tbody>
</table>

The “Estimates for Smoothing Components” table in Output 5.1.4 shows that the effective degrees of freedom for the spline term of Range is approximately 8 after the GCV criterion is optimized with respect to the smoothing parameter. The roughness penalty is small, suggesting that there is an important contribution from the penalized part of thin-plate regression splines beyond nonpenalized polynomials.

Output 5.1.4  Estimates for Smoothing Components

<table>
<thead>
<tr>
<th>Estimates for Smoothing Components</th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
</tr>
<tr>
<td>-----------</td>
</tr>
<tr>
<td>Spline(Range)</td>
</tr>
</tbody>
</table>

Because the optimal model is obtained by searching in a functional space that is constrained by the maximum degrees of freedom for a spline term, you might wonder whether PROC GAMMOD produces a much different model if you increase the value. The following statements fit another model in which the maximum degrees of freedom is increased to 20:
Output 5.1.5 displays fit summary statistics for the second model. The model fit statistics from the second model are very close to the ones from the first model, indicating that the second model is not much different from the first model.

**Output 5.1.5  Fit Statistics**

**Scatter Plot Smoothing**

The GAMMOD Procedure

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
<td>250.96488</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>0.05315</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
<td>10.06143</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
<td>209.02182</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>-481.86006</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>-480.79981</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>-447.66969</td>
</tr>
<tr>
<td>GCV (smaller is better)</td>
<td>0.00657</td>
</tr>
</tbody>
</table>

Output 5.1.6 shows that the effective degrees of freedom for the spline term of Range is slightly larger than 8, which is understandable because increasing the maximum degrees of freedom expands the functional space for model searching. Functions in the expanded space can provide a better fit to the data, but they are also penalized more because the roughness penalty value for the second model is much larger than the one for the first model. This suggests that functions in the expanded space do not help much, given the nonlinear relationship between Range and LogRatio.

**Output 5.1.6  Estimates for Smoothing Components**

<table>
<thead>
<tr>
<th>Estimates for Smoothing Components</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
<td></td>
</tr>
<tr>
<td>Spline(Range)</td>
<td></td>
</tr>
<tr>
<td>Effective DF</td>
<td>8.06143</td>
</tr>
<tr>
<td>Smoothing Parameter</td>
<td>23032.9</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>0.0532</td>
</tr>
<tr>
<td>Number of Parameters</td>
<td>19</td>
</tr>
<tr>
<td>Rank of Penalty Matrix</td>
<td>20</td>
</tr>
<tr>
<td>Number of Knots</td>
<td>221</td>
</tr>
</tbody>
</table>

The two fitted models are both based on thin-plate regression splines, in which polynomials that have degrees higher than 2 are penalized. You might wonder whether allowing higher-order polynomials yields a much different model. The following statements fit a third spline model by penalizing polynomials that have degrees higher than 3:

```plaintext
proc gammod data=mycas.Lidar seed=12345;
    model LogRatio = spline(Range/maxdf=20);
    output out=mycas.LidarOut2 pred=p2;
run;
```
The fit summary statistics shown in Output 5.1.7 are close to the ones from the previous two models, albeit slightly smaller.

### Output 5.1.7  Fit Statistics

**Scatter Plot Smoothing**

**The GAMMOD Procedure**

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
<td>249.79779</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>9.440383E-9</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
<td>10.00000</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
<td>211.00000</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>-479.59559</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>-478.54379</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>-445.61397</td>
</tr>
<tr>
<td>GCV (smaller is better)</td>
<td>0.00664</td>
</tr>
</tbody>
</table>

As shown in Output 5.1.8, the effective degrees of freedom for the spline term where polynomials with degrees less than 4 are allowed without penalization is 8. The roughness penalty is quite small compared to the previous two fits. This also suggests that there are important contributions from the penalized part of the thin-plate regression splines even after the nonpenalized polynomials are raised to order 3.

### Output 5.1.8  Estimates for Smoothing Components

<table>
<thead>
<tr>
<th>Component</th>
<th>Effective DF</th>
<th>Smoothing Parameter</th>
<th>Roughness Penalty</th>
<th>Number of Parameters</th>
<th>Rank of Penalty Matrix</th>
<th>Number of Knots</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spline(Range)</td>
<td>8.00000</td>
<td>1.0000</td>
<td>9.44E-9</td>
<td>9</td>
<td>10</td>
<td>221</td>
</tr>
</tbody>
</table>

The following statements use the DATA step to merge the predictions from the three scatter plot smoothing fits by PROC GAMMOD and use the SGPLOT procedure to visualize them:

```plaintext
data LidarPred;
   merge mycas.Lidar mycas.LidarOut mycas.LidarOut2 mycas.LidarOut3;
run;
proc sort data=LidarPred; by Range;run;
proc sgplot data=LidarPred;
   scatter x=Range y=LogRatio / markerattrs=GraphData1(size=7);
   series x=Range y=p / lineattrs =GraphData2(thickness=2)
      legendlabel="Spline 1";
   series x=Range y=p2 / lineattrs =GraphData3(thickness=2)
      legendlabel="Spline 2";
   series x=Range y=p3 / lineattrs =GraphData4(thickness=2)
      legendlabel="Spline 3";
run;
```

Output 5.1.9 displays the scatter plot smoothing fits by PROC GAMMOD under three different spline specifications.
Example 5.2: Nonparametric Logistic Regression

This example shows how you can use PROC GAMMOD to build a nonparametric logistic regression model for a data set that contains a binary response and then use that model to classify observations.

The example uses the Pima Indians Diabetes data set, which can be obtained from the UCI Machine Learning Repository (Lichman 2013). It is extracted from a larger database that was originally owned by the National Institute of Diabetes and Digestive and Kidney Diseases. Data are for female patients who are at least 21 years old, are of Akimel O’otham (Pima Indian) heritage, and live near Phoenix, Arizona. The objective of this study is to investigate the relationship between a diabetes diagnosis and variables that represent physiological measurements and medical attributes. Some missing or invalid observations are removed from the analysis. The reduced data set contains 532 records. The following DATA step creates the data set DiabetesStudy:

```sas
title 'Diabetes Study';
data DiabetesStudy;
  input NPreg Glucose Pressure Triceps BMI Pedigree Age Diabetes Test@@;
datalines;
  6 148 72 35 33.6 0.627 50 1 1 1 85 66 29 26.6 0.351 31 0 1
  1 89 66 23 28.1 0.167 21 0 0 3 78 50 32 31 0.248 26 1 0
```
The data set contains nine variables, including the binary response variable Diabetes. Table 5.17 describes the variables.

Table 5.17  Variables in the DiabetesStudy Data Set

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NPreg</td>
<td>Number of pregnancies</td>
</tr>
<tr>
<td>Glucose</td>
<td>Two-hour plasma glucose concentration in an oral glucose tolerance test</td>
</tr>
<tr>
<td>Pressure</td>
<td>Diastolic blood pressure (mm Hg)</td>
</tr>
<tr>
<td>Triceps</td>
<td>Triceps skin fold thickness (mm)</td>
</tr>
<tr>
<td>BMI</td>
<td>Body mass index (weight in kg/(height in m)^2)</td>
</tr>
<tr>
<td>Pedigree</td>
<td>Diabetes pedigree function</td>
</tr>
<tr>
<td>Age</td>
<td>Age (years)</td>
</tr>
<tr>
<td>Diabetes</td>
<td>0 if test negative for diabetes, 1 if test positive</td>
</tr>
<tr>
<td>Test</td>
<td>0 for training role, 1 for test</td>
</tr>
</tbody>
</table>

The Test variable splits the data set into training and test subsets. The training observations (whose Test value is 0) hold approximately 59.4% of the data. To build a model that is based on the training data and evaluate its performance by predicting the test data, you use the following statements to create a new variable, Result, whose value is the same as that of the Diabetes variable for a training observation and is missing for a test observation:

```plaintext
data mycas.DiabetesStudy;
  set DiabetesStudy;
  Result = Diabetes;
  if Test=1 then Result=.;
run;
```

A typical starting point of your analysis for modeling the binary response might be a parametric logistic regression model. But it is restricted in the sense that all variables affect the response in strictly linear fashion. If you are uncertain that a variable is an important factor and its contribution is linear in predicting the response, you might want to choose a nonparametric logistic regression model to fit the data. You can use PROC GAMMOD to form a nonparametric model by including the spline transformation of each explanatory variable, as shown in the following statements:

```plaintext
proc gammod data=mycas.DiabetesStudy seed=12345;
  model Result(event='1') = spline(NPreg) spline(Glucose)
             spline(Pressure) spline(Triceps)
             spline(BMI) spline(Pedigree)
             spline(Age) / dist=binary;
run;
```
Because the response variable Result is binary, the DIST=BINARY option in the MODEL statement specifies a binary distribution for the response variable. By default, PROC GAMMOD models the probability of the first ordered response category, which is a negative diabetes testing result in this case. The EVENT= option specifically requests that PROC GAMMOD model the probability of positive diabetes testing results. The "Response Profile" table in Output 5.2.1 shows the frequencies of the response in both categories.

**Output 5.2.1** Response Profile

**Diabetes Study**

**The GAMMOD Procedure**

<table>
<thead>
<tr>
<th>Response Profile</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ordered Value</td>
<td>Result Frequency</td>
</tr>
<tr>
<td>1 0</td>
<td>208</td>
</tr>
<tr>
<td>2 1</td>
<td>122</td>
</tr>
</tbody>
</table>

Probability modeled is Result = 1.

Output 5.2.2 lists the summary statistics from the nonparametric logistic regression model, which include spline transformations of all variables.

**Output 5.2.2** Fit Statistics

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
<td>-138.57851</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>1.208687E-8</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
<td>16.00000</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
<td>314.37615</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>309.15702</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>310.89504</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>369.94250</td>
</tr>
<tr>
<td>UBRE (smaller is better)</td>
<td>0.02357</td>
</tr>
</tbody>
</table>

The “Tests for Smoothing Components” table in Output 5.2.3 shows approximate tests results. Although some spline terms are significant, others are not. The null testing hypothesis is whether the total contribution from a variable is 0. So you can form a reduced model by removing those nonsignificant spline terms from the model. In this case, spline transformations for NPreg, Pressure, BMI, and Triceps are dropped from the model because their p-values are larger than the 0.1 nominal level.
Example 5.2: Nonparametric Logistic Regression

Output 5.2.3 Tests for Smoothing Components

<table>
<thead>
<tr>
<th>Component</th>
<th>Effective DF</th>
<th>Effective DF for Test</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spline(NPreg)</td>
<td>1.00000</td>
<td>1</td>
<td>0.0186</td>
<td>0.8916</td>
</tr>
<tr>
<td>Spline(Glucose)</td>
<td>1.00000</td>
<td>1</td>
<td>44.5949</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Spline(Pedigree)</td>
<td>1</td>
<td>1</td>
<td>2.8310</td>
<td>0.0925</td>
</tr>
<tr>
<td>Spline(Triceps)</td>
<td>1.00000</td>
<td>1</td>
<td>1.2128</td>
<td>0.2708</td>
</tr>
<tr>
<td>Spline(BMI)</td>
<td>1.00000</td>
<td>1</td>
<td>5.8112</td>
<td>0.0159</td>
</tr>
<tr>
<td>Spline(Pedigree)</td>
<td>1.00000</td>
<td>1</td>
<td>6.1108</td>
<td>0.0134</td>
</tr>
<tr>
<td>Spline(Age)</td>
<td>9.00000</td>
<td>9</td>
<td>19.0721</td>
<td>0.0246</td>
</tr>
</tbody>
</table>

The following statements use PROC GAMMOD to fit a reduced nonparametric logistic regression model. The OUTPUT statement requests predicted probabilities for both training and test data. The COPYVARS option in the OUTPUT statement requests that the Diabetes and Test variables also be included in the output data table so that you can use them to identify test observations and compute misclassification errors.

ods graphics on;
proc gammod data=mycas.DiabetesStudy plots seed=12345;
  model Result(event='1') = spline(Glucose) spline(Pedigree) spline(Age) / dist=binary;
  output out=mycas.DiabetesStudyOut copyvars=(Diabetes Test);
run;

Output 5.2.4 shows the summary statistics from the reduced nonparametric logistic regression model. The values of the information criteria are better than those of the parametric logistic regression model.

Output 5.2.4 Fit Statistics

Diabetes Study

The GAMMOD Procedure

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
<td>-149.85766</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>2.85613</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
<td>8.05241</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
<td>320.61183</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>312.96402</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>313.41826</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>343.55588</td>
</tr>
<tr>
<td>UBRE (smaller is better)</td>
<td>-0.00230</td>
</tr>
</tbody>
</table>

In the “Estimates for Smoothing Components” table in Output 5.2.5, PROC GAMMOD reports that the effective degrees of freedom value for spline transformations of Glucose is quite close to 1. This suggests a strictly linear form for Glucose. For Pedigree, the degrees of freedom value demonstrates a moderate amount of nonlinearity. For Age, the degrees of freedom value is much larger than 1. The measure suggests a nonlinear pattern in the dependency of the response on Age.
Chapter 5: The GAMMOD Procedure

Output 5.2.5 Estimates for Smoothing Components

<table>
<thead>
<tr>
<th>Component</th>
<th>Effective DF</th>
<th>Smoothing Parameter</th>
<th>Roughness Penalty</th>
<th>Number of Parameters</th>
<th>Rank of Penalty Matrix</th>
<th>Number of Knots</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spline(Glucose)</td>
<td>1.00000</td>
<td>9.636E17</td>
<td>2.66E-14</td>
<td>9</td>
<td>10</td>
<td>110</td>
</tr>
<tr>
<td>Spline(Pedigree)</td>
<td>1.51071</td>
<td>0.4383</td>
<td>0.5086</td>
<td>9</td>
<td>10</td>
<td>283</td>
</tr>
<tr>
<td>Spline(Age)</td>
<td>4.54170</td>
<td>69.8812</td>
<td>2.3475</td>
<td>9</td>
<td>10</td>
<td>42</td>
</tr>
</tbody>
</table>

The “Tests for Smoothing Components” table in Output 5.2.6 shows that all spline transformations are significant in predicting diabetes testing results.

Output 5.2.6 Tests for Smoothing Components

<table>
<thead>
<tr>
<th>Component</th>
<th>Effective DF</th>
<th>Effective DF for Test</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spline(Glucose)</td>
<td>1.00000</td>
<td>1</td>
<td>53.0363</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Spline(Pedigree)</td>
<td>1.51071</td>
<td>2</td>
<td>9.9354</td>
<td>0.0070</td>
</tr>
<tr>
<td>Spline(Age)</td>
<td>4.54170</td>
<td>6</td>
<td>23.0661</td>
<td>0.0008</td>
</tr>
</tbody>
</table>

The smoothing component panel (which is produced by the PLOTS option and is shown in Output 5.2.7) visualizes the spline transformations for the four variables in addition to 95% Bayesian curvewise confidence bands. For Glucose, the spline transformation is almost a straight line. For Pedigree, the spline transformation shows a slightly nonlinear trend. For Age, the dependency is obviously nonlinear.
The following statements compute the misclassification error on the test data from the reduced nonparametric logistic regression model that PROC GAMMOD produces:

```latex
\begin{verbatim}
data test;
  set mycas.DiabetesStudyOut(where=(Test=1));
  if ((Pred>0.5 & Diabetes=1) | (Pred<0.5 & Diabetes=0))
    then Error=0;
  else Error=1;
run;

proc freq data=test;
  tables Diabetes*Error/nocol norow;
run;
\end{verbatim}
```

Output 5.2.8 shows the misclassification errors for observations in the test set and observations of each response category.
Example 5.3: Nonparametric Tweedie Regression

This example illustrates how you can use the GAMMOD procedure to fit a nonparametric regression model with spline effects for a response variable that has a Tweedie distribution.

You can view this model as a generalized linear model because the Tweedie distribution belongs to the exponential family. The Tweedie distribution is particularly useful for modeling response variables that are continuous for positive values and take the value 0 with a positive probability. For example, in the insurance industry the Tweedie distribution is often assumed for claims, which are positive for customers who have filed claims and are 0 for other customers. You can use the Tweedie distribution to model such response variables without special transformations.

The GENSELECT procedure can fit Tweedie regression models that incorporate linear effects for the covariates. However, as demonstrated in this example, the assumption of linearity can be too restrictive, and you might want to use the GAMMOD procedure to explore the nonlinear dependency structures in the data.

The following DATA step simulates a response variable $Y$ by using a Tweedie distribution and four continuous predictors. Each continuous predictor is sampled independently from the uniform distribution $U(0,1)$. The linear predictor $\eta$ for the true model is formed by applying additive nonlinear transformations to $x_1$, $x_2$, and $x_3$:

$$
\eta = \frac{2\sin(\pi x_1) + 0.8\exp(2x_2) + 0.2x_3^{11}(10(1-x_3))^6 + 10(10x_3)^3(1-x_3)^{10}}{20}
$$

The predictor $x_4$ is a nuisance parameter that does not enter the model. The parameters for the Tweedie distribution are $\phi = 0.4$ and $p = 1.5$, and the link function is $\log \mu = \eta$, where the expected value is $E(Y) = \mu$ and the variance is $\text{Var}(Y) = \phi \mu^p$. The power parameter $p$ controls the variance of the distribution. When $p$ is between 1 and 2, as in this example, a Tweedie random variable can be generated from a compound Poisson distribution (Smyth 1996).

```plaintext
text 'Nonparametric Tweedie Model';
%let phi=0.4;
%let power=1.5;

data mycas.one;
  do i=1 to 1000;
```
Example 5.3: Nonparametric Tweedie Regression

/* Sample the predictors */
x1=ranuni(1);
x2=ranuni(1);
x3=ranuni(1);
x4=ranuni(1);

/* Apply nonlinear transformations to predictors */
f1=2*sin(3.14159265*x1);
f2=exp(2*x2)*0.8;
f3=0.2*x3**11*(10*(1-x3))**6+10*(10*x3)**3*(1-x3)**10;
xb=f1+f2+f3;
xb=xb/20;
mu=exp(xb);

/* Compute parameters of compound Poisson distribution */
lambda=mu**(2-&power)/(&phi*(2-&power));
alpha=(2-&power)/(&power-1);
gamma=&phi*(&power-1)*(mu**(&power-1));

/* Simulate the response */
rpoi=ranpoi(1,lambda);
if rpoi=0 then y=0;
else do;
y=0;
do j=1 to rpoi;
y=y+rangam(1,alpha);
end;
y=y*gamma;
end;
output;
end;
run;

You can use PROC GENSELECT to fit a parametric model for $Y$ by using the following statements:

    proc genselect data=mycas.one;
      model y=x1 x2 x3 x4/dist=tweedie;
    run;

Equivalently, you can also use PROC GAMMOD to fit a parametric linear model by using the PARAM option in the MODEL statement, as shown in the following statements.

    proc gammod data=mycas.one seed=1234;
      model y=param(x1 x2 x3 x4)/dist=tweedie;
    run;

The “Fit Statistics” table in Output 5.3.1 shows the summary statistics for the fitted parametric Tweedie model.
Output 5.3.1 Fit Statistics

Nonparametric Tweedie Model

The GAMMOD Procedure

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
</tr>
<tr>
<td>Roughness Penalty</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
</tr>
</tbody>
</table>

The “Parameter Estimates” table in Output 5.3.2 shows the estimates for regression parameters in addition to dispersion and power parameters (\(\phi\) and \(\rho\)).

Output 5.3.2 Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>0.441832</td>
<td>0.067334</td>
<td>43.0565</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>x1</td>
<td>1</td>
<td>-0.043725</td>
<td>0.064965</td>
<td>0.4530</td>
<td>0.5009</td>
</tr>
<tr>
<td>x2</td>
<td>1</td>
<td>0.202242</td>
<td>0.064216</td>
<td>9.9188</td>
<td>0.0016</td>
</tr>
<tr>
<td>x3</td>
<td>1</td>
<td>-0.253920</td>
<td>0.066625</td>
<td>14.5250</td>
<td>0.0001</td>
</tr>
<tr>
<td>x4</td>
<td>1</td>
<td>-0.061098</td>
<td>0.066040</td>
<td>0.8559</td>
<td>0.3549</td>
</tr>
<tr>
<td>Dispersion</td>
<td>1</td>
<td>0.416001</td>
<td>0.016987</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Power</td>
<td>1</td>
<td>1.524581</td>
<td>0.048675</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

If you are uncertain about the relationship between the linked mean for the fitted Tweedie model and the covariates, you can add spline terms to the model to explore possible nonlinear dependence. The following statements fit a nonparametric Tweedie model and produce a plot of fitted smoothing components.

```
proc gammod data=mycas.one seed=1234 plots;
model y=spline(x1) spline(x2) spline(x3) spline(x4)/dist=tweedie;
run;
```

The “Fit Statistics” table in Output 5.3.3 shows the summary statistics for the fitted nonparametric Tweedie model. Compared to the parametric model, the nonparametric model has more effective degrees of freedom, but smaller AIC and AICC values. The penalized likelihood value is larger for the nonparametric model. These statistics indicate that the nonparametric model provides a better fit.
Example 5.3: Nonparametric Tweedie Regression

Output 5.3.3  Fit Statistics
Nonparametric  Tweedie  Model

The GAMMOD Procedure

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Penalized Log Likelihood</td>
<td>-1157.17502</td>
</tr>
<tr>
<td>Roughness Penalty</td>
<td>2.62230</td>
</tr>
<tr>
<td>Effective Degrees of Freedom</td>
<td>14.1192</td>
</tr>
<tr>
<td>Effective Degrees of Freedom for Error</td>
<td>983.62098</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>2339.96615</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>2340.39965</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>2409.25974</td>
</tr>
<tr>
<td>GCV (smaller is better)</td>
<td>0.39845</td>
</tr>
</tbody>
</table>

The “Regression Parameter Estimates” table in Output 5.3.4 lists the estimate for the intercept, in addition to the estimates for the dispersion and power parameters for the Tweedie model. Both variance parameters are close to the true values.

Output 5.3.4  Regression Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter Estimates</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameter</td>
<td>DF</td>
</tr>
<tr>
<td>Intercept</td>
<td>1</td>
</tr>
<tr>
<td>Dispersion</td>
<td>1</td>
</tr>
<tr>
<td>Power</td>
<td>1</td>
</tr>
</tbody>
</table>

The “Estimates for Smoothing Components” table in Output 5.3.5 shows the fitted information for the spline terms in the model. The degrees of freedom value and the roughness penalty value suggest some moderate nonlinear relationship between the linked mean and the three covariates \(x_1\), \(x_2\), and \(x_3\). The spline term for the nuisance parameter \(x_4\) has a linear form.

Output 5.3.5  Estimates for Smoothing Components

<table>
<thead>
<tr>
<th>Estimates for Smoothing Components</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Component</td>
<td>Effective DF</td>
</tr>
<tr>
<td>Spline(x1)</td>
<td>2.10969</td>
</tr>
<tr>
<td>Spline(x2)</td>
<td>2.38340</td>
</tr>
<tr>
<td>Spline(x3)</td>
<td>5.62068</td>
</tr>
<tr>
<td>Spline(x4)</td>
<td>1.00002</td>
</tr>
</tbody>
</table>

The “Tests for Smoothing Components” table in Output 5.3.6 shows the approximate Wald test for the four spline terms. The spline term for the nuisance predictor \(x_4\) is not significant.
Output 5.3.6 Tests for Smoothing Components

<table>
<thead>
<tr>
<th>Component</th>
<th>Effective DF</th>
<th>Effective DF for Test</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spline(x1)</td>
<td>2.10969</td>
<td>3</td>
<td>4.76</td>
<td>0.0027</td>
</tr>
<tr>
<td>Spline(x2)</td>
<td>2.38340</td>
<td>3</td>
<td>13.64</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Spline(x3)</td>
<td>5.62608</td>
<td>7</td>
<td>49.02</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Spline(x4)</td>
<td>1.00002</td>
<td>1</td>
<td>0.88</td>
<td>0.3484</td>
</tr>
</tbody>
</table>

Output 5.3.7 displays the “Smoothing Component Panel” for all the spline terms used in the model. For $x_1$, $x_2$, and $x_3$, the fitted curves are reasonably smooth and close to the true functions. For $x_4$, the spline plot shows a strictly linear fit, with 95% Bayesian confidence bands covering the horizontal line at 0. This reinforces the conclusion that $x_4$ does not contribute to the model and can be removed from further analysis.

Output 5.3.7 Smoothing Component Panel
References


# Chapter 6
## The GENSELECT Procedure

## Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: GENSELECT Procedure</td>
<td>356</td>
</tr>
<tr>
<td>PROC GENSELECT Features</td>
<td>356</td>
</tr>
<tr>
<td>PROC GENSELECT Compared with Other SAS Procedures</td>
<td>357</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>358</td>
</tr>
<tr>
<td>Getting Started: GENSELECT Procedure</td>
<td>359</td>
</tr>
<tr>
<td>Poisson Regression for Count Data</td>
<td>359</td>
</tr>
<tr>
<td>Syntax: GENSELECT Procedure</td>
<td>364</td>
</tr>
<tr>
<td>PROC GENSELECT Statement</td>
<td>364</td>
</tr>
<tr>
<td>BY Statement</td>
<td>367</td>
</tr>
<tr>
<td>CLASS Statement</td>
<td>367</td>
</tr>
<tr>
<td>CODE Statement</td>
<td>368</td>
</tr>
<tr>
<td>DISPLAY Statement</td>
<td>368</td>
</tr>
<tr>
<td>DISPLAYOUT Statement</td>
<td>369</td>
</tr>
<tr>
<td>EFFECT Statement</td>
<td>370</td>
</tr>
<tr>
<td>FREQ Statement</td>
<td>371</td>
</tr>
<tr>
<td>MODEL Statement</td>
<td>372</td>
</tr>
<tr>
<td>OUTPUT Statement</td>
<td>378</td>
</tr>
<tr>
<td>PARTITION Statement</td>
<td>383</td>
</tr>
<tr>
<td>SELECTION Statement</td>
<td>384</td>
</tr>
<tr>
<td>WEIGHT Statement</td>
<td>385</td>
</tr>
<tr>
<td>Details: GENSELECT Procedure</td>
<td>386</td>
</tr>
<tr>
<td>Missing Values</td>
<td>386</td>
</tr>
<tr>
<td>Exponential Family Distributions</td>
<td>386</td>
</tr>
<tr>
<td>Response Distributions</td>
<td>387</td>
</tr>
<tr>
<td>Response Probability Distribution Functions</td>
<td>388</td>
</tr>
<tr>
<td>Log-Likelihood Functions</td>
<td>393</td>
</tr>
<tr>
<td>Existence of Maximum Likelihood Estimates</td>
<td>397</td>
</tr>
<tr>
<td>The LASSO Method of Model Selection</td>
<td>398</td>
</tr>
<tr>
<td>Model Fit and Assessment Statistics</td>
<td>399</td>
</tr>
<tr>
<td>Predicted Values and Regression Diagnostics</td>
<td>400</td>
</tr>
<tr>
<td>Joint Tests and Type 3 Tests</td>
<td>403</td>
</tr>
<tr>
<td>Multithreading</td>
<td>404</td>
</tr>
<tr>
<td>Optimization Algorithms</td>
<td>404</td>
</tr>
<tr>
<td>Displayed Output</td>
<td>405</td>
</tr>
<tr>
<td>ODS Table Names</td>
<td>408</td>
</tr>
<tr>
<td>ODS Graphics</td>
<td>409</td>
</tr>
</tbody>
</table>
Overview: GENSELECT Procedure

The GENSELECT procedure fits and performs model selection for generalized linear models in SAS Viya. The models that PROC GENSELECT supports can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The models can also include constructed effects such as splines. The procedure offers a number of effect-selection methods, including stepwise methods and modern LASSO methods. It also offers extensive capabilities for customizing the model selection by using a wide variety of selection and stopping criteria, from computationally efficient significance-level-based criteria to modern, computationally intensive validation-based criteria. PROC GENSELECT also provides a variety of diagnostics that are conditional on the selected model.

PROC GENSELECT fits models for standard distributions in the exponential family, such as the normal, Poisson, binomial, gamma, and Tweedie distributions. In addition, the procedure fits multinomial models for ordinal and nominal response data, and it fits models for the beta, generalized Poisson, and negative binomial distributions.

PROC GENSELECT Features

The GENSELECT procedure does the following:

- estimates the parameters of a generalized linear regression model by using maximum likelihood techniques
- provides model-building syntax in the CLASS statement and the effect-based MODEL statement, which are familiar from SAS/STAT procedures (in particular, the GLM, GENMOD, LOGISTIC, GLIMMIX, and MIXED procedures)
- enables you to split classification effects into individual components by using the SPLIT option in the CLASS statement
- permits any degree of interaction effects that involve classification and continuous variables
- provides multiple link functions
- provides cumulative link models for ordinal response data and generalized logit modeling for unordered multinomial data
- provides response-variable options for binary and multinomial data as in the LOGISTIC procedure
- enables model building (variable selection) through the SELECTION statement
• provides a WEIGHT statement for weighted analysis
• provides a FREQ statement for grouped analysis
• provides a CODE statement to produce SAS code that can score a new data set
• provides an OUTPUT statement to produce a data table that contains predicted probabilities and other observationwise statistics
• uses ODS Graphics to create model selection plots as part of its output. For more information about ODS Graphics, see the section “ODS Graphics” on page 409.

Because the GENSELECT procedure runs on CAS, it also does the following:

• enables you to run on a cluster of machines that distribute the data and the computations
• enables you to run in single-machine mode on CAS
• exploits all the available cores and concurrent threads. For information about how PROC GENSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

PROC GENSELECT Compared with Other SAS Procedures

The GENSELECT procedure provides generalized linear modeling functionality that is comparable to that of the HPGENSELECT and GENMOD procedures in SAS/STAT software.

PROC GENSELECT Compared with the HPGENSELECT Procedure

The functionality of the GENSELECT procedure closely resembles that of the HPGENSELECT procedure, which is a high-performance procedure. The GENSELECT procedure is the next generation of the HPGENSELECT procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations.

Both the GENSELECT and HPGENSELECT procedures fit and perform model selection for generalized linear models. The models can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The GENSELECT procedure is additionally capable of constructing complex effects, including univariate spline and polynomial expansions. The default parameterization of CLASS variables in both procedures is the GLM parameterization.

If you do not specify a link function with the LINK= option, the GENSELECT procedure uses the logarithm link function as the default for both the gamma and the inverse Gaussian distributions. The HPGENSELECT procedure uses the reciprocal link function as the default for the gamma distribution, and the reciprocal squared as the default for the inverse Gaussian distribution.

With the GENSELECT and HPGENSELECT procedures, you request model selection by using the SELECTION statement. Both procedures offer the same methods of effect selection, but the GENSELECT procedure also produces selection plots by using ODS Graphics.

Both procedures use a modification of the Newton-Raphson algorithm with a ridged Hessian by default. You can choose different optimization techniques, including first-order methods that do not require a crossproducts matrix or Hessian, by using the TECHNIQUE= option. The default method for the Tweedie distribution is a quasi-Newton method.
Chapter 6: The GENSELECT Procedure

PROC GENSELECT Compared with the GENMOD Procedure

The GENMOD procedure fits generalized linear models. The GENSELECT procedure fits and performs model selection for generalized linear models. The models can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The default parameterization of CLASS variables in both procedures is the GLM parameterization.

If you do not specify a link function with the LINK= option, the GENSELECT procedure uses the logarithm link function as the default for both the gamma and the inverse Gaussian distributions. The GENMOD procedure uses the reciprocal link function as the default for the gamma distribution, and the reciprocal squared as the default for the inverse Gaussian distribution.

Both procedures use a modification of the Newton-Raphson algorithm with a ridged Hessian by default. You can instead choose Fisher scoring in PROC GENMOD.

The GENMOD procedure offers a wide variety of postfitting analyses, such as contrasts, estimates, tests of model effects, and least squares means. The GENSELECT procedure is limited in postfitting functionality because it is primarily designed for large-data tasks, such as predictive model building, model fitting, and scoring.

The GENSELECT procedure is specifically designed to operate in SAS Viya, and it performs computations in multiple threads. The GENMOD procedure executes in a single thread on a single machine.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
proc cas sessref=mysess terminate;
run;
```
cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: GENSELECT Procedure

Poisson Regression for Count Data

This example illustrates how you can use PROC GENSELECT to perform Poisson regression for count data. The input data must be a table on your CAS server, and a CAS session must be set up. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.” The following DATA step creates the data table getStarted, which consists of 100 observations on a count response variable (Y); a continuous variable (Total) to be used in a later analysis; and five categorical variables (C1–C5), each of which has four numerical levels, in your CAS session:

```
data mycas.getStarted;
  input C1-C5 Y Total;
datalines;
0 3 1 1 3 2 28.361
2 3 0 3 1 2 39.831
1 3 2 2 2 1 17.133
1 2 0 0 3 2 12.769
0 2 1 0 1 1 29.464
0 2 1 0 2 1 4.152
1 2 1 0 1 0 0.000
0 2 1 1 2 1 20.199
1 2 0 0 1 0 0.000
0 1 1 3 3 2 53.376
2 2 2 2 1 1 31.923
0 3 2 0 3 2 37.987
2 2 2 0 0 1 1.082
0 2 0 2 0 1 6.323
1 3 0 0 0 0 0.000
1 2 1 2 3 2 4.217
0 1 2 3 1 1 26.084
1 1 0 0 1 0 0.000
1 3 2 2 2 0 0.000
2 1 3 1 1 2 52.640
1 3 0 1 2 1 3.257
2 0 2 3 0 5 88.066
2 2 2 1 0 1 15.196
3 1 3 1 0 1 11.955
3 1 3 1 2 3 91.790
3 1 1 2 3 7 232.417
3 1 1 1 0 1 2.124
3 1 0 0 0 2 32.762
```
<p>| | | | | | | |</p>
<table>
<thead>
<tr>
<th></th>
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<tbody>
<tr>
<td>1</td>
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<td>1</td>
<td>2</td>
<td>1</td>
<td>42.753</td>
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<td>2</td>
<td>3</td>
<td>1</td>
<td>23.854</td>
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<td>0</td>
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<td>0</td>
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<td>3</td>
<td>4</td>
<td>105.449</td>
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<td>0</td>
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<td>2</td>
<td>3</td>
<td>0</td>
<td>6</td>
<td>101.536</td>
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<td>0</td>
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<td>0</td>
<td>0.000</td>
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<td>1</td>
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</tr>
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<td>0</td>
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<td>0</td>
<td>4</td>
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<td>2</td>
<td>0</td>
<td>1</td>
<td>3</td>
<td>53.798</td>
</tr>
</tbody>
</table>
These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements fit a log-linked Poisson model to these data by using classification effects for the variables C1–C5:

```plaintext
proc genselect data=mycas.getStarted;
   class C1-C5;
      model Y = C1-C5 / Distribution=Poisson Link=Log;
run;
```

The output from this analysis is presented in Figure 6.1 through Figure 6.7.

**Figure 6.1** displays the “Model Information” table. The variable Y is an integer-valued variable that is modeled by using a Poisson probability distribution, and the mean of Y is modeled by using a log link function. The GENSELECT procedure uses a Newton-Raphson algorithm to fit the model. The CLASS variables C1–C5 are parameterized by using GLM parameterization, which is the default.

**Figure 6.1 Model Information**

**The GENSELECT Procedure**

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Optimization Technique</td>
</tr>
</tbody>
</table>

Each of the CLASS variables C1–C5 has four unique formatted levels, which are displayed in the “Class Level Information” table in Figure 6.2.
Chapter 6: The GENSELECT Procedure

Figure 6.2 Class Level Information

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class Levels</td>
</tr>
<tr>
<td>C1</td>
</tr>
<tr>
<td>C2</td>
</tr>
<tr>
<td>C3</td>
</tr>
<tr>
<td>C4</td>
</tr>
<tr>
<td>C5</td>
</tr>
</tbody>
</table>

Figure 6.3 displays the “Number of Observations” table. All 100 observations in the data set are used in the analysis.

Figure 6.3 Number of Observations

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>100</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Used</td>
<td>100</td>
</tr>
</tbody>
</table>

Figure 6.4 displays the “Dimensions” table for this model. This table summarizes some important sizes of various model components. For example, it shows that there are 21 columns in the design matrix $X$: 1 column for the intercept and 20 columns for the effects that are associated with the classification variables $C_1$–$C_5$. However, the rank of the crossproducts matrix is only 16. Because the classification variables $C_1$–$C_5$ use GLM parameterization and because the model contains an intercept, there is one singularity in the crossproducts matrix of the model for each classification variable. Consequently, only 16 parameters enter the optimization.

Figure 6.4 Dimensions in Poisson Regression

<table>
<thead>
<tr>
<th>Dimensions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Columns in Design</td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Max Effect Columns</td>
</tr>
<tr>
<td>Rank of Design</td>
</tr>
<tr>
<td>Parameters in Optimization</td>
</tr>
</tbody>
</table>

Figure 6.5 displays the final convergence status of the Newton-Raphson algorithm. The FCONV= convergence criterion is satisfied.

Figure 6.5 Convergence Status

Convergence criterion (FCONV=1E-7) satisfied.

The “Fit Statistics” table is shown in Figure 6.6. The $-2$ log likelihood at the converged estimates is 290.16169. You can use this value to compare the model to nested model alternatives by means of a likelihood ratio test. To compare models that are not nested, information criteria such as AIC (Akaike’s information criterion), AICC (Akaike’s bias-corrected information criterion), and BIC (Schwarz Bayesian information criterion) are used. These criteria penalize the $-2$ log likelihood for the number of parameters.
The “Parameter Estimates” table in Figure 6.7 shows that many parameters have fairly large \( p \)-values, indicating that one or more of the model effects might not be necessary.
Syntax: GENSELECT Procedure

The following statements are available in the GENSELECT procedure:

```plaintext
PROC GENSELECT <options> ;
   BY variables ;
   CLASS variable <(options)> . . . variable <(options)> < / global-options> ;
   CODE <options> ;
   DISPLAY <table-list> < / options> ;
   DISPLAYOUT table-spec-list < / options> ;
   EFFECT name=effect-type(variables < / options>) ;
   FREQ variable ;
   MODEL response < (response-options) > = < effects > < / model-options > ;
   MODEL events/trials < (response-options) > = < effects > < / model-options > ;
   OUTPUT OUT=CAS-libref.data-table <keyword < = name > . . . < keyword < = name > > < options > ;
   PARTITION < partition-options > ;
   SELECTION < METHOD=method < (method-options) > > < options > ;
   WEIGHT variable ;
```

The PROC GENSELECT statement and at least one MODEL statement are required. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statements.

PROC GENSELECT Statement

```plaintext
PROC GENSELECT <options> ;
```

The PROC GENSELECT statement invokes the procedure. Table 6.1 summarizes the available options in the PROC GENSELECT statement by function. They are then described fully in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>ALPHA=</td>
<td>Specifies a global significance level</td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td>MAXOPTBATCH=</td>
<td>Specifies the maximum number of observations to be computed in each batch</td>
</tr>
<tr>
<td><strong>Options Related to Output</strong></td>
<td></td>
</tr>
<tr>
<td>CORRB</td>
<td>Displays the “Parameter Estimates Correlation Matrix” table</td>
</tr>
<tr>
<td>COVB</td>
<td>Displays the “Parameter Estimates Covariance Matrix” table</td>
</tr>
<tr>
<td>ITHIST</td>
<td>Displays the “Iteration History” table</td>
</tr>
<tr>
<td>NOCHECK</td>
<td>Disables checking for infinite parameters</td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Limits or suppresses the display of classification variable levels</td>
</tr>
<tr>
<td>NOSTDERR</td>
<td>Suppresses computation of the covariance matrix and standard errors</td>
</tr>
<tr>
<td>PARTFIT</td>
<td>Displays the fit statistics that are produced when your data are partitioned</td>
</tr>
<tr>
<td>STB</td>
<td>Displays standardized estimates</td>
</tr>
</tbody>
</table>
The optimization options are fully described in the section “Optimization Options” on page 42 in Chapter 2, “Shared Concepts.” The following list describes the other options available in the PROC GENSELECT statement:

**ALPHA=number**

specifies a global significance level for the construction of confidence intervals. The confidence level is $1 - \text{number}$. The value of number must be between 0 and 1. You can override this global significance level by specifying this option in the OUTPUT statement. By default, ALPHA=0.05.

**MAXOPTBATCH=number**

specifies the maximum number of observations to be included in a batch. The GENSELECT procedure reads at most number observations from the data table into memory, performs the appropriate log-likelihood, gradient, and Hessian computations on that batch of observations, then discards those observations and reads in the next batch of data for processing. Generally, a smaller MAXOPTBATCH value decreases memory usage but might lead to longer computation times, whereas a larger MAXOPTBATCH value might lead to shorter computation times but increases memory usage. By default, MAXOPTBATCH=256.

**CORRB**

creates the “Parameter Estimates Correlation Matrix” table. The correlation matrix is computed by normalizing the covariance matrix $\Sigma$. That is, if $\sigma_{ij}$ is an element of $\Sigma$, then the corresponding element of the correlation matrix is $\sigma_{ij}/\sigma_i \sigma_j$, where $\sigma_i = \sqrt{\sigma_{ii}}$. 
COVB
creates the “Parameter Estimates Covariance Matrix” table. The covariance matrix is computed as the inverse of the negative of the matrix of second derivatives of the log-likelihood function with respect to the model parameters (the Hessian matrix).

DATA=CAS-libref.data-table
names the input data table for PROC GENSELECT to use. The default is the most recently created data table. CAS-libref specifies the CAS library where the input data table resides, and data-table specifies the name of the input data table.

ITHIST
generates the “Iteration History” table.

LASSORHO=r
specifies the base regularization parameter for the LASSO model selection method. The regularization parameter for step \( i \) is \( r^i \). By default, LASSORHO=0.8.

LASSOSTEPS=n
specifies the maximum number of steps for LASSO model selection. By default, LASSOSTEPS=20.

LASSOTOL=r
specifies the convergence tolerance for the optimization algorithm that solves for the LASSO parameter estimates at each step of LASSO model selection. By default, LASSOTOL=1E–6.

NOCHECK
disables the checking process that determines whether maximum likelihood estimates of the regression parameters exist. For more information, see the section “Existence of Maximum Likelihood Estimates” on page 397.

NOCHECK<number>
suppresses the display of the “Class Level Information” table if you do not specify number. If you specify number, the values of the classification variables are displayed for only those variables whose number of levels is less than number. Specifying number helps to reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

NOSTDERR
suppresses computation of the covariance matrix and the standard errors of the regression coefficients. When the model contains many variables (thousands), the inversion of the Hessian matrix to derive the covariance matrix and the standard errors of the regression coefficients can be time-consuming. The CORRB, COVB, and TYPE3 options are not available when the NOSTDERR option is specified. This option also disables the quasi-complete separation check; for more information, see the section “Existence of Maximum Likelihood Estimates” on page 397.

PARTFIT
displays fit statistics in the “Fit Statistics” table that are usually produced when your data are partitioned. This option is not required when you specify a PARTITION statement. The statistic that is added to the table is the average square error (or Brier score).
STB displays the standardized estimates of the parameters in the “Parameter Estimates” table. The standardized estimate of $\hat{\beta}_i$ is given by $\hat{\beta}_i / (s_i/s_i)$, where $s_i$ is the total sample standard deviation for the $i$th explanatory variable and

$$s = \begin{cases} \pi/\sqrt{3} & \text{LOGIT and GLOGIT links} \\ 1 & \text{PROBIT link} \\ \pi/\sqrt{6} & \text{CLOGLOG and LOGLOG links} \\ 1 & \text{all other links} \end{cases}$$

The sample standard deviations for parameters that are associated with CLASS variables are computed using their codings. The standardized estimates are not computed for the intercept parameters.

**BY Statement**

```
BY variables ;
```

You can specify a BY statement in PROC GENSELECT to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in *SAS Language Reference: Concepts*.

**CLASS Statement**

```
CLASS variable<(options)> . . . < variable<(options)> > < / global-options > ;
```

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required. Table 6.2 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>
CODE Statement

**CODE <options> ;**

The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a file, to a catalog entry, or to a CAS table. To score new data, you can then include the file or the catalog entry in a DATA step, or you can specify the CAS table in the `runCodeTable` action in the `dataStep` action set (for more information, see *SAS Viya: System Programming Guide*).

Table 6.3 summarizes the **options** available in the CODE statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
</tbody>
</table>

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

DISPLAY Statement

**DISPLAY <table-list> < /options> ;**

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the **table-list** as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 408. A path is a table name that is prefixed with dot-separated grouping information. For example, a
A SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (`/`). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (`/`):

- **CASESENSITIVE**
  - performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  - displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  - suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  - displays the display table names, labels, and paths.

---

**DISPLAYOUT Statement**

```
DISPLAYOUT table-spec-list < / options > ;
```

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.
- `key` specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following `options` after a slash (`/`):
INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

---

**EFFECT Statement**

\[
\text{EFFECT name=} \text{effect-type} (\text{variables < / options>}) ;
\]

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as *constructed effects* to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following *effect-types*:

- **COLLECTION** specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.

- **MULTIMEMBER | MM** specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.

- **POLYNOMIAL | POLY** specifies a multivariate polynomial effect in the specified numeric variables.

- **SPLINE** specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 6.4 summarizes the *options* available in the EFFECT statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
</tbody>
</table>
Table 6.4  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
</tbody>
</table>

**Polynomial Effects Options**
- **DEGREE=** Specifies the degree of the polynomial
- **DETAILS** Displays details of the specified polynomial
- **MDEGREE=** Specifies the maximum degree of any variable in a term of the polynomial
- **NOSEPARATE** Treats the polynomial as a single effect with multiple degrees of freedom
- **STANDARDIZE=** Specifies centering and scaling suboptions for the variables that define the polynomial

**Spline Effects Options**
- **BASIS=** Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect
- **DATABOUNDARY** Uses the extremes of the data as boundary knots for a B-spline basis
- **DEGREE=** Specifies the degree of the spline effect
- **DETAILS** Displays the knots and locations for each spline basis function
- **KNOTMAX=** Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value
- **KNOTMETHOD=** Specifies how to construct the knots for the spline effect
- **KNOTMIN=** Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value
- **NATURALCUBIC** Specifies a natural cubic spline basis for the spline effect
- **SEPARATE** Treats the spline basis for each variable as a separate effect when multiple variables are specified
- **SPLIT** Treats each design matrix column as a separate effect for selection methods

For more information about the syntax of these effect-types and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”

---

**FREQ Statement**

```
FREQ variable;
```

The `variable` in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC GENSELECT treats each observation as if it appears `f` times, where `f` is the value of the FREQ `variable` for the observation. If `f` is not an integer, it is truncated to an integer. If `f` is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.
The MODEL statement defines the statistical model in terms of a response variable (the target) or an events/trials specification, model effects that are constructed from variables in the input data table, and model-options. An intercept is included in the model by default. You can remove the intercept by specifying the NOINT option.

You can specify a single response variable that contains your response values. When you have binomial data, you can specify the events/trials form of the response, where one variable contains the number of positive responses (or events) and another variable contains the number of trials. Note that the values of both events and (trials – events) must be nonnegative and the value of trials must be positive.

For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

There are two sets of options in the MODEL statement. The response-options determine how the GENSELECT procedure models probabilities for binary and multinomial data. The model-options control other aspects of model formation and inference. Table 6.5 summarizes these options.

### Table 6.5  MODEL Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the response categories</td>
</tr>
<tr>
<td>EVENT=</td>
<td>Specifies the event category</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference category</td>
</tr>
<tr>
<td>CENTER</td>
<td>Centers and scales continuous main effects</td>
</tr>
<tr>
<td>CLB</td>
<td>Requests confidence limits</td>
</tr>
<tr>
<td>INCLUDE=</td>
<td>Includes effects in all models for model selection</td>
</tr>
<tr>
<td>INFORMATIVE</td>
<td>Models missing values by using extra indicator variables</td>
</tr>
<tr>
<td>LINK=</td>
<td>Specifies the link function</td>
</tr>
<tr>
<td>NOINT</td>
<td>Suppresses the intercept</td>
</tr>
<tr>
<td>OFFSET=</td>
<td>Specifies the offset variable</td>
</tr>
<tr>
<td>PHI=</td>
<td>Specifies a fixed dispersion parameter</td>
</tr>
<tr>
<td>START=</td>
<td>Includes effects in the initial model for model selection</td>
</tr>
<tr>
<td>TYPE3</td>
<td>Displays the Type 3 or joint tests of effects</td>
</tr>
</tbody>
</table>

### Response Variable Options

Response variable options determine how the GENSELECT procedure models probabilities for binary and multinomial data.
You can specify the following *response-options* by enclosing them in parentheses after the *response* or *trials* variable.

**DESCENDING**

*DESC*

reverses the order of the response categories. If you specify both the DESCENDING and ORDER= options, PROC GENSELECT orders the response categories according to the ORDER= option and then reverses that order.

**EVENT=’category’ | FIRST | LAST**

specifies the event category for the binary and multinomial response model. PROC GENSELECT models the probability of the event category. The EVENT= option has no effect when there are more than two response categories.

You can specify one of the following:

*’category’*

specifies the value (formatted, if a format is applied) of the event category in quotation marks.

**FIRST**

designates the first ordered category as the event.

**LAST**

designates the last ordered category as the event.

By default, EVENT=FIRST.

For example, the following statements specify that observations whose formatted value is 1 represent events in the data. The probability that PROC GENSELECT models is thus the probability that the variable def takes the (formatted) value 1.

```plaintext
proc genselect data=mycas.MyData;
    class A B C;
    model def(event =’1’) = A B C x1 x2 x3;
run;
```

**ORDER=FORMATTED | FREQ | INTERNAL**

specifies the sort order for the levels of the *response* variable. You can specify the following values:

**FORMATTED**

sorts the levels by external formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. For numeric variables for which you have supplied no explicit format (that is, for which there is no corresponding FORMAT statement in the current PROC GENSELECT run or in the DATA step that created the data table), the levels are ordered by their internal (numeric) value. The sort order is machine-dependent.

**FREQ**

sorts the levels by descending frequency count (levels that have the most observations come first in the order).

**INTERNAL**

sorts the levels by unformatted value. The sort order is machine-dependent.
By default, ORDER=FORMATTED.

For more information about sort order, see the chapter on the SORT procedure in the SAS Visual Data Management and Utility Procedures Guide and the discussion of BY-group processing in SAS Language Reference: Concepts.

**REF='category' | FIRST | LAST**

specifies the reference category for the generalized logit model and the binary response model. For the generalized logit model, each logit contrasts a nonreference category with the reference category. For the binary response model, specifying one response category as the reference is the same as specifying the other response category as the event. You can specify one of the following:

- `'category'` specifies the value (formatted, if a format is applied) of the reference category in quotation marks.
- `FIRST` designates the first ordered category as the reference.
- `LAST` designates the last ordered category as the reference.

By default, REF=LAST.

**Model Options**

You can specify the following *model-options* after a slash (/):

- **CENTER** requests that continuous main effects be centered and scaled internally. (Continuous main effects are centered and scaled to aid in computing maximum likelihood estimates.) Parameter estimates and related statistics are always reported on the original scale.

- **CLB** constructs confidence limits for each parameter estimate. The confidence level is 0.95 by default; you can change it by specifying the ALPHA= option.

- **DISTRIBUTION=** *keyword*

  specifies the response distribution for the model. The *keywords* and the associated distributions are shown in Table 6.6. For information about default and commonly used link functions for each distribution function, see Table 6.8.
Table 6.6 Built-In Distribution Functions

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Distribution Function</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETA</td>
<td>Beta</td>
</tr>
<tr>
<td>BINARY</td>
<td>Binary</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Binary or binomial</td>
</tr>
<tr>
<td>EXPONENTIAL</td>
<td>Exponential</td>
</tr>
<tr>
<td>GAMMA</td>
<td>Gamma</td>
</tr>
<tr>
<td>GENPOISSON</td>
<td>GPOISSON</td>
</tr>
<tr>
<td>GEOMETRIC</td>
<td>Geometric</td>
</tr>
<tr>
<td>IGAUSSIAN</td>
<td>IG</td>
</tr>
<tr>
<td>MULTINOMIAL</td>
<td>Multinomial. For ordinal responses, it fits a model that has a cumulative link function. For nominal responses, it fits a model that has a generalized logit link function.</td>
</tr>
<tr>
<td>NEGATIVEBINOMIAL</td>
<td>NB</td>
</tr>
<tr>
<td>NORMAL</td>
<td>Normal</td>
</tr>
<tr>
<td>POISSON</td>
<td>Poisson</td>
</tr>
<tr>
<td>$T^{&lt;v&gt;}$</td>
<td>$t$ with $v$ degrees of freedom. If you do not specify $v$, a value of $v = 3$ is used.</td>
</tr>
<tr>
<td>TWEEDIE&lt; (Tweedie-options)&gt;</td>
<td>Tweedie</td>
</tr>
<tr>
<td>WEIBULL</td>
<td>Two-parameter Weibull</td>
</tr>
</tbody>
</table>

When DISTRIBUTION=TWEEDIE, you can specify the following Tweedie-options:

**EQL**
uses extended quasi-likelihood instead of Tweedie log likelihood in parameter estimation.

**INITIALP=value**
specifies a starting value for iterative estimation of the Tweedie power parameter.

**OPTMETHOD=Tweedie-optimization-option**
requests an optimization method for iterative estimation of the Tweedie model parameters. You can specify the following Tweedie-optimization-options:

**EQL**
uses extended quasi-likelihood for a sample of the data, followed by extended quasi-likelihood for the full data. This is equivalent to the EQL Tweedie-option.

**EQLLHOOD**
uses extended quasi-likelihood for a sample of the data, followed by Tweedie log likelihood for the full data. This is the default method.

**FINALLHOOD**
uses a four-stage approach to estimating the Tweedie model parameters. The four stages are as follows:

1. extended quasi-likelihood for a sample of the data
Chapter 6: The GENSELECT Procedure

2. Tweedie log likelihood for a sample of the data
3. extended quasi-likelihood for the full data
4. Tweedie log likelihood for the full data

**LHOOD**
uses Tweedie log likelihood for a sample of the data, followed by Tweedie log likelihood for the full data.

**P=value**
specifies a value to use as a fixed Tweedie power parameter.

**SAMPLEFRAC=value**
specifies a value to use as the fraction of the data that are used to compute starting values for the Tweedie distribution. The value must be between 0 and 1.

**INCLUDE=n**
**INCLUDE=single-effect**
**INCLUDE=(effect-list)**
forces effects to be included in all models. If you specify INCLUDE=n, then the first n effects that are listed in the MODEL statement are included in all models. If you specify INCLUDE=single-effect or if you specify a list of effects within parentheses, then the specified effects are forced into all models. The effects that you specify in the INCLUDE= option must be explanatory effects that are specified in the MODEL statement before the slash (/).

**INFORMATIVE**
models missing values by using extra model effects. These effects consist of dummy variables that take the value 1 when the value of a continuous model variable involved in the effect is missing, and take the value 0 otherwise. The missing value in the original model effect is replaced by the average value of the effect for the nonmissing values. For continuous-by-class effects, such as A*x, where A is a classification variable and x is a continuous variable, informative missingness creates multiple dummy columns and substitutes the effect mean of x that corresponds to the respective level of A. Missing values for classification variables are treated as valid levels. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

**LINK=keyword**
specifies the link function for the model. The keywords and their associated link functions are shown in Table 6.7. Default and commonly used link functions for the available distributions are shown in Table 6.8.
Table 6.7  Built-In Link Functions

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Link Function</th>
<th>( g(\mu) = \eta = )</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLOGLOG</td>
<td>Complementary log-log or cumulative complementary log-log</td>
<td>( \log(-\log(1 - \mu)) )</td>
</tr>
<tr>
<td>GLOGIT</td>
<td>Generalized logit</td>
<td></td>
</tr>
<tr>
<td>IDENTITY</td>
<td>Identity</td>
<td>( \mu )</td>
</tr>
<tr>
<td>INVERSE</td>
<td>Reciprocal</td>
<td>( \frac{1}{\mu} )</td>
</tr>
<tr>
<td>POWERMINUS2</td>
<td>Reciprocal square</td>
<td>( \frac{1}{\mu^2} )</td>
</tr>
<tr>
<td>POWER(p)</td>
<td>Power</td>
<td>( \mu^p )</td>
</tr>
<tr>
<td>LOG</td>
<td>Logarithm</td>
<td>( \log(\mu) )</td>
</tr>
<tr>
<td>LOGIT</td>
<td>Logit or cumulative logit</td>
<td>( \log(\mu/(1 - \mu)) )</td>
</tr>
<tr>
<td>LOGLOG</td>
<td>Log-log or cumulative log-log</td>
<td>( -\log(-\log(\mu)) )</td>
</tr>
<tr>
<td>PROBIT</td>
<td>Probit or cumulative probit</td>
<td>( \Phi^{-1}(\mu) )</td>
</tr>
</tbody>
</table>

For the probit and cumulative probit links, \( \Phi^{-1}(\cdot) \) denotes the quantile function of the standard normal distribution.

If you do not specify the \texttt{LINK=} option, a default link function is used, as shown in Table 6.8. For binary or multinomial distributions, only the link functions shown in Table 6.8 are available. For the other distributions, you can use any link function shown in Table 6.7 by specifying the \texttt{LINK=} option. Other commonly used link functions for each distribution are shown in Table 6.8.

Table 6.8  Default and Commonly Used Link Functions

<table>
<thead>
<tr>
<th>Value of the DISTRIBUTION= Option</th>
<th>Default Link Function</th>
<th>Other Commonly Used Link Functions</th>
</tr>
</thead>
<tbody>
<tr>
<td>BETA</td>
<td>Logit</td>
<td>Probit, complementary log-log, log-log</td>
</tr>
<tr>
<td>BINARY</td>
<td>Logit</td>
<td>Probit, complementary log-log, log-log</td>
</tr>
<tr>
<td>BINOMIAL</td>
<td>Logit</td>
<td>Probit, complementary log-log, log-log</td>
</tr>
<tr>
<td>EXPONENTIAL</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>GAMMA</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>GENPOISSON</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>GEOMETRIC</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>INVERSEGAUSSIAN</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>MULTINOMIAL</td>
<td>Cumulative logit</td>
<td>Cumulative probit, cumulative complementary log-log, cumulative log-log, generalized logit</td>
</tr>
<tr>
<td>NEGATIVEBINOMIAL</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>NORMAL</td>
<td>Identity</td>
<td>Log</td>
</tr>
<tr>
<td>POISSON</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>T</td>
<td>Identity</td>
<td>Log</td>
</tr>
<tr>
<td>TWEEDIE</td>
<td>Log</td>
<td></td>
</tr>
<tr>
<td>WEIBULL</td>
<td>Log</td>
<td></td>
</tr>
</tbody>
</table>
NOINT
requests that no intercept be included in the model. An intercept is included by default. The NOINT
option is not available for multinomial models.

OFFSET=variable
specifies a variable to be used as an offset to the linear predictor. An offset plays the role of an effect
whose coefficient is known to be 1. The offset variable cannot appear in the CLASS statement or
elsewhere in the MODEL statement. Observations that have missing values for the offset variable are
excluded from the analysis.

PHI=number
specifies a fixed dispersion parameter for those distributions that have a dispersion parameter. The
dispersion parameter that is used in all computations is fixed at number and not estimated.

START=n
START=single-effect
START=(effects)

begins the selection process from the designated initial model for the forward selection method. If you
specify START=n, then the starting model includes the first n effects that are listed in the MODEL
statement. If you specify START=single-effect or START=(effects), then the starting model includes
those specified effects. The effects that you specify in the START= option must be explanatory effects
that are specified in the MODEL statement before the slash (/). This option is not available when you
specify METHOD=BACKWARD in the SELECTION statement.

TYPE3
requests that Wald statistics for Type 3 contrasts be computed for each effect that is specified in the
MODEL statement. For more information, see the section “Joint Tests and Type 3 Tests” on page 403.

OUTPUT Statement

OUTPUT OUT=\text{CAS-libref.data-table} < ALL > < ALPHA=number > < COPYVARS=(variables) >
< keyword =name > ...< keyword =name >;

The OUTPUT statement creates a data table that contains observationwise statistics that PROC GENSELECT
computes after fitting the model. In order to avoid data duplication for large data tables, the variables in the
input data table are not included in the output data table unless you specify them in the COPYVAR= option.

If the response variable has more than two categories, you can request the “Statistic Options” listed in
Table 6.9; the other diagnostic statistics are not available. These statistics are computed for every response
category, and the automatic variable _LEVEL_ identifies the response category on which the computed values
are based. That is, every observation generates several rows in the output data set. If you also specify the
OBSCAT option, then the observationwise statistics are computed only for the observed response category,
which is indicated by the value of the _LEVEL_ variable.

The output statistics are computed based on the final parameter estimates. If the optimization does not
converge, then the output data table is not created.
For observations in which only the response variable is missing, values of the linear predictor and the predicted values are computed even though these observations do not affect the model fit. This enables, for example, predicted values to be computed for new observations.

You must specify the following option:

**OUT=** CAS-libref.data-table

names the output data table for PROC GENSELECT to use. You must specify this option before any other options. **CAS-libref.data-table** is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about **CAS-libref**, see the section “Using CAS Sessions and CAS Engine Librefs” on page 358.

- **data-table** specifies the name of the output data table.

You can also specify the following syntax elements:

- **ALL**
- **ALLSTAT**
  adds all available statistics to the output data table.

- **ALPHA=** number
  specifies the significance level for the construction of confidence intervals in the output data table. The confidence level is \( 1 - \text{number} \). The value of number must be between 0 and 1. By default, number is equal to the value of the **ALPHA=** option in the PROC GENSELECT statement, or 0.05 if that option is not specified.

- **COPYVAR=** variable
- **COPYVARS=(** variables **)**
  transfers one or more variables from the input data table to the output data table.

- **OBSCAT**
  requests (for multinomial models) that observationwise statistics be produced only for the observed response level. If you do not specify this option and the response variable has \( J \) levels, then the following outputs are created: for cumulative link models, \( J - 1 \) records are output for every observation in the input data that corresponds to the \( J - 1 \) lower-ordered response categories; for generalized logit models, \( J \) records are output that correspond to all \( J \) response categories.

- **PREDPROBS**
  creates variables (for multinomial models) for each response category that corresponds to the requested **IPRED** and **PREDICTED** keywords.

- **keyword <=** name >
  specifies a statistic to include in the output data table and optionally names the variable name. If you do not provide a name, the GENSELECT procedure assigns a default name based on the type of statistic requested.

Table 6.9 summarizes the keywords available in the OUTPUT statement.
### Table 6.9 OUTPUT Statement Keywords

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Default Names</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Statistic Options</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>Specifies the individual predicted probabilities</td>
<td><em>IPRED</em></td>
</tr>
<tr>
<td>LCL</td>
<td>Specifies the lower confidence limit for the linear predictor</td>
<td><em>LCL</em></td>
</tr>
<tr>
<td>LCLM</td>
<td>Specifies the lower confidence limit for the event probability</td>
<td><em>LCLM</em></td>
</tr>
<tr>
<td>PREDICTED</td>
<td>Specifies the predicted probabilities</td>
<td><em>PRED</em></td>
</tr>
<tr>
<td>STDXBETA</td>
<td>Specifies the standard error estimate of the linear predictor</td>
<td><em>STDXBETA</em></td>
</tr>
<tr>
<td>UCL</td>
<td>Specifies the upper confidence limit for the linear predictor</td>
<td><em>UCL</em></td>
</tr>
<tr>
<td>UCLM</td>
<td>Specifies the upper confidence limit for the event probability</td>
<td><em>UCLM</em></td>
</tr>
<tr>
<td>XBETA</td>
<td>Specifies the linear predictor</td>
<td><em>XBETA</em></td>
</tr>
<tr>
<td><strong>Diagnostic Options</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CBAR</td>
<td>Specifies the confidence interval displacement</td>
<td><em>CBAR</em></td>
</tr>
<tr>
<td>DIFCHISQ</td>
<td>Specifies the deletion chi-square goodness-of-fit change</td>
<td><em>DIFCHISQUARE</em></td>
</tr>
<tr>
<td>DIFDEV</td>
<td>Specifies the deletion deviance change</td>
<td><em>DIFDEVIANCE</em></td>
</tr>
<tr>
<td>H</td>
<td>Specifies the leverage</td>
<td><em>HATDIAG</em></td>
</tr>
<tr>
<td>RESCHI</td>
<td>Specifies the Pearson chi-square residual</td>
<td><em>RESCHI</em></td>
</tr>
<tr>
<td>RESDEV</td>
<td>Specifies the deviance residual</td>
<td><em>RESDEV</em></td>
</tr>
<tr>
<td>RESLIK</td>
<td>Specifies the likelihood residual</td>
<td><em>RESLIK</em></td>
</tr>
<tr>
<td>RESRAW</td>
<td>Specifies the raw residual</td>
<td><em>RESRAW</em></td>
</tr>
<tr>
<td>RESWORK</td>
<td>Specifies the working residual</td>
<td><em>RESWORK</em></td>
</tr>
<tr>
<td>STDRESCHI</td>
<td>Specifies the standardized Pearson chi-square residual</td>
<td><em>STDRESCHI</em></td>
</tr>
<tr>
<td>STDRESDEV</td>
<td>Specifies the standardized deviance residual</td>
<td><em>STDRESDEV</em></td>
</tr>
<tr>
<td><strong>Miscellaneous Options for Binary and Multinomial Response Data</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>INTO</td>
<td>Names the level into which the observation is classified</td>
<td><em>INTO</em></td>
</tr>
<tr>
<td>LEVEL</td>
<td>Names the response level for a row of the output</td>
<td><em>LEVEL</em></td>
</tr>
</tbody>
</table>

The following list describes these *keywords*. For more information, see the section “Predicted Values and Regression Diagnostics” on page 400.

**CBAR**

specifies the confidence interval displacement diagnostic that measures the overall change in the global regression estimates that results from deleting an individual observation. The default name is _CBAR_.

**DIFCHISQ**

specifies the change in the chi-square goodness-of-fit statistic that results from deleting the individual observation. The default name is _DIFCHISQUARE_.

**DIFDEV**

specifies the change in the deviance that results from deleting the individual observation. The default name is _DIFDEVIANCE_.

**H**

specifies the diagonal element of the hat matrix (leverage) for detecting extreme points in the design space. The default name is _HATDIAG_.
INDIVIDUAL
IPRED
IPROB
IP
specifies the individual predicted values for multinomial response variables. For a response variable Y with three levels, 1, 2, and 3, the individual probabilities are \( \Pr(Y = 1) \), \( \Pr(Y = 2) \), and \( \Pr(Y = 3) \). The default name is _IPRED_.

INTO< (cutpoint)>
names the variable that contains the level of the response into which an observation is classified. The default name is _INTO_. Multinomial models classify observations into the level that has the largest model-predicted probability. For binary or binomial response variables, if the predicted probability of an observation equals or exceeds the cutpoint, the observation is classified as an event; otherwise it is classified as a nonevent. You can specify the cutpoint value as a number between 0 and 1. The default value is 0.5.

LCL
LOWERXBETA
names the variable that contains the lower confidence limits for the linear predictor. The default name is _LCL_. You can set the confidence level by specifying the ALPHA= option.

LCLM
LOWERMEAN
LOWER
specifies the lower confidence limits for the mean. The default name is _LCL_. You can set the confidence level by specifying the ALPHA= option.

LEVEL
names the variable that contains the level of the response for a given row of the output. The default name is _LEVEL_.

PREDICTED
PRED
PROB
P
specifies the predicted values for the response variable. It specifies the predicted probabilities of events for binary and nominal response variables and the cumulative predicted probabilities for ordinal response variables. For a response variable Y with three levels, 1, 2, and 3, the cumulative probabilities are \( \Pr(Y \leq 1) \) and \( \Pr(Y \leq 2) \), but by default the last level, \( \Pr(Y \leq 3) = 1 \), is not output. The default name is _PRED_.

RESCHI
PEARSON
specifies the Pearson residual for identifying poorly fitted observations. The default name is _RESCHI_.

RESDEV
specifies the deviance residual for identifying poorly fitted observations. The default name is _RESDEV_.

RESLIK
specifies the likelihood residual for identifying poorly fitted observations. The default name is _RESLIK_.

RESRAW
RESIDUAL
R
specifies the raw residual for identifying poorly fitted observations. The default name is _RESRAW_.

RESWORK
specifies the working residual for identifying poorly fitted observations. The default name is _RESWORK_.

ROLE
specifies the numeric variable that indicates the role played by each observation in fitting the model. The default name is _ROLE_. Table 6.10 shows how this variable is interpreted for each observation.

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by specifying a PARTITION statement, then the role variable value is 1 for observations that are used in fitting the model and 0 for observations that have at least one missing or invalid value for the response, regressor, frequency, or weight variables.

STDRESCHI
specifies the standardized Pearson (chi-square) residual for identifying observations that are poorly accounted for by the model. The default name is _STDRESCHI_.

STDRESDEV
specifies the standardized deviance residual for identifying poorly fitted observations. The default name is _STDRESDEV_.

STDXBETA
specifies the standard error estimates of XBETA. The default name is _STDXBETA_.

Table 6.10  Role Interpretation
UCL
UPPERXBETA
specifies the variable that contains the upper confidence limits for the linear predictor. The default name is _UCL_. You can set the confidence level by specifying the ALPHA= option.

UCLM
UPPERMEAN
UPPER
specifies the variable that contains the upper confidence limits for the mean. The default name is _UCLM_. You can set the confidence level by specifying the ALPHA= option.

XBETA
LINP
specifies the linear predictor. The default name is _XBETA_.

PARTITION Statement

PARTITION statement-option;

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:

FRACTION(<TEST=fraction> <VALIDATE=fraction> <SEED=number>)
randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The SEED= option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify SEED=number or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

ROLE=variable (<TEST='value'> <TRAIN='value'> <VALIDATE='value'>)
ROLEVAR=variable (<TEST='value'> <TRAIN='value'> <VALIDATE='value'>)
names the variable in the input data table whose values are used to assign roles to each observation. This variable cannot also appear as an analysis variable in other statements or options. The TEST=, TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

For more information, see the section “Partition Fit Statistics” on page 399.
Chapter 6: The GENSELECT Procedure

SELECTION Statement

SELECTION <METHOD=method < (method-options)> > < options >

The SELECTION statement performs model selection by examining whether effects should be added to or removed from the model according to rules that are defined by model selection methods. The statement is fully documented in the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

The GENSELECT procedure supports the following effect-selection methods in the SELECTION statement:

- **BACKWARD** performs backward elimination. This method starts with all effects in the model and deletes effects.
- **BACKWARD(FAST)** performs fast backward elimination when SELECT=SL. This method starts with all effects in the model and deletes effects without refitting the model.
- **FORWARD** performs forward selection. This method starts with no effects in the model and adds effects.
- **LASSO** performs model selection by the group LASSO method. This method adds and removes effects by using a sequence of LASSO steps. For more information, see the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.”
- **NONE** results in no model selection. This method fits the full model.

By default, METHOD=STEPWISE.

The SELECT=, CHOOSE=, and STOP= method-options default to SBC. These defaults differ from their corresponding defaults in the HPGENSELECT procedure in SAS/STAT software.

You can specify the following criteria in the SELECT=, CHOOSE=, and STOP= method-options:

- **AIC** uses Akaike’s information criterion (Akaike 1974).
- **AICC** uses a small-sample bias corrected version of Akaike’s information criterion, as promoted in Hurvich and Tsai (1989) and Burnham and Anderson (1998).
- **SBC | BIC** uses the Schwarz Bayesian criterion (Schwarz 1978).
- **SL** uses the significance level of the score test as the criterion (not available for the CHOOSE= option).
- **VALIDATE** uses the average square error (ASE) that is computed on the validation data as the criterion (not available for the SELECT= option).

For more information, see the section “Information Criteria” on page 399. If you specify the PARTITION statement, then the AIC, AICC, SBC, and SL statistics are computed on the training data; otherwise they are computed on the full data table.

Forward selection where you also specify the NOINT option is available only for the following models: binary, binomial, exponential, geometric, and Poisson.

If you specify METHOD=LASSO and do not specify the CHOOSE= option, then the model in the last LASSO step is chosen as the selected model.
WEIGHT Statement

WEIGHT variable;

The variable in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

**NOTE:** If you use the fast backward elimination method, then the $-2$ log-likelihood, AIC, AICC, and SBC statistics are approximated at each step where the model is not refit, and hence they do not match the values that are computed when that model is fit outside the selection routine. Similarly, if you specify SELECT=AIC, AICC, or SBC, the selection criteria are estimated (Lawless and Singhal 1978), and hence they do not match the values that are computed when that model is fit outside the selection routine.

**NOTE:** The default model hierarchy method is HIERARCHY=NONE for the forward and fast backward selection methods. The backward elimination method always uses the HIERARCHY=SINGLE method-option.

The LASSO method produces a summary table that displays the effects that are added or removed at each step; the LASSO regularization parameter; and the AIC, AICC, and SBC fit statistics. For the other methods, you can specify the following values for the DETAILS= option:

- **SUMMARY** produces a summary table that shows the effect that is added or removed at each step along with the SELECT=, CHOOSE=, and STOP= criteria. The summary table is produced by default if the DETAILS= option is not specified.
- **STEPS** produces the preceding summary table and displays the results from fitting each model at each step.
- **ALL** produces the preceding tables and a detailed listing of all candidates at each step along with their ranking in terms of the selection criterion for addition to or removal from the model.

If you specify the PLOTS=CRITERIA or PLOTS=ALL option, then a plot of the fit criterion by the selection step is created for the AIC, AICC, and SBC statistics. If you also specify a PARTITION statement or the PARTFIT option, then the same type of plot is created for the ASE (for each role).

If you specify the PLOTS=FITBYROLE or PLOTS=ALL option and a PARTITION statement, then a plot of the ASE by the selection step for each role is created.

The PLOTS= option is not available for the LASSO method.
Details: GENSELECT Procedure

Missing Values

Any observation that has missing values for the response, frequency, weight, offset, or explanatory variables is excluded from the analysis; however, missing values are valid for response and explanatory variables that are specified along with the MISSING option in the CLASS statement. Observations that have a nonpositive weight or a frequency less than 1 are also excluded.

The estimated linear predictor and the fitted probabilities are not computed for any observation that has missing offset or explanatory variable values. However, if only the response value is missing, the linear predictor and the fitted probabilities can be computed and output to a data set by using the OUTPUT statement.

You can also model the missing values by specifying the INFORMATIVE option in the MODEL statement. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

Exponential Family Distributions

Many of the probability distributions that the GENSELECT procedure fits are members of an exponential family of distributions, which have probability distributions that are expressed as follows for some functions $b$ and $c$ that determine the specific distribution:

$$f(y) = \exp \left\{ \frac{y\theta - b(\theta)}{\phi} + c(y, \phi) \right\}$$

For fixed $\phi$, this is a one-parameter exponential family of distributions. The response variable can be discrete or continuous, so $f(y)$ represents either a probability mass function or a probability density function. A more useful parameterization of generalized linear models is by the mean and variance of the distribution:

$$E(Y) = b'(\theta)$$
$$\text{Var}(Y) = b''(\theta)\phi$$

In generalized linear models, the mean $\mu$ of the response distribution is related to linear regression parameters through a link function,

$$g(\mu_i) = x_i'\beta$$

for the $i$th observation, where $x_i$ is a fixed known vector of explanatory variables and $\beta$ is a vector of regression parameters. The GENSELECT procedure parameterizes models in terms of the regression parameters $\beta$ and either the dispersion parameter $\phi$ or a parameter that is related to $\phi$, depending on the model. For exponential family models, the distribution variance is $\text{Var}(Y) = \phi V(\mu)$, where $V(\mu)$ is a variance function that depends only on $\mu$.

Other distributions that are not exponential family models but are sometimes useful in statistical modeling are also included in the GENSELECT procedure.
Response Distributions

The response distribution is the probability distribution of the response (target) variable. The GENSELECT procedure can fit data for the following exponential family distributions:

- binary distribution
- binomial distribution
- gamma distribution
- geometric distribution
- exponential distribution
- inverse Gaussian distribution
- multinomial for ordinal or nominal responses
- negative binomial distribution
- normal (Gaussian) distribution
- Poisson distribution
- Tweedie distribution

The following distributions are not exponential family members but are also included in the GENSELECT procedure:

- beta distribution
- generalized Poisson distribution
- t distribution
- Weibull distribution

Expressions for the probability distributions (probability density functions for continuous variables or probability mass functions for discrete variables) are shown in the section “Response Probability Distribution Functions” on page 388. The expressions for the log-likelihood functions of these distributions are presented in the section “Log-Likelihood Functions” on page 393.

The binary (or Bernoulli) distribution is the elementary distribution of a discrete random variable that can take two values, which have the probabilities \( p \) and \( 1 - p \). Suppose the random variable is denoted as \( Y \) and

\[
\Pr(Y = 1) = p \\
\Pr(Y = 0) = 1 - p
\]

The value that is associated with probability \( p \) is often called the event or “success”; the complementary event is called the nonevent or “failure.” A Bernoulli experiment is a random draw from a binary distribution and generates events with probability \( p \).
If $Y_1, \ldots, Y_n$ are $n$ independent Bernoulli random variables, then their sum follows a binomial distribution. In other words, if $Y_i = 1$ denotes an event (success) in the $i$th Bernoulli trial, a binomial random variable is the number of events (successes) in $n$ independent Bernoulli trials. If you use the events/trials syntax in the MODEL statement and you specify the DISTRIBUTION=BINOMIAL option, the GENSELECT procedure fits the model as if the data had arisen from a binomial distribution. For example, the following statements fit a binomial regression model that has the regressors $x_1$ and $x_2$. The variables $e$ and $t$ represent the events and trials, respectively, for the binomial distribution:

```
proc genselect;
  model e/t = x1 x2 / distribution=Binomial;
run;
```

If the events/trials syntax is used, then both variables must be numeric and the value of the events variable cannot be less than 0 or exceed the value of the trials variable. A “Response Profile” table is not produced for binomial data, because the response variable is not subject to levelization.

If the response variable is listed in a CLASS statement and a response distribution is not specified in a DISTRIBUTION= option, then a binary distribution or a multinomial distribution that uses the default or specified link function is assumed. If the response variable is not listed in a CLASS statement and a response distribution is not specified in a DISTRIBUTION= option, then a normal distribution that uses the default or specified link function is assumed.

The multinomial distribution is a generalization of the binary distribution and allows for more than two outcome categories. Because there are more than two possible outcomes for the multinomial distribution, the terminology of “successes,” “failures,” “events,” and “nonevents” no longer applies. With multinomial data, these outcomes are generically referred to as “categories” or levels.

Whenever the GENSELECT procedure determines that the response variable is listed in a CLASS statement and has more than two levels (unless the events/trials syntax is used), it fits the model as if the data had arisen from a multinomial distribution. By default, the procedure then assumes that the response categories are ordered, and it fits a cumulative link model by applying the default or specified link function.

If the response categories are unordered, then you should fit a generalized logit model by choosing LINK=GLOGIT in the MODEL statement.

---

**Response Probability Distribution Functions**

**Beta Distribution**

\[
\begin{align*}
  f(y) & = \frac{\Gamma(\phi)}{\Gamma(\mu \phi)\Gamma((1-\mu)\phi)} y^{\mu \phi - 1}(1-y)^{(1-\mu)\phi - 1} \quad \text{for } 0 < y < 1 \\
  E(Y) & = \mu \\
  \text{Var}(Y) & = \frac{\mu(1-\mu)/(1+\phi)}{\phi > 0}
\end{align*}
\]

This parameterization of the beta distribution comes from Ferrari and Cribari-Neto (2004).
Binary Distribution

\[
f(y) = \begin{cases} 
  p & \text{for } y = 1 \\
  1 - p & \text{for } y = 0
\end{cases}
\]

\[E(Y) = p\]

\[\text{Var}(Y) = p(1 - p)\]

Binomial Distribution

\[
f(y) = \binom{n}{r} p^r (1 - p)^{n-r} \text{ for } y = \frac{r}{n}, \ r = 0, 1, 2, \ldots, n
\]

\[E(Y) = \mu\]

\[\text{Var}(Y) = \frac{\mu(1 - \mu)}{n}\]

Exponential Distribution

\[
f(y) = \frac{1}{\mu} \exp\left(\frac{-y}{\mu}\right) \text{ for } 0 < y < \infty
\]

\[E(Y) = \mu\]

\[\text{Var}(Y) = \mu^2\]

The exponential distribution is a special case of the gamma where \( \nu = 1 \).

Gamma Distribution

\[
f(y) = \frac{1}{\Gamma(\nu)\mu^\nu} \left(\frac{y}{\mu}\right)^\nu \exp\left(-\frac{y}{\mu}\right) \text{ for } 0 < y < \infty
\]

\[\phi = \frac{1}{\nu}\]

\[E(Y) = \mu\]

\[\text{Var}(Y) = \frac{\mu^2}{\nu}, \ \nu > 0\]

For the gamma distribution, \( \nu = \frac{1}{\phi} \) is the estimated dispersion parameter that is displayed in the output. The parameter \( \nu \) is sometimes called the gamma index parameter.
Generalized Poisson Distribution

\[ \xi = 1 - \exp(-\phi), \quad \phi \geq 0 \]
\[ \mu^* = \mu - \xi (\mu - y) \]
\[ f(y) = (\mu^*)^{(y-1)} \frac{((1-\xi)\mu)}{\Gamma(y+1)} \exp(-\mu^*) \quad \text{for } y = 0, 1, 2, \ldots \]
\[ \text{E}(Y) = \mu \]
\[ \text{Var}(Y) = \frac{\mu}{(1 - \xi)^2} \]

The generalized Poisson distribution provides an overdispersed alternative to the Poisson distribution; \( \phi = \xi = 0 \) produces the mass function of a regular Poisson random variable. For more information about the generalized Poisson distribution and a comparison with the negative binomial distribution, see Joe and Zhu (2005). For the generalized Poisson distribution, \( \phi \) is the estimated dispersion parameter that is displayed in the output.

Geometric Distribution

\[ f(y) = \frac{\mu^y}{(1 + \mu)^{y+1}} \quad \text{for } y = 0, 1, 2, \ldots \]
\[ \text{E}(Y) = \mu \]
\[ \text{Var}(Y) = \mu + \mu^2 \]

The geometric distribution is a special case of the negative binomial where \( \phi = 1 \).

Inverse Gaussian Distribution

\[ f(y) = \frac{1}{\sqrt{2\pi y^3}\sigma} \exp \left[ -\frac{1}{2y} \left( \frac{y - \mu}{\mu\sigma} \right)^2 \right] \quad \text{for } 0 < y < \infty \]
\[ \phi = \sigma^2 \]
\[ \text{Var}(Y) = \phi \mu^3 \]

Multinomial Distribution

\[ f(y_1, y_2, \ldots, y_k) = \frac{m!}{y_1! y_2! \cdots y_k!} p_1^{y_1} p_2^{y_2} \cdots p_k^{y_k} \]
Negative Binomial Distribution

\[ f(y) = \frac{\Gamma(y + 1/k)}{\Gamma(y + 1)\Gamma(1/k)} \frac{(k\mu)^y}{(1 + k\mu)^{y+1/k}} \text{ for } y = 0, 1, 2, \ldots \]

\[ \phi = k \]

\[ E(Y) = \mu \]

\[ \text{Var}(Y) = \mu + \phi \mu^2 \]

For the negative binomial distribution, \( k \) is the estimated dispersion parameter that is displayed in the output.

Normal Distribution

\[ f(y) = \frac{1}{\sqrt{2\pi}\sigma} \exp\left[ -\frac{1}{2} \left( \frac{y - \mu}{\sigma} \right)^2 \right] \text{ for } -\infty < y < \infty \]

\[ \phi = \sigma^2 \]

\[ E(Y) = \mu \]

\[ \text{Var}(Y) = \phi \]

Poisson Distribution

\[ f(y) = \frac{\mu^y e^{-\mu}}{y!} \text{ for } y = 0, 1, 2, \ldots \]

\[ E(Y) = \mu \]

\[ \text{Var}(Y) = \mu \]

(Shifted) \( t \) Distribution

\[ z = \frac{\Gamma(0.5(v + 1))}{\sqrt{\pi v\phi} \Gamma(0.5v)} \]

\[ f(y) = z \left( 1 + \frac{(y - \mu)^2}{v\phi} \right)^{-0.5(v+1)} \text{ for } -\infty < y < \infty \]

\[ E(Y) = \mu \]

\[ \text{Var}(Y) = \phi v/(v - 2), \quad v \geq 3 \]
You can specify the degrees of freedom parameter \( \nu \) in the \texttt{DISTRIBUTION=t(\nu)} option. If you do not specify it, a value of \( \nu = 3 \) is used.

Note that this form of the \( t \) distribution is not a noncentral distribution, but that of a shifted central \( t \) random variable.

**Tweedie Distribution**

The Tweedie model is a generalized linear model from the exponential family. The Tweedie distribution is characterized by three parameters: the mean \( \mu \), the dispersion \( \phi \), and the power \( p \). The variance of the distribution is \( \phi \mu^p \). For values of \( p \) in the range \( 1 < p < 2 \), a Tweedie random variable can be represented as a Poisson sum of gamma distributed random variables. That is,

\[
Y = \sum_{i=1}^{N} Y_i
\]

where \( N \) has a Poisson distribution that has mean \( \lambda = \frac{\mu^{2-p}}{\phi(2-p)} \) and the \( Y_i \)s have independent, identical gamma distributions, each of which has an expected value \( E(Y_i) = \phi(2-p)\mu^{p-1} \) and an index parameter \( \nu_i = \frac{2-p}{p-1} \).

In this case, \( Y \) has a discrete mass at 0, \( \Pr(Y = 0) = \Pr(N = 0) = \exp(-\lambda) \), and the probability density of \( Y \), \( f(y) \), is represented by an infinite series for \( y > 0 \). The GENSELECT procedure restricts the power parameter to satisfy \( 1.1 \leq p \) for numerical stability in model fitting. The Tweedie distribution does not have a general closed form representation for all values of \( p \). For more information about the Tweedie distribution, see Frees (2010).

The distribution mean and variance are:

\[
E(Y) = \mu \\
\text{Var}(Y) = \phi \mu^p
\]

**Weibull Distribution**

\[
f(y) = \frac{1}{\mu \phi} \left( \frac{y}{\mu} \right)^{1-1} \exp \left( -\frac{y}{\mu} \right)^{\frac{1}{\phi}} \text{ for } 0 < y < \infty
\]

\[
E(Y) = \mu \Gamma(1 + \phi) \\
\text{Var}(Y) = \mu^2 \left[ \Gamma(1 + 2\phi) - \Gamma^2(1 + \phi) \right], \quad \phi > 0
\]
Log-Likelihood Functions

The GENSELECT procedure forms the log-likelihood functions of the various models as

\[ L(\mu; y) = \sum_{i=1}^{n} f_i l(\mu_i; y_i, w_i) \]

where \( l(\mu_i; y_i, w_i) \) is the log-likelihood contribution of the \( i \)th observation that has weight \( w_i \), and \( f_i \) is the value of the frequency variable. For the determination of \( w_i \) and \( f_i \), see the WEIGHT and FREQ statements.

The individual log-likelihood contributions for the various distributions are as follows.

In the following, the mean parameter \( \mu_i \) for each observation \( i \) is related to the regression parameters \( \beta_i \) through the linear predictor \( \eta_i = \mathbf{x}_i' \beta \) by

\[ \mu_i = g^{-1}(\eta_i) \]

where \( g \) is the link function.

**Beta Distribution**

\[
l(\mu_i; y_i, w_i) = \log \left\{ \frac{\Gamma(\phi/w_i)}{\Gamma(\mu_i\phi/w_i)\Gamma((1-\mu_i)\phi/w_i)} \right\}
+ (\mu_i\phi/w_i - 1) \log\{y_i\}
+ ((1 - \mu_i)\phi/w_i - 1) \log\{1 - y_i\}
\]

where \( \phi \) is the dispersion parameter that is displayed in the output.

**Binary Distribution**

\[
\eta_i = \mathbf{x}_i' \beta \\
\mu_i = g^{-1}(\eta_i) \\
l(\mu_i; y_i) = y_i \log\{\mu_i\} + (1 - y_i) \log\{1 - \mu_i\}
\]

Here, \( \mu_i \) is the probability of an event, and the variable \( y_i \) takes the value 1 for an event and 0 for a nonevent. The inverse link function \( g^{-1}(\cdot) \) maps from the scale of the linear predictor \( \eta_i \) to the scale of the mean. For example, for the logit link (the default),

\[ \mu_i = \frac{\exp\{\eta_i\}}{1 + \exp\{\eta_i\}} \]

You can control which binary outcome in your data is modeled as the event by specifying the response-options in the MODEL statement, and you can choose the link function by specifying the LINK= option in the MODEL statement.

If you specify a WEIGHT statement and \( w_i \) denotes the weight for the current observation, the log-likelihood function is computed as

\[ l(\mu_i; y_i, w_i) = w_i l(\mu_i; y_i) \]
Binomial Distribution

\[ \eta_i = x_i^T \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = w_i \left( y_i \log \{\mu_i\} + (n_i - y_i) \log \{1 - \mu_i\} \right) + w_i \left( \log \{\Gamma(n_i + 1)\} - \log \{\Gamma(y_i + 1)\} - \log \{\Gamma(n_i - y_i + 1)\} \right) \]

where \( y_i \) and \( n_i \) are the values of the events and trials of the \( i \)th observation, respectively. The value \( \mu_i \) measures the probability of events (successes) in the underlying Bernoulli distribution whose aggregate follows the binomial distribution.

Exponential Distribution

\[ l(\mu_i; y_i, w_i) = w_i \log \left\{ \frac{w_i y_i}{\mu_i} \right\} - \frac{w_i y_i}{\mu_i} - \log \{y_i \Gamma(w_i)\} \]

Gamma Distribution

\[ \eta_i = x_i^T \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = \frac{w_i}{\phi} \log \left( \frac{w_i y_i}{\phi \mu_i} \right) - \frac{w_i y_i}{\phi \mu_i} - \log(y_i) - \log \left( \Gamma \left( \frac{w_i}{\phi} \right) \right) \]

For the gamma distribution, \( \nu = \frac{1}{\phi} \) is the estimated dispersion parameter that is displayed in the output.

Generalized Poisson Distribution

\[ \xi_i = (1 - \exp\{-\phi\})/w_i \]
\[ \mu_i^* = \mu_i - \xi(\mu_i - y_i) \]
\[ l(\mu_i^*; y_i, w_i) = \log \{\mu_i^* - \xi y_i\} + (y_i - 1) \log \{\mu_i^*\} - \mu_i^* - \log \{\Gamma(y_i + 1)\} \]

where \( \phi \) is the dispersion parameter that is displayed in the output.

Geometric Distribution

\[ l(\mu_i; y_i, w_i) = y_i \log \left( \frac{\mu_i}{w_i} \right) - (y_i + w_i) \log \left( \frac{1 + \mu_i}{w_i} \right) + \log \left\{ \frac{\Gamma(y_i + w_i)}{\Gamma(w_i) \Gamma(y_i + 1)} \right\} \]
Inverse Gaussian Distribution

\[ \eta_i = x'_i \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = - \frac{1}{2} \left[ \frac{w_i(y_i - \mu_i)^2}{y_i \mu^2 \phi} + \log \left( \frac{\phi y_i^3}{w_i} \right) + \log(2\pi) \right] \]

where \( \phi \) is the dispersion parameter that is displayed in the output.

Multinomial Distribution

The multinomial distribution that the GENSELECT procedure models is a generalization of the binary distribution; it is the distribution of a single draw from a discrete distribution that has \( J \) possible values. Thus, the log-likelihood function for the \( i \)th observation is

\[ l(\pi_i; y_i, w_i) = w_i \sum_{j=1}^{J} y_{ij} \log(\pi_{ij}) \]

In this expression, \( J \) denotes the number of response categories (the number of possible outcomes) and \( \pi_{ij} \) is the probability that the \( i \)th observation takes on the response value associated with category \( j \). The category probabilities must satisfy

\[ \sum_{j=1}^{J} \pi_j = 1 \]

and the constraint is satisfied by modeling \( J - 1 \) categories.

If your response \( Y \) has more than two values and they can be ordered (for example, \( Y \in \{1, \ldots, J - 1, J\} \)), then the GENSELECT procedure fits ordinal response models of the form

\[ g(\pi_j \mid x) = \alpha_j + \beta'x, \quad j = 1, \ldots, J - 1 \]

where \( g \) is the link function and \( \pi_j = \Pr(Y \leq j) \) are cumulative probabilities of the ordered response categories.

If your response \( Y \) has more than two values and they have no natural ordering, then the GENSELECT procedure fits a generalized or baseline-category logit model, which has the form

\[ \log \left( \frac{\Pr(Y = j \mid x)}{\Pr(Y = J \mid x)} \right) = \alpha_j + \beta'_j x, \quad j = 1, \ldots, J - 1 \]

where the \( \beta_1, \ldots, \beta_{J-1} \) are \( J - 1 \) vectors of slope parameters. These models are a special case of the discrete choice or conditional logit models introduced by McFadden (1974).

In models that have ordered response categories, the probabilities are expressed in cumulative form, so the last category is redundant. In generalized logit models (multinomial models that have unordered categories), one category is chosen as the reference category, and the linear predictor in the reference category is set to 0. For more information, see the \texttt{REF= response-option} in the MODEL statement.
**Negative Binomial Distribution**

\[ \eta_i = x_i^\top \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = y_i \log \left( \frac{k\mu_i}{w_i} \right) - (y_i + w_i/k) \log \left( 1 + \frac{k\mu_i}{w_i} \right) + \log \left( \frac{\Gamma(y_i + w_i/k)}{\Gamma(y_i + 1)\Gamma(w_i/k)} \right) \]

where \( k \) is the negative binomial dispersion parameter that is displayed in the output.

**Normal Distribution**

\[ \eta_i = x_i^\top \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = -\frac{1}{2} \left[ \frac{w_i(y_i - \mu_i)^2}{\phi} + \log \left( \frac{\phi}{w_i} \right) + \log(2\pi) \right] \]

where \( \phi \) is the dispersion parameter that is displayed in the output.

**Poisson Distribution**

\[ \eta_i = x_i^\top \beta \]
\[ \mu_i = g^{-1}(\eta_i) \]
\[ l(\mu_i; y_i, w_i) = w_i[y_i \log(\mu_i) - \mu_i - \log(y_i!)] \]

**t Distribution**

\[ z_i = -0.5 \log \left\{ \frac{\phi}{w_i} \right\} + \log \left\{ \Gamma(0.5(v + 1)) \right\} \]
\[ - \log \left\{ \Gamma(0.5v) \right\} - 0.5 \times \log \left\{ \pi v \right\} \]
\[ l(\mu_i; y_i, w_i) = - \left( \frac{v + 1}{2} \right) \log \left\{ 1 + \frac{w_i(y_i - \mu_i)^2}{v \cdot \phi} \right\} + z_i \]

where \( \phi \) is the dispersion parameter that is displayed in the output.

**Tweedie Distribution**

The Tweedie distribution does not in general have a closed form log-likelihood function in terms of the mean, dispersion, and power parameters. The form of the log likelihood is

\[ L(\mu; y) = \sum_{i=1}^{n} f_i l(\mu_i; y_i, w_i) \]

where

\[ l(\mu_i, y_i, w_i) = \log(f(y_i; \mu_i, p, \frac{\phi}{w_i})) \]

and \( f(y, \mu, p, \phi) \) is the Tweedie probability distribution, which is described in the section “Tweedie Distribution” on page 392. Evaluation of the Tweedie log likelihood for model fitting is performed numerically as described in Dunn and Smyth (2005, 2008).
**Quasi-likelihood**

The extended quasi-likelihood (EQL) is constructed according to the definition of McCullagh and Nelder (1989, Chapter 9) as

$$Q_p(y, \mu, \phi, p) = \sum_i q(y_i, \mu_i, \phi, p)$$

where the contribution from an observation is

$$q(y_i, \mu_i, \phi, p) = -0.5 \log(2\pi \frac{\phi}{w_i} y_i^p) - w_i \left( \frac{y_i^{2-p} - (2-p)y_i \mu_i^{1-p} + (1-p)\mu_i^{2-p}}{(1-p)(1-p)} \right)/\phi$$

where $1 < p < 2$. This EQL is used in computing initial values for the iterative maximization of the Tweedie log likelihood, as specified using the OPTMETHOD= Tweedie optimization-option in Table 6.6. If you specify the OPTMETHOD=EQL in Table 6.6, then the parameter estimates are computed by using the EQL instead of the log likelihood.

**Weibull Distribution**

$$l(\mu_i; y_i, w_i) = -w_i \left\{ \frac{\phi - 1}{\phi} \log \left( \frac{y_i}{\mu_i} \right) + \log(\mu_i\phi) + \exp \left[ \log \left( \frac{y_i}{\mu_i} \right) / \phi \right] \right\}$$

where $\phi$ is the dispersion parameter that is displayed in the output.

---

**Existence of Maximum Likelihood Estimates**

The likelihood equation for a logistic regression model does not always have a finite solution. Sometimes there is a nonunique maximum on the boundary of the parameter space, at infinity. The existence, finiteness, and uniqueness of maximum likelihood estimates for the logistic regression model depend on the patterns of data points in the observation space (Albert and Anderson 1984; Santner and Duffy 1986).

Consider a binary response model. Let $Y_j$ be the response of the $j$th subject, and let $x_j$ be the vector of explanatory variables (including the constant 1 that is associated with the intercept). There are three mutually exclusive and exhaustive types of data configurations:

**Complete separation**  There is a complete separation of data points if there exists a vector $b$ that correctly allocates all observations to their response groups; that is,

$$\begin{align*}
    \begin{cases}
        b'x_j > 0 & Y_j = 0 \\
        b'x_j < 0 & Y_j = 1 
    \end{cases}
\end{align*}$$

This configuration produces nonunique infinite estimates. If the iterative process of maximizing the likelihood function is allowed to continue, then the log likelihood diminishes to 0 and the dispersion matrix becomes unbounded.

**Quasi-complete separation**  The data are not completely separable, but there is a vector $b$ such that

$$\begin{align*}
    \begin{cases}
        b'x_j \geq 0 & Y_j = 0 \\
        b'x_j \leq 0 & Y_j = 1 
    \end{cases}
\end{align*}$$
and equality holds for at least one subject in each response group. This configuration also yields nonunique infinite estimates. If the iterative process of maximizing the likelihood function is allowed to continue, then the dispersion matrix becomes unbounded and the log likelihood diminishes to a nonzero constant.

**Overlap** If neither complete nor quasi-complete separation exists in the sample points, there is an overlap of sample points. In this configuration, the maximum likelihood estimates exist and are unique.

The GENSELECT procedure uses a simple empirical approach to recognize the data configurations that lead to infinite parameter estimates. The basis of this approach is that any convergence method of maximizing the log likelihood must yield a solution that indicates complete separation, if such a solution exists. Upon convergence, if the predicted response equals the observed response for every observation, there is a complete separation of data points.

If the data are not completely separated, if an observation is identified to have an extremely large probability (≥ 0.95) of predicting the observed response, and if there have been at least eight iterations, then there are two possible situations. First, there is overlap in the data set, the observation is an atypical observation of its own group, and the iterative process stopped when a maximum was reached. Second, there is quasi-complete separation in the data set, and the asymptotic dispersion matrix is unbounded. If any of the diagonal elements of the dispersion matrix for the standardized observation vector (all explanatory variables standardized to zero mean and unit variance) exceeds 5,000, then PROC GENSELECT declares quasi-complete separation; if any of the diagonal elements exceeds 1,000, then the procedure displays a message indicating that quasi-complete separation might be detectable by increasing the number of iterations. If either complete separation or quasi-complete separation is detected, a note is displayed in the procedure output.

Checking for quasi-complete separation is less foolproof than checking for complete separation. If neither type of separation is discovered and your parameter estimates have large standard errors, then your data might be separable. The NOCHECK option in the MODEL statement turns off the process of checking for infinite parameter estimates; the MINITER= option in the PROC GENSELECT statement increases the number of iterations.

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### The LASSO Method of Model Selection

#### LASSO Selection

The GENSELECT procedure implements the group LASSO method, which is described in the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.” The current section provides some background about the LASSO method that you need in order to understand the group LASSO method.

LASSO (least absolute shrinkage and selection operator) selection arises from a constrained form of ordinary least squares regression in which the sum of the absolute values of the regression coefficients is constrained to be smaller than a specified parameter. More precisely, let $\mathbf{X} = (\mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_m)$ denote the matrix of covariates, and let $\mathbf{y}$ denote the response. Then for a given parameter $t$, the LASSO regression coefficients $\hat{\beta} = (\hat{\beta}_1, \hat{\beta}_2, \ldots, \hat{\beta}_m)$ are the solution to the constrained least squares problem:

$$
\min \| \mathbf{y} - \mathbf{X} \hat{\beta} \|^2 \quad \text{subject to} \quad \sum_{j=1}^{m} |\hat{\beta}_j| \leq t
$$
For generalized linear models, the LASSO regression coefficients \( \beta = (\beta_1, \beta_2, \ldots, \beta_m) \) are the solution to the constrained optimization problem,

\[
\min\{-L(\mu; y)\} \quad \text{subject to} \quad \sum_{j=1}^{m} |\beta_j| \leq t
\]

where \( L \) is the log-likelihood function defined in the section “Log-Likelihood Functions” on page 393.

Provided that the LASSO parameter \( t \) is small enough, some of the regression coefficients will be exactly zero. Hence, you can think of the LASSO method as selecting a subset of the regression coefficients for each LASSO parameter. By increasing the LASSO parameter in discrete steps, you obtain a sequence of regression coefficients for which the nonzero coefficients at each step correspond to selected parameters. For more information about the LASSO method, see, for example, Hastie, Tibshirani, and Friedman (2009).

Some distributions involve a dispersion parameter (the parameter \( \phi \) in the expressions for the log likelihood). These parameters are not estimated by the LASSO optimization algorithm, and they are set to either the default value or a value that you specify. You can use the MODEL statement option PHI= to set the dispersion to a fixed value.

**Partition Fit Statistics**

Specifying a PARTITION statement modifies the display of many tables by adding separate rows or columns for the training, validation, and test data tables. In addition, the “Fit Statistics” table displays the average square error, which is useful for assessing the model and which should be very similar for the different roles when the training data are representative of the other data partitions. For more information, see the section “Model Fit and Assessment Statistics” on page 399.

**Model Fit and Assessment Statistics**

The statistics that are defined in this section are useful for assessing the fit of the model to your data; they are displayed in the “Fit Statistics” table. The statistics are computed for each data role when you specify a PARTITION statement.

**Information Criteria**

The calculation of the information criteria uses the following formulas, where \( p \) denotes the number of effective parameters in the candidate model, \( F \) denotes the sum of frequencies used, and \( l \) is the log likelihood evaluated at the converged estimates:

\[
\begin{align*}
\text{AIC} &= -2l + 2p \\
\text{AICC} &= \begin{cases} 
-2l + 2pF/(F - p - 1) & \text{when } F > p + 2 \\
-2l + 2p(p + 2) & \text{otherwise}
\end{cases} \\
\text{SBC} &= -2l + p \log(F)
\end{align*}
\]

If you do not specify a FREQ statement, \( F \) equals \( n \), the number of observations used.
These measures are most useful for comparing competing models that are not necessarily nested—that is, models that cannot be reduced to one another by simple constraints on the parameter space. Smaller values of the measures indicate better models.

**Average Square Error**

The average square error (ASE) is the average of the squared differences between the responses and the predictions. When you have a discrete number of response levels, the ASE is modified as shown in Table 6.11 (Brier 1950; Murphy 1973); it is also called the Brier score or Brier reliability.

<table>
<thead>
<tr>
<th>Response Type</th>
<th>ASE (Brier Score)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binary</td>
<td>$\frac{1}{F} \sum_i f_i (y_i (1 - \hat{\pi}_i)^2 + (1 - y_i) \hat{\pi}_i^2)$</td>
</tr>
<tr>
<td>Binomial</td>
<td>$\frac{1}{F} \sum_i f_i (r_i / t_i - \hat{\pi}_i)^2$</td>
</tr>
<tr>
<td>Multinomial</td>
<td>$\frac{1}{F} \sum_i f_i \sum_j (y_{ij} - \hat{\pi}_{ij})^2$</td>
</tr>
</tbody>
</table>

In Table 6.11, $F = \sum_i f_i$, $r_i$ is the number of events, $t_i$ is the number of trials in binomial response models, $y_i = 1$ for events and 0 for nonevents in binary response models, and $\hat{\pi}_i$ is the predicted probability of an event. For polytomous response models, $y_{ij} = 1$ if the $i$th observation has response level $j$, and $\pi_{ij}$ is the model-predicted probability of response level $j$ for observation $i$.

**Predicted Values and Regression Diagnostics**

You can produce observationwise predicted values, confidence limits, and regression diagnostics developed by Williams (1987) and Pregibon (1981) by specifying the OUTPUT statement. For multinomial response data, you can likewise produce observationwise predicted probabilities, confidence limits, and raw residuals.

Given a vector of covariates $x_i$ for the $i$th observation in your data table, and the model-predicted parameter estimates $\hat{\beta}$, you can write the linear predictor $\hat{\eta}_i = x_i' \hat{\beta}$. The mean of the $i$th observation $\mu_i(\hat{\beta})$, or the model-predicted event probability $\hat{\pi}_i$, is $\mu_i(\hat{\beta}) = \hat{\pi}_i = g^{-1}(\hat{\eta}_i)$, where the link function $g$ is chosen by specifying the LINK= option. The variance function of the distribution is $V(\mu)$, and $\Sigma$ is the estimated covariance of $\hat{\beta}$. Denote the frequency of the $i$th observation as $f_i$ and the weight as $w_i$.

For ordinal response models, the predicted cumulative probabilities are computed by using the appropriate model-predicted intercept parameters $\hat{\alpha}_j$ and letting $\beta$ consist of the slope parameters: $\hat{\eta}_{ij} = g(Pr(Y \leq j | x_i)) = \hat{\alpha}_j + x_i' \hat{\beta}$ and $\hat{\pi}_{ij} = Pr(Y \leq j | x_i) = g^{-1}(\hat{\eta}_{ij})$ for $1 \leq j < J$.

For nominal response models, the predicted probabilities are computed by using the appropriate model-predicted intercept parameters $\hat{\alpha}_j$ and letting $\beta_j$ consist of the slope parameters: $\hat{\eta}_{ij} = g(Pr(Y = j | x_i)) = \hat{\alpha}_j + x_i' \hat{\beta}_j$ and $\hat{\pi}_{ij} = Pr(Y = j | x_i) = g^{-1}(\hat{\eta}_{ij})$ for $1 \leq j < J$.

**Confidence Intervals**

Approximate confidence intervals for predicted values can be computed as follows. The variance of the linear predictor is estimated by

$$\sigma^2 = x_i' \Sigma x_i$$
For multinomial models, the variance also depends on the response function. Let \( \delta_j \) be a \((J - 1)\) column vector whose \( j \)th entry is equal to 1 and all other entries are equal to 0. Redefine \( x_i = (\delta_j', x_i')', \eta_i = \eta_{ij} \), and \( \pi_i = \pi_{ij} \). Then

\[
\hat{\sigma}^2(\eta_i) = x_i' \Sigma x_i
\]

The asymptotic \( 100(1 - \alpha)\% \) confidence interval for \( \eta_i \) is

\[
\hat{\eta}_i \pm z_{\alpha/2} \hat{\sigma}(\hat{\eta}_i)
\]

where \( z_{\alpha/2} \) is the \( 100(1 - \alpha/2)\)th percentile point of a standard normal distribution.

The predicted value and the \( 100(1 - \alpha)\% \) confidence limits for \( p_i \) are obtained by back-transforming the corresponding measures for the linear predictor. So the confidence limits are

\[
g^{-1} \left[ \hat{\eta}_i \pm z_{\alpha/2} \hat{\sigma}(\hat{\eta}_i) \right]
\]

### Hat-Matrix Diagonals

The diagonal elements of the hat matrix are useful in detecting extreme points in the design space, where they tend to have larger values. For the generalized linear model, the variance of the \( i \)th individual observation is

\[
v_i = \frac{\phi V(\mu_i)}{f_i w_i}
\]

For the \( i \)th observation, let

\[
w_{ei} = v_i^{-1} (g'(\mu_i))^{-2}
\]

where \( g'(\mu_i) \) is the derivative of the link function evaluated at \( \mu_i \). Let \( W \) be the diagonal matrix, with \( w_{ei} \) denoting the \( i \)th diagonal element, which is used in computing the expected information matrix. Define the leverage, or hat-matrix diagonal, \( h_i \), as the \( i \)th diagonal element of the matrix

\[
W^{1/2} X (X'WX)^{-1} X' W^{1/2}
\]

For binary or binomial models, if the estimated probability is extreme (less than 0.1 and greater than 0.9, approximately), then the hat-matrix diagonal might be greatly reduced in value. Consequently, when an observation has a very large or very small estimated probability, its leverage is not a good indicator of the observation’s distance from the design space (Hosmer and Lemeshow 2000, p. 171).

### Residuals

Residuals are useful in identifying observations that are not explained well by the model. For the binomial distribution, the raw residual is defined as

\[
r_i = y_i / t_i - \hat{p}_i
\]

where \( y_i \) is the number of event responses out of \( t_i \) trials for the \( i \)th observation. For single-trial syntax, \( t_i = 1 \) and \( y_i = 1 \) if the ordered response is 1 and \( y_i = 0 \) otherwise. For multinomial response data, the raw residual is

\[
y_{ij} - \hat{\pi}_{ij}
\]
where \( y_{ij} = 1 \) if the \( i \)th observation has response level \( j \) and \( y_{ij} = 0 \) otherwise, and \( \hat{\pi}_{ij} \) are the model-predicted probabilities of response level \( j \) for observation \( i \).

For other generalized linear models, the raw residual is

\[
    r_i = y_i - \hat{p}_i
\]

where \( y_i \) is the observed response and \( \hat{p}_i \) is the predicted value.

The Pearson residual is the square root of the \( i \)th observation’s contribution to Pearson’s chi-square:

\[
    r_{Pi} = r_i \sqrt{\frac{f_i w_i}{V(\mu_i)}}
\]

The deviance residual is the square root of the contribution of the \( i \)th observation to the deviance, with the sign of the raw residual,

\[
    r_{Di} = (\text{sign}(r_i)) \sqrt{d_i}
\]

For example, for the binomial distribution,

\[
    d_i = 2 f_i w_i t_i \left[ y_i/t_i \log \left( \frac{y_i/t_i}{\mu_i} \right) + (1 - y_i/t_i) \log \left( \frac{1 - y_i/t_i}{1 - \mu_i} \right) \right]
\]

The working residual is

\[
    r_{Wi} = r_i \left( \frac{\partial \mu_i}{\partial \eta_i} \right)^{-1}
\]

The Pearson residuals, standardized to have unit asymptotic variance, are

\[
    r_{SPi} = \frac{r_{Pi}}{\sqrt{1 - h_i}}
\]

The deviance residuals, standardized to have unit asymptotic variance, are

\[
    r_{SDi} = \frac{r_{Di}}{\sqrt{1 - h_i}}
\]

The likelihood residuals, which estimate components of a likelihood ratio test of deleting an individual observation, are a weighted combination of the standardized Pearson and deviance residuals,

\[
    r_{Li} = \text{sign}(r_i) \sqrt{h_i r_{SPi}^2 + (1 - h_i) r_{SDi}^2}
\]
Other Regression Diagnostics

The CBAR statistic is a confidence interval displacement diagnostic that provides a scalar measure of the influence of an individual observation on $\hat{\beta}$. This diagnostic is based on the same idea as Cook’s distance in linear regression theory (Cook and Weisberg 1982), but it uses the one-step estimate:

$$C_i = r^2_P h_i / (1 - h_i)$$

The DIFDEV and DIFCHISQ statistics are diagnostics for detecting ill-fitted observations—observations that contribute heavily to the disagreement between the data and the predicted values of the fitted model. DIFDEV is the change in the deviance that results from deleting an individual observation, and DIFCHISQ is the change in the Pearson chi-square statistic that results from the same deletion. By using the one-step estimate, DIFDEV and DIFCHISQ for the $i$th observation are computed as follows:

$$DIFDEV_i = r^2_D h_i$$
$$DIFCHISQ_i = C_i / h_i$$

Joint Tests and Type 3 Tests

Linear hypotheses for $\beta$ are expressed in matrix form as

$$H_0: L\beta = c$$

where $L$ is a matrix of coefficients for the linear hypotheses and $c$ is a vector of constants. The vector of regression coefficients $\beta$ includes slope parameters and intercept parameters. The Wald chi-square statistic for testing $H_0$ is computed as

$$\chi^2_W = (L\hat{\beta} - c)' [L\hat{\Sigma}(\hat{\beta})L']^{-1} (L\hat{\beta} - c)$$

where $\hat{\Sigma}(\hat{\beta})$ is the estimated covariance matrix. Under $H_0$, $\chi^2_W$ has an asymptotic chi-square distribution with $r$ degrees of freedom, where $r$ is the rank of $L$.

For models that use less-than-full-rank parameterization (as specified by the PARAM=GLM option in the CLASS statement), a Type 3 test of an effect of interest (main effect or interaction) is a test of the Type III estimable functions that are defined for that effect. When the model contains no missing cells, the Type 3 test of a main effect is equivalent to testing the hypothesis of equal marginal means. For more information about Type III estimable functions, see the chapter “The GLM Procedure” and the section “The Four Types of Estimable Functions” in SAS/STAT User’s Guide. Also see Littell, Freund, and Spector (1991).

For models that use full-rank parameterization, all parameters are estimable when there are no missing cells, so it is unnecessary to define estimable functions. The standard test of an effect of interest in this case is the joint test that the values of the parameters associated with that effect are 0. For a model that uses effects parameterization (as specified by the PARAM=EFFECT option in the CLASS statement), the joint test for a main effect is equivalent to testing the equality of marginal means. For a model that uses reference parameterization (as specified by the PARAM=REF option in the CLASS statement), the joint test is equivalent to testing the equality of cell means at the reference level of the other model effects. For more information about the coding scheme and the associated interpretation of results, see Muller and Fetterman (2002, Chapter 14).
If there is no interaction term, the Type 3 test of an effect for a model that uses GLM parameterization is the same as the joint test of the effect for the model that uses full-rank parameterization. In this situation, the joint test is also called the Type 3 test. For a model that contains an interaction term and no missing cells, the Type 3 test of a component main effect under GLM parameterization is the same as the joint test of the component main effect under effect parameterization. Both test the equality of cell means. But this Type 3 test differs from the joint test under reference parameterization, which tests the equality of cell means at the reference level of the other component main effect. If some cells are missing, you can obtain meaningful tests only by testing a Type III estimation function, so in this case you should use GLM parameterization.

The results of a Type 3 test or a joint test do not depend on the order in which you specify the terms in the MODEL statement.

### Multithreading

The GENSELECT procedure allocates data to different threads and calculates the likelihood function, gradient, and Hessian by accumulating the values from all threads. For more information about how PROC GENSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

### Optimization Algorithms

Several optimization techniques are available in PROC GENSELECT. You can choose a particular optimizer by using the TECHNIQUE= option in the PROC GENSELECT statement. Table 6.12 summarizes the optimization techniques available in PROC GENSELECT.

<table>
<thead>
<tr>
<th>TECHNIQUE=</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>Trust region method</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>Newton-Raphson method with line search</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>Newton-Raphson method with ridging</td>
</tr>
<tr>
<td>QUANEW</td>
<td>Quasi-Newton methods</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>Double-dogleg method</td>
</tr>
<tr>
<td>CONGRA</td>
<td>Conjugate gradient methods</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>Nelder-Mead simplex method</td>
</tr>
</tbody>
</table>

There is no algorithm for optimizing general nonlinear functions that always finds the global optimum for a general nonlinear optimization problem in a reasonable amount of time. Because no single optimization technique is always superior to others, PROC GENSELECT provides a variety of optimization techniques that work well in various circumstances. However, you can devise problems for which none of the techniques in PROC GENSELECT can find the correct solution. Moreover, nonlinear optimization can be computationally expensive in terms of time and memory, so you must be careful when matching an algorithm to a problem. The section “Choosing an Optimization Algorithm” on page 80 in Chapter 2, “Shared Concepts,” is helpful in choosing a suitable optimization algorithm.
Displayed Output

The following sections describe the output that PROC GENSELECT produces. The output is organized into various tables, which are discussed in their order of appearance.

Model Information

The “Model Information” table displays basic information about the model, such as the response variable, the frequency variable, the link function, and the model category that the GENSELECT procedure selected based on your input and options. The “Model Information” table also displays the distribution of the data that is assumed by the GENSELECT procedure. For information about how the procedure determines the response distribution, see the section “Response Distributions” on page 387. If you specify the CODE statement, then the table displays the name of the variable in the scoring code that contains the classifications. If you do not also specify the PCATALL option, then the table also displays the name of the variable in the scoring code that contains the predicted probabilities.

Number of Observations

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis. If a FREQ statement is present, the table displays the sum of the frequencies that are read and used. If the events/trials syntax is used, the number of events and trials is also displayed. If you specify a PARTITION statement, the table displays the values for each role.

Response Profile

The “Response Profile” table displays the ordered value from which the GENSELECT procedure determines the probability being modeled as an event in a binary model and displays the ordering of categories in a multinomial model. For each response category level, the frequency used in the analysis is reported. You can affect the ordering of the response values by specifying response-options in the MODEL statement. For a binary model, the note that follows the “Response Profile” table indicates which outcome is modeled as the event. For an ordinal multinomial model, the note that follows the “Response Profile” table indicates how the ordered response levels are accumulated; for a nominal multinomial model, the note indicates the reference response level. If you specify a PARTITION statement, the table displays the values for each role.

Class Level Information

The “Class Level Information” table lists the levels of every variable specified in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by specifying the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by specifying the NOCLPRINT= option in the PROC GENSELECT statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.
Selection Information

When you specify the SELECTION statement, the GENSELECT procedure by default produces a series of tables that display information about the model selection. The “Selection Information” table informs you about the model selection method, selection and stop criteria, and other parameters that govern the selection. You can suppress this table by specifying DETAILS=NONE in the SELECTION statement.

Iteration History

When you specify the ITHIST option in the PROC GENSELECT statement, the “Iteration History” table displays, for each iteration of the optimization, the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element. The objective function that is used in the optimization in the GENSELECT procedure is normalized by default to enable comparisons across data tables that have different sampling intensity. You can control normalization by specifying the NORMALIZE= option in the PROC GENSELECT statement.

Convergence Status

The convergence status table is a small ODS table in the default output. In the listing, it appears as a message that indicates whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message indicates the reason for the failure. If you save the convergence status table to an output data set, a numeric Status variable is added that enables you to assess convergence programmatically. The values of the Status variable indicate the following:

- 0 Convergence was achieved, or an optimization was not performed (because TECHNIQUE=NONE is specified).
- 1 The objective function could not be improved.
- 2 Convergence was not achieved because of a user interruption or because a limit was exceeded, such as the maximum number of iterations or the maximum number of function evaluations. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC GENSELECT statement.
- 3 Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

Entry and Removal Candidates

When you specify DETAILS=ALL or DETAILS=STEPS in the SELECTION statement, the GENSELECT procedure produces the “Entry Candidates” or “Removal Candidates” table, which displays the effect names and values of the criterion used to select entering or departing effects at each step of the selection process. For each step, the effects are displayed in sorted order from best to worst of the selection criterion.

Selection Summary

When you specify the SELECTION statement, the GENSELECT procedure produces the “Selection Summary” table, which displays information about which effects were added to or removed from the model in the various steps of the model selection process. The statistic that led to the entry or removal decision is also
displayed. You can request further details about the model selection steps by specifying DETAILS=STEPS or DETAILS=ALL in the SELECTION statement. You can suppress the display of the “Selection Summary” table by specifying DETAILS=NONE in the SELECTION statement.

If you specify the LASSO selection method, then this table displays information about which effect was added to or removed from the model, the number of effects in the model, the lambda value, and the information criteria.

**Stop Reason**

When you specify the SELECTION statement, the GENSELECT procedure produces a simple table that tells you why model selection stopped.

**Selection Reason**

When you specify the SELECTION statement, the GENSELECT procedure produces a simple table that tells you why the final model was selected.

**Selected Effects**

When you specify the SELECTION statement, the GENSELECT procedure produces a simple table that tells you which effects were included in the final model.

**Dimensions**

The “Dimensions” table displays size measures that are derived from the model and the environment. It displays the number of columns in the current design matrix, the number of effects in the current design, the largest number of design columns associated with an effect, the rank of the matrix, and the number of parameters in the current model, including any dispersion parameters.

**Fit Statistics**

The “Fit Statistics” table displays a variety of likelihood-based measures of fit. All statistics are presented in “smaller is better” form. The values that the “Fit Statistics” table displays are not based on a normalized log-likelihood function. If you specify a PARTITION statement or the PARTFIT option, the table displays the values for each role along with statistics for comparing the training, validation, and testing results.

For more information about the statistics displayed in this table, see the section “Model Fit and Assessment Statistics” on page 399.

**Parameter Estimates**

The parameter estimates, their estimated (asymptotic) standard errors, and $p$-values for the hypothesis that the parameter is 0 are presented in the “Parameter Estimates” table. If you request confidence intervals by specifying the CLB option in the MODEL statement, confidence limits are produced for the estimates.

**Parameter Estimates Covariance Matrix**

When you specify the COVB option in the PROC GENSELECT statement, the GENSELECT procedure displays the covariance matrix of the parameter estimates. The covariance matrix is computed as the inverse
of the negative of the matrix of second derivatives of the log-likelihood function with respect to the model parameters (the Hessian matrix), evaluated at the parameter estimates.

**Parameter Estimates Correlation Matrix**

When you specify the `CORRB` option in the `PROC GENSELECT` statement, the GENSELECT procedure displays the correlation matrix of the parameter estimates.

**Score Code Variables for Predicted Values**

When you specify the `PCATALL` option in the `CODE` statement and you specify the `DISTRIBUTION=BINARY` option in the `MODEL` statement, the GENSELECT procedure produces the “Score Code Variables for Predicted Probability” table. For each level of the response variable, this table displays the corresponding variable in the scoring code that contains the predicted probability.

**Timing**

The “Timing” table displays the amount of time (in seconds) that PROC GENSELECT required to perform different tasks in the analysis.

**Output CAS Tables**

When you specify the `OUTPUT` statement, the GENSELECT procedure produces the output data table along with a table that lists the CAS library, the data table name, and the number of rows and columns in that data table.

**ODS Table Names**

Each table that the GENSELECT procedure creates has a name associated with it. You must use this name to refer to the table when you use the `DISPLAY` statement, the `DISPLAYOUT` statement, or ODS statements. These names are listed in Table 6.13.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassInfo</td>
<td>Level information from the <code>CLASS</code> statement</td>
<td><code>CLASS</code></td>
<td>Default</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Status of optimization at conclusion of optimization</td>
<td><code>PROC GENSELECT</code></td>
<td>Default</td>
</tr>
<tr>
<td>CorrB</td>
<td>Correlation matrix of parameter estimates</td>
<td><code>PROC GENSELECT</code></td>
<td><code>CORRB</code></td>
</tr>
<tr>
<td>CovB</td>
<td>Covariance matrix of parameter estimates</td>
<td><code>PROC GENSELECT</code></td>
<td><code>COVB</code></td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td><code>PROC GENSELECT</code></td>
<td>Default</td>
</tr>
<tr>
<td>EntryCandidates</td>
<td>Details about candidates for entry into the model</td>
<td><code>SELECTION</code></td>
<td><code>METHOD=FORWARD DETAILS=STEP</code></td>
</tr>
</tbody>
</table>
Table 6.13 continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>PROC GENSELECT</td>
<td>Default</td>
</tr>
<tr>
<td>IterHistory</td>
<td>Iteration history</td>
<td>PROC GENSELECT</td>
<td>ITHIST</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Information about the modeling environment</td>
<td>PROC GENSELECT</td>
<td>Default</td>
</tr>
<tr>
<td>ModelAnova</td>
<td>Model analysis of variance (Type III)</td>
<td>MODEL</td>
<td>TYPE3</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used, and number of events and trials, if applicable</td>
<td>PROC GENSELECT</td>
<td>Default</td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Library and name of the output data table, and number of rows and columns in the table</td>
<td>OUTPUT DISPLAYOUT</td>
<td>OUT=</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in MODEL statements</td>
<td>PROC GENSELECT</td>
<td>Default</td>
</tr>
<tr>
<td>PredProbName</td>
<td>Displays the predicted probability variable in the scoring code associated with each response level</td>
<td>CODE</td>
<td>PCATALL</td>
</tr>
<tr>
<td>RemovalCandidates</td>
<td>Details about candidates for removal from the model</td>
<td>SELECTION</td>
<td>METHOD=BACKWARD DETAILS=STEP</td>
</tr>
<tr>
<td>ResponseProfile</td>
<td>Response categories for binary and multinomial data</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>SelectedEffects</td>
<td>List of effects selected for the model</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionInfo</td>
<td>Information about the settings for model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionReason</td>
<td>Reason why the particular model was selected</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Summary information about model selection steps</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>StopReason</td>
<td>Reason for termination of model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times for tasks performed by the procedure</td>
<td>PROC GENSELECT</td>
<td>Default</td>
</tr>
</tbody>
</table>

**ODS Graphics**

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in *SAS/STAT User’s Guide*.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON
statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.

When ODS Graphics is enabled, the SELECTION statement can produce plots to help evaluate the selection process. For information about these plots, see the section “Model Selection Plots” on page 69 in Chapter 2, “Shared Concepts.”

PROC GENSELECT assigns a name to each graph that it creates using ODS. You can use these names to reference the graphs when using ODS. The names are listed in Table 6.14.

**Table 6.14**  Graphs Produced by PROC GENSELECT

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CoefficientPanel</td>
<td>Coefficients and CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>ChooseCriterionPlot</td>
<td>CHOOSE= criterion by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CoefficientPlot</td>
<td>Coefficients by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CriterionPanel</td>
<td>Fit criteria by step</td>
<td>CRITERIA</td>
</tr>
<tr>
<td>AICCPlot</td>
<td>Corrected Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICPlot</td>
<td>Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>SBCPlot</td>
<td>Schwarz Bayesian information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TEST_ASEPlot</td>
<td>Average square error on testing data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TRAIN_ASEPlot</td>
<td>Average square error on training data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>VAL_ASEPlot</td>
<td>Average square error on validation data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>FitByRolePlot</td>
<td>Progression of average square error by role</td>
<td>FITBYROLE</td>
</tr>
</tbody>
</table>

**Examples: GENSELECT Procedure**

**Example 6.1: Model Selection**

The following statements examine the same data set that is used in the section “Getting Started: GENSELECT Procedure” on page 359, but they request model selection via the forward selection technique. Model effects are added in the order of their significance until no more effects significantly improve the current model.
The DETAILS=ALL option in the SELECTION statement requests that all tables that are related to model selection be produced.

The data set getStarted is shown in the section “Getting Started: GENSELECT Procedure” on page 359. It contains 100 observations on a count response variable (Y), a continuous variable (Total) to be used in Example 6.2, and five categorical variables (C1–C5), each of which has four numerical levels.

A log-linked Poisson regression model is specified by using classification effects for variables C1–C5. The following statements request model selection by the forward selection method:

```sas
ods graphics on;
proc genselect data=mycas.getStarted;
   class C1-C5;
   model Y = C1-C5 / Distribution=Poisson;
   selection method=forward details=all plots=all;
run;
ods graphics off;
```

The model selection tables are shown in Output 6.1.1 through Output 6.1.3. Selection graphics produced by the PLOTS= option are displayed in Output 6.1.6 and Output 6.1.7.

The “Selection Information” table in Output 6.1.1 summarizes the settings for the model selection. The effect that produces the smallest approximate SBC is added to the model. The forward selection stops three steps after the smallest SBC is obtained, or when all effects have been added to the model.

```
Output 6.1.1  Selection Information

The GENSELECT Procedure

<table>
<thead>
<tr>
<th>Selection Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
</tbody>
</table>
```

The “Selection Summary” table in Output 6.1.2 shows the effects that were added to the model and the approximate SBC. Step 0 refers to the null model that contains only an intercept. In the next step, effect C2 resulted in the smallest approximate SBC among the candidate effects. In step 2, the smallest SBC when an effect is added to a model that contains the intercept and C2 was achieved by adding C5 to the model. Similarly, in steps 3, 4, and 5, effects were added in order of the minimum SBC among remaining candidates. Finally, the model in step 2 was chosen as the best because it had the smallest SBC among all the candidate models.
Output 6.1.2 Selection Summary Information

<table>
<thead>
<tr>
<th>Step</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>SBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Intercept</td>
<td>1</td>
<td>354.7980</td>
</tr>
<tr>
<td>1</td>
<td>C2</td>
<td>2</td>
<td>342.8795</td>
</tr>
<tr>
<td>2</td>
<td>C5</td>
<td>3</td>
<td>333.8182*</td>
</tr>
<tr>
<td>3</td>
<td>C1</td>
<td>4</td>
<td>341.7993</td>
</tr>
<tr>
<td>4</td>
<td>C4</td>
<td>5</td>
<td>351.8375</td>
</tr>
<tr>
<td>5</td>
<td>C3</td>
<td>6</td>
<td>363.8674</td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

Selection stopped at a local minimum of the STOP criterion.

The model at step 2 is selected.

Selected Effects: Intercept C2 C5

For each step of the selection process, the DETAILS=ALL option displays the candidate effects for entering the model along with their SELECT= criterion. Output 6.1.3 displays this table for the first step; the other steps are not shown here.

Output 6.1.3 Step1 Entry Candidates

<table>
<thead>
<tr>
<th>Rank</th>
<th>Effect</th>
<th>SBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>C2</td>
<td>342.8795</td>
</tr>
<tr>
<td>2</td>
<td>C5</td>
<td>347.5376</td>
</tr>
<tr>
<td>3</td>
<td>C1</td>
<td>355.7067</td>
</tr>
<tr>
<td>4</td>
<td>C4</td>
<td>361.7379</td>
</tr>
<tr>
<td>5</td>
<td>C3</td>
<td>365.7339</td>
</tr>
</tbody>
</table>

The DETAILS=ALL option also displays the dimensions, fit statistics, and parameter estimates at each step of the selection process; these details are not shown here.

Output 6.1.4 displays information about the selected model. Notice that the –2 log-likelihood value in the “Fit Statistics” table is larger than the value for the full model in Figure 6.6. This is expected because the selected model contains only a subset of the parameters. Because the selected model is more parsimonious than the full model, the information criteria AIC, AICC, and BIC are smaller than in the full model, indicating a better fit.

Output 6.1.4 Fit Statistics

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>303.58036</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>317.58036</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>318.79775</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>335.81655</td>
</tr>
</tbody>
</table>
The parameter estimates of the selected model are shown in Output 6.1.5. Notice that the effects are listed in the “Parameter Estimates” table in the order in which they were specified in the MODEL statement and not the order in which they were added to the model.

### Output 6.1.5 Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>0.528024</td>
<td>0.215231</td>
<td>6.0186</td>
<td>0.0142</td>
</tr>
<tr>
<td>C2 0</td>
<td>1</td>
<td>0.962636</td>
<td>0.236921</td>
<td>16.5088</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>C2 1</td>
<td>1</td>
<td>0.845132</td>
<td>0.233634</td>
<td>13.0851</td>
<td>0.0003</td>
</tr>
<tr>
<td>C2 2</td>
<td>1</td>
<td>0.213247</td>
<td>0.248896</td>
<td>0.7341</td>
<td>0.3916</td>
</tr>
<tr>
<td>C2 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C5 0</td>
<td>1</td>
<td>-0.763491</td>
<td>0.207082</td>
<td>13.5933</td>
<td>0.0002</td>
</tr>
<tr>
<td>C5 1</td>
<td>1</td>
<td>-0.785915</td>
<td>0.201271</td>
<td>15.2471</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>C5 2</td>
<td>1</td>
<td>-0.541212</td>
<td>0.208661</td>
<td>6.7275</td>
<td>0.0095</td>
</tr>
<tr>
<td>C5 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

The coefficient panel in Figure 6.1.6 enables you to visualize the selection process. In this plot, standardized coefficients of all the effects that are selected at some step of the stepwise method are plotted as a function of the step number. This enables you to assess the relative importance of the effects that are selected at any step of the selection process and to know when effects entered the model. The lower plot in the panel shows how the criterion that is used to choose the selected model changes as effects enter or leave the model.
The criterion panel in Figure 6.1.7 provides a graphical view of the progression of the fit criteria as the selection process evolves.
Example 6.2: Gamma Model

The following statements examine the data set `getStarted`, which is used in the section “Getting Started: GENSELECT Procedure” on page 359, but they request that a log-linked gamma model be fit by using the continuous variable `Total` as the response instead of the count variable `Y`. The following statements fit a log-linked gamma model to these data by using classification effects for the variables C1–C5. The CLB MODEL statement option requests that 95% confidence limits be computed and displayed along with the parameter estimates. The CODE statement requests that a text file named “Scoring Parameters.txt” be created. This file contains a SAS program that has information from the model that allows scoring of a new data set based on the parameter estimates from the current model.

```
proc genselect data=mycas.getStarted;
   class C1-C5;
   model Total = C1-C5 / Distribution=Gamma Link=Log CLB;
   code File='ScoringParameters.txt';
run;
```

The “Parameter Estimates” table in Output 6.2.1 shows the resulting regression model parameter estimates and the estimated gamma dispersion parameter.
Chapter 6: The GENSELECT Procedure

Output 6.2.1 Parameter Estimates

The GENSELECT Procedure

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
<th>95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>4.028096</td>
<td>0.454883</td>
<td>78.4153</td>
<td>&lt;.0001</td>
<td>3.13654 - 4.91965</td>
</tr>
<tr>
<td>C1 0</td>
<td>1</td>
<td>-0.064442</td>
<td>0.256719</td>
<td>0.0630</td>
<td>0.8018</td>
<td>-0.56760 - 0.43872</td>
</tr>
<tr>
<td>C1 1</td>
<td>1</td>
<td>-1.308470</td>
<td>0.318002</td>
<td>16.9305</td>
<td>&lt;.0001</td>
<td>-1.93174 - -0.68520</td>
</tr>
<tr>
<td>C1 2</td>
<td>1</td>
<td>0.295802</td>
<td>0.257834</td>
<td>1.3162</td>
<td>0.2513</td>
<td>-0.20954 - 0.80115</td>
</tr>
<tr>
<td>C1 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C2 0</td>
<td>1</td>
<td>1.154556</td>
<td>0.295110</td>
<td>15.3060</td>
<td>&lt;.0001</td>
<td>0.57615 - 1.73296</td>
</tr>
<tr>
<td>C2 1</td>
<td>1</td>
<td>0.824472</td>
<td>0.295273</td>
<td>7.7966</td>
<td>0.0052</td>
<td>0.24575 - 1.40320</td>
</tr>
<tr>
<td>C2 2</td>
<td>1</td>
<td>-0.287943</td>
<td>0.288421</td>
<td>0.9967</td>
<td>0.3181</td>
<td>-0.85324 - 0.27735</td>
</tr>
<tr>
<td>C2 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C3 0</td>
<td>1</td>
<td>-0.008546</td>
<td>0.283509</td>
<td>0.0009</td>
<td>0.9760</td>
<td>-0.56421 - 0.54712</td>
</tr>
<tr>
<td>C3 1</td>
<td>1</td>
<td>-0.319783</td>
<td>0.276053</td>
<td>1.3419</td>
<td>0.2467</td>
<td>-0.86084 - 0.22127</td>
</tr>
<tr>
<td>C3 2</td>
<td>1</td>
<td>-0.071452</td>
<td>0.296418</td>
<td>0.0581</td>
<td>0.8095</td>
<td>-0.65242 - 0.50952</td>
</tr>
<tr>
<td>C3 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C4 0</td>
<td>1</td>
<td>-0.143018</td>
<td>0.288101</td>
<td>0.2464</td>
<td>0.6196</td>
<td>-0.70769 - 0.42165</td>
</tr>
<tr>
<td>C4 1</td>
<td>1</td>
<td>-0.219348</td>
<td>0.290441</td>
<td>0.5704</td>
<td>0.4501</td>
<td>-0.78860 - 0.34991</td>
</tr>
<tr>
<td>C4 2</td>
<td>1</td>
<td>0.091763</td>
<td>0.278635</td>
<td>0.1085</td>
<td>0.7419</td>
<td>-0.45435 - 0.63788</td>
</tr>
<tr>
<td>C4 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C5 0</td>
<td>1</td>
<td>-1.227558</td>
<td>0.267605</td>
<td>21.0425</td>
<td>&lt;.0001</td>
<td>-1.75205 - -0.70306</td>
</tr>
<tr>
<td>C5 1</td>
<td>1</td>
<td>-0.560699</td>
<td>0.252238</td>
<td>4.9413</td>
<td>0.0262</td>
<td>-1.05508 - -0.06632</td>
</tr>
<tr>
<td>C5 2</td>
<td>1</td>
<td>-0.252965</td>
<td>0.259908</td>
<td>0.9473</td>
<td>0.3304</td>
<td>-0.76238 - 0.25645</td>
</tr>
<tr>
<td>C5 3</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Dispersion</td>
<td>1</td>
<td>1.672305</td>
<td>0.238205</td>
<td></td>
<td></td>
<td>1.26494 - 2.21086</td>
</tr>
</tbody>
</table>

Now suppose you want to compute predicted values for some different data. If $x$ is a vector of explanatory variables that might not be in the original data and $\hat{\beta}$ is the vector of estimated regression parameters from the model, then $\mu = g^{-1}(x'\hat{\beta})$ is the predicted value of the mean, where $g$ is the log link function in this case.

The following data contain new values of the regression variables C1–C5, from which you can compute predicted values based on information in the SAS program that is created by the CODE statement. This is called scoring the new data set.

```sas
   data ScoringData;
     input C1-C5;
   datalines;
     3 3 1 0 2
     1 1 2 2 0
     3 2 2 2 0
     1 1 2 3 2
     1 1 2 3 3
     3 1 1 0 1
     0 2 1 0 0
     2 1 3 1 3
     3 2 3 2 0
     3 0 2 0 1
   ;
```
The following SAS DATA step creates the new data set Scores, which contains a variable `P_Total` that represents the predicted values of `Total`, along with the variables `C1`–`C5`. The resulting data are shown in Output 6.2.2.

```sas
data Scores;
  set ScoringData;
  %inc 'ScoringParameters.txt';
run;
proc print data=Scores;
run;
```

**Output 6.2.2** Predicted Values for Scoring Data

<table>
<thead>
<tr>
<th>Obs</th>
<th>C1</th>
<th>C2</th>
<th>C3</th>
<th>C4</th>
<th>C5</th>
<th>P_Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>3</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>2</td>
<td>27.449</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>10.349</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>0</td>
<td>12.590</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>25.020</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>3</td>
<td>32.222</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>46.020</td>
</tr>
<tr>
<td>7</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>7.282</td>
</tr>
<tr>
<td>8</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>3</td>
<td>138.244</td>
</tr>
<tr>
<td>9</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>2</td>
<td>0</td>
<td>13.523</td>
</tr>
<tr>
<td>10</td>
<td>3</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>1</td>
<td>82.063</td>
</tr>
</tbody>
</table>

**References**


Chapter 7
The KCLUS Procedure

Contents

Overview: KCLUS Procedure ........................................ 420
   PROC KCLUS Features ............................................ 420
   Using CAS Sessions and CAS Engine Librefs .................. 421
Getting Started: KCLUS Procedure ................................ 421
Syntax: KCLUS Procedure .......................................... 425
   PROC KCLUS Statement ......................................... 425
   CODE Statement .................................................. 431
   DISPLAY Statement ............................................. 431
   DISPLAYOUT Statement ......................................... 432
   FREQ Statement ................................................. 432
   INPUT Statement ................................................. 433
   SCORE Statement ................................................. 433
Details: KCLUS Procedure .......................................... 434
   Obtaining the Statistics for Clustering ....................... 434
   Missing Values .................................................. 434
   Initial Seed Selection .......................................... 435
   Standardization ................................................. 435
   Finding the Number of Clusters ................................ 435
   Clustering Nominal Variables .................................. 436
      Dissimilarity Measures ...................................... 436
      Computing Cluster Centers ................................ 437
   Clustering Both Interval and Nominal Variables ............ 438
      Mixed Distance Measure .................................... 438
      Weight of Nominal Distance ................................ 438
Score Output for Clustering Both Interval and Nominal Variables .... 438
Displayed Output ................................................ 439
   Number of Observations ....................................... 439
   Model Information .............................................. 439
   Cluster Summary ............................................... 439
   Iteration History ............................................... 440
   Descriptive Statistics ......................................... 440
   Within-Cluster Statistics ..................................... 440
   Cluster Summary for Nominal Variables ....................... 441
   Frequencies for Nominal Variables ........................... 441
   Cluster Summary for Mixed Variables ......................... 441
   Standardization ................................................. 442
Overview: KCLUS Procedure

The KCLUS procedure performs clustering (a common step in data exploration) in SAS Viya.

You can use the KCLUS procedure to read and write data in distributed form, and to perform clustering and scoring in parallel by making full use of multicore computers or distributed computing environments.

The KCLUS procedure performs a cluster analysis on the basis of distances that are computed from quantitative or qualitative variables (or both). The observations are divided into clusters such that every observation belongs to one and only one cluster.

The KCLUS procedure uses the $k$-means algorithm for clustering interval input variables, uses the $k$-modes algorithm for clustering nominal input variables, and uses $k$-prototypes algorithm for clustering mixed input that contains both interval and nominal variables.

The KCLUS procedure accomplishes the clustering by updating the cluster centroids and the cluster membership of the data iteratively until the convergence criterion (for example, the least squares criterion for the Euclidean distance in $k$-means clustering) is satisfied or until the maximum iteration number is reached.

PROC KCLUS produces brief summaries of the cluster analysis in two output data tables:

- The OUT= data table is produced by the SCORE statement. This data table contains the cluster membership and distance variables for each observation in the input data table. It can be used for more detailed examination of the clusters.
- The OUTSTAT= data table is produced by the PROC KCLUS statement. This data table can be used for more detailed examination of between-cluster statistics.

PROC KCLUS Features

PROC KCLUS enables you to use parallel execution for clustering in a distributed computing environment. The following list summarizes the basic features of PROC KCLUS:
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: KCLUS Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table
name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

This example shows how to use the KCLUS procedure to compute clusters of observations in a CAS table. Suppose you want to group the observations in the input CAS table mycas.inpData, in which the variables are raw measures on interval scales.

The following DATA step creates the input data table, mycas.inpData, in your CAS session. This data table contains four variables: the first two variables are the input variables among which x has missing values, the third variable is the frequency variable, and the last variable is an index variable.

```
data mycas.inpData;
  title 'Using PROC KCLUS to Analyze Data';
  drop n;
  id=1;
  do n=1 to 1000;
    x=2*rannor(12345)+20;
    y=4*rannor(12345)+20;
    freq = 1;
    id = id + 1;
    output;
  end;
  do n=1 to 1000;
    x=3*rannor(12345)+10;
    y=5*rannor(12345)+10;
    freq=2;
    id = id + 1;
    output;
  end;
  do n=1 to 700;
    x=10*rannor(12345);
    y=10*rannor(12345);
    freq=1;
    id = id + 1;
    output;
  end;
  do n=1 to 200;
    x=.;
    y=10*rannor(12345);
    freq=1;
    id = id + 1;
    output;
  end;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements run PROC KCLUS and output the results to ODS tables:

```
proc kclus data=mycas.inpData maxclusters=3;
  input x y;
  freq freq;
run;
```
Figure 7.1 shows that the “Number of Observations Used” is less than the “Number of Observations Read”. By default, the KCLUS procedure ignores observations that have missing values, and it does not use them in the analysis. The two additional rows, “Sum of Frequencies Read” and “Sum of Frequencies Used” are displayed when the FREQ statement is specified. They provide information about the frequency values that are read and used.

**Figure 7.1 Number of Observations**

**Using PROC KCLUS to Analyze Data**

**The KCLUS Procedure**

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
<td>2900</td>
</tr>
<tr>
<td>Number of Observations Used</td>
<td>2700</td>
</tr>
<tr>
<td>Sum of Frequencies Read</td>
<td>3900</td>
</tr>
<tr>
<td>Sum of Frequencies Used</td>
<td>3700</td>
</tr>
</tbody>
</table>

Figure 7.2 shows the values of the parameters that are used in clustering. Because the number of clusters is not estimated by default and MAXCLUSTERS=3, three clusters are generated. Figure 7.2 shows the number of clusters and the default values for other options.

**Figure 7.2 Model Information**

<table>
<thead>
<tr>
<th>Model Information</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximum Iterations</td>
<td>10</td>
</tr>
<tr>
<td>Stop Criterion</td>
<td>Cluster Change</td>
</tr>
<tr>
<td>Stop Criterion Value</td>
<td>0</td>
</tr>
<tr>
<td>Clusters</td>
<td>3</td>
</tr>
<tr>
<td>Initialization</td>
<td>Forgy</td>
</tr>
<tr>
<td>Seed</td>
<td>987467829</td>
</tr>
<tr>
<td>Distance</td>
<td>Euclidean</td>
</tr>
<tr>
<td>Standardization</td>
<td>None</td>
</tr>
<tr>
<td>Interval Imputation</td>
<td>None</td>
</tr>
</tbody>
</table>

For each cluster, Figure 7.3 shows the number of observations; the maximum, minimum, and average distances from that cluster’s centroid to the observations in that cluster; the sum of squares error; and the standard deviation. Figure 7.3 also displays information about the nearest cluster to that cluster and the distance between their centroids.
Figure 7.3  Cluster Summary

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Frequency</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Average</th>
<th>SSE</th>
<th>Standard Deviation</th>
<th>Nearest Cluster</th>
<th>Distance to Nearest Cluster Centroid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1175</td>
<td>0.0202</td>
<td>29.2308</td>
<td>4.4741</td>
<td>3196.81</td>
<td>5.2160</td>
<td>2</td>
<td>13.8882</td>
</tr>
<tr>
<td>2</td>
<td>2038</td>
<td>0.2289</td>
<td>31.7970</td>
<td>5.2019</td>
<td>78608.4</td>
<td>6.2106</td>
<td>1</td>
<td>13.8882</td>
</tr>
<tr>
<td>3</td>
<td>487</td>
<td>0.5652</td>
<td>30.4447</td>
<td>10.7298</td>
<td>73156.7</td>
<td>12.2564</td>
<td>2</td>
<td>18.3687</td>
</tr>
</tbody>
</table>

Figure 7.4 shows the sum of squared errors (SSE) for each iteration. If the variables are interval, then the “Iteration History” table displays SSE Change and Stop Criterion columns. The SSE Change column displays the change in within-cluster distances. The Stop Criterion column displays the stopping criterion for each iteration. If the input variables are nominal, then the “Iteration History” table displays Within Distance Change and Stop Criterion columns. If the input variables are both interval and nominal, then the “Iteration History” table also displays Within Distance Change and Stop Criterion columns, but with the distance in the sense of mixed distance with both the interval and nominal parts as detailed in Clustering Both Interval and Nominal Variables.

Figure 7.4  Iteration History

<table>
<thead>
<tr>
<th>Iteration Number</th>
<th>SSE</th>
<th>SSE Change</th>
<th>Stop Criterion</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>260987</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>190242</td>
<td>-70745</td>
<td>4.666667</td>
</tr>
<tr>
<td>2</td>
<td>185578</td>
<td>-4664.513827</td>
<td>2.407407</td>
</tr>
<tr>
<td>3</td>
<td>184388</td>
<td>-1190.314300</td>
<td>1.333333</td>
</tr>
<tr>
<td>4</td>
<td>184034</td>
<td>-353.882617</td>
<td>0.703704</td>
</tr>
<tr>
<td>5</td>
<td>183866</td>
<td>-167.400789</td>
<td>0.666667</td>
</tr>
<tr>
<td>6</td>
<td>183768</td>
<td>-98.177548</td>
<td>0.333333</td>
</tr>
<tr>
<td>7</td>
<td>183739</td>
<td>-29.222378</td>
<td>0.074074</td>
</tr>
<tr>
<td>8</td>
<td>183733</td>
<td>-5.722173</td>
<td>0</td>
</tr>
</tbody>
</table>

Figure 7.5 and Figure 7.6 show statistics for each variable in the INPUT statement. Figure 7.5 shows the variable statistics for all the observations in the input data table, and Figure 7.6 shows the variable statistics for the observations that belong to a specific cluster.

Figure 7.5  Descriptive Statistics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>x</td>
<td>11.020648</td>
<td>8.189686</td>
</tr>
<tr>
<td>y</td>
<td>10.756547</td>
<td>9.180654</td>
</tr>
</tbody>
</table>
The following statements are available in the KCLUS procedure:

```plaintext
PROC KCLUS <options>;
    CODE <options>;
    DISPLAY <table-list> </options>;
    DISPLAYOUT table-spec-list </options>;
    FREQ variable;
    INPUT variables <LEVEL= NOMINAL | INTERVAL>;
    SCORE OUT=CAS-libref.data-table <options>;
```

The `PROC KCLUS` statement and an `INPUT` statement are required. You can specify multiple `INPUT` statements.

The following sections describe the `PROC KCLUS` statement and then describe the other statements in alphabetical order.

### PROC KCLUS Statement

```
PROC KCLUS <options>;
```

The `PROC KCLUS` statement invokes the procedure. Table 7.1 summarizes the `options` available in the `PROC KCLUS` statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input and Output Data Set Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
<tr>
<td>OUTSTAT(OUTITER)=</td>
<td>Specifies the output data table to contain cluster centroids</td>
</tr>
<tr>
<td>PRINTALLDISTANCES</td>
<td>Outputs the interval distance, nominal distance, and total distance</td>
</tr>
<tr>
<td></td>
<td>(this option can be used only for mixed input variables)</td>
</tr>
</tbody>
</table>
Table 7.1  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Clustering Options</strong></td>
<td></td>
</tr>
<tr>
<td>DISTANCE=</td>
<td>Specifies the distance measure for similarity measurement (used for interval input variables)</td>
</tr>
<tr>
<td>DISTANCENOM=</td>
<td>Specifies the distance measure for similarity measurement (used for nominal input variables)</td>
</tr>
<tr>
<td>INIT=</td>
<td>Specifies the method for obtaining the initial estimate of cluster centers</td>
</tr>
<tr>
<td>MAXCLUSTERS=</td>
<td>Specifies the number of clusters</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Specifies the maximum number of iterations</td>
</tr>
<tr>
<td>SEED=</td>
<td>Specifies the seed that is used for pseudorandom number generation</td>
</tr>
<tr>
<td>STOPCRITERION=</td>
<td>Specifies the stop criterion method to use for convergence</td>
</tr>
<tr>
<td>KPROTOTYPEPARAMS=</td>
<td>Specifies the (k)-prototypes parameters for clustering interval and nominal variables at the same time (this option can be used only for mixed input variables)</td>
</tr>
<tr>
<td><strong>Data Processing Options</strong></td>
<td></td>
</tr>
<tr>
<td>IMPUTE=</td>
<td>Specifies the imputation method for interval input variables</td>
</tr>
<tr>
<td>IMPUTENOM=</td>
<td>Specifies the imputation method for nominal input variables</td>
</tr>
<tr>
<td>STANDARDIZE=</td>
<td>Specifies the method for standardizing interval input variables</td>
</tr>
<tr>
<td><strong>Number of Clusters Estimation Options</strong></td>
<td></td>
</tr>
<tr>
<td>NOC=</td>
<td>Specifies the method for estimating the number of clusters</td>
</tr>
<tr>
<td><strong>Performance Options</strong></td>
<td></td>
</tr>
<tr>
<td>NTHREADS=</td>
<td>Specifies the number of threads for the computation</td>
</tr>
</tbody>
</table>

You can specify the following options:

**DATA=**`CAS-libref.data-table`

names the input data table for PROC KCLUS to use. The default is the most recently created data table. `CAS-libref.data-table` is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 421.

- **data-table** specifies the name of the input data table.

**DISTANCE=**`EUCLIDEAN | MANHATTAN`

specifies the distance measure for similarity that is used for interval input variables.

You can choose from the following measures:

- **EUCLIDEAN** calculates the Euclidean distance.
- **MANHATTAN** calculates the Manhattan distance.

By default, **DISTANCE=EUCLIDEAN**.
PROC KCLUS Statement

DISTANCENOM=BINARY | GLOBALFREQ | RELATIVEFREQ
specifies the distance measure for similarity that is used for nominal input variables.

You can choose from the following measures:

BINARY calculates a simple matching distance.
GLOBALFREQ calculates the distance based on the frequency of levels of nominal input variables in the input data table.
RELATIVEFREQ calculates the distance based on the frequency of levels of nominal input variables in each cluster.

By default, DISTANCENOM=BINARY. For more information about these distance functions, see the section “Clustering Nominal Variables” on page 436.

INIT=FORGY | RAND
specifies the method for obtaining the initial estimate of cluster centers.

You can choose from the following methods:

FORGY selects the initial cluster centers randomly from observations.
RAND assigns all observations randomly to one of the clusters.

By default, INIT=FORGY.

IMPUTE=MEAN | NONE
specifies the imputation method to be used when the INPUT statement specifies interval variables.

You can choose from the following methods:

MEAN imputes missing values of variables in observations by using the mean value for that variable.
NONE does not do any imputation and excludes observations that have missing values.

If IMPUTE=NONE and the number of observations that have nonmissing values is less than the value of the MAXCLUSTERS= option, then the number of clusters is set to the number of observations that have nonmissing values.

By default, IMPUTE=NONE.

IMPUTENOM=MODE | NONE
specifies the imputation method to be used when the INPUT statement specifies nominal variables.

You can choose from the following methods:

MODE imputes missing values of variables in observations by using the mode value for that variable.
NONE does not do any imputation and excludes observations that have any missing values.

If IMPUTENOM=NONE and the number of observations that have nonmissing values is less than the value of the MAXCLUSTERS= option, then the number of clusters is set to the number of observations that have nonmissing values.

By default, IMPUTENOM=NONE.
**MAXCLUSTERS=**`number`

specifies either the number of clusters to be used (if the **NOC=** option is not specified or **NOC=NONE**) or the maximum number of clusters to be searched (if **NOC=ABC**).

By default, **MAXCLUSTERS=6**.

**MAXITER=**`number`

specifies the maximum number of iterations for the algorithm to perform. In each iteration of the \(k\)-means or \(k\)-modes clustering method, each observation is assigned to the nearest cluster centroid, and the centroids are recomputed.

By default, **MAXITER=10**.

**NOC=**`NONE | ABC < suboptions>`

specifies the method for estimating the number of clusters.

You can specify the following values:

- **ABC < suboptions>** estimates the number of clusters by using the aligned box criterion (ABC) method. For more information about this method, see the section “Finding the Number of Clusters” on page 435.

  You can specify one or more of the following **suboptions**:

  - **ALIGN=**`keyword` specifies the method for aligning the reference data based on the input data.
    
    You can specify the following **keywords**:
    
    - **NONE** generates the reference data from a uniform distribution over the range of values for each subset of the input data table.
    - **PCA** generates the reference data from a uniform distribution over a box that is aligned with the principal components of each subset of the input data table.

    By default, **ALIGN=NONE**.

  - **B=**`number` specifies the number of reference data to be created for each cluster candidate. By default, **B=1**.

  - **CRITERION=**`keyword` specifies the criterion to be used to estimate the number of clusters that use the statistics obtained by the ABC method.
    
    You can specify the following **keywords**:
    
    - **ALL** uses all the following options and selects the number of clusters based on which number of clusters is chosen the most often. If each option selects a different number of clusters, then the number selected by **GLOBALPEAK** is used.
**PROC KCLUS Statement**

**FIRSTMAXWITHSTD** uses the smallest $k$ such that the gap value for that $k$ is greater than the one-standard-error adjusted gap value for $k+1$.

**FIRSTPEAK** uses the first peak value among the peak values in gap statistics.

**GLOBALPEAK** uses the maximum peak value among all the peak values in gap statistics.

By default, CRITERION=GLOBALPEAK.

**MINCLUSTERS=number** specifies the minimum number of clusters for searching for the best number of clusters. By default, MINCLUSTERS=2.

**NONE** does not estimate the number of clusters and uses the value specified in MAXCLUSTERS= option.

By default, NOC=NONE.

**NTHREADS=number-of-threads** specifies the number of threads that are used in the computation. The default value is the number of CPUs available in the machine.

**OUTSTAT < (OUTITER) >=CAS-libref.data-table** creates the output data table that contains the cluster centroids for each cluster. CAS-libref.data-table is a two-level name, where CAS-libref refers to the caslib and session identifier, and data-table specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 421.

This data table includes the iteration number as _ITERATION_, the cluster ID as _CLUSTER_ID_ and the cluster centroids, which consist of the variables that are specified in the INPUT statement. If you specify STANDARDIZE=RANGE or STANDARDIZE=STD, the data table also contains the standardized values of the cluster centroids, which are displayed by adding the S_ prefix to the variables in the INPUT statement.

You can also specify the following suboption:

**OUTITER** also outputs the cluster centroids to the OUTSTAT= data table for each iteration.

**SEED=number** specifies an integer to be used to start the pseudorandom number generator. If you do not specify a seed or if you specify a value less than or equal to 0, the seed is generated from reading the time of day from the computer’s clock.

**STANDARDIZE=NONE | RANGE | STD** specifies the method for standardizing the interval input variables. PROC KCLUS uses the location and scale measures specific to the method. You can specify the following values:

**NONE** does not standardize and uses the actual values for the input variables.
RANGE standardizes the input variables by using the range method. PROC KCLUS uses the minimum as the location and the range as the scale.

STD standardizes the input variables by using the traditional standardization method. PROC KCLUS uses the mean as the location and the standard deviation as the scale.

By default, STANDARDIZE=NONE.

STOPCRITERION=convergence_method( VALUE=number )
specifies the method to use for convergence. If you do not specify this option, the algorithm stops after it reaches the maximum number of iterations (which is specified in MAXITER= option).

You can specify the following convergence_methods:

CLUSTER_CHANGE( VALUE=number )
uses the percentile of observations that do not change their cluster membership for that iteration. The optional VALUE= suboption enables you to specify the percentile of observations.

By default or if VALUE=0, PROC KCLUS runs until the cluster centroids no longer change.

WCSD_CHANGE( VALUE=number )
uses the within-cluster distance change as a convergence criterion. The optional VALUE= suboption enables you to specify the change in SSE for the k-means algorithm or specify the sum of within-cluster distances for the k-modes algorithm and the k-prototypes algorithm. For the k-prototypes algorithm, the distance is a mixed distance that includes both the interval and nominal parts.

KPROTOTYPEPARAMS=gamma_method
specifies the method for obtaining the γ parameter in the k-prototypes clustering algorithm (Huang 1997) for clustering mixed input data that contain both interval and nominal variables.

You can specify either of the following gamma_methods:

USERGAMMA(VALUE=number)
specifies the γ parameter value (in the VALUE= suboption) for the k-prototypes clustering algorithm. The value of γ should be an appropriate positive number that balances the difference between the scales of the nominal and interval input variables.

AUTOGAMMA
estimates the γ parameter value for the k-prototypes clustering algorithm. You can use this option when you do not have a clear idea of how large the γ value would be. When you specify the AUTOGAMMA option, the value of γ is inferred to be the average of the standard deviations of the interval input variables.

By default, KPROTOTYPEPARAMS=USERGAMMA(VALUE=0.5).

PRINTALLDISTANCES
prints the distance that is contributed by the interval variables (as _DISTANCEINT_) and the distance that is contributed by the nominal variables (as _DISTANCEOM_) in the mixed distance that is used by the k-prototypes algorithm to the output table that is specified in the SCORE statement. For more information, see the section “Score Output for Clustering Both Interval and Nominal Variables” on page 438.
CODE Statement

```
CODE < options > ;
```

The CODE statement generates the SAS DATA step code that mimics the computations that are done by the SCORE statement.

You can specify the following options:

- `FILE=filename`
  - specifies the filename of the file to write the SAS score code to.

- `LABELID=number`
  - specifies a number used to construct array names and statement labels in the generated code. You can specify a value in the range 0 to 1024; by default, LABELID=0.

DISPLAY Statement

```
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 443. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following options after a slash (/):
CASESENSITIVE
performs a case-sensitive comparison of table names in the \textit{table-list} to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the \textit{table-list} in quotation marks.

EXCLUDE
displays all display tables except those that you specify in the \textit{table-list}.

EXCLUDEALL
suppresses display of all tables. This option takes precedence over the other options.

TRACE
displays the display table names, labels, and paths.

\textbf{DISPLAYOUT Statement}

\begin{verbatim}
DISPLAYOUT table-spec-list < / options > ;
\end{verbatim}

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see \textit{SAS Output Delivery System: Procedures Guide}.

The \textit{table-spec-list} specifies a list of CAS output tables to create. Each entry in the list has either a \textit{key=value} format or a \textit{key} format:

\begin{itemize}
  \item \textit{key=value} specifies \textit{key} as the ODS table name, path, or partial pathname, and specifies \textit{value} as the CAS output table name.
  \item \textit{key} specifies \textit{key} as the ODS table name and also as the CAS output table name.
\end{itemize}

Table names and partial pathnames are discussed under the \textbf{DISPLAY} statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following \textit{options} after a slash (/):

\begin{itemize}
  \item \textbf{INCLUDEALL} creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the \textit{table-spec-list} specification is ignored.
  \item \textbf{NOREPLACE} does not replace any existing CAS output table of the same name.
  \item \textbf{REPEATED} replicates all CAS output tables on all nodes.
\end{itemize}

\textbf{FREQ Statement}

\begin{verbatim}
FREQ variable ;
\end{verbatim}
The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC KCLUS treats each observation as if it appears $f$ times, where $f$ is the value of the FREQ variable for the observation. If $f$ is not an integer, it is truncated to an integer. If $f$ is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

**INPUT Statement**

```plaintext
INPUT variables < LEVEL= NOMINAL | INTERVAL > ;
```

The INPUT statement specifies the names of the variables to be used in clustering. It names one or more input variables that use common options. If you want to use different options for different variables, you can specify multiple INPUT statements.

To trigger the $k$-prototypes clustering algorithm for clustering mixed input data that contain both interval and nominal input variables, either you can use two INPUT statements with one INPUT statement that includes the LEVEL=INTERVAL option for interval input variables and another INPUT statement that includes the LEVEL=NOMINAL option for nominal input variables, or you can use a single INPUT statement without the LEVEL= option specified. In the latter case, PROC KCLUS detects the types of the input variables and uses the $k$-prototypes clustering algorithm if the input variables include both interval and nominal types.

You can include the following option in each INPUT statement:

- **LEVEL= NOMINAL | INTERVAL**
  - specifies the level of measurement of the variables. For clustering, only interval, binary, and nominal variables are accepted.
  - By default, LEVEL=INTERVAL for numeric variables, and LEVEL=NOMINAL for categorical character variables.

**SCORE Statement**

```plaintext
SCORE OUT=CAS-libref.data-table < option > ;
OUTPUT OUT=CAS-libref.data-table < option > ;
```

The SCORE statement writes the cluster membership information of each observation to the output data table that is specified in the OUT= option. This information includes the variables that are specified in the COPYVARS= option and additional variables, as described in the section “Score Output for Clustering Both Interval and Nominal Variables” on page 438.

You must specify the following option:

- **OUT=CAS-libref.data-table**
  - names the output data table for PROC KCLUS to use. You must specify this option before any other options. *CAS-libref.data-table* is a two-level name, where
    - *CAS-libref* refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and
a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS-libref, see the section “Using CAS Sessions and CAS Engine Librefs” on page 421.

**data-table**

specifies the name of the output data table.

The output data table contains the scored data. When you specify this option, all variables that are specified in the COPYVARS= option, followed by the _CLUSTER_ID_ variable and the _DISTANCE_ variable, are added to the output data table that is specified in this option.

You can also specify the following option:

**COPYVAR=variable**

**COPYVARS=(variables)**

lists one or more variables from the input data table that are transferred to the scored output data table, provided that the output data table produces one or more records per input observation. By default, the KCLUS procedure does not transfer any variables from the input data table to the output data table. The COPYVARS= option accepts numeric and character variables. You can also use COPYVARS=(_ALL_) option to include all the input variables.

---

**Details: KCLUS Procedure**

**Obtaining the Statistics for Clustering**

The KCLUS procedure calculates the following cluster-based statistics (in addition to the variable-based statistics) about the data in the input data table.

- summary statistics for each cluster (for example, the number of observations)
- summary statistics for the variables in each cluster (for example, the mean value of an interval input variable in a cluster)

You can use these statistics in addition to the output data tables to further analyze the clustering results.

**Missing Values**

Observations that have missing values affect the clustering results because the distance measures that are computed for these observations do not reflect the actual values. To solve this problem, you can use the IMPUTE= option for interval input variables and the IMPUTENOM= option for nominal input variables in the PROC KCLUS statement. If IMPUTE=NONE, observations that have missing values for interval input variables are not considered in cluster analysis. If IMPUTE=MEAN, observations that have missing values for interval input variables are considered by replacing the missing values with the average value for that missing variable, and the mean is calculated based on all nonmissing values of this variable. Similarly, if IMPUTENOM=NONE, observations that have missing values for nominal input variables are not considered...
in cluster analysis. If IMPUTENOM=MODE, observations that have missing values for nominal input variables are considered by replacing the missing values with the mode value for that missing variable. However, observations that have all missing values are not considered in cluster analysis.

**Initial Seed Selection**

When INIT=FORGY in the PROC KCLUS statement (the default), random observations from the input data table are selected as initial cluster centroids by default. The initial aim of PROC KCLUS is to select the observations that have no missing values.

You can change the observations that are selected from the input data table by using the SEED= option. You can use this option to set the seed value for the random number generator, which is used for generating random observation indices.

Because the random number generator creates indices for the observations, the initial cluster centroids will be different depending on where and how you run the procedure and where the input data reside. When the data are distributed or the computation is done in parallel, the indices of the observations will change depending on the number of nodes and number of threads that are used. Thus, you might get different initial cluster centroids.

**Standardization**

Because variables that have large variances tend to affect the distance measure more than variables that have small variances, it is recommended that you standardize the variables before clustering the observations. The STANDARDIZE= option in the PROC KCLUS statement provides a convenient way to standardize the INPUT variables. This option standardizes all the variables by using the method that is specified in that option and adds the standardized values to the output data tables.

**Finding the Number of Clusters**

To estimate the number of clusters (NOC), you can specify NOC=ABC in the PROC KCLUS statement. This option uses the aligned box criterion (ABC) method to estimate an interim number of clusters and then runs the $k$-means clustering method to produce the final clusters. The NOC= option works only for interval variables. If the NOC= option is not specified, PROC KCLUS uses the MAXCLUSTERS= option in the PROC KCLUS statement to set the number of the clusters, and then runs the $k$-means clustering method to produce the final clusters.

The ABC method estimates the number of clusters for well-separated clusters. Similar to the gap statistics method that is presented in Tibshirani, Walther, and Hastie (2001), the ABC method uses within-cluster dispersion from the results of clustering as an error measure, making the ABC method independent of the method that is used for clustering. In order to estimate the number of clusters, the ABC method compares the change in the error measure with the change that is expected under an appropriate reference null distribution.

The cubic clustering criterion (CCC), proposed in Sarle (1983), is based on the assumption that a uniform distribution on a hyperrectangle is divided into clusters that are shaped approximately like hypercubes. In recent and widely accepted work, Tibshirani, Walther, and Hastie (2001) propose a gap statistics method that
Chapter 7: The KCLUS Procedure

uses Monte Carlo simulation (instead of a heuristic) to generate a hypercube reference distribution. The ABC method improves on the CCC and gap statistics methods by generating more restricted and aligned reference distributions that consider different features in the input data table.

Although the ABC method calculates the reference distribution differently than the other methods do, the computation of the error measure is similar to the method presented in Tibshirani, Walther, and Hastie (2001). The error measure—also called the gap and represented as $\text{Gap}(k)$—is obtained by subtracting the logarithm of the within-cluster sum of squares error from the logarithm of its expectation for clustering solutions over a range of possible $k$ values. The simulation-adjusted standard deviation of the reference distribution—represented as $s(k)$—is obtained by using the standard deviation of the logarithm of the within-cluster sum of squares errors for reference data. The one-standard-error adjusted gap is obtained by subtracting $s(k)$ from the gap. For more information, see Tibshirani, Walther, and Hastie (2001).

A notable feature of the ABC algorithm is that it also applies to clustering both interval and nominal inputs. In the $k$-prototypes clustering algorithm, the ABC algorithm is performed with a mixed distance to which both the interval and nominal inputs contribute.

The number of clusters is estimated by considering the $\text{Gap}(k)$ and $s(k)$ values for each cluster candidate $k$. You can choose one of four methods for estimating the number of clusters by specifying the CRITERION= suboption in the NOC=ABC option in the PROC KCLUS statement:

- The FIRSTPEAK option selects the first peak value among all the values in $\text{Gap}(k)$.
- The GLOBALPEAK option selects the peak value that has the maximum value among the peak values in $\text{Gap}(k)$.
- The FIRSTMAXWITHSTD option considers the standard deviation in each cluster in addition to the values in $\text{Gap}(k)$. It considers the values in the one-standard-error adjusted gap to estimate the number of clusters. It selects the smallest $k$ such that the gap value for that $k$ is greater than the one-standard-error adjusted gap value for $k+1$.
- The ALL option uses all the preceding options and selects the number of clusters based on which number of clusters is chosen the most often. If each option selects a different number, then the number selected by the GLOBALPEAK option is used.

Clustering Nominal Variables

The $k$-means algorithm works only with interval inputs. One way to apply the $k$-means algorithm to nominal data is to use data transformation methods to transform the nominal data into a new feature space. However, this approach can be very inefficient, and it does not produce good results. For clustering nominal inputs, the KCLUS procedure implements the $k$-modes clustering algorithm, which extends the $k$-means algorithm by using different dissimilarity measures and a different method for computing cluster centers (Huang 1997).

Dissimilarity Measures

In the $k$-modes clustering algorithm, distance measures depend on the level of nominal variables. Let $X$ and $Y$ be two observations, which are described by $F$ nominal variables. Each nominal variable $j$ in $F$ has a different number of distinct values, which are called levels (or sometimes called categories).
The dissimilarity measure between observations $X$ and $Y$ is

$$d(X,Y) = \sum_{j=1}^{F} \delta(x_j, y_j)$$

where $\delta(x_j, y_j)$ is the dissimilarity measure between two nominal variables $j$.

PROC KCLUS supports the following dissimilarity measures:

- The simple matching dissimilarity measure calculates the total number of mismatches of the corresponding variables of two observations. If the number of mismatches is small, then the observations are similar to each other. The dissimilarity measure between two nominal variables $j$ is

$$\delta(x_j, y_j) = \begin{cases} 0 & \text{if } x_j = y_j \\ 1 & \text{if } x_j \neq y_j \end{cases}$$

This algorithm is very efficient. However, it might lead to clusters that have weak intrasimilarity, depending on the number of levels and the number of observations that have these levels. For more information, see Huang (1997). Specify DISTANCENUM=BINARY in the PROC KCLUS statement to use this distance measure.

- The global frequency-based dissimilarity measure takes into account the frequencies of levels of each variable in the input data table. The dissimilarity measure between two nominal variables $j$ is

$$\delta(x_j, y_j) = \begin{cases} 0 & \text{if } x_j = y_j \\ \frac{(n_{x_j} + n_{y_j})}{n_{x_j} \cdot n_{y_j}} & \text{if } x_j \neq y_j \end{cases}$$

where $n_{x_j}$ is the number of observations that have level $x_j$ of variable $j$ in the input data table and $n_{y_j}$ is the number of observations that have level $y_j$ of variable $j$ in the input data table. You can use this measure to find underrepresented clusters because it assigns more importance to rare categories than to frequent ones. For more information, see Huang (1997). Specify DISTANCENUM=GLOBALFREQ in the PROC KCLUS statement to use this distance measure.

- The cluster frequency-based dissimilarity measure takes into account the relative frequencies of levels of each variable in each cluster. The dissimilarity measure between two nominal variables $j$ is

$$\delta(x_j, y_j) = \begin{cases} 1 - \frac{n_{x_j}}{n_c} & \text{if } x_j = y_j \\ 1 & \text{if } x_j \neq y_j \end{cases}$$

where $n_c$ is the number of observations in cluster $c$ and $n_{x_j}$ is the number of objects that have level $x_j$ of variable $j$ in cluster $c$.

This distance measure enables the algorithm to assign less similar observations to the clusters that have weak intrasimilarity. Thus, the generated clusters have strong intrasimilarities. For more information, see Ng et al. (2007). Specify DISTANCENUM=RELATIVEFREQ in the PROC KCLUS statement to use this distance measure.

### Computing Cluster Centers

The $k$-modes algorithm uses modes instead of means as cluster centers. The KCLUS procedure uses a frequency-based method to update the modes after each iteration in order to minimize the clustering cost function. Cluster centers are updated using the same approach for all the distance measures.
Clustering Both Interval and Nominal Variables

For clustering inputs that include only interval or only nominal variables, the KCLUS procedure implements the $k$-means or $k$-modes clustering algorithm, respectively. For clustering inputs that include both interval and nominal variables, the KCLUS procedure implements the $k$-prototypes clustering algorithm (Huang 1997). The $k$-prototypes clustering algorithm uses a mixed distance that combines the distance contributed by the interval inputs and the distance contributed by the nominal inputs. This mixed distance is characterized with a weight parameter, $\gamma$, to balance the scales of the interval and nominal distances.

Mixed Distance Measure

The mixed distance measure $d_{mixed}$ is defined as

$$d_{mixed} = d_{int}^2 + \gamma \times d_{nom}$$

where $d_{int}$ is the distance of the interval input variables and $d_{nom}$ is the distance of the nominal input variables. The interval distance measure, $d_{int}$, is specified in the DISTANCE= option, and the nominal distance measure, $d_{nom}$, is specified in the DISTANCENOM= option.

Weight of Nominal Distance

A weight parameter, $\gamma$, is used to balance any possible difference between the scales of the nominal variables and the interval variables. You can specify this value in the KPROTOYPEPARAMS= option. By default, the weight is 0.5.

Score Output for Clustering Both Interval and Nominal Variables

The KCLUS procedure writes the cluster membership information to the output table that is specified in the OUT= option in the SCORE statement. This information always includes the variables that are specified in the COPYVARS= option and the following variables:

- _CLUSTER_ID_ (the ID of the closest cluster)
- _DISTANCE_ (the distance between the observation and the centroid of that cluster)

In addition, cluster membership information can include one or more of the following variables:

- _STANDARDIZED_DISTANCE_ (the distance between the standardized values of the observation and the standardized values of cluster centroid). This variable is included if you specify STANDARDIZE=RANGE or STANDARDIZE=STD in the PROC KCLUS statement.
- _DISTANCEINT_ (the interval part of the distance between the observation and the centroid of that cluster). This variable is included if the $k$-prototypes clustering algorithm is used and you specify the PRINTALLDISTANCES option in the PROC KCLUS statement.
- _DISTANCENOM_ (the nominal part of the distance between the observation and the centroid of that cluster). This variable is included if the $k$-prototypes clustering algorithm is used and you specify the PRINTALLDISTANCES option in the PROC KCLUS statement.
- `_DISTANCE_`, which is equal to `_DISTANCEINT_^2 + \gamma \times _DISTANCENOM_`.
- `_STANDARDIZED_DISTANCEINT_` (the interval part of the distance between the standardized values of the observation and the standardized values of cluster centroid). This variable is included if the \(k\)-prototypes clustering algorithm is used and you specify the both the `PRINTALLDISTANCES` and the `STANDARDIZE=` options in the `PROC KCLUS` statement.
- `_STANDARDIZED_DISTANCE_`, which is equal to `_STANDARDIZED_DISTANCEINT_^2 + \gamma \times _DISTANCENOM_`.

**Displayed Output**

The KCLUS procedure displays various tables for cluster analysis.

The following sections describe the output in the order of their appearance when the related options are specified.

**Number of Observations**

The “Number of Observations” table displays the number of observations that are read from the input data table and the number of observations that are used in the clustering. The Number of Observations Read column displays the count of raw data that are read from the input data table, and the Number of Observations Used column displays the count of data that are actually used in the clustering. The latter count is affected by the missing values in the raw data and the setting of the `IMPUTE=` and `IMPUTENOM=` options in the `PROC KCLUS` statement. When the `FREQ` statement is specified, then the Sum of Frequencies Read and Sum of Frequencies Used are also displayed.

**Model Information**

The “Model Information” table provides basic information about the parameters that are used in the cluster analysis. This information includes the clustering algorithm, maximum number of iterations, stop criterion method and the value for that criterion, number of clusters, initialization technique, seed value, distance method, standardization method, imputation method, and the value of \( \gamma \) when the \(k\)-prototypes clustering algorithm is used.

**Cluster Summary**

The “Cluster Summary” table displays the following for each cluster when the variables in `INPUT` statement are interval:

- cluster number
- frequency (the number of observations in the cluster)
- maximum, minimum, and average distances from the cluster centroid to the observations in the cluster
- SSE (sum of squared errors between the observations and the closest cluster centroids to them)
• standard deviation (the root mean square distances between the observations and the cluster centroids that are closest to them)

• nearest cluster (the ID of the cluster whose centroid is closest to the current cluster’s)

• distance between the cluster centroid of the current cluster and the nearest cluster

If the number of observations in a cluster is zero, then this cluster is not displayed in the “Cluster Summary” table.

**Iteration History**

The “Iteration History” table displays the following when the variables that are specified in the **INPUT** statement are interval:

• iteration number

• SSE (sum of squared distances between the observations and the closest cluster centroids)

• SSE change

• stop criterion

The “Iteration History” table displays the following when the variables that are specified in the **INPUT** statement are nominal:

• iteration number

• WithinDist (sum of distances between the observations and the closest cluster centroids)

• within distance change

• stop criterion

**Descriptive Statistics**

The “Descriptive Statistics” table displays the mean and standard deviation for each interval variable that is specified in the **INPUT** statement. The calculation of the mean and standard deviation for an interval variable uses all the data in its own column and discards the missing values. So the calculation of mean and standard deviation for one interval variable is independent of the calculation for other interval variables.

**Within-Cluster Statistics**

The “Within Cluster Statistics” table displays the following for each interval variable that is specified in the **INPUT** statement in each cluster:

• mean of the values for each variable in that cluster

• standard deviations of the values for each variable in that cluster
Cluster Summary for Nominal Variables

The “Cluster Summary for Nominal Variables” table displays the following for each cluster when the variables that are specified in the INPUT statement are nominal:

- cluster number
- frequency (the number of observations in the cluster)
- maximum, minimum, and average distances from the cluster centroid to the observations in the cluster
- within-cluster distance
- nearest cluster (the ID of the cluster whose centroid is closest to the current cluster’s centroid)
- distance between the cluster centroid of the current cluster and the nearest cluster

If the number of observations in a cluster is 0, then this cluster is not displayed in the “Cluster Summary for Nominal Variables” table.

Frequencies for Nominal Variables

The “Frequencies for Nominal Variables” table displays the following for each nominal variable in the INPUT statement in each cluster:

- levels of each variable in that cluster
- frequencies of the levels of each variable in the input data table.
- frequencies of the levels of each variable in that cluster

Cluster Summary for Mixed Variables

The “Cluster Summary for Mixed Variables” table displays the following for each cluster when the k-prototypes clustering algorithm is performed:

- cluster number
- frequency (the number of observations in the cluster)
- maximum, minimum, and average distances from the cluster centroid to the observations in the cluster
- within-cluster distance
- nearest cluster (the ID of the cluster whose centroid is closest to the current cluster’s centroid)
- distance between the cluster centroid of the current cluster and the nearest cluster

If the number of observations in a cluster is 0, then that cluster is not displayed in the “Cluster Summary for Mixed Variables” table.
Standardization

The “Standardization” table displays the following:

- variable name
- location value that is used for standardization
- scale value that is used for standardization

Aligned Box Criterion Parameters

The “ABC Parameters” table displays the following:

- minimum number of clusters that are searched
- maximum number of clusters that are searched
- reference distribution count
- alignment method used for determining the region for generating the reference data

Aligned Box Criterion Statistics

The “ABC Statistics” table displays the following:

- number of clusters ($k$)
- logarithm of within-cluster sum of squares ($W_k^*$) for the input data for $k$ number of clusters
- logarithm of within-cluster sum of squares ($W_k$) for the reference data for $k$ number of clusters
- gap between the error measure from the reference data and the input data
- simulation-adjusted standard deviation ($s$) that is obtained from the reference data
- one-standard-error adjusted gap

Estimated Number of Clusters

The “Estimated Number of Clusters” table displays the following:

- criterion used for estimating the number of clusters from the measures that are calculated in the specified method
- estimated number of clusters for the input data table
Output CAS Tables

The “Output CAS Table” lists the number of observations and the number of variables that are included in the output data table.

ODS Table Names

Each table created by the KCLUS procedure has a name associated with it. You must use this name to refer to the table when you use ODS statements. These names are listed in Table 7.2.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABCParameters</td>
<td>Parameters that are specified in the NOC= option</td>
<td>PROC</td>
<td>NOC=ABC</td>
</tr>
<tr>
<td>ABCResults</td>
<td>Estimated number of clusters and the criteria that are used to calculate them</td>
<td>PROC</td>
<td>NOC=ABC</td>
</tr>
<tr>
<td>ABCStats</td>
<td>Statistics that are computed for estimating the number of clusters</td>
<td>PROC</td>
<td>NOC=ABC</td>
</tr>
<tr>
<td>ClusterSum</td>
<td>Cluster summary for interval input variables</td>
<td>INPUT</td>
<td>LEVEL=INTERVAL</td>
</tr>
<tr>
<td>ClusterSumIntNom</td>
<td>Cluster summary for mixed input variables</td>
<td>INPUT</td>
<td>LEVEL=INTERVAL and LEVEL=NOMINAL</td>
</tr>
<tr>
<td>ClusterSumNom</td>
<td>Cluster summary for nominal input variables</td>
<td>INPUT</td>
<td>LEVEL=NOMINAL</td>
</tr>
<tr>
<td>DescStats</td>
<td>Descriptive statistics for interval input variables</td>
<td>INPUT</td>
<td>LEVEL=INTERVAL</td>
</tr>
<tr>
<td>FreqNom</td>
<td>Frequencies for nominal variables in the input table and within each cluster</td>
<td>INPUT</td>
<td>LEVEL=NOMINAL</td>
</tr>
<tr>
<td>IterStats</td>
<td>Iteration history</td>
<td>PROC</td>
<td>Default output</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Model information</td>
<td>PROC</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations</td>
<td>PROC</td>
<td>Default output</td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Summary table for output data; contains number of observations and number of variables</td>
<td>PROC</td>
<td>Default output</td>
</tr>
<tr>
<td>Standardization</td>
<td>Information about the standardization method and its parameters</td>
<td>PROC</td>
<td>STANDARDIZE=RANGE or STANDARDIZE=STD</td>
</tr>
<tr>
<td>WithinClusStats</td>
<td>Statistics for interval input variables within clusters</td>
<td>INPUT</td>
<td>LEVEL=INTERVAL</td>
</tr>
</tbody>
</table>
Examples: KCLUS Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

**Example 7.1: Cluster Analysis**

This example uses the Iris data set in the Sashelp library to demonstrate how to use PROC KCLUS to perform cluster analysis. The iris data published by Fisher (1936) have been widely used for examples in discriminant and cluster analyses. The sepal length, sepal width, petal length, and petal width are measured in millimeters on 50 iris specimens from each of three species: *Iris setosa*, *I. versicolor*, and *I. virginica*. Mezzich and Solomon (1980) discuss a variety of cluster analyses that use the Iris data.

You can load the Sashelp.Iris data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sas
data mycas.iris;
  set sashelp.iris;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements perform clustering:

```sas
proc kclus data=mycas.iris maxclusters=3 outstat(outiter)=kclusOutstat1;
  input SepalLength SepalWidth PetalLength PetalWidth;
  score out=mycas.kclusOut1 copyvars=(SepalLength SepalWidth PetalLength PetalWidth Species);
run;
```

In this example, PROC KCLUS generates the data table mycas.kclusOut1, which contains the cluster membership information for each observation in the input data table. For each observation, the mycas.kclusOut1 data table includes the variables that are specified in the COPYVARS= option in the SCORE statement and two new variables: _CLUSTER_ID_, which is the ID of the closest cluster, and _DISTANCE_, which is the distance between the observation and the centroid of the closest cluster. This example uses the variables in both the INPUT statement and the COPYVARS= option in order to transfer these variables to the output data table to do further analysis.

PROC KCLUS generates several ODS tables, some of which are shown in Output 7.1.1 through Output 7.1.6.

**Output 7.1.1** Number of Observations

**Using PROC KCLUS to Analyze Data**

<table>
<thead>
<tr>
<th>The KCLUS Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
</tbody>
</table>
Example 7.1: Cluster Analysis

Output 7.1.2 Model Information

<table>
<thead>
<tr>
<th>Model Information</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Maximum Iterations</td>
<td>10</td>
</tr>
<tr>
<td>Stop Criterion</td>
<td>Cluster Change</td>
</tr>
<tr>
<td>Stop Criterion Value</td>
<td>0</td>
</tr>
<tr>
<td>Clusters</td>
<td>3</td>
</tr>
<tr>
<td>Initialization</td>
<td>Forgy</td>
</tr>
<tr>
<td>Seed</td>
<td>1301482243</td>
</tr>
<tr>
<td>Distance</td>
<td>Euclidean</td>
</tr>
<tr>
<td>Standardization</td>
<td>None</td>
</tr>
<tr>
<td>Interval Imputation</td>
<td>None</td>
</tr>
</tbody>
</table>

Output 7.1.3 Cluster Summary

<table>
<thead>
<tr>
<th>Cluster Summary for Interval Variables</th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Distance from Cluster</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Centroid to Observation</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Frequency</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Average</th>
<th>SSE</th>
<th>Standard Deviation</th>
<th>Nearest Cluster</th>
<th>Distance to Nearest Cluster Centroid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>50</td>
<td>0.6618</td>
<td>12.4803</td>
<td>4.8171</td>
<td>1515.1</td>
<td>5.5047</td>
<td>2</td>
<td>33.4949</td>
</tr>
<tr>
<td>2</td>
<td>61</td>
<td>2.3571</td>
<td>16.4680</td>
<td>7.3111</td>
<td>3829.1</td>
<td>7.9229</td>
<td>3</td>
<td>17.8842</td>
</tr>
<tr>
<td>3</td>
<td>39</td>
<td>2.3945</td>
<td>15.5156</td>
<td>7.3185</td>
<td>2541.4</td>
<td>8.0724</td>
<td>2</td>
<td>17.8842</td>
</tr>
</tbody>
</table>

Output 7.1.4 Iteration History

<table>
<thead>
<tr>
<th>Iteration History</th>
<th></th>
<th></th>
<th>Stop Criterion</th>
</tr>
</thead>
<tbody>
<tr>
<td>Iteration Number</td>
<td>SSE</td>
<td>SSE Change</td>
<td></td>
</tr>
<tr>
<td>0</td>
<td>17261</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>7917.110683</td>
<td>-9343.883917</td>
<td>1.333333</td>
</tr>
<tr>
<td>2</td>
<td>7892.139072</td>
<td>-24.985111</td>
<td>0.666667</td>
</tr>
<tr>
<td>3</td>
<td>7885.566583</td>
<td>-6.564390</td>
<td>0</td>
</tr>
</tbody>
</table>

Output 7.1.5 Descriptive Statistics

<table>
<thead>
<tr>
<th>Descriptive Statistics</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Mean</td>
<td>Standard Deviation</td>
</tr>
<tr>
<td>SepalLength</td>
<td>58.433333</td>
<td>8.280661</td>
</tr>
<tr>
<td>SepalWidth</td>
<td>30.573333</td>
<td>4.358663</td>
</tr>
<tr>
<td>PetalLength</td>
<td>37.580000</td>
<td>17.652982</td>
</tr>
<tr>
<td>PetalWidth</td>
<td>11.993333</td>
<td>7.622377</td>
</tr>
</tbody>
</table>
Chapter 7: The KCLUS Procedure

Output 7.1.6 Within-Cluster Statistics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Cluster</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>SepalLength</td>
<td>1</td>
<td>50.0600</td>
<td>3.5249</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>58.8361</td>
<td>4.4803</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>68.5385</td>
<td>4.8820</td>
</tr>
<tr>
<td>SepalWidth</td>
<td>1</td>
<td>34.2800</td>
<td>3.7906</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>27.4098</td>
<td>2.9290</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>30.7692</td>
<td>2.8696</td>
</tr>
<tr>
<td>PetalLength</td>
<td>1</td>
<td>14.6200</td>
<td>1.7366</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>43.8852</td>
<td>5.1157</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>57.1538</td>
<td>5.1018</td>
</tr>
<tr>
<td>PetalWidth</td>
<td>1</td>
<td>2.4600</td>
<td>1.0539</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>14.3443</td>
<td>2.9994</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>20.5385</td>
<td>2.9633</td>
</tr>
</tbody>
</table>

The following statements extract the first 10 observations from the output data table; they are shown in Output 7.1.7.

```plaintext
proc print noobs data=mycas.kclusOut1(obs=10);
run;
```

Output 7.1.7 First 10 Observations in the Output Data Table

<table>
<thead>
<tr>
<th>SepalLength</th>
<th>SepalWidth</th>
<th>PetalLength</th>
<th>PetalWidth</th>
<th>Species</th>
<th><em>CLUSTER_ID</em></th>
<th><em>DISTANCE</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>50</td>
<td>33</td>
<td>14</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>1.4959946524</td>
</tr>
<tr>
<td>46</td>
<td>34</td>
<td>14</td>
<td>3</td>
<td>Setosa</td>
<td>1</td>
<td>4.1518670499</td>
</tr>
<tr>
<td>46</td>
<td>36</td>
<td>10</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>6.4029680618</td>
</tr>
<tr>
<td>51</td>
<td>33</td>
<td>17</td>
<td>5</td>
<td>Setosa</td>
<td>1</td>
<td>3.8259639308</td>
</tr>
<tr>
<td>55</td>
<td>35</td>
<td>13</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>5.2685861481</td>
</tr>
<tr>
<td>48</td>
<td>31</td>
<td>16</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>4.1373904819</td>
</tr>
<tr>
<td>52</td>
<td>34</td>
<td>14</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>2.1066561181</td>
</tr>
<tr>
<td>49</td>
<td>36</td>
<td>14</td>
<td>1</td>
<td>Setosa</td>
<td>1</td>
<td>2.5686572368</td>
</tr>
<tr>
<td>44</td>
<td>32</td>
<td>13</td>
<td>2</td>
<td>Setosa</td>
<td>1</td>
<td>6.6901420015</td>
</tr>
<tr>
<td>50</td>
<td>35</td>
<td>16</td>
<td>6</td>
<td>Setosa</td>
<td>1</td>
<td>3.8675573687</td>
</tr>
</tbody>
</table>
```

PROC KCLUS creates the output statistics data table, which contains the cluster centroids. This data table includes the iteration number as _ITERATION_, the cluster ID as _CLUSTER_ID_, and the cluster centroids, which consist of the variables that are specified in the INPUT statement. Because the OUTITER= suboption is included in the OUTSTAT= option in the PROC KCLUS statement, cluster centroids for each iteration are added to the kclusOutstat1 data table.

The following statements extract the centroids before the first iteration and after the last iteration:
Example 7.2: Finding the Number of Clusters

This example uses the same data table that is loaded into your CAS session in Example 7.1.

You can find the number of clusters in the data table by specifying NOC=ABC in the PROC KCLUS statement as follows:

```sas
data mycas.iris;
  set sashelp.iris;
run;

proc kclus data=mycas.iris maxclusters=9 seed=1234
  NOC=ABC(B=10 minclusters=2 align=PCA criterion=FIRSTPEAK);
  input SepalLength SepalWidth PetalLength PetalWidth;
  ods output ABCStats=ABCStats1;
run;
```

PROC KCLUS generates several ODS tables, some of which are shown in Output 7.2.1 through Output 7.2.4. Output 7.2.1 shows the parameters that are used in the aligned box criterion (ABC) method.

---

### Example 7.2: Finding the Number of Clusters

Output 7.1.8 and Output 7.1.9 show the results.

#### Output 7.1.8 Cluster Centroids before the First Iteration

**Using PROC KCLUS to Analyze Data**

<table>
<thead>
<tr>
<th>ITERATION</th>
<th><em>CLUSTER_ID</em></th>
<th>SepalLength</th>
<th>SepalWidth</th>
<th>PetalLength</th>
<th>PetalWidth</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1</td>
<td>43</td>
<td>30</td>
<td>11</td>
<td>1</td>
</tr>
<tr>
<td>0</td>
<td>2</td>
<td>65</td>
<td>28</td>
<td>46</td>
<td>15</td>
</tr>
<tr>
<td>0</td>
<td>3</td>
<td>67</td>
<td>30</td>
<td>50</td>
<td>17</td>
</tr>
</tbody>
</table>

#### Output 7.1.9 Cluster Centroids after the Last Iteration

**Using PROC KCLUS to Analyze Data**

<table>
<thead>
<tr>
<th>ITERATION</th>
<th><em>CLUSTER_ID</em></th>
<th>SepalLength</th>
<th>SepalWidth</th>
<th>PetalLength</th>
<th>PetalWidth</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>1</td>
<td>51.9375</td>
<td>36.3125</td>
<td>14.7500</td>
<td>2.7188</td>
</tr>
<tr>
<td>7</td>
<td>2</td>
<td>63.1458</td>
<td>28.9583</td>
<td>49.7396</td>
<td>17.0313</td>
</tr>
<tr>
<td>7</td>
<td>3</td>
<td>47.3182</td>
<td>29.2727</td>
<td>17.7273</td>
<td>3.5000</td>
</tr>
</tbody>
</table>

---

---
Output 7.2.1  Aligned Box Criterion Parameters

Using PROC KCLUS to Analyze Data

The KCLUS Procedure

<table>
<thead>
<tr>
<th>Minimum Cluster</th>
<th>Maximum Cluster</th>
<th>Distribution Count</th>
<th>Alignment Method</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>9</td>
<td>10</td>
<td>PCA</td>
</tr>
</tbody>
</table>

Output 7.2.2 shows the statistics that are obtained for each candidate number of clusters.

Output 7.2.2  Aligned Box Criterion Statistics

<table>
<thead>
<tr>
<th>Number of Clusters</th>
<th>Input</th>
<th>Reference</th>
<th>Gap</th>
<th>Simulation Adjusted Standard Deviation</th>
<th>One Standard Error Adjusted Gap</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>9.6313</td>
<td>10.1237</td>
<td>0.4923</td>
<td>0.0531</td>
<td>0.4392</td>
</tr>
<tr>
<td>3</td>
<td>8.9727</td>
<td>9.4894</td>
<td>0.5167</td>
<td>0.3678</td>
<td>0.1489</td>
</tr>
<tr>
<td>4</td>
<td>8.6811</td>
<td>8.9211</td>
<td>0.2400</td>
<td>0.0408</td>
<td>0.1992</td>
</tr>
<tr>
<td>5</td>
<td>8.5528</td>
<td>8.8012</td>
<td>0.2485</td>
<td>0.0536</td>
<td>0.1948</td>
</tr>
<tr>
<td>6</td>
<td>8.2784</td>
<td>8.4730</td>
<td>0.1945</td>
<td>0.0587</td>
<td>0.1359</td>
</tr>
<tr>
<td>7</td>
<td>8.2133</td>
<td>8.3702</td>
<td>0.1569</td>
<td>0.0517</td>
<td>0.1053</td>
</tr>
<tr>
<td>8</td>
<td>8.0750</td>
<td>8.5884</td>
<td>0.5134</td>
<td>0.0419</td>
<td>0.4715</td>
</tr>
<tr>
<td>9</td>
<td>8.0444</td>
<td>8.1240</td>
<td>0.0796</td>
<td>0.0639</td>
<td>0.0158</td>
</tr>
</tbody>
</table>

Output 7.2.3  Estimated Number of Clusters

<table>
<thead>
<tr>
<th>Estimated Number of Clusters</th>
<th>Number of Clusters</th>
</tr>
</thead>
<tbody>
<tr>
<td>FirstPeak</td>
<td>3</td>
</tr>
</tbody>
</table>
Example 7.3: Clustering Nominal Variables

Output 7.2.4 Cluster Summary Table for Each Cluster

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Frequency</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Average</th>
<th>SSE</th>
<th>Standard Deviation</th>
<th>Nearest Cluster</th>
<th>Distance to Nearest Cluster Centroid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>62</td>
<td>2.1994</td>
<td>16.6064</td>
<td>7.3815</td>
<td>3982.1</td>
<td>8.0142</td>
<td>2</td>
<td>17.9718</td>
</tr>
<tr>
<td>2</td>
<td>38</td>
<td>2.5958</td>
<td>15.2971</td>
<td>7.1984</td>
<td>2387.9</td>
<td>7.9272</td>
<td>1</td>
<td>17.9718</td>
</tr>
<tr>
<td>3</td>
<td>50</td>
<td>0.6618</td>
<td>12.4803</td>
<td>4.8171</td>
<td>1515.1</td>
<td>5.5047</td>
<td>1</td>
<td>33.5693</td>
</tr>
</tbody>
</table>

When you use the NOC= option, the KCLUS procedure first estimates the number of clusters, \(k\), and then it displays the cluster analysis results for each of the \(k\) clusters as shown in Output 7.2.4.

Example 7.3: Clustering Nominal Variables

In this example, PROC KCLUS clusters nominal variables in the Baseball data set. The Baseball data set includes 322 observations, and each observation has 24 variables. Among these 24 variables, the 5 nominal ones are selected as the input data to show an example of running \(k\)-modes clustering on a nominal data set. You can load the Sashelp.Baseball data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```plaintext
data mycas.baseball;
  set sashelp.baseball;
  keep Team League Division Position Div;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements run the \(k\)-modes clustering algorithm with a frequency-based distance measure (DISTANCENOM=RELATIVEFREQ) and verify whether the clusters that the procedure obtains match the labels of the observations in the data table:

```plaintext
proc kclus data=mycas.baseball maxiter=10 maxc=5 DISTANCENOM=RELATIVEFREQ
  outstat(outiter)=kclusOutstat2;
  input Team League Division Position Div / level=nominal;
  score out=mycas.kclusOut2 copyvars=(Team League Division Position Div);
  ods output FreqNom=FreqNom1;
run;
```

Output 7.3.1 shows the cluster summary table that is produced for five clusters.
Output 7.3.1 Cluster Summary Table for Five Clusters

Using PROC KCLUS to Analyze Data

The KCLUS Procedure

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Frequency</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Average</th>
<th>Within Cluster Distance</th>
<th>Nearest Cluster</th>
<th>Distance to Nearest Cluster Centroid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>90</td>
<td>1.7111</td>
<td>2.0000</td>
<td>1.9580</td>
<td>176.2</td>
<td>2</td>
<td>3.8824</td>
</tr>
<tr>
<td>2</td>
<td>85</td>
<td>1.7059</td>
<td>2.0000</td>
<td>1.9550</td>
<td>166.2</td>
<td>1</td>
<td>3.8667</td>
</tr>
<tr>
<td>3</td>
<td>59</td>
<td>1.6271</td>
<td>2.0000</td>
<td>1.9282</td>
<td>113.8</td>
<td>4</td>
<td>2.0000</td>
</tr>
<tr>
<td>4</td>
<td>16</td>
<td>0.9375</td>
<td>1.6250</td>
<td>1.3867</td>
<td>22.1875</td>
<td>3</td>
<td>2.0000</td>
</tr>
<tr>
<td>5</td>
<td>72</td>
<td>1.6806</td>
<td>2.0000</td>
<td>1.9466</td>
<td>140.2</td>
<td>2</td>
<td>3.8824</td>
</tr>
</tbody>
</table>

Output 7.3.2 shows the frequencies of levels for the nominal input variable Team and information about how the levels of variables are distributed in each cluster; this information is important for revealing intracluster similarity. The following statement prints the observations from the frequency table, as shown in Output 7.3.2:

```
proc print noobs data=FreqNom1(obs=12);
run;
```

Output 7.3.2 Frequencies for Nominal Variables

Using PROC KCLUS to Analyze Data

<table>
<thead>
<tr>
<th>Variable</th>
<th>Level</th>
<th>Frequency Read</th>
<th>_1</th>
<th>_2</th>
<th>_3</th>
<th>_4</th>
<th>_5</th>
</tr>
</thead>
<tbody>
<tr>
<td>Team</td>
<td>Atlanta</td>
<td>11</td>
<td>0</td>
<td>0</td>
<td>10</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Baltimore</td>
<td>15</td>
<td>0</td>
<td>15</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Boston</td>
<td>10</td>
<td>0</td>
<td>10</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>California</td>
<td>13</td>
<td>13</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Chicago</td>
<td>24</td>
<td>13</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>11</td>
</tr>
<tr>
<td>Team</td>
<td>Cincinnati</td>
<td>12</td>
<td>0</td>
<td>0</td>
<td>11</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Cleveland</td>
<td>12</td>
<td>0</td>
<td>12</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Detroit</td>
<td>12</td>
<td>0</td>
<td>12</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Houston</td>
<td>11</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>11</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Kansas City</td>
<td>14</td>
<td>14</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Los Angeles</td>
<td>14</td>
<td>0</td>
<td>0</td>
<td>13</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Team</td>
<td>Milwaukee</td>
<td>14</td>
<td>0</td>
<td>14</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Example 7.4: Clustering Mixed Variables

In this example, PROC KCLUS uses the $k$-prototypes clustering algorithm to cluster mixed input data that contain both interval and nominal variables in the Baseball data set, which is the same data set that is used in Example 7.3. You can execute the following SAS code to load the input data table, mycas.baseball.

```sas
data mycas.baseball;
  Set sashelp.baseball;
  Keep CrAtBat CrHits CrRuns CrRbi CrBB Team League Division Position Div;
Run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements run the $k$-prototypes clustering algorithm on mixed input data. The first INPUT statement uses the LEVEL=INTERVAL option to specify the input variables CrAtBat, CrHits, CrRuns, CrRbi, and CrBB as the interval input variables; the second INPUT statement uses the LEVEL=NOMINAL option to specify the input variables Team, League, Division, Position, and Div as the nominal input variables.

The KPROTOTYPEPARAMS=USERGAMMA(VALUE=10) option specifies $\gamma = 10$ for the $k$-prototypes clustering algorithm. The NOC=ABC option uses the ABC algorithm to search for the best number of clusters in a range of 2 to 10. The PRINTALLDISTANCES option prints two additional variables, _DISTANCEINT_ and _DISTANCENOM_, in the output table kclusout4.

```sas
proc kclus data=mycas.baseball maxiter=10 maxc=10 distancenom=relativefreq
  outstat(outiter)=kclusOutstat4 printalldistances
  noc=abc(B=10 minclusters=2 align=none criterion=all)
  kprototypeparams=usergamma(value=10);
  input CrAtBat CrHits CrRuns CrRbi CrBB / level=interval;
  input Team League Division Position Div / level=nominal;
  score out=mycas.kclusOut4 copyvars=(CrAtBat CrHits CrRuns CrRbi CrBB Team League Division Position Div);
  ods output FreqNom=FreqNom4;
run;
```

Output 7.4.1 shows the “Model Information” table. The clustering algorithm in use is the $k$-prototypes, and the $\gamma$ value is 10. Since PROC KCLUS is implementing the $k$-prototypes algorithm on mixed input data, the distance measures for both the interval and nominal variables are displayed in the table, as Euclidean and RelativeFreq, respectively.
Output 7.4.1 Model Information for \( k \)-Prototypes Clustering Algorithm

Using PROC KCLUS to Analyze Data

The KCLUS Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Clustering Algorithm</td>
<td>( k )-prototypes</td>
</tr>
<tr>
<td>Gamma Value</td>
<td>10</td>
</tr>
<tr>
<td>Maximum Iterations</td>
<td>10</td>
</tr>
<tr>
<td>Stop Criterion</td>
<td>Cluster Change</td>
</tr>
<tr>
<td>Stop Criterion Value</td>
<td>0</td>
</tr>
<tr>
<td>Clusters</td>
<td>9</td>
</tr>
<tr>
<td>Initialization</td>
<td>Forgy</td>
</tr>
<tr>
<td>Seed</td>
<td>1344669769</td>
</tr>
<tr>
<td>Distance</td>
<td>Euclidean</td>
</tr>
<tr>
<td>Distance for Nominal Variables</td>
<td>RelativeFreq</td>
</tr>
<tr>
<td>Number of Clusters Estimation</td>
<td>ABC</td>
</tr>
<tr>
<td>Standardization</td>
<td>None</td>
</tr>
<tr>
<td>Interval Imputation</td>
<td>None</td>
</tr>
<tr>
<td>Nominal Imputation</td>
<td>None</td>
</tr>
</tbody>
</table>

Output 7.4.2 shows the cluster summary table that is produced for the \( k \)-prototypes algorithm.

Output 7.4.2 Cluster Summary Table for \( k \)-Prototypes Clustering Algorithm

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Frequency</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Average</th>
<th>Within Cluster Distance</th>
<th>Nearest Cluster</th>
<th>Distance to Nearest Cluster Centroid</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>29</td>
<td>41716.4</td>
<td>2463136</td>
<td>567051</td>
<td>16444476</td>
<td>9</td>
<td>3561949</td>
</tr>
<tr>
<td>2</td>
<td>39</td>
<td>632.5</td>
<td>42746.1</td>
<td>12940.6</td>
<td>504683</td>
<td>5</td>
<td>149138</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>2266864</td>
<td>10194126</td>
<td>5154060</td>
<td>15462181</td>
<td>1</td>
<td>16431341</td>
</tr>
<tr>
<td>4</td>
<td>46</td>
<td>1219.0</td>
<td>116650</td>
<td>39041.5</td>
<td>1795908</td>
<td>2</td>
<td>222343</td>
</tr>
<tr>
<td>5</td>
<td>38</td>
<td>276.8</td>
<td>32704.3</td>
<td>9088.9</td>
<td>345377</td>
<td>2</td>
<td>149138</td>
</tr>
<tr>
<td>6</td>
<td>46</td>
<td>3962.8</td>
<td>206478</td>
<td>70851.3</td>
<td>3259159</td>
<td>4</td>
<td>489878</td>
</tr>
<tr>
<td>7</td>
<td>40</td>
<td>14835.3</td>
<td>710325</td>
<td>224020</td>
<td>8960815</td>
<td>8</td>
<td>1805148</td>
</tr>
<tr>
<td>8</td>
<td>51</td>
<td>3919.0</td>
<td>447387</td>
<td>147933</td>
<td>7544608</td>
<td>6</td>
<td>1146577</td>
</tr>
<tr>
<td>9</td>
<td>30</td>
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<td>713299</td>
<td>275928</td>
<td>8277848</td>
<td>7</td>
<td>2653048</td>
</tr>
</tbody>
</table>
References


Overview: LOGSELECT Procedure

The LOGSELECT procedure fits and performs model selection for logistic regression models in SAS Viya, including binary, binomial, and multinomial response models.

The models that PROC LOGSELECT supports can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The models can also include constructed effects such as splines. The procedure offers a number of effect-selection methods, including stepwise methods and modern LASSO methods. It also offers extensive capabilities for customizing the model selection by using a wide variety of selection and stopping criteria, from computationally efficient significance-level-based criteria to modern, computationally intensive validation-based criteria. PROC LOGSELECT also provides a variety of logistic regression diagnostics that are conditional on the selected model.

Logistic regression analysis is often used to investigate the relationship between discrete responses and a set of explanatory variables. The LOGSELECT procedure fits logistic regression models in the broader sense; the procedure permits several link functions and can handle ordinal and nominal response data that have more than two response categories (multinomial data).

The logistic model shares a common feature with a more general class of linear models: a function \( g = g(\mu) \) of the mean of the response variable is assumed to be linearly related to the explanatory variables. Because the mean \( \mu \) implicitly depends on the stochastic behavior of the response and the explanatory variables are assumed to be fixed, the function \( g \) provides the link between the random (stochastic) component and the systematic (deterministic) component of the response variable \( Y \). For this reason, Nelder and Wedderburn (1972) refer to \( g(\mu) \) as a link function. The LOGSELECT procedure fits a broad class of binary response models of the form

\[
g(\pi \mid x) = \alpha + \beta'x
\]

where the link functions that are available in PROC LOGSELECT and that are widely used in practice are the logit, probit, log-log, and complementary log-log functions, and the predicted probability of an event, \( \pi \), is the mean \( \mu \) of the response variable. One advantage of the logit function over other link functions is that differences on the logistic scale are interpretable regardless of whether the data are sampled prospectively or retrospectively (McCullagh and Nelder 1989, Chapter 4).

If your response \( Y \) has more than two values and they can be ordered (for example, \( Y \in \{1, \ldots, J - 1, J\} \)), then the LOGSELECT procedure uses the preceding link functions and fits ordinal response models of the form

\[
g(\pi_j \mid x) = \alpha_j + \beta'x, \quad j = 1, \ldots, J - 1
\]

where \( \pi_j = \Pr(Y \leq j) \) are cumulative probabilities of the ordered response categories.
If your response $Y$ has more than two values and they have no natural ordering, then the LOGSELECT procedure fits a generalized or baseline-category logit model, which has the form

$$
\log \left( \frac{\Pr(Y = j | x)}{\Pr(Y = J | x)} \right) = \alpha_j + \beta_j x, \quad j = 1, \ldots, J - 1
$$

where the $\beta_1, \ldots, \beta_{J-1}$ are $J-1$ vectors of slope parameters. These models are a special case of the discrete choice or conditional logit models introduced by McFadden (1974).

Texts that discuss logistic regression include Agresti (2013); Allison (2012); Collett (2003); Cox and Snell (1989); Hosmer and Lemeshow (2013); Stokes, Davis, and Koch (2012).

### PROC LOGSELECT Features

The LOGSELECT procedure estimates the parameters of a logistic regression model by using maximum likelihood techniques. It also does the following:

- provides model-building syntax with the CLASS, EFFECT, and effect-based MODEL statements, which are familiar from SAS/STAT analytic procedures (in particular, the GLM, LOGISTIC, GLIMMIX, and MIXED procedures)
- provides response-variable options as in the LOGISTIC procedure
- performs maximum likelihood estimation
- provides the logit, probit, log-log, and complementary log-log link functions
- provides cumulative link models for ordinal response data and generalized logit modeling for unordered multinomial data
- enables model building (variable selection) through the SELECTION statement
- provides a WEIGHT statement for weighted analysis
- provides a FREQ statement for grouped analysis
- provides a CODE statement to produce SAS code that can score a new data set
- provides an OUTPUT statement to produce a data table that contains predicted probabilities and other observation-wise statistics
- uses ODS Graphics to create model selection plots as part of its output. For more information about ODS Graphics, see the section “ODS Graphics” on page 501.

Because the LOGSELECT procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on CAS
- exploits all the available cores and concurrent threads. For information about how PROC LOGSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

### PROC LOGSELECT Compared with Other SAS Procedures

The LOGSELECT procedure provides logistic regression modeling functionality that is comparable to that of the HPLOGISTIC and LOGISTIC procedures in SAS/STAT software.
PROC LOGSELECT Compared with the HPLOGISTIC Procedure

The functionality of the LOGSELECT procedure closely resembles that of the HPLOGISTIC procedure, which is a high-performance procedure. The LOGSELECT procedure is the next generation of the HPLOGISTIC procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations. Both procedures perform computations in multiple threads.

Both the LOGSELECT and HPLOGISTIC procedures fit and perform model selection for logistic regression models. The models can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The HPLOGISTIC procedure provides GLM and reference parameterizations of classification variables; the LOGSELECT procedure provides the full set of parameterizations that are available in PROC LOGISTIC and other modeling procedures. The LOGSELECT procedure is additionally capable of creating complex constructed effects, including univariate spline and polynomial expansions.

With the LOGSELECT and HPGLOGISTIC procedures, you request model selection by using the SELECTION statement. Both procedures offer the same methods of effect selection, but the LOGSELECT procedure also provides LASSO selection and produces selection plots by using ODS Graphics.

The LOGSELECT procedure provides more regression diagnostics than the HPLOGISTIC procedure. This release of the LOGSELECT procedure is more limited in postfitting functionality than the HPLOGISTIC procedure.

PROC LOGSELECT Compared with the LOGISTIC Procedure

The LOGSELECT procedure provides the full set of parameterizations that are available in PROC LOGISTIC. The LOGSELECT procedure uses the GLM parameterization for the CLASS variables by default. The LOGISTIC procedure uses the EFFECT parameterization for the CLASS variables by default. In either procedure, you can use the PARAM= option in the CLASS statement to change the parameterization.

The LOGISTIC procedure uses Fisher scoring by default. The LOGSELECT procedure uses a modification of the Newton-Raphson algorithm with a ridged Hessian by default. You can choose different optimization techniques, including first-order methods that do not require a crossproducts matrix or Hessian, by using the TECHNIQUE= option in the PROC LOGSELECT statement.

The LOGSELECT procedure provides a richer set of model selection options than the LOGISTIC procedure, including LASSO selection, information-criterion-based selection and stopping criteria, and validation-based criteria.

The LOGSELECT procedure uses ODS Graphics to display plots that help interpret the selection process; the LOGISTIC procedure displays many diagnostic and fit plots.

The LOGISTIC procedure offers a wide variety of postfitting analyses, such as contrasts, estimates, tests of model effects, least squares means, and odds ratios. This release of the LOGSELECT procedure is limited in postfitting functionality, because for large data sets the focus is primarily on model fitting and scoring.

The LOGSELECT procedure is specifically designed to operate in SAS Viya and performs computations in multiple threads. The LOGISTIC procedure executes in a single thread on a single machine.
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: LOGSELECT Procedure

Binary Logistic Regression

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following DATA step creates the data table getStarted, which consists of 100 observations on a dichotomous response variable (y), a character variable (C), and 10 continuous variables (x1–x10), in your CAS session:
data mycas.getStarted;
  input C$ y x1-x10;
  datalines;
  D 0 10.2 6 1.6 38 15 2.4 20 0.8 8.5 3.9
  F 1 12.2 6 2.6 42 61 1.5 10 0.6 8.5 0.7
  D 1 7.7 1 2.1 38 61 1 90 0.6 7.5 5.2
  J 1 10.9 7 3.5 46 42 0.3 0 0.2 6 3.6
  E 0 17.3 6 3.8 26 47 0.9 10 0.4 1.5 4.7
  A 0 18.7 4 1.8 2 34 1.7 80 1 9.5 2.2
  B 0 7.2 1 0.3 48 61 1.1 10 0.8 3.5 4
  D 0 0.1 3 2.4 0 65 1.6 70 0.8 3.5 0.7
  H 1 2.4 4 0.7 38 22 0.2 20 0 3 4.2
  J 0 15.6 7 1.4 0 98 0.3 0 1 5 5.2
  J 0 11.1 3 2.4 42 55 2.2 60 0.6 4.5 0.7
  F 0 4 6 0.9 4 36 2.1 30 0.8 9 4.6
  A 0 6.2 2 1.8 14 79 1.1 70 0.2 0 5.1
  H 0 3.7 3 0.8 12 66 1.3 40 0.4 0.5 3.3
  A 1 9.2 3 2.3 48 51 2.3 50 0 6 5.4
  G 0 14 3 2 18 12 2.2 0 0 3 3.4
  E 1 19.5 6 3.7 26 81 0.1 30 0.6 5 4.8
  C 0 11 3 2.8 38 9 1.7 50 0.8 6.5 0.9
  I 0 15.3 7 2.2 20 98 2.7 100 0.4 7 0.8
  H 1 7.4 4 0.5 28 65 1.3 60 0.2 9.5 5.4
  F 0 11.4 2 1.4 42 12 2.4 10 0.4 1 4.5
  C 1 19.4 1 0.4 42 4 2.4 10 0 6.5 0.1
  G 0 5.9 4 2.6 12 57 0.8 50 0.4 2 5.8
  G 1 15.8 6 3.7 34 8 1.3 90 0.6 2.5 5.7
  I 0 10 3 1.9 16 80 3 90 0.4 9.5 1.9
  E 0 15.7 1 2.7 32 25 1.7 20 0.2 8.5 6
  G 0 11 5 2.9 48 53 0.1 50 1 3.5 1.2
  J 1 16.8 0 0.9 14 86 1.4 40 0.8 9 5
  D 1 11 4 3.2 48 63 2.8 90 0.6 0 2.2
  J 1 4.8 7 3.6 24 1 2.2 20 1 8.5 0.5
  J 1 10.4 5 2 42 56 1 20 0 3.5 4.2
  G 0 12.7 7 3.6 8 56 2.1 70 1 4.5 1.5
  G 0 6.8 1 3.2 30 27 0.6 0 0.8 2 5.6
  E 0 8.8 0 3.2 2 67 0.7 10 0.4 1 5
  I 1 0.2 0 2.9 10 41 2.3 60 0.2 9 0.3
  J 1 4.6 7 3.9 50 61 2.1 50 0.4 3 4.9
  J 1 2.3 2 3.2 36 98 0.1 40 0.6 4.5 4.3
  I 0 10.8 3 2.7 28 58 0.8 80 0.8 3 6
  B 0 9.3 2 3.3 44 44 0.3 50 0.8 5.5 0.4
  F 0 9.2 6 0.6 4 64 0.1 0 0.6 4.5 3.9
  D 0 7.4 0 2.9 14 0 0.2 30 0.8 7.5 4.5
  G 0 18.3 3 3.1 8 60 0.3 60 0.2 7 1.9
  F 0 5.3 4 0.2 48 63 2.3 80 0.2 8 5.2
  C 0 2.6 5 2.2 24 4 1.3 20 0 2 1.4
  F 0 13.8 4 3.6 4 7 1.1 10 0.4 3.5 1.9
  B 1 12.4 6 1.7 30 44 1.1 60 0.2 6 1.5
  I 0 1.3 1 1.3 8 53 1.1 70 0.6 7 0.8
  F 0 18.2 7 1.7 26 92 2.2 30 1 8.5 4.8
  J 0 5.2 2 2.2 18 12 1.4 90 0.8 4 4.9
  G 1 9.4 2 0.8 22 86 0.4 30 0.4 1 5.9
| J  | 1   | 10.4 | 2  | 1.7 | 26  | 31  | 2.4 | 10  | 0.2  | 7   | 1.6 |
| J  | 0   | 13   | 1  | 1.8 | 14  | 11  | 2.3 | 50  | 0.6  | 5.5 | 2.6 |
| A  | 0   | 17.9 | 4  | 3.1 | 46  | 58  | 2.6 | 90  | 0.6  | 1.5 | 3.2 |
| D  | 1   | 19.4 | 6  | 3   | 20  | 50  | 2.8 | 100 | 0.2  | 9   | 1.2 |
| I  | 0   | 19.6 | 3  | 3.6 | 22  | 19  | 1.2 | 0   | 0.6  | 5   | 4.1 |
| I  | 1   | 6    | 2  | 1.5 | 30  | 30  | 2.2 | 20  | 0.4  | 8.5 | 5.3 |
| G  | 0   | 13.8 | 1  | 2.7 | 0   | 52  | 2.4 | 20  | 0.8  | 6   | 2   |
| B  | 0   | 14.3 | 4  | 2.9 | 30  | 11  | 0.6 | 90  | 0.6  | 0.5 | 4.9 |
| E  | 0   | 15.6 | 0  | 0.4 | 38  | 79  | 0.4 | 80  | 0.4  | 1   | 3.3 |
| D  | 0   | 14   | 2  | 1   | 22  | 61  | 3   | 90  | 0.6  | 2   | 0.1 |
| C  | 1   | 9.4  | 5  | 0.4 | 12  | 53  | 1.7 | 40  | 0    | 3   | 1.1 |
| H  | 0   | 13.2 | 1  | 1.6 | 40  | 15  | 0.7 | 40  | 0.2  | 9   | 5.5 |
| A  | 0   | 13.5 | 5  | 2.4 | 18  | 89  | 1.6 | 20  | 0.4  | 9.5 | 4.7 |
| E  | 0   | 2.6  | 4  | 2.3 | 38  | 6   | 0.8 | 20  | 0.4  | 5   | 5.3 |
| E  | 0   | 12.4 | 3  | 1.3 | 26  | 8   | 2.8 | 10  | 0.8  | 6   | 5.8 |
| D  | 0   | 7.6  | 2  | 0.9 | 44  | 89  | 1.3 | 50  | 0.8  | 6   | 0.4 |
| I  | 0   | 12.7 | 1  | 2.3 | 42  | 6   | 2.4 | 10  | 0.4  | 1   | 3   |
| C  | 1   | 10.7 | 4  | 3.2 | 28  | 23  | 2.2 | 90  | 0.8  | 5.5 | 2.8 |
| H  | 0   | 10.1 | 2  | 2.3 | 10  | 62  | 0.9 | 50  | 0.4  | 2.5 | 3.7 |
| C  | 1   | 16.6 | 1  | 0.5 | 12  | 88  | 0.1 | 20  | 0.6  | 5.5 | 1.8 |
| I  | 1   | 0.2  | 3  | 2.2 | 8   | 71  | 1.7 | 80  | 0.4  | 0.5 | 5.5 |
| C  | 0   | 10.8 | 4  | 3.5 | 30  | 70  | 2.3 | 60  | 0.4  | 4.5 | 5.9 |
| F  | 0   | 7.1  | 4  | 3   | 14  | 63  | 2.4 | 70  | 0    | 7   | 3.1 |
| D  | 0   | 16.5 | 1  | 3.3 | 30  | 80  | 1.6 | 40  | 0    | 3.5 | 2.7 |
| H  | 0   | 17.1 | 7  | 2.1 | 30  | 45  | 1.5 | 60  | 0.6  | 0.5 | 2.8 |
| D  | 0   | 4.3  | 1  | 1.5 | 24  | 44  | 0   | 70  | 0    | 5   | 0.5 |
| H  | 0   | 15   | 2  | 0.2 | 14  | 87  | 1.8 | 50  | 0    | 4.5 | 4.7 |
| G  | 0   | 19.7 | 3  | 1.9 | 36  | 99  | 1.5 | 10  | 0.6  | 3   | 1.7 |
| H  | 1   | 2.8  | 6  | 0.6 | 34  | 21  | 2   | 60  | 1    | 9   | 4.7 |
| G  | 0   | 16.6 | 3  | 3.3 | 46  | 1   | 1.4 | 70  | 0.6  | 1.5 | 5.3 |
| E  | 0   | 11.7 | 5  | 2.7 | 48  | 4   | 0.9 | 60  | 0.8  | 4.5 | 1.6 |
| F  | 0   | 15.6 | 3  | 0.2 | 4   | 79  | 0.5 | 0   | 0.8  | 1.5 | 2.9 |
| C  | 1   | 5.3  | 6  | 1.4 | 8   | 64  | 2   | 80  | 0.4  | 9   | 4.2 |
| B  | 1   | 8.1  | 7  | 1.7 | 40  | 36  | 1.4 | 60  | 0.6  | 6   | 3.9 |
| I  | 0   | 14.8 | 2  | 3.2 | 8   | 37  | 0.4 | 10  | 0    | 4.5 | 3   |
| D  | 0   | 7.4  | 4  | 3   | 12  | 3   | 0.6 | 60  | 0.6  | 7   | 0.7 |
| D  | 0   | 4.8  | 3  | 2.3 | 44  | 41  | 1.9 | 60  | 0.2  | 3   | 3.1 |
| A  | 0   | 4.5  | 0  | 0.2 | 4   | 48  | 1.7 | 80  | 0.8  | 9   | 4.2 |
| D  | 0   | 6.9  | 6  | 3.3 | 14  | 92  | 0.5 | 40  | 0.4  | 7.5 | 5   |
| B  | 0   | 4.7  | 4  | 0.9 | 14  | 99  | 2.4 | 80  | 1    | 0.5 | 0.7 |
| I  | 1   | 7.5  | 4  | 2.1 | 20  | 79  | 0.4 | 40  | 0.4  | 2.5 | 0.7 |
| C  | 0   | 6.1  | 0  | 1.4 | 38  | 18  | 2.3 | 60  | 0.8  | 4.5 | 0.7 |
| C  | 0   | 18.3 | 1  | 1   | 26  | 98  | 2.7 | 20  | 1    | 8.5 | 0.5 |
| F  | 0   | 16.4 | 7  | 1.2 | 32  | 94  | 2.9 | 40  | 0.4  | 5.5 | 2.1 |
| I  | 0   | 9.4  | 2  | 2.3 | 32  | 42  | 0.2 | 70  | 0.4  | 8.5 | 0.3 |
| F  | 1   | 17.9 | 4  | 1.3 | 32  | 42  | 2   | 40  | 0.2  | 1   | 5.4 |
| H  | 0   | 14.9 | 3  | 1.6 | 36  | 74  | 2.6 | 60  | 0.2  | 1   | 2.3 |
| C  | 0   | 12.7 | 0  | 2.6 | 0   | 88  | 1.1 | 80  | 0.8  | 0.5 | 2.1 |
| F  | 0   | 5.4  | 4  | 1.5 | 2   | 1   | 1.8 | 70  | 0.4  | 5.5 | 3.6 |
| J  | 1   | 12.1 | 4  | 1.8 | 20  | 59  | 1.3 | 60  | 0.4  | 3   | 3.8 |

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.
The following statements fit a logistic model to these data by using a classification effect for variable C and 10 regressor effects for x1–x10. The ITHIST option displays a table that summarizes the steps of the optimization.

```plaintext
proc logselect data=mycas.getStarted ithist;
   class C;
   model y = C x1-x10;
run;
```

The output from this analysis is presented in Figure 8.1 through Figure 8.10.

Figure 8.1 displays the “Model Information” table. The LOGSELECT procedure uses a Newton-Raphson algorithm to model a binary distribution with a logit link function for the variable y. The CLASS variable C is parameterized using the GLM parameterization, which is the default.

**Figure 8.1 Model Information**

The LOGSELECT Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Optimization Technique</td>
</tr>
</tbody>
</table>

Figure 8.2 displays the “Number of Observations” table. All 100 observations in the data table are used in the analysis.

**Figure 8.2 Number of Observations**

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>Number of Observations Used</th>
</tr>
</thead>
<tbody>
<tr>
<td>100</td>
<td>100</td>
</tr>
</tbody>
</table>

The “Response Profile” table in Figure 8.3 is produced by default. It shows the breakdown of the response variable levels by frequency. By default for binary data, the LOGSELECT procedure models the probability of the event with the lower-ordered value in the “Response Profile” table, as indicated by the note that follows the table. In this example, the values that are represented by y = 0 are modeled as the “successes” in the Bernoulli experiments.

**Figure 8.3 Response Profile**

<table>
<thead>
<tr>
<th>Response Profile</th>
<th>Total Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ordered Value y</td>
<td></td>
</tr>
<tr>
<td>1 0</td>
<td>69</td>
</tr>
<tr>
<td>2 1</td>
<td>31</td>
</tr>
</tbody>
</table>

Probability modeled is $y = 0$.

You can use the response-variable options in the MODEL statement to choose which value of the response variable to model.
The **CLASS** variable \( C \) has 10 unique formatted levels that are displayed in the “Class Level Information” table in **Figure 8.4**.

**Figure 8.4** Class Level Information

<table>
<thead>
<tr>
<th>Class Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>( C )</td>
<td>A B C D E F G H I J</td>
</tr>
</tbody>
</table>

The “Iteration History” table is shown in **Figure 8.5**. The Newton-Raphson algorithm with ridging converged after four iterations, not counting the initial setup iteration.

**Figure 8.5** Iteration History

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Evaluations</th>
<th>Objective Function</th>
<th>Change</th>
<th>Maximum Gradient</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>4</td>
<td>0.4493546916</td>
<td>0.410972</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>0.4436453992</td>
<td>0.00570929</td>
<td>0.081339</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0.4435038109</td>
<td>0.00014159</td>
<td>0.003302</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>0.4435025933</td>
<td>0.00000022</td>
<td>5.623E-6</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0.4435025933</td>
<td>0.00000000</td>
<td>1.59E-11</td>
</tr>
</tbody>
</table>

**Figure 8.6** displays the final convergence status of the Newton-Raphson algorithm. The \( \text{GCONV=} \) relative convergence criterion is satisfied.

**Figure 8.6** Convergence Status

Convergence criterion (\( \text{GCONV=}1\text{E}-8 \)) satisfied.

**Figure 8.7** displays the “Dimensions” table for this model. This table summarizes some important sizes of various model components. For example, it shows that the design matrix \( X \) has 21 columns, which correspond to 1 column for the intercept, 10 columns for the effect associated with the classification variable \( C \), and 1 column each for the continuous variables \( x_1 \)–\( x_{10} \). However, the rank of the crossproducts matrix is only 20. Because the classification variable \( C \) uses GLM parameterization and because the model contains an intercept, there is one singularity in the crossproducts matrix of the model. Consequently, only 20 parameters enter the optimization.

**Figure 8.7** Dimensions in Binomial Logistic Regression

<table>
<thead>
<tr>
<th>Dimensions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Columns in Design</td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Max Effect Columns</td>
</tr>
<tr>
<td>Rank of Design</td>
</tr>
<tr>
<td>Parameters in Optimization</td>
</tr>
</tbody>
</table>
Figure 8.8 shows the global test for the null hypothesis that all model effects jointly do not affect the probability of success of the binary response. The test is significant \((p = 0.0135)\). One or more of the model effects thus significantly affect the probability of observing an event.

**Figure 8.8 Null Test**

<table>
<thead>
<tr>
<th>Test</th>
<th>DF</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Likelihood Ratio</td>
<td>19</td>
<td>35.1194</td>
<td>0.0135</td>
</tr>
</tbody>
</table>

The “Fit Statistics” table is shown in Figure 8.9. The \(-2\) log likelihood at the converged estimates is 88.7007. You can use this value to compare the model to nested model alternatives by means of a likelihood ratio test. To compare models that are not nested, you can use information criteria such as AIC (Akaike’s information criterion), AICC (Akaike’s bias-corrected information criterion), and SBC (Schwarz Bayesian information criterion). These criteria penalize the \(-2\) log likelihood for the number of parameters. Because of the large number of parameters relative to the number of observations, the discrepancy between the \(-2\) log likelihood and, for example, AIC is substantial in this case.

**Figure 8.9 Fit Statistics**

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>(-2) Log Likelihood</td>
<td>88.70072</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>128.70072</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>139.33363</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>180.80412</td>
</tr>
</tbody>
</table>

However, the “Parameter Estimates” table in Figure 8.10 shows that many parameters have fairly large \(p\)-values, indicating that one or more of the model effects might not be necessary.
Finally, the procedure displays the table in Figure 8.11, which shows the amount of time (in seconds) that PROC LOGSELECT required to perform different tasks in the analysis.

**Figure 8.11** Procedure Timing

<table>
<thead>
<tr>
<th>Task</th>
<th>Seconds</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Setup and Parsing</td>
<td>0.05</td>
<td>33.30%</td>
</tr>
<tr>
<td>Levelization</td>
<td>0.06</td>
<td>41.12%</td>
</tr>
<tr>
<td>Model Initialization</td>
<td>0.00</td>
<td>1.08%</td>
</tr>
<tr>
<td>SSCP Computation</td>
<td>0.00</td>
<td>1.12%</td>
</tr>
<tr>
<td>Model Fitting</td>
<td>0.03</td>
<td>18.48%</td>
</tr>
<tr>
<td>Cleanup</td>
<td>0.00</td>
<td>1.59%</td>
</tr>
<tr>
<td>Total</td>
<td>0.15</td>
<td>100.00%</td>
</tr>
</tbody>
</table>
Syntax: LOGSELECT Procedure

The following statements are available in the LOGSELECT procedure:

```
PROC LOGSELECT < options > ;
   BY variables ;
   CLASS variable < (options) > . . . < variable < (options) > > < / global-options > ;
   CODE < options > ;
   DISPLAY < table-list > < / options > ;
   DISPLAYOUT table-spec-list < / options > ;
   EFFECT name=effect-type(variables < / options > ) ;
   FREQ variable ;
   MODEL response < (response-options) > = < effects > < / model-options > ;
   MODEL events/trials < (response-options) > = < effects > < / model-options > ;
   OUTPUT OUT=CAS-libref.data-table < options > < keyword = name > . . . < keyword = name > ;
   PARTITION partition-options ;
   SELECTION < METHOD=method > < (method-options) > > < options > ;
   WEIGHT variable ;
```

The PROC LOGSELECT statement and at least one MODEL statement are required. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statements.

PROC LOGSELECT Statement

```
PROC LOGSELECT < options > ;
```

The PROC LOGSELECT statement invokes the procedure. Table 8.1 summarizes the available `options` in the PROC LOGSELECT statement by function.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALPHA=</td>
<td>Specifies a global significance level</td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td>MAXOPTBATCH=</td>
<td>Specifies the maximum number of observations to be computed in each batch</td>
</tr>
</tbody>
</table>

Output Options
```
CORRB         | Displays the “Parameter Estimates Correlation Matrix” table |
COVB          | Displays the “Parameter Estimates Covariance Matrix” table |
ITHIST        | Displays the “Iteration History” table                |
NOCHECK       | Disables checking for infinite parameters             |
NOCLPRINT     | Limits or suppresses the display of class levels       |
NOSTDERR      | Suppresses computation of the covariance matrix and standard errors |
PARTFIT       | Displays the fit statistics that are produced when your data are partitioned |
STB           | Displays standardized estimates                       |
```
Table 8.1  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Optimization Options</strong></td>
<td></td>
</tr>
<tr>
<td>ABSCONV=</td>
<td>Tunes the absolute function convergence criterion</td>
</tr>
<tr>
<td>ABSFCNV=</td>
<td>Tunes the absolute function difference convergence criterion</td>
</tr>
<tr>
<td>ABSCGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>ABSXCONV=</td>
<td>Tunes the absolute parameter convergence criterion</td>
</tr>
<tr>
<td>FCONV=</td>
<td>Tunes the relative function difference convergence criterion</td>
</tr>
<tr>
<td>FCONV2=</td>
<td>Tunes the second relative function difference convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>GCONV2=</td>
<td>Tunes the second relative gradient convergence criterion</td>
</tr>
<tr>
<td>XCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Specifies the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit of CPU time (in seconds) for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>NORMALIZE=</td>
<td>Specifies whether the objective function is normalized during optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
<tr>
<td><strong>LASSO Options</strong></td>
<td></td>
</tr>
<tr>
<td>LASSORHO=</td>
<td>Specifies the base regularization parameter for the LASSO method</td>
</tr>
<tr>
<td>LASSOSTEPS=</td>
<td>Specifies the maximum number of steps for the LASSO method</td>
</tr>
<tr>
<td>LASSOTOL=</td>
<td>Specifies the convergence criterion for the LASSO method</td>
</tr>
</tbody>
</table>

The optimization options are fully described in the section “Optimization Options” on page 42 in Chapter 2, “Shared Concepts.” The following list describes the other options available in the PROC LOGSELECT statement:

**ALPHA=number**

specifies a global significance level for the construction of confidence intervals. The confidence level is 1–number. The value of number must be between 0 and 1. You can override the global specification by specifying the ALPHA= option in the OUTPUT statement. By default, ALPHA=0.05.

**CORRB**

creates the “Parameter Estimates Correlation Matrix” table. The correlation matrix is computed by normalizing the covariance matrix \( \Sigma \). That is, if \( \sigma_{ij} \) is an element of \( \Sigma \), then the corresponding element of the correlation matrix is \( \frac{\sigma_{ij}}{\sigma_i \sigma_j} \), where \( \sigma_i = \sqrt{\sigma_{ii}} \).

**COVB**

creates the “Parameter Estimates Covariance Matrix” table. The covariance matrix is computed as the inverse of the negative of the matrix of second derivatives of the log-likelihood function with respect to the model parameters (the Hessian matrix).

**DATA=CAS-libref.data-table**

names the input data table for PROC LOGSELECT to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where
CAS-libref refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS-libref, see the section “Using CAS Sessions and CAS Engine Librefs” on page 459.

data-table specifies the name of the input data table.

ITHIST generates the “Iteration History” table.

LASSORHO=r specifies the base regularization parameter for the LASSO model selection method. The regularization parameter for step $i$ is $r^i$. By default, LASSORHO=0.8.

LASSOSTEPS=n specifies the maximum number of steps for LASSO model selection. By default, LASSOSTEPS=20.

LASSOTOL=r specifies the convergence tolerance for the optimization algorithm that solves for the LASSO parameter estimates at each step of LASSO model selection. By default, LASSOTOL=1E–6.

MAXOPTBATCH=number specifies the maximum number of observations to be included in a batch. The LOGSELECT procedure reads at most number observations from the data table into memory, performs the appropriate log-likelihood, gradient, and Hessian computations on that batch of observations, then discards those observations and reads in the next batch of data for processing. Generally, a smaller MAXOPTBATCH value decreases memory usage but might lead to longer computation times, whereas a larger MAXOPTBATCH value might lead to shorter computation times but increases memory usage. By default, MAXOPTBATCH=256.

NOCHECK disables the checking process that determines whether maximum likelihood estimates of the regression parameters exist. For more information, see the section “Existence of Maximum Likelihood Estimates” on page 488.

NOCLPRINT<=number> suppresses the display of the “Class Level Information” table if you do not specify number. If you specify number, the values of the classification variables are displayed for only those variables whose number of levels is less than number. Specifying number helps to reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

NOSTDERR suppresses computation of the covariance matrix and the standard errors of the regression coefficients. When the model contains many variables (thousands), the inversion of the Hessian matrix to derive the covariance matrix and the standard errors of the regression coefficients can be time-consuming. The CORRB, COVB, and TYPE3 options are not available when the NOSTDERR option is specified. This option also disables the quasi-complete separation check; for more information, see the section “Existence of Maximum Likelihood Estimates” on page 488.
PARTFIT displays fit statistics in the “Fit Statistics” table that are usually produced when your data are partitioned. This option is not required when you specify a PARTITION statement.

The additional statistics include the R-square, the adjusted R-square, McFadden’s R-square, the average square error (Brier score), the misclassification rate, the null-model log likelihood, and the difference in means.

STB displays the standardized estimates of the parameters in the “Parameter Estimates” table. The standardized estimate of \( \hat{\beta}_i \) is given by \( \frac{\hat{\beta}_i}{s/s_i} \), where \( s_i \) is the total sample standard deviation for the \( i \)th explanatory variable and

\[
s = \begin{cases} 
\pi/\sqrt{3} & \text{LOGIT and GLOGIT links} \\
1 & \text{PROBIT link} \\
\pi/\sqrt{6} & \text{CLOGLOG and LOGLOG links}
\end{cases}
\]

The sample standard deviations for parameters that are associated with CLASS variables are computed using their codings. The standardized estimates are not computed for the intercept parameters.

BY Statement

BY variables;

You can specify a BY statement in PROC LOGSELECT to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in SAS Language Reference: Concepts.

CLASS Statement

CLASS variable < (options)> ... < variable < (options)> > < / global-options >;

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required. Table 8.2 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>
CODE Statement

```
CODE <options> ;
```

The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a file, to a catalog entry, or to a CAS table. To score new data, you can then include the file or the catalog entry in a DATA step, or you can specify the CAS table in the runCodeTable action in the dataStep action set (for more information, see SAS Viya: System Programming Guide).

Table 8.3 summarizes the options available in the CODE statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZEx=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>IPROB</td>
<td>Computes individual predicted probabilities for ordinal response models</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
<tr>
<td>PCATALL</td>
<td>Generates probabilities for all levels of categorical response variables</td>
</tr>
</tbody>
</table>

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

DISPLAY Statement

```
DISPLAY <table-list> < / options> ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the table-list as a list of table names, paths, partial pathnames, and regular expressions.
The table names that you can specify are listed in the section “ODS Table Names” on page 500. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path Bygroup1.Summary:SelectionSummary. A partial pathname does not include all groups; for example, SelectionSummary and Summary:SelectionSummary are partial pathnames for Bygroup1.Summary:SelectionSummary.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both SelectionSummary and Summary:SelectionSummary select Bygroup1.Summary:SelectionSummary.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the Bygroup1.Summary:SelectionSummary table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the Bygroup1.Summary:SelectionSummary table is not selected.

You can specify the following options after a slash (/):

**CASESENSITIVE**
- performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

**EXCLUDE**
- displays all display tables except those that you specify in the `table-list`.

**EXCLUDEALL**
- suppresses display of all tables. This option takes precedence over the other options.

**TRACE**
- displays the display table names, labels, and paths.

---

**DISPLAYOUT Statement**

```plaintext
DISPLAYOUT table-spec-list < / options > ;
```

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.

- `key` specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):
INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

## EFFECT Statement

EFFECT name=effect-type (variables < / options>);  

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as constructed effects to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following effect-types:

- **COLLECTION** specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.
- **MULTIMEMBER | MM** specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.
- **POLYNOMIAL | POLY** specifies a multivariate polynomial effect in the specified numeric variables.
- **SPLINE** specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 8.4 summarizes the options available in the EFFECT statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
</tbody>
</table>
Table 8.4  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
</tbody>
</table>

**Polynomial Effects Options**

- **DEGREE=** Specifies the degree of the polynomial
- **DETAILS** Displays details of the specified polynomial
- **MDEGREE=** Specifies the maximum degree of any variable in a term of the polynomial
- **NOSEPARATE** Treats the polynomial as a single effect with multiple degrees of freedom
- **STANDARDIZE=** Specifies centering and scaling suboptions for the variables that define the polynomial

**Spline Effects Options**

- **BASIS=** Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect
- **DATABOUNDARY** Uses the extremes of the data as boundary knots for a B-spline basis
- **DEGREE=** Specifies the degree of the spline effect
- **DETAILS** Displays the knots and locations for each spline basis function
- **KNOTMAX=** Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value
- **KNOTMETHOD=** Specifies how to construct the knots for the spline effect
- **KNOTMIN=** Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value
- **NATURALCUBIC** Specifies a natural cubic spline basis for the spline effect
- **SEPARATE** Treats the spline basis for each variable as a separate effect when multiple variables are specified
- **SPLIT** Treats each design matrix column as a separate effect for selection methods

For more information about the syntax of these effect-types and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”

---

**FREQ Statement**

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC LOGSELECT treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.
The **MODEL Statement**

```
MODEL response < (response-options) > = < effects > < / model-options > ;

MODEL events / trials < (response-options) > = < effects > < / model-options > ;
```

The **MODEL** statement defines the statistical model in terms of a *response* variable (the target) or an *events/trials* specification, model *effects* that are constructed from variables in the input data table, and *model-options*. An intercept is included in the model by default. You can remove the intercept by specifying the **NOINT** option.

You can specify a single *response* variable that contains your response values. When you have binomial data, you can specify the *events/trials* form of the response, where one variable contains the number of positive responses (or events) and another variable contains the number of trials. Note that the values of both *events* and *(trials – events)* must be nonnegative and the value of *trials* must be positive.

For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

There are two sets of options in the **MODEL** statement. The *response-options* determine how the LOGSELECT procedure models probabilities for binary and multinomial data. The *model-options* control other aspects of model formation and inference. **Table 8.5** summarizes these options.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Response Variable Options</strong></td>
<td></td>
</tr>
<tr>
<td>DESCENDING</td>
<td>Reverses the response categories</td>
</tr>
<tr>
<td>EVENT=</td>
<td>Specifies the event category</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference category</td>
</tr>
<tr>
<td><strong>Model Options</strong></td>
<td></td>
</tr>
<tr>
<td>CLB</td>
<td>Requests confidence limits</td>
</tr>
<tr>
<td>INCLUDE=</td>
<td>Includes effects in all models for model selection</td>
</tr>
<tr>
<td>INFORMATIVE</td>
<td>Models missing values by using extra indicator variables</td>
</tr>
<tr>
<td>LINK=</td>
<td>Specifies the link function</td>
</tr>
<tr>
<td>NOINT</td>
<td>Suppresses the intercept</td>
</tr>
<tr>
<td>OFFSET=</td>
<td>Specifies the offset variable</td>
</tr>
<tr>
<td>START=</td>
<td>Includes effects in the initial model for model selection</td>
</tr>
<tr>
<td>TYPE3</td>
<td>Displays the Type 3 or joint tests of effects</td>
</tr>
</tbody>
</table>

**Response Variable Options**

Response variable options determine how the LOGSELECT procedure models probabilities for binary and multinomial response data. You can specify the following *response-options* by enclosing them in parentheses after the *response* or *trials* variable.
DESCENDING
DESC
reverses the order of the response categories. If you specify both the DESCENDING and ORDER= options, PROC LOGSELECT orders the response categories according to the ORDER= option and then reverses that order.

EVENT='category' | FIRST | LAST
specifies the event category for the binary response model. PROC LOGSELECT models the probability of the event category. The EVENT= option has no effect when there are more than two response categories.

You can specify one of the following:

'category'
    specifies the value (formatted, if a format is applied) of the event category in quotation marks.

FIRST
designates the first ordered category as the event.

LAST
designates the last ordered category as the event.

By default, EVENT=FIRST.

For example, the following statements specify that observations with the formatted value ‘1’ represent events in the data. The probability that the LOGSELECT procedure models is thus the probability that the variable def takes on the (formatted) value ‘1’.

        proc logselect data=mycas.MyData;
            class A B C;
            model def(event =’1’) = A B C x1 x2 x3;
        run;

ORDER=FORMATTED | FREQ | INTERNAL
specifies the sort order for the levels of the response variable. When ORDER=FORMATTED (the default) for numeric variables for which you have supplied no explicit format (that is, for which there is no corresponding FORMAT statement in the current PROC LOGSELECT run or in the DATA step that created the data table), the levels are ordered by their internal (numeric) value. The following table shows how the ORDER= option is interpreted:

<table>
<thead>
<tr>
<th>ORDER=</th>
<th>Levels Sorted By</th>
</tr>
</thead>
<tbody>
<tr>
<td>FORMATTED</td>
<td>External formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value; the sort order is machine-dependent.</td>
</tr>
<tr>
<td>FREQ</td>
<td>Descending frequency count (levels with the most observations come first in the order)</td>
</tr>
<tr>
<td>INTERNAL</td>
<td>Unformatted value; the sort order is machine-dependent.</td>
</tr>
</tbody>
</table>

By default, ORDER=FORMATTED.
For more information about sort order, see the chapter on the SORT procedure in the *SAS Visual Data Management and Utility Procedures Guide* and the discussion of BY-group processing in *SAS Language Reference: Concepts*.

REF='category' | FIRST | LAST
specifies the reference category for the generalized logit model and the binary response model. For the generalized logit model, each logit contrasts a nonreference category with the reference category. For the binary response model, specifying one response category as the reference is the same as specifying the other response category as the event. You can specify one of the following:

'category'
specifies the value (formatted, if a format is applied) of the reference category in quotation marks.

FIRST
designates the first ordered category as the reference.

LAST
designates the last ordered category as the reference.

By default, REF=LAST.

**Model Options**

CLB
constructs confidence limits for each of the parameter estimates. The confidence level is 0.95 by default; you can change it by specifying the ALPHA= option.

INCLUDE=n
INCLUDE=single-effect
INCLUDE=(effect-list)
forces effects to be included in all models. If you specify INCLUDE=n, then the first n effects that are listed in the MODEL statement are included in all models. If you specify INCLUDE=single-effect or if you specify INCLUDE=(effect-list), then the specified effects are forced into all models. The effects that you specify in this option must be explanatory effects that are specified in the MODEL statement before the slash (/).

INFORMATIVE
models missing values by using extra model effects. These effects consist of dummy variables that take the value 1 when the value of a continuous model variable involved in the effect is missing, and take the value 0 otherwise. The missing value in the original model effect is replaced by the average value of the effect for the nonmissing values. For continuous-by-class effects, such as A*x, where A is a classification variable and x is a continuous variable, informative missingness creates multiple dummy columns and substitutes the effect mean of x that corresponds to the respective level of A. Missing values for classification variables are treated as valid levels. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

LINK=keyword
specifies the link function for the model. The default link is the logit. The keywords and the associated link functions are shown in Table 8.6.
Table 8.6  Built-In Link Functions of the LOGSELECT Procedure

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Link Function</th>
<th>$g(\pi) = \eta =$</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLOGLOG</td>
<td>Complementary log-log</td>
<td>$\log(-\log(1 - \pi))$</td>
</tr>
<tr>
<td>GLOGIT</td>
<td>Generalized logit</td>
<td>$\log(\pi_j / \pi_{J-1})$</td>
</tr>
<tr>
<td>LOGIT</td>
<td>Logit</td>
<td>$\log(\pi/(1 - \pi))$</td>
</tr>
<tr>
<td>LOGLOG</td>
<td>Log-log</td>
<td>$- \log(-\log(\pi))$</td>
</tr>
<tr>
<td>PROBIT</td>
<td>Probit</td>
<td>$\Phi^{-1}(\pi)$</td>
</tr>
</tbody>
</table>

For the probit and cumulative probit links, $\Phi^{-1}(\cdot)$ denotes the quantile function of the standard normal distribution.

If the response variable has more than two categories, the LOGSELECT procedure fits a model that has a cumulative link function that is based on the specified link. However, if you specify LINK=GLOGIT, the procedure assumes a generalized logit model for nominal (unordered) data.

NOINT
requests that no intercept be included in the model. An intercept is included by default. The NOINT option is not available for multinomial models.

OFFSET=variable
specifies a variable to be used as an offset to the linear predictor. An offset plays the role of an effect whose coefficient is known to be 1. The offset variable cannot appear in the CLASS statement or elsewhere in the MODEL statement. Observations that have missing values for the offset variable are excluded from the analysis.

START=n
START=single-effect
START=effects
begins the selection process from the designated initial model for the forward and stepwise selection methods. If you specify START=n, then the starting model includes the first n effects that are listed in the MODEL statement. If you specify START=single-effect or if you specify START=(effects), then the starting model includes those specified effects. The effects that you specify in the START= option must be explanatory effects that are specified in the MODEL statement before the slash (/). This option is not available when you specify METHOD=BACKWARD in the SELECTION statement.

TYPE3
requests that Wald statistics for Type 3 contrasts be computed for each effect that is specified in the MODEL statement. For more information, see the section “Joint Tests and Type 3 Tests” on page 494.

**OUTPUT Statement**

```
OUTPUT OUT=CAS-libref.data-table
  < options >
  < keyword =name > . . . < keyword =name > ;
```
The OUTPUT statement creates a data table that contains observationwise statistics that PROC LOGSELECT computes after fitting the model. In order to avoid data duplication for large data tables, the variables in the input data table are not included in the output data table unless you specify them in the COPYVAR= option.

If the response variable has more than two categories, you can request the “Statistic Options” listed in Table 8.7; the other diagnostic statistics are not available. These statistics are computed for every response category, and the automatic variable _LEVEL_ identifies the response category on which the computed values are based. That is, every observation generates several rows in the output data set. If you also specify the OBSCAT option, then the observationwise statistics are computed only for the observed response category, which is indicated by the value of the _LEVEL_ variable. If you specify the PREDPROBS option, then only the PRED and IPRED variables are output to the data table, and a variable is created to contain the values that correspond to each response category. PROC LOGSELECT names these variables by concatenating the PRED= or IPRED= name with the response category.

The output statistics are computed based on the final parameter estimates. If the optimization does not converge, then the output data table is not created.

For observations in which only the response variable is missing, values of the linear predictor and the predicted probabilities are computed even though these observations do not affect the model fit. This enables, for example, predicted probabilities to be computed for new observations.

You must specify the following option:

```
OUT=CAS-libref.data-table
```

names the output data table for PROC LOGSELECT to use. You must specify this option before any other options. `CAS-libref.data-table` is a two-level name, where

- `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 459.

- `data-table` specifies the name of the output data table.

You can also specify the following options:

- **ALL**
- **ALLSTAT**
  adds all available statistics to the output data table.

- **ALPHA=number**
  specifies the significance level for the construction of confidence intervals in the output data table. The confidence level is $1 - \text{number}$. The value of `number` must be between 0 and 1. By default, `number` is equal to the value of the `ALPHA=` option in the PROC LOGSELECT statement, or 0.05 if that option is not specified.

- **COPYVAR=variable**
- **COPYVARS=(variables)**
  transfers one or more `variables` from the input data table to the output data table.
**FIXEDOFFSET=** number

specifies a value to use as an offset to the linear predictor instead of obtaining the value from the offset variable. This option is ignored unless you also specify the `OFFSET=` variable in the MODEL statement.

**OBSCAT**

requests (for multinomial models) that observationwise statistics be produced only for the observed response level. If you do not specify this option and the response variable has \( J \) levels, then the following outputs are created: for cumulative link models, \( J-1 \) records are output for every observation in the input data that corresponds to the \( J-1 \) lower-ordered response categories; for generalized logit models, \( J \) records are output that correspond to all \( J \) response categories.

**PREDPROBS**

creates variables (for multinomial models) for each response category that corresponds to the requested `IPRED` and `PREDICTED` keywords.

```
keyword <= name >
```

specifies a statistic to include in the output data table and optionally names the variable `name`. If you do not provide a `name`, the LOGSELECT procedure assigns a default name based on the type of statistic requested.

Table 8.7 summarizes the `keywords` that are available in the OUTPUT statement.

**Table 8.7 OUTPUT Statement Keywords**

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Default Names</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Statistic Options</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>INDIVIDUAL</td>
<td>Specifies the individual predicted probabilities</td>
<td><em>IPRED</em></td>
</tr>
<tr>
<td>LCL</td>
<td>Specifies the lower confidence limit for the linear predictor</td>
<td><em>LCL</em></td>
</tr>
<tr>
<td>LCLM</td>
<td>Specifies the lower confidence limit for the event probability</td>
<td><em>LCLM</em></td>
</tr>
<tr>
<td>PREDICTED</td>
<td>Specifies the predicted probabilities</td>
<td><em>PRED</em></td>
</tr>
<tr>
<td>RESRAW</td>
<td>Specifies the raw residual</td>
<td><em>RESRAW</em></td>
</tr>
<tr>
<td>STDXBETA</td>
<td>Specifies the standard error estimate of the linear predictor</td>
<td><em>STDXBETA</em></td>
</tr>
<tr>
<td>UCL</td>
<td>Specifies the upper confidence limit for the linear predictor</td>
<td><em>UCL</em></td>
</tr>
<tr>
<td>UCLM</td>
<td>Specifies the upper confidence limit for the event probability</td>
<td><em>UCLM</em></td>
</tr>
<tr>
<td>XBETA</td>
<td>Specifies the linear predictor</td>
<td><em>XBETA</em></td>
</tr>
<tr>
<td><strong>Diagnostic Options for Binary and Binomial Response Data</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CBAR</td>
<td>Specifies the confidence interval displacement</td>
<td><em>CBAR</em></td>
</tr>
<tr>
<td>DIFCHISQ</td>
<td>Specifies the deletion chi-square goodness-of-fit change</td>
<td><em>DIFCHISQUARE</em></td>
</tr>
<tr>
<td>DIFDEV</td>
<td>Specifies the deletion deviance change</td>
<td><em>DIFDEVIANCE</em></td>
</tr>
<tr>
<td>H</td>
<td>Specifies the leverage</td>
<td><em>HATDIAG</em></td>
</tr>
<tr>
<td>RESCHI</td>
<td>Specifies the Pearson chi-square residual</td>
<td><em>RESCHI</em></td>
</tr>
<tr>
<td>RESDEV</td>
<td>Specifies the deviance residual</td>
<td><em>RESDEV</em></td>
</tr>
<tr>
<td>RESLIK</td>
<td>Specifies the likelihood residual</td>
<td><em>RESLIK</em></td>
</tr>
<tr>
<td>RESWORK</td>
<td>Specifies the working residual</td>
<td><em>RESWORK</em></td>
</tr>
<tr>
<td>STDRESCHI</td>
<td>Specifies the standardized Pearson chi-square residual</td>
<td><em>STDRESCHI</em></td>
</tr>
<tr>
<td>STDRESDEV</td>
<td>Specifies the standardized deviance residual</td>
<td><em>STDRESDEV</em></td>
</tr>
</tbody>
</table>
The following list describes these *keywords*. For more information, see the section “Predicted Probabilities and Regression Diagnostics” on page 492.

**CBAR**
specifies the confidence interval displacement diagnostic that measures the overall change in the global regression estimates that results from deleting an individual observation. The default name is `_CBAR_`.

**DIFCHISQ**
specifies the change in the chi-square goodness-of-fit statistic that results from deleting the individual observation. The default name is `_DIFCHISQUARE_`.

**DIFDEV**
specifies the change in the deviance that results from deleting the individual observation. The default name is `_DIFDEVIANCE_`.

**H**
specifies the diagonal element of the hat matrix (leverage) for detecting extreme points in the design space. The default name is `_HATDIAG_`.

**INDIVIDUAL**

**IPRED**

**IPROB**

**IP**
specifies the individual predicted values for multinomial response variables. For a response variable $Y$ with three levels, 1, 2, and 3, the individual probabilities are $Pr(Y = 1)$, $Pr(Y = 2)$, and $Pr(Y = 3)$. The default name is `_IPRED_`.

**INTO< (cutpoint) >**

names the variable that contains the level of the response into which an observation is classified. The default name is `_INTO_`. Multinomial models classify observations into the level that has the largest model-predicted probability. For binary or binomial response variables, if the predicted probability of an observation equals or exceeds the cutpoint, the observation is classified as an event; otherwise it is classified as a nonevent. You can specify the *cutpoint* value as a number between 0 and 1. The default value is 0.5.

**LCL**

**LOWERXBETA**

names the variable that contains the lower confidence limits for the linear predictor. You can set the confidence level by specifying the **ALPHA=** option. The default name is `_LCL_`.
LCLM
LOWERMEAN
LOWER
specifies the lower confidence limits for the probability of the event. You can set the confidence
level by specifying the ALPHA= option. The default name is _LCLM_.

LEVEL
names the variable that contains the level of the response for a given row of the output. The
default name is _LEVEL_.

PREDICTED
PRED
PROB
P
specifies the predicted values (predicted probabilities of events) for binary and nominal response
variables and the cumulative predicted probabilities for ordinal response variables. For a response
variable Y with three levels, 1, 2, and 3, the cumulative probabilities are \( P_r(Y \leq 1) \) and \( P_r(Y \leq 2) \),
but by default the last level, \( P_r(Y \leq 3) = 1 \), is not output. The default name is _PRED_.

RESCHI
PEARSON
specifies the Pearson residual for identifying poorly fitted observations. The default name is
_RESCHI_.

RESDEV
specifies the deviance residual for identifying poorly fitted observations. The default name is
_RESDEV_.

RESLIK
specifies the likelihood residual for identifying poorly fitted observations. The default name is
_RESLIK_.

RESRAW
RESIDUAL
R
specifies the raw residual for identifying poorly fitted observations. The default name is
_RESRAW_.

RESWORK
specifies the working residual for identifying poorly fitted observations. The default name is
_RESWORK_.

ROLE
specifies the numeric variable that indicates the role played by each observation in fitting the
model. The default name is _ROLE_. Table 8.8 shows how this variable is interpreted for each
observation.
Table 8.8  Role Interpretation

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by specifying a PARTITION statement, then the role variable value is 1 for observations that are used in fitting the model and 0 for observations that have at least one missing or invalid value for the response, regressor, frequency, or weight variables.

**STDRESCHI**

specifies the standardized Pearson (chi-square) residual for identifying observations that are poorly accounted for by the model. The default name is _STDRESCHI_.

**STDRESDEV**

specifies the standardized deviance residual for identifying poorly fitted observations. The default name is _STDRESDEV_.

**STDXBETA**

specifies the standard error estimates of XBETA. The default name is _STDXBETA_.

**UCL**

**UPPERXBETA**

specifies the variable that contains the upper confidence limits for the linear predictor. The default name is _UCL_. You can set the confidence level by specifying the ALPHA= option.

**UCLM**

**UPPERMEAN**

**UPPER**

specifies the variable that contains the upper confidence limits for the probability of the event response. The default name is _UCLM_. You can set the confidence level by specifying the ALPHA= option.

**XBETA**

**LINP**

specifies the linear predictor. The default name is _XBETA_.

---

**PARTITION Statement**

```
PARTITION partition-option;
```

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in
the input data table and a set of formatted values of that variable to determine the role of each observation, or
you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:

**FRACTION(< TEST=fraction> < VALIDATE=fraction> < SEED=number>)**
randomly assigns specified proportions of the observations in the input data table to the roles. You
specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions
must be less than 1 and the remaining fraction of the observations are assigned to the training role. The
SEED= option specifies an integer that is used to start the pseudorandom number generator for random
partitioning of data for training, testing, and validation. If you do not specify SEED=number or if
number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s
clock.

**ROLE=variable (< TEST=value > < TRAIN=value > < VALIDATE=value >)**
**ROLEVAR=variable (< TEST=value > < TRAIN=value > < VALIDATE=value >)**

names the variable in the input data table whose values are used to assign roles to each observation.
This variable cannot also appear as an analysis variable in other statements or options. The TEST=,
TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to
assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose
role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

For more information, see the section “Partition Fit Statistics” on page 490. For an illustration, see Example 8.3.

## SELECTION Statement

**SELECTION < METHOD=method< (method-options) >>< options> ;**

The SELECTION statement performs model selection by examining whether effects should be added to or
removed from the model according to rules that are defined by model selection methods. The statement is
fully documented in the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

The LOGSELECT procedure supports the following effect-selection methods in the SELECTION statement:

**BACKWARD**
performs backward elimination. This method starts with all effects in the model and deletes effects.

**BACKWARD(FAST)**
performs fast backward elimination. This method starts with all effects in the model and deletes effects without refitting the model.

**FORWARD**
performs forward selection. This method starts with no effects in the model and adds effects.

**LASSO**
performs model selection by the group LASSO method. This method adds and removes effects by using a sequence of LASSO steps. For more information, see the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.”

**NONE**
results in no model selection. This method fits the full model.
**STEPWISE** performs stepwise selection. This method is similar to the FORWARD method except that effects already in the model do not necessarily stay there.

By default, METHOD=STEPWISE.

The SELECT=, CHOOSE=, and STOP= *method-options* default to SBC. These defaults differ from their corresponding defaults in the HPROCLOGISTIC procedure in SAS/STAT software.

You can specify the following criteria in the SELECT=, CHOOSE=, and STOP= *method-options*:

- **AIC** uses Akaike’s information criterion (Akaike 1974) computed on the *training data*.
- **AICC** uses a small-sample bias-corrected version of Akaike’s information criterion, as promoted in Hurvich and Tsai (1989) and Burnham and Anderson (1998), computed on the *training data*.
- **SBC** uses the Schwarz Bayesian criterion (Schwarz 1978) computed on the *training data*.
- **SL** uses the significance level of the score test computed on the *training data* as the criterion (not available for the CHOOSE= option).
- **VALIDATE** uses the average square error (ASE) computed on the *validation data* as the criterion (not available for the SELECT= option).

For more information, see the section “Information Criteria” on page 490.

If you specify METHOD=LASSO and you do not specify either the CHOOSE= or STOP= option, then the model in the last LASSO step is chosen as the selected model.

**NOTE:** If you use the fast backward elimination method, then the $-2$ log likelihood, AIC, AICC, and SBC statistics are approximated at each step where the model is not refit, and hence they do not match the values that are computed when that model is fit outside the selection routine. Similarly, if you specify SELECT=AIC, AICC, or SBC, the selection criteria are estimated (Lawless and Singhal 1978), and hence they do not match the values that are computed when that model is fit outside the selection routine.

**NOTE:** The default model hierarchy method is HIERARCHY=NONE for the stepwise, forward, and fast backward selection methods. The backward elimination method always uses the HIERARCHY=SINGLE *method-option*.

The LASSO method produces a summary table that displays the effects that are added or removed at each step; the LASSO regularization parameter; and the AIC, AICC, and SBC fit statistics. For the other methods, you can specify the following values for the DETAILS= option:

- **SUMMARY** produces a summary table that shows the effect that is added or removed at each step along with the SELECT=, CHOOSE=, and STOP= criteria. The summary table is produced by default if the DETAILS= option is not specified.
- **STEPS** produces the preceding summary table and displays the results from fitting each model at each step.
- **ALL** produces the preceding tables and a detailed listing of all candidates at each step along with their ranking in terms of the selection criterion for addition to or removal from the model.

If you specify the PLOTS=CRITERIA or PLOTS=ALL option, then a plot of the fit criterion by the selection step is created for the AIC, AICC, and SBC statistics. If you also specify a PARTITION statement or the
PARTFIT option, then the same type of plot is created for the ASE (for each role), max-rescaled R-square, McFadden’s R-square, misclassification rate, and difference of means statistics.

If you specify the PLOTS=FITBYROLE or PLOTS=ALL option and a PARTITION statement, then a plot of the ASE by the selection step for each role is created.

The PLOTS= option is not available for the LASSO method.

---

**WEIGHT Statement**

```plaintext
WEIGHT variable;
```

The `variable` in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

---

**Details: LOGSELECT Procedure**

**Missing Values**

Any observation that has missing values for the response, frequency, weight, offset, or explanatory variables is excluded from the analysis; however, missing values are valid for response and explanatory variables that are specified along with the MISSING option in the CLASS statement. Observations that have a nonpositive weight or a frequency less than 1 are also excluded.

The estimated linear predictor and the fitted probabilities are not computed for any observation that has missing offset or explanatory variable values. However, if only the response value is missing, the linear predictor and the fitted probabilities can be computed and output to a data table by using the OUTPUT statement.

You can also model the missing values by specifying the INFORMATIVE option in the MODEL statement. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

**Response Distributions**

The response distribution is the probability distribution of the response (target) variable. The LOGSELECT procedure can fit data for the following distributions:

- binary distribution
- binomial distribution
- multinomial distribution

The expressions for the log-likelihood functions of these distributions are given in the next section.
The binary (or Bernoulli) distribution is the elementary distribution of a discrete random variable that can take two values, which have the probabilities \( p \) and \( 1 - p \). Suppose the random variable is denoted as \( Y \) and

\[
\begin{align*}
\Pr(Y = 0) &= p \\
\Pr(Y = 1) &= 1 - p
\end{align*}
\]

The value that is associated with probability \( p \) is often called the *event* or “success”; the complementary event is called the *nonevent* or “failure.” A Bernoulli experiment is a random draw from a binary distribution and generates events with probability \( p \).

If \( Y_1, \ldots, Y_n \) are \( n \) independent Bernoulli random variables, then their sum follows a binomial distribution. In other words, if \( Y_i = 1 \) denotes an event (success) in the \( i \)th Bernoulli trial, a binomial random variable is the number of events (successes) in \( n \) independent Bernoulli trials. If you use the events/trials syntax in the `MODEL` statement, the LOGSELECT procedure fits the model as if the data had arisen from a binomial distribution. For example, the following statements fit a binomial regression model with regressors \( x_1 \) and \( x_2 \).

```plaintext
proc logselect;
   model e/t = x1 x2;
run;
```

If the events/trials syntax is used, then both variables must be numeric and the value of the events variable cannot be less than 0 or exceed the value of the trials variable.

The multinomial distribution is a generalization of the binary distribution and allows for more than two outcome categories. Because there are more than two possible outcomes for the multinomial distribution, the terminology of “successes,” “failures,” “events,” and “nonevents” no longer applies. With multinomial data, these outcomes are generically referred to as “categories” or levels.

Whenever the LOGSELECT procedure determines that the response variable has more than two levels (unless the events/trials syntax is used), it fits the model as if the data had arisen from a multinomial distribution. By default, the procedure then assumes that the response categories are ordered, and it fits a cumulative link model by applying the default or specified link function. If the response categories are unordered, then you should fit a generalized logit model by specifying `LINK=GLOGIT` in the `MODEL` statement.

---

**Log-Likelihood Functions**

The LOGSELECT procedure forms the log-likelihood functions of the various models as

\[
L(\mu; y) = \sum_{i=1}^{n} f_i l(\mu_i; y_i, w_i)
\]

where \( \mu_i \) is the probability that the \( i \)th observation is an event, \( l(\mu_i; y_i, w_i) \) is the log-likelihood contribution of the \( i \)th observation, \( w_i \) is the weight, and \( f_i \) is its frequency. For the determination of \( w_i \) and \( f_i \), see the `WEIGHT` and `FREQ` statements. The individual log-likelihood contributions for the various distributions are described in the following sections.
Binary Distribution

The LOGSELECT procedure computes the log-likelihood function \( l(\mu_i(\beta); y_i) \) for the \( i \)th binary observation as

\[
\eta_i = x_i'\beta \\
\mu_i(\beta) = g^{-1}(\eta_i) \\
l(\mu_i(\beta); y_i) = y_i \log\{\mu_i\} + (1 - y_i) \log\{1 - \mu_i\}
\]

where the variable \( y_i \) takes the value 1 for an event and 0 for a nonevent. The inverse link function \( g^{-1}() \) maps from the scale of the linear predictor \( \eta_i \) to the scale of the mean. For example, for the logit link (the default),

\[
\mu_i(\beta) = \frac{\exp\{\eta_i\}}{1 + \exp\{\eta_i\}}
\]

You can control which binary outcome in your data is modeled as the event by using the response-options in the MODEL statement, and you can choose the link function by using the LINK= option in the MODEL statement.

If a WEIGHT statement is specified and \( w_i \) denotes the weight for the current observation, the log-likelihood function is computed as

\[
l(\mu_i(\beta); y_i, w_i) = w_i l(\mu_i(\beta); y_i)
\]

Binomial Distribution

The LOGSELECT procedure computes the log-likelihood function \( l(\mu_i(\beta); y_i) \) for the \( i \)th binomial observation as

\[
\eta_i = x_i'\beta \\
\mu_i(\beta) = g^{-1}(\eta_i) \\
l(\mu_i(\beta); y_i, w_i) = w_i \left( y_i \log\{\mu_i\} + (n_i - y_i) \log\{1 - \mu_i\} \right)
\]

where \( y_i \) and \( n_i \) are the values of the events and trials of the \( i \)th observation, respectively. The value \( \mu_i \) measures the probability of events (successes) in the underlying Bernoulli distribution whose aggregate follows the binomial distribution.

Multinomial Distribution

The multinomial distribution that the LOGSELECT procedure models is a generalization of the binary distribution; it is the distribution of a single draw from a discrete distribution that has \( J \) possible values. Thus, the log-likelihood function for the \( i \)th observation is

\[
l(\mu; y_i, w_i) = w_i \sum_{j=1}^{J} y_{ij} \log\{\mu_{ij}\}
\]
In this expression, \( J \) denotes the number of response categories (the number of possible outcomes) and \( \mu_{ij} \) is the probability that the \( i \)th observation takes on the response value associated with category \( j \). The category probabilities must satisfy
\[
\sum_{j=1}^{J} \mu_{ij} = 1
\]
and the constraint is satisfied by modeling \( J - 1 \) categories. In models that have ordered response categories, the probabilities are expressed in cumulative form, so the last category is redundant. In generalized logit models (multinomial models that have unordered categories), one category is chosen as the reference category, and the linear predictor in the reference category is set to 0. For more information, see the \texttt{REF= response-option} in the MODEL statement.

**Existence of Maximum Likelihood Estimates**

The likelihood equation for a logistic regression model does not always have a finite solution. Sometimes there is a nonunique maximum on the boundary of the parameter space, at infinity. The existence, finiteness, and uniqueness of maximum likelihood estimates for the logistic regression model depend on the patterns of data points in the observation space (Albert and Anderson 1984; Santner and Duffy 1986).

Consider a binary response model. Let \( Y_j \) be the response of the \( j \)th subject, and let \( x_j \) be the vector of explanatory variables (including the constant 1 that is associated with the intercept). There are three mutually exclusive and exhaustive types of data configurations:

- **Complete separation** There is a complete separation of data points if there exists a vector \( b \) that correctly allocates all observations to their response groups; that is,
  \[
  \begin{cases}
  b'x_j > 0 & Y_j = 0 \\
  b'x_j < 0 & Y_j = 1 
  \end{cases}
  \]
  This configuration produces nonunique infinite estimates. If the iterative process of maximizing the likelihood function is allowed to continue, then the log likelihood diminishes to 0 and the dispersion matrix becomes unbounded.

- **Quasi-complete separation** The data are not completely separable, but there is a vector \( b \) such that
  \[
  \begin{cases}
  b'x_j \geq 0 & Y_j = 0 \\
  b'x_j \leq 0 & Y_j = 1 
  \end{cases}
  \]
  and equality holds for at least one subject in each response group. This configuration also yields nonunique infinite estimates. If the iterative process of maximizing the likelihood function is allowed to continue, then the dispersion matrix becomes unbounded and the log likelihood diminishes to a nonzero constant.

- **Overlap** If neither complete nor quasi-complete separation exists in the sample points, there is an overlap of sample points. In this configuration, the maximum likelihood estimates exist and are unique.

The LOGSELECT procedure uses a simple empirical approach to recognize the data configurations that lead to infinite parameter estimates. The basis of this approach is that any convergence method of maximizing the log likelihood must yield a solution that indicates complete separation, if such a solution exists. Upon
convergence, if the predicted response equals the observed response for every observation, there is a complete separation of data points.

If the data are not completely separated, if an observation is identified to have an extremely large probability ($\geq 0.95$) of predicting the observed response, and if there have been at least eight iterations, then there are two possible situations. First, there is overlap in the data set, the observation is an atypical observation of its own group, and the iterative process stopped when a maximum was reached. Second, there is quasi-complete separation in the data set, and the asymptotic dispersion matrix is unbounded. If any of the diagonal elements of the dispersion matrix for the standardized observation vector (all explanatory variables standardized to zero mean and unit variance) exceeds 5,000, then PROC LOGSELECT declares quasi-complete separation; if any of the diagonal elements exceeds 1,000, then the procedure displays a message indicating that quasi-complete separation might be detectable by increasing the number of iterations. If either complete separation or quasi-complete separation is detected, a note is displayed in the procedure output.

Checking for quasi-complete separation is less foolproof than checking for complete separation. If neither type of separation is discovered and your parameter estimates have large standard errors, then your data might be separable. The NOCHECK option in the MODEL statement turns off the process of checking for infinite parameter estimates; the MINITER= option in the PROC LOGSELECT statement increases the number of iterations.

The LASSO Method of Model Selection

LASSO Selection

The LOGSELECT procedure implements the group LASSO method, which is described in the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.” The current section provides some background about the LASSO method that you need in order to understand the group LASSO method.

LASSO (least absolute shrinkage and selection operator) selection arises from a constrained form of ordinary least squares regression in which the sum of the absolute values of the regression coefficients is constrained to be smaller than a specified parameter. More precisely, let $X = (x_1, x_2, \ldots, x_m)$ denote the matrix of covariates, and let $y$ denote the response. Then for a given parameter $t$, the LASSO regression coefficients $\beta = (\beta_1, \beta_2, \ldots, \beta_m)$ are the solution to the following constrained least squares problem:

$$\min \|y - X\beta\|^2 \quad \text{subject to } \sum_{j=1}^{m} |\beta_j| \leq t$$

For generalized linear models, the LASSO regression coefficients $\beta = (\beta_1, \beta_2, \ldots, \beta_m)$ are the solution to the following constrained optimization problem,

$$\min \{-L(\mu; y)\} \quad \text{subject to } \sum_{j=1}^{m} |\beta_j| \leq t$$

where $L$ is the log-likelihood function defined in the section “Log-Likelihood Functions” on page 486.

Provided that the LASSO parameter $t$ is small enough, some of the regression coefficients will be exactly zero. Hence, you can think of the LASSO method as selecting a subset of the regression coefficients for each LASSO parameter. By increasing the LASSO parameter in discrete steps, you obtain a sequence of regression coefficients for which the nonzero coefficients at each step correspond to selected parameters. For more information about the LASSO method, see, for example, Hastie, Tibshirani, and Friedman (2009).
Partition Fit Statistics

Specifying a PARTITION statement modifies the display of many tables by adding separate rows or columns for the training, validation, and test data tables, and adds statistics to the “Fit Statistics” table. These additional statistics are useful for assessing the model and should be very similar for the different roles when the training data are representative of the other data partitions: average square error, misclassification rate, and the difference of means. The $R^2$, maximum-rescaled $R^2$, and McFadden’s $R^2$ are also computed. For more information, see the section “Model Fit and Assessment Statistics” on page 490.

Model Fit and Assessment Statistics

The statistics that are defined in this section are useful for assessing the fit of the model to your data; they are displayed in the “Fit Statistics” table. The statistics are computed for each data role when you specify a PARTITION statement.

Information Criteria

The calculation of the information criteria uses the following formulas, where $p$ denotes the number of effective parameters in the candidate model, $F$ denotes the sum of frequencies used, and $I$ is the log likelihood evaluated at the converged estimates:

- AIC = $-2I + 2p$
- AICC = \begin{cases} -2I + 2pF/(F - p - 1) & \text{when } F > p + 2 \\ -2I + 2p(p + 2) & \text{otherwise} \end{cases}$
- SBC = $-2I + p \log(F)$

If you do not specify a FREQ statement, $F$ equals $n$, the number of observations used.

Generalized Coefficient of Determination

The goal of a coefficient of determination, also known as an R-square measure, is to express the agreement between a stipulated model and the data in terms of variation in the data that is explained by the model. In linear models, the R-square measure is based on residual sums of squares; because these are additive, a measure bounded between 0 and 1 is easily derived.

In more general models where parameters are estimated by the maximum likelihood principle, Cox and Snell (1989, pp. 208–209) and Magee (1990) proposed the following generalization of the coefficient of determination:

$$R^2 = 1 - \left( \frac{L(\mathbf{0})}{L(\hat{\mathbf{\theta}})} \right)^{\frac{2}{n}}$$

Here, $L(\mathbf{0})$ is the likelihood of the intercept-only model, $L(\hat{\mathbf{\theta}})$ is the likelihood of the specified model, and $n$ denotes the number of observations used in the analysis. This number is adjusted for frequencies if a FREQ statement is present, and it is based on the trials variable for binomial models.
As discussed in Nagelkerke (1991), this generalized R-square measure has properties similar to those of the coefficient of determination in linear models. If the model effects do not contribute to the analysis, \( L(\hat{\beta}) \) approaches \( L(0) \) and \( R^2 \) approaches zero.

However, \( R^2 \) does not have an upper limit of 1. Nagelkerke suggested a rescaled generalized coefficient of determination, \( R^2_N \), which achieves an upper limit of 1 by dividing \( R^2 \) by its maximum value:

\[
R^2_{\text{max}} = 1 - \{L(0)\}^{-\frac{1}{2}}
\]

\[
R^2_N = \frac{R^2}{R^2_{\text{max}}}
\]

Another measure, from McFadden (1974), is also bounded by 0 and 1:

\[
R^2_M = 1 - \left( \frac{\log L(\hat{\beta})}{\log L(0)} \right)
\]

These measures are most useful for comparing competing models that are not necessarily nested—that is, models that cannot be reduced to one another by simple constraints on the parameter space. Larger values of the measures indicate better models.

**Average Square Error**

The average square error (ASE) is the average of the squared differences between the responses and the predictions. When you have a discrete number of response levels, the ASE is modified as shown in Table 8.9 (Brier 1950; Murphy 1973); it is also called the Brier score or Brier reliability.

**Table 8.9 Average Square Error Computations**

<table>
<thead>
<tr>
<th>Response Type</th>
<th>ASE (Brier Score)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Binary</td>
<td>( \frac{1}{F} \sum_i f_i {y_i (1 - \hat{\pi}_i)^2 + (1 - y_i)\hat{\pi}_i^2} )</td>
</tr>
<tr>
<td>Binomial</td>
<td>( \frac{1}{F} \sum_i f_i {r_i / t_i - \hat{\pi}_i}^2 )</td>
</tr>
<tr>
<td>Multinomial</td>
<td>( \frac{1}{F} \sum_i f_i \sum_j (y_{ij} - \hat{\pi}_{ij})^2 )</td>
</tr>
</tbody>
</table>

In Table 8.9, \( F = \sum_i f_i \), \( r_i \) is the number of events, \( t_i \) is the number of trials in binomial response models, \( y_i = 1 \) for events and 0 for nonevents in binary response models, and \( \hat{\pi}_i \) is the predicted probability of an event. For polytomous response models, \( y_{ij} = 1 \) if the \( i \)th observation has response level \( j \), and \( \pi_{ij} \) is the model-predicted probability of response level \( j \) for observation \( i \).

**Difference of Means**

For a binary response model, write the mean of the model-predicted probabilities of event \((Y=0)\) observations as \( \overline{X}_1 = \frac{\sum_{i=1}^{n} (\hat{\pi}_i | y_i = 0)}{n_0} \) and of nonevent \((Y=1)\) observations as \( \overline{X}_2 = \frac{\sum_{i=1}^{n} (\hat{\pi}_i | y_i = 1)}{n_0} \), where \( \hat{\pi}_i \) is the predicted probability of an event. The difference of means is \( \overline{X}_1 - \overline{X}_2 \), which Tjur (2009) relates to other R-square measures and calls the coefficient of discrimination, because it is a measure of the model’s ability to distinguish between the event and nonevent distributions. The difference of means is also the \( d' \) or \( \Delta m \) statistic (with unit standard error) that is discussed in the signal detection literature (McNicol 2005).
Predicted Probabilities and Regression Diagnostics

For binary response data, you can produce observationwise predicted probabilities, confidence limits, and regression diagnostics developed by Pregibon (1981) by specifying the OUTPUT statement. For multinomial response data, you can likewise produce observationwise predicted probabilities, confidence limits, and raw residuals.

For a binary response model, given a vector of covariates \( x_i \) for the \( i \)th observation in your data table and the model-predicted parameter estimates \( \hat{\beta} \), you can write the linear predictor \( \hat{\eta}_i = x_i' \hat{\beta} \). The mean of the \( i \)th observation \( \mu_i(\hat{\beta}) \), or the model-predicted event probability \( \hat{\pi}_i \), is \( \mu_i(\hat{\beta}) = \hat{\pi}_i = g^{-1}(\eta_i) \), where the link function \( g \) is chosen by specifying the LINK= option. The variance of the binary distribution is \( V(\mu) = \mu(1-\mu) = \hat{\pi}_i(1-\hat{\pi}_i) = V(\pi) \), and \( \Sigma \) is the estimated covariance of \( \hat{\beta} \). Denote the frequency of the \( i \)th observation as \( f_i \) and the weight as \( w_i \).

For ordinal response models, the predicted cumulative probabilities are computed in the same fashion by using the appropriate model-predicted intercept parameters \( \hat{\alpha}_j \) and letting \( \beta \) consist of the slope parameters: \( \hat{\eta}_{ij} = g(Pr(Y \leq j | x_i)) = \hat{\alpha}_j + x_i' \hat{\beta}_j \) and \( \hat{\pi}_{ij} = Pr(Y \leq j | x_i) = g^{-1}(\eta_{ij}) \) for \( 1 \leq j < J \).

For nominal response models, the predicted probabilities are computed by using the appropriate model-predicted intercept parameters \( \hat{\alpha}_j \) and letting \( \beta_j \) consist of the slope parameters: \( \hat{\eta}_{ij} = g(Pr(Y = j | x_i)) = \hat{\alpha}_j + x_i' \hat{\beta}_j \) and \( \hat{\pi}_{ij} = Pr(Y = j | x_i) = g^{-1}(\eta_{ij}) \) for \( 1 \leq j < J \).

Confidence Intervals

Approximate confidence intervals for predicted probabilities can be computed as follows. The variance of the linear predictor is estimated by

\[
\hat{\sigma}^2(\eta_i) = x_i'\Sigma x_i
\]

For multinomial models, the variance also depends on the response function. Let \( \delta_j \) be a \((J-1)\) column vector whose \( j \)th entry is equal to 1 and all other entries are equal to 0. Redefine \( x_i = (\delta'_j, x_i')' \), \( \eta_i = \eta_{ij} \), and \( \pi_i = \pi_{ij} \). Then

\[
\hat{\sigma}^2(\eta_i) = x_i'\Sigma x_i
\]

The asymptotic 100(1 - \( \alpha \))% confidence interval for \( \eta_i \) is

\[
\hat{\eta}_i \pm z_{\alpha/2} \hat{\sigma}(\eta_i)
\]

where \( z_{\alpha/2} \) is the 100(1 - \( \alpha/2 \))th percentile point of a standard normal distribution.

The predicted probability and the 100(1 - \( \alpha \))% confidence limits for \( \pi_i \) are obtained by back-transforming the corresponding measures for the linear predictor. So the confidence limits are

\[
g^{-1}\left[ \hat{\eta}_i \pm z_{\alpha/2} \hat{\sigma}(\eta_i) \right]
\]
Hat-Matrix Diagonals

The diagonal elements of the hat matrix are useful in detecting extreme points in the design space, where they tend to have larger values. For the generalized linear model, the variance of the $i$th individual observation is

$$v_i = \frac{V(\pi_i)}{f_i w_i}$$

For the $i$th observation, let

$$w_{ei} = v_i^{-1}(g'(\pi_i))^{-2}$$

where $g'(\pi_i)$ is the derivative of the link function evaluated at $\pi_i$. The weight matrix $W_e$ is a diagonal matrix, with $w_{ei}$ denoting the $i$th diagonal element, which is used in computing the expected information matrix. Define the leverage, or hat-matrix diagonal, $h_i$, as the $i$th diagonal element of the matrix

$$W_e^{1/2}X(X'W_eX)^{-1}X'W_e^{1/2}$$

If the estimated probability is extreme (less than 0.1 and greater than 0.9, approximately), then the hat-matrix diagonal might be greatly reduced in value. Consequently, when an observation has a very large or very small estimated probability, its leverage is not a good indicator of the observation’s distance from the design space (Hosmer and Lemeshow 2000, p. 171).

Residuals

Residuals are useful in identifying observations that are not explained well by the model. For binary and binomial response data, the raw residual is

$$r_i = y_i/t_i - \hat{\pi}_i$$

where $y_i$ is the number of event responses out of $t_i$ trials for the $i$th observation. For single-trial syntax, $t_i = 1$ and $y_i = 1$ if the ordered response is 1 and $y_i = 0$ otherwise. For multinomial response data, the raw residual is

$$y_{ij} - \hat{\pi}_{ij}$$

where $y_{ij} = 1$ if the $i$th observation has response level $j$ and $y_{ij} = 0$ otherwise, and $\hat{\pi}_{ij}$ are the model-predicted probabilities of response level $j$ for observation $i$.

The Pearson residual is the square root of the $i$th observation’s contribution to Pearson’s chi-square:

$$r_{pi} = r_i \sqrt{\frac{f_i w_i}{V(\pi_i)}}$$

The deviance residual is the square root of the contribution of the $i$th observation to the deviance, with the sign of the raw residual,

$$r_{Di} = (\text{sign}(r_i)) \sqrt{d_i}$$

where

$$d_i = 2f_i w_i t_i \left[ \frac{y_i}{t_i} \log \left( \frac{y_i}{t_i} \pi_i \right) + \left( 1 - \frac{y_i}{t_i} \right) \log \left( \frac{1 - y_i/t_i}{1 - \pi_i} \right) \right] \left( \frac{1}{\pi_i} - \frac{1}{t_i} \right)$$
The working residual is

\[ r_{W_i} = r_i \left( \frac{\partial \pi_i}{\partial \eta_i} \right)^{-1} \]

The Pearson residuals, standardized to have unit asymptotic variance, are

\[ r_{SP_i} = \frac{r_{P_i}}{\sqrt{1 - h_i}} \]

The deviance residuals, standardized to have unit asymptotic variance, are

\[ r_{SD_i} = \frac{r_{D_i}}{\sqrt{1 - h_i}} \]

The likelihood residuals, which estimate components of a likelihood ratio test of deleting an individual observation, are a weighted combination of the standardized Pearson and deviance residuals:

\[ r_{Li} = \text{sign}(r_i) \sqrt{h_i r_{SP_i}^2 + (1 - h_i) r_{SD_i}^2} \]

Other Regression Diagnostics

The CBAR statistic is a confidence interval displacement diagnostic that provides a scalar measure of the influence of an individual observation on \( \hat{\beta} \). This diagnostic is based on the same idea as the Cook distance in linear regression theory (Cook and Weisberg 1982), but it uses the one-step estimate:

\[ \overline{C}_i = r_{P_i}^2 h_i / (1 - h_i) \]

The DIFDEV and DIFCHISQ statistics are diagnostics for detecting ill-fitted observations—observations that contribute heavily to the disagreement between the data and the predicted values of the fitted model. DIFDEV is the change in the deviance that results from deleting an individual observation, and DIFCHISQ is the change in the Pearson chi-square statistic that results from the same deletion. By using the one-step estimate, DIFDEV and DIFCHISQ for the \( i \)th observation are computed as follows:

\[
\begin{align*}
\text{DIFDEV}_i &= r_{D_i}^2 + \overline{C}_i \\
\text{DIFCHISQ}_i &= \overline{C}_i / h_i
\end{align*}
\]

Joint Tests and Type 3 Tests

Linear hypotheses for \( \beta \) are expressed in matrix form as

\[ H_0: L\beta = e \]

where \( L \) is a matrix of coefficients for the linear hypotheses and \( e \) is a vector of constants. The vector of regression coefficients \( \beta \) includes slope parameters and intercept parameters. The Wald chi-square statistic for testing \( H_0 \) is computed as

\[ \chi^2_W = (L\hat{\beta} - e)'[L\hat{V}(\hat{\beta})L']^{-1}(L\hat{\beta} - e) \]
where \( \hat{V}(\hat{\beta}) \) is the estimated covariance matrix. Under \( H_0, \chi^2_w \) has an asymptotic chi-square distribution with \( r \) degrees of freedom, where \( r \) is the rank of \( \mathbf{L} \).

For models that use less-than-full-rank parameterization (as specified by the PARAM=GLM option in the CLASS statement), a Type 3 test of an effect of interest (main effect or interaction) is a test of the Type III estimable functions that are defined for that effect. When the model contains no missing cells, the Type 3 test of a main effect is equivalent to testing the hypothesis of equal marginal means. For more information about Type III estimable functions, see the chapter “The GLM Procedure” and the section “The Four Types of Estimable Functions” in *SAS/STAT User’s Guide*. Also see Littell, Freund, and Spector (1991).

For models that use full-rank parameterization, all parameters are estimable when there are no missing cells, so it is unnecessary to define estimable functions. The standard test of an effect of interest in this case is the joint test that the values of the parameters associated with that effect are 0. For a model that uses effects parameterization (as specified by the PARAM=EFFECT option in the CLASS statement), the joint test for a main effect is equivalent to testing the equality of marginal means. For a model that uses reference parameterization (as specified by the PARAM=REF option in the CLASS statement), the joint test is equivalent to testing the equality of cell means at the reference level of the other model effects. For more information about the coding scheme and the associated interpretation of results, see Muller and Fetterman (2002, Chapter 14).

If there is no interaction term, the Type 3 test of an effect for a model that uses GLM parameterization is the same as the joint test of the effect for the model that uses full-rank parameterization. In this situation, the joint test is also called the Type 3 test. For a model that contains an interaction term and no missing cells, the Type 3 test of a component main effect under GLM parameterization is the same as the joint test of the component main effect under effect parameterization. Both test the equality of cell means. But this Type 3 test differs from the joint test under reference parameterization, which tests the equality of cell means at the reference level of the other component main effect. If some cells are missing, you can obtain meaningful tests only by testing a Type III estimation function, so in this case you should use GLM parameterization.

The results of a Type 3 test or a joint test do not depend on the order in which you specify the terms in the MODEL statement.

**Multithreading**

The LOGSELECT procedure allocates data to different threads and calculates the likelihood function, gradient, and Hessian by accumulating the values from all threads. For more information about how PROC LOGSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

**Optimization Algorithms**

Several optimization techniques are available in PROC LOGSELECT. You can choose a particular optimizer by using the TECHNIQUE= option in the PROC LOGSELECT statement. Table 8.10 summarizes the optimization techniques available in PROC LOGSELECT.
Table 8.10  Optimization Techniques

<table>
<thead>
<tr>
<th>TECHNIQUE=</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>Trust region method</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>Newton-Raphson method with line search</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>Newton-Raphson method with ridging</td>
</tr>
<tr>
<td>QUANEW</td>
<td>Quasi-Newton methods</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>Double-dogleg method</td>
</tr>
<tr>
<td>CONGRA</td>
<td>Conjugate gradient methods</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>Nelder-Mead simplex method</td>
</tr>
</tbody>
</table>

There is no algorithm for optimizing general nonlinear functions that always finds the global optimum for a general nonlinear optimization problem in a reasonable amount of time. Because no single optimization technique is always superior to others, PROC LOGSELECT provides a variety of optimization techniques that work well in various circumstances. However, you can devise problems for which none of the techniques in PROC LOGSELECT can find the correct solution. Moreover, nonlinear optimization can be computationally expensive in terms of time and memory, so you must be careful when matching an algorithm to a problem. The section “Choosing an Optimization Algorithm” on page 80 in Chapter 2, “Shared Concepts,” is helpful in choosing a suitable optimization algorithm.

Displayed Output

The following sections describe the output that PROC LOGSELECT produces. The output is organized into various tables, which are discussed in their order of appearance.

Model Information

The “Model Information” table displays basic information about the model, such as the response variable, the frequency variable, the link function, and the distribution of the data that is assumed by the LOGSELECT procedure. For information about how PROC LOGSELECT determines the response distribution, see the section “Response Distributions” on page 485. If you specify the CODE statement, then the table displays the name of the variable in the scoring code that contains the classifications. If you do not also specify the PCATALL option, then the table also displays the name of the variable in the scoring code that contains the predicted probabilities.

Number of Observations

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis. If a FREQ statement is present, the table displays the sum of the frequencies that are read and used. If a WEIGHT statement is specified, the table displays the sum of $f_i w_i$ that are read and used. If you specify a PARTITION statement, the table displays the values for each role.
Response Profile

The “Response Profile” table displays the ordered value from which the LOGSELECT procedure determines the probability being modeled as an event in a binary model and displays the ordering of categories in a multinomial model. For each response category level, the frequency used in the analysis is reported. You can affect the ordering of the response values by specifying response-options in the MODEL statement. For a binary model, the note that follows the “Response Profile” table indicates which outcome is modeled as the event. For an ordinal multinomial model, the note that follows the “Response Profile” table indicates how the ordered response levels are accumulated; for a nominal multinomial model, the note indicates the reference response level. If you specify a PARTITION statement, the table displays the values for each role.

Class Level Information

The “Class Level Information” table lists the levels of every variable specified in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by using the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by using the NOCLPRINT= option in the PROC LOGSELECT statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.

Selection Information

When you specify the SELECTION statement, the LOGSELECT procedure by default produces a series of tables that display information about the model selection. The “Selection Information” table informs you about the model selection method, selection and stop criteria, and other parameters that govern the selection. You can suppress this table by specifying DETAILS=NONE in the SELECTION statement.

Iteration History

When you specify the ITHIST option in the PROC LOGSELECT statement, the “Iteration History” table displays, for each iteration of the optimization, the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element. The objective function that is used in the optimization in the LOGSELECT procedure is normalized by default to enable comparisons across data tables that have different sampling intensity. You can control normalization by specifying the NORMALIZE= option in the PROC LOGSELECT statement.

Convergence Status

The convergence status table is a small ODS table that appears as a message that indicates whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message indicates the reason for the failure. If you save the convergence status table to an output data set, a numeric Status variable is added that enables you to assess convergence programmatically. The values of the Status variable indicate the following:

<table>
<thead>
<tr>
<th>Status</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Convergence was achieved, or an optimization was not performed (because TECHNIQUE=NONE is specified).</td>
</tr>
<tr>
<td>1</td>
<td>The objective function could not be improved.</td>
</tr>
</tbody>
</table>
2 Convergence was not achieved because of a user interruption or because a limit was exceeded, such as the maximum number of iterations or the maximum number of function evaluations. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC LOGSELECT statement.

3 Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

**Entry and Removal Candidates**

When you specify DETAILS=ALL or DETAILS=STEPS in the SELECTION statement, the LOGSELECT procedure produces the “Entry Candidates” or “Removal Candidates” table, which displays the effect names and values of the criterion used to select entering or departing effects at each step of the selection process. For each step, the effects are displayed in sorted order from best to worst of the selection criterion.

**Selection Summary**

When you specify the SELECTION statement, the LOGSELECT procedure produces the “Selection Summary” table, which displays information about which effects were added to or removed from the model in the various steps of the model selection process. The statistic that led to the entry or removal decision is also displayed. You can request further details about the model selection steps by specifying DETAILS=STEPS or DETAILS=ALL in the SELECTION statement. You can suppress the display of the “Selection Summary” table by specifying DETAILS=NONE in the SELECTION statement.

If you specify the LASSO selection method, then this table displays information about which effect was added to the model, the number of effects in the model, the lambda value, and the information criteria.

**Stop Reason**

When you specify the SELECTION statement, the LOGSELECT procedure produces a simple table that tells you why model selection stopped.

**Selection Reason**

When you specify the SELECTION statement, the LOGSELECT procedure produces a simple table that tells you why the final model was selected.

**Selected Effects**

When you specify the SELECTION statement, the LOGSELECT procedure produces a simple table that tells you which effects are in the final model.

**Dimensions**

The “Dimensions” table displays size measures that are derived from the model. It displays the number of columns in the current design matrix, the number of effects in the current design, the largest number of design columns associated with an effect, the rank of the matrix, and the number of parameters in the current model, including any scale parameters.
Global Test

The “Global Test” table provides a likelihood ratio test for the hypothesis of whether the final model provides a better fit than a model without effects (an “intercept-only” model).

If you specify the NOINT option in the MODEL statement, the reference model is one where the linear predictor is 0 for all observations.

Fit Statistics

The “Fit Statistics” table displays a variety of likelihood-based measures of fit. The values that the “Fit Statistics” table displays are not based on a normalized log-likelihood function. If you specify a PARTITION statement or the PARTFIT option, the table displays the values for each role along with statistics for comparing the training, validation, and testing results.

For more information about the statistics displayed in this table, see the section “Model Fit and Assessment Statistics” on page 490.

Parameter Estimates

The parameter estimates, their estimated (asymptotic) standard errors, and p-values for the hypothesis that the parameter is 0 are presented in the “Parameter Estimates” table. If you request confidence intervals by specifying the CLB option in the MODEL statement, confidence limits are produced for the estimates.

Parameter Estimates Covariance Matrix

When you specify the COVB option in the PROC LOGSELECT statement, the LOGSELECT procedure displays the covariance matrix of the parameter estimates. The covariance matrix is computed as the inverse of the negative of the matrix of second derivatives of the log-likelihood function with respect to the model parameters (the Hessian matrix), evaluated at the parameter estimates.

Parameter Estimates Correlation Matrix

When you specify the CORRB option in the PROC LOGSELECT statement, the LOGSELECT procedure displays the correlation matrix of the parameter estimates.

Model Analysis of Variance (Type III)

When you specify the TYPE3 option in the MODEL statement, the LOGSELECT procedure produces the “Model Analysis of Variance (Type III)” table. This table displays tests that all parameters for a particular effect are equal to zero. For more information, see the section “Joint Tests and Type 3 Tests” on page 494.

Score Code Variables for Predicted Probability

When you specify the PCATALL option in the CODE statement, the LOGSELECT procedure produces the “Score Code Variables for Predicted Probability” table. For each level of the response variable, this table displays the corresponding variable in the scoring code that contains the predicted probability.
Timing

The “Timing” table displays the amount of time (in seconds) that PROC LOGSELECT required to perform different tasks in the analysis.

Output CAS Tables

When you specify an OUTPUT statement or a DISPLAYOUT statement to create output tables on your CAS server, the LOGSELECT procedure produces the “Output CAS Tables” table. This table displays the names, the number of rows and columns, and the CAS libraries in which the output table is created for every output table that you requested.

ODS Table Names

Each table that the LOGSELECT procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement, the DISPLAYOUT statement, or ODS statements. These names are listed in Table 8.11.

**NOTE:** The EFFECT statement also create tables which are not listed in this section. For information about these tables, see “ODS Table Names” on page 33 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
<td>Default</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Status of optimization at conclusion of optimization</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>CorrB</td>
<td>Correlation matrix of parameter estimates</td>
<td>PROC LOGSELECT</td>
<td>CORRB</td>
</tr>
<tr>
<td>CovB</td>
<td>Covariance matrix of parameter estimates</td>
<td>PROC LOGSELECT</td>
<td>COVB</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>EntryCandidates</td>
<td>Details about candidates for entry into the model</td>
<td>SELECTION</td>
<td>METHOD=FORWARD or</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>STEPWISE and DETAILS=STEP</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>GlobalTest</td>
<td>Test of the model versus the null model</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>IterHistory</td>
<td>Iteration history</td>
<td>PROC LOGSELECT</td>
<td>ITHIST</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Information about the modeling environment</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>ModelAnova</td>
<td>Model analysis of variance (Type III)</td>
<td>MODEL</td>
<td>TYPE3</td>
</tr>
</tbody>
</table>
Table 8.11  continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>NObs</td>
<td>Number of observations read and used, and number of events and trials, if</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td></td>
<td>applicable</td>
<td></td>
<td></td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Library and name of the output data table, and number of rows and columns</td>
<td>OUTPUT DISPLAYOUT</td>
<td>OUT=</td>
</tr>
<tr>
<td></td>
<td>in the table</td>
<td></td>
<td></td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in MODEL</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td></td>
<td>statements</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PredProbName</td>
<td>Displays the predicted probability variable in the scoring code associated</td>
<td>CODE</td>
<td>PCATALL</td>
</tr>
<tr>
<td></td>
<td>with each response level</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RemovalCandidates</td>
<td>Details about candidates for removal from the model</td>
<td>SELECTION</td>
<td>METHOD=BACKWARD or</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>STEPWISE and DETAILS=STEP</td>
</tr>
<tr>
<td>ResponseProfile</td>
<td>Response categories for binary and multinomial data</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>SelectedEffects</td>
<td>List of effects selected for the model</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionInfo</td>
<td>Information about the settings for model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionReason</td>
<td>Reason why the particular model was selected</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Summary information about model selection steps</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>StopReason</td>
<td>Reason for termination of model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times for tasks performed by the procedure</td>
<td>Default</td>
<td></td>
</tr>
</tbody>
</table>

**ODS Graphics**

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in SAS/STAT User’s Guide.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.
When ODS Graphics is enabled, the SELECTION statement can produce plots to help evaluate the selection process. For information about these plots, see the section “Model Selection Plots” on page 69 in Chapter 2, “Shared Concepts.”

PROC LOGSELECT assigns a name to each graph that it creates using ODS. You can use these names to reference the graphs when using ODS. The names are listed in Table 8.12.

### Table 8.12  Graphs Produced by PROC LOGSELECT

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CoefficientPanel</td>
<td>Coefficients and CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>ChooseCriterionPlot</td>
<td>CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>CoefficientPlot</td>
<td>Coefficients by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CriterionPanel</td>
<td>Fit criteria by step</td>
<td>CRITERIA</td>
</tr>
<tr>
<td>AdjRSqPlot</td>
<td>Max-rescaled (adjusted) R-square by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICCPlot</td>
<td>Corrected Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICPlot</td>
<td>Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>DiffMeanPlot</td>
<td>Difference of means by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>McFaddenPlot</td>
<td>McFadden’s R-square by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>MisclassPlot</td>
<td>Misclassification rate by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>SBCPlot</td>
<td>Schwarz Bayesian information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TEST_ASEPlot</td>
<td>Average square error on testing data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TRAIN_ASEPlot</td>
<td>Average square error on training data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>VAL_ASEPlot</td>
<td>Average square error on validation data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>FitByRolePlot</td>
<td>Progression of average square error by role</td>
<td>FITBYROLE</td>
</tr>
</tbody>
</table>

### Examples: LOGSELECT Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
Example 8.1: Model Selection

The following statements examine the same data as in the section “Getting Started: LOGSELECT Procedure” on page 459, but they request model selection via the forward selection technique. Effects that provide the best improvement to the selection criterion, SBC, are added until no more effects can improve the selection criterion. The DETAILS=ALL option in the SELECTION statement produces all tables that are related to model selection. The PLOTS=ALL option produces graphics to help you interpret the selection process. ODS Graphics must be enabled before you can request plots. For more information about ODS Graphics, see the section “ODS Graphics” on page 501.

```plaintext
ods graphics on;
proc logselect data=mycas.getStarted;
   class C;
   model y = C x1-x10;
   selection method=forward details=all plots=all;
run;
ods graphics off;
```

The model selection tables are shown in Output 8.1.1 through Output 8.1.3. Results from the selected model are shown in Output 8.1.4 and Output 8.1.5. Selection graphics that the PLOTS= option produces are displayed in Output 8.1.6 and Output 8.1.7.

The “Selection Information” table in Output 8.1.1 summarizes the settings for the model selection. Effects are added to the model only if they produce a significant improvement, which is determined by comparing the values of their SBCs. The forward selection stops three steps after the smallest SBC is obtained or when all effects have been added to the model.

**Output 8.1.1 Selection Information**

**The LOGSELECT Procedure**

<table>
<thead>
<tr>
<th>Selection Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
</tbody>
</table>

For each step of the selection process, the DETAILS=ALL option displays the candidate effects for entering the model along with their SELECT= criterion. Output 8.1.2 displays this table for the first step; the other steps are not shown here.
The DETAILS=ALL option also displays the dimensions, global test, fit statistics, and parameter estimates at each step of the selection process; these details are not shown here.

When the selection procedure is complete, the “Selection Summary” table in Output 8.1.3 shows the effects that were added to the model and the value of their selection criterion (and the choose and stop criteria, if they are specified). Step 0 refers to the null model that contains only an intercept. In the next step, effect $x_8$ made the most significant contribution to the model among the candidate effects, according to the SBC statistic. In step 2, $x_2$ made the most significant contribution when an effect was added to a model that contains the intercept and $x_8$. In the three subsequent steps, no effect could be added to the model that would reduce the SBC, so variable selection stopped because the stop horizon (see Output 8.1.1) indicates that at most three steps beyond the minimum SBC value are taken.

In Output 8.1.3, the “Selection Summary” table is followed by three small tables that summarize why the process stopped and which model is selected.

### Output 8.1.3  Selection Summary Information

<table>
<thead>
<tr>
<th>Step</th>
<th>Effect</th>
<th>Entered</th>
<th>Effects In</th>
<th>SBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Intercept</td>
<td>1</td>
<td>1</td>
<td>128.4253</td>
</tr>
<tr>
<td>1</td>
<td>$x_8$</td>
<td>2</td>
<td>2</td>
<td>128.7318</td>
</tr>
<tr>
<td>2</td>
<td>$x_2$</td>
<td>3</td>
<td>3</td>
<td>128.2892*</td>
</tr>
<tr>
<td>3</td>
<td>$x_4$</td>
<td>4</td>
<td>4</td>
<td>130.0901</td>
</tr>
<tr>
<td>4</td>
<td>$x_9$</td>
<td>5</td>
<td>5</td>
<td>131.9534</td>
</tr>
<tr>
<td>5</td>
<td>$x_1$</td>
<td>6</td>
<td>6</td>
<td>134.7945</td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

Selection stopped at a local minimum of the STOP criterion.

The model at step 2 is selected.

**Selected Effects:** Intercept $x_2$ $x_8$
Output 8.1.4 displays information about the selected model. Notice that the \(-2\) log-likelihood value in the “Fit Statistics” table is larger than the value for the full model in Figure 8.9. This is expected because the selected model contains only a subset of the parameters. Because the selected model is more parsimonious than the full model, the discrepancy between the \(-2\) log likelihood and the information criteria is less severe than previously noted.

**Output 8.1.4 Fit Statistics and Null Test**

<table>
<thead>
<tr>
<th>Dimensions</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Columns in Design</td>
<td>3</td>
</tr>
<tr>
<td>Number of Effects</td>
<td>3</td>
</tr>
<tr>
<td>Max Effect Columns</td>
<td>1</td>
</tr>
<tr>
<td>Rank of Design</td>
<td>3</td>
</tr>
<tr>
<td>Parameters in Optimization</td>
<td>3</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Test</th>
<th>DF</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Likelihood Ratio</td>
<td>2</td>
<td>9.4237</td>
<td>0.0090</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>(-2) Log Likelihood</td>
<td>114.39646</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>120.39646</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>120.64646</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>128.21197</td>
</tr>
</tbody>
</table>

The parameter estimates of the selected model are shown in **Output 8.1.5**. Notice that the effects are listed in the “Parameter Estimates” table in the order in which they were specified in the MODEL statement and not in the order in which they were added to the model.

**Output 8.1.5 Parameter Estimates**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>0.858377</td>
<td>0.550302</td>
<td>2.4331</td>
<td>0.1188</td>
</tr>
<tr>
<td>x2</td>
<td>1</td>
<td>-0.250240</td>
<td>0.114578</td>
<td>4.7700</td>
<td>0.0290</td>
</tr>
<tr>
<td>x8</td>
<td>1</td>
<td>1.783956</td>
<td>0.790845</td>
<td>5.0885</td>
<td>0.0241</td>
</tr>
</tbody>
</table>

You can construct the prediction equation for this model from the parameter estimates as follows. The estimated linear predictor for an observation is

\[
\hat{\eta} = 0.8584 - 0.2502 \times x_2 + 1.7840 \times x_8
\]

The predicted probability that variable \(y\) takes the value 0 is

\[
\hat{Pr}(Y = 0) = \frac{1}{1 + \exp\{-\hat{\eta}\}}
\]
The coefficient panel in Figure 8.1.6 enables you to visualize the selection process. In this plot, standardized coefficients of all the effects that are selected at some step of the stepwise method are plotted as a function of the step number. This enables you to assess the relative importance of the effects that are selected at any step of the selection process and to know when effects entered the model. The lower plot in the panel shows how the criterion that is used to choose the selected model changes as effects enter or leave the model.

**Output 8.1.6  Coefficient Progression**

![Coefficient Progression for y](image)

The criterion panel in Figure 8.1.7 provides a graphical view of the progression of the fit criteria as the selection process evolves. Notice at Step 0 that the SBC criterion seems to be at its minimum. Because the stop horizon value is 3 (see Output 8.1.1), three more steps are taken in case Step 0 is a local optimum. In this example, the global optimum is found two steps later.
Example 8.2: Modeling Binomial Data

If $Y_1, \ldots, Y_n$ are independent binary (Bernoulli) random variables with common success probability $\pi$, then their sum is a binomial random variable. In other words, a binomial random variable with parameters $n$ and $\pi$ can be generated as the sum of $n$ Bernoulli($\pi$) random experiments. The LOGSELECT procedure uses a special syntax, the events/trials syntax, to express data in binomial form.

Consider the following data, taken from Cox and Snell (1989, pp. 10–11), of the number of ingots not ready for rolling ($r$) out of $n$ tested for a number of combinations of heating time and soaking time. If each test is carried out independently and if for a particular combination of heating and soaking time there is a constant probability that the tested ingot is not ready for rolling, then the random variable $r$ follows a binomial($n, \pi$) distribution, where the success probability $\pi$ is a function of heating and soaking time.

```static
data Ingots;
  input Heat Soak r n @@;
  Obsnum= _n_;
datalines;
7 1.0 0 10 14 1.0 0 31 27 1.0 1 56 51 1.0 3 13
7 1.7 0 17 14 1.7 0 43 27 1.7 4 44 51 1.7 0 1
```

**Example 8.2: Modeling Binomial Data**

If $Y_1, \ldots, Y_n$ are independent binary (Bernoulli) random variables with common success probability $\pi$, then their sum is a binomial random variable. In other words, a binomial random variable with parameters $n$ and $\pi$ can be generated as the sum of $n$ Bernoulli($\pi$) random experiments. The LOGSELECT procedure uses a special syntax, the events/trials syntax, to express data in binomial form.

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```static
data Ingots;
  input Heat Soak r n @@;
  Obsnum= _n_;
datalines;
7 1.0 0 10 14 1.0 0 31 27 1.0 1 56 51 1.0 3 13
7 1.7 0 17 14 1.7 0 43 27 1.7 4 44 51 1.7 0 1
```
The following statements show the use of the events/trials syntax to model the binomial response. The events variable in this situation is \( r \) (the number of ingots not ready for rolling), and the trials variable is \( n \) (the number of ingots that are tested). The dependency of the probability of not being ready for rolling is modeled as a function of heating time, soaking time, and their interaction. The OUTPUT statement stores the linear predictors and the predicted probabilities in the mycas.Out data table along with the other variables from the input data table.

```plaintext
proc logselect data=mycas.Ingots;
  model r/n = Heat Soak Heat*Soak;
  output out=mycas.Out xbeta predicted=Pred copyvars=(Heat Soak);
run;
```

The “Model Information” table shows that the data are modeled as binomially distributed with a logit link function (Output 8.2.1). This is the default link function in the LOGSELECT procedure for binary and binomial data. The procedure estimates the parameters of the model by a Newton-Raphson algorithm.

**Output 8.2.1** Model Information and Number of Observations

### The LOGSELECT Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source: INGOTS</td>
</tr>
<tr>
<td>Response Variable (Events): r</td>
</tr>
<tr>
<td>Response Variable (Trials): n</td>
</tr>
<tr>
<td>Distribution: Binomial</td>
</tr>
<tr>
<td>Link Function: Logit</td>
</tr>
<tr>
<td>Optimization Technique: Newton-Raphson with Ridging</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>19</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Used</td>
<td>19</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Response Profile</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ordered Value</td>
</tr>
<tr>
<td>---------------</td>
</tr>
<tr>
<td>1 Event</td>
</tr>
<tr>
<td>2 Nonevent</td>
</tr>
</tbody>
</table>

The second table in **Output 8.2.1** shows that all 19 observations in the input data table were used in the analysis and the “Response Profile” table shows that the total number of events and nonevents equals 12 and 387, respectively.

**Output 8.2.2** displays the convergence status table for this run. The LOGSELECT procedure satisfies the GCONV= convergence criterion.
Output 8.2.2 Convergence Status

Convergence criterion (GCONV=1E-8) satisfied.

Output 8.2.3 displays the “Dimensions” table for the model. The design matrix of the model (the $X$ matrix) has four columns, which correspond to the intercept, the Heat effect, the Soak effect, and the interaction of the Heat and Soak effects. The model is nonsingular because the rank of the crossproducts matrix equals the number of columns in $X$. All parameters are estimable, and all participate in the optimization.

**Output 8.2.3 Dimensions in Binomial Logistic Regression**

<table>
<thead>
<tr>
<th>Dimensions</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Columns in Design</td>
<td>4</td>
</tr>
<tr>
<td>Number of Effects</td>
<td>4</td>
</tr>
<tr>
<td>Max Effect Columns</td>
<td>1</td>
</tr>
<tr>
<td>Rank of Design</td>
<td>4</td>
</tr>
<tr>
<td>Parameters in Optimization</td>
<td>4</td>
</tr>
</tbody>
</table>

Output 8.2.4 displays the “Fit Statistics” table for this run. Evaluated at the converged estimates, $-2$ times the value of the log-likelihood function equals 27.9569. Further fit statistics are also displayed, all of them in “smaller is better” form. The AIC, AICC, and SBC criteria are used to compare non-nested models and to penalize the model fit for the number of observations and parameters. You can use the $-2$ log-likelihood value to compare nested models by way of a likelihood ratio test.

**Output 8.2.4 Fit Statistics**

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>27.9569</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>35.95689</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>38.81403</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>39.73464</td>
</tr>
</tbody>
</table>

Output 8.2.5 shows the test of the global hypothesis that the effects jointly do not affect the probability of ingot readiness. You can obtain the chi-square test statistic by comparing the $-2$ log-likelihood value of the model with covariates to the value in the intercept-only model. The test is significant, with a $p$-value of 0.0082. One or more of the effects in the model have a significant impact on the probability of ingot readiness.

**Output 8.2.5 Null Test**

<table>
<thead>
<tr>
<th>Testing Global Null Hypothesis: BETA=0</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Test</td>
<td>DF</td>
<td>Chi-Square</td>
</tr>
<tr>
<td>Likelihood Ratio</td>
<td>3</td>
<td>11.7663</td>
</tr>
</tbody>
</table>

The “Parameter Estimates” table in Output 8.2.6 displays the estimates and standard errors of the model effects.
You can construct the prediction equation of the model from the “Parameter Estimates” table. For example, an observation with Heat equal to 14 and Soak equal to 1.7 has the linear predictor

\[ \hat{\eta} = -5.9902 + 0.09634 \times 14 + 0.2996 \times 1.7 - 0.00884 \times 14 \times 1.7 = -4.3425 \]

The probability that an ingot with these characteristics is not ready for rolling is

\[ \hat{\pi} = \frac{1}{1 + \exp\{-(-4.3425)\}} = 0.01284 \]

PROC LOGSELECT computes these linear predictors and probabilities and stores them in the mycas.Out data set. The following PROC PRINT statement produces Output 8.2.7, which shows the probability that an ingot with Heat equal to 14 and Soak equal to 1.7 is not ready for rolling:

```plaintext
proc print data=mycas.Out;
  where Heat=14 & Soak=1.7;
run;
```

**Output 8.2.7** Predicted Probability for Heat=14 and Soak=1.7

<table>
<thead>
<tr>
<th>Obs</th>
<th>Pred <em>XBETA</em></th>
<th>Heat</th>
<th>Soak</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0.012836</td>
<td>14</td>
<td>1.7</td>
</tr>
</tbody>
</table>

Binomial data are a form of grouped binary data in which “successes” in the underlying Bernoulli trials are totaled. You can thus unwind data for which you use the events/trials syntax and fit these data by using techniques for binary data.

The following DATA step expands the Ingots data set, which contains 12 events in 387 trials, into a data table that has 387 observations:

```plaintext
data mycas.Ingots_binary;
  set Ingots;
  do i=1 to n;
    if i <= r then y=1; else y = 0;
    output;
  end;
run;
```

The following statements fit the model that contains the Heat effect, the Soak effect, and their interaction to the data table. The `event='1'` response-variable option in the `MODEL` statement ensures that the LOGSELECT procedure models the probability that the variable y takes the value 1.
Example 8.2: Modeling Binomial Data

```
proc logselect data=mycas.Ingots_binary;
   model y(event='1') = Heat Soak Heat*Soak;
run;
```

Output 8.2.8 displays the “Model Information,” “Number of Observations,” and “Response Profile” tables. The data are now modeled as binary (Bernoulli distributed) with a logit link function. The “Response Profile” table shows that the binary response breaks down into 375 observations where $y=0$ and 12 observations where $y=1$.

**Output 8.2.8** Model Information in Binary Model

**The LOGSELECT Procedure**

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Optimization Technique</td>
</tr>
</tbody>
</table>

Number of Observations Read 387
Number of Observations Used 387

<table>
<thead>
<tr>
<th>Response Profile</th>
<th>Ordered Value</th>
<th>y</th>
<th>Total Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>375</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>12</td>
<td></td>
</tr>
</tbody>
</table>

Probability modeled is $y = 1$.

Output 8.2.9 displays the result of the test of the global null hypothesis and the parameter estimates. These results match those in Output 8.2.5 and Output 8.2.6.

**Output 8.2.9** Null Test and Parameter Estimates

<table>
<thead>
<tr>
<th>Testing Global Null Hypothesis: BETA=0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test</td>
</tr>
<tr>
<td>DF</td>
</tr>
<tr>
<td>----</td>
</tr>
<tr>
<td>Likelihood Ratio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameter</td>
</tr>
<tr>
<td>---------------</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>Heat</td>
</tr>
<tr>
<td>Soak</td>
</tr>
<tr>
<td>Heat * Soak</td>
</tr>
</tbody>
</table>
Chapter 8: The LOGSELECT Procedure

Example 8.3: Partitioning Data

The Sashelp.JunkMail data set comes from a study that classifies whether an email is junk email (coded as 1) or not (coded as 0). The data were collected by Hewlett-Packard Labs and donated by George Forman. The data set, which is specified in the following DATA step, contains 4,601 observations, with 2 binary variables and 57 continuous explanatory variables. The response variable, Class, is a binary indicator of whether an email is considered spam or not. The partitioning variable, Test, is a binary indicator that is used to divide the data into training and testing sets. The 57 explanatory variables are continuous variables that represent frequencies of some common words and characters and lengths of uninterrupted sequences of capital letters in emails.

```plaintext
data mycas.JunkMail;
  set Sashelp.JunkMail;
run;
```

In the following program, the PARTITION statement divides the data into two parts. The training data have a Test value of 0 and contain about two-thirds of the data; the rest of the data are used to evaluate the fit. A forward selection method selects the best model based on the training observations.

```plaintext
proc logselect data=mycas.JunkMail;
  model Class(event='1')=Make Address All _3d Our Over Remove Internet Order Mail Receive Will People Report Addresses Free Business Email You Credit Your Font _000 Money HP HPL George _650 Lab Labs Telnet _857 Data _415 _85 Technology _1999 Parts PM Direct CS Meeting Original Project RE Edu Table Conference Semicolon Paren Bracket Exclamation Dollar Pound CapAvg CapLong CapTotal;
  partition rolevar=Test(train='0' test='1');
  selection method=forward;
run;
```

Selected results from the analysis are shown in Output 8.3.1 and Output 8.3.2.

The “Number of Observations” and “Response Profile” tables in Output 8.3.1 are divided into training and testing columns.

Output 8.3.1  Partitioned Counts

The LOGSELECT Procedure

<table>
<thead>
<tr>
<th>Description</th>
<th>Number of Observations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total</td>
<td>Training</td>
</tr>
<tr>
<td>Number of Observations Read</td>
<td>4601</td>
</tr>
<tr>
<td>Number of Observations Used</td>
<td>4601</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Ordered Value</th>
<th>Class</th>
<th>Total</th>
<th>Frequency</th>
<th>Training</th>
<th>Testing</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>0</td>
<td>2788</td>
<td>1847</td>
<td>941</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1813</td>
<td>1218</td>
<td>595</td>
<td></td>
</tr>
</tbody>
</table>

Probability modeled is Class = 1.
The likelihood-based fit statistics for the selected model are displayed in the “Fit Statistics” table in Output 8.3.2, which has columns for the training and testing subsets.

**Output 8.3.2  Partitioned Fit Statistics**

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th>Training</th>
<th>Testing</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>1242.59491</td>
<td>823.68742</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>1292.59491</td>
<td>873.68742</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>1293.02268</td>
<td>874.54835</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>1443.28998</td>
<td>1007.11085</td>
</tr>
<tr>
<td>Average Square Error</td>
<td>0.05659</td>
<td>0.06353</td>
</tr>
<tr>
<td>-2 Log L (Intercept-only)</td>
<td>4118.98701</td>
<td>2050.73514</td>
</tr>
<tr>
<td>R-Square</td>
<td>0.60877</td>
<td>0.55016</td>
</tr>
<tr>
<td>Max-rescaled R-Square</td>
<td>0.82359</td>
<td>0.74661</td>
</tr>
<tr>
<td>McFadden's R-Square</td>
<td>0.69833</td>
<td>0.59835</td>
</tr>
<tr>
<td>Misclassification Rate</td>
<td>0.07471</td>
<td>0.07813</td>
</tr>
<tr>
<td>Difference of Means</td>
<td>0.75122</td>
<td>0.73431</td>
</tr>
</tbody>
</table>

These statistics are computed for both the training and testing data. The statistics include the likelihood-based R-square statistics as well as several prediction-based statistics that are described in the section “Model Fit and Assessment Statistics” on page 490. The ASE, the misclassification rate, and the difference of means should be very similar between the two groups when the training data are representative of the testing data; for this model, the values of these statistics seem similar between the two disjoint subsets.

If you want to display all the fit statistics without partitioning your data table, you can specify the PARTFIT option as follows:

```plaintext
proc logselect data=mycas.JunkMail(where Test=0) partfit;
  model Class(event='1')= Our Over Remove Internet Order Will
      Free Business You Your Font _000 Money HP George Parts
      Meeting RE Edu Semicolon Exclamation Dollar CapAvg
      CapLong;
run;
```

The resulting “Fit Statistics” table is identical to the Training column in Output 8.3.2.

---

**Example 8.4: Ordinal Logistic Regression**

Consider a study of the effects of various cheese additives on taste. Researchers tested four cheese additives and obtained 52 response ratings for each additive. Each response was measured on a scale of nine categories ranging from strong dislike (1) to excellent taste (9). The data, given in McCullagh and Nelder (1989, p. 175) in the form of a two-way frequency table of additive by rating, are saved in the data table mycas.Cheese by using the following program. The variable `y` contains the response rating. The variable `Additive` specifies the cheese additive (1, 2, 3, or 4). The variable `freq` gives the frequency with which each additive received each rating.
Chapter 8: The LOGSELECT Procedure

data mycas.Cheese;
  do Additive = 1 to 4;
    do y = 1 to 9;
      input freq @@;
      output;
    end;
  end;
  label y='Taste Rating';
datalines;
0 0 1 7 8 8 19 8 1
6 9 12 11 7 6 1 0 0
1 1 6 8 23 7 5 1 0
0 0 0 1 3 7 14 16 11
;

The response variable $y$ is ordinally scaled. A cumulative logit model is used to investigate the effects of the cheese additives on taste. The following statements invoke PROC LOGSELECT to fit this model with $y$ as the response variable and three indicator variables as explanatory variables, with the fourth additive as the reference level. With this parameterization, each Additive parameter compares an additive to the fourth additive.

```
proc logselect data=mycas.Cheese;
  freq freq;
  class Additive(ref='4') / param=ref ;
  model y=Additive;
run;
```

Results from the logistic analysis are shown in Output 8.4.1 through Output 8.4.3.

The “Response Profile” table in Output 8.4.1 shows that the strong dislike ($y=1$) end of the rating scale is associated with lower Ordered Values in the “Response Profile” table; hence the probability of disliking the additives is modeled.

**Output 8.4.1** Proportional Odds Model Regression Analysis

**The LOGSELECT Procedure**

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Number of Response Levels</td>
</tr>
<tr>
<td>Frequency Variable</td>
</tr>
<tr>
<td>Distribution</td>
</tr>
<tr>
<td>Link Type</td>
</tr>
<tr>
<td>Link Function</td>
</tr>
<tr>
<td>Optimization Technique</td>
</tr>
</tbody>
</table>

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
<td>36</td>
</tr>
<tr>
<td>Number of Observations Used</td>
<td>28</td>
</tr>
<tr>
<td>Sum of Frequencies Read</td>
<td>208</td>
</tr>
<tr>
<td>Sum of Frequencies Used</td>
<td>208</td>
</tr>
</tbody>
</table>
Example 8.4: Ordinal Logistic Regression

Output 8.4.1 continued

<table>
<thead>
<tr>
<th>Response Profile</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Ordered Value</strong></td>
</tr>
<tr>
<td>1 1</td>
</tr>
<tr>
<td>2 2</td>
</tr>
<tr>
<td>3 3</td>
</tr>
<tr>
<td>4 4</td>
</tr>
<tr>
<td>5 5</td>
</tr>
<tr>
<td>6 6</td>
</tr>
<tr>
<td>7 7</td>
</tr>
<tr>
<td>8 8</td>
</tr>
<tr>
<td>9 9</td>
</tr>
</tbody>
</table>

Probabilities modeled are cumulated over the lower Ordered Values.

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class</td>
</tr>
<tr>
<td>Additive</td>
</tr>
</tbody>
</table>

Output 8.4.2 Proportional Odds Model Regression Analysis

Convergence criterion (GCONV=1E-8) satisfied.

<table>
<thead>
<tr>
<th>Dimensions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Columns in Design</td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Max Effect Columns</td>
</tr>
<tr>
<td>Rank of Design</td>
</tr>
<tr>
<td>Parameters in Optimization</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Testing Global Null Hypothesis: BETA=0</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test</td>
</tr>
<tr>
<td>Likelihood Ratio</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
</tr>
</tbody>
</table>

The positive value (1.6128) for the parameter estimate for Additive=1 in Output 8.4.3 indicates a tendency toward the lower-numbered categories of the first cheese additive relative to the fourth. In other words, the fourth additive tastes better than the first additive. Similarly, the second and third additives are both less favorable than the fourth additive. The relative magnitudes of these slope estimates imply the preference ordering: fourth, first, third, second.
Output 8.4.3  Proportional Odds Model Regression Analysis

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept 1</td>
<td>1</td>
<td>0.564010</td>
<td>157.5844</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 2</td>
<td>1</td>
<td>-0.029480</td>
<td>159.9230</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 3</td>
<td>1</td>
<td>0.425651</td>
<td>133.8992</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 4</td>
<td>1</td>
<td>0.388022</td>
<td>98.7968</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 5</td>
<td>1</td>
<td>0.345268</td>
<td>53.2940</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 6</td>
<td>1</td>
<td>0.312208</td>
<td>25.2408</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Intercept 7</td>
<td>1</td>
<td>0.273819</td>
<td>0.0596</td>
<td>0.8071</td>
<td></td>
</tr>
<tr>
<td>Intercept 8</td>
<td>1</td>
<td>1.492974</td>
<td>19.7794</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Additive 1</td>
<td>1</td>
<td>0.380544</td>
<td>17.9617</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Additive 2</td>
<td>1</td>
<td>0.476721</td>
<td>108.4546</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>Additive 3</td>
<td>1</td>
<td>0.421830</td>
<td>62.0444</td>
<td>&lt;.0001</td>
<td></td>
</tr>
</tbody>
</table>

References


Chapter 9
The NLMOD Procedure

Contents

<table>
<thead>
<tr>
<th>Topic</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: NLMOD Procedure</td>
<td>520</td>
</tr>
<tr>
<td>PROC NLMOD Features</td>
<td>520</td>
</tr>
<tr>
<td>PROC NLMOD Compared with the Other SAS Procedures</td>
<td>520</td>
</tr>
<tr>
<td>PROC NLMOD Compared with the HPNLMOD Procedure</td>
<td>521</td>
</tr>
<tr>
<td>PROC NLMOD Compared with the NLIN Procedure</td>
<td>521</td>
</tr>
<tr>
<td>PROC NLMOD Compared with the NLMIXED Procedure</td>
<td>521</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>521</td>
</tr>
<tr>
<td>Getting Started: NLMOD Procedure</td>
<td>522</td>
</tr>
<tr>
<td>Least Squares Model</td>
<td>522</td>
</tr>
<tr>
<td>Binomial Model</td>
<td>523</td>
</tr>
<tr>
<td>Syntax: NLMOD Procedure</td>
<td>525</td>
</tr>
<tr>
<td>PROC NLMOD Statement</td>
<td>526</td>
</tr>
<tr>
<td>BOUNDS Statement</td>
<td>528</td>
</tr>
<tr>
<td>BY Statement</td>
<td>528</td>
</tr>
<tr>
<td>DISPLAY Statement</td>
<td>528</td>
</tr>
<tr>
<td>DISPLAYOUT Statement</td>
<td>529</td>
</tr>
<tr>
<td>ESTIMATE Statement</td>
<td>530</td>
</tr>
<tr>
<td>ID Statement</td>
<td>530</td>
</tr>
<tr>
<td>MODEL Statement</td>
<td>530</td>
</tr>
<tr>
<td>PARAMETERS Statement</td>
<td>531</td>
</tr>
<tr>
<td>PREDICT Statement</td>
<td>534</td>
</tr>
<tr>
<td>RESTRICT Statement</td>
<td>535</td>
</tr>
<tr>
<td>Programming Statements</td>
<td>535</td>
</tr>
<tr>
<td>Details: NLMOD Procedure</td>
<td>537</td>
</tr>
<tr>
<td>Least Squares Estimation</td>
<td>537</td>
</tr>
<tr>
<td>Built-In Log-Likelihood Functions</td>
<td>538</td>
</tr>
<tr>
<td>Multithreading</td>
<td>540</td>
</tr>
<tr>
<td>Optimization Algorithms</td>
<td>540</td>
</tr>
<tr>
<td>Displayed Output</td>
<td>540</td>
</tr>
<tr>
<td>ODS Table Names</td>
<td>543</td>
</tr>
<tr>
<td>Examples: NLMOD Procedure</td>
<td>544</td>
</tr>
<tr>
<td>Example 9.1: Segmented Model</td>
<td>544</td>
</tr>
<tr>
<td>References</td>
<td>548</td>
</tr>
</tbody>
</table>
Overview: NLMOD Procedure

The NLMOD procedure fits nonlinear regression models with standard or general distributions in SAS Viya. PROC NLMOD enables you to specify the model by using SAS programming statements, which give you greater flexibility in modeling the relationship between the response variable and independent (regressor) variables than SAS procedures that use a more structured MODEL statement. The NLMOD procedure uses either nonlinear least squares or maximum likelihood to fit nonlinear regression models.

PROC NLMOD Features

The NLMOD procedure does the following:

- is highly multithreaded during all phases of analytic execution
- computes analytical derivatives of user-provided expressions for more robust parameter estimations
- evaluates user-provided expressions and their confidence limits by using the ESTIMATE and PREDICT statements
- estimates parameters without specifying a particular distribution function by using the least squares method
- estimates parameters by using the maximum likelihood method when either a built-in distribution function is specified or a likelihood function is provided

Because the NLMOD procedure runs on CAS, it also does the following:

- enables you to run in distributed mode on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on CAS
- exploits all the available cores and concurrent threads, regardless of execution mode. For information about how PROC NLMOD uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

PROC NLMOD Compared with the Other SAS Procedures

The NLMOD procedure provides nonlinear regression modeling functionality that is comparable to that of the HPNLMOD, NLIN, and NLMIXED procedures in SAS/STAT software.
PROC NLMOD Compared with the HPNLMOD Procedure

The functionality of the NLMOD procedure is identical to the HPNLMOD procedure, which is a high-performance procedure. The NLMOD procedure is the next generation of the HPNLMOD procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations. Both procedures perform computations in multiple threads.

Both the NLMOD and HPNLMOD procedures fit nonlinear regression models.

PROC NLMOD Compared with the NLIN Procedure

Like the NLIN procedure in SAS/STAT software, the NLMOD procedure estimates parameters by using least squares minimization for models that are specified by SAS programming statements. However, PROC NLMOD can also perform maximum likelihood estimation when information about the response variable’s distribution is provided. PROC NLMOD also has a RESTRICT statement for specifying restrictions on parameter estimates that are more general than those available in PROC NLIN. Because the NLMOD and NLIN procedures use different optimization techniques, the available options that control the estimation process and resulting parameter estimates can differ between these procedures when equivalent models and data are analyzed.

PROC NLMOD Compared with the NLMIXED Procedure

Although it does not support the specification of random effects, PROC NLMOD is similar to the NLMIXED procedure in SAS/STAT. Both procedures perform maximum likelihood estimation by using the same programming syntax and set of distributions to specify the model’s mean term. In addition, both PROC NLMOD and PROC NLMIXED use the same optimization techniques and options. However, PROC NLMIXED does not support least squares parameter estimation.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```
The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```r
   cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

### Getting Started: NLMOD Procedure

The most common use of the NLMOD procedure is to estimate the parameters in a model in which the response variable is a nonlinear function of one or more of the parameters.

#### Least Squares Model

The Michaelis-Menten model of enzyme kinetics (Ratkowsky 1990, p. 59) relates a substrate’s concentration to its catalyzed reaction rate. You can analyze the Michaelis-Menten model by using a least squares estimation because it does not specify how the reaction rate is distributed around its predicted value. The relationship between reaction rate and substrate concentration is

$$f(x_i, \theta) = \frac{\theta_1 x_i}{\theta_2 + x_i}, \text{ for } i = 1, 2, \ldots, n$$

where $x_i$ represents the concentration for $n$ trials and $f(x, \theta)$ is the reaction rate. The vector $\theta$ contains the rate parameters.

The input data must be a table on your CAS server, and a CAS session must be set up. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.” The following DATA step creates the Enzyme data table, which consists of experimental measurements of reaction rate and concentration, in your CAS session:

```r
data mycas.Enzyme;
   input conc rate @@;
datalines;
   0.26 124.7  0.30 126.9
   0.48 135.9  0.50 137.6
   0.54 139.6  0.68 141.1
   0.82 142.8  1.14 147.6
   1.28 149.8  1.38 149.4
   1.80 153.9  2.30 152.5
   2.44 154.5  2.48 154.7
;
```
These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following SAS statements estimate the parameters $\theta_1$ and $\theta_2$:

```sas
proc nlmom data=mycas.Enzyme;
   parms theta1=0 theta2=0;
   model rate ~ residual(theta1*conc / (theta2 + conc));
run;
```

The least squares estimation that PROC NLMOD performs for this enzyme kinetics problem produces the analysis of variance table in Figure 9.1. The table displays the degrees of freedom, sums of squares, and mean squares along with the model $F$ test.

**Figure 9.1** Nonlinear Least Squares Analysis of Variance

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Approx Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>2</td>
<td>290116</td>
<td>145058</td>
<td>88537.2</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>12</td>
<td>19.6606</td>
<td>1.6384</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Uncorrected Total</td>
<td>14</td>
<td>290135</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

An intercept was not specified for this model.

Finally, Figure 9.2 displays the parameter estimates, standard errors, $t$ statistics, and 95% confidence intervals for $\theta_1$ and $\theta_2$.

**Figure 9.2** Parameter Estimates and Approximate 95% Confidence Intervals

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>DF</th>
<th>$t$ Value</th>
<th>Approx Pr &gt;</th>
<th>Approx 95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>theta1</td>
<td>158.1</td>
<td>0.6737</td>
<td>12</td>
<td>234.67</td>
<td>&lt;.0001</td>
<td>156.6 159.6</td>
</tr>
<tr>
<td>theta2</td>
<td>0.0741</td>
<td>0.00313</td>
<td>12</td>
<td>23.69</td>
<td>&lt;.0001</td>
<td>0.0673 0.0809</td>
</tr>
</tbody>
</table>

In the enzyme kinetics model, no information was supplied about the distribution of the reaction rate around the model’s mean value. Therefore, the residual model distribution was specified to perform a least squares parameter fit.

**Binomial Model**

In the example “Probit Model with Likelihood Function” in the chapter “The NLIN Procedure” in SAS/STAT User’s Guide, cancer remission is modeled by expressing the maximum likelihood function for a binary distribution as a nonlinear least squares optimization. The following statements show an equivalent formulation of this model that uses PROC NLMOD and specifies the binary distribution explicitly:
data mycas.Remiss;
    input remiss cell smear infil li blast temp;
    label remiss = 'complete remission';
    like = 0;
    label like = 'dummy variable for nlin';
    datalines;
1 0.8 .83 .66 1.9 1.10 .996
1 0.9 .36 .32 1.4 0.74 .992
0 0.8 .88 .70 0.8 0.176 .982
0 1 .87 .87 0.7 1.053 .986
1 0.9 .75 .68 1.3 0.519 .980
0 1 .65 .65 0.6 0.519 .982
1 0.95 .97 .92 1 1.23 .992
0 0.95 .87 .83 1.9 1.354 1.020
0 1 .45 .45 0.8 0.322 .999
0 0.95 .36 .34 0.5 0 1.038
0 0.85 .39 .33 0.7 0.279 .988
0 0.7 .76 .53 1.2 0.146 .982
0 0.8 .46 .37 0.4 0.38 1.006
0 0.2 .39 .08 0.8 0.114 .990
0 1 .90 .90 1.1 1.037 .990
1 1 .84 .84 1.9 2.064 1.020
0 0.65 .42 .27 0.5 0.114 1.014
0 1 .75 .75 1 1.322 1.004
0 0.5 .44 .22 0.6 0.114 .990
1 1 .63 .63 1.1 1.072 .986
0 1 .33 .33 0.4 0.176 1.010
0 0.9 .93 .84 0.6 1.591 1.020
1 1 .58 .58 1 0.531 1.002
0 0.95 .32 .30 1.6 0.886 .988
1 1 .60 .60 1.7 0.964 .990
1 1 .69 .69 0.9 0.398 .986
0 1 .73 .73 0.7 0.398 .986
;
proc nlmod data=mycas.Remiss corr;
    parms int=-10 a=-2 b=-1 c=6;
    linp = int + a*cell + b*li + c*temp;
    p = probnorm(linp);
    model remiss ~ binary(1-p);
run;

This binary distribution model displays information about the quality of the estimation that is different from the information displayed in the section “Least Squares Model” on page 522. No analysis of variance table is produced for this model; fit statistics based on the value of the likelihood function are displayed in Figure 9.3.
Parameter estimates for the binary distribution model that uses the same quantities as in the section “Least Squares Model” on page 522 are displayed in Figure 9.4.

**Figure 9.4** Parameter Estimates and Approximate 95% Confidence Intervals

| Parameter | Estimate | Standard Error | DF | t Value | Approx Pr > |t| | Approx 95% Confidence Limits |
|-----------|----------|----------------|----|---------|-------------|------------------|-----------------------------|
| int       | -36.7548 | 32.3607        | 27 | -1.14   | 0.2660      | -103.2           | 29.6439                    |
| a         | -5.6296  | 4.6376         | 27 | -1.21   | 0.2353      | -15.145         | 3.8858                    |
| b         | -2.2513  | 0.9790         | 27 | -2.30   | 0.0294      | -4.2599         | -0.2426                   |
| c         | 45.1815  | 34.9095        | 27 | 1.29    | 0.2065      | -26.4469        | 116.8                     |

**Syntax: NLMOD Procedure**

The following statements are available in the NLMOD procedure:

```
PROC NLMOD <options> ;
   BOUNDS constraint < , constraint ... > ;
   BY variables ;
   DISPLAY <table-list>< /options> ;
   DISPLAYOUT table-spec-list< /options> ;
   ESTIMATE 'label' expression <options> ;
   ID variables ;
   MODEL dependent-variable ~ distribution ;
   PARAMETERS <parameter-specification>< , . . . , parameter-specification>< /options> ;
   PREDICT 'label' expression <options> ;
   RESTRICT restriction1 < , restriction2 . . . > ;
   Programming Statements ;
```

The PROC NLMOD statement and exactly one MODEL statement are required.
**PROC NLMOD Statement**

```plaintext
PROC NLMOD <options> ;
```

The PROC NLMOD statement invokes the procedure. Table 9.1 summarizes important options in the PROC NLMOD statement by function. These and other options in the PROC NLMOD statement are then described fully in alphabetical order.

**Table 9.1  PROC NLMOD Statement Options**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
<tr>
<td>OUT=</td>
<td>Specifies the output data table</td>
</tr>
<tr>
<td><strong>Output Options</strong></td>
<td></td>
</tr>
<tr>
<td>CORR</td>
<td>Specifies the correlation matrix</td>
</tr>
<tr>
<td>COV</td>
<td>Specifies the covariance matrix</td>
</tr>
<tr>
<td>ECORR</td>
<td>Specifies the correlation matrix of additional estimates</td>
</tr>
<tr>
<td>ECOV</td>
<td>Specifies the covariance matrix of additional estimates</td>
</tr>
<tr>
<td>DF</td>
<td>Specifies the default degrees of freedom</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>NOITPRINT</td>
<td>Suppresses output about iterations within the optimization process</td>
</tr>
<tr>
<td><strong>Optimization Options</strong></td>
<td></td>
</tr>
<tr>
<td>ABSCONV=</td>
<td>Tunes an absolute function convergence criterion</td>
</tr>
<tr>
<td>ABSFCONV=</td>
<td>Tunes an absolute difference function convergence criterion</td>
</tr>
<tr>
<td>ABSGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>FCONV=</td>
<td>Tunes the relative function convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Chooses the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit (in seconds) of CPU time for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
<tr>
<td><strong>Tolerance Options</strong></td>
<td></td>
</tr>
<tr>
<td>SINGULAR=</td>
<td>Tunes the general singularity criterion</td>
</tr>
</tbody>
</table>

The optimization options are fully described in the section “Optimization Options” on page 42 in Chapter 2, “Shared Concepts.” Other options available in the PROC NLMOD statement are described in the following sections.
You can specify the following options in the PROC NLMOD statement:

**ALPHA=** \( \alpha \)

specifies the level of significance \( \alpha \) that is used in constructing \( 100(1 - \alpha)\% \) confidence intervals. The value must be strictly between 0 and 1; the default value of \( \alpha = 0.05 \) results in 95% intervals. This value is used as the default confidence level for limits that are computed in the “Parameter Estimates” table and is used in the LOWER and UPPER options in the PREDICT statement.

**CORR**

requests the approximate correlation matrix for the parameter estimates.

**COV**

requests the approximate covariance matrix for the parameter estimates.

**DATA=** CAS-libref.data-table

names the input data table to be used by PROC NLMOD. The default is the most recently created data table. CAS-libref specifies the CAS library where the input data table resides, and data-table specifies the name of the input data table.

**DF=n**

specifies the default number of degrees of freedom to use in the calculation of \( p \)-values and confidence limits for additional parameter estimates.

**ECORR**

requests the approximate correlation matrix for all expressions that are specified in ESTIMATE statements.

**ECOV**

requests the approximate covariance matrix for all expressions that are specified in ESTIMATE statements.

**NOITPRINT**

suppresses the display of the “Iteration History” table.

**NOPRINT**

suppresses the generation of ODS output.

**OUT=** CAS-libref.data-table

names the output data table to be created when one or more PREDICT statements are specified. CAS-libref specifies the CAS library where the output data table is to be created, and data-table specifies the name of the output data table. A single OUT= data table is created to contain all predicted values when more than one PREDICT statement is specified. An error message is generated if a PREDICT statement is specified and an OUT= data table is not specified. The variables in the input data table are not included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the ID statement are included.

**SINGULAR=** number

tunes the general singularity criterion that is applied in sweeps and inversions. The default is \( 1E4 \) times the machine epsilon; this product is approximately \( 1E-12 \) on most computers.
BOUNDDS Statement

BOUNDDS constraint <, constraint . . . >;

where constraint represents

< number operator > parameter-list < operator number >

Boundary constraints are specified in a BOUNDS statement. One- or two-sided boundary constraints are allowed. Elements in a list of boundary constraints are separated by commas. For example:

bounds 0 <= a1-a9 x <= 1, -1 <= c2-c5;
bounds b1-b10 y >= 0;

You can specify more than one BOUNDS statement. If you specify more than one lower (or upper) bound for the same parameter, the maximum (or minimum) of these is taken.

If the maximum $l_j$ of all lower bounds is larger than the minimum of all upper bounds $u_j$ for the same parameter $\theta_j$, the boundary constraint is replaced by $\theta_j := l_j := \min(u_j)$, which is defined by the minimum of all upper bounds specified for $\theta_j$.

BY Statement

BY variables ;

You can specify a BY statement in PROC NLMOD to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in SAS Language Reference: Concepts.

DISPLAY Statement

DISPLAY < table-list > < / options > ;

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the table-list as a list of table names, paths, partial pathnames, and regular expressions. The table names that you can specify are listed in the section “ODS Table Names” on page 543. A path is a table name that is prefixed with dot-separated grouping information. For example, a
SelectionSummary table that a procedure produces during a selection routine might have the path Bygroup1.Summary.SelectionSummary. A partial pathname does not include all groups; for example, SelectionSummary and Summary.SelectionSummary are partial pathnames for Bygroup1.Summary.SelectionSummary.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both SelectionSummary and Summary.SelectionSummary select Bygroup1.Summary.SelectionSummary.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is not selected.

You can specify the following options after a slash (/):

**CASESENSITIVE**
performs a case-sensitive comparison of table names in the table-list to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the table-list in quotation marks.

**EXCLUDE**
displays all display tables except those that you specify in the table-list.

**EXCLUDEALL**
suppresses display of all tables. This option takes precedence over the other options.

**TRACE**
displays the display table names, labels, and paths.

---

**DISPLAYOUT Statement**

**DISPLAYOUT** table-spec-list < /options > ;

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The table-spec-list specifies a list of CAS output tables to create. Each entry in the list has either a key=value format or a key format:

- **key=value** specifies key as the ODS table name, path, or partial pathname, and specifies value as the CAS output table name.
- **key** specifies key as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

**INCLUDEALL**
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.
NOREPLACE

does not replace any existing CAS output table of the same name.

REPEATED

replicates all CAS output tables on all nodes.

---

**ESTIMATE Statement**

```
ESTIMATE 'label' expression < options > ;
```

The ESTIMATE statement enables you to compute an additional estimate that is a function of the parameter values. You must provide a quoted string to identify the estimate and then provide a valid SAS expression. Multiple ESTIMATE statements are permitted, and results from all ESTIMATE statements are listed in a common table. PROC NLMOD computes approximate standard errors for the estimates by using the delta method (Billingsley 1986). It uses these standard errors to compute corresponding $t$ statistics, $p$-values, and confidence limits.

The **ECOV** option in the PROC NLMOD statement produces a table that contains the approximate covariance matrix of all the additional estimates that you specify. The **ECORR** option produces the corresponding correlation matrix.

You can specify the following **options**:

- **ALPHA=$\alpha$**
  
specifies the alpha level to be used to compute confidence limits. The default value corresponds to the **ALPHA=** option in the PROC NLMOD statement.

- **DF=$d$**
  
specifies the degrees of freedom to be used to compute $p$-values and confidence limits. The default value corresponds to the **DF=** option in the PROC NLMOD statement.

---

**ID Statement**

```
ID variables ;
```

The ID statement lists one or more variables from the input data table that are transferred to output data tables that PROC NLMOD creates, provided that the output data table contains one or more records per input observation. For example, when you use an **OUT=** option in PROC NLMOD statement to produce prediction statistics, ID variables are added to the output data table.

By default, PROC NLMOD do not include all variables from the input data table in output data tables.

---

**MODEL Statement**

```
MODEL dependent-variable ~ distribution ;
```

The MODEL statement is the mechanism for either using a distribution specification to specify the distribution of the data or using the RESIDUAL distribution to specify a predicted value. You must specify a single
dependent variable from the input data table, a tilde (~), and then a distribution and its parameters. You can specify the following values for distribution:

RESIDUAL($m$) or LS($m$) specifies no particular distribution. Instead the sum of squares of the differences between $m$ and the dependent variable is minimized.

NORMAL($m$, $v$) specifies a normal (Gaussian) distribution that has mean $m$ and variance $v$.

BINARY($p$) specifies a binary (Bernoulli) distribution that has probability $p$.

BINOMIAL($n$, $p$) specifies a binomial distribution that has count $n$ and probability $p$.

GAMMA($a$, $b$) specifies a gamma distribution that has shape $a$ and scale $b$.

NEGBIN($n$, $p$) specifies a negative binomial distribution that has count $n$ and probability $p$.

POISSON($m$) specifies a Poisson distribution that has mean $m$.

GENERAL($ll$) specifies a general log-likelihood function that you construct by using SAS programming statements.

The MODEL statement must follow any SAS programming statements that you specify for computing parameters of the preceding distributions. For information about the built-in log-likelihood functions, see the section “Built-In Log-Likelihood Functions” on page 538.

---

**PARAMETERS Statement**

PARAMETERS < parameter-specification > <,..., parameter-specification> </ options> ;

PARMS < parameter-specification > <,..., parameter-specification> </ options> ;

The purpose of the PARAMETERS statement is to provide starting values for the NLMOD procedure. You can provide values that define a single point in the parameter space or that define a set of points. For more information about the parameter-specification, see the section “Assigning Starting Values by Using a Parameter Specification” on page 532.

You can specify the following options after a slash (/):

BEST=$i > 0$

specifies the maximum number of parameter grid points and the corresponding objective function values to display in the “Parameters” table. If you specify this option, the parameter grid points are listed in ascending order of objective function value. By default, all parameter grid points are displayed.

PDATA=CASE-libref.data-table

DATA=CASE-libref.data-table

specifies the data table that provides parameter starting values. CASE-libref specifies the CAS library where the input data table resides, and data-table specifies the name of the input data table.

START=value

DEFSTART=value

specifies a default starting value for all parameters.

Four methods are available for providing starting values to the optimization process. In order of precedence, the methods are as follows:

1. Specify values directly in the PARAMETERS statement.
Chapter 9: The NLMOD Procedure

2. Specify values in the PDATA= data table option.

3. Specify a single value for all parameters by using the START= option.

4. Use the default value 1.0.

The names that you assign to parameters must be valid SAS names and must not be the same as names of variables in the input data table (see the DATA= option in the PROC NLMOD statement). Parameters that are assigned starting values through the PARAMETERS statement can be omitted from the estimation if the expression in the MODEL statement does not depend on them.

Assigning Starting Values by Using a Parameter Specification

A parameter-specification has the following general form, where name identifies the parameter and value-list provides the set of starting values for the parameter:

\[ \text{name} = \text{value-list} \]

Often the value-list contains only a single value, but you can use more general and flexible list specifications such as these:

- \( m \) a single value
- \( m_1, m_2, \ldots, m_n \) several values
- \( m \) TO \( n \) a sequence in which \( m \) equals the starting value, \( n \) equals the ending value, and the increment is 1
- \( m \) TO \( n \) BY \( i \) a sequence in which \( m \) equals the starting value, \( n \) equals the ending value, and the increment is \( i \)
- \( m_1, m_2 \) TO \( m_3 \) mixed values and sequences

When you specify more than one value for a parameter, PROC NLMOD sorts the values in ascending order and removes duplicate values from the parameter list before forming the grid for the parameter search. If you specify several values for each parameter, PROC NLMOD evaluates the model at each point on the grid. The iterations then commence from the point on the grid that yields the smallest objective function value.

For example, the following PARMS statement specifies five parameters and sets their possible starting values as shown in the table:

\[
\text{parms} \quad b0 = 0 \\
\quad b1 = 4 \text{ to } 8 \\
\quad b2 = 0 \text{ to } .6 \text{ by } .2 \\
\quad b3 = 1, 10, 100 \\
\quad b4 = 0, .5, 1 \text{ to } 4;
\]

<table>
<thead>
<tr>
<th>Possible Starting Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>B0</td>
</tr>
<tr>
<td>0</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
</tbody>
</table>
The objective function values are calculated for each of the $1 \times 5 \times 4 \times 3 \times 6 = 360$ combinations of possible starting values.

If you specify a starting value by using a *parameter-specification*, any starting values that are provided for this parameter through the PDATA= data table are ignored. The *parameter-specification* overrides the information in the PDATA= data table.

### Assigning Starting Values from a Data Table That Resides in a CAS Library

The PDATA= option in the PARAMETERS statement enables you to assign starting values for parameters by using a data table. You must specify the CAS library where your data table resides and the data table name. The data table must contain at least two variables: a character variable named Parameter (or Parm) that identifies the parameter, and a numeric variable named Estimate (or Est) that contains the starting values. For example, the PDATA= option enables you to use the contents of the “ParameterEstimates” table from one PROC NLMOD run to supply starting values for a subsequent run, as follows:

```plaintext
proc nlmod data=mycas.D(obs=30);
  parameters alpha=100 beta=3 gamma=4;
  Switch = 1/(1+gamma*exp(beta*log(dose))));
  model y ~ residual(alpha*Switch);
  displayout ParameterEstimates=pest;
run;

proc nlmod data=mycas.D;
  parameters / pdata=mycas.pest;
  Switch = 1/(1+gamma*exp(beta*log(dose))));
  model y ~ residual(alpha*Switch);
run;
```

You can specify multiple values for a parameter in the PDATA= data table, and the parameters can appear in any order. The starting values are collected by parameter and arranged in ascending order, and duplicate values are removed. The parameter names in the PDATA= data table are not case-sensitive. For example, the following DATA step defines starting values for three parameters and a starting grid that has $1 \times 3 \times 1 = 3$ points:

```plaintext
data mycas.Test;
  input Parameter $ Estimate;
datalines;
  alpha 100
  BETA 4
  beta 4.1
  beta 4.2
  beta 4.1
  gamma 30
;
```
The PREDICT statement enables you to construct predictions of an expression across all the observations in the input data table. Multiple PREDICT statements are permitted. Results for all PREDICT statements are displayed in the output data table that you specify in the OUT= option in the PROC NLMOD statement. The variables in the input data table are not included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the ID statement are included.

You must specify the following arguments:

'label'
identifies the predicted expression.

expression | MEAN
provides the predicted value. You can specify the predicted value either by using a SAS programming expression that contains the input data table variables and parameters or by using the keyword MEAN. If you specify the keyword MEAN, the predicted mean value for the distribution specified in the MODEL statement is used. Predicted values are computed using the final parameter estimates. Standard errors of prediction are computed using the delta method (Billingsley 1986; Cox 1998).

You can also specify the following options:

ALPHA= \( \alpha \)
specifies the alpha level to be used to compute confidence limits. The default value corresponds to the ALPHA= option in the PROC NLMOD statement.

DF= \( d \)
specifies the degrees of freedom to be used to compute confidence limits. The default value corresponds to the DF= option in the PROC NLMOD statement.

LOWER= name
specifies a variable that contains the lower confidence limit of the predicted value.

PRED= name
specifies a variable that contains the predicted value.

PROBT= name
specifies a variable that contains the \( p \)-value of the predicted value.

STDERR= name
specifies a variable that contains the standard error of the predicted value.

TVALUE= name
specifies a variable that contains the \( t \) statistic for the predicted value.

UPPER= name
specifies a variable that contains the upper confidence limit of the predicted value.
RESTRICT Statement

RESTRICT  restriction1 <, restriction2 . . . > ;

The RESTRICT statement imposes linear restrictions on the model’s parameters estimates. You can specify any number of RESTRICT statements.

Each restriction is written as an expression, optionally followed by an equality operator (=) or an inequality operator (<, >, <=, >=), followed by a second expression:

expression < operator expression>

The operator can be =, <, >, <=, or >=. The operator and second expression are optional. When they are omitted, the operator defaults to = and the second expression defaults to the value 0.

Restriction expressions can be composed of parameter names, arithmetic operators, functions, and constants. You cannot use comparison operators (such as = or <) or logical operators (such as & ) in RESTRICT statement expressions. Parameters that are named in restriction expressions must be among the parameters that are estimated by the model. Restriction expressions cannot refer to other variables that are defined in the program or in the DATA= data table. The restriction expressions must be linear functions of the parameters.

The following example illustrates how to use the RESTRICT statement to impose a linear constraint on parameters:

proc nlmod;
   parms alpha beta;
   f = (x/alpha + beta)**2
   model y ~ residual(f);
   restrict beta < 2*(alpha + constant('pi'));
run;

The preceding RESTRICT statement represents the following model constraint:

\[ \beta < 2(\alpha + \pi) \]

Programming Statements

Programming statements define the arguments of the MODEL, ESTIMATE, and PREDICT statements in PROC NLMOD. Most of the programming statements that you can use in the SAS DATA step can also be used in the NLMOD procedure. For a description of SAS programming statements, see SAS Language Reference: Concepts. You can use the following programming statements:
ABORT;
CALL name[ ( expression [, expression ... ] ) ];
DELETE;
DO[variable = expression
    [TO expression] [BY expression]
    [ , expression [ TO expression] [ BY expression ] ... ]
] [WHILE expression] [UNTIL expression];
END;
GOTO statement_label;
IF expression;
IF expression THEN program_statement;
   ELSE program_statement;
   variable = expression;
   variable + expression;
LINK statement_label;
PUT [variable] [=] [...];
RETURN;
SELECT[(expression)];
STOP;
SUBSTR( variable, index, length )= expression;
WHEN (expression) program_statement;
   OTHERWISE program_statement;

For the most part, these SAS programming statements work the same as they do in the SAS DATA step, as documented in SAS Language Reference: Concepts. However, they differ as follows:

- The ABORT statement does not allow any arguments.
- The DO statement does not allow a character index variable. Thus, PROC NLMOD supports the first of the following statements, but not the second:
  
  do i = 1,2,3;
  do i = 'A','B','C';

- In contrast to other procedures that share PROC NLMOD’s programming syntax, PROC NLMOD does not support the LAG function. Because observations are not processed sequentially when high-performance analytical procedures perform the parameter optimization, information for computing lagged values is not available.
- The PUT statement, used mostly for program debugging in PROC NLMOD, supports only some of the features of the DATA step PUT statement, and it has some new features that the DATA step PUT statement does not have:
  - The PROC NLMOD PUT statement does not support line pointers, factored lists, iteration factors, overprinting, _INFILE_, the colon (:) format modifier, or “$”.
  - The PROC NLMOD PUT statement supports expressions, but the expression must be enclosed in parentheses. For example, the following statement displays the square root of x:
put (sqrt(x));

- The PROC NLMOD PUT statement supports the item _PDV_, which displays a formatted listing of all variables in the program. For example, the following statement displays a much more readable listing of the variables than the _ALL_ print item:

    put _pdv_;

- The WHEN and OTHERWISE statements enable you to specify more than one programming statement. That is, DO/END groups are not necessary for multiple WHEN statements. For example, the following syntax is valid:

    select;
    when (exp1) stmt1;
    stmt2;
    when (exp2) stmt3;
    stmt4;
    end;

When you write your programming statements, avoid defining variables that begin with an underscore (_), because they might conflict with internal variables that PROC NLMOD creates. The MODEL statement must follow any SAS programming statements that define or modify terms that are used to specify the model.

---

**Details: NLMOD Procedure**

**Least Squares Estimation**

Models that are estimated by PROC NLMOD can be represented by using the equations

\[
Y = f(\beta; z_1, \ldots, z_k) + \epsilon
\]

\[
E[\epsilon] = 0
\]

\[
\text{Var}[\epsilon] = \sigma^2 I
\]

where

- \(Y\) is the \((n \times 1)\) vector of observed responses.
- \(f\) is the nonlinear prediction function of parameters and regressor variables.
- \(\beta\) is the vector of model parameters to be estimated.
- \(z_1, \ldots, z_k\) are the \((n \times 1)\) vectors of each of the \(k\) regressor variables.
Chapter 9: The NLMOD Procedure

\( \epsilon \) is the \((n \times 1)\) vector of residuals.

\( \sigma^2 \) is the variance of the residuals.

In these models, the distribution of the residuals is not specified and the model parameters are estimated using the least squares method. For the standard errors and confidence limits in the “ParameterEstimates” table to apply, the errors are assumed to be homoscedastic and uncorrelated and to have zero mean.

### Built-In Log-Likelihood Functions

For models in which the distribution of model errors is specified, the NLMOD procedure estimates parameters by maximizing the value of a log-likelihood function for the specified distribution. The log-likelihood functions that PROC NLMOD uses for the supported error distributions are as follows:

\( Y \sim \text{normal}(m, v) \)

\[
l(m, v; y) = -\frac{1}{2} \left( \log(2\pi) + \frac{(y-m)^2}{v} + \log(v) \right)
\]

\( E[Y] = m \)

\( \text{Var}[Y] = v \)

\( v > 0 \)

\( Y \sim \text{binary}(p) \)

\[
l_1(p; y) = \begin{cases} y \log(p) & y > 0 \\ 0 & \text{otherwise} \end{cases}
\]

\[
l_2(p; y) = \begin{cases} (1 - y) \log(1 - p) & y < 1 \\ 0 & \text{otherwise} \end{cases}
\]

\( l(p; y) = l_1(p; y) + l_2(p; y) \)

\( E[Y] = p \)

\( \text{Var}[Y] = p(1 - p) \)

\( 0 < p < 1 \)

\( Y \sim \text{binomial}(n, p) \)

\[
l_c = \log\{\Gamma(n + 1)\} - \log\{\Gamma(y + 1)\} - \log\{\Gamma(n - y + 1)\}
\]

\[
l_1(n, p; y) = \begin{cases} y \log(p) & y > 0 \\ 0 & \text{otherwise} \end{cases}
\]

\[
l_2(n, p; y) = \begin{cases} (n - y) \log(1 - p) & n - y > 0 \\ 0 & \text{otherwise} \end{cases}
\]

\( l(n, p; y) = l_c + l_1(n, p; y) + l_2(n, p; y) \)

\( E[Y] = np \)

\( \text{Var}[Y] = np(1 - p) \)

\( 0 < p < 1 \)
The natural text is:

$Y \sim \text{gamma}(a, b)$

\[
l(a, b; y) = -a \log \{b\} - \log \{\Gamma(a)\} + (a - 1) \log \{y\} - y/b
\]

\[
E[Y] = ab
\]

\[
\text{Var}[Y] = ab^2
\]

\[
a > 0
\]

\[
b > 0
\]

This parameterization of the gamma distribution differs from the parameterization that the GENSELECT procedure uses. The scale parameter in PROC NLMOD is expressed as the inverse of the scale parameter that PROC GENSELECT uses. The PROC NLMOD parameter represents the scale of the magnitude of the residuals. You can estimate the scale parameter in PROC GENSELECT by using the following statements:

```plaintext
proc genselect;
    model y = x / dist=gamma s;
run;
```

PROC NLMOD uses the following statements to estimate the equivalent scale parameter:

```plaintext
proc nlmod;
    parms b0=1 b1=0 scale=14;
    linp = b0 + b1*x;
    mu = exp(linp);
    b = mu*scale;
    model y ~ gamma(1/scale,b);
run;
```

$Y \sim \text{negbin}(n, p)$

\[
l(n, p; y) = \log \{\Gamma(n + y)\} - \log \{\Gamma(n)\} - \log \{\Gamma(y + 1)\}
\]

\[
+ n \log \{p\} + y \log \{1 - p\}
\]

\[
E[Y] = n \left( \frac{1 - p}{p} \right)
\]

\[
\text{Var}[Y] = n \left( \frac{1 - p}{p^2} \right)
\]

\[
n \geq 0
\]

\[
0 < p < 1
\]

The value of parameter $n$ can be a real number; it does not have to be an integer.

$Y \sim \text{Poisson}(m)$

\[
l(m; y) = y \log \{m\} - m - \log \{\Gamma(y + 1)\}
\]

\[
E[Y] = m
\]

\[
\text{Var}[Y] = m
\]

\[
m > 0
\]
Multithreading

The NLMOD procedure allocates data to different threads and calculates the likelihood function, gradient, and Hessian by accumulating the values from all threads. For more information about how PROC NLMOD uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

Optimization Algorithms

Several optimization techniques are available in PROC NLMOD. You can choose a particular optimizer by using the TECHNIQUE= option in the PROC NLMOD statement. Table 9.3 summarizes the optimization techniques available in PROC NLMOD.

<table>
<thead>
<tr>
<th>TECHNIQUE=</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>Trust region method</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>Newton-Raphson method with line search</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>Newton-Raphson method with ridging</td>
</tr>
<tr>
<td>QUANEW</td>
<td>Quasi-Newton methods</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>Double-dogleg method</td>
</tr>
<tr>
<td>CONGRA</td>
<td>Conjugate gradient methods</td>
</tr>
<tr>
<td>LEVMAR</td>
<td>Levenberg-Marquardt method</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>Nelder-Mead simplex method</td>
</tr>
</tbody>
</table>

There is no algorithm for optimizing general nonlinear functions that always finds the global optimum for a general nonlinear optimization problem in a reasonable amount of time. Because no single optimization technique is always superior to others, PROC NLMOD provides a variety of optimization techniques that work well in various circumstances. However, you can devise problems for which none of the techniques in PROC NLMOD can find the correct solution. Moreover, nonlinear optimization can be computationally expensive in terms of time and memory, so you must be careful when matching an algorithm to a problem. The section “Choosing an Optimization Algorithm” on page 80 in Chapter 2, “Shared Concepts,” is helpful in choosing a suitable optimization algorithm.

Displayed Output

The following sections describe the output that PROC NLMOD produces by default. The output is organized into various tables, which are discussed in their order of appearance.

Specifications

The “Specifications” table displays basic information about the model, such as the data source, the dependent variable, the distribution being modeled, and the optimization technique.
Number of Observations

The “Number of Observations” table displays the number of observations that are read from the input data table and the number of observations that are used in the analysis.

Dimensions

The “Dimensions” table displays the number of parameters that are estimated in the model and the number of upper and lower bounds that are imposed on the parameters.

Parameters

The “Parameters” table displays the initial values of parameters that are used to start the estimation process. You can limit this information by specifying the BEST= option in the PARAMETERS statement when you specify a large number of initial parameter value combinations. The parameter combinations and their corresponding objective function values are listed in increasing order of objective function value.

Iteration History

For each iteration of the optimization, the “Iteration History” table displays the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element.

Convergence Status

The convergence status table is a small ODS table that appears as a message that indicates whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message indicates the reason for the failure. If you save the convergence status table to an output data set, a numeric Status variable is added that enables you to programmatically assess convergence. The values of the Status variable indicate the following:

0  Convergence was achieved or an optimization was not performed because TECHNIQUE=NONE.
1  The objective function could not be improved.
2  Convergence was not achieved because of a user interruption or because a limit (such as the maximum number of iterations or the maximum number of function evaluations) was reached. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC NLMOD statement.
3  Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

Linear Constraints

The “Linear Constraints” table summarizes the linear constraints that are applied to the model by using the RESTRICT statements. The table lists all the constraints that are specified in the model, along with information about whether each constraint represents an inequality or equality condition and whether that constraint is active for the final parameter estimates.
Fit Statistics

The “Fit Statistics” table displays a variety of measures of fit, depending on whether the model was estimated using least squares or maximum likelihood. In both cases, smaller values of the fit statistics indicate better fit.

For least squares estimations, the table displays the sum of squares of errors and the variance of errors.

For maximum likelihood estimations, the table uses the following formulas to display information criteria, where \( p \) denotes the number of effective parameters, \( n \) denotes the number of observations used, and \( l \) is the log likelihood that is evaluated at the converged estimates:

\[
\text{AIC} = -2l + 2p \\
\text{AICC} = \begin{cases} 
-2l + 2pn/(n - p - 1) & n > p + 2 \\
-2l + 2p(p + 2) & \text{otherwise}
\end{cases} \\
\text{BIC} = -2l + p \log(n)
\]

The information criteria values that are displayed in the “Fit Statistics” table are not based on a normalized log-likelihood function.

ANOVA

The “Analysis of Variance” (ANOVA) table is displayed only for least squares estimations. It displays the number of degrees of freedom and the sum of squares that are attributed to the model, the error, and the total.

The ANOVA table also reports the variance of the model and the errors, the \( F \) statistic, and its probability for the model.

Parameter Estimates

The “Parameter Estimates” table displays the parameter estimates, their estimated (asymptotic) standard errors \( t \) statistics, and associated \( p \)-values for the hypothesis that the parameter is 0. Confidence limits, which are displayed for each parameter, are based on the value of the \text{ALPHA=} \text{option that you specify in the } \text{PROC NLMOD statement.}

Additional Estimates

The “Additional Estimates” table displays the same information as the “Parameter Estimates” table for the expressions that appear in the optional ESTIMATE statements. The table is generated when you specify one or more ESTIMATE statements. Because you can specify a separate \text{ALPHA=} \text{option for each } \text{ESTIMATE statement, the “Additional Estimates” table also includes a column that indicates each confidence interval’s corresponding significance level.}

Covariance

The “Covariance” table appears when you specify the \text{COV option in the } \text{PROC NLMOD statement. It displays a matrix of covariances between each pair of estimated parameters.}

Correlation

The “Correlation” table appears when you specify the \text{CORR option in the } \text{PROC NLMOD statement. It displays the correlation matrix for the estimated parameters.}
Additional Estimates Covariance

The “Covariance of Additional Estimates” table appears when you specify the ECOV option in the PROC NLMOD statement. It displays a matrix of covariances between each pair of expressions that are specified in ESTIMATE statements.

Additional Estimates Correlation

The “Correlation of Additional Estimates” table appears when you specify the ECORR option in the PROC NLMOD statement. It displays the correlation matrix for the expressions that are specified in ESTIMATE statements.

Procedure Task Timing

The “Timing” table displays the amount of time (in seconds) that PROC NLMOD required to perform different tasks in the analysis.

ODS Table Names

Each table that the NLMOD procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement, the DISPLAYOUT statement, or ODS statements. These names are listed in Table 9.4.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>AdditionalEstimates</td>
<td>Functions of estimated parameters and their associated statistics</td>
<td>ESTIMATE</td>
<td>Default</td>
</tr>
<tr>
<td>ANOVA</td>
<td>Least squares analysis of variance information</td>
<td>MODEL</td>
<td>RESIDUAL</td>
</tr>
<tr>
<td>Constraints</td>
<td>Information about the model’s linear constraints</td>
<td>RESTRICT</td>
<td>Default</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Optimization success and convergence information</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>CorrB</td>
<td>Parameter correlation matrix</td>
<td>PROC NLMOD</td>
<td>CORR</td>
</tr>
<tr>
<td>CovB</td>
<td>Parameter covariance matrix</td>
<td>PROC NLMOD</td>
<td>COV</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Number of parameters and their bounds</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>ECorrB</td>
<td>Additional estimates’ correlation matrix</td>
<td>PROC NLMOD</td>
<td>ECORR</td>
</tr>
<tr>
<td>ECovB</td>
<td>Additional estimates’ covariance matrix</td>
<td>PROC NLMOD</td>
<td>ECOV</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Statistics about the quality of the fit</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>Table Name</td>
<td>Description</td>
<td>Statement</td>
<td>Option</td>
</tr>
<tr>
<td>------------------</td>
<td>-----------------------------------------------------------------------------</td>
<td>------------------</td>
<td>------------</td>
</tr>
<tr>
<td>IterHistory</td>
<td>Optimizer iteration information</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Library and name of the output data tables, and number of rows and columns in the table</td>
<td>PROC NLMOD OUT=</td>
<td>DISPLAYOUT</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Parameter estimates and associated statistics</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>Parameters</td>
<td>Initial parameter values</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>Specifications</td>
<td>Basic model characteristics</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times for tasks performed by the procedure</td>
<td>PROC NLMOD</td>
<td>Default</td>
</tr>
</tbody>
</table>

### Examples: NLMOD Procedure

#### Example 9.1: Segmented Model

Suppose you are interested in fitting a model that consists of two segments that connect in a smooth fashion. For example, the following model states that the mean of $Y$ is a quadratic function in $x$ for values of $x$ less than $x_0$ and that the mean of $Y$ is constant for values of $x$ greater than $x_0$:

$$E[Y|x] = \begin{cases} 
\alpha + \beta x + \gamma x^2 & \text{if } x < x_0 \\
c & \text{if } x \geq x_0 
\end{cases}$$

In this model equation, $\alpha$, $\beta$, and $\gamma$ are the coefficients of the quadratic segment, and $c$ is the plateau of the mean function. The NLMOD procedure can fit such a segmented model even when the join point, $x_0$, is unknown.

Suppose you also want to impose conditions on the two segments of the model. First, the curve should be continuous—that is, the quadratic and the plateau section need to meet at $x_0$. Second, the curve should be smooth—that is, the first derivative of the two segments with respect to $x$ needs to coincide at $x_0$.

The continuity condition requires that

$$c = E[Y|x_0] = \alpha + \beta x_0 + \gamma x_0^2$$

The smoothness condition requires that

$$\frac{\partial E[Y|x_0]}{\partial x} = \beta + 2\gamma x_0 = 0$$
If you solve for $x_0$ and substitute your result in the expression for $c$, the two conditions jointly imply that

$$x_0 = -\beta/2\gamma$$
$$c = \alpha - \beta^2/4\gamma$$

Although there are five unknowns, the model contains only three independent parameters. Together the continuity and smoothness restrictions completely determine two parameters, given the other three.

The following DATA step creates the data table for this example in your CAS session:

```plaintext
data mycas.A;
  input y x @@;
  datalines;
.46 1 .47 2 .57 3 .61 4 .62 5 .68 6 .69 7
.78 8 .70 9 .74 10 .77 11 .78 12 .74 13 .80 13
.80 15 .78 16
;
```

The following PROC NLMOD statements fit this segmented model:

```plaintext
proc nlmmod data=mycas.A out=mycas.B;
  parms alpha=.45 beta=.05 gamma=-.0025;
  x0 = -.5*beta / gamma;
  if (x < x0) then
    yp = alpha + beta*x + gamma*x*x;
  else
    yp = alpha + beta*x0 + gamma*x0*x0;
  model y ~ residual(yp);
  estimate 'join point' -beta/2/gamma;
  estimate 'plateau value c' alpha - beta**2/(4*gamma);
  predict 'predicted' yp pred=yp;
  predict 'response' y pred=y;
  predict 'x' x pred=x;
run;
```

The parameters of the model are $\alpha$, $\beta$, and $\gamma$, which are represented in the PROC NLMOD statements by the variables alpha, beta, and gamma, respectively. To model the two segments, a conditional statement assigns the appropriate expression to the mean function, depending on the value of $x_0$. The ESTIMATE statements compute the values of $x_0$ and $c$. The PREDICT statement computes predicted values for plotting and saves them to data table b.

The results from fitting this model are shown in Output 9.1.1 through Output 9.1.3. The iterative optimization converges after six iterations (Output 9.1.1). Output 9.1.2 shows the estimated parameters. Output 9.1.3 indicates that the joint point is 12.7477 and the plateau value is 0.7775.
### Output 9.1.1 Nonlinear Least Squares Iterative Phase

**Quadratic Model with Plateau**

The **NLMOD** Procedure

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Evaluations</th>
<th>Objective Function</th>
<th>Change</th>
<th>Max Gradient</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>5</td>
<td>0.0035144531</td>
<td>7.184063</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>0.0007352716</td>
<td>0.00277918</td>
<td>2.145337</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>0.0006292751</td>
<td>0.00010600</td>
<td>0.032551</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>0.0006291261</td>
<td>0.000000015</td>
<td>0.002952</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>0.0006291244</td>
<td>0.000000000</td>
<td>0.000238</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>0.0006291244</td>
<td>0.000000000</td>
<td>0.000023</td>
</tr>
<tr>
<td>6</td>
<td>2</td>
<td>0.0006291244</td>
<td>0.000000000</td>
<td>2.313E-6</td>
</tr>
</tbody>
</table>

Convergence criterion (GCONV=1E-8) satisfied.

### Output 9.1.2 Least Squares Analysis of the Quadratic Model

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Approx Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>2</td>
<td>0.1769</td>
<td>0.0884</td>
<td>114.22</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>13</td>
<td>0.0101</td>
<td>0.000774</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>15</td>
<td>0.1869</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

### Output 9.1.3 Additional Estimates for the Quadratic Model

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>DF</th>
<th>t Value</th>
<th>Approx Pr &gt;</th>
<th>Approximate 95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>alpha</td>
<td>0.3921</td>
<td>0.0267</td>
<td>13</td>
<td>14.70</td>
<td>&lt;.0001</td>
<td>0.3345 0.4497</td>
</tr>
<tr>
<td>beta</td>
<td>0.0605</td>
<td>0.00842</td>
<td>13</td>
<td>7.18</td>
<td>&lt;.0001</td>
<td>0.0423 0.0787</td>
</tr>
<tr>
<td>gamma</td>
<td>-0.00237</td>
<td>0.000551</td>
<td>13</td>
<td>-4.30</td>
<td>0.0009</td>
<td>-0.00356 -0.00118</td>
</tr>
</tbody>
</table>

The following statements produce a graph, shown in **Output 9.1.4**, of the observed and predicted values along with reference lines for the join point and plateau estimates:
data B;
   set mycas.B;
run;

proc sort data = B;
   by x;
run;

proc sgplot data=B noautolegend;
   yaxis label='Observed or Predicted';
   reline 0.7775 / axis=y label='Plateau' labelpos=min;
   reline 12.7477 / axis=x label='Join point' labelpos=min;
   scatter y=y x=x;
   series y=yp x=x;
run;

**Output 9.1.4** Observed and Predicted Values for the Quadratic Model
References


Chapter 10
The PCA Procedure

Contents
Overview: PCA Procedure .................................................. 550
PROC PCA Features ......................................................... 550
PROC PCA Compared with Other SAS Procedures ....................... 551
PROC PCA Compared with the HPRINCOMP Procedure ............... 551
PROC PCA Compared with the PRINCOMP Procedure ............... 552
Using CAS Sessions and CAS Engine Librefs ......................... 553
Getting Started: PCA Procedure ........................................ 554
Syntax: PCA Procedure ...................................................... 558
PROC PCA Statement ....................................................... 558
BY Statement ............................................................... 563
CODE Statement .......................................................... 563
DISPLAY Statement ....................................................... 564
DISPLAYOUT Statement .................................................. 565
FREQ Statement ............................................................ 566
OUTPUT Statement ........................................................ 566
PARTIAL Statement ......................................................... 568
VAR Statement ............................................................. 568
WEIGHT Statement ........................................................ 568
Details: PCA Procedure ..................................................... 568
Computing Principal Components ....................................... 568
   Eigenvalue Decomposition .......................................... 569
   NIPALS ................................................................. 570
   ITERGS ............................................................... 570
   RANDOM ............................................................. 570
Missing Values ............................................................. 571
OUTSTAT= Data Table ..................................................... 571
Displayed Output .......................................................... 573
   Model Information .................................................. 573
   Number of Variables ............................................... 573
   Number of Observations .......................................... 573
   Simple Statistics ................................................... 573
   Centering and Scaling Information ............................... 573
   Explained Variation of Variables ................................. 574
   Correlation Matrix .................................................. 574
   Regression Statistics .............................................. 574
   Regression Coefficients .......................................... 574
Overview: PCA Procedure

The PCA procedure performs principal component analysis in SAS Viya.

Principal component analysis is a multivariate technique for examining relationships among several quantitative variables. It provides an optimal way to reduce dimensionality by projecting the data onto a lower-dimensional orthogonal subspace that explains as much variation as possible in those variables. The choice between using factor analysis and using principal component analysis depends in part on your research objectives. You should use the PCA procedure if you are interested in summarizing data and detecting linear relationships. You can use principal component analysis to reduce the number of variables in regression, clustering, and so on.

PROC PCA Features

The PCA procedure does the following:

- provides a PARTIAL statement for analyzing a partial correlation or covariance matrix
- provides a FREQ statement for grouped analysis
- provides a WEIGHT statement for weighted analysis
- provides a CODE statement for scoring new data
- produces an output data table that contains principal component scores and other observationwise statistics
- produces an output data table that contains means, standard deviations, number of observations, correlations or covariances, eigenvalues, and eigenvectors
- produces a scree plot of eigenvalues and proportion variance explained and a pattern profile plot
The PCA procedure implements the following methods:

- eigenvalue decomposition, which uses the correlation or covariance of the data matrix and calculates all the principal components simultaneously
- the nonlinear iterative partial least squares (NIPALS) method, which uses the data matrix and extracts the principal components successively
- the iterative method based on the Gram-Schmidt orthogonalization (ITERGS) of Andrecut (2009), which uses the data matrix and extracts the principal components successively. The algorithm applies reorthogonalization correction to both the scores and the loadings at each iteration step.
- the iterative method based on random projection (RANDOM) of Halko, Martinsson, and Tropp (2011), which uses the data matrix and extracts all requested principal components simultaneously. Because of the nature of the algorithm, the principal components are an approximation of the actual principal components.

Because the PCA procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on CAS
- exploits all the available cores and concurrent threads. For information about how PROC PCA uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”
Table 10.1 Comparison of PROC PCA and PROC HPPRINCOMP

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PCA</th>
<th>PROC HPPRINCOMP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supports various methods to extract principal components by using the METHOD= option in the PROC statement</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports BY statement</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports DISPLAY and DISPLAYOUT statements</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports CODE and OUTPUT statements</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports ID statement</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports PLOTS= option</td>
<td>Yes, with limited number of options</td>
<td>No</td>
</tr>
<tr>
<td>Includes input variables in output data table</td>
<td>Not by default, in order to avoid data duplication for large data tables. To include input variables, specify them in the COPYVARS= option in the OUTPUT statement.</td>
<td>Not by default, in order to avoid data duplication for large data sets. To include input variables, specify them in the ID statement.</td>
</tr>
<tr>
<td>Threading</td>
<td>Specifically designed for CAS; executes on multiple threads</td>
<td>Primarily designed for a distributed environment; executes on multiple threads</td>
</tr>
</tbody>
</table>

PROC PCA Compared with the PRINCOMP Procedure

The PCA procedure and the PRINCOMP procedure have the similarities and differences shown in Table 10.2.

Table 10.2 Comparison of PROC PCA and PROC PRINCOMP

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PCA</th>
<th>PROC PRINCOMP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supports various methods to extract principal components by using the METHOD= option in the PROC statement</td>
<td>Yes</td>
<td>No, supports only eigenvalue decomposition</td>
</tr>
<tr>
<td>Supports BY statement</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports DISPLAY and DISPLAYOUT statements</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports CODE and OUTPUT statements</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports ID statement</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports PLOTS= option</td>
<td>Limited number of options</td>
<td>Full set of options</td>
</tr>
</tbody>
</table>
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
runc;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

### Table 10.2 continued

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PCA</th>
<th>PROC PRINCOMP</th>
</tr>
</thead>
<tbody>
<tr>
<td>Accepts input data</td>
<td>Only CAS input data tables</td>
<td>Ordinary SAS data sets and certain types of special SAS data sets</td>
</tr>
<tr>
<td>Includes input variables in output data table</td>
<td>Not by default, in order to avoid data duplication for large data tables. To include input variables, specify them in the COPYVARS= option in the OUTPUT statement.</td>
<td>Yes</td>
</tr>
<tr>
<td>Threading</td>
<td>Specifically designed for CAS; executes on multiple threads</td>
<td>Executes on a single thread</td>
</tr>
</tbody>
</table>

---

**Using CAS Sessions and CAS Engine Librefs**

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
runc;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
## Getting Started: PCA Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following DATA step creates the Crime data table, which provides crime rates per 100,000 people in seven categories for each of the 50 US states in 1977, in your CAS session:

```sas
data mycas.Crime;
  title 'Crime Rates per 100,000 Population by State';
  input State $1-15 Murder Rape Robbery Assault
      Burglary Larceny Auto_Theft;
  datalines;
Alabama  14.2  25.2  96.8 278.3 1135.5 1881.9  280.7
Alaska   10.8  51.6  96.8 284.0 1331.7  3369.8  753.3
Arizona  9.5  34.2 138.2 312.8 2346.1  4467.4  439.5
Arkansas  8.8  27.6  83.2 297.0 1935.2  3903.2  477.1
California 11.5  49.4 287.0 358.0 2139.4  3499.8  663.5
Colorado  6.3  42.0 170.7 292.9 1935.2  3903.2  477.1
Connecticut  4.2 16.8 129.5 184.2 1331.7  2620.7  593.2
Delaware  10.2  39.6 187.9 449.1 1859.9  3840.5  351.4
Florida   11.7  31.1 140.5 256.5 1351.1  2170.2  297.9
Georgia   7.2  25.5 128.0 64.1 1911.5  3920.4  489.4
Idaho     5.5  19.4  39.6 172.5 1050.8  2599.6  237.6
Illinois  9.9  21.8 211.3 209.0 1085.0  2828.5  528.6
Indiana   7.4  26.5 123.2 153.5 1086.2  2498.7  374.4
Iowa      2.3  10.6  41.2  89.8  812.5  2685.1  219.9
Kansas    6.6  22.0 100.7 180.5 1270.4  2739.3  244.3
Kentucky  10.1  19.1  81.1 123.3  872.2  1662.1  245.4
Louisiana 15.5  30.9 142.9 335.5 1165.5  2469.9  337.7
Maine     2.4  13.5  38.7 170.0 1253.1  2350.7  246.9
Maryland  8.0  34.8 292.1 358.9 1400.0  3177.7  428.5
Massachusetts 3.1  20.8 169.1 231.6 1532.2  2311.3 1140.1
Michigan  9.3  38.9 261.9 274.6 1522.7  3159.0  545.5
Minnesota 2.7  19.5  85.9 1134.7 2559.3  343.1
Mississippi 14.3  19.6  65.7 189.1  915.6  1239.9 144.4
Missouri  9.6  28.3 189.0 233.5 1318.3  2424.2  378.4
Montana   5.4  16.7  39.2 156.8  804.9  2773.2  309.2
Nebraska  3.9  18.1  64.7 112.7  760.0  2316.1  249.1
Nevada    15.8  49.1 323.1 355.0 2453.1  4212.6  559.2
New Hampshire 3.2  10.7  23.2  76.0 1041.7  2343.9  293.4
New Jersey  5.6  21.0 180.4 185.1 1435.8  2774.5  511.5
New Mexico  8.8  39.1 109.6 343.4 1418.7  3008.6  259.5
New York   10.7  29.4 472.6 319.1 1728.0  2782.0  745.8
North Carolina 10.6  17.0 61.3 318.3 1154.1  2037.8  192.1
North Dakota  0.9  9.0  13.3  43.8  446.1  1843.0  144.7
Ohio      7.8  27.3 190.5 181.1 1216.0  2696.8  400.4
Oklahoma  8.6  29.2  73.8 205.0 1288.2  2228.1  326.8
Oregon    4.9  39.9 124.1 286.9 1636.4  3506.1  388.9
```


### Pennsylvania
- 5.6 19.0 130.3 128.0 877.5 1624.1 333.2
### Rhode Island
- 3.6 10.5 86.5 201.0 1489.5 2844.1 791.4
### South Carolina
- 11.9 33.0 105.9 485.3 1613.6 2342.4 245.1
### South Dakota
- 2.0 13.5 17.9 155.7 570.5 1704.4 147.5
### Tennessee
- 10.1 29.7 145.8 1259.7 1776.5 314.0
### Texas
- 13.3 33.8 152.4 208.2 1603.1 2988.7 397.6
### Utah
- 3.5 20.3 68.8 147.3 1171.6 3004.6 334.5
### Vermont
- 1.4 15.9 30.8 101.2 1348.2 2201.0 265.2
### Virginia
- 9.0 23.3 92.1 165.7 2201.0 265.2
### Washington
- 4.3 39.6 106.2 224.8 1605.6 3386.9 360.3
### West Virginia
- 6.0 13.2 42.2 597.4 1341.7 163.3
### Wyoming
- 2.8 12.9 52.2 63.7 846.9 2614.2 220.7

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements invoke the PCA procedure, which requests a principal component analysis of the data and produces Figure 10.1 through Figure 10.4:

```plaintext
proc pca data=mycas.Crime;
run;
```

**Figure 10.1** displays the “Model Information,” “Number of Variables,” “Number of Observations,” and “Simple Statistics” tables.

The “Model Information” table identifies the data source and shows that the principal component extraction method is eigenvalue decomposition, which is the default.

The “Number of Variables” table indicates that there are seven variables to be analyzed and seven principal components to be computed. By default, if you omit the **VAR** statement, all numeric variables that are not listed in other statements are used in the analysis.

The “Number of Observations” table shows that of the 50 observations in the input data, only 48 observations are used in the analysis, because some observations have incomplete data.

The “Simple Statistics” table displays the mean and standard deviation of the analysis variables.

---

**Figure 10.1** Model Information and Simple Statistics

**Crime Rates per 100,000 Population by State**

### The PCA Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Component Extraction Method</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of Variables</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Principal Components</td>
<td>7</td>
</tr>
<tr>
<td>Number of Observations Read</td>
<td>50</td>
</tr>
<tr>
<td>Number of Observations Used</td>
<td>48</td>
</tr>
</tbody>
</table>
Figure 10.1 continued

<table>
<thead>
<tr>
<th>Simple Statistics</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
<td>Mean</td>
</tr>
<tr>
<td>Murder</td>
<td>7.51667</td>
</tr>
<tr>
<td>Rape</td>
<td>26.07500</td>
</tr>
<tr>
<td>Robbery</td>
<td>127.55625</td>
</tr>
<tr>
<td>Assault</td>
<td>214.58750</td>
</tr>
<tr>
<td>Burglary</td>
<td>1316.37917</td>
</tr>
<tr>
<td>Larceny</td>
<td>2696.88542</td>
</tr>
<tr>
<td>Auto_Theft</td>
<td>383.97917</td>
</tr>
</tbody>
</table>

Figure 10.2 displays the “Correlation Matrix” table. By default, the PROC PCA statement requests that principal components be computed from the correlation matrix, so the total variance is equal to the number of variables, 7.

<table>
<thead>
<tr>
<th>Correlation Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variable</td>
</tr>
<tr>
<td>Murder</td>
</tr>
<tr>
<td>Rape</td>
</tr>
<tr>
<td>Robbery</td>
</tr>
<tr>
<td>Assault</td>
</tr>
<tr>
<td>Burglary</td>
</tr>
<tr>
<td>Larceny</td>
</tr>
<tr>
<td>Auto_Theft</td>
</tr>
</tbody>
</table>

Figure 10.3 displays the “Eigenvalues” table. The first principal component accounts for about 57.8% of the total variance, the second principal component accounts for about 18.1%, and the third principal component accounts for about 10.7%. Note that the eigenvalues sum to the total variance.

The eigenvalues indicate that two or three components provide a good summary of the data: two components account for 76% of the total variance, and three components account for 87%. Subsequent components account for less than 5% each.

<table>
<thead>
<tr>
<th>Eigenvalues of the Correlation Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>Eigenvalue</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
</tbody>
</table>
Figure 10.4 displays the “Eigenvectors” table. From the eigenvectors matrix, you can represent the first principal component, Prin1, as a linear combination of the original variables:

\[
\text{Prin1} = -0.30289 \times (\text{Murder}) - 0.43410 \times (\text{Rape}) - 0.39705 \times (\text{Robbery}) - 0.28834 \times (\text{Auto_Theft})
\]

Similarly, the second principal component, Prin2, is

\[
\text{Prin2} = 0.61893 \times (\text{Murder}) + 0.17053 \times (\text{Rape}) - 0.04713 \times (\text{Robbery}) - 0.50400 \times (\text{Auto_Theft})
\]

where the variables are standardized.

The first component is a measure of the overall crime rate, because the first eigenvector shows approximately equal loadings on all variables. The second eigenvector has high negative loadings on the variables Auto_Theft and Larceny and high positive loadings on the variables Murder and Assault. There is also a small negative loading on the variable Burglary and a small positive loading on the variable Rape. This component seems to measure the preponderance of property crime compared to violent crime. The interpretation of the third component is not obvious.
Syntax: PCA Procedure

The following statements are available in the PCA procedure:

```plaintext
PROC PCA < options > ;
   BY variables ;
   CODE < options > ;
   DISPLAY < table-list > </ options > ;
   DISPLAYOUT table-spec-list </ options > ;
   FREQ variable ;
   OUTPUT OUT=CAS-libref.data-table
      < COPYVARS=(variables) >
      < keyword < =prefix > . . . < keyword < =prefix > > > ;
       PARTIAL variables ;
       VAR variables ;
       WEIGHT variable ;
```

The rest of this section provides detailed syntax information about each of the preceding statements, beginning with the PROC PCA statement. The remaining statements are described in alphabetical order.

PROC PCA Statement

```plaintext
PROC PCA < options > ;
```

The PROC PCA statement invokes the PCA procedure. Optionally, it also identifies the input and output data sets, specifies the analyses to be performed, and controls displayed output. Table 10.3 summarizes the options available in the PROC PCA statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Specify Data Sets</td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td>OUTSTAT=</td>
<td>Specifies the CAS output data table that contains various statistics</td>
</tr>
<tr>
<td>Specify Details of Analysis</td>
<td></td>
</tr>
<tr>
<td>COV</td>
<td>Computes the principal components from the covariance matrix</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the principal component extraction method to be used</td>
</tr>
<tr>
<td>N=</td>
<td>Specifies the number of principal components to be computed</td>
</tr>
<tr>
<td>NOINT</td>
<td>Omits the intercept from the model</td>
</tr>
<tr>
<td>PREFIX=</td>
<td>Specifies a prefix for naming the principal components</td>
</tr>
<tr>
<td>PARPREFIX=</td>
<td>Specifies a prefix for naming the residual variables</td>
</tr>
<tr>
<td>SINGULAR=</td>
<td>Specifies the singularity criterion</td>
</tr>
<tr>
<td>STD</td>
<td>Standardizes the principal component scores</td>
</tr>
<tr>
<td>VARDEF=</td>
<td>Specifies the divisor used to calculate variances and standard deviations</td>
</tr>
</tbody>
</table>

Table 10.3  PROC PCA Statement Options
The following list provides details about these options.

**COVARIANCE**

**COV**

computes the principal components from the covariance matrix. If you omit this option, the correlation matrix is analyzed. The COV option causes variables that have large variances to be more strongly associated with components that have large eigenvalues, and it causes variables that have small variances to be more strongly associated with components that have small eigenvalues. You should not specify this option unless the units in which the variables are measured are comparable or the variables are standardized in some way.

**DATA=** *CAS-libref.data-table*

names the input data table for PROC PCA to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where

*CAS-libref* refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 553.

*data-table* specifies the name of the input data table.

**METHOD=EIG | ITERGS< (iter-options) > | NIPALS< (nipals-options) > | RANDOM< (rand-options) >**

specifies the principal component extraction method to be used. You can specify the following values:

**EIG**

requests eigenvalue decomposition.

**ITERGS< (iter-options) >**

requests the iterative method based on Gram-Schmidt orthogonalization (ITERGS) of Andrecut (2009). You can specify the following `iter-options`.

**EPSILON=n**

specifies the convergence criterion for the iterative method. By default, EPSILON=1E–12.

**MAXITER=n**

specifies the maximum number of iterations for the iterative method. By default, MAX-ITER=500.
NOCENTER suppresses centering of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

NOSCALE suppresses scaling of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

NIPALS<(nipals-options)> requests the nonlinear iterative partial least squares (NIPALS) method. You can specify the following nipals-options.

EPSILON=n specifies the convergence criterion for the iterative method. By default, EPSILON=1E–12.

MAXITER=n specifies the maximum number of iterations for the iterative method. By default, MAXITER=500.

NOCENTER suppresses centering of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

NOSCALE suppresses scaling of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

RANDOM<(rand-options)> requests the iterative method based on random projection (RANDOM) of Halko, Martinsson, and Tropp (2011). You can specify the following rand-options.

NITER=n specifies the number of iterations. By default, NITER=1.

NOCENTER suppresses centering of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

NOSCALE suppresses scaling of the numeric variables to be analyzed. This option is useful if the analysis variables are already centered and scaled.

SEED=n specifies the random number generator seed. By default, SEED=1.

By default, METHOD=EIG. If you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM, the following options in the PROC PCA statement are not supported: COV, NOINT, OUTSTAT=, PARPREFIX=, SINGULAR=, and STD.
N=number
specifies the number of principal components to be computed. If you specify METHOD=ITERGS,
METHOD=NIPALS, or METHOD=EIG, the default is the number of variables. If you specify
METHOD=RANDOM, the default is 1. The number must be an integer greater than or equal to 0. If
N=0, the default is used.

NOINT
omits the intercept from the model. In other words, this option requests that the covariance or
correlation matrix not be corrected for the mean. When you specify this option, the covariance matrix
and, hence, the standard deviations are not corrected for the mean. If you want to obtain the standard
deviations corrected for the mean, you can obtain them by using a procedure such as PROC MEANS
in Base SAS.

If you specify this option and also create an OUTSTAT= data table, the data table’s type is UCORR or
UCOV rather than CORR or COV. For more information, see the section “OUTSTAT= Data Table” on
page 571.

OUTSTAT=CAS-libref.data-table
creates an output data table to contain means, standard deviations, number of observations, correlations
or covariances, eigenvalues, and eigenvectors. CAS-libref specifies the CAS library where the output
data table is to be created, and data-table specifies the name of the output data table. If you specify the
COV option, the data table’s type is COV or UCOV, depending on the NOINT option, and it contains
covariances; otherwise, the data table’s type is CORR or UCORR, depending on the NOINT option,
and it contains correlations. If you specify the PARTIAL statement, the OUTSTAT= data table also
contains R-squares.

For more information about the OUTSTAT= data table, see the section “OUTSTAT= Data Table” on
page 571.

PLOTS < (global-plot-options) > < = plot-request < (options) > >
PLOTS < (global-plot-options) > < = (plot-request < (options) > < ... plot-request < (options) > ) >
controls the plots that are produced through ODS Graphics. When you specify only one plot-request,
you can omit the parentheses around it. Some examples follow:

- plots
- plots=none
- plots=(eigen profile)
- plots(unpack)=scree

ODS Graphics must be enabled before you can request plots. For example:

- ods graphics on;
- proc pca plots=all;
  var x1--x10;
- run;
- ods graphics off;

You must specify the PLOTS option in order for the PCA procedure to produce plots. If you do not
specify a plot-request, PROC PCA produces the scree plot by default.

You can specify the following global-plot-options:
UNPACKPANEL

UNPACK
suppresses paneling in the scree plot. By default, multiple plots can appear in an output panel. Specify UNPACKPANEL if you want each plot to appear in a separate panel. You can specify PLOTS(UNPACKPANEL) to unpack the default plots. You can also specify UNPACKPANEL as a suboption of the SCREE option (such as PLOTS=SCREE(UNPACKPANEL)).

You can specify the following plot-requests:

ALL
produces all appropriate plots. You can specify other options along with ALL; for example, to request all plots and unpack only the scree plot, specify PLOTS=(ALL SCREE(UNPACKPANEL)).

EIGEN < ( UNPACKPANEL ) >
EIGENVALUE < ( UNPACKPANEL ) >
SCREE < ( UNPACKPANEL ) >
produces the scree plot of eigenvalues and proportion variance explained. By default, both plots appear in the same panel. Specify PLOTS=SCREE(UNPACKPANEL) if you want each plot to appear in a separate panel.

NONE
suppresses the display of all plots.

PATTERNPROFILE
PROFILE
produces the pattern profile plot. Each component has its own profile. The Y-axis value represents the correlation between the variable (corresponding to the X-axis value) and the profiled principal component.

PREFIX=name
specifies a prefix for naming the principal components. By default, the names are Prin1, Prin2, ..., Prin_n. If you specify PREFIX=Abc, the components are named Abc1, Abc2, Abc3, and so on. The number of characters in the prefix plus the number of digits required to designate the variables should not exceed the current name length that is defined by the VALIDVARNAME= system option.

PARPREFIX=name
PPREFIX=name
RPREFIX=name
specifies a prefix for naming the residual variables in the OUTSTAT= data table. By default, the prefix is R_. The number of characters in the prefix plus the maximum length of the variable names should not exceed the current name length that is defined by the VALIDVARNAME= system option.

SINGULAR=p
SING=p
specifies the singularity criterion, where $0 < p < 1$. If a variable in a PARTIAL statement has an R-square as large as $1 - p$ when predicted from the variables listed before it in the statement, the variable is assigned a standardized coefficient of 0. By default, SINGULAR=1E–8.
STANDARD STD
standardizes the principal component scores in the OUT= data table in the OUTPUT statement to unit variance. If you omit this option, the scores have a variance equal to the corresponding eigenvalue. Note that this option has no effect on the eigenvalues themselves.

VARDEF=DF | N | WDF | WEIGHT | WGT
specifies the divisor to be used to calculate variances and standard deviations. By default, VARDEF=DF. The following table displays the values and associated divisors:

<table>
<thead>
<tr>
<th>Value</th>
<th>Divisor</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>DF</td>
<td>Error degrees of freedom</td>
<td>$n - i$</td>
</tr>
<tr>
<td></td>
<td></td>
<td>$n - p - i$</td>
</tr>
<tr>
<td>N</td>
<td>Number of observations</td>
<td>$n$</td>
</tr>
<tr>
<td>WEIGHT WGT</td>
<td>Sum of weights</td>
<td>$\sum_{j=1}^{n} w_j$</td>
</tr>
<tr>
<td>WDF</td>
<td>Sum of weights minus one</td>
<td>$(\sum_{j=1}^{n} w_j) - i$</td>
</tr>
<tr>
<td></td>
<td></td>
<td>$(\sum_{j=1}^{n} w_j) - p - i$</td>
</tr>
</tbody>
</table>

In the formulas for VARDEF=DF and VARDEF=WDF, $p$ is the number of degrees of freedom of the variables in the PARTIAL statement, and $i$ is 0 if you specify the NOINT option and 1 otherwise.

**BY Statement**

BY variables ;

You can specify a BY statement in PROC PCA to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in *SAS Language Reference: Concepts*.

**CODE Statement**

CODE < options > ;

The CODE statement writes SAS DATA step code for computing the principal component scores either to a file or to a catalog entry. This code can then be included in a DATA step to score new data.

The CODE statement is not supported when you specify the PARTIAL statement. If you specify more than one CODE statement, only the first one specified is used.

Table 10.5 summarizes the options available in the CODE statement.
Table 10.5  CODE Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file where the generated code is saved</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
</tbody>
</table>

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

DISPLAY Statement

DISPLAY < table-list > < / options > ;

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the table-list as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 575. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path Bygroup1.Summary.SelectionSummary. A partial pathname does not include all groups; for example, SelectionSummary and Summary.SelectionSummary are partial pathnames for Bygroup1.Summary.SelectionSummary.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both SelectionSummary and Summary.SelectionSummary select Bygroup1.Summary.SelectionSummary.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the Bygroup1.Summary.SelectionSummary table is not selected.
You can specify the following \textit{options} after a slash (/):

\textbf{CASESENSITIVE}

performs a case-sensitive comparison of table names in the \textit{table-list} to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the \textit{table-list} in quotation marks.

\textbf{EXCLUDE}

displays all display tables except those that you specify in the \textit{table-list}.

\textbf{EXCLUDEALL}

suppresses display of all tables. This option takes precedence over the other options.

\textbf{TRACE}

displays the display table names, labels, and paths.

\textbf{DISPLAYOUT Statement}

\texttt{DISPLAYOUT table-spec-list \textbackslash options \};

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see \textit{SAS Output Delivery System: Procedures Guide}.

The \textit{table-spec-list} specifies a list of CAS output tables to create. Each entry in the list has either a \texttt{key=value} format or a \texttt{key} format:

\texttt{key=value} specifies \texttt{key} as the ODS table name, path, or partial pathname, and specifies \texttt{value} as the CAS output table name.

\texttt{key} specifies \texttt{key} as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the \texttt{DISPLAY} statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following \textit{options} after a slash (/):

\textbf{INCLUDEALL}

creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the \textit{table-spec-list} specification is ignored.

\textbf{NOREPLACE}

does not replace any existing CAS output table of the same name.

\textbf{REPEATED}

replicates all CAS output tables on all nodes.
FREQ Statement

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC PCA treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

The FREQ statement is not supported if you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM in the PROC PCA statement.

OUTPUT Statement

OUTPUT OUT=\texttt{CAS-libref.data-table} < COPYVARS=(variables) > < keyword <=prefix>> . . . < keyword <=prefix>> ;

The OUTPUT statement creates a data table that contains observationwise statistics, which are computed after PROC PCA fits the model. If you do not specify a keyword, then only the principal component scores are included.

The variables in the input data table are not included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the COPYVARS= option are included.

You must specify the following option:

\texttt{OUT=} \texttt{CAS-libref.data-table}

names the output data table for PROC PCA to use. You must specify this option before any other options. \texttt{CAS-libref.data-table} is a two-level name, where

\begin{itemize}
\item \texttt{CAS-libref} refers to a collection of information that is defined in the LIBNAME statement and includes the \texttt{caslib}, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about \texttt{CAS-libref}, see the section “Using CAS Sessions and CAS Engine Librefs” on page 553.
\item \texttt{data-table} specifies the name of the output data table.
\end{itemize}

You can also specify the following syntax elements:

\texttt{COPYVAR=} \texttt{variable}

\texttt{COPYVARS=} \texttt{(variables)}

transfers one or more variables from the input data table to the output data table.

\texttt{keyword <=prefix>}

specifies a statistic to include in the output data table and optionally a prefix for naming the output variables. If you do not provide a prefix, the PCA procedure assigns a default prefix based on the type.
of statistic requested. For example, for the VAR statement variables x1 and x2, RESIDUAL produces two residual value variables, R_x1 and R_x2.

You can specify the following *keywords* to add statistics to the OUTPUT data table:

**H**
requests the approximate leverage. The default prefix is H.

**STD**
requests standardized (centered and scaled) VAR statement variable values for each VAR statement variable. The default prefix is Std.

**STDSSE**
requests the sum of squares of residuals for standardized VAR statement variables. The default prefix is StdSSE.

**TSQUARE**
**T2**
requests scaled sum of squares of score values. The default prefix is TSquare.

**RESIDUAL**
**RESID**
**R**
requests residuals for each VAR statement variable. The default prefix is R.

**SCORE**
requests principal component scores for each principal component. The default prefix is Score.

If you specify METHOD=EIG, the only valid *keywords* are RESIDUAL (if you also specify the PARTIAL statement; PROC PCA computes the residuals by predicting the VAR statement variables from the PARTIAL statement variables) and SCORE. Other *keywords* are ignored. The output variables that contain the principal component scores have mean 0 and a variance equal to the corresponding eigenvalue, unless you specify the STANDARD option to standardize the scores to unit variance. Also, if you specify the COV option, PROC PCA computes the principal component scores from the corrected variables or (if the NOINT option is specified) uncorrected variables rather than from the standardized variables.

The output variables that contain the requested statistic are named as follows, according to the *keyword* that you specify:

- The *keywords* RESIDUAL and STD define an output variable for each VAR statement variable, so the variables that correspond to each VAR statement variable are named by appending the name of the VAR statement variable to the prefix. For example, if the model has the VAR statement variables x1 and x2, then RESIDUAL=R produces the variables R_x1 and R_x2.
- The *keyword* SCORE defines an output variable for each principal component, so the variables that correspond to each successive component are named by appending the component number to the prefix. For example, if the model has three principal components, then SCORE=T produces the variables T1, T2, and T3.
- The *keywords* H, STDSSE, and TSQUARE each define a single output variable, so the variable name matches the prefix.
PARTIAL Statement

PARTIAL variables ;

If you want to analyze a partial correlation or covariance matrix, use the PARTIAL statement to specify the names of the numeric variables to be partialed out. The PCA procedure computes the principal components of the residuals by predicting the VAR statement variables from the PARTIAL statement variables. If you request an OUTSTAT= data table, the residual variables are named by prefixing either the characters _R_ (by default) or the string specified in the PARPREFIX= option to the VAR statement variable names.

The PARTIAL statement is not supported if you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM in the PROC PCA statement.

VAR Statement

VAR variables ;

The VAR statement lists the numeric variables to be analyzed. If you omit the VAR statement, all numeric variables that are not specified in other statements are analyzed.

WEIGHT Statement

WEIGHT variable ;

The variable in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

The WEIGHT statement is not supported if you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM in the PROC PCA statement.

Details: PCA Procedure

Computing Principal Components

The PCA procedure implements several methods of calculating principal components: eigenvalue decomposition (EIG), the nonlinear iterative partial least squares (NIPALS) method, the iterative method based on the Gram-Schmidt orthogonalization (ITERGS) of Andrecut (2009), and the iterative method based on random projection (RANDOM) of Halko, Martinsson, and Tropp (2011). The EIG, NIPALS, and ITERGS methods provide exact principal component solutions, whereas the RANDOM method gives approximate principal components.

Each method has computational strengths; Table 10.6 provides guidelines for selecting an efficient (fast) method. The guidelines include the concept of a “small to moderate” and “moderate to large” number of
variables. This concept depends on the number of data set observations, the number of principal components required, the PCA method parameter settings, and the grid computing environment. As a simple illustration of the efficiency relationship between the EIG and RANDOM methods, consider a scenario in which one principal component is extracted from a data set that consists of 1,000,000 observations that are distributed across a grid of 16 servers. Figure 10.5 depicts execution time for RANDOM divided by the execution time of EIG (labeled “Execution Time Ratio”) as a function of the number of data set variables. Where execution time ratio is greater than 1, EIG is more efficient than RANDOM. For this scenario, “small to moderate” means approximately 700 variables or less and “moderate to large” means anything more than 700 variables.

**Table 10.6** Guidelines for PCA Method Selection

<table>
<thead>
<tr>
<th>Method</th>
<th>Efficient in These Scenarios</th>
</tr>
</thead>
<tbody>
<tr>
<td>EIG</td>
<td>Small to moderate number of variables, and/or computing all principal components</td>
</tr>
<tr>
<td>NIPALS</td>
<td>Computing only the first few principal components</td>
</tr>
<tr>
<td>ITERGS</td>
<td>Computing only the first few principal components</td>
</tr>
<tr>
<td>RANDOM</td>
<td>Moderate to large number of variables</td>
</tr>
</tbody>
</table>

**Figure 10.5** Illustration of Efficiency Crossover Point for EIG and RANDOM Methods

---

**Eigenvalue Decomposition**

Let $X$ be a centered and scaled data matrix that has $k$ numeric variables. The eigenvalue decomposition method bases the component extraction on the eigenvalue decomposition of the covariance matrix $X'X$, which extracts all the $k$ principal components simultaneously. Each principal component is a linear combination
of the original variables, and each component is orthogonal, with coefficients equal to the eigenvectors of the covariance matrix $X'X$. The eigenvectors are usually normalized to have unit length. The principal components are sorted by descending order of the eigenvalues, which are equal to the variances of the components.

**NIPALS**

The nonlinear iterative partial least squares (NIPALS) method extracts the principal components successively based on the data matrix $X$. The NIPALS method starts by calculating the loadings, $p$, as $p' = (t' t)^{-1} t' X$, where $t$ is the score vector. It then calculates an improved score vector, $t = X p$. The method iteratively computes the improved $p$ and $t$ until convergence is reached.

This process accounts for how the first principal component is extracted. The second component is extracted in the same way, by replacing $X$ with the residual from the first component: $E = X - t p'$.

For large data matrices or matrices that have a high degree of column collinearity, the NIPALS method suffers from loss of orthogonality because of the machine-precision errors that accumulate at each iteration step. In practice, the NIPALS method is used to extract only the first few principal components.

**ITERGS**

The iterative method based on Gram-Schmidt orthogonalization (ITERGS) of Andrecut (2009) overcomes the issue of loss of orthogonality in the NIPALS method by applying Gram-Schmidt reorthogonalization correction to both the loadings and the scores at each iteration step:

$$p_c = p - P_k P'_k p$$
$$t_c = t - T_k T'_k t$$

Here, $p_c$ and $t_c$ are the corrected loading vector and score vector, respectively. $P_k$ is the matrix that is formed by using the first $k$ loadings. $T_k$ is the matrix that is formed by using the first $k$ scores.

The ITERGS method stabilizes the iterative process at the cost of increased computational effort.

**RANDOM**

The iterative method based on random projection (RANDOM) of Halko, Martinsson, and Tropp (2011) computes approximate scores and loadings by using a two-step process. The first step calculates an approximate basis for the range of $X$ (that is, $X \approx Q Q'X$), where $Q$ has orthonormal columns. The second step computes a sketch of $X$ from $B = Q'X$. The singular value decomposition of $B$ gives an equivalent representation $USV^T$, and simple manipulations of these matrices provide the approximate loadings $P = V$ and the scores $T = QS$.

The iterative part of this method is the construction of the orthonormal basis matrix $Q$. Conceptually, you can obtain $Q$ by QR factorization of $Y = (XX^T)^iX\Omega$, where $\Omega$ is a random Gaussian projection matrix and $i$ is the number of iterations. Here the notion of iteration refers to multiplication of a sample matrix by $X^T$ and then $X$. This conceptual approach is susceptible to rounding error, so in practice you orthonormalize the columns of the sample matrix for numerical stability. Here, the initial sample matrix is the subspace defined by the QR factorization of a random projection of the data matrix $X\Omega = Q_0 R_0$. Each iteration
$(j = 1, 2, \ldots, i)$ then consists of alternating projection and orthonormalization steps of

\[
\hat{Y}_j = X^T Q_{j-1} \\
\hat{Q}_j R_j = \hat{Y}_j
\]

and

\[
Y_j = X \hat{Q}_j \\
Q_j R_j = Y_j
\]

When $j = i$, $Q_j$ is the desired orthonormal basis matrix.

---

**Missing Values**

Observations that have missing values for any variable in the VAR, PARTIAL, FREQ, or WEIGHT statement are omitted from the analysis and are given missing values for principal component scores in the OUT= data table that is specified in the OUTPUT statement.

---

**OUTSTAT= Data Table**

The following table relates the type of the OUTSTAT= data table to the options that are specified in the PROC PCA statement:

<table>
<thead>
<tr>
<th>Options</th>
<th>Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>Default</td>
<td>CORR</td>
</tr>
<tr>
<td>COV</td>
<td>COV</td>
</tr>
<tr>
<td>NOINT</td>
<td>UCORR</td>
</tr>
<tr>
<td>COV NOINT</td>
<td>UCOV</td>
</tr>
</tbody>
</table>

Note that the default (neither the COV nor NOINT option) produces a data table of type CORR.

The new data table contains the following variables:

- the BY variables, if any
- two new variables, _TYPE_ and _NAME_, both character variables
- the variables that are analyzed (that is, those in the VAR statement); or, if there is no VAR statement, all numeric variables not listed in any other statement; or, if there is a PARTIAL statement, the residual variables that contain the residuals computed by predicting the VAR statement variables from the PARTIAL statement variables.

Each observation in the new data table contains some type of statistic, as indicated by the _TYPE_ variable. The values of the _TYPE_ variable are as follows:
Chapter 10: The PCA Procedure

_TYPE_ | Contents
--- | ---
MEAN | mean of each variable. If you specify the PARTIAL statement, this observation is omitted.
STD | standard deviations. If you specify the COV option, this observation is omitted. If you specify the PARTIAL statement, the standard deviation of a variable is computed as its root mean squared error as predicted from the PARTIAL statement variables.
USTD | uncorrected standard deviations. When you specify the NOINT option in the PROC PCA statement, the OUTSTAT= data table contains standard deviations not corrected for the mean. However, if you also specify the COV option in the PROC PCA statement, this observation is omitted.
N | number of observations on which the analysis is based. This value is the same for each variable. If you specify the PARTIAL statement and the value of the VARDEF= option is DF or unspecified, then the number of observations is decremented by the degrees of freedom for the PARTIAL statement variables.
SUMWGT | the sum of the weights of the observations. This value is the same for each variable. If you specify the PARTIAL statement and VARDEF=WDF, then the sum of the weights is decremented by the degrees of freedom for the PARTIAL statement variables. This observation is output only if the value is different from that in the observation for which _TYPE_ = 'N'.
CORR | correlations between each variable and the variable specified by the _NAME_ variable. The number of observations for which _TYPE_ = 'CORR' is equal to the number of variables being analyzed. If you specify the COV option, no _TYPE_ = 'CORR' observations are produced. If you use the PARTIAL statement, then the partial correlations, not the raw correlations, are output.
UCORR | uncorrected correlation matrix. When you specify the NOINT option without the COV option in the PROC PCA statement, the OUTSTAT= data table contains a matrix of correlations not corrected for the means. However, if you also specify the COV option in the PROC PCA statement, this observation is omitted.
COV | covariances between each variable and the variable specified by the _NAME_ variable. _TYPE_ = 'COV' observations are produced only if you specify the COV option. If you specify the PARTIAL statement, the partial covariances, not the raw covariances, are output.
UCOV | uncorrected covariance matrix. When you specify the NOINT and COV options in the PROC PCA statement, the OUTSTAT= data table contains a matrix of covariances not corrected for the means.
EIGENVAL | eigenvalues. If the N= option requests less than the maximum number of principal components, only the specified number of eigenvalues are produced, and missing values fill out the observation.
SCORE | eigenvectors. The _NAME_ variable contains the name of the corresponding principal component as constructed from the PREFIX= option. The number of observations for which _TYPE_ = 'SCORE' equals the number of principal components computed. The eigenvectors have unit length unless you specify the STD option, in which case the unit-length eigenvectors are divided by the square roots of the eigenvalues to produce scores that have unit standard deviations.
To obtain the principal component scores, if the COV option is not specified, these coefficients should be multiplied by the standardized data. For the COV option, these coefficients should be multiplied by the centered data. To center and standardize the data, you should use means that are obtained from the observation for which _TYPE_='MEAN' and standard deviations that are obtained from the observation for which _TYPE_='STD'.

**USCORE**
scoring coefficients to be applied without subtracting the mean from the raw variables. Observations for which _TYPE_='USCORE' are produced when you specify the NOINT option in the PROC PCA statement.

To obtain the principal component scores, these coefficients should be multiplied by the data that are standardized by the uncorrected standard deviations obtained from the observation for which _TYPE_='USTD'.

**RSQUARED**
R-squares for each VAR statement variable as predicted by the PARTIAL statement variables.

**B**
regression coefficients for each VAR statement variable as predicted by the PARTIAL statement variables. This observation is produced only if you specify the COV option.

**STB**
standardized regression coefficients for each VAR statement variable as predicted by the PARTIAL statement variables. If you specify the COV option, this observation is omitted.

---

**Displayed Output**

The following sections describe the output that PROC PCA produces. The output is organized into various tables, which are discussed in their order of appearance.

**Model Information**

The “Model Information” table displays basic information about the model, including the input data table and the principal component extraction method that is used in the analysis.

**Number of Variables**

The “Number of Variables” table displays the number of VAR statement variables, the number of PARTIAL statement variables, and the number of principal components to be extracted.

**Number of Observations**

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis. If you specify a FREQ statement, the table also displays the sum of frequencies read and used.

**Simple Statistics**

If you specify METHOD=EIG, the PCA procedure produces a “Simple Statistics” table that displays the mean and standard deviation (std) for each variable. If you specify the NOINT option, the uncorrected standard deviation (ustd) is displayed.
Chapter 10: The PCA Procedure

Centering and Scaling Information
If you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM, the PCA procedure produces a “Centering and Scaling Information” table that displays the centering and scaling information for each variable.

Explained Variation of Variables
If you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM, the PCA procedure produces an “Explained Variation of Variables” table that displays the fraction of variation that is accounted for in each variable by each successive principal component.

Correlation Matrix
If you specify METHOD=EIG, the PCA procedure produces a “Correlation Matrix” table that displays the correlation matrix or, if you specify the COV option, the covariance matrix.

Regression Statistics
When you specify the PARTIAL statement, the PCA procedure produces a “Regression Statistics” table that displays the R-square and root mean squared error (RMSE) for each VAR statement variable as predicted by the PARTIAL statement variables.

Regression Coefficients
When you specify the PARTIAL statement, the PCA procedure produces a “Regression Coefficients” table that displays standardized regression coefficients or, if you specify the COV option, regression coefficients for predicting the VAR statement variables from the PARTIAL statement variables.

Partial Correlation Matrix
When you specify the PARTIAL statement, the PCA procedure produces a “Partial Correlation Matrix” table that displays the partial correlation matrix or, if you specify the COV option, the partial covariance matrix.

Total Variance
If you specify METHOD=EIG and the COV option, the PCA procedure produces a simple table that displays the total variance.

Eigenvalues
The “Eigenvalues” table displays eigenvalues of the correlation or covariance matrix (if you specify METHOD=EIG) or eigenvalues of the data matrix (if you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM), along with the difference between successive eigenvalues, the proportion of variance explained by each eigenvalue, and the cumulative proportion of variance explained.

Eigenvectors
If you specify METHOD=EIG, the PCA procedure produces an “Eigenvectors” table that displays the eigenvectors.
Loadings

If you specify METHOD=ITERGS, METHOD=NIPALS, or METHOD=RANDOM, the PCA procedure produces a “Loadings” table that displays the loadings.

Timing Information

The “Timing” table displays the elapsed time of each main task of the procedure.

ODS Table Names

Each table that the PCA procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement, the DISPLAYOUT statement, or the Output Delivery System (ODS) statements. These names are listed in Table 10.7.

Table 10.7 ODS Tables Produced by PROC PCA

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CenScaleInfo</td>
<td>Centering and scaling information</td>
<td>METHOD=ITERGS</td>
</tr>
<tr>
<td>Corr</td>
<td>Correlation matrix</td>
<td>METHOD=EIG</td>
</tr>
<tr>
<td>Cov</td>
<td>Covariance matrix</td>
<td>METHOD=EIG and COV</td>
</tr>
<tr>
<td>Eigenvalues</td>
<td>Eigenvalues</td>
<td>Default output</td>
</tr>
<tr>
<td>Eigenvectors</td>
<td>Eigenvectors</td>
<td>METHOD=EIG</td>
</tr>
<tr>
<td>Loadings</td>
<td>Loadings</td>
<td>METHOD=ITERGS</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Model information</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>Default output</td>
</tr>
<tr>
<td>NVars</td>
<td>Number of variables, partial variables, and principal components</td>
<td>Default output</td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Library and name of output data tables, and number of rows and columns in the table</td>
<td>DISPLAYOUT statement</td>
</tr>
<tr>
<td>ParCorr</td>
<td>Partial correlation matrix</td>
<td>PARTIAL statement</td>
</tr>
<tr>
<td>ParCov</td>
<td>Uncorrected partial covariance matrix</td>
<td>PARTIAL statement and COV</td>
</tr>
<tr>
<td>RegCoef</td>
<td>Regression coefficients</td>
<td>PARTIAL statement and COV</td>
</tr>
<tr>
<td>RSquareRMSE</td>
<td>Regression statistics: R-squares and RMSEs</td>
<td>PARTIAL statement</td>
</tr>
<tr>
<td>SimpleStatistics</td>
<td>Simple statistics</td>
<td>METHOD=EIG</td>
</tr>
<tr>
<td>StdRegCoef</td>
<td>Standardized regression coefficients</td>
<td>PARTIAL statement</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times of tasks that are performed by the procedure</td>
<td>Default output</td>
</tr>
<tr>
<td>TotalVariance</td>
<td>Total variance</td>
<td>METHOD=EIG and COV</td>
</tr>
<tr>
<td>Variation</td>
<td>Explained variation of variables</td>
<td>METHOD=ITERGS</td>
</tr>
</tbody>
</table>
**ODS Graphics**

You can refer to every graph produced through ODS Graphics by name. The names of the graphs that PROC PCA generates are listed in Table 10.8, along with a description of each graph and the required statements and options.

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>PatternProfilePlot</td>
<td>Component pattern profile plot</td>
<td>PLOTS=_PATTERNPROFILE</td>
</tr>
<tr>
<td>ScreePlot</td>
<td>Scree and variance plots</td>
<td>Default output</td>
</tr>
<tr>
<td>VariancePlot</td>
<td>Variance proportion-explained plot</td>
<td>PLOTS=SCREE(UNPACKPANEL)</td>
</tr>
</tbody>
</table>

**Examples: PCA Procedure**

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

**Example 10.1: Analyzing Mean Temperatures of US Cities**

This example analyzes mean daily temperatures of selected US cities in January and July. The following DATA step creates the data:

```sas
data mycas.Temperature;
  length Cityid $ 2;
  title 'Mean Temperature of Selected Cities in January and July';
  input City $1-15 January July;
  Cityid = substr(City,1,2);
  datalines;
  Mobile  51.2  81.6
  Phoenix 51.2  91.2
  Little Rock 39.5  81.4
  Sacramento 45.1  75.2
  Denver  29.9  73.0
  ... more lines ...
  Cheyenne 26.6  69.1
;```

Example 10.1: Analyzing Mean Temperatures of US Cities

The following statements invoke the PCA procedure, which requests a principal component analysis of these data and outputs the scores to an output data table. The Cityid variable is also included in the output data table (COPYVARS= Cityid).

```plaintext
title 'Mean Temperature of Selected Cities in January and July';
proc pca data=mycas.Temperature cov;
   var July January;
   output out=mycas.Scores copyVars=Cityid;
run;
```

Output 10.1.1 displays the PROC PCA output. The standard deviation of January (11.712) is higher than the standard deviation of July (5.128). The COV option in the PROC PCA statement requests that the principal components be computed from the covariance matrix. The total variance is 163.474. The first principal component accounts for about 94% of the total variance, and the second principal component accounts for only about 6%. The eigenvalues sum to the total variance.

Note that January receives a higher loading on Prin1 because it has a higher standard deviation than July. Also note that the PCA procedure calculates the scores by using the centered variables rather than the standardized variables.

Output 10.1.1 Results of Principal Component Analysis

### Mean Temperature of Selected Cities in January and July

#### The PCA Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
<td>TEMPERATURE</td>
</tr>
<tr>
<td>Component Extraction Method</td>
<td>Eigenvalue Decomposition</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of Variables</th>
<th>2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Principal Components</td>
<td>2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>64</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Used</td>
<td>64</td>
</tr>
</tbody>
</table>

#### Simple Statistics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Mean</th>
<th>Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td>July</td>
<td>75.60781</td>
<td>5.12762</td>
</tr>
<tr>
<td>January</td>
<td>32.09531</td>
<td>11.71243</td>
</tr>
</tbody>
</table>

#### Covariance Matrix

<table>
<thead>
<tr>
<th>Variable</th>
<th>July</th>
<th>January</th>
</tr>
</thead>
<tbody>
<tr>
<td>July</td>
<td>26.29248</td>
<td>46.82829</td>
</tr>
<tr>
<td>January</td>
<td>46.82829</td>
<td>137.18109</td>
</tr>
</tbody>
</table>

| Total Variance | 163.47356647 |

#### Eigenvalues of the Covariance Matrix

<table>
<thead>
<tr>
<th>Eigenvalue</th>
<th>Difference</th>
<th>Proportion</th>
<th>Cumulative</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>154.310607</td>
<td>0.9439</td>
<td>0.9439</td>
</tr>
<tr>
<td>2</td>
<td>9.162960</td>
<td>0.0561</td>
<td>1.0000</td>
</tr>
</tbody>
</table>
Example 10.2: Extracting Principal Components with NIPALS

This example demonstrates the NIPALS method in PROC PCA, which extracts principal components successively. The data that this example uses are from the Getting Started section; they provide crime rates per 100,000 people in seven categories for each of the 50 US states in 1977. The following DATA step generates the data:

```plaintext
data mycas.Crime;
  title 'Crime Rates per 100,000 Population by State';
  input State $1-15 Murder Rape Robbery Assault Burglary Larceny Auto_Theft;
  datalines;
  Alabama 14.2 25.2 96.8 278.3 1135.5 1881.9 280.7
  Alaska 10.8 51.6 96.8 284.0 1331.7 3369.8 753.3
  Arizona 9.5 34.2 138.2 312.3 2346.1 4467.4 439.5
  Arkansas 8.8 27.6 83.2 203.4 972.6 1862.1 183.4
  California 11.5 49.4 287.0 358.0 2139.4 3499.8 663.5
  ... more lines ...
  Wisconsin 2.8 12.9 52.2 63.7 846.9 2614.2 220.7
  Wyoming . 21.9 39.7 173.9 811.6 2772.2 282.0
;
```

The following statements use PROC PCA to extract principal components by using the NIPALS method, and produce default plots:

```plaintext
ods graphics on;
proc pca data=mycas.Crime method=nipals plots;
run;
```

Output 10.2.1 displays the PROC PCA output. The “Model Information” table shows that the NIPALS method is used to extract principal components. The “Explained Variation of Variables” table lists the fraction of variation that is accounted for in each variable by each of the seven principal components. All the variation in each variable is accounted for by seven principal components because there are only seven variables. The eigenvalues indicate that two or three components provide a good summary of the data: two components account for 76% of the total variance, and three components account for 87%. Subsequent components account for less than 5% each.

Note that in the Getting Started section, the principal components are extracted from the same data by using the eigenvalue decomposition method; the “Eigenvalues” table that is generated there matches the one generated by the NIPALS method. Also, the eigenvectors in the “Eigenvectors” table match the loading factors in the “Loadings” table.
Example 10.2: Extracting Principal Components with NIPALS

Output 10.2.1 Results of Principal Component Analysis Using NIPALS

Crime Rates per 100,000 Population by State

The PCA Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Component Extraction Method</td>
</tr>
</tbody>
</table>

| Number of Variables | 7 |
| Number of Principal Components | 7 |

| Number of Observations Read | 50 |
| Number of Observations Used  | 48 |

Centering and Scaling Information

<table>
<thead>
<tr>
<th>Variable</th>
<th>Subtracted off</th>
<th>Divided by</th>
</tr>
</thead>
<tbody>
<tr>
<td>Murder</td>
<td>7.51667</td>
<td>3.93059</td>
</tr>
<tr>
<td>Rape</td>
<td>26.07500</td>
<td>10.81304</td>
</tr>
<tr>
<td>Robbery</td>
<td>127.55625</td>
<td>88.49374</td>
</tr>
<tr>
<td>Assault</td>
<td>214.58750</td>
<td>100.64360</td>
</tr>
<tr>
<td>Burglary</td>
<td>1316.37917</td>
<td>423.31261</td>
</tr>
<tr>
<td>Larceny</td>
<td>2696.88542</td>
<td>714.75023</td>
</tr>
<tr>
<td>Auto_Theft</td>
<td>383.97917</td>
<td>194.37033</td>
</tr>
</tbody>
</table>

Explained Variation of Variables

<table>
<thead>
<tr>
<th>Variable</th>
<th>Prin1</th>
<th>Prin2</th>
<th>Prin3</th>
<th>Prin4</th>
<th>Prin5</th>
<th>Prin6</th>
<th>Prin7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Murder</td>
<td>0.37117</td>
<td>0.85539</td>
<td>0.87790</td>
<td>0.89562</td>
<td>0.97555</td>
<td>0.99143</td>
<td>1.00000</td>
</tr>
<tr>
<td>Rape</td>
<td>0.76242</td>
<td>0.79917</td>
<td>0.84059</td>
<td>0.84199</td>
<td>0.85065</td>
<td>0.99041</td>
<td>1.00000</td>
</tr>
<tr>
<td>Robbery</td>
<td>0.63783</td>
<td>0.64064</td>
<td>0.82164</td>
<td>0.92942</td>
<td>0.99788</td>
<td>0.99992</td>
<td>1.00000</td>
</tr>
<tr>
<td>Assault</td>
<td>0.63517</td>
<td>0.79127</td>
<td>0.79341</td>
<td>0.91781</td>
<td>0.98822</td>
<td>0.99513</td>
<td>1.00000</td>
</tr>
<tr>
<td>Burglary</td>
<td>0.78913</td>
<td>0.84414</td>
<td>0.88183</td>
<td>0.88207</td>
<td>0.88544</td>
<td>0.94800</td>
<td>1.00000</td>
</tr>
<tr>
<td>Larceny</td>
<td>0.51373</td>
<td>0.72178</td>
<td>0.93718</td>
<td>0.95479</td>
<td>0.95492</td>
<td>0.95530</td>
<td>1.00000</td>
</tr>
<tr>
<td>Auto_Theft</td>
<td>0.33638</td>
<td>0.65746</td>
<td>0.90481</td>
<td>0.96197</td>
<td>0.99623</td>
<td>0.99706</td>
<td>1.00000</td>
</tr>
</tbody>
</table>

Eigenvalues

<table>
<thead>
<tr>
<th></th>
<th>Eigenvalue</th>
<th>Difference</th>
<th>Proportion</th>
<th>Cumulative</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.045824</td>
<td>2.781795</td>
<td>0.5780</td>
<td>0.5780</td>
</tr>
<tr>
<td>2</td>
<td>1.264030</td>
<td>0.516529</td>
<td>0.1806</td>
<td>0.7586</td>
</tr>
<tr>
<td>3</td>
<td>0.747500</td>
<td>0.421175</td>
<td>0.1068</td>
<td>0.8653</td>
</tr>
<tr>
<td>4</td>
<td>0.326325</td>
<td>0.061119</td>
<td>0.0466</td>
<td>0.9120</td>
</tr>
<tr>
<td>5</td>
<td>0.265207</td>
<td>0.036843</td>
<td>0.0379</td>
<td>0.9498</td>
</tr>
<tr>
<td>6</td>
<td>0.228364</td>
<td>0.105613</td>
<td>0.0326</td>
<td>0.9825</td>
</tr>
<tr>
<td>7</td>
<td>0.122750</td>
<td>0.0175</td>
<td>1.0000</td>
<td></td>
</tr>
</tbody>
</table>
PROC PCA produces the scree plot as shown in Output 10.2.2 by default when ODS Graphics is enabled and no plot request is specified in the PLOTS option. You can obtain more plots by specifying the plot requests in the PLOTS option in the PROC PCA statement.

The scree plot on the left shows that the eigenvalue of the first component is approximately 4 and the eigenvalue of the second component is largely decreased to under 1.5. The variance-explained plot on the right shows that the first two principal components account for nearly 80% of the total variance.

In addition to the scree plot, PROC PCA also produces the pattern profile plot. The following statements request this plot:

```
proc pca data=mycas.Crime method=nipals plots=patternprofile;
run;
```

Output 10.2.3 shows a component pattern profile. As shown in the pattern plots, the nearly horizontal profile of the first component indicates that the first component is mostly correlated evenly across all variables.
Example 10.3: Approximating Principal Components with the RANDOM Method

This example illustrates that the iterative method based on random projection (RANDOM) of Halko, Martinsson, and Tropp (2011) provides a good approximation to the true principal components by using simulated data. The data for this example are the result of multiplying the low-rank matrices $A$ and $B$ and adding random noise. Matrix $A$ is 1,000,000 rows by 50 columns, and matrix $B$ is 50 rows by 5,000 columns, so the final data table consists of 1,000,000 observations and 5,000 variables.

The following DATA step generates the data:

```plaintext
data mycas.testdata / sessref=mysess single=no;
title;
keep x:;
drop rank number_of_obs number_of_var sigma ii idum;
drop rv1 rv2 rsq fac row col;
drop nobs_per_thread nextras start_obs obs j k;
array B[50,5000]; /* dimensions: rank, number_of_var */
array A[50];     /* dimension: rank */
array x[5000] x1-x5000; /* dimension: number_of_var */

target_nthreads = min(_nthreads_,96);
if (_threadid_ = 1) then
   put "Number of threads = " target_nthreads;
rank=50;
number_of_obs=1000000;
number_of_var=5000;
```
sigma=0.1;

call streaminit(1);

if (_threadid_ <= target_nthreads) then do;
   ii = 0;
   idum = 0;
   do while (ii < rank * number_of_var);
      idum = mod(mod(1664525*idum,4294967296)+1013904223,4294967296);
      rv1 = 2.0*(idum/4294967296)-1.0;
      idum = mod(mod(1664525*idum,4294967296)+1013904223,4294967296);
      rv2 = 2.0*(idum/4294967296)-1.0;
      rsq = rv1*rv1+rv2*rv2;
      if ((rsq < 1.0) and (rsq ^= 0.0)) then do;
         fac = sqrt(-2.0*log(rsq)/rsq);
         row = int(ii/number_of_var)+1;
         col = mod(ii, number_of_var)+1;
         B[row, col] = rv1*fac;
         ii = ii + 1;
      if (ii < rank * number_of_var) then do;
         row = int(ii/number_of_var)+1;
         col = mod(ii, number_of_var)+1;
         B[row, col] = rv2*fac;
         ii = ii + 1;
      end;
   end;
   nobs_per_thread = int(number_of_obs /target_nthreads);
   nextras = number_of_obs - nobs_per_thread*target_nthreads;
   if (_threadid_ <= nextras) then do;
      nobs_per_thread = nobs_per_thread+1;
      start_obs = (_threadid_-1)*nobs_per_thread+1;
   end;
   else
      start_obs = nextras+(_threadid_-1)*nobs_per_thread+1;
   do obs = start_obs to (start_obs+nobs_per_thread-1);
      do j = 1 to rank;
         A[j] = rand('Normal');
      end;
      do k = 1 to number_of_var;
         x[k] = sigma*rand('Normal');
         do j = 1 to rank;
            x[k] = x[k] + A[j]*B[j, k];
         end;
      end;
   output;
   end;
end;
run;
The following statements use PROC PCA to extract principal components by using the RANDOM and EIG methods. The suboptions for the RANDOM method specify 1, 5, or 10 iterations. Both the EIG and RANDOM methods extract 25 principal components. The DISPLAY statement suppresses the default output except for eigenvalues, and the DISPLAYOUT statement saves the computed eigenvalues to specific CAS output tables.

```
ods graphics off;

proc pca data=mycas.testdata n=25 method=random(niter=1) plots=none;
   var x; 
   display Eigenvalues; 
   displayout Eigenvalues=oneiter;
run;

proc pca data=mycas.testdata n=25 method=random(niter=5) plots=none;
   var x; 
   display Eigenvalues; 
   displayout Eigenvalues=fiveiter;
run;

proc pca data=mycas.testdata n=25 method=random(niter=10) plots=none;
   var x; 
   display Eigenvalues; 
   displayout Eigenvalues=teniter;
run;

proc pca data=mycas.testdata n=25 method=eig plots=none;
   var x; 
   display Eigenvalues; 
   displayout Eigenvalues=trueeig;
run;
```

To assess the accuracy of the RANDOM method, compare the estimated eigenvalues to those computed by the EIG method. Using the DATA step and PROC SGPLOT (code not shown), you can combine the estimated eigenvalue data sets with the true eigenvalue data set and plot the results. Output 10.3.1 shows this composite plot and demonstrates the following heuristic rules for the RANDOM method:

- One iteration usually provides a reasonable approximation of the true eigenvalues.
- Three to five iterations usually provide the best trade-off between approximation accuracy and computational cost.
- Beyond five iterations, the improvement in approximation accuracy is usually small compared to the computational cost.

For additional examples that show the impact of the number of iterations for both simulated and real data, see Halko, Martinsson, and Tropp (2011).
**Output 10.3.1** RANDOM Method Performance with Varying Number of Iterations

**Effect of Varying NITER**

<table>
<thead>
<tr>
<th>Eigenvalue</th>
<th>Principal Component</th>
</tr>
</thead>
<tbody>
<tr>
<td>120</td>
<td>0</td>
</tr>
<tr>
<td>110</td>
<td>5</td>
</tr>
<tr>
<td>100</td>
<td>10</td>
</tr>
<tr>
<td>90</td>
<td>15</td>
</tr>
<tr>
<td>80</td>
<td>20</td>
</tr>
<tr>
<td>70</td>
<td>25</td>
</tr>
</tbody>
</table>

1 Iteration  | 5 Iterations  | 10 Iterations | True Eigenvalues

**NOTE:** The heuristic rules provide guidance for selecting the number of iterations for data tables that are (approximately) low-rank. You might need to increase the number of iterations beyond what is recommended for data tables that are not low-rank.

**References**


Chapter 11
The PHSELECT Procedure

Contents

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: PHSELECT Procedure</td>
<td>588</td>
</tr>
<tr>
<td>PROC PHSELECT Features</td>
<td>588</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>589</td>
</tr>
<tr>
<td>Getting Started: PHSELECT Procedure</td>
<td>590</td>
</tr>
<tr>
<td>Cox Regression</td>
<td>590</td>
</tr>
<tr>
<td>Syntax: PHSELECT Procedure</td>
<td>595</td>
</tr>
<tr>
<td>PROC PHSELECT Statement</td>
<td>595</td>
</tr>
<tr>
<td>BY Statement</td>
<td>598</td>
</tr>
<tr>
<td>CLASS Statement</td>
<td>598</td>
</tr>
<tr>
<td>CODE Statement</td>
<td>598</td>
</tr>
<tr>
<td>DISPLAY Statement</td>
<td>600</td>
</tr>
<tr>
<td>DISPLAYOUT Statement</td>
<td>601</td>
</tr>
<tr>
<td>EFFECT Statement</td>
<td>602</td>
</tr>
<tr>
<td>FREQ Statement</td>
<td>604</td>
</tr>
<tr>
<td>MODEL Statement</td>
<td>604</td>
</tr>
<tr>
<td>OUTPUT Statement</td>
<td>605</td>
</tr>
<tr>
<td>PARTITION Statement</td>
<td>608</td>
</tr>
<tr>
<td>SELECTION Statement</td>
<td>609</td>
</tr>
<tr>
<td>STRATA Statement</td>
<td>611</td>
</tr>
<tr>
<td>WEIGHT Statement</td>
<td>611</td>
</tr>
<tr>
<td>Details: PHSELECT Procedure</td>
<td>611</td>
</tr>
<tr>
<td>Missing Values</td>
<td>611</td>
</tr>
<tr>
<td>Cox Proportional Hazards Regression Model</td>
<td>611</td>
</tr>
<tr>
<td>Partial Likelihood for the Cox Model</td>
<td>612</td>
</tr>
<tr>
<td>The LASSO Method of Model Selection</td>
<td>612</td>
</tr>
<tr>
<td>Model Fit and Assessment Statistics</td>
<td>613</td>
</tr>
<tr>
<td>Predicted Values and Regression Diagnostics</td>
<td>614</td>
</tr>
<tr>
<td>Joint Tests and Type 3 Tests</td>
<td>616</td>
</tr>
<tr>
<td>Multithreading</td>
<td>617</td>
</tr>
<tr>
<td>Optimization Algorithms</td>
<td>617</td>
</tr>
<tr>
<td>Displayed Output</td>
<td>617</td>
</tr>
<tr>
<td>ODS Table Names</td>
<td>621</td>
</tr>
<tr>
<td>ODS Graphics</td>
<td>622</td>
</tr>
<tr>
<td>Examples: PHSELECT Procedure</td>
<td>623</td>
</tr>
<tr>
<td>Example 11.1: Model Selection</td>
<td>623</td>
</tr>
<tr>
<td>Example 11.2: Stratified Analysis</td>
<td>627</td>
</tr>
<tr>
<td>References</td>
<td>629</td>
</tr>
</tbody>
</table>
Overview: PHSELECT Procedure

The PHSELECT procedure fits the Cox proportional hazards regression models for survival data and performs variable selection in SAS Viya.

The models that PROC PHSELECT supports can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The models can also include constructed effects such as splines. The procedure offers a number of effect-selection methods, including stepwise methods and modern LASSO methods. It also offers extensive capabilities for customizing the model selection by using a wide variety of selection and stopping criteria, from computationally efficient significance-level-based criteria to modern, computationally intensive validation-based criteria. PROC PHSELECT also provides a variety of Cox regression diagnostics that are conditional on the selected model.

PROC PHSELECT Features

The PHSELECT procedure estimates the parameters of a Cox regression model by maximizing the partial likelihood. It also does the following:

- provides model-building syntax through the CLASS, EFFECT, and effect-based MODEL statements, which are familiar from SAS/STAT analytic procedures (in particular, the GLM, LOGISTIC, GLIMMIX, and PHREG procedures)
- enables model building (variable selection) through the SELECTION statement
- enables you to split classification effects into individual components by using the SPLIT option in the CLASS statement
- permits any degree of interaction effects that involve classification and continuous variables
- provides a WEIGHT statement for weighted analysis
- provides a FREQ statement for grouped analysis
- provides a STRATA statement for stratified analysis
- provides a CODE statement to produce SAS code that can score a new data set
- provides an OUTPUT statement to produce a data table that contains predicted values and other observationwise statistics
- uses ODS Graphics to create model selection plots as part of its output. For more information about ODS Graphics, see the section “ODS Graphics” on page 622.

Because the PHSELECT procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode
- exploits all the available cores and concurrent threads. For information about how PROC PHSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”
PROC PHSELECT Compared with the PHREG Procedure

The PHSELECT procedure provides the full set of parameterizations that are available in the PHREG procedure. The PHSELECT procedure uses the GLM parameterization for the CLASS variables by default. The PHREG procedure uses the REF parameterization for the CLASS variables by default. In either procedure, you can use the PARAM= option in the CLASS statement to change the parameterization.

The PHSELECT procedure uses a quasi-Newton algorithm by default. You can choose different optimization techniques, including second-order methods that require a crossproducts matrix, by using the TECHNIQUE= option in the PROC PHSELECT statement. The PHREG procedure uses the Newton-Raphson optimization algorithm exclusively.

The PHREG procedure can fit a variety of models, but it has very limited model selection capability. The PHSELECT procedure provides a richer set of model selection options, including LASSO selection, information-criterion-based selection and stopping criteria, and validation-based criteria.

The PHSELECT procedure uses ODS Graphics to display plots that help interpret the selection process; the PHREG procedure use ODS graphics to display predicted survival curves.

The PHSELECT procedure is specifically designed to operate in SAS Viya and performs computations in multiple threads. The PHREG procedure executes in a single thread on a single machine.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

    proc options option=(CASHOST CASPORT);
    run;

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

    cas mysess;
    libname mycas cas sessref=mysess;

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:
Chapter 11: The PHSELECT Procedure

Getting Started: PHSELECT Procedure

Cox Regression

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following DATA step creates the data table `mycas.getStarted` in your CAS session. This data table consists of 100 observations on a failure time variable (`Time`), an indicator variable (`Status`) that has two values (0 for censored observations and 1 for event observations), three classification variables (`C1–C3`), and four continuous variables (`X1–X4`). This DATA step assumes that your CAS engine libref is named `mycas`, but you can substitute any appropriately defined CAS engine libref.

```sas
data mycas.getStarted;
  input Time Status C1$ C2 C3$ X1-X4;
datalines;
  53 0 Low 1 M 1.11 2.000 3.6128 12.0
  12 0 High 1 M 1.40 1.362 3.8388 8.8
  11 1 Low 1 F 1.57 1.672 3.8865 7.5
  7 1 Medium 0 M 1.04 2.000 3.7324 5.1
  2 1 Low 1 M 1.52 2.000 3.8751 9.8
  41 0 High 1 M 1.76 1.447 3.7243 12.8
  6 1 Critical 1 F 1.36 1.462 3.5441 9.0
  6 1 Critical 1 M 1.42 1.690 3.9294 10.4
  16 1 Medium 1 M 1.32 0.699 3.6990 8.8
  41 1 Medium 1 M 1.00 1.477 3.4771 10.2
  2 1 High 0 M 1.30 2.000 3.7243 5.1
  58 1 Medium 1 M 1.20 1.580 3.6990 12.1
  11 1 High 1 M 1.08 1.903 3.5051 9.6
  12 0 Critical 1 F 1.15 1.146 3.6435 11.6
  16 0 High 1 F 1.15 0.903 3.8573 13.0
  54 1 Medium 1 M 1.26 1.699 3.7243 9.0
  51 1 Low 0 M 1.57 1.041 3.4150 7.7
  67 1 Medium 1 M 1.32 1.041 3.6435 12.8
  1 1 Low 1 M 1.94 1.954 3.9868 12.0
  19 0 Medium 1 M 1.32 2.000 3.7709 13.0
  1 1 Medium 1 M 2.22 1.954 3.6628 9.4
  35 1 Medium 0 M 1.11 1.176 3.6532 7.0
  41 1 High 1 M 1.15 1.342 3.5185 5.0
  58 1 Medium 1 M 1.20 1.580 3.6990 12.1
  11 1 Medium 1 M 1.11 1.279 3.8808 14.0
```

<p>| | | | | |</p>
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<td>1</td>
<td>Low</td>
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<td>F</td>
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<td>1</td>
<td>High</td>
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<td>F</td>
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<td>2</td>
<td>1</td>
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<td>0</td>
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<td>Medium</td>
<td>1</td>
<td>M</td>
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<td>Medium</td>
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<td>F</td>
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<tr>
<td>66</td>
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<td>High</td>
<td>1</td>
<td>M</td>
</tr>
<tr>
<td>18</td>
<td>1</td>
<td>Critical</td>
<td>1</td>
<td>F</td>
</tr>
</tbody>
</table>
The following statements fit a Cox proportional hazards model to these data by using three classification effects for the variables \(C_1-C_3\) and four regressor effects for the variables \(X_1-X_4\). The \texttt{ITHIST} option displays a table that summarizes the steps of the optimization.

```r
proc phselect data=mycas.getStarted ithist;
  class C1-C3;
  model Time*Status(0) = C1-C3 X1-X4;
run;
```

The output from this analysis is presented in Figure 11.1 through Figure 11.8.

**Figure 11.1** displays the “Model Information” table. The variable \(Time\) is the failure time variable. The variable \(Status\) is the censoring variable; the value 0 indicates censored observations. The PHSELECT procedure uses a quasi-Newton algorithm to maximize the partial likelihood to estimate the regression coefficients.

**Figure 11.1** Model Information

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Response Variable</td>
</tr>
<tr>
<td>Censoring Variable</td>
</tr>
<tr>
<td>Censoring Values</td>
</tr>
<tr>
<td>Optimization Technique</td>
</tr>
</tbody>
</table>

**Figure 11.2** displays the “Number of Observations” table. All 100 observations in the data table are used in the analysis; of them, 26 are censored and 74 are uncensored.
The classification variables C1–C3 are parameterized using the GLM parameterization, which is the default. The variable C1 has four unique formatted levels; each of the two variables C2 and C3 has two levels. The classification levels are displayed in the “Class Level Information” table in Figure 11.3.

<table>
<thead>
<tr>
<th>Class</th>
<th>Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1</td>
<td>4</td>
<td>Critical</td>
</tr>
<tr>
<td></td>
<td></td>
<td>High</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Low</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Medium</td>
</tr>
<tr>
<td>C2</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1</td>
</tr>
<tr>
<td>C3</td>
<td>2</td>
<td>F</td>
</tr>
<tr>
<td></td>
<td></td>
<td>M</td>
</tr>
</tbody>
</table>

The “Iteration History” table is shown in Figure 11.4. The quasi-Newton algorithm converged after 12 iterations, not counting the initial setup iteration.

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Evaluations</th>
<th>Objective Function</th>
<th>Change</th>
<th>Max Gradient</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>4</td>
<td>272.56284984</td>
<td>.</td>
<td>65.17039</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>267.70594206</td>
<td>4.85690778</td>
<td>7.86724</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>261.80868056</td>
<td>5.89726150</td>
<td>4.723085</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>256.62059571</td>
<td>5.18808485</td>
<td>4.650619</td>
</tr>
<tr>
<td>4</td>
<td>2</td>
<td>255.59346125</td>
<td>1.02713446</td>
<td>1.0462</td>
</tr>
<tr>
<td>5</td>
<td>2</td>
<td>255.44142594</td>
<td>0.15203531</td>
<td>1.018105</td>
</tr>
<tr>
<td>6</td>
<td>3</td>
<td>255.40692196</td>
<td>0.03450398</td>
<td>0.353611</td>
</tr>
<tr>
<td>7</td>
<td>3</td>
<td>255.39461736</td>
<td>0.01230460</td>
<td>0.415741</td>
</tr>
<tr>
<td>8</td>
<td>3</td>
<td>255.39362761</td>
<td>0.00009065</td>
<td>0.074411</td>
</tr>
<tr>
<td>9</td>
<td>3</td>
<td>255.39339211</td>
<td>0.00023460</td>
<td>0.062435</td>
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<tr>
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<td>255.39336653</td>
<td>0.00002558</td>
<td>0.004922</td>
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<tr>
<td>11</td>
<td>3</td>
<td>255.39336262</td>
<td>0.00000391</td>
<td>0.002273</td>
</tr>
<tr>
<td>12</td>
<td>3</td>
<td>255.39336237</td>
<td>0.00000026</td>
<td>0.000452</td>
</tr>
</tbody>
</table>

Figure 11.5 displays the final convergence status of the quasi-Newton algorithm. The GCONV=1E-8 convergence criterion is satisfied.
Chapter 11: The PHSELECT Procedure

Figure 11.6 displays the “Dimensions” table for this model. This table summarizes some important sizes of various model components. For example, it shows that the design matrix $X$ has 12 columns: 4 columns for the effects that are associated with the classification variable $C1$, 2 columns for each of the classification variables $C2$ and $C3$, and 1 column for each of the continuous variables $X1$–$X4$. However, the rank of the crossproducts matrix is only 9. Because the classification variables $C1$–$C3$ use GLM parameterization, there is one singularity in the crossproducts matrix of the model for each classification variable. Consequently, only nine parameters enter the optimization.

<table>
<thead>
<tr>
<th>Dimensions</th>
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</thead>
<tbody>
<tr>
<td>Number of Effects</td>
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<td>Max Effect Columns</td>
</tr>
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<td>Columns in Design</td>
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<tr>
<td>Rank of Design</td>
</tr>
</tbody>
</table>

The “Fit Statistics” table is shown in Figure 11.7. The $-2$ log likelihood at the converged estimates is 510.78672. You can use this value to compare the model to nested model alternatives by means of a likelihood ratio test. To compare models that are not nested, you can use information criteria such as Akaike’s information criterion (AIC), Akaike’s bias-corrected information criterion (AICC), and the Schwarz Bayesian information criterion (BIC). These criteria penalize the $-2$ log partial likelihood for the number of parameters.

<table>
<thead>
<tr>
<th>Fit Statistics</th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
</tr>
</tbody>
</table>

The “Parameter Estimates” table in Figure 11.8 shows that many parameters have fairly large $p$-values, indicating that one or more of the model effects might not be necessary.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1 Critical</td>
<td>1</td>
<td>0.400493</td>
<td>0.489562</td>
<td>0.6692</td>
<td>0.4133</td>
</tr>
<tr>
<td>C1 High</td>
<td>1</td>
<td>-0.990602</td>
<td>0.325145</td>
<td>9.2821</td>
<td>0.0023</td>
</tr>
<tr>
<td>C1 Low</td>
<td>1</td>
<td>-0.665495</td>
<td>0.339148</td>
<td>3.8504</td>
<td>0.0497</td>
</tr>
<tr>
<td>C1 Medium</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C2 0</td>
<td>1</td>
<td>0.410704</td>
<td>0.398833</td>
<td>1.0604</td>
<td>0.3031</td>
</tr>
<tr>
<td>C2 1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C3 F</td>
<td>1</td>
<td>-0.172550</td>
<td>0.337940</td>
<td>0.2607</td>
<td>0.6096</td>
</tr>
<tr>
<td>C3 M</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>X1</td>
<td>1</td>
<td>1.970488</td>
<td>0.524142</td>
<td>14.1335</td>
<td>0.0002</td>
</tr>
<tr>
<td>X2</td>
<td>1</td>
<td>0.726605</td>
<td>0.415141</td>
<td>3.0634</td>
<td>0.0801</td>
</tr>
<tr>
<td>X3</td>
<td>1</td>
<td>0.725390</td>
<td>0.585658</td>
<td>1.5341</td>
<td>0.2155</td>
</tr>
<tr>
<td>X4</td>
<td>1</td>
<td>-0.131226</td>
<td>0.057103</td>
<td>5.2810</td>
<td>0.0216</td>
</tr>
</tbody>
</table>
Finally, the procedure displays the table in Figure 11.9, which shows the amount of time (in seconds) that PROC PHSELECT required to perform different tasks in the analysis.

Figure 11.9 Procedure Timing

<table>
<thead>
<tr>
<th>Task</th>
<th>Seconds</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Setup and Parsing</td>
<td>0.02</td>
<td>16.78%</td>
</tr>
<tr>
<td>Levelization</td>
<td>0.01</td>
<td>8.78%</td>
</tr>
<tr>
<td>Model Initialization</td>
<td>0.00</td>
<td>0.91%</td>
</tr>
<tr>
<td>SSCP Computation</td>
<td>0.00</td>
<td>0.91%</td>
</tr>
<tr>
<td>Model Fitting</td>
<td>0.05</td>
<td>60.08%</td>
</tr>
<tr>
<td>Cleanup</td>
<td>0.01</td>
<td>6.01%</td>
</tr>
<tr>
<td>Total</td>
<td>0.09</td>
<td>100.00%</td>
</tr>
</tbody>
</table>

Syntax: PHSELECT Procedure

The following statements are available in the PHSELECT procedure:

```latex
PROC PHSELECT < options> ;
   BY variables ;
   CLASS variable < (options) > . . . < variable < (options) > > < / global-options > ;
   CODE < options> ;
   DISPLAY < table-list > < / options > ;
   DISPLAYOUT table-spec-list < / options > ;
   EFFECT name=effect-type(variables < / options > ) ;
   FREQ variable ;
   MODEL response < * censor(list) > = < effects > < / model-options > ;
   OUTPUT OUT=CAS-libref.data-table < options > < keyword <= name > > . . . < keyword <= name > > ;
   PARTITION partition-options ;
   SELECTION < METHOD = method < (method-options) > > < options > ;
   STRATA variable < MISSING > ;
   WEIGHT variable ;
```

The PROC PHSELECT statement and the MODEL statement are required. The CLASS statement can appear multiple times. If you use a CLASS statement, it must precede the MODEL statements.

PROC PHSELECT Statement

```latex
PROC PHSELECT < options> ;
```

The PROC PHSELECT statement invokes the procedure. Table 11.1 summarizes the available options in the PROC PHSELECT statement by function. They are then described fully in alphabetical order.
Table 11.1 PROC PHSELECT Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALPHA=</td>
<td>Specifies a global significance level</td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
</tbody>
</table>

**Output Options**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>CORRB</td>
<td>Displays the “Parameter Estimates Correlation Matrix” table</td>
</tr>
<tr>
<td>COVB</td>
<td>Displays the “Parameter Estimates Covariance Matrix” table</td>
</tr>
<tr>
<td>ITHIST</td>
<td>Displays the “Iteration History” table</td>
</tr>
<tr>
<td>LOGLIKENULL</td>
<td>Displays the “–2 Log Likelihood for Null Model” table</td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Limits or suppresses the display of class levels</td>
</tr>
<tr>
<td>NOSTDERR</td>
<td>Suppresses computation of the covariance matrix and standard errors</td>
</tr>
</tbody>
</table>

**Optimization Options**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ABSCONV=</td>
<td>Tunes the absolute function convergence criterion</td>
</tr>
<tr>
<td>ABSFCNV=</td>
<td>Tunes the absolute function difference convergence criterion</td>
</tr>
<tr>
<td>ABSGCONV=</td>
<td>Tunes the absolute gradient convergence criterion</td>
</tr>
<tr>
<td>ABSXCONV=</td>
<td>Tunes the absolute parameter convergence criterion</td>
</tr>
<tr>
<td>FCONV=</td>
<td>Tunes the relative function difference convergence criterion</td>
</tr>
<tr>
<td>FCONV2=</td>
<td>Tunes the second relative function difference convergence criterion</td>
</tr>
<tr>
<td>GCONV=</td>
<td>Tunes the relative gradient convergence criterion</td>
</tr>
<tr>
<td>GCONV2=</td>
<td>Tunes the second relative gradient convergence criterion</td>
</tr>
<tr>
<td>XCONV=</td>
<td>Tunes the relative parameter convergence criterion</td>
</tr>
<tr>
<td>HESSIAN</td>
<td>Uses analytic Hessian instead of finite-difference Hessian</td>
</tr>
<tr>
<td>MAXFUNC=</td>
<td>Specifies the maximum number of function evaluations in any optimization</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Specifies the maximum number of iterations in any optimization</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the upper limit of CPU time (in seconds) for any optimization</td>
</tr>
<tr>
<td>MINITER=</td>
<td>Specifies the minimum number of iterations in any optimization</td>
</tr>
<tr>
<td>TECHNIQUE=</td>
<td>Selects the optimization technique</td>
</tr>
</tbody>
</table>

**LASSO Options**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LASSORHO=</td>
<td>Specifies the base regularization parameter for the LASSO method</td>
</tr>
<tr>
<td>LASSOSTEPS=</td>
<td>Specifies the maximum number of steps for the LASSO method</td>
</tr>
<tr>
<td>LASSOTOL=</td>
<td>Specifies the convergence criterion for the LASSO method</td>
</tr>
</tbody>
</table>

The optimization options, with the exception of the HESSIAN option, are fully described in the section “Optimization Options” on page 42 in Chapter 2, “Shared Concepts.” The following list describes the other options available in the PROC PHSELECT statement:

**ALPHA=number**

specifies a global significance level for the construction of confidence intervals. The confidence level is 1–number. The value of number must be between 0 and 1. By default, ALPHA=0.05.

**CORRB**

creates the “Parameter Estimates Correlation Matrix” table. The correlation matrix is computed by normalizing the covariance matrix $\Sigma$. That is, if $\sigma_{ij}$ is an element of $\Sigma$, then the corresponding element of the correlation matrix is $\sigma_{ij}/\sigma_i\sigma_j$, where $\sigma_i = \sqrt{\sigma_{ii}}$. 
COVB
creates the “Parameter Estimates Covariance Matrix” table. The covariance matrix is computed as the
inverse of the negative Hessian matrix, which is the matrix of second derivatives of the log-likelihood
function with respect to the model parameters.

DATA=\texttt{CAS-libref.data-table}
names the input data table for PROC PHSELECT to use. The default is the most recently created data
table. \texttt{CAS-libref.data-table} is a two-level name, where

\texttt{CAS-libref} refers to a collection of information that is defined in the LIBNAME statement and
includes the \texttt{caslib}, which includes a path to the data, and a session identifier, which
defaults to the active session but which can be explicitly defined in the LIBNAME
statement. For more information about \texttt{CAS-libref}, see the section “Using CAS
Sessions and CAS Engine Librefs” on page 589.

\texttt{data-table} specifies the name of the input data table.

HESSIAN
computes the Hessian matrix by using the analytic expression for the second-order derivatives of the log
partial likelihood function instead of using the finite-difference method. When you specify this option,
the optimization technique defaults to the Newton-Raphson method with ridging (TECH=NRRIDG),
but you can use the TECH= option to specify the technique of your choice. The HESSIAN option
requires a large amount of memory for each machine in the cluster.

ITHIST
generates the “Iteration History” table.

LASSORHO=\texttt{r}
specifies the base regularization parameter for the LASSO model selection method. The regularization
parameter for step \texttt{i} is \texttt{r}^\texttt{i}. By default, LASSORHO=0.8.

LASSOSTEPS=\texttt{n}
specifies the maximum number of steps for LASSO model selection. By default, LASSOSTEPS=20.

LASSOTOL=\texttt{r}
specifies the convergence tolerance for the optimization algorithm that solves for the LASSO parameter
estimates at each step of LASSO model selection. By default, LASSOTOL=1E–6.

LOGLIKENULL
creates the “–2 Log Likelihood for the Null Model” table. If you also specify the PARTITION
statement, the table displays the –2 log likelihood for the null model for each data partition.

NOCLPRINT\(<=\texttt{number}\)
suppresses the display of the “Class Level Information” table if you do not specify \texttt{number}. If you
specify \texttt{number}, the values of the classification variables are displayed for only those variables whose
number of levels is less than \texttt{number}. Specifying \texttt{number} helps reduce the size of the “Class Level
Information” table if some classification variables have a large number of levels.
NOSTDERR
suppresses computation of the covariance matrix and the standard errors of the regression coefficients.
When the model contains many variables (such as thousands), inverting the Hessian matrix to derive
the covariance matrix and the standard errors of the regression coefficients can be time-consuming.
The CORRB, COVB, and TYPE3 options are not available when you specify this option.

BY Statement

BY variables;
You can specify a BY statement in PROC PHSELECT to obtain separate analyses of observations in groups
that are defined by the values of the BY variables. If you specify more than one BY statement, only the last
one specified is used. For more information, see the discussion of BY-group processing in SAS Language
Reference: Concepts.

CLASS Statement

CLASS variable <(options)> . . . <variable <(options)>> < / global-options> ;
The CLASS statement names the classification variables to be used as explanatory variables in the analysis.
You can list the response variable for binary models in the CLASS statement, but this is not required.
Table 11.2 summarizes the values that you can use for either an option or a global-option. The options are
fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>

CODE Statement

CODE <options>;
The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a
file, to a catalog entry, or to a CAS table. The predicted values include survival probabilities and cumulative
hazards at specific time points. To score new data, you can then include the file or the catalog entry in a
DATA step, or you can specify the CAS table in the runCodeTable action in the dataStep action set (for
more information, see SAS Viya: System Programming Guide).
Table 11.3 summarizes the options available in the CODE statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>CUMHAZ</td>
<td>Generates cumulative hazard values at specified time points</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOSURVIVAL</td>
<td>Suppresses the generation of survival probabilities</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
<tr>
<td>SHOWTIME</td>
<td>Creates variables that contain the time points at which predictions are made</td>
</tr>
<tr>
<td>TIMEPOINT=</td>
<td>Specifies the time points at which survival probabilities or cumulative hazards are predicted</td>
</tr>
</tbody>
</table>

The following CODE statement options are particularly important:

**CUMHAZ**

generates SAS code to predict the cumulative hazard function at the time points that you specify in the **TIMEPOINT=** option.

**FILE=filename**

names the external file that saves the generated code. When enclosed in a quoted string (for example, `FILE="c:\mydir\scorecode.sas"`), this option specifies the path and filename for writing the code to an external file. If you do not specify a path but your SAS client has a default path, then the code is written to an external file named **filename** at that location. You can also specify an unquoted **filename** of no more than eight characters. If the **filename** is assigned as a fileref in a Base SAS FILENAME statement, the file specified in the FILENAME statement is opened; otherwise, if your SAS client has a default path, an external file named **filename** is created. This option cannot be specified with the **OUT=** option.

**NOSURVIVAL**

suppresses SAS code for survival probabilities prediction. If you do not specify this option, PROC PHSELECT generates SAS code to predict survival probabilities at the time points that you specify in the **TIMEPOINT=** option.

**SHOWTIME**

creates variables that contain the time points at which predictions are made. If T is the name of the failure time variable, these time point variables are named T_1, T_2, and so on.

**TIMEPOINT=list | QUANTILE(probability-list)**

specifies the time points at which survival probabilities or cumulative hazards are predicted. You can specify a list of numbers that represent exact time points. For example:
code cumhaz timepoint = 40 to 60 by 10;

If \( T \) is the name of the failure time variable, the preceding specification requests the predicted cumulative hazard and survival probability at the time points \( T=40, T=50, \) and \( T=60 \). If you also specify the SHOWTIME option, these time points are saved in the variables \( T_1, T_2, \) and \( T_3 \), respectively. The predicted variables are named and labeled as shown in Table 11.4.

<table>
<thead>
<tr>
<th>( T )</th>
<th>Name</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>40</td>
<td>C_T_1</td>
<td>Cumulative Hazard at ( T_1 )</td>
</tr>
<tr>
<td>50</td>
<td>C_T_2</td>
<td>Cumulative Hazard at ( T_2 )</td>
</tr>
<tr>
<td>60</td>
<td>C_T_3</td>
<td>Cumulative Hazard at ( T_3 )</td>
</tr>
<tr>
<td>40</td>
<td>S_T_1</td>
<td>Survival Probability at ( T_1 )</td>
</tr>
<tr>
<td>50</td>
<td>S_T_2</td>
<td>Survival Probability at ( T_2 )</td>
</tr>
<tr>
<td>60</td>
<td>S_T_3</td>
<td>Survival Probability at ( T_3 )</td>
</tr>
</tbody>
</table>

Alternatively, you can use the keyword QUANTILE to specify a list of quantile probabilities. For example:

\[
\text{code timepoint = quantile(.2, .5, .8);}
\]

The PHSELECT procedure computes the 20th, 50th, and 80th percentiles from the Kaplan-Meier curve (or the Breslow curve if you also specify the ENTRY= option in the MODEL statement) and use them as the time points for the prediction.

By default, TIMEPOINT=QUANTILE(0.25, 0.50, 0.75).

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

**DISPLAY Statement**

```
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE
statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 621. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`. When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

- **CASESENSITIVE**
  - performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  - displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  - suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  - displays the display table names, labels, and paths.

---

**DISPLAYOUT Statement**

`DISPLAYOUT table-spec-list <options> ;`

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.

- `key` specifies `key` as the ODS table name and also as the CAS output table name.
Table names and partial pathnames are discussed under the `DISPLAY` statement. The `DISPLAYOUT` statement does not support regular expressions.

You can specify the following options after a slash (/):

**INCLUDEALL**
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the `table-spec-list` specification is ignored.

**NOREPLACE**
does not replace any existing CAS output table of the same name.

**REPEATED**
replicates all CAS output tables on all nodes.

---

**EFFECT Statement**

```
EFFECT name=effect-type (variables < / options>) ;
```

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as *constructed effects* to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following effect-types:

- **COLLECTION**
specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.

- **MULTIMEMBER | MM**
specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.

- **POLYNOMIAL | POLY**
specifies a multivariate polynomial effect in the specified numeric variables.

- **SPLINE**
specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 11.5 summarizes the options available in the EFFECT statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
</tbody>
</table>

---
### Table 11.5 continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
</tbody>
</table>

#### Polynomial Effects Options
- **DEGREE=** Specifies the degree of the polynomial
- **DETAILS** Displays details of the specified polynomial
- **MDEGREE=** Specifies the maximum degree of any variable in a term of the polynomial
- **NOSEPARATE** Treats the polynomial as a single effect with multiple degrees of freedom
- **STANDARDIZE=** Specifies centering and scaling suboptions for the variables that define the polynomial

#### Spline Effects Options
- **BASIS=** Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect
- **DATABOUNDARY** Uses the extremes of the data as boundary knots for a B-spline basis
- **DEGREE=** Specifies the degree of the spline effect
- **DETAILS** Displays the knots and locations for each spline basis function
- **KNOTMAX=** Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value
- **KNOTMETHOD=** Specifies how to construct the knots for the spline effect
- **KNOTMIN=** Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value
- **NATURALCUBIC** Specifies a natural cubic spline basis for the spline effect
- **SEPARATE** Treats the spline basis for each variable as a separate effect when multiple variables are specified
- **SPLIT** Treats each design matrix column as a separate effect for selection methods

For more information about the syntax of these *effect-types* and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”
**FREQ Statement**

```
FREQ variable ;
```

The `variable` in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC PHSELECT treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ `variable` for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

**MODEL Statement**

```
MODEL response < * censor (list) > = effects < / options > ;
```

The MODEL statement identifies the variables to be used as the failure time variable, the optional censoring variable, and the explanatory effects, including covariates, main effects, interactions, and nested effects.

The name of the failure time variable precedes the equal sign. This name can optionally be followed by an asterisk, the name of the censoring variable, and a list of censoring values (separated by blanks or commas) enclosed in parentheses.

The censoring variable must be numeric, and the failure time variables must contain nonnegative values. Any observation that has a negative failure time is excluded from the analysis, as is any observation that has a missing value for any of the variables listed in the MODEL statement. Failure time variables in SAS date format are not recommended, because the dates might be translated into negative numbers and consequently the corresponding observations would be discarded.

If the censoring variable takes one of these values, the corresponding failure time is considered to be censored. Following the equal sign are the explanatory effects (sometimes called independent variables or covariates) for the model.

For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

Table 11.6 summarizes the `options` available in the MODEL statement. You can specify these `options` after a slash (/).

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Options</td>
<td></td>
</tr>
<tr>
<td>CLB</td>
<td>Requests confidence limits</td>
</tr>
<tr>
<td>ENTRY=</td>
<td>Specifies the left-truncation time variable</td>
</tr>
<tr>
<td>INCLUDE=</td>
<td>Includes effects in all models for model selection</td>
</tr>
<tr>
<td>INFORMATIVE</td>
<td>Models missing values by using extra indicator variables</td>
</tr>
<tr>
<td>OFFSET=</td>
<td>Specifies the offset variable</td>
</tr>
<tr>
<td>START=</td>
<td>Includes effects in the initial model for model selection</td>
</tr>
<tr>
<td>TYPE3</td>
<td>Displays the Type 3 or joint tests of effects</td>
</tr>
</tbody>
</table>
The following list describes these options:

**CLB**
constructs confidence limits for each of the parameter estimates. The confidence level is 0.95 by default; you can change it by specifying the **ALPHA=** option in the PROC PHSELECT statement.

**ENTRY=** variable
specifies the left-truncation time variable. The left-truncation time is the time at which an individual starts to be observed.

**INCLUDE=** n | single-effect | (effects)
forces effects to be included in all models. If you specify **INCLUDE=** n, then the first n effects that you list in the **MODEL** statement are included in all models. If you specify **INCLUDE=** single-effect or **INCLUDE=**(effects), then the specified effects are forced into all models. The effects that you specify in this option must be explanatory effects that you specify in the **MODEL** statement before the slash (/).

**INFORMATIVE**
models missing values by using extra model effects. These effects consist of dummy variables that take the value 1 when the value of a continuous model variable involved in the effect is missing, and take the value 0 otherwise. The missing value in the original model effect is replaced by the average value of the effect for the nonmissing values. For continuous-by-class effects, such as A*x, where A is a classification variable and x is a continuous variable, informative missingness creates multiple dummy columns and substitutes the effect mean of x that corresponds to the respective level of A. Missing values for classification variables are treated as valid levels. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

**OFFSET=** variable
specifies a variable to be used as an offset to the linear predictor. An offset plays the role of an effect whose coefficient is known to be 1. The offset variable cannot appear in the **CLASS** statement or elsewhere in the **MODEL** statement. Observations that have missing values for the offset variable are excluded from the analysis.

**START=** n | single-effect | (effects)
begins the selection process from the designated initial model for the forward and stepwise selection methods. If you specify **START=** n, then the starting model includes the first n effects that you list in the **MODEL** statement. If you specify **START=** single-effect or **START=**(effects), then the starting model includes those specified effects. The effects that you specify in the **START=** option must be explanatory effects that you specify in the **MODEL** statement before the slash (/). This option is not available when you specify **METHOD=** BACKWARD in the **SELECTION** statement.

**TYPE3**
requests that Wald statistics for Type 3 contrasts be computed for each effect that you specify in the **MODEL** statement. For more information, see the section “Joint Tests and Type 3 Tests” on page 616.

---

**OUTPUT Statement**

```
OUTPUT OUT=CAS-libref.data-table
< COPYVARS=(variables) >
< keyword < =name > > . . . < keyword < =name > > ;
```
The OUTPUT statement creates a data table that contains observationwise statistics that PROC PHSELECT computes after fitting the model. In order to avoid data duplication for large data tables, the variables in the input data table are *not* included in the output data table unless you specify them in the COPYVAR= option.

The output statistics are computed based on the final parameter estimates. If the optimization does not converge, then the output data table is not created.

For observations in which only the censoring variable is missing, values of the linear predictor and the predicted survival probabilities are computed even though these observations do not affect the model fit. This enables, for example, predicted survival probabilities to be computed for new observations.

You must specify the following option:

```plaintext
OUT=CAS-libref.data-table
```

names the output data table for PROC PHSELECT to use. You must specify this option before any other options. *CAS-libref.data-table* is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 589.

- **data-table** specifies the name of the output data table.

You can also specify the following syntax elements:

```plaintext
COPYVAR=variable
COPYVARS=(variables)
```

transfers one or more *variables* from the input data table to the output data table.

```plaintext
keyword <= name >
```

specifies a statistic to include in the output data table. Four statistics (DFBETA, RESSCH, RESSCO, and WTRESSCH) are multidimensional; each has a dimension equal to the number of parameters in the model. For the one-dimensional statistic, you can name the variable *name*. For the multidimensional statistic, *name* is used as the prefix; for example, if X1–X10 are the explanatory variables in the model, specifying RESSCH=sch creates the variables schX1–schX10 as the 10-dimensional Schoenfeld residual variables. If you do not provide a *name*, the PHSELECT procedure assigns a default name based on the type of statistic that is requested.

Table 11.7 summarizes the *keywords* available in the OUTPUT statement.

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Default Names</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Statistic Options</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CUMHAZ</td>
<td>Specifies the predicted cumulative hazard</td>
<td><em>CUMHAZ</em></td>
</tr>
<tr>
<td>STDXBETA</td>
<td>Specifies the standard error estimate of the linear predictor</td>
<td><em>STDXBETA</em></td>
</tr>
<tr>
<td>SURVIVAL</td>
<td>Specifies the predicted survival probability</td>
<td><em>SURVIVAL</em></td>
</tr>
<tr>
<td>XBETA</td>
<td>Specifies the linear predictor</td>
<td><em>XBETA</em></td>
</tr>
</tbody>
</table>
### Table 11.7 continued

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
<th>Default Names</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Diagnostic Options</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>DFBETA</td>
<td>Specifies the standardize deletion parameter differences</td>
<td><em>DFBETA</em></td>
</tr>
<tr>
<td>LD</td>
<td>Specifies the likelihood displacement</td>
<td><em>LD</em></td>
</tr>
<tr>
<td>RESDEV</td>
<td>Specifies the deviance residual</td>
<td><em>RESDEV</em></td>
</tr>
<tr>
<td>REMART</td>
<td>Specifies the martingale residual</td>
<td><em>RESMART</em></td>
</tr>
<tr>
<td>RESSCH</td>
<td>Specifies the Schoenfeld residuals</td>
<td><em>RESSCH</em></td>
</tr>
<tr>
<td>RESSCO</td>
<td>Specifies the score residuals</td>
<td><em>RESSCO</em></td>
</tr>
<tr>
<td>WTRESSCH</td>
<td>Specifies the weighted Schoenfeld residuals</td>
<td><em>WTRESSCH</em></td>
</tr>
<tr>
<td><strong>Other Option</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ROLE</td>
<td>Specifies the observation role</td>
<td><em>ROLE</em></td>
</tr>
</tbody>
</table>

The following list describes these *keywords*. For more information, see the section “Predicted Values and Regression Diagnostics” on page 614.

**CUMHAZ**
- specifies the predicted cumulative hazard function at the observed time. The default *name* is _CUMHAZ_.

**DFBETA**
- requests the approximate changes in the parameter estimates \((\hat{\beta} - \hat{\beta}_{(j)})\) when the *j*th observation is omitted. These variables are a weighted transform of the score residual variables and are useful in assessing local influence. The default *name* that is used as a prefix is _DFBETA_.

**LD**
- specifies the approximate likelihood displacement when the observation is omitted. This diagnostic can be used to assess the impact of each observation on the overall fit of the model. The default *name* is _LD_.

**RESDEV**
- specifies the deviance residual. This variable is a transform of **RESMART** to achieve a more symmetric distribution. The default *name* is _RESDEV_.

**RESMART**
- specifies the martingale residual, which, at the observed time \(t\), can be interpreted as the difference over \([0, t]\) in the observed number of events minus the expected number of events. The default *name* is _RESMART_.

**RESSCH**
- requests the Schoenfeld residuals, which are useful in assessing the proportional hazards assumption. Schoenfeld residuals are computed only at uncensored times and are missing for censored times. If an effect in the MODEL statement is not included in the final model, the corresponding Schoenfeld residuals are set to missing. The default *name* that is used as a prefix is _RESSCH_.
RESSCO requests the score residuals, which are a decomposition of the first partial derivative of the log likelihood. They can be used to assess the leverage that each subject exerts in the parameter estimation. The default name that is used as a prefix is _RESSCO_.

ROLE specifies the numeric variable that indicates the role that each observation plays in fitting the model. The default name is _ROLE_. Table 11.8 shows how this variable is interpreted for each observation.

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by specifying a PARTITION statement, then the role variable value is 1 for observations that are used in fitting the model and 0 for observations that have at least one missing or invalid value for the response, regressor, frequency, or weight variables.

STDXBETA specifies the standard error estimates of XBETA. The default name is _STDXBETA_.

SURVIVAL requests the predicted survival probabilities at the observed times. The default name is _SURVIVAL_.

WTRESSCH requests the weighted Schoenfeld residuals, which are useful in investigating the nature of nonproportionality if the proportional hazard assumption does not hold. If an effect in the MODEL statement is not included in the final model, the corresponding weighted Schoenfeld residuals are set to missing. The default name that is used as a prefix is _WTRESSCH_.

XBETA specifies the linear predictor. The default name is _XBETA_.

**PARTITION Statement**

```
PARTITION partition-option;
```

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:
FRACTION(<TEST=\text{fraction}> <VALIDATE=\text{fraction}> <SEED=\text{number}>)
randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The SEED= option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify SEED=\text{number} or if \text{number} is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

ROLE=\text{variable} (<TEST='\text{value}'> <TRAIN='\text{value}'> <VALIDATE='\text{value}'>)
ROLEVAR=\text{variable} (<TEST='\text{value}'> <TRAIN='\text{value}'> <VALIDATE='\text{value}'>)
names the \text{variable} in the input data table whose values are used to assign roles to each observation. This \text{variable} cannot also appear as an analysis variable in other statements or options. The TEST=, TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

**SELECTION Statement**

**SELECTION <METHOD=\text{method}< (method-options)> >> <options> ;**

The SELECTION statement performs model selection by examining whether effects should be added to or removed from the model according to rules that are defined by model selection methods. You can use the PLOT= option to produce graphical summaries of the selection process or the HIERARCHY= option to specify whether and how a requirement of model hierarchy is applied. The statement is fully documented in the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

The PHSELECT procedure supports the following effect-selection \text{methods} in the SELECTION statement:

- **BACKWARD** performs backward elimination. This method starts with all effects in the model and deletes effects.
- **BACKWARD(FAST)** performs fast backward elimination. This method starts with all effects in the model and deletes effects without refitting the model.
- **FORWARD** performs forward selection. This method starts with no effects in the model and adds effects.
- **LASSO** performs model selection by the group LASSO method. This method adds and removes effects by using a sequence of LASSO steps. For more information, see the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.”
- **NONE** results in no model selection. This method fits the full model.
- **STEPWISE** performs stepwise selection. This method is similar to the FORWARD method, except that effects already in the model do not necessarily stay there.

By default, METHOD=STEPWISE.
The SELECT=, CHOOSE=, and STOP= method-options default to the Schwartz Bayesian criterion (SBC). You can specify the following criteria in the SELECT=, CHOOSE=, and STOP= method-options:

- **AIC** uses Akaike’s information criterion (Akaike 1974) on the training data.
- **AICC** uses a small-sample bias-corrected version of Akaike’s information criterion, as promoted by Hurvich and Tsai (1989) and Burnham and Anderson (1998), on the training data.
- **SBC** or **BIC** uses the Schwarz Bayesian criterion (Schwarz 1978) on the training data.
- **SL** uses the significance level of the score test as the criterion on the training data (not available for the CHOOSE= option).
- **VALIDATE** uses the –2 log-likelihood (M2LL) value computed on the validation data as the criterion (not available for the SELECT= option).

If you specify METHOD=LASSO and do not specify either the CHOOSE= or STOP= option, then the model in the last LASSO step is chosen as the selected model.

**NOTE:** If you use the fast backward elimination method, then the –2 log-likelihood, AIC, AICC, and SBC statistics are approximated at each step where the model is not refit, and hence they do not match the values that are computed when that model is fit outside the selection routine. Similarly, if you specify SELECT=AIC, AICC, or SBC, the selection criteria are estimated (Lawless and Singhal 1978), and hence they do not match the values that are computed when that model is fit outside the selection routine.

**NOTE:** The default model hierarchy method is HIERARCHY=None for the stepwise, forward, and fast backward selection methods. The backward elimination method always uses the HIERARCHY=SINGLE method-option.

If you specify DETAILS=ALL, the LASSO method produces a table that displays the effects that are added or removed at each step and the corresponding fit statistics. For the other methods, you can specify the following values for the DETAILS= option:

- **SUMMARY** produces a summary table that shows the effect that is added or removed at each step along with the criteria specified in the SELECT=, CHOOSE=, and STOP= method-options. The summary table is produced by default if you do not specify the DETAILS= option.
- **STEPS** produces the preceding summary table and displays the results from fitting each model at each step.
- **ALL** produces the preceding tables and a detailed listing of all candidates at each step along with their ranking in terms of the selection criterion for addition to or removal from the model.

If you specify the PLOTS=CRITERIA or PLOTS=ALL option, then a plot of the fit criterion by the selection step is created for the AIC, AICC, and SBC statistics. If you also specify a PARTITION statement, then the same type of plot is created for the M2LL statistics.

If you specify the PLOTS=FITBYROLE or PLOTS=ALL option and a PARTITION statement, then a plot of the M2LL by the selection step for each role is created.

The PLOTS= option is not available for the LASSO method.
**STRATA Statement**

```
STRATA variable < / MISSING > ;
```

The STRATA statement specifies a `variable` whose values determine the stratification of the data. Strata are formed according to the nonmissing values of the STRATA `variable` unless you specify the MISSING option.

**WEIGHT Statement**

```
WEIGHT variable ;
```

The `variable` in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

**Details: PHSELECT Procedure**

### Missing Values

Any observation that has missing values for the response, frequency, weight, offset, or explanatory variables is excluded from the analysis; however, missing values are valid for response and explanatory variables that are specified along with the MISSING option in the CLASS statement. Observations that have a nonpositive weight or a frequency less than 1 are also excluded.

The estimated linear predictor and the fitted probabilities are not computed for any observation that has missing offset or explanatory variable values. However, if only the response value is missing, the linear predictor and the fitted probabilities can be computed and output to a data table by using the OUTPUT statement.

You can also model the missing values by specifying the INFORMATIVE option in the MODEL statement. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

### Cox Proportional Hazards Regression Model

The Cox proportional hazards regression model is a semiparametric model that assumes a parametric form for the effects of the explanatory variables, but it allows an unspecified form for the underlying survivor function. The survival time of each member of a population is assumed to follow its own hazard function, \( \lambda_j(t) \), expressed as

\[
\lambda_j(t) = \lambda(t; Z_j) = \lambda_0(t) \exp(Z_j' \beta)
\]

where \( \lambda_0(t) \) is an arbitrary and unspecified baseline hazard function, \( Z_j \) is the vector of explanatory variables for the \( j \)th individual, and \( \beta \) is the vector of unknown regression parameters that is associated with the explanatory variables.
Chapter 11: The PHSELECT Procedure

The population under study can consist of a number of subpopulations, each of which has its own baseline hazard function. A stratified analysis is needed to adjust for such subpopulation differences. Under the stratified model, the hazard function for the \( j \)th individual in the \( i \)th stratum is expressed as

\[
\lambda_{ij}(t) = \lambda_{i0}(t) \exp(Z'_{ij} \beta)
\]

where \( \lambda_{i0}(t) \) is the baseline hazard function for the \( i \)th stratum and \( Z_{ij} \) is the vector of explanatory variables for the individual. The regression coefficients are assumed to be the same for all individuals across all strata.

To estimate \( \beta \), Cox (1972, 1975) introduced the partial likelihood function, which eliminates the unknown baseline hazard functions and accounts for censored survival times.

---

**Partial Likelihood for the Cox Model**

Let \( Z_l \) denote the vector explanatory variables for the \( l \)th individual, and let \( w_l \) be the associated weight. Let \( t_1 < t_2 < \cdots < t_k \) denote the \( k \) distinct, ordered event times. Let \( d_l \) denote the multiplicity of failures at \( t_l \); that is, \( d_l \) is the size of the set \( D_l \) of individuals that fail at \( t_l \). Let \( R_i \) be the risk set at \( t_i \). Using this notation, the following equations describe the partial likelihood functions that PROC PHSELECT uses to estimate \( \beta \).

**Breslow Likelihood**

\[
L(\beta) = \prod_{i=1}^{k} \frac{e^{\beta' \sum_{j \in D_i} Z_j}}{\sum_{l \in R_i} e^{\beta' Z_l} d_l}
\]

If you incorporate weights, the Breslow likelihood becomes

\[
L(\beta) = \prod_{i=1}^{k} \frac{e^{\beta' \sum_{j \in D_i} w_j Z_j}}{\sum_{l \in R_i} w_l e^{\beta' Z_l} \sum_{j \in D_i} w_j}
\]

In a stratified analysis, the partial likelihood is the product of the partial likelihood functions for the individual strata.

The regression coefficients are estimated by maximizing the log of the partial likelihood function with respect to \( \beta \).

---

**The LASSO Method of Model Selection**

**LASSO Selection**

The PHSELECT procedure implements the group LASSO method, which is described in the section “Group LASSO Selection” on page 67 in Chapter 2, “Shared Concepts.” The current section provides some background about the LASSO method that you need in order to understand the group LASSO method.
LASSO (least absolute shrinkage and selection operator) selection arises from a constrained form of ordinary least squares regression in which the sum of the absolute values of the regression coefficients is constrained to be smaller than a specified parameter. More precisely, let $\mathbf{Z} = (z_1, z_2, \ldots, z_m)$ denote the matrix of covariates, and let $\mathbf{y}$ denote the response. Then for a given parameter $t$, the LASSO regression coefficients $\mathbf{\beta} = (\beta_1, \beta_2, \ldots, \beta_m)$ are the solution to the following constrained least squares problem:

$$
\min ||\mathbf{y} - \mathbf{Z}\mathbf{\beta}||^2 \quad \text{subject to} \quad \sum_{j=1}^{m} |\beta_j| \leq t
$$

For the Cox proportional hazards regression model, the LASSO regression coefficients $\mathbf{\beta} = (\beta_1, \beta_2, \ldots, \beta_m)$ are the solution to the following constrained optimization problem,

$$
\min \{-l(\mathbf{\beta})\} \quad \text{subject to} \quad \sum_{j=1}^{m} |\beta_j| \leq t
$$

where $l(\mathbf{\beta})$ is the log of the partial likelihood function $L(\mathbf{\beta})$ defined in the section “Partial Likelihood for the Cox Model” on page 612.

Provided that the LASSO parameter $t$ is small enough, some of the regression coefficients will be exactly 0. Hence, you can think of the LASSO method as selecting a subset of the regression coefficients for each LASSO parameter. By increasing the LASSO parameter in discrete steps, you obtain a sequence of regression coefficients for which the nonzero coefficients at each step correspond to selected parameters. For more information about the LASSO method, see, for example, Hastie, Tibshirani, and Friedman (2009).

---

**Model Fit and Assessment Statistics**

The statistics that are defined in this section are useful for assessing the fit of the model to your data; they are displayed in the “Fit Statistics” table. The statistics are computed for each data role when you specify a PARTITION statement.

**Information Criteria**

The calculation of the information criteria uses the following formulas, where $p$ denotes the number of effective parameters in the candidate model, $F$ denotes the sum of the frequencies of the uncensored observations that are used, and $\ell$ is the log partial likelihood that is evaluated at the converged estimates:

$$
\text{AIC} = -2\ell + 2p
$$

$$
\text{AICC} = \begin{cases} 
-2\ell + 2pF/(F - p - 1) & \text{when } F > p + 2 \\
-2\ell + 2p(p + 2) & \text{otherwise}
\end{cases}
$$

$$
\text{SBC} = -2\ell + p \log(F)
$$

If you do not specify a FREQ statement, $F$ equals $n$, the number of uncensored observations that are used.
Predicted Values and Regression Diagnostics

For the $i$th observation, let $\{(X_i, \Delta_i, Z_i)\}$ represent the failure time, the event indicator, and the vector of covariate values, respectively. Let $\hat{\beta}$ be the vector of regression coefficients. For $t \geq 0$, let

$$
Y_i(t) = I(X_i \geq t)
$$
$$
N_i(t) = I(X_i \leq t)
$$
$$
S^{(0)}(\beta, t) = \sum_i Y_i(t)e^{\beta'Z_i}
$$
$$
S^{(1)}(\beta, t) = \sum_i Y_i(t)e^{\beta'Z_i}Z_i
$$
$$
\tilde{Z}(\beta, t) = \frac{S^{(1)}(\beta, t)}{S^{(0)}(\beta, t)}
$$
$$
d\Lambda_0(\beta, t) = \sum_i \frac{dN_i(t)}{S^{(0)}(\beta, t)}
$$
$$
dM_i(\beta, t) = dN_i(t) - Y_i(t)e^{\beta'Z_i(t)}d\Lambda_0(\beta, t)
$$

Let $\hat{\beta}$ be the estimator of $\beta$, and let $I(\hat{\beta})$ be the observed information matrix.

Predicted Values

Let $z$ be a vector of covariates. The linear predictor and its standard error estimate are, respectively,

$$
z'\hat{\beta} \quad \text{and} \quad \sqrt{z'\hat{\Sigma}^{-1}(\hat{\beta})z}
$$

The predicted cumulative hazard at a time point $t$ is

$$
\hat{\Lambda}(t, z) = e^{\hat{\beta}'z(t)}
$$

and the predicted survival probability is

$$
\hat{S}(t, z) = e^{-\hat{\Lambda}(t, z)}
$$

Residuals

The martingale residual for the $i$th observation is

$$
\hat{M}_i = \Delta_i - \hat{\Lambda}(X_i, Z_i)
$$

The deviance residual is a transform of the martingale residual,

$$
\hat{D}_i = \text{sign}(\hat{M}_i)\sqrt{2[-\hat{M}_i - \Delta_i \log(\Delta_i - \hat{M}_i)]}
$$

The square root shrinks large negative martingale residuals, and the logarithmic transformation expands martingale residuals that are close to unity.
The Schoenfeld (1982) residual vector is calculated per event time. If the \( i \)th observation is uncensored, the Schoenfeld residual vector is

\[
\hat{U}_i = Z_i - \tilde{Z} (\hat{\beta}, X_i)
\]

Otherwise, the elements of the Schoenfeld residual vector are set to missing values. Under the proportional hazards assumption, the Schoenfeld residuals have the sample path of a random walk; therefore, they are useful in assessing time trend or lack of proportionality. Harrell (1986) proposed a \( z \)-transform of the Pearson correlation between these residuals and the rank order of the failure time as a test statistic for nonproportional hazards.

The score residual vector for the \( i \)th observation is

\[
\hat{L}_i = \int_0^\infty [Z_i(s) - \tilde{Z} (\hat{\beta}, s)] dM_i (\hat{\beta}, s)
\]

The score residuals are a decomposition of the first partial derivative of the log likelihood. They are useful in assessing the influence of each observation on individual parameter estimates. Therneau, Grambsch, and Fleming (1990) have considered a Kolmogorov-type test based on the cumulative sum of the residuals for detecting nonproportional hazards.

### Other Regression Diagnostics

The vector of weighted Schoenfeld residuals, \( W_i \), is computed as

\[
W_i = n_e \mathcal{I}^{-1}(\hat{\beta}) \hat{U}_i
\]

where \( n_e \) is the total number of events and \( \hat{U}_i \) is the vector of Schoenfeld residuals for the \( i \) observation. The weighted Schoenfeld residuals are useful in assessing the proportional hazards assumption. The idea is that most of the common alternatives to the proportional hazards can be cast in terms of a time-varying coefficient model,

\[
\lambda(t, Z) = \lambda_0(t) \exp(\beta_1(t) Z_1 + \beta_2(t) Z_2 + \cdots)
\]

where \( \lambda(t, Z) \) and \( \lambda_0(t) \) are hazard rates. Let \( \hat{\beta}_j \) and \( r_{ij} \) be the \( j \)th component of \( \hat{\beta} \) and \( r_i \), respectively. Grambsch and Therneau (1994) suggest using a smoothed plot of \( (\hat{\beta}_j r_{ij}) \) versus \( t_i \) to discover the functional form of the time-varying coefficient \( \beta_j(t) \). A zero slope indicates that the coefficient does not vary with time.

The DFBETA diagnostics approximate the changes in the parameter estimates, \( \delta_i \hat{\beta}_i = \hat{\beta} - \hat{\beta}_{(-i)} \), when the \( i \)th observation is left out. The \( j \)th component of \( \delta_i \hat{\beta} \) can be used to assess any unusual effect of the \( i \)th observation on \( \hat{\beta}_j \). The exact computation of \( \delta_i \hat{\beta} \) involves refitting the model each time a subject is omitted. Cain and Lange (1984) derived the following approximation of \( \delta_i \beta \) as weighted score residuals,

\[
\text{DFBETA}_i = \mathcal{I}^{-1}(\hat{\beta}) \hat{L}_i
\]

where \( \hat{L}_i \) is the score residual vector of the \( i \)th observation.

The LD statistic approximates the likelihood displacement, which is the amount by which minus twice the log likelihood \( -2 \log L(\hat{\beta}) \), under a fitted model, changes when each observation in turn is left out. When the \( i \)th subject is omitted, the likelihood displacement is

\[
2 \log L(\hat{\beta}) - 2 \log L(\hat{\beta}_{(-i)})
\]
where \( \hat{\beta}_{(\cdot\cdot)} \) is the vector of parameter estimates that you obtain by fitting the model without the \( i \)th observation. Instead of refitting the model without the \( i \)th observation, Pettitt and Bin Daud (1989) propose that the likelihood displacement for the \( i \)th observation be approximated by

\[
LD_i = \hat{L}_i \mathcal{I}^{-1}(\hat{\beta}) \hat{L}_i
\]

where \( \hat{L}_i \) is the score residual vector of the \( i \)th observation.

### Joint Tests and Type 3 Tests

Linear hypotheses for \( \beta \) are expressed in matrix form as

\[
H_0: L\beta = c
\]

where \( L \) is a matrix of coefficients for the linear hypotheses and \( c \) is a vector of constants. The vector of regression coefficients \( \beta \) includes slope parameters and intercept parameters. The Wald chi-square statistic for testing \( H_0 \) is computed as

\[
\chi^2_W = (L\hat{\beta} - c)' [L\hat{\hat{V}}(\hat{\beta})L']^{-1} (L\hat{\beta} - c)
\]

where \( \hat{\hat{V}}(\hat{\beta}) \) is the estimated covariance matrix. Under \( H_0 \), \( \chi^2_W \) has an asymptotic chi-square distribution with \( r \) degrees of freedom, where \( r \) is the rank of \( L \).

For models that use less-than-full-rank parameterization (as specified by the PARAM=GLM option in the CLASS statement), a Type 3 test of an effect of interest (main effect or interaction) is a test of the Type III estimable functions that are defined for that effect. When the model contains no missing cells, the Type 3 test of a main effect is equivalent to testing the hypothesis of equal marginal means. For more information about Type III estimable functions, see the chapter “The GLM Procedure” and the section “The Four Types of Estimable Functions” in SAS/STAT User’s Guide. Also see Littell, Freund, and Spector (1991).

For models that use full-rank parameterization, all parameters are estimable when there are no missing cells, so it is unnecessary to define estimable functions. The standard test of an effect of interest in this case is the joint test that the values of the parameters associated with that effect are 0. For a model that uses effects parameterization (as specified by the PARAM=EFFECT option in the CLASS statement), the joint test for a main effect is equivalent to testing the equality of marginal means. For a model that uses reference parameterization (as specified by the PARAM=REF option in the CLASS statement), the joint test is equivalent to testing the equality of cell means at the reference level of the other model effects. For more information about the coding scheme and the associated interpretation of results, see Muller and Fetterman (2002, Chapter 14).

If there is no interaction term, the Type 3 test of an effect for a model that uses GLM parameterization is the same as the joint test of the effect for the model that uses full-rank parameterization. In this situation, the joint test is also called the Type 3 test. For a model that contains an interaction term and no missing cells, the Type 3 test of a component main effect under GLM parameterization is the same as the joint test of the component main effect under effect parameterization. Both test the equality of cell means. But this Type 3 test differs from the joint test under reference parameterization, which tests the equality of cell means at the reference level of the other component main effect. If some cells are missing, you can obtain meaningful tests only by testing a Type III estimation function, so in this case you should use GLM parameterization.

The results of a Type 3 test or a joint test do not depend on the order in which you specify the terms in the MODEL statement.
Multithreading

The PHSELECT procedure allocates data to different threads and calculates the likelihood function, gradient, and Hessian by accumulating the values from all threads. For more information about how PROC PHSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

Optimization Algorithms

Several optimization techniques are available in PROC PHSELECT. You can choose a particular optimizer by using the TECHNIQUE= option in the PROC PHSELECT statement. Table 11.9 summarizes the optimization techniques available in PROC PHSELECT.

<table>
<thead>
<tr>
<th>TECHNIQUE=</th>
<th>Algorithm</th>
</tr>
</thead>
<tbody>
<tr>
<td>TRUREG</td>
<td>Trust region method</td>
</tr>
<tr>
<td>NEWRAP</td>
<td>Newton-Raphson method with line search</td>
</tr>
<tr>
<td>NRRIDG</td>
<td>Newton-Raphson method with ridging</td>
</tr>
<tr>
<td>QUANEW</td>
<td>Quasi-Newton methods</td>
</tr>
<tr>
<td>DBLDOG</td>
<td>Double-dogleg method</td>
</tr>
<tr>
<td>CONGRA</td>
<td>Conjugate gradient methods</td>
</tr>
<tr>
<td>NMSIMP</td>
<td>Nelder-Mead simplex method</td>
</tr>
</tbody>
</table>

There is no algorithm for optimizing general nonlinear functions that always finds the global optimum for a general nonlinear optimization problem in a reasonable amount of time. Because no single optimization technique is always superior to others, PROC PHSELECT provides a variety of optimization techniques that work well in various circumstances. However, you can devise problems for which none of the techniques in PROC PHSELECT can find the correct solution. Moreover, nonlinear optimization can be computationally expensive in terms of time and memory, so you must be careful when matching an algorithm to a problem. The section “Choosing an Optimization Algorithm” on page 80 in Chapter 2, “Shared Concepts,” is helpful in choosing a suitable optimization algorithm.

In addition, PROC PHSELECT uses the finite-difference method to compute second-order derivatives, unless you specify the HESSIAN option. The HESSIAN option requires extra memory, the size of which also depends on the number of distinct uncensored failure times in the data.

Displayed Output

The following sections describe the output that PROC PHSELECT produces. The output is organized into various tables, which are discussed in their order of appearance.
Model Information

The “Model Information” table displays basic information about the model, such as the response variable, the frequency variable, the link function, and the distribution of the data that is assumed by the PHSELECT procedure.

Number of Observations

The “Number of Observations” table displays the number of observations that are read from the input data table and the number of observations that are used in the analysis. If you specify a FREQ statement, the table displays the sum of the frequencies that are read and used. If you specify a WEIGHT statement, the table displays the sum of \( f_i w_i \) that are read and used. If you specify a PARTITION statement, the table displays the values for each role.

–2 Log Likelihood for Null Model

When you specify the LOGLIKENULL option in the PROC PHSELECT statement, the PHSELECT procedure displays the –2 log-likelihood value of the null model for the training data. If you also specify a PARTITION statement, PROC PHSELECT displays the corresponding statistic for the validation data and the test data.

Class Level Information

The “Class Level Information” table lists the levels of every variable that you specify in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by using the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by using the NOCLPRINT= option in the PROC PHSELECT statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.

Selection Information

When you specify the SELECTION statement, the PHSELECT procedure by default produces a series of tables that display information about the model selection. The “Selection Information” table informs you about the model selection method, selection and stop criteria, and other parameters that govern the selection. You can suppress this table by specifying DETAILS=NONE in the SELECTION statement.

Iteration History

When you specify the ITHIST option in the PROC PHSELECT statement, the “Iteration History” table displays, for each iteration of the optimization, the number of function evaluations (including gradient and Hessian evaluations), the value of the objective function, the change in the objective function from the previous iteration, and the absolute value of the largest (projected) gradient element.

Convergence Status

The convergence status table is a small ODS table that appears as a message that indicates whether the optimization succeeded and which convergence criterion was met. If the optimization fails, the message
indicates the reason for the failure. If you save the convergence status table to an output data set, a numeric Status variable is added that enables you to assess convergence programmatically. The values of the Status variable indicate the following:

0  Convergence was achieved, or an optimization was not performed (because TECHNIQUE=NONE is specified).
1  The objective function could not be improved.
2  Convergence was not achieved because of a user interruption or because a limit was exceeded, such as the maximum number of iterations or the maximum number of function evaluations. To modify these limits, see the MAXITER=, MAXFUNC=, and MAXTIME= options in the PROC PHSELECT statement.
3  Optimization failed to converge because function or derivative evaluations failed at the starting values or during the iterations or because a feasible point that satisfies the parameter constraints could not be found in the parameter space.

Entry and Removal Candidates
When you specify DETAILS=ALL or DETAILS=STEPS in the SELECTION statement, the PHSELECT procedure produces the “Entry Candidates” or “Removal Candidates” table, which displays the effect names and values of the criterion used to select entering or departing effects at each step of the selection process. For each step, the effects are displayed in sorted order from best to worst of the selection criterion.

Selection Summary
When you specify the SELECTION statement, the PHSELECT procedure produces the “Selection Summary” table, which displays information about which effects were added to or removed from the model in the various steps of the model selection process. The statistic that led to the entry or removal decision is also displayed. You can request further details about the model selection steps by specifying DETAILS=STEPS or DETAILS=ALL in the SELECTION statement. You can suppress the display of this table by specifying DETAILS=NONE in the SELECTION statement.

If you specify the LASSO selection method, then this table displays information about which effect was added to the model, the number of effects in the model, the lambda value, and the information criteria.

Stop Reason
When you specify the SELECTION statement, the PHSELECT procedure produces a simple table that tells you why model selection stopped.

Selection Reason
When you specify the SELECTION statement, the PHSELECT procedure produces a simple table that tells you why the final model was selected.

Selected Effects
When you specify the SELECTION statement, the PHSELECT procedure produces a simple table that tells you which effects are in the final model.
Dimensions

The “Dimensions” table displays size measures that are derived from the model. It displays the number of columns in the current design matrix, the number of effects in the current design, the largest number of design columns associated with an effect, the rank of the matrix, and the number of parameters in the current model, including any scale parameters.

Fit Statistics

The “Fit Statistics” table displays a variety of likelihood-based measures of fit. The values that the “Fit Statistics” table displays are not based on a normalized log-likelihood function. If you specify a PARTITION statement, the table displays the values for each role along with statistics for comparing the training, validation, and testing results. For more information about the statistics that this table displays, see the section “Model Fit and Assessment Statistics” on page 613.

Parameter Estimates

The parameter estimates, their estimated (asymptotic) standard errors, and p-values for the hypothesis that the parameter is 0 are displayed in the “Parameter Estimates” table. If you request confidence intervals by specifying the CLB option in the MODEL statement, confidence limits are displayed for the parameters.

Parameter Estimates Covariance Matrix

When you specify the COVB option in the PROC PHSELECT statement, the PHSELECT procedure displays the covariance matrix of the parameter estimates. The covariance matrix is computed as the inverse of the negative of the matrix of second derivatives of the log-likelihood function with respect to the model parameters (the Hessian matrix), evaluated at the parameter estimates.

Parameter Estimates Correlation Matrix

When you specify the CORRB option in the PROC PHSELECT statement, the PHSELECT procedure displays the correlation matrix of the parameter estimates.

Model Analysis of Variance (Type III)

When you specify the TYPE3 option in the MODEL statement, the PHSELECT procedure produces the “Model Analysis of Variance (Type III)” table. This table displays tests that all parameters for a particular effect are equal to zero. For more information, see the section “Joint Tests and Type 3 Tests” on page 616.

Timing

The “Timing” table displays the amount of time (in seconds) that PROC PHSELECT required to perform different tasks in the analysis.

Output CAS Tables

When you specify an OUTPUT statement or a DISPLAYOUT statement to create output tables on your CAS server, the PHSELECT procedure produces the “Output CAS Tables” table. This table displays the names, the number of rows and columns, and the CAS libraries in which the output table is created for every output table that you request.
ODS Table Names

Each table that the PHSELECT procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement, the DISPLAYOUT statement, or ODS statements. These names are listed in Table 11.10.

**NOTE:** The EFFECT statement also creates tables that are not listed in this section. For information about these tables, see the section “ODS Table Names” on page 33 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
<td>Default</td>
</tr>
<tr>
<td>ConvergenceStatus</td>
<td>Status of optimization at conclusion of optimization</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>CorrB</td>
<td>Correlation matrix of parameter estimates</td>
<td>PROC PHSELECT</td>
<td>CORRB</td>
</tr>
<tr>
<td>CovB</td>
<td>Covariance matrix of parameter estimates</td>
<td>PROC PHSELECT</td>
<td>COVB</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>EntryCandidates</td>
<td>Details about candidates for entry into the model</td>
<td>SELECTION</td>
<td>METHOD=FORWARD orSTEPWISE and DETAILS=STEP</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>IterHistory</td>
<td>Iteration history</td>
<td>PROC PHSELECT</td>
<td>ITHIST</td>
</tr>
<tr>
<td>LogLikeNull</td>
<td>−2 log likelihood for null model</td>
<td>PROC PHSELECT</td>
<td>LOGLIKENULL</td>
</tr>
<tr>
<td>ModelAnova</td>
<td>Model analysis of variance (Type III)</td>
<td>MODEL</td>
<td>TYPE3</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Information about the modeling environment</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used, and breakdown of censored and uncensored values</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>OutputCASTable</td>
<td>Library and name of the output data table, and number of rows and columns in the table</td>
<td>OUTPUT</td>
<td>OUT=</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in MODEL statements</td>
<td>Default</td>
<td></td>
</tr>
<tr>
<td>RemovalCandidates</td>
<td>Details about candidates for removal from the model</td>
<td>SELECTION</td>
<td>METHOD=BACKWARD or STEPWISE and DETAILS=STEP</td>
</tr>
<tr>
<td>SelectedEffects</td>
<td>List of effects selected for the model</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
</tbody>
</table>
### Table 11.10  continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SelectionInfo</td>
<td>Information about the settings for model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionReason</td>
<td>Reason why the particular model was selected</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Summary information about model selection steps</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>StopReason</td>
<td>Reason for termination of model selection</td>
<td>SELECTION</td>
<td>Default</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times for tasks performed by the procedure</td>
<td></td>
<td>Default</td>
</tr>
</tbody>
</table>

### ODS Graphics

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in *SAS/STAT User's Guide*.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.

When ODS Graphics is enabled, the SELECTION statement can produce plots to help evaluate the selection process. For information about these plots, see the section “Model Selection Plots” on page 69 in Chapter 2, “Shared Concepts.”

PROC PHSELECT assigns a name to each graph that it creates using ODS. You can use these names to refer to the graphs when using ODS. The names are listed in Table 11.11.

### Table 11.11  Graphs Produced by PROC PHSELECT

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS= Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CoefficientPanel</td>
<td>Coefficients and CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>ChooseCriterionPlot</td>
<td>CHOOSE= criterion by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CoefficientPlot</td>
<td>Coefficients by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
</tbody>
</table>
Examples: PHSELECT Procedure

Table 11.11  continued

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS= Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CriterionPanel</td>
<td>Fit criteria by step</td>
<td>CRITERIA</td>
</tr>
<tr>
<td>TEST_M2LLPlot</td>
<td>–2 log likelihood on testing data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TRAIN_M2LLPlot</td>
<td>–2 log likelihood on training data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>VAL_M2LLPlot</td>
<td>–2 log likelihood on validation data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>FitByRolePlot</td>
<td>Progression of average square error by role</td>
<td>FITBYROLE</td>
</tr>
</tbody>
</table>

Examples: PHSELECT Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following examples assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

**Example 11.1: Model Selection**

The following statements examine the same data as in the section “Getting Started: PHSELECT Procedure” on page 590, but they request model selection via the forward selection technique. Effects that provide the best improvement to the selection criterion, the Schwartz Bayesian criterion (SBC), are added until no more effects can improve the selection criterion. The DETAILS=ALL option in the SELECTION statement produces all tables that are related to model selection. The PLOTS=ALL option produces graphics to help you interpret the selection process. ODS Graphics must be enabled before you can request plots. (For more information about ODS Graphics, see the section “ODS Graphics” on page 622.)

```sas
ods graphics on;
proc phselect data=mycas.getStarted;
   class C1-C3;
   model Time*Status(0) = C1-C3 X1-X4;
   selection method=forward(stop=sbc select=sbc) details=all plots=all;
run;
```

The model selection tables are shown in Output 11.1.1 through Output 11.1.3. Results from the selected model are shown in Output 11.1.4 and Output 11.1.5. Selection graphics that the PLOTS= option produces are displayed in Output 11.1.6 and Output 11.1.7.
The "Selection Information" table in Output 11.1.1 summarizes the settings for the model selection. Effects are added to the model only if they produce a significant improvement, which is determined by comparing their SBC values. The forward selection stops three steps after the smallest SBC is obtained or when all effects have been added to the model.

**Output 11.1.1 Selection Information**

**The PHSELECT Procedure**

<table>
<thead>
<tr>
<th>Selection Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Description</td>
</tr>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
</tbody>
</table>

For each step of the selection process, the DETAILS=ALL option displays the candidate effects for entering the model along with their SELECT= criterion. Output 11.1.2 displays this table for the first step; the other steps are not shown here.

**Output 11.1.2 Step 1 Entry Candidates**

**The PHSELECT Procedure**

**Forward Selection: Step 1**

**Effect Entered: X1**

<table>
<thead>
<tr>
<th>Entry Candidates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Rank</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
</tbody>
</table>

The DETAILS=ALL option also displays the dimensions, fit statistics, and parameter estimates at each step of the selection process; these details are not shown here.

When the selection procedure is complete, the "Selection Summary" table in Output 11.1.3 shows the effects that were added to the model and the value of their selection criterion (and the choose and stop criteria, if they are specified). In step 1, effect X1 made the most significant contribution to the model among the candidate effects, according to the SBC statistic. In step 2, X4 made the most significant contribution when an effect was added to a model that contains X1. In the three subsequent steps, no effect could be added to the model that would reduce the SBC value, so variable selection stopped because the stop horizon (see Output 11.1.1) indicates that at most three steps beyond the minimum SBC value are taken.

In Output 11.1.3, the "Selection Summary" table is followed by three small tables that summarize why the process stopped and which model is selected.
Output 11.1.3 Selection Summary Information

The PHSELECT Procedure

Selection Details

<table>
<thead>
<tr>
<th>Selection Summary</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>SBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step</td>
<td>X1</td>
<td>1</td>
<td>536.7462</td>
</tr>
<tr>
<td>2</td>
<td>X4</td>
<td>2</td>
<td>535.1652*</td>
</tr>
<tr>
<td>3</td>
<td>C1</td>
<td>3</td>
<td>538.2917</td>
</tr>
<tr>
<td>4</td>
<td>X2</td>
<td>4</td>
<td>539.2661</td>
</tr>
<tr>
<td>5</td>
<td>X3</td>
<td>5</td>
<td>542.4842</td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

Selection stopped at a local minimum of the SBC criterion.

The model at step 2 is selected.

Selected Effects: X1 X4

Output 11.1.4 displays information about the selected model. Notice that the –2 log-likelihood value in the “Fit Statistics” table is larger than the value for the full model in Figure 11.7. This is expected because the selected model contains only a subset of the parameters. Because the selected model is more parsimonious than the full model, the discrepancy between the –2 log likelihood and the information criteria is less severe than that shown in Figure 11.7 in the “Getting Started” example.

Output 11.1.4 Dimensions and Fit Statistics

The PHSELECT Procedure

Selected Model

<table>
<thead>
<tr>
<th>Dimensions</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Effects</td>
<td>2</td>
</tr>
<tr>
<td>Max Effect Columns</td>
<td>1</td>
</tr>
<tr>
<td>Columns in Design</td>
<td>2</td>
</tr>
<tr>
<td>Rank of Design</td>
<td>2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Fit Statistics</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>526.74445</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>530.74445</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>530.91346</td>
</tr>
<tr>
<td>SBC (smaller is better)</td>
<td>535.35258</td>
</tr>
</tbody>
</table>

The parameter estimates of the selected model are shown in Output 11.1.5. Notice that the effects are listed in the “Parameter Estimates” table in the order in which they are specified in the MODEL statement and not necessarily in the order in which they are added to the model.
The coefficient panel in Figure 11.1.6 enables you to visualize the selection process. In this plot, standardized coefficients of all the effects that are selected at some step of the stepwise method are plotted as a function of the step number. This enables you to assess the relative importance of the effects that are selected at any step of the selection process and to know when effects entered the model. The lower plot in the panel shows how the criterion that is used to choose the selected model changes as effects enter or leave the model.

The criterion panel in Figure 11.1.7 provides a graphical view of the progression of the fit criteria as the selection process evolves. Notice at Step 2 that the SBC value seems to be at its minimum. Because the stop horizon value is 3 (see Output 11.1.1), three more steps are taken to determine if Step 2 is a global optimum. None of these three subsequent steps have a smaller SBC value than in Step 2, so the global optimum is at step 2.
Example 11.2: Stratified Analysis

In the `getStarted` data set that is presented in the section “Getting Started: PHSELECT Procedure” on page 590, suppose the variable C3 represents the gender of the subjects. It is conceivable that males and females belong to different subpopulations and might have different baseline hazard functions. A stratified analysis is conducted by specifying C3 as the stratifying variable in the STRATA statement. The CODE statement requests that a text file named `ScoreCode.txt` be created. This file contains SAS DATA step code to predict survival probabilities at time points that are specified by the TIMEPOINT= option. By default, PROC PHSELECT uses the estimated quartiles of the KM curve (no covariates) of the training data. The SHOWTIME option produces variables that contain these estimated time points.

```sas
proc phselect data=mycas.getStarted;
   class C1 C2;
   model Time*Status(0) = C1 C2 X1-X4;
   strata C3;
   code file='ScoreCode.txt' showtime;
run;
```
Chapter 11: The PHSELECT Procedure

The “Parameter Estimates” table in Output 11.2.1 shows the resulting regression parameter estimates of the stratified analysis.

**Output 11.2.1** Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>Chi-Square</th>
<th>Pr &gt; ChiSq</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1 Critical</td>
<td>1</td>
<td>0.301314</td>
<td>0.512375</td>
<td>0.3458</td>
<td>0.5565</td>
</tr>
<tr>
<td>C1 High</td>
<td>1</td>
<td>-1.030679</td>
<td>0.334457</td>
<td>9.4966</td>
<td>0.0021</td>
</tr>
<tr>
<td>C1 Low</td>
<td>1</td>
<td>-0.649179</td>
<td>0.342083</td>
<td>3.6014</td>
<td>0.0577</td>
</tr>
<tr>
<td>C1 Medium</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C2 0</td>
<td>1</td>
<td>0.519843</td>
<td>0.405972</td>
<td>1.6396</td>
<td>0.2004</td>
</tr>
<tr>
<td>C2 1</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>X1</td>
<td>1</td>
<td>1.970290</td>
<td>0.534947</td>
<td>13.5656</td>
<td>0.0002</td>
</tr>
<tr>
<td>X2</td>
<td>1</td>
<td>0.752247</td>
<td>0.419589</td>
<td>3.2142</td>
<td>0.0730</td>
</tr>
<tr>
<td>X3</td>
<td>1</td>
<td>0.959931</td>
<td>0.600959</td>
<td>2.5515</td>
<td>0.1102</td>
</tr>
<tr>
<td>X4</td>
<td>1</td>
<td>-0.117182</td>
<td>0.059406</td>
<td>3.8910</td>
<td>0.0485</td>
</tr>
</tbody>
</table>

You can use the DATA step code from the CODE statement to compute direct adjusted survival probabilities by taking the average of individual predicted survival probabilities. The method of direct adjustment controls for possible confounders that result from an imbalance of subject characteristics between groups. This adjustment is especially useful in nonrandomized studies. In the following statements, the DATA step code is applied to the `getStarted` data set to obtain the predicted survival probabilities for individuals in that data set and the predicted probabilities at each time point are averaged by gender:

```latex
\begin{verbatim}
data Scores;
  set mycas.getStarted;
  %inc 'ScoreCode.txt';
run;

proc print data=Scores (obs=1);
  var Time_:;
run;

proc means data=Scores mean;
  class C3;
  var S_Time_:;
run;
\end{verbatim}
```

Output 11.2.2 displays the time points at which the survival probabilities were predicted. These time points, Time_1=7, Time_2=19, and Time_3=54, are the quartiles of the failure times based on the Kaplan-Meier curve. Output 11.2.3 displays the direct adjusted survival probabilities at these quartiles. The predicted survival probability at Time_1 for females is slightly lower than that for males, but at Time_3 the direction is reversed. Also revealed is that the `getStarted` data set has 76 males but only 24 females.

**Output 11.2.2** Quartiles of the Observed Failure Times

<table>
<thead>
<tr>
<th>Obs</th>
<th>Time_1</th>
<th>Time_2</th>
<th>Time_3</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>7</td>
<td>19</td>
<td>54</td>
</tr>
</tbody>
</table>
Output 11.2.3  Direct Adjusted Survival Probabilities

The MEANS Procedure

<p>| | | | | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>C3</td>
<td>N</td>
<td>Obs</td>
<td>Variable</td>
<td>Label</td>
</tr>
<tr>
<td>-----</td>
<td>-----</td>
<td>-----</td>
<td>----------</td>
<td>------------------------------</td>
</tr>
<tr>
<td>F</td>
<td>24</td>
<td>S_Time_1 Survival Probability at Time_1</td>
<td>0.7016195</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>S_Time_2 Survival Probability at Time_2</td>
<td>0.3693234</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>S_Time_3 Survival Probability at Time_3</td>
<td>0.2765601</td>
<td></td>
</tr>
<tr>
<td>M</td>
<td>76</td>
<td>S_Time_1 Survival Probability at Time_1</td>
<td>0.7485799</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>S_Time_2 Survival Probability at Time_2</td>
<td>0.4568778</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>S_Time_3 Survival Probability at Time_3</td>
<td>0.2354066</td>
<td></td>
</tr>
</tbody>
</table>

References


Chapter 12
The PLSMOD Procedure

Contents

Overview: PLSMOD Procedure .......................................................... 632
PROC PLSMOD Features ................................................................. 632
PROC PLSMOD Compared with Other SAS Procedures ......................... 633
    PROC PLSMOD Compared with the HPPLS Procedure ...................... 633
    PROC PLSMOD Compared with the PLS Procedure ......................... 634
Using CAS Sessions and CAS Engine Librefs .................................... 635
Getting Started: PLSMOD Procedure .............................................. 636
    Fitting a PLS Model .............................................................. 637
    Selecting the Number of Factors by Test Set Validation ................. 639
    Predicting New Observations .................................................. 643
Syntax: PLSMOD Procedure ......................................................... 644
    PROC PLSMOD Statement ...................................................... 644
    BY Statement ................................................................ 647
    CLASS Statement ................................................................ 647
    DISPLAY Statement ................................................................ 648
    DISPLAYOUT Statement .......................................................... 649
    EFFECT Statement ................................................................. 649
    MODEL Statement ................................................................. 651
    OUTPUT Statement ............................................................... 651
    PARTITION Statement ............................................................. 654
Details: PLSMOD Procedure ........................................................... 655
    Regression Methods ............................................................... 655
        Partial Least Squares ........................................................ 655
        SIMPLS .......................................................................... 656
        Principal Component Regression ......................................... 656
        Reduced Rank Regression ................................................... 656
        Relationships between Methods ......................................... 657
    Test Set Validation ................................................................. 659
    Centering and Scaling ............................................................ 661
    Missing Values ...................................................................... 661
    Displayed Output ................................................................. 662
        Model Information ........................................................... 662
        Dimensions .................................................................... 662
        Number of Observations .................................................... 662
        Class Level Information ..................................................... 662
        Centering and Scaling Information ...................................... 662
Overview: PLSMOD Procedure

The PLSMOD procedure fits reduced-rank linear models in SAS Viya by using any one of a number of linear predictive methods, including partial least squares (PLS).

Ordinary least squares regression, as implemented in SAS/STAT procedures such as the GLM and REG procedures, has the single goal of minimizing sample response prediction error, and it seeks linear functions of the predictors that explain as much variation in each response as possible. The PLSMOD procedure implements techniques that have the additional goal of accounting for variation in the predictors, under the assumption that directions in the predictor space that are well sampled should provide better prediction for new observations when the predictors are highly correlated. All the techniques that the PLSMOD procedure implements work by extracting successive linear combinations of the predictors, called factors (also called components, latent vectors, or latent variables), that optimally address one or both of these two goals: explaining response variation and explaining predictor variation. In particular, the method of partial least squares balances the two objectives by seeking factors that explain both response and predictor variation.

The name “partial least squares” also applies to a more general statistical method that is not implemented in this procedure. The partial least squares method was originally developed in the 1960s by the econometrician Herman Wold (1966) for modeling “paths” of causal relation between any number of “blocks” of variables. However, the PLSMOD procedure fits only predictive partial least squares models that have one “block” of predictors and one “block” of responses. If you are interested in fitting more general path models, consider using the CALIS procedure in SAS/STAT.

PROC PLSMOD Features

The main features of the PLSMOD procedure are as follows:

- provides model-building syntax with classification variables, continuous variables, interactions, and nestings
- provides effect-construction syntax for polynomial and spline effects
- supports partitioning of data into training and testing roles
PROC PLSMOD Compared with Other SAS Procedures

The PLSMOD procedure implements the following methods:

- principal component regression, which extracts factors to explain as much predictor sample variation as possible
- reduced rank regression, which extracts factors to explain as much response variation as possible. This technique, also known as (maximum) redundancy analysis, differs from multivariate linear regression only when there are multiple responses.
- partial least squares regression, which balances the two objectives of explaining response variation and explaining predictor variation. Two different formulations for partial least squares are available: the original predictive method of Wold (1966) and the straightforward implementation of a statistically inspired modification of the partial least squares (SIMPLS) method of De Jong (1993).

Because the PLSMOD procedure runs on SAS Cloud Analytic Services (CAS), it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode
- exploits all the available cores and concurrent threads. For information about how PROC PLSMOD uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”
Table 12.1  Comparison of PROC PLSMOD and PROC HPPLS

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PLSMOD</th>
<th>PROC HPPLS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supports general factor extraction methods</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports EFFECT statement</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports DISPLAY and DISPLAYOUT statements</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports BY statement</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports ID statement</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports MISSING=, VARSCALE, and PLOTS options</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Supports cross validation methods</td>
<td>Only test set validation by using the PARTITION statement</td>
<td>Only test set validation by using the PARTITION statement</td>
</tr>
<tr>
<td>Includes input variables in output data table</td>
<td>Not by default, in order to avoid data duplication for large data tables. To include input variables, specify them in the COPYVARS= option in the OUTPUT statement.</td>
<td>Not by default, in order to avoid data duplication for large data sets. To include input variables, specify them in the ID statement.</td>
</tr>
<tr>
<td>Supports parameterization of classification variables</td>
<td>Full set of parameterizations (supports all values of the PARAM= option in the CLASS statement)</td>
<td>Supports only PARAM=GLM or PARAM=REFERENCE</td>
</tr>
<tr>
<td>Threading</td>
<td>Specifically designed for CAS; executes on multiple threads</td>
<td>Primarily designed for a distributed environment; executes on multiple threads</td>
</tr>
</tbody>
</table>

PROC PLSMOD Compared with the PLS Procedure

The PLSMOD procedure and the PLS procedure have the similarities and differences shown in Table 12.2.

Table 12.2  Comparison of PROC PLSMOD and PROC PLS

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PLSMOD</th>
<th>PROC PLS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Supports general factor extraction methods</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports EFFECT statement</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports DISPLAY and DISPLAYOUT statements</td>
<td>Yes</td>
<td>No</td>
</tr>
<tr>
<td>Supports BY statement</td>
<td>Yes</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports ID statement</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports MISSING=, VARSCALE, and PLOTS options</td>
<td>No</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports cross validation methods</td>
<td>Only test set validation by using the PARTITION statement</td>
<td>Various methods</td>
</tr>
</tbody>
</table>

[54x751]634  Chapter 12: The PLSMOD Procedure
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

---

**Table 12.2 continued**

<table>
<thead>
<tr>
<th>Feature</th>
<th>PROC PLSMOD</th>
<th>PROC PLS</th>
</tr>
</thead>
<tbody>
<tr>
<td>Syntax of OUTPUT statement</td>
<td>No prefix needed; default prefix used if none is provided. If you do not specify any keywords, the output data table includes predicted values for response variables.</td>
<td>You must provide keyword and prefix</td>
</tr>
<tr>
<td>Includes input variables in output data table</td>
<td>Not by default, in order to avoid data duplication for large data tables. To include input variables, specify them in the COPYVARS= option in the OUTPUT statement.</td>
<td>Yes</td>
</tr>
<tr>
<td>Supports parameterization of classification variables</td>
<td>Full set of parameterizations (supports all values of the PARAM= option in the CLASS statement)</td>
<td>Only GLM parameterization</td>
</tr>
<tr>
<td>Threading</td>
<td>Specifically designed for CAS; executes on multiple threads</td>
<td>Executes on a single thread</td>
</tr>
</tbody>
</table>

---
Getting Started: PLSMOD Procedure

The example in this section illustrates basic features of the PLSMOD procedure. The data are reported in Umetrics (1995); the original source is Lindberg, Persson, and Wold (1983). Suppose you are researching pollution in the Baltic Sea and you want to use the fluorescence spectra of seawater samples to determine the amounts of three compounds present: lignin sulfonate (ls: pulp industry pollution), humic acids (ha: natural forest products), and optical whitener from detergent (dt). Spectrometric calibration is a type of problem in which partial least squares can be very effective. The predictors are the spectra emission intensities at different frequencies in a sample spectrum, and the responses are the amounts of various chemicals in the sample.

For the purpose of calibrating the model, samples that have known compositions are used. The calibration data consist of 16 samples of known concentrations of ls, ha, and dt, with spectra based on 27 frequencies (or, equivalently, wavelengths). In order to demonstrate the use of test set validation, the data contain a variable Role, which is used to assign observations to the training and testing roles. In this case, the training role has nine samples and the testing role has seven samples.

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following DATA step creates the mycas.Sample data table, which provides the calibration data, in your CAS session. These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

```sas
data mycas.Sample;
  input obsnam $ v1-v27 ls ha dt Role $5. @@;
  datalines;
  EM1  2766  2610  3306  3630  3600  3438  3213  3051  2907  2844  2796
       2787  2760  2754  2670  2520  2310  2100  1917  1755  1602  1467
       1353  1260  1167  1101  1017  3.0110  0.0000  0.00 TRAIN
  EM2  1492  1419  1369  1158  958  887  905  929  920  887  800
       710  617  535  451  368  296  241  190  157  128  106
       89   70   65   56   50  0.0000  0.4005  0.00 TEST
  EM3  2450  2379  2400  2055  1689  1355  1109  908  750  673  644
       640  630  618  571  512  440  368  305  247  196  156
       120   98   80   61   50  0.0000  0.0000  90.63 TRAIN
  EM4  2751  2883  3492  3570  3282  2937  2634  2370  2187  2070  2007
       1974  1950  1890  1824  1680  1527  1350  1206  1080  984  888
       810  732  669  630  582  1.4820  0.1580  40.00 TEST
  EM5  2652  2691  3225  3285  3033  2784  2520  2340  2235  2148  2094
       2049  2007  1917  1800  1650  1464  1299  1140  1020  909  810
       726  657  594  549  507  1.1160  0.4104  30.45 TEST
```

---

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
To isolate a few underlying spectral factors that provide a good predictive model, you can fit a PLS model to the 16 samples by using the following SAS statements:

```sas
proc plsmod data=mycas.sample;
  model ls ha dt = v1-v27;
run;
```

By default, the PLSMOD procedure extracts at most 15 factors. The default output from this analysis is presented in Figure 12.1 and Figure 12.2.

**Figure 12.1** displays the “Model Information,” “Dimensions,” and “Number of Observations” tables.

The “Model Information” table identifies the data source and shows that the factor extraction method is partial least squares regression (which is the default) and that the nonlinear iterative partial least squares (NIPALS) algorithm (which is also the default) is used to compute extracted PLS factors.
The “Dimensions” table shows the number of response variables, the number of effects, the number of predictor parameters, and the number of factors to extract.

The “Number of Observations” table shows that all 16 of the sample observations in the input data are used in the analysis; all the samples are used because they all contain complete data.

**Figure 12.1** Model Information, Dimensions, and Number of Observations

<table>
<thead>
<tr>
<th>The PLSMOD Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Model Information</strong></td>
</tr>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Factor Extraction Method</td>
</tr>
<tr>
<td>PLS Algorithm</td>
</tr>
<tr>
<td>Validation Method</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Dimensions</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Response Variables</td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Number of Predictor Parameters</td>
</tr>
<tr>
<td>Number of Factors</td>
</tr>
</tbody>
</table>

Number of Observations Read | 16 |
Number of Observations Used  | 16 |

Figure 12.2 lists the amount of variation, both individual and cumulative, that is accounted for by each of the 15 factors. All the variation in both the predictors and the responses is accounted for by only 15 factors because there are only 16 sample observations. More important, almost all the variation is accounted for by even fewer factors—one or two for the predictors and three to eight for the responses.
Selecting the Number of Factors by Test Set Validation

A PLS model is not complete until you choose the number of factors. You can choose the number of factors by using test set validation, in which the data table is divided into two groups called the training data and test data. You fit the model to the training data, and then you check the capability of the model to predict responses for the test data. The predicted residual sum of squares (PRESS) statistic is based on the residuals that are generated by this process.

To select the number of extracted factors by test set validation, you use the PARTITION statement to specify how to logically divide observations in the input data table into two subsets for model training and testing. For example, you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, as in the following SAS statements:

```sas
proc plsmod data=mycas.sample;
    model ls ha dt = v1-v27;
    partition roleVar = Role(train='TRAIN' test='TEST');
run;
```

The resulting output is shown in Figure 12.3 through Figure 12.5.
Figure 12.3  Model Information, Dimensions, and Number of Observations with Test Set Validation

The PLSMOD Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Factor Extraction Method</td>
</tr>
<tr>
<td>PLS Algorithm</td>
</tr>
<tr>
<td>Validation Method</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Dimensions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Response Variables</td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Number of Predictor Parameters</td>
</tr>
<tr>
<td>Maximum Number of Factors</td>
</tr>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
<tr>
<td>Number of Observations Used for Training</td>
</tr>
<tr>
<td>Number of Observations Used for Testing</td>
</tr>
</tbody>
</table>

Figure 12.4  Test-Set-Validated PRESS Statistics for Number of Factors

The PLSMOD Procedure

<table>
<thead>
<tr>
<th>Number of Extracted Factors</th>
<th>Root Mean PRESS</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>1.426362</td>
</tr>
<tr>
<td>1</td>
<td>1.276694</td>
</tr>
<tr>
<td>2</td>
<td>1.181752</td>
</tr>
<tr>
<td>3</td>
<td>0.656999</td>
</tr>
<tr>
<td>4</td>
<td>0.43457</td>
</tr>
<tr>
<td>5</td>
<td>0.420916</td>
</tr>
<tr>
<td>6</td>
<td>0.585031</td>
</tr>
<tr>
<td>7</td>
<td>0.576586</td>
</tr>
<tr>
<td>8</td>
<td>0.563935</td>
</tr>
<tr>
<td>9</td>
<td>0.563935</td>
</tr>
</tbody>
</table>

Minimum Root Mean PRESS 0.420916
Minimizing Number of Factors 5
In Figure 12.3, the “Model Information” table indicates that test set validation is used. The “Dimensions” table shows that the maximum number of factors to extract is nine. The “Number of Observations” table shows that nine sample observations are assigned for training roles and seven are assigned for testing roles.

Figure 12.4 provides details about the results from test set validation. These results show that the absolute minimum PRESS is achieved with five extracted factors. Notice, however, that this is not much smaller than the PRESS for three factors. By using the CVTEST option, you can perform a statistical model comparison that is suggested by Van der Voet (1994) to test whether this difference is significant, as shown in the following SAS statements:

```sas
proc plsmod data=mycas.sample cvtest(pval=0.15 seed=12345);
   model ls ha dt = v1-v27;
   partition roleVar = Role(train='TRAIN' test='TEST');
run;
```

The model comparison test is based on a rerandomization of the data. By default, the seed for this randomization is based on the system clock, but it is specified here. The resulting output is presented in Figure 12.6 through Figure 12.8.

---

**Figure 12.5** PLS Variation Summary for Test-Set-Validated Model

<table>
<thead>
<tr>
<th>Number of Extracted Factors</th>
<th>Model Effects Current</th>
<th>Total</th>
<th>Response Variables Current</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>95.92495</td>
<td>95.92495</td>
<td>37.27071</td>
<td>37.27071</td>
</tr>
<tr>
<td>2</td>
<td>3.86407</td>
<td>99.78903</td>
<td>32.38167</td>
<td>69.65238</td>
</tr>
<tr>
<td>3</td>
<td>0.10170</td>
<td>99.89073</td>
<td>20.76882</td>
<td>90.42120</td>
</tr>
<tr>
<td>4</td>
<td>0.08979</td>
<td>99.98052</td>
<td>4.66666</td>
<td>95.08787</td>
</tr>
<tr>
<td>5</td>
<td>0.01142</td>
<td>99.99194</td>
<td>3.88184</td>
<td>98.96971</td>
</tr>
</tbody>
</table>

---

**Figure 12.6** Model Information with Model Comparison Test

**The PLSMOD Procedure**

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Factor Extraction Method</td>
</tr>
<tr>
<td>PLS Algorithm</td>
</tr>
<tr>
<td>Validation Method</td>
</tr>
<tr>
<td>Validation Testing Criterion</td>
</tr>
<tr>
<td>Number of Random Permutations</td>
</tr>
<tr>
<td>Random Number Seed for Permutation</td>
</tr>
</tbody>
</table>
The "Model Information" table in Figure 12.6 displays information about the options that are used in the model comparison test. In Figure 12.7, the \( p \)-value in comparing the test-set-validated residuals from models that have five and three factors indicates that the difference between the two models is insignificant; therefore, the model with fewer factors is preferred. The variation summary in Figure 12.8 shows that more than 99% of the predictor variation and more than 90% of the response variation are accounted for by the three factors.
Predicting New Observations

Now that you have chosen a three-factor PLS model for predicting pollutant concentrations that are based on sample spectra, suppose that you have two new samples. The following SAS statements create a data table that contains the spectra for the new samples:

```sas
data newobs;
  input obsnam $ v1-v27 @@;
datalines;
  EM17  3933 4518 5637 6006 5721 5187 4641 4149 3789
        3579 3447 3381 3327 3234 3078 2832 2571 2274
        2040 1818 1629 1470 1350 1245 1134 1050 987
  EM25  2904 2997 3255 3150 2922 2778 2700 2646 2571
        2487 2370 2250 2127 2052 1713 1419 1200 984
        795 648 525 426 351 291 240 204 162;
;
You can apply the PLS model to these samples to estimate pollutant concentration by appending the new samples to the original 16 and specifying that the predicted values for all 18 samples be output to a data table, as shown in the following statements:

```sas
data mycas.all;
  set mycas.sample newobs;
run;

proc plsmod data=mycas.all nfac=2;
  model ls ha dt = v1-v27;
  partition roleVar = Role(train='TRAIN' test='TEST');
  output out=mycas.result pred=p copyvars=(obsnam);
run;

proc print data=mycas.result;
  where (obsnam in ('EM17','EM25'));
  var obsnam p_ls p_ha p_dt;
run;
```

The COPYVARS= option in the OUTPUT statement requests that the variable obsnam from the input data table be copied to the output data table. The new observations are not used in calculating the PLS model because they have no response values. Their predicted concentrations are shown in Figure 12.9.

**Figure 12.9** Predicted Concentrations for New Observations

<table>
<thead>
<tr>
<th>Obs</th>
<th>obsnam</th>
<th>p_ls</th>
<th>p_ha</th>
<th>p_dt</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>EM17</td>
<td>2.63326</td>
<td>0.22343</td>
<td>80.2027</td>
</tr>
<tr>
<td>2</td>
<td>EM25</td>
<td>0.69865</td>
<td>0.14308</td>
<td>98.9937</td>
</tr>
</tbody>
</table>
Syntax: PLSMOD Procedure

The following statements are available in the PLSMOD procedure:

```plaintext
PROC PLSMOD <options> ;
   BY variables ;
   CLASS variable <(options)> . . . <variable <(options)>> </global-options> ;
   DISPLAY <table-list> </options> ;
   DISPLAYOUT table-spec-list </options> ;
   EFFECT name = effect-type (variables <options>) ;
   MODEL response-variables = predictor-effects </options> ;
   OUTPUT OUT=CAS-libref.data-table
      <COPYVARS=(variables)>
      <keyword = prefix> . . . <keyword = prefix> ;
   PARTITION partition-options ;
```

The PROC PLSMOD statement and a single MODEL statement are required. All other statements are optional. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statement. The following sections describe the PROC PLSMOD statement and then describe the other statements in alphabetical order.

PROC PLSMOD Statement

```plaintext
PROC PLSMOD <options> ;
```

The PROC PLSMOD statement invokes the PLSMOD procedure. Table 12.3 summarizes the options available in the PROC PLSMOD statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the CAS input data table</td>
</tr>
<tr>
<td><strong>Model Fitting Options</strong></td>
<td></td>
</tr>
<tr>
<td>CVTEST</td>
<td>Requests that van der Voet's (1994) randomization-based model comparison test be performed</td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies the general factor extraction method to be used</td>
</tr>
<tr>
<td>NFAC=</td>
<td>Specifies the number of factors to extract</td>
</tr>
<tr>
<td>NOCENTER</td>
<td>Suppresses centering of the responses and predictors before fitting</td>
</tr>
<tr>
<td>NOCVSTDIZE</td>
<td>Suppresses re-centering and rescaling of the responses and predictors when cross validating</td>
</tr>
<tr>
<td>NOSCALE</td>
<td>Suppresses scaling of the responses and predictors before fitting</td>
</tr>
<tr>
<td><strong>Output Options</strong></td>
<td></td>
</tr>
<tr>
<td>CENSCALE</td>
<td>Displays the centering and scaling information</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the details of the fitted model</td>
</tr>
</tbody>
</table>
The following list provides details about these options.

**CENSCALE**
lists the centering and scaling information for each response and predictor.

**CVTEST < (cvtest-options) >**
requests that van der Voet’s (1994) randomization-based model comparison test be performed to test models that have different numbers of extracted factors against the model that minimizes the predicted residual sum of squares. For more information, see the section “Test Set Validation” on page 659. You can also specify the following *cvtest-options* in parentheses:

- **NSAMP=number**
  specifies the number of randomizations to perform. By default, NSAMP=1000.

- **PVAL=number**
  specifies the cutoff probability for declaring an insignificant difference. By default, PVAL=0.10.

- **SEED=number**
  specifies the seed value for the random number stream. If you do not specify this option or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

  Analyses that use the same (nonzero) seed are not completely reproducible if they are executed on a different number of compute nodes, because the random number streams in separate compute nodes are independent.

- **STAT=PRESS | T2**
  specifies the test statistic for the model comparison. You can specify the following values:

  - **PRESS**
    uses the predicted residual sum of squares.

  - **T2**
    uses Hotelling’s $T^2$ statistic.

  By default, STAT=T2.

**DATA=CAS-libref.data-table**
names the input data table for PROC PLSMOD to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where

- **CAS-libref**
  refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 635.
data-table specifies the name of the input data table.

DETAILS
lists the details of the fitted model for each successive factor. The listed details are different for different extraction methods. For more information, see the section “Displayed Output” on page 662.

METHOD=PLS< (PLS-options) > | SIMPLS | PCR | RRR
specifies the general factor extraction method to be used. You can specify the following values:

PCR
uses principal component regression.

PLS< (PLS-options) >
uses partial least squares. You can also specify the following optional PLS-options in parentheses:

ALGORITHM=NIPALS | SVD | EIG
names the specific algorithm to use to compute extracted PLS factors. You can specify the following values:

NIPALS requests the usual iterative NIPALS algorithm.

SVD bases the extraction on the singular value decomposition of $X'Y$. This algorithm is the most accurate but least efficient approach.

EIG bases the extraction on the eigenvalue decomposition of $Y'XX'Y$.

By default, ALGORITHM=NIPALS.

EPSILON=number
specifies the convergence criterion for the NIPALS algorithm. By default, EPSILON=$10^{-12}$.

MAXITER=number
specifies the maximum number of iterations for the NIPALS algorithm. By default, MAXITER=200.

RRR
uses reduced rank regression.

SIMPLS
uses the straightforward implementation of a statistically inspired modification of the partial least squares (SIMPLS) method of De Jong (1993).

By default, METHOD=PLS(NIPALS).

NFAC=number
specifies the number of factors to extract. The default is $\min\{15, p, N\}$, where $p$ is the number of predictors (or the number of response variables when METHOD=RRR) and $N$ is the number of runs (observations). You probably do not need to extract this many factors for most applications. Extracting too many factors can lead to an overfitted model (one that matches the training data too well), sacrificing predictive ability. Thus, if you use the default, you should also either specify the PARTITION statement to select the appropriate number of factors for the final model or consider the analysis to be preliminary and examine the results to determine the appropriate number of factors for a subsequent analysis.
NOCENTER suppresses centering of the responses and predictors before fitting. This option is useful if the analysis variables are already centered and scaled. For more information, see the section “Centering and Scaling” on page 661.

NOCLPRINT<=number> suppresses the display of the “Class Level Information” table if you do not specify number. If you specify number, the values of the classification variables are displayed only for variables whose number of levels is less than number. Specifying a number helps to reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

NOCVSTDIZE suppresses re-centering and rescaling of the responses and predictors before each model is fit in the cross validation. For more information, see the section “Centering and Scaling” on page 661.

NOSCALE suppresses scaling of the responses and predictors before fitting. This option is useful if the analysis variables are already centered and scaled. For more information, see the section “Centering and Scaling” on page 661.

VARSS lists, in addition to the average response and predictor sum of squares accounted for by each successive factor, the amount of variation accounted for in each response and predictor.

BY Statement

BY variables ;

You can specify a BY statement in PROC PLSMOD to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in SAS Language Reference: Concepts.

CLASS Statement

CLASS variable <(options)> . . . < variable <(options)>> </global-options> ;

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required. Table 12.4 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
</tbody>
</table>
Table 12.4 continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>

**DISPLAY Statement**

```
DISPLAY <table-list> < / options> ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 663. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “/!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

**CASESENSITIVE**

performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.
EXCLUDE
displays all display tables except those that you specify in the table-list.

EXCLUDEALL
suppresses display of all tables. This option takes precedence over the other options.

TRACE
displays the display table names, labels, and paths.

DISPLAYOUT Statement

DISPLAYOUT table-spec-list < / options > ;

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The table-spec-list specifies a list of CAS output tables to create. Each entry in the list has either a key=value format or a key format:

key=value specifies key as the ODS table name, path, or partial pathname, and specifies value as the CAS output table name.

key specifies key as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

EFFECT Statement

EFFECT name=effect-type (variables < / options > ) ;

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as constructed effects to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following effect-types:
specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.

specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.

specifies a multivariate polynomial effect in the specified numeric variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 12.5 summarizes the options available in the EFFECT statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
<tr>
<td><strong>Polynomial Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the polynomial</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays details of the specified polynomial</td>
</tr>
<tr>
<td>MDEGREE=</td>
<td>Specifies the maximum degree of any variable in a term of the polynomial</td>
</tr>
<tr>
<td>NOSEPARATE</td>
<td>Treats the polynomial as a single effect with multiple degrees of freedom</td>
</tr>
<tr>
<td>STANDARDIZE=</td>
<td>Specifies centering and scaling suboptions for the variables that define the polynomial</td>
</tr>
<tr>
<td><strong>Spline Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>BASIS=</td>
<td>Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect</td>
</tr>
<tr>
<td>DATABOUNDARY</td>
<td>Uses the extremes of the data as boundary knots for a B-spline basis</td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the spline effect</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the knots and locations for each spline basis function</td>
</tr>
<tr>
<td>KNOTMAX=</td>
<td>Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value</td>
</tr>
<tr>
<td>KNOTMETHOD=</td>
<td>Specifies how to construct the knots for the spline effect</td>
</tr>
</tbody>
</table>
Table 12.5  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>KNOTMIN=</td>
<td>Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value</td>
</tr>
<tr>
<td>NATURALCUBIC</td>
<td>Specifies a natural cubic spline basis for the spline effect</td>
</tr>
<tr>
<td>SEPARATE</td>
<td>Treats the spline basis for each variable as a separate effect when multiple variables are specified</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Treats each design matrix column as a separate effect for selection methods</td>
</tr>
</tbody>
</table>

For more information about the syntax of these effect-types and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”

**MODEL Statement**

MODEL response-variables = predictor-effects < / options> ;

The MODEL statement names the responses and the predictors, which determine, respectively, the Y and X matrices of the model. You can simply list the names of the predictor variables as the model effects, but you can also specify other types of effects, including polynomial effects and interactions. For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

The MODEL statement is required. You can specify only one MODEL statement.

You can specify the following options after a slash (/).

INTERCEPT

overrides the default, in which the responses and predictors are centered. When responses and predictors are centered, no intercept is required in the model.

SOLUTION

lists the coefficients of the final predictive model for the responses. The coefficients for predicting the centered and scaled responses that are based on the centered and scaled predictors are displayed, in addition to the coefficients for predicting the raw responses that are based on the raw predictors.

**OUTPUT Statement**

OUTPUT OUT=CAS-libref.data-table
  < COPYVARS=(variables)>
  < keyword =prefix>>...< keyword =prefix>> ;

The OUTPUT statement creates a data table that contains observationwise statistics, which are computed after fitting the model. If you do not specify any keywords, then only the predicted values for responses are included.
The variables in the input data table are not included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the COPYVARS= option are included.

You must specify the following option:

**OUT=** `CAS-libref.data-table`

names the output data table for PROC PLSMOD to use. You must specify this option before any other options. `CAS-libref.data-table` is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 635.

- **data-table** specifies the name of the output data table.

You can also specify the following syntax elements:

- **COPYVAR=** `variable`
  - **COPYVARS=(** `variables` **)**

  copies one or more variables from the input data table to the output data table.

- **keyword <=** `prefix >**

  specifies a statistic to include in the output data table and optionally a prefix for naming the output variables. If you do not provide a `prefix`, the PLSMOD procedure assigns a default prefix based on the type of statistic requested. For example, for response variables `y1` and `y2`, a specification of PREDICTED produces two predicted value variables, `Pred_y1` and `Pred_y2`.

You can specify the following keywords to add statistics to the OUTPUT data table:

- **H**
  - requests the approximate leverage. The default prefix is `H`.

- **PREDICTED**
  - **PRED**
  - **P**

  requests predicted values for each response. The default prefix is `Pred`.

- **PRESS**

  requests approximate predicted residuals for each response. The default prefix is `PRESS`.

- **ROLE**

  requests numeric values that indicate the role played by each observation in fitting the model. The default prefix is `_ROLE_`. Table 12.6 shows the interpretation of this variable for each observation.
<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by using a PARTITION statement, then the role variable value is 1 for observations that are used in fitting the model, and 0 for observations that have at least one missing or invalid value for the responses or predictors.

**STDX**
requests standardized (centered and scaled) predictor values for each predictor. The default prefix is StdX.

**STDXSSE**
requests the sum of squares of residuals for standardized predictors. The default prefix is StdXSSE.

**STDY**
requests standardized (centered and scaled) response values for each response. The default prefix is StdY.

**STDYSSE**
requests the sum of squares of residuals for standardized responses. The default prefix is StdYSSE.

**TSQUARE**

**T2**
requests a scaled sum of squares of score values. The default prefix is TSquare.

**XRESIDUAL**

**XRESID**

**XR**
requests residuals for each predictor. The default prefix is XResid.

**XSCORE**
requests extracted factors (X-scores, latent vectors, latent variables, and T) for each selected model factor. The default prefix is XScore.

**YRESIDUAL**

**YRESID**

**YR**
requests residuals for each response. The default prefix is YResid.
YSCORE
requests extracted responses (Y-scores and U) for each selected model factor. The default prefix is YScore.

The output variables that contain the requested statistic are named as follows, according to the keyword that you specify:

- The keywords XRESIDUAL and STDX define an output variable for each predictor, so the variables that correspond to each predictor are named by appending a number (which starts from 1) to the prefix. For each defined variable, a label is also generated automatically; the label contains the prefix of the variable and the name of the predictor. For example, if the model has three predictors, then a specification of XRESIDUAL=XR produces the variables XR1, XR2, and XR3.

- The keywords PREDICTED, YRESIDUAL, STDY, and PRESS define an output variable for each response, so the variables that correspond to each response are named by appending an underscore followed by the name of the response variable to the prefix. For example, if the model has response variables y1 and y2, then a specification of PREDICTED=P produces the variables P_y1 and P_y2.

- The keywords XSCORE and YSCORE define an output variable for each selected model factor, so the variables that correspond to each successive factor are named by appending the factor number to the prefix. For example, if the model has three selected factors, then a specification of XSCORE=T produces the variables T1, T2, and T3.

- The keywords H, TSQUARE, STDXSSE, STDYSSE, and ROLE each define a single output variable, so the variable name matches the prefix.

---

**PARTITION Statement**

**PARTITION partition-options ;**

The PARTITION statement specifies how to logically partition observations in the input data table into disjoint subsets for model training and testing. Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for random assignment of observations to each role.

You must specify exactly one of the following partition-options:

**FRACTION( < TEST=fraction > < SEED=number > )**
requests that specified proportions of the observations in the input data table be randomly assigned training and testing roles. You specify the proportions for testing by using the TEST= suboption; the specified fraction must be less than 1 and the remaining fraction of the observations are assigned to the training role. If you do not specify the TEST= suboption, all observations are assigned to the training role. The SEED= suboption specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training and testing. If you do not specify SEED=number or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

Because fraction is a per-observation probability (which means that any particular observation has a probability of fraction of being assigned the testing role), using the FRACTION option can cause
different numbers of observations to be assigned training and testing roles. You can specify the SEED= suboption to create the same partition data tables for a particular number of compute nodes. However, changing the number of compute nodes changes the initial distribution of data, resulting in different partition data tables.

**ROLEVAR | ROLE=variable (TEST='value' < TRAIN='value'>)**

names the variable in the input data table whose values are used to assign roles to each observation. This variable cannot also appear as an analysis variable in other statements or options. The TEST= and TRAIN= suboptions specify the formatted values of this variable that are used to assign observation roles. If you specify only the TEST= suboption, then all observations whose role is not determined by the TEST= suboption are assigned to training.

For more information, see the section “Test Set Validation” on page 659. For an illustration, see Example 12.1.

---

**Details: PLSMOD Procedure**

**Regression Methods**

All the predictive methods that PROC PLSMOD implements work essentially by finding linear combinations of the predictors (factors) to use to predict the responses linearly. The methods differ only in how the factors are derived, as explained in the following sections.

**Partial Least Squares**

Partial least squares (PLS) works by extracting one factor at a time. Let \( X = X_0 \) be the centered and scaled matrix of predictors, and let \( Y = Y_0 \) be the centered and scaled matrix of response values. The PLS method starts with a linear combination \( t = X_0 w \) of the predictors, where \( t \) is called a score vector and \( w \) is its associated weight vector. The PLS method predicts both \( X_0 \) and \( Y_0 \) by regression on \( t \):

\[
\hat{X}_0 = tp', \quad \text{where} \quad p' = (t't)^{-1}t'X_0 \\
\hat{Y}_0 = tc', \quad \text{where} \quad c' = (t't)^{-1}t'Y_0
\]

The vectors \( p \) and \( c \) are called the X- and Y-loadings, respectively.

The specific linear combination \( t = X_0 w \) is the combination that has maximum covariance \( t'u \) with some response linear combination \( u = Y_0 q \). Another characterization is that the X-weight, \( w \), and the Y-weight, \( q \), are proportional to the first left- and right-singular vectors, respectively, of the covariance matrix \( X_0'Y_0 \) or, equivalently, the first eigenvectors of \( X_0'Y_0'X_0'Y_0'X_0' \) and \( Y_0'X_0'Y_0'X_0' \), respectively.

This accounts for how the first PLS factor is extracted. The second factor is extracted in the same way by replacing \( X_0 \) and \( Y_0 \) with the X- and Y-residuals from the first factor:

\[
X_1 = X_0 - \hat{X}_0 \\
Y_1 = Y_0 - \hat{Y}_0
\]
These residuals are also called the deflated $X$ and $Y$ blocks. The process of extracting a score vector and deflating the data matrices is repeated for as many extracted factors as you want.

**SIMPLS**

The fact that each extracted PLS factor is defined in terms of different $X$-variables $X_i$ leads to difficulties in comparing different scores, weights, and so on. The SIMPLS method of De Jong (1993) overcomes these difficulties by computing each score $t_i = Xr_i$ in terms of the original (centered and scaled) predictors $X$. The SIMPLS $X$-weight vectors $r_i$ are similar to the eigenvectors of $SS' = X'YY'X$, but they satisfy a different orthogonality condition. The $r_1$ vector is just the first eigenvector $e_1$ (so that the first SIMPLS score is the same as the first PLS score). However, the second eigenvector maximizes

$$e_1' SS'e_2 \quad \text{subject to} \quad e_1'e_2 = 0$$

whereas the second SIMPLS weight $r_2$ maximizes

$$r_1'SS'r_2 \quad \text{subject to} \quad r_1'X'Xr_2 = t_1't_2 = 0$$

The SIMPLS scores are identical to the PLS scores for one response but slightly different for more than one response; see De Jong (1993) for details. The $X$- and $Y$-loadings are defined as in PLS, but it is easy to compute the overall model coefficients $B$ because the scores are all defined in terms of $X$:

$$\hat{Y} = \sum_i t_i c_i'$$
$$= \sum_i Xr_i c_i'$$
$$= XB, \text{ where } B = RC'$$

**Principal Component Regression**

Like the SIMPLS method, principal component regression (PCR) defines all the scores in terms of the original (centered and scaled) predictors $X$. However, unlike both the PLS and SIMPLS methods, the PCR method chooses the $X$-weights and $X$-scores without regard to the response data. The $X$-scores are chosen to explain as much variation in $X$ as possible; equivalently, the $X$-weights for the PCR method are the eigenvectors of the predictor covariance matrix $X'X$. Again, the $X$- and $Y$-loadings are defined as in PLS; but, as in SIMPLS, it is easy to compute overall model coefficients for the original (centered and scaled) responses $Y$ in terms of the original predictors $X$.

**Reduced Rank Regression**

As discussed in the preceding sections, partial least squares depends on selecting the factors $t = Xw$ of the predictors and $u = Yq$ of the responses that have maximum covariance, whereas principal component regression effectively ignores $u$ and selects $t$ to have maximum variance, subject to orthogonality constraints. In contrast, reduced rank regression selects $u$ to account for as much variation in the predicted responses as possible, effectively ignoring the predictors for the purpose of factor extraction. In reduced rank regression, the $Y$-weights, $q_i$, are the eigenvectors of the covariance matrix $\hat{Y}_{LS}' \hat{Y}_{LS}$ of the responses that are predicted by ordinary least squares regression, and the $X$-scores are the projections of the $Y$-scores, $Yq_i$, onto the $X$ space.
Relationships between Methods

When you develop a predictive model, it is important to consider not only the explanatory power of the model for current responses, but also how well the predictive functions are sampled, because the sampling affects how well the model can extrapolate to future observations. All the techniques that the PLSMOD procedure implements work by extracting successive factors (linear combinations of the predictors) that optimally address one or both of these two goals: explaining response variation and explaining predictor variation. In particular, principal component regression selects factors that explain as much predictor variation as possible, reduced rank regression selects factors that explain as much response variation as possible, and partial least squares balances the two objectives, seeking factors that explain both response and predictor variation.

To see the relationships between these methods, consider how each one extracts a single factor from the following artificial data table, `artData`, which consists of two predictors and one response:

```sas
data artData;
  input x1 x2 y;
  datalines;
3.37651 2.30716 0.75615
0.74193 -0.88845 1.15285
4.18747 2.17373 1.42392
0.96097 0.57301 0.27433
-1.11161 -0.75225 -0.25410
-1.38029 -1.31343 -0.04728
1.28153 -0.13751 1.00341
-1.39242 -2.03615 0.45518
0.63741 0.06183 0.40699
-2.52533 -1.23726 -0.91080
2.44277 3.61077 -0.82590
;
```

```sas
data mycas.artData;
  set artData;
run;
```

```sas
proc plsmod data=mycas.artData nfac=1 method=rrr;
  model y = x1 x2;
run;
```

```sas
proc plsmod data=mycas.artData nfac=1 method=pcr;
  model y = x1 x2;
run;
```

```sas
proc plsmod data=mycas.artData nfac=1 method=pls;
  model y = x1 x2;
run;
```

The amount of model and response variation that are explained by the first factor for each method is shown in Figure 12.10 through Figure 12.12.
Notice that although the first reduced rank regression factor explains all of the response variation, it accounts for only about 15% of the predictor variation. In contrast, the first principal component regression factor accounts for most of the predictor variation (93%) but only 9% of the response variation. The first partial least squares factor accounts for only slightly less predictor variation than principal components but about three times as much response variation.

Figure 12.13 illustrates how partial least squares balances the goals of explaining response and predictor variation in this case.
The ellipse shows the general shape of the 11 observations in the predictor space, with the contours of increasing y overlaid. Also shown are the directions of the first factor for each of the three methods. Notice that although the predictors vary most in the $x_1 = x_2$ direction, the response changes most in the orthogonal $x_1 = -x_2$ direction. This explains why the first principal component accounts for little variation in the response and why the first reduced rank regression factor accounts for little variation in the predictors. The direction of the first partial least squares factor represents a compromise between the other two directions.

**Test Set Validation**

None of the regression methods that the PLSMOD procedure implements fit the observed data any better than ordinary least squares (OLS) regression; in fact, all the methods approach OLS as more factors are extracted. Basing the model on more extracted factors improves the model fit to the observed data, but extracting too many factors can cause overfitting—that is, tailoring the model too much to the current data to the detriment of future predictions. So the crucial point is that when there are many predictors, OLS can overfit the observed data; biased regression methods that use fewer extracted factors can provide better predictability of future observations. However, as the preceding observations imply, the quality of the observed data fit cannot be
used to choose the number of factors to extract; the number of extracted factors must be chosen on the basis of how well the model fits observations that are not involved in the modeling procedure itself.

PROC PLSMOD implements the test set validation method of choosing the number of extracted factors. When you have sufficient data, you can subdivide your data into two parts: training data and test data. During the validation process, the model is fit on the training data, and the predicted residual sum of squares (PRESS) for models that have different numbers of extracted factors is found by using the test data. The number of factors chosen is usually the one that minimizes PRESS.

You use the PARTITION statement to logically subdivide the DATA= data table into separate roles. You can name the fractions of the data that you want to reserve as training data and test data. For example, the following statements randomly subdivide the inData data table, reserving 50% each for training and testing:

```
proc plsmod data=mycas.inData;
  partition fraction(test=0.5);
  ...
run;
```

In some cases you might need to exercise more control over the partitioning of the input data table. You can do this by naming both a variable in the input data table and a formatted value of that variable for each role. For example, the following statements assign roles to the observations in the inData data table based on the value of the variable Group in that data table. Observations whose value of Group is 'group 1' are assigned for training, and those whose value is 'group 2' are assigned to testing. All other observations are ignored.

```
proc plsmod data=mycas.inData;
  partition roleVar=Group(train='group 1' test='group 2')
  ...
run;
```

By default, the number of extracted factors is chosen to be the one that minimizes PRESS. However, models that have fewer factors often have PRESS statistics that are only marginally larger than the absolute minimum. To address this, Van der Voet (1994) proposed a statistical test for comparing the predicted residuals from different models; when you apply van der Voet’s test, the number of factors chosen is the fewest while still producing residuals that are insignificantly larger than the residuals of the model that has a minimum PRESS.

To see how van der Voet’s test works, let $R_{i,j,k}$ be the $j$th predicted residual for response $k$ for the model that has $i$ extracted factors. Then, the PRESS statistic is $\sum_{jk} R^2_{i,j,k}$. Also, let $i_{min}$ be the number of factors for which PRESS is minimized. The critical value for van der Voet’s test is based on the differences between squared predicted residuals:

\[
D_{i,j,k} = R^2_{i,j,k} - R^2_{i_{min},j,k}
\]

One alternative for the critical value is $C_i = \sum_{jk} D_{i,j,k}$, which is simply the difference between the PRESS statistics for $i$ and $i_{min}$ factors; alternatively, van der Voet suggests Hotelling’s $T^2$ statistic $C_i = \mathbf{d}_i' S_i^{-1} \mathbf{d}_i$, where $\mathbf{d}_i$ is the sum of the vectors $\mathbf{d}_{i,j} = \{D_{i,j1}, \ldots, D_{i,jN_y}\}'$ and $S_i$ is the sum of squares and crossproducts matrix,
Theoretically, the significance level for van der Voet’s test is obtained by comparing $C_i$ with the distribution of values that result from randomly exchanging $R_{i,j}^2$ and $R_{i_{max},jk}^2$. In practice, a Monte Carlo sample of such values is simulated and the significance level is approximated as the proportion of simulated critical values that are greater than $C_i$. If you apply van der Voet’s test by specifying the CVTEST option, then, by default, the number of extracted factors that are chosen is the smallest number of factors that have an approximate significance level that is greater than 0.1.

Centering and Scaling

By default, the predictors and the responses are centered and scaled to have mean 0 and standard deviation 1. Centering the predictors and the responses ensures that the criterion for choosing successive factors is based on how much variation they explain in either the predictors or the responses or in both. (For more information about how different methods explain variation, see the section “Regression Methods” on page 655.) Without centering, both the value of the mean variable and the variation around that mean are involved in selecting factors. Scaling serves to place all predictors and responses on an equal footing relative to their variation in the data. For example, if Time and Temp are two of the predictors, then scaling says that a change of std(Time) in Time is approximately equivalent to a change of std(Temp) in Temp.

Usually, both the predictors and responses should be centered and scaled. However, if their values already represent variation around a nominal or target value, then you can use the NOCENTER option in the PROC PLSMOD statement to suppress centering. Likewise, if the predictors or responses are already all on comparable scales, then you can use the NOSCALE option to suppress scaling.

If the predictors involve crossproduct terms, PROC PLSMOD does not standardize the variables before it standardizes the crossproduct. That is, if the $i$th values of two predictors are denoted $x_{1i}^j$ and $x_{2i}^j$, then the default standardized $i$th value of the crossproduct is

$$\frac{x_{1i}^j x_{2i}^j - \text{mean}_j(x_{1j}^j x_{2j}^j)}{\text{std}_j(x_{1j}^j x_{2j}^j)}$$

When test set validation is performed for the number of effects, some practitioners disagree as to whether the training data should be retransformed. By default, PROC PLSMOD does retransform the training data, but you can suppress this behavior by specifying the NOCVSTDIZE option in the PROC PLSMOD statement.

Missing Values

Observations that have any missing independent variables (including all classification variables) are excluded from the analysis, and no predictions are computed for such observations. However, if you specify the MISSING option in the CLASS statement, missing values are treated as valid values for the classification variable. Observations that have no missing independent variables but do have missing response variables are
also excluded from the analysis, but predictions are computed. If you use the PARTITION statement and specify the ROLEVAR= option, observations that contain missing values for the ROLEVAR= variable are excluded from the analysis, but predictions are computed for them.

---

**Displayed Output**

The following sections describe the output that PROC PLSDMOD produces. The output is organized into various tables, which are discussed in the order of their appearance.

**Model Information**

The “Model Information” table displays basic information about the model, such as the input data table, the factor extraction method, the validation method, and the type of parameterization used for classification variables that are named in the CLASS statement. If you use the PARTITION statement, the table also displays the random number seed for partitioning, the validation testing criterion, the number of random permutations, and the random number seed for permutation, depending on whether you specify the FRACTION option in the PARTITION statement and the CVTEST option in the PROC PLSDMOD statement.

**Dimensions**

The “Dimensions” table displays information about the number of response variables, the number of effects, and the number of predictor parameters. It also displays the number of factors to extract.

**Number of Observations**

The “Number of Observations” table displays the number of observations that are read from the input data table and the number of observations that are used in the analysis. If you use a PARTITION statement, the table also displays the number of observations that are used for each data role.

**Class Level Information**

The “Class Level Information” table lists the levels of every variable that is specified in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by specifying the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by specifying the NOCLPRINT= option in the PROC PLSDMOD statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.

**Centering and Scaling Information**

If you specify the CENSCALE option in the PROC PLSDMOD statement, the PLSDMOD procedure produces “Model Effect Centering and Scaling” and “Response Variable Centering and Scaling” tables, which display the centering and scaling information for each predictor and response.
Test Set Validation

If you use the PARTITION statement to perform a test set validation for choosing the number of extracted factors, the PLSMOD procedure produces a “Test Set Validation Residual Summary” table to display a residual summary of the validation for each number of factors. It also produces a “Test Set Validation Results” table to display information about the optimal number of factors.

Percentage Variation Accounted for by Extracted Factors

By default, the PLSMOD procedure produces the “Percentage Variation Accounted for by Extracted Factors” table to display the amount of predictor variation and response variation that are accounted for by each factor. If you specify the VARSS option in the PROC PLSMOD statement, the PLSMOD procedure also produces the “Model Effect Percentage Variation Accounted for by Extracted Factors” table and the “Response Variable Percentage Variation Accounted for by Extracted Factors” table to display the amount of variation that is accounted for in each predictor and response, in addition to the average predictor and response sum of squares that are accounted for by each successive factor.

Model Details

If you specify the DETAILS option in the PROC PLSMOD statement, the PLSMOD procedure produces tables to display details about the fitted model for each successive factor. These tables include the following:

- “Model Effect Loadings” table, which displays the predictor loadings
- “Model Effect Weights” table, which displays predictor weights
- “Response Variable Weights” table, which displays the response weights
- “Coded Regression Coefficients” tables, which display the coded regression coefficients, if you specify METHOD=SIMPLS, METHOD=PCR, or METHOD=RRR in the PROC PLSMOD statement.

Parameter Estimates

If you specify the SOLUTION option in the MODEL statement, the PLSMOD procedure produces a “Parameter Estimates” table to display the coefficients of the final predictive model for the responses. The coefficients for predicting the centered and scaled responses that are based on the centered and scaled predictors are displayed, in addition to the coefficients for predicting the raw responses based on the raw predictors.

Timing Information

The “Timing” table displays the elapsed time of each main task of the procedure.

ODS Table Names

Each table that the PLSMOD procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement, the DISPLAYOUT statement, or the Output Delivery System (ODS) statements. These names are listed in Table 12.7.
### Table 12.7 ODS Tables Produced by PROC PLSMOD

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement and Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CVResults</td>
<td>Results of test set validation</td>
<td>PARTITION statement</td>
</tr>
<tr>
<td>CenScaleParms</td>
<td>Parameter estimates for centered and scaled data</td>
<td>SOLUTION option in MODEL statement</td>
</tr>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS statement</td>
</tr>
<tr>
<td>CodedCoef</td>
<td>Coded regression coefficients</td>
<td>DETAILS option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td>Default output</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Model information</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>Default output</td>
</tr>
<tr>
<td>OutputCasTables</td>
<td>Library and name of output data tables, and number of rows and columns in the table</td>
<td>DISPLAYOUT statement or OUTPUT statement</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Parameter estimates for raw data</td>
<td>SOLUTION option in MODEL statement</td>
</tr>
<tr>
<td>PercentVariation</td>
<td>Predictor and response variation that are accounted for by each factor</td>
<td>Default output</td>
</tr>
<tr>
<td>ResidualSummary</td>
<td>Residual summary from test set validation</td>
<td>PARTITION statement</td>
</tr>
<tr>
<td>Timing</td>
<td>Absolute and relative times spent by tasks that are performed by the procedure</td>
<td>Default output</td>
</tr>
<tr>
<td>XEffectCenScale</td>
<td>Centering and scaling information for predictor effects</td>
<td>CENSCALE option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>XLoadings</td>
<td>Loadings for predictor effects</td>
<td>DETAILS option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>XPercentVariation</td>
<td>Variation that is accounted for by each factor for predictor effects</td>
<td>VARSS option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>XWeights</td>
<td>Weights for predictor effects</td>
<td>DETAILS option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>YPercentVariation</td>
<td>Variation that is accounted for by each factor for responses</td>
<td>VARSS option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>YVariableCenScale</td>
<td>Centering and scaling information for responses</td>
<td>CENSCALE option in PROC PLSMOD statement</td>
</tr>
<tr>
<td>YWeights</td>
<td>Weights for responses</td>
<td>DETAILS option in PROC PLSMOD statement</td>
</tr>
</tbody>
</table>
Example 12.1: Choosing a PLS Model by Test Set Validation

This example demonstrates issues in spectrometric calibration. The data (Umetrics 1995) consist of spectrographic readings on 33 samples that contain known concentrations of two amino acids, tyrosine and tryptophan. The spectra are measured at 30 frequencies across the overall range of frequencies. For example, Output 12.1.1 shows the observed spectra for three samples: one with only tryptophan, one with only tyrosine, and one with a mixture of the two, all at a total concentration of $10^{-6}$.

Output 12.1.1 Spectra for Three Samples of Tyrosine and Tryptophan
Of the 33 samples, 18 are used as a training set and 15 as a test set. The data originally appear in McAvoy et al. (1989).

These data were created in a lab, where the concentrations are fixed in order to provide a wide range of applicability for the model. This example uses a linear function of the logarithms of the spectra to predict the logarithms of tyrosine and tryptophan concentration and the logarithm of the total concentration. Actually, because zeros are possible in both the responses and the predictors, slightly different transformations are used. The following statements create a data table named ex1Data for these data. The data table also contains a variable Role that is used to assign samples to the training and testing roles.

```plaintext
data ex1Data;
  input obsnam $ Role : $5. tot tyr f1-f30 @@;
  try = tot - tyr;
  if (tyr) then tyr_log = log10(tyr); else tyr_log = -8;
  if (try) then try_log = log10(try); else try_log = -8;
  tot_log = log10(tot);
  datalines;
17mix35 TRAIN 0.00003 0
-6.215 -5.809 -5.114 -3.963 -2.897 -2.269 -1.675 -1.235
-0.900 -0.659 -0.497 -0.395 -0.335 -0.315 -0.333 -0.377
-0.453 -0.549 -0.658 -0.797 -0.878 -0.954 -1.060 -1.266
-1.520 -1.804 -2.044 -2.269 -2.496 -2.714
19mix35 TRAIN 0.00003 3E-7
-5.516 -5.294 -4.823 -3.858 -2.827 -2.249 -1.683 -1.218
-0.907 -0.658 -0.501 -0.400 -0.345 -0.323 -0.342 -0.387
-0.461 -0.554 -0.665 -0.803 -0.887 -0.960 -1.072 -1.272
-1.541 -1.814 -2.058 -2.289 -2.496 -2.712
21mix35 TRAIN 0.00003 7.5E-7
-5.519 -5.294 -4.501 -3.863 -2.827 -2.280 -1.716 -1.262
-0.939 -0.694 -0.536 -0.444 -0.384 -0.369 -0.377 -0.421
-0.495 -0.596 -0.706 -0.824 -0.917 -0.988 -1.103 -1.294
-1.565 -1.841 -2.084 -2.320 -2.521 -2.729
23mix35 TRAIN 0.00003 1.5E-6
... more lines ...
-5.138 -5.463 -5.461 -5.461 -5.461 -5.461 -5.461 -5.461
tyro2 TEST 0.0001 0.0001
-1.081 -0.710 -0.470 -0.337 -0.327 -0.433 -0.602 -0.841
-4.668 -4.668 -4.865 -4.865 -5.109 -5.111
;

data mycas.ex1Data;
  set ex1Data;
run;
```

The following statements fit a PLS model that has 10 factors:

```plaintext
proc plsmod data=mycas.ex1Data nfac=10;
  model tot_log tyr_log try_log = f1-f30;
run;
```
The “Model Information” table in Output 12.1.2 shows that no validation method is used. The “Number of Observations” table confirms that all 33 sample observations are used in the analysis.

**Output 12.1.2** Model Information and Number of Observations

<table>
<thead>
<tr>
<th>The PLSMOD Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Model Information</strong></td>
</tr>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Factor Extraction Method</td>
</tr>
<tr>
<td>PLS Algorithm</td>
</tr>
<tr>
<td>Validation Method</td>
</tr>
<tr>
<td><strong>Number of Observations Read</strong></td>
</tr>
<tr>
<td><strong>Number of Observations Used</strong></td>
</tr>
</tbody>
</table>

The table in **Output 12.1.3** indicates that only four or five factors are required to explain almost all the variation in both the predictors and the responses.

**Output 12.1.3** Amount of Variation Explained

<table>
<thead>
<tr>
<th>Percentage Variation Accounted for by Partial Least Squares Factors</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Model Effects</strong></td>
</tr>
<tr>
<td><strong>Number of Extracted Factors</strong></td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
<tr>
<td>8</td>
</tr>
<tr>
<td>9</td>
</tr>
<tr>
<td>10</td>
</tr>
</tbody>
</table>

In order to choose the optimal number of PLS factors, you can explore how well models that are based on data in training roles and have different numbers of factors fit the data in testing roles. To do so, you can use the PARTITION statement to assign observations to training and testing roles based on the values of the input variable named `Role`, as follows:

```plaintext
proc plsmod data=mycas.ex1Data nfac=10 cvtest(stat=press seed=12345);
    model tot_log tyr_log try_log = f1-f30;
    partition roleVar = Role(train='TRAIN' test='TEST');
run;
```

**Output 12.1.4** shows the “Model Information” table and the “Number of Observations” table. The “Model Information” table indicates that test set validation is used, and it displays information about the options
that are used in the model comparison test. The “Number of Observations” table confirms that there are 18 observations for the training role and 15 for the testing role.

**Output 12.1.4** Model Information and Number of Observations with Test Set Validation

The PLSMOD Procedure

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Data Source</td>
</tr>
<tr>
<td>Factor Extraction Method</td>
</tr>
<tr>
<td>PLS Algorithm</td>
</tr>
<tr>
<td>Validation Method</td>
</tr>
<tr>
<td>Validation Testing Criterion</td>
</tr>
<tr>
<td>Number of Random Permutations</td>
</tr>
<tr>
<td>Random Number Seed for Permutation</td>
</tr>
</tbody>
</table>

| Number of Observations Read | 33 |
| Number of Observations Used | 33 |
| Number of Observations Used for Training | 18 |
| Number of Observations Used for Testing | 15 |

Output 12.1.5 displays the results of the test set validation. They indicate that although five PLS factors produce the minimum predicted residual sum of squares, the residuals for four factors are insignificantly different from the residuals for five factors. Thus, the smaller model is preferred.

**Output 12.1.5** Test Set Validation for the Number of PLS Factors

The PLSMOD Procedure

<table>
<thead>
<tr>
<th>Test Set Validation for the Number of Extracted Factors</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Extracted Factors</td>
</tr>
<tr>
<td>-----------------------------</td>
</tr>
<tr>
<td>0</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
<tr>
<td>8</td>
</tr>
<tr>
<td>9</td>
</tr>
<tr>
<td>10</td>
</tr>
</tbody>
</table>

Minimum Root Mean PRESS | 0.500034
Minimizing Number of Factors | 5
Smallest Number of Factors with \( p > 0.1 \) | 4
Output 12.1.5 continued

<table>
<thead>
<tr>
<th>Number of Extracted Factors</th>
<th>Current Model Effects</th>
<th>Total Model Effects</th>
<th>Current Response Variables</th>
<th>Total Response Variables</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>81.16545</td>
<td>48.33854</td>
<td>16.81113</td>
<td>80.88508</td>
</tr>
<tr>
<td>2</td>
<td>16.8113</td>
<td>32.54654</td>
<td>97.97676</td>
<td>92.32888</td>
</tr>
<tr>
<td>3</td>
<td>1.76391</td>
<td>11.44380</td>
<td>99.74067</td>
<td>96.16519</td>
</tr>
<tr>
<td>4</td>
<td>0.19507</td>
<td>3.83631</td>
<td>99.93574</td>
<td>96.16519</td>
</tr>
</tbody>
</table>

References


Chapter 13
The QTRSELECT Procedure

Contents

Overview: QTRSELECT Procedure ........................................ 672
PROC QTRSELECT Features ............................................. 672
PROC QTRSELECT Compared with Other SAS Procedures ............. 673
Using CAS Sessions and CAS Engine Librefs .......................... 674
Getting Started: QTRSELECT Procedure ............................... 675
Syntax: QTRSELECT Procedure ........................................ 683
PROC QTRSELECT Statement .......................................... 683
BY Statement .......................................................... 684
CLASS Statement ...................................................... 684
CODE Statement ....................................................... 685
DISPLAY Statement .................................................... 686
DISPLAYOUT Statement ............................................... 687
EFFECT Statement ...................................................... 687
MODEL Statement ...................................................... 689
OUTPUT Statement ..................................................... 691
PARTITION Statement .................................................. 693
SELECTION Statement .................................................. 694
WEIGHT Statement ..................................................... 695
Details: QTRSELECT Procedure ........................................ 695
Quantile Regression ..................................................... 695
Criteria Used in Model Selection ...................................... 697
Diagnostic Statistics .................................................... 700
Classification Variables and the SPLIT Option ....................... 701
Using Validation and Test Data ........................................ 702
Computational Method .................................................. 705
Displayed Output ....................................................... 705
ODS Table Names ....................................................... 708
ODS Graphics .......................................................... 709
Examples: QTRSELECT Procedure ..................................... 710
Example 13.1: Simulation Study ....................................... 710
Example 13.2: Growth Charts for Body Mass Index .................. 713
Example 13.3: Pollution and Mortality ................................ 715
References ............................................................... 722
Overview: QTRSELECT Procedure

The QTRSELECT procedure fits and performs model selection for quantile regression models in SAS Viya. Quantile regression uses a linear function model to fit the quantiles of a response variable conditional on the explanatory variables. The model does not assume a particular parametric distribution for the response. The models that PROC QTRSELECT supports can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The models can also include constructed effects such as splines. The procedure offers a number of effect-selection methods, including stepwise methods. It also offers extensive capabilities for customizing the model selection by using a wide variety of selection and stopping criteria, including significance-level-based criteria, information criteria, and modern validation-based criteria. PROC QTRSELECT also provides a variety of quantile regression diagnostics that are conditional on the selected model.

PROC QTRSELECT Features

The main features of the QTRSELECT procedure are as follows:

- **Model specification**
  - supports quantile regression for single or multiple quantile levels
  - supports multiple parameterizations for classification effects
  - supports any degree of interactions (crossed effects) and nested effects
  - supports hierarchical model selection strategy among effects that have a containment relationship
  - supports partitioning of data into training, validation, and testing roles
  - provides a WEIGHT statement for weighted analysis

- **Selection control**
  - provides multiple effect-selection methods
  - offers selection of individual levels of classification effects
  - provides effect selection based on a variety of selection criteria
  - provides stopping rules based on a variety of model evaluation criteria
  - supports stopping and selection rules based on external validation

- **Display and output**
  - provides a CODE statement to produce SAS code that can score a new data set
  - produces output data tables that contain predicted values, residuals, and confidence limits
  - uses ODS Graphics to create model selection plots as part of its output. For more information about ODS Graphics, see the section “ODS Graphics” on page 709

The QTRSELECT procedure supports the following effect-selection methods. For a more detailed description of these methods, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”
- Forward selection starts with no effects in the model and adds effects.
- Backward elimination starts with all effects in the model and deletes effects.
- Stepwise regression is similar to forward selection, except that effects already in the model do not necessarily stay there.

Because the QTRSELECT procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on CAS
- exploits all the available cores and concurrent threads. For information about how PROC QTRSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

---

PROC QTRSELECT Compared with Other SAS Procedures

The QTRSELECT procedure provides quantile regression functionality that is comparable to that of the HPQUANTSELECT, QUANTSELECT, and QUANTREG procedures in SAS/STAT software.

PROC QTRSELECT Compared with the HPQUANTSELECT Procedure

The functionality of the QTRSELECT procedure closely resembles that of the HPQUANTSELECT procedure, which is a high-performance procedure. The QTRSELECT procedure is the next generation of the HPQUANTSELECT procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations.

Both the QTRSELECT and HPQUANTSELECT procedures fit and perform effect selection for quantile regression models. The models can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The QTRSELECT procedure is additionally capable of constructing complex effects including univariate spline and polynomial expansions, and producing effect-selection plots by using ODS Graphics.

With the QTRSELECT and HPQUANTSELECT procedures, you request model selection by using the SELECTION statement. Both procedures offer the same methods of effect selection.

PROC QTRSELECT Compared with the QUANTSELECT Procedure

Both the QTRSELECT and QUANTSELECT procedures fit and perform model selection for quantile regression models. The models can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. Both procedures support the forward, backward, and stepwise effect-selection methods and the ability to use separate validation and test data as specified in the PARTITION statement.

PROC QTRSELECT provides confidence limits and Wald tests for parameters, and prediction limits for quantiles.

PROC QUANTSELECT provides LASSO and adaptive LASSO effect-selection methods and effect selection for quantile process regression.
PROC QTRSELECT Compared with the QUANTREG Procedure

The QTRSELECT procedure chooses and fits quantile regression models. The QUANTREG procedure fits quantile regression models, but it does not offer model selection.

PROC QTRSELECT provides a variety of effect-selection methods, fit statistics, graphical effect-selection summary, and a cloud-enabled interior-point algorithm. It also supports partitioning the data into training, validation, and testing roles.

PROC QUANTREG provides simplex and smoothing algorithms, a rank-score test, a likelihood test, Markov-chain-marginal-bootstrap covariance estimation, many diagnostic and fit plots, and quantile process regression.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
**Getting Started: QTRSELECT Procedure**

The following example is modeled on the example in the section “Getting Started: QUANTSELECT Procedure” in the *SAS/STAT User’s Guide*. The Sashelp.baseball data set contains salary and performance information for Major League Baseball (MLB) players, excluding pitchers, who played in at least one game in both the 1986 and 1987 seasons. The salaries (*Time Inc. 1987*) are for the 1987 season, and the performance measures are for the 1986 season (*Reichler 1987*).

The following statements display the variables in the data set. Figure 13.1 shows the results.

```sas
proc contents varnum data=sashelp.baseball;
   ods select position;
run;
```

**Figure 13.1** Sashelp.Baseball Data Set

### The CONTENTS Procedure

<table>
<thead>
<tr>
<th>Variables in Creation Order</th>
<th># Variable</th>
<th>Type</th>
<th>Len</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Name</td>
<td>Char</td>
<td>18</td>
<td></td>
<td>Player’s Name</td>
</tr>
<tr>
<td>2 Team</td>
<td>Char</td>
<td>14</td>
<td></td>
<td>Team at the End of 1986</td>
</tr>
<tr>
<td>3 nAtBat</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Times at Bat in 1986</td>
</tr>
<tr>
<td>4 nHits</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Hits in 1986</td>
</tr>
<tr>
<td>5 nHome</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Home Runs in 1986</td>
</tr>
<tr>
<td>6 nRuns</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Runs in 1986</td>
</tr>
<tr>
<td>7 nRBI</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>RBIs in 1986</td>
</tr>
<tr>
<td>8 nBB</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Walks in 1986</td>
</tr>
<tr>
<td>9 YrMajor</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Years in the Major Leagues</td>
</tr>
<tr>
<td>10 CrAtBat</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career Times at Bat</td>
</tr>
<tr>
<td>11 CrHits</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career Hits</td>
</tr>
<tr>
<td>12 CrHome</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career Home Runs</td>
</tr>
<tr>
<td>13 CrRuns</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career Runs</td>
</tr>
<tr>
<td>14 CrRbi</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career RBIs</td>
</tr>
<tr>
<td>15 CrBB</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Career Walks</td>
</tr>
<tr>
<td>16 League</td>
<td>Char</td>
<td>8</td>
<td></td>
<td>League at the End of 1986</td>
</tr>
<tr>
<td>17 Division</td>
<td>Char</td>
<td>8</td>
<td></td>
<td>Division at the End of 1986</td>
</tr>
<tr>
<td>18 Position</td>
<td>Char</td>
<td>8</td>
<td></td>
<td>Position(s) in 1986</td>
</tr>
<tr>
<td>19 n Outs</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Put Outs in 1986</td>
</tr>
<tr>
<td>20 n Assts</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Assists in 1986</td>
</tr>
<tr>
<td>21 n Error</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Errors in 1986</td>
</tr>
<tr>
<td>22 Salary</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>1987 Salary in $ Thousands</td>
</tr>
<tr>
<td>23 Div</td>
<td>Char</td>
<td>16</td>
<td></td>
<td>League and Division</td>
</tr>
<tr>
<td>24 log Salary</td>
<td>Num</td>
<td>8</td>
<td></td>
<td>Log Salary</td>
</tr>
</tbody>
</table>

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
You can load the Sashelp.Baseball data set into your CAS session by using your CAS engine libref with the following DATA step:

```sas
   data mycas.baseball;
   set sashelp.baseball;
   run;
```

These statements assume that your CAS engine libref is named `mycas`, as in the section “Using CAS Sessions and CAS Engine Librefs” on page 674, but you can substitute any appropriately defined CAS engine libref.

Suppose you want to investigate how the MLB players’ salaries for the 1987 season depend on performance measures for the players’ previous season and MLB career. You might worry that some players who are outliers could dominate your least squares analysis. To address this concern, you can use the following statements to obtain a median regression model, which is equivalent to the 50th conditional percentile or the quantile regression model at quantile level 0.5:

```sas
   proc qtrselect data=mycas.baseball;
   class league division;
   model Salary = nAtBat nHits nHome nRuns nRBI nBB
                yrMajor crAtBat crHits crHome crRuns crRbi
                crBB league division nOuts nAssts nError;
   run;
```

If you do not use the SELECTION statement, the QTRSELECT procedure fits the full model that is specified by the MODEL statement without any effect selection.

**Figure 13.2** Number of Observations, Class Level Information, and Dimensions Tables

<table>
<thead>
<tr>
<th>The QTRSELECT Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
</tbody>
</table>

**Class Level Information**

<table>
<thead>
<tr>
<th>Class</th>
<th>Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>League</td>
<td>2</td>
<td>American National</td>
</tr>
<tr>
<td>Division</td>
<td>2</td>
<td>East West</td>
</tr>
</tbody>
</table>

**Dimensions**

<table>
<thead>
<tr>
<th>Description</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Effects</td>
<td>19</td>
</tr>
<tr>
<td>Number of Parameters</td>
<td>21</td>
</tr>
</tbody>
</table>

**Figure 13.2** displays the “Number of Observations,” “Class Level Information,” and “Dimensions” tables. The “Number of Observations” table shows that, of the 322 observations, PROC QTRSELECT uses only 263 observations for model fitting and ignores 59 incomplete observations.

The “Class Level Information” table shows level information for two CLASS effects that the CLASS statement identifies: League and Division. League has two levels: American League and National League. Division also has two levels: East Division and West Division.

The “Dimensions” table shows that the MODEL statement identifies 19 effects for model fitting besides the intercept effect. Because the 19 effects include two CLASS effects and each level of a CLASS effect corresponds to a parameter, the 19 effects contain a total of 21 parameters.
The QTRSELECT Procedure

Quantile Level = 0.5

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>-67.753223</td>
<td>39.95908</td>
<td>-1.70</td>
<td>0.0912</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nAtBat</td>
<td>1</td>
<td>-1.571116</td>
<td>0.44700</td>
<td>-3.51</td>
<td>0.0005</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nHits</td>
<td>1</td>
<td>8.821920</td>
<td>1.94990</td>
<td>4.52</td>
<td>&lt;0.001</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nHome</td>
<td>1</td>
<td>-5.917572</td>
<td>4.91015</td>
<td>-1.21</td>
<td>0.2293</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nRuns</td>
<td>1</td>
<td>-5.170765</td>
<td>2.14914</td>
<td>-2.41</td>
<td>0.0169</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nRBI</td>
<td>1</td>
<td>0.775465</td>
<td>2.15469</td>
<td>0.36</td>
<td>0.7192</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nBB</td>
<td>1</td>
<td>5.288663</td>
<td>1.67603</td>
<td>3.16</td>
<td>0.0018</td>
<td></td>
<td></td>
</tr>
<tr>
<td>YrMajor</td>
<td>1</td>
<td>6.618769</td>
<td>6.61798</td>
<td>1.00</td>
<td>0.3182</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrAtBat</td>
<td>1</td>
<td>-0.044629</td>
<td>0.15485</td>
<td>-0.29</td>
<td>0.7734</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrHits</td>
<td>1</td>
<td>0.078964</td>
<td>0.73594</td>
<td>0.11</td>
<td>0.9146</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrHome</td>
<td>1</td>
<td>3.782307</td>
<td>1.90065</td>
<td>1.99</td>
<td>0.0477</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrRuns</td>
<td>1</td>
<td>1.231052</td>
<td>0.77137</td>
<td>1.60</td>
<td>0.1118</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrRbi</td>
<td>1</td>
<td>-0.706950</td>
<td>0.76888</td>
<td>-0.92</td>
<td>0.3588</td>
<td></td>
<td></td>
</tr>
<tr>
<td>CrBB</td>
<td>1</td>
<td>-0.689111</td>
<td>0.41382</td>
<td>-1.67</td>
<td>0.0971</td>
<td></td>
<td></td>
</tr>
<tr>
<td>League American</td>
<td>1</td>
<td>-34.391364</td>
<td>24.37175</td>
<td>-1.41</td>
<td>0.1595</td>
<td></td>
<td></td>
</tr>
<tr>
<td>League National</td>
<td>0</td>
<td>0</td>
<td>0.0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Division East</td>
<td>1</td>
<td>60.308558</td>
<td>27.28730</td>
<td>2.21</td>
<td>0.0280</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Division West</td>
<td>0</td>
<td>0</td>
<td>0.0</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nOuts</td>
<td>1</td>
<td>0.232729</td>
<td>0.12110</td>
<td>1.92</td>
<td>0.0558</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nAssts</td>
<td>1</td>
<td>0.098240</td>
<td>0.18888</td>
<td>0.52</td>
<td>0.6035</td>
<td></td>
<td></td>
</tr>
<tr>
<td>nError</td>
<td>1</td>
<td>-0.815744</td>
<td>3.51436</td>
<td>-0.23</td>
<td>0.8166</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Figure 13.3 displays the “Fit Statistics” table, which shows the values of model fitting criteria for the fitted median model. For more information about model fitting criteria for quantile regression, see the section “Details: QTRSELECT Procedure” on page 695.

Figure 13.4 displays the “Parameter Estimates” table, which shows the parameter estimates of the fitted median model. You can see that, of the 19 effective parameters whose degrees of freedom are not zero, the fitted model contains 13 insignificant parameters whose 95% confidence intervals cover zeros. Because more than half of the 19 effective parameters are insignificant, you might worry that the model is overfitted.
It is well known that both overfitting and underfitting harm the prediction performance of a model. You can prevent overfitting and underfitting by using a good effect-selection technique. The following statements apply the forward selection method and the SL (significance level) criterion to choose a parsimonious model for the mycas.baseball data table:

```sas
proc qtrselect data=mycas.baseball;
  class league division;
  model Salary = nAtBat nHits nHome nRuns nRBI nBB
                   yrMajor crAtBat crHits crHome crRuns crRbi
                   crBB league division nOuts nAssts nError
       / clb;
  selection method=forward(select=sl sle=0.1);
run;
```

The CLB option in the MODEL statement requests 95% confidence limits for the parameter estimates. The SLE=0.1 option in the SELECTION statement specifies the significance level for entry. A candidate effect can enter the model at a certain selection step only if the following conditions are met:

- Its $p$-value is the smallest among all the valid candidate effects.
- Its $p$-value is smaller than 0.1 (the significance level for entry).

For more information about using significance levels in effect selection, see the section “Statistical Tests for Significance Level” on page 699.

**Figure 13.5 Selection Information**

<table>
<thead>
<tr>
<th>Selection Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Entry Significance Level (SLE)</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
</tbody>
</table>

Figure 13.5 displays the “Selection Information” table. The “Selection Information” provides details about the method and criteria used to perform the model selection. The requested selection method is the forward selection method where the decisions about what effects to add at any step and when to terminate the selection are both based on the significance level criterion.
### Figure 13.6 Selection Summary

**The QTRSELECT Procedure**

**Quantile Level = 0.5**

**Selection Details**

<table>
<thead>
<tr>
<th>Step</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Intercept</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>CrHome</td>
<td>2</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>2</td>
<td>nHits</td>
<td>3</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>3</td>
<td>CrHits</td>
<td>4</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>4</td>
<td>nOuts</td>
<td>5</td>
<td>0.0185</td>
</tr>
<tr>
<td>5</td>
<td>nABat</td>
<td>6</td>
<td>0.0182</td>
</tr>
<tr>
<td>6</td>
<td>Division</td>
<td>7</td>
<td>0.0118</td>
</tr>
<tr>
<td>7</td>
<td>nBB</td>
<td>8</td>
<td>0.0647</td>
</tr>
<tr>
<td>8</td>
<td>nRuns</td>
<td>9</td>
<td>0.0558</td>
</tr>
</tbody>
</table>

Figure 13.6 displays the “Selection Summary” table. Each row in the “Selection Summary” table shows the effect that enters the model at the corresponding step of the effect selection process together with its $p$-value for adding the effect into the model at that step.

### Figure 13.7 Stopping and Selection Reasons

Selection stopped because no candidate for entry is significant at the 0.1 level.

The model at step 8 is selected.

**Selected Effects:** Intercept nABat nHits nRuns nBB CrHits CrHome Division nOuts

Figure 13.7 displays the “Stop Reason,” “Selection Reason,” and “Selected Effects” tables. The “Stop Reason” and “Selection Reason” tables indicate that effect selection stopped because no candidate for entry was significant at the 0.1 level after step 8. The “Selected Effects” table lists the effects that are included in the selected model.

### Figure 13.8 Details of the Selected Model

**The QTRSELECT Procedure**

**Quantile Level = 0.5**

**Selected Model**

<table>
<thead>
<tr>
<th>Objective Function</th>
<th>26568</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>0.39232</td>
</tr>
<tr>
<td>Adj R1</td>
<td>0.37318</td>
</tr>
<tr>
<td>AIC</td>
<td>2445.64547</td>
</tr>
<tr>
<td>AICC</td>
<td>2446.35693</td>
</tr>
<tr>
<td>SBC</td>
<td>2477.79485</td>
</tr>
<tr>
<td>ACL</td>
<td>101.01768</td>
</tr>
</tbody>
</table>
Chapter 13: The QTRSELECT Procedure

Figure 13.8 continued

The “Fit Statistics” and “Parameter Estimates” tables in Figure 13.8 give details of the final selected model. You can see that all nine effective parameters (excluding Division West) are significant at the 5% significance level, corresponding to the 95% confidence limits.

Like the sample median, a median regression model is robust to extreme observations, because it depends only on a small middle subset of all the observations in the data table. However, it is less representative of the entire conditional distribution of the response variable. You might want to further investigate the mycas.baseball data table at other quantile levels. The following statements select quantile regression models at the quantile levels 0.1 and 0.9, which correspond to the 10% and 90% conditional percentiles of the players’ salaries:

```sas
proc qtrselect data=mycas.baseball alpha=0.1;
    class league division;
    model Salary = nAtBat nHits nHome nRuns nRBI nBB
        yrMajor crAtBat crHits crHome crRuns crRbi
crBB league division nOuts nAssts nError
        / quantile=0.1 0.9 stb clb;
    selection method=backward(select=sl sls=0.1);
run;
```

The ALPHA=0.1 option in the PROC statement sets the significance level to 0.1. Combined with the CLB option in the MODEL statement, the ALPHA=0.1 option requests 90% confidence limits for parameter estimates. The QUANTILE= option in the MODEL statement specifies two quantile levels, 0.1 and 0.9, for fitting quantile regression models. The METHOD=BACKWARD option in the SELECTION statement specifies the backward elimination method for effect selection.

Figure 13.9 Parameter Estimates at Quantile Level 0.1

The QTRSELECT Procedure

Quantile Level = 0.1

Selection Details

Selected Effects: Intercept nAtBat nHits nBB CrRuns CrBB Division nAssts
Figure 13.9 displays the “Selected Effects” and “Parameter Estimates” tables at quantile level 0.1.

You might want to compute the 90th percentile predictions for players’ salaries and find out which players were overpaid based on the quantile regression model at quantile level 0.9. The following statements repeat the backward elimination method at quantile level 0.9, compute and sort the overpaid players’ salaries, and output the observations for the top 10 overpaid players in the mycas.baseball data table:

```plaintext
proc qtrselect data=mycas.baseball alpha=0.1;
class league division;
model Salary = nAtBat nHits nHome nRuns nRBI nBB yrMajor crAtBat crHits crHome crRuns crRbi crBB league division nOuts nAssts nError /
quantile=0.9 clb;
selection method=backward(select=s1 sls=0.1);
```

Figure 13.10 Parameter Estimates at Quantile Level 0.9

Selected Effects: Intercept nHits nBB CrAtBat CrHits CrHome CrRbi League Division nOuts

You might want to compute the 90th percentile predictions for players’ salaries and find out which players were overpaid based on the quantile regression model at quantile level 0.9. The following statements repeat the backward elimination method at quantile level 0.9, compute and sort the overpaid players’ salaries, and output the observations for the top 10 overpaid players in the mycas.baseball data table:

```plaintext
proc qtrselect data=mycas.baseball alpha=0.1;
class league division;
model Salary = nAtBat nHits nHome nRuns nRBI nBB yrMajor crAtBat crHits crHome crRuns crRbi crBB league division nOuts nAssts nError /
quantile=0.9 clb;
selection method=backward(select=s1 sls=0.1);
```
The LCLM and UCLM options, respectively, request lower and upper bounds of $100(1 - \alpha)\%$ confidence intervals for the expected conditional quantile predictions of players’ salaries at quantile level 0.9.

![Figure 13.11 Top 10 Overpaid Baseball Players at Quantile Level 0.9](image)

<table>
<thead>
<tr>
<th>Obs</th>
<th>Name</th>
<th>Salary</th>
<th>Overpaid</th>
<th>PredictedSalary</th>
<th>LCLM</th>
<th>UCLM</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Smith, Ozzie</td>
<td>1940.0</td>
<td>1084.54</td>
<td>855.46</td>
<td>611.09</td>
<td>1099.83</td>
</tr>
<tr>
<td>2</td>
<td>Wiggins, Alan</td>
<td>700.0</td>
<td>220.74</td>
<td>479.26</td>
<td>345.93</td>
<td>612.60</td>
</tr>
<tr>
<td>3</td>
<td>Murray, Eddie</td>
<td>2460.0</td>
<td>213.10</td>
<td>2246.90</td>
<td>1982.06</td>
<td>2511.74</td>
</tr>
<tr>
<td>4</td>
<td>Strawberry, Darryl</td>
<td>1220.0</td>
<td>187.64</td>
<td>1032.36</td>
<td>914.99</td>
<td>1149.72</td>
</tr>
<tr>
<td>5</td>
<td>Gibson, Kirk</td>
<td>1300.0</td>
<td>177.24</td>
<td>1122.76</td>
<td>1011.97</td>
<td>1233.56</td>
</tr>
<tr>
<td>6</td>
<td>Trevino, Alex</td>
<td>512.5</td>
<td>149.70</td>
<td>362.80</td>
<td>273.17</td>
<td>452.43</td>
</tr>
<tr>
<td>7</td>
<td>Ramirez, Rafael</td>
<td>875.0</td>
<td>141.09</td>
<td>733.91</td>
<td>599.52</td>
<td>868.31</td>
</tr>
<tr>
<td>8</td>
<td>Romero, Ed</td>
<td>375.0</td>
<td>128.71</td>
<td>246.29</td>
<td>144.88</td>
<td>347.70</td>
</tr>
<tr>
<td>9</td>
<td>Mattingly, Don</td>
<td>1975.0</td>
<td>124.82</td>
<td>1850.18</td>
<td>1557.81</td>
<td>2142.55</td>
</tr>
<tr>
<td>10</td>
<td>Puhl, Terry</td>
<td>900.0</td>
<td>104.34</td>
<td>795.66</td>
<td>625.51</td>
<td>965.81</td>
</tr>
</tbody>
</table>

Output 13.11 shows the information about the top 10 overpaid players according to the final selected quantile regression model at quantile level 0.9. Ozzie Smith is in first place. This might be because, although Smith was known for his defensive brilliance, the model weights offensive performance measures much more than defensive performance measures.
**Syntax: QTRSELECT Procedure**

The following statements are available in the QTRSELECT procedure:

```
PROC QTRSELECT < options > ;
   BY variables ;
   CLASS variable < (options) > . . . < variable < (options) > > < / global-options > ;
   CODE < options > ;
   DISPLAY < table-list > < / options > ;
   DISPLAYOUT table-spec-list < / options > ;
   EFFECT name=effect-type(variables < / options > ) ;
   MODEL dependent = < effects > < / model-options > ;
   OUTPUT OUT=CAS-libref.data-table < keyword = name >= name > . . . < keyword = name > < / options > ;
   PARTITION partition-options ;
   SELECTION < METHOD=method < (method-options) > > < options > ;
   WEIGHT variable ;
```

The PROC QTRSELECT statement and a single MODEL statement are required. All other statements are optional. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statement.

The rest of this section provides detailed syntax information about each of the preceding statements, beginning with the PROC QTRSELECT statement. The remaining statements are described in alphabetical order.

---

**PROC QTRSELECT Statement**

```
PROC QTRSELECT < options > ;
```

The PROC QTRSELECT statement invokes the procedure. Table 13.1 summarizes the options in the PROC QTRSELECT statement by function.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
<tr>
<td><strong>Other Options</strong></td>
<td></td>
</tr>
<tr>
<td>ALPHA=</td>
<td>Sets the significance level to be used for the construction of confidence intervals</td>
</tr>
<tr>
<td>COV=SPARSITY</td>
<td>Specifies the sparsity-function method for estimating the covariance matrix of the parameter estimates</td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Limits or suppresses the display of class levels</td>
</tr>
</tbody>
</table>

You can specify the following options:
Chapter 13: The QTRSELECT Procedure

**ALPHA=number**
sets the significance level to be used for the construction of confidence intervals. The value must be between 0 and 1; the default value of 0.05 results in 95% intervals. This option affects the keywords LCLM, UCLM, and STDP in the OUTPUT statement and the CLB option in the MODEL statement.

**COV=SPARSITY<(BF | HS)></COV=SPARSITY>(HS)>
**
specifies the sparsity-function bandwidth method for estimating the covariance matrix of the parameter estimates. You can specify the following suboptions:

- **BF** uses the Bofinger bandwidth method.
- **HS** uses the Hall-Sheather bandwidth method.

By default, COV=SPARSITY(HS). For more information, see the section “Details: QTRSELECT Procedure” on page 695.

**DATA=CAS-libref.data-table**
names the input data table for PROC QTRSELECT to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 674.
- **data-table** specifies the name of the input data table.

**NOCLPRINT<=number>**
suppresses the display of the “Class Level Information” table if you do not specify *number*. If you specify *number*, the values of the classification variables are displayed for only those variables whose number of levels is less than *number*. Specifying *number* helps reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

---

**BY Statement**

**BY variables ;**

You can specify a BY statement in PROC QTRSELECT to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in *SAS Language Reference: Concepts*.

---

**CLASS Statement**

**CLASS variable <(options)> . . . < variable <(options)> ></global-options> ;**

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required.
Table 13.2 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>

**CODE Statement**

```sas
CODE <options> ;
```

The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a file, to a catalog entry, or to a CAS table. To score new data, you can then include the file or the catalog entry in a DATA step, or you can specify the CAS table in the `runCodeTable` action in the `dataStep` action set (for more information, see SAS Viya: System Programming Guide).

Table 13.3 summarizes the options available in the CODE statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
</tbody>
</table>

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

The predicted values in the SAS DATA step code are computed based on the parameter estimates for the selected models. If you specify multiple quantile levels by using the QUANTILES option in the MODEL statement, then one variable of the predicted values is generated for each specified quantile level.
Chapter 13: The QTRSELECT Procedure

DISPLAY Statement

```
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 708. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

- **CASESENSITIVE**
  performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  displays the display table names, labels, and paths.
**DISPLAYOUT Statement**

```
DISPLAYOUT table-spec-list < / options> ;
```

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.
- `key` specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following `options` after a slash (/):

- **INCLUDEALL**
  - creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the `table-spec-list` specification is ignored.

- **NOREPLACE**
  - does not replace any existing CAS output table of the same name.

- **REPEATED**
  - replicates all CAS output tables on all nodes.

**EFFECT Statement**

```
EFFECT name=effect-type (variables < / options>) ;
```

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as *constructed effects* to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following `effect-types`:

- **COLLECTION**
  - specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.

- **MULTIMEMBER | MM**
  - specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.

- **POLYNOMIAL | POLY**
  - specifies a multivariate polynomial effect in the specified numeric variables.
specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 13.4 summarizes the options available in the EFFECT statement.

**Table 13.4 EFFECT Statement Options**

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Collection Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the constituents of the collection effect</td>
</tr>
<tr>
<td><strong>Multimember Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the levels of the multimember effect</td>
</tr>
<tr>
<td>NOEFFECT</td>
<td>Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns</td>
</tr>
<tr>
<td>STDIZE</td>
<td>Standardizes the design matrix entries so that each observation has a sum of 1</td>
</tr>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
<tr>
<td><strong>Polynomial Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the polynomial</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays details of the specified polynomial</td>
</tr>
<tr>
<td>MDEGREE=</td>
<td>Specifies the maximum degree of any variable in a term of the polynomial</td>
</tr>
<tr>
<td>NOSEPARATE</td>
<td>Treats the polynomial as a single effect with multiple degrees of freedom</td>
</tr>
<tr>
<td>STANDARDIZE=</td>
<td>Specifies centering and scaling suboptions for the variables that define the polynomial</td>
</tr>
<tr>
<td><strong>Spline Effects Options</strong></td>
<td></td>
</tr>
<tr>
<td>BASIS=</td>
<td>Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect</td>
</tr>
<tr>
<td>DATABOUNDARY</td>
<td>Uses the extremes of the data as boundary knots for a B-spline basis</td>
</tr>
<tr>
<td>DEGREE=</td>
<td>Specifies the degree of the spline effect</td>
</tr>
<tr>
<td>DETAILS</td>
<td>Displays the knots and locations for each spline basis function</td>
</tr>
<tr>
<td>KNOTMAX=</td>
<td>Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value</td>
</tr>
<tr>
<td>KNOTMETHOD=</td>
<td>Specifies how to construct the knots for the spline effect</td>
</tr>
<tr>
<td>KNOTMIN=</td>
<td>Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value</td>
</tr>
<tr>
<td>NATURALCUBIC</td>
<td>Specifies a natural cubic spline basis for the spline effect</td>
</tr>
<tr>
<td>SEPARATE</td>
<td>Treats the spline basis for each variable as a separate effect when multiple variables are specified</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Treats each design matrix column as a separate effect for selection methods</td>
</tr>
</tbody>
</table>
For more information about the syntax of these effect-types and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”

**MODEL Statement**

```
MODEL dependent=<effects> / <model-options> ;
```

The MODEL statement names the dependent variable and the explanatory effects, including covariates, main effects, interactions, and nested effects. If you omit the explanatory effects, the procedure fits an intercept-only model.

After the keyword MODEL, the dependent (response) variable is specified, followed by an equal sign. The explanatory effects follow the equal sign.

For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

The `model-options` control other aspects of model formation and inference. Table 13.5 summarizes these options.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model Options</td>
<td></td>
</tr>
<tr>
<td>CLB</td>
<td>Requests confidence limits</td>
</tr>
<tr>
<td>INCLUDE=</td>
<td>Includes effects in all models for model selection</td>
</tr>
<tr>
<td>INFORMATIVE</td>
<td>Models missing values by using extra indicator variables</td>
</tr>
<tr>
<td>NOINT</td>
<td>Suppresses the intercept</td>
</tr>
<tr>
<td>QUANTILES</td>
<td>Specifies quantile levels for the quantile regression</td>
</tr>
<tr>
<td>START=</td>
<td>Includes effects in the initial model for model selection</td>
</tr>
<tr>
<td>STB</td>
<td>Displays standardized estimates</td>
</tr>
</tbody>
</table>

**Model Options**

You can specify the following options in the MODEL statement after a slash (/):

- **CLB**
  requests the 100(1 − α)% upper and lower confidence limits for the parameter estimates. By default, the 95% limits are computed; you can use the `ALPHA=` option in the `PROC QTRSELECT` statement to change the α level.

- **INCLUDE=n**
  - `INCLUDE=single-effect`
  - `INCLUDE=(effects)`
  forces effects to be included in all models. If you specify INCLUDE=n, then the first n effects listed in the MODEL statement are included in all models. If you specify INCLUDE=single-effect or INCLUDE=(single-effect), then the specified effects are forced into all models.
INFORMATIVE

models missing values by using extra model effects. These effects consist of dummy variables that take the value 1 when the value of a continuous model variable involved in the effect is missing, and take the value 0 otherwise. The missing value in the original model effect is replaced by the average value of the effect for the nonmissing values. For continuous-by-class effects, such as A*x, where A is a classification variable and x is a continuous variable, informative missingness creates multiple dummy columns and substitutes the effect mean of x that corresponds to the respective level of A. Missing values for classification variables are treated as valid levels. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

NOINT

suppresses the intercept term that is otherwise included in the model.

QUANTILES<(quantile-level-options)><=number-list>
QUANTILE<(quantile-level-options)><=number-list>
Q<(quantile-level-options)><=number-list>

specifies the quantile levels for the quantile regression. You can request any values of quantile levels in (0, 1) by specifying a number-list. By default, the QTRSELECT procedure uses QUANTILES=0.5, which corresponds to median regression.

You can also specify the following quantile-level-options:

NTAU=n
NQ=n

specifies the following n quantile levels for the quantile regression:

\[
\left\{ \frac{1}{n+1}, \ldots, \frac{n}{n+1} \right\}
\]

If you specify both a QUANTILES=number-list and NTAU=n, the QTRSELECT procedure uses all the specified quantile levels.

SORT

sorts all the specified quantile levels in ascending order. This option affects the order of the prediction variables in the SAS DATA step code that is created by the CODE statement, and the order of the appropriate keyword variables in the SAS data set that is created by the OUTPUT statement.

START=n
START=single-effect
START=(effects)

begins the selection process in the FORWARD and STEPWISE selection methods from the initial model that you designate. If you specify START=n, then the starting model consists of the first n effects listed in the MODEL statement. If you specify START=single-effect or START=(single-effect), then the starting model consists of these specified effects.

STB

produces standardized regression coefficients. A standardized regression coefficient is computed by dividing a parameter estimate by the ratio of the sample standard deviation of the dependent variable to the sample standard deviation of the regressor. If you use the INCLUDE= option to force some effects
to be in the model, then the QTRSELECT procedure computes the sample standard deviation against all the effects that are forced in, as follows. Let \( X_1 \) denote the design submatrix of \( p_1 \) regressors that consists of all the effects that are forced in, and let \( z \) denote the dependent variable or any regressor. Then the sample standard deviation of \( z \) is computed as

\[
s_z = \sqrt{z' \left[ I - X_1 (X_1' X_1)^{-1} X_1' \right] z} / n - p_1
\]

**OUTPUT Statement**

```
OUTPUT OUT=CAS-libref.data-table
  <COPYVARS=(variables)>
  <keyword =name> . . . <keyword =name> ;
```

The OUTPUT statement creates a data table that contains observationwise statistics, which are computed after the model is fitted. The variables in the input data table are *not* included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the `COPYVARS=` option are included.

The output statistics are computed based on the parameter estimates for the selected model. If you specify multiple quantile levels by using the `QUANTILES` option in the `MODEL` statement, then for each appropriate keyword that is specified in the `OUTPUT` statement, one variable is generated for each specified quantile level. For observations in which only the response variable is missing, predicted values are computed even though these observations do not affect the model fit. This enables, for example, predicted values to be computed for new observations.

You must specify the following option:

```
OUT=CAS-libref.data-table
```
	names the output data table for PROC QTRSELECT to use. You must specify this option before any other options. *CAS-libref.data-table* is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the `LIBNAME` statement and includes the `caslib`, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the `LIBNAME` statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 674.

- **data-table** specifies the name of the output data table.

You can also specify the following syntax elements:

```
COPYVAR=variable
COPYVARS=(variables)
```

transfers one or more *variables* from the input data table to the output data table.
keyword < =name >
specifies the statistics to include in the output data table and optionally names the new variables that contain the statistics. Specify a keyword for each desired statistic (see the following list of keywords), followed optionally by an equal sign and a variable to contain the statistic.

If you specify keyword=name, the new variable that contains the requested statistic has the specified name. If you omit the optional =name after a keyword, then a default name is used.

You can specify the following values for keyword to request statistics that are available with all selection methods:

- PREDICTED< =name >
- PRED< =name >
- P< =name >
  requests predicted values for the response variable. The default name is Pred.

- RESIDUAL< =name >
- RESID< =name >
- R< =name >
  requests the residual, calculated as ACTUAL – PREDICTED. The default name is Residual.

- ROLE< =name >
  requests a numeric variable that indicates the role played by each observation in fitting the model. The default name is _ROLE_. For each observation, the interpretation of this variable is shown in Table 13.6.

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by using a PARTITION statement, then the role variable value is 1 for observations used in fitting the model, and 0 for observations that have at least one missing or invalid value for the response, regressor, frequency, or weight variables.

If you specify multiple quantile levels by using the QUANTILES option in the MODEL statement, then for each appropriate keyword that is specified in the OUTPUT statement, one variable is generated for each specified quantile level. These variables appear in the same order as the specified quantile levels. For example, the following statements generate the mycas.out data table, which contains the two predicted quantile variables p1 and p2:

```plaintext
proc qtrselect data=mycas.one;
  model y = x1-x4 /quantiles=0.5 0.3;
  output out=mycas.out pred=p;
run;
```
The variable $p_1$ is for quantile level 0.5, and the variable $p_2$ is for quantile level 0.3.

By using the SORT suboption in the QUANTILES option, the following statements generate the mycas.out data table in sorted order:

```
proc qtrselect data=mycas.one;
    model y = x1-x4 /quantiles(sort)=0.5 0.3;
    output out=mycas.out pred=p;
run;
```

The variable $p_1$ is for quantile level 0.3, and the variable $p_2$ is for quantile level 0.5, because the sorted quantile levels are (0.3 0.5).

In addition to the preceding statistics, you can also use the keywords listed in Table 13.7 in the OUTPUT statement to obtain additional statistics. For computational formulas, see the section “Diagnostic Statistics” on page 700. All the statistics available in the OUTPUT statement are conditional on the selected model and do not take into account the variability introduced when you do model selection.

### Table 13.7 Keywords for OUTPUT Statement

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCLM</td>
<td>Lower bound of a $100(1 - \alpha)%$ confidence interval for the quantile prediction variable</td>
</tr>
<tr>
<td>STDP</td>
<td>Standard error of the quantile prediction variable</td>
</tr>
<tr>
<td>UCLM</td>
<td>Upper bound of a $100(1 - \alpha)%$ confidence interval for the quantile prediction variable</td>
</tr>
</tbody>
</table>

---

**PARTITION Statement**

```
PARTITION partition-option ;
```

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:

- **FRACTION(<TEST=fraction> <VALIDATE=fraction> <SEED=number>)**
  
randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The SEED= option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify SEED=number or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.
ROLE=variable (< TEST='value' > < TRAIN='value' > < VALIDATE='value' >)

ROLEVAR=variable (< TEST='value' > < TRAIN='value' > < VALIDATE='value' >)

names the variable in the input data table whose values are used to assign roles to each observation. This variable cannot also appear as an analysis variable in other statements or options. The TEST=, TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

### SELECTION Statement

**SELECTION < METHOD=method < (method-options) >>< options> ;**

The SELECTION statement performs model selection by examining whether effects should be added to or removed from the model according to rules that are defined by model selection methods. The statement is fully documented in the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

The QTRSELECT procedure supports the following values of the METHOD= option in the SELECTION statement:

- **BACKWARD** specifies the backward elimination method, which starts with all effects in the model and deletes effects.
- **FORWARD** specifies the forward selection method, which starts with no effects in the model and adds effects.
- **NONE** specifies no model selection.
- **STEPWISE** specifies the stepwise regression method, which is similar to the forward selection method except that effects already in the model do not necessarily stay there.

By default, METHOD=STEPWISE.

The DETAILS=ALL and DETAILS=STEPS options produce the “Fit Statistics,” and “Parameter Estimates” tables, which provide information about the model that is selected at each step of the selection process.

By default, the QTRSELECT procedure displays the stop horizon steps in the “Selection Summary” table, and uses these steps for choosing the final model of the model selection process. Therefore, it is possible that the final model occurs after the step that has the best stop criterion value. To exclude the stop horizon steps for choosing the final model, you can specify the following option:

**HIDESTOPSTEPS**

**HSS**

hides the stop horizon steps in the “Selection Summary” table, and excludes these steps in choosing the final model.

If you specify the PLOTS=CRITERIA or PLOTS=ALL option, then a plot of the fit criteria by the selection step is created for the AIC, AICC, SBC, R1, and adjusted R1 statistics. If you also specify a PARTITION statement, then the same type of plot is created for the ACL criteria for training, validation, and testing roles. If you specify the PLOTS=FITBYROLE option and a PARTITION statement, then a plot of the ACL criterion by the selection step for each role is created.
WEIGHT Statement

WEIGHT variable;

The variable in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.

The QTRSELECT procedure uses each valid weight as the scale factor of its relevant observation. Let X denote the design matrix before weights are used, and let W denote the diagonal matrix whose diagonal elements are the weights. Then PROC QTRSELECT uses the weighted design matrix WX for its computation. For example, the weighted version of X'X is X'WX but not X'WX.

Details: QTRSELECT Procedure

Quantile Regression

This section describes the basic concepts and notations for quantile regression and quantile regression model selection.

Let \{(y_i, x_i) : i = 1, \ldots, n\} denote a data set of observations, where y_i are responses and x_i are regressors. Koenker and Bassett (1978) define the regression quantile at quantile level \(\tau \in (0, 1)\) as any solution to the minimization problem

\[
\min_{\beta \in \mathbb{R}^p} \sum_{i=1}^{n} \rho_\tau (y_i - x_i' \beta)
\]

where \(\rho_\tau(r) = \tau r^+ + (1 - \tau) r^-\) is a check loss function in which \(r^+ = \max(r, 0)\) and \(r^- = \max(-r, 0)\).

If you specify weights \(w_i, i = 1, \ldots, n\), in the WEIGHT statement, then weighted quantile regression is carried out by solving

\[
\min_{\beta \in \mathbb{R}^p} \sum_{i=1}^{n} \rho_\tau (w_i(y_i - x_i' \beta))
\]

The QTRSELECT procedure fits a quantile regression model by using a predictor-corrector interior point algorithm, which was originally designed to solve support vector machine classifiers for large data sets (Gertz and Griffin 2005, 2010).

Linear Model with Independent and Identically Distributed Errors

A linear model with independent and identically distributed (iid) errors assumes that the distribution of the response \(Y_i\) conditional on \(x_i\) follows the linear model,

\[Y_i = x_i' \beta + \epsilon_i\]
where $\epsilon_i$ for $i = 1, \ldots, n$ are iid in the distribution function $F$. General linear regression uses this model for deriving its statistical inferences and model selection criteria. Although quantile regression can analyze heterogeneous data without the iid errors assumption, this model is helpful for deriving some quantile regression model selection criteria. For more information about using a linear model with iid errors in deriving the quasi-likelihood information criteria, see the section “Criteria Used in Model Selection” on page 697.

**Linear-in-Parameter Model with Non-iid Settings**

The more general form of a linear quantile regression model is

$$Q_Y(\tau|x) = x' \beta(\tau)$$

where the iid assumption is not necessary.

Let $s_i(\tau) = 1/f_i(F_i^{-1}(\tau))$ denote the sparsity function of the $i$th observation. Under some regularity conditions, the asymptotic distribution of the general form of quantile regression estimates is

$$\sqrt{n}(\hat{\beta}(\tau) - \beta(\tau)) \rightarrow N(0, \tau(1-\tau)H^- \Omega H^-)$$

where $H = \lim_{n \to \infty} n^{-1} \sum x_i x_i' / s_i(\tau)$ and $\Omega = \lim_{n \to \infty} n^{-1} \sum x_i x_i'$.

The sparsity function of the $i$th observation, $s_i(\tau)$, can be estimated as

$$\hat{s}_i(\tau) = \frac{\hat{F}_i^{-1}(\tau + h_n) - \hat{F}_i^{-1}(\tau - h_n)}{2h_n}$$

where $\hat{F}_i^{-1}(\tau \pm h_n) = x'_i \hat{\beta}(\tau \pm h_n)$ are the quantile predictions of the $i$th observation at quantile levels $(\tau \pm h_n)$.

Accordingly, the covariance matrix of $\hat{\beta}(\tau)$ can be estimated as

$$\hat{\text{COV}}(\hat{\beta}(\tau)) = n^{-1} \tau(1-\tau) \hat{H}_n \hat{\Omega}_n \hat{H}_n^{-1}$$

where $\hat{H}_n = n^{-1} \sum (x_i x_i' / \hat{s}_i(\tau))$ and $\hat{\Omega}_n = n^{-1} \sum x_i x_i'$.

You can specify the bandwidth method for computing $h_n$ by using either the COV=SPARSITY(BF) option for the Bofinger bandwidth method or the COV=SPARSITY(HF) option for the Hall-Sheather bandwidth method:

- The Bofinger bandwidth optimizes the mean square error for standard density estimation:
  $$h_n = n^{-1/5} (4.5 v^2(\tau))^{1/5}$$

- The Hall-Sheather bandwidth is based on Edgeworth expansions for studentized quantiles:
  $$h_n = n^{-1/3} z_\alpha^{2/3} (1.5 v(\tau))^{1/3}$$

$z_\alpha$ satisfies $T(z_\alpha, df) = 1 - \alpha/2$ for the construction of $1 - \alpha$ confidence intervals, where $T$ is the cumulative distribution function for the $t$ distribution and $df$ is the residual degrees of freedom.
The quantity

\[ v(\tau) = \frac{s(\tau)}{s^{(2)}(\tau)} = \frac{f^2}{2(f^{(1)}/f)^2 + [(f^{(1)}/f)^2 - f^{(2)}/f]} \]

is not sensitive to \( f \) and can be estimated by assuming \( f \) is Gaussian as

\[ \hat{v}(\tau) = \frac{\exp(-q^2)}{2\pi(q^2 + 1)} \]

where \( q = \Phi^{-1}(\tau) \).

**More Statistics for Parameter Estimates**

Let \( \hat{\beta}_j(\tau) \) denote the \( j \)th parameter estimate, and let \( \hat{\beta}(\tau) = \left( \hat{\beta}_1(\tau), \ldots, \hat{\beta}_p(\tau) \right) \) denote the vector of the parameter estimates.

PROC QTRSELECT outputs the standard error, \( t \) value, and \( \Pr > |t| \) probability for each \( \hat{\beta}_j(\tau) \) in the parameter estimates table. If you specify the CLB option in the MODEL statement, PROC QTRSELECT also outputs confidence limits in the parameter estimates table. Table 13.8 summarizes these statistics for \( \hat{\beta}_j(\tau) \).

**Table 13.8 More Statistics for \( \hat{\beta}_j(\tau) \)**

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Definition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard error: ( \hat{\sigma}_j )</td>
<td>( \sqrt{\text{COV} \left( \hat{\beta}(\tau) \right)_{jj}} )</td>
</tr>
<tr>
<td>(1 - ( \alpha ))% confidence limits</td>
<td>( \left( \hat{\beta}<em>j(\tau) \pm t</em>{1,1-\frac{\alpha}{2}} \hat{\sigma}_j \right) )</td>
</tr>
<tr>
<td>( t ) value</td>
<td>( \hat{\beta}_j(\tau)/\hat{\sigma}_j )</td>
</tr>
<tr>
<td>( \Pr &gt;</td>
<td>t</td>
</tr>
</tbody>
</table>

Here \( \text{COV} \left( \hat{\beta}(\tau) \right)_{jj} \) is the \( (j, j) \) element of \( \text{COV} \left( \hat{\beta}(\tau) \right) \), and \( t_{1,1-\frac{\alpha}{2}} \) denotes the \( (1 - \frac{\alpha}{2}) \)-level student’s \( t \) score with 1 degree of freedom.

**Criteria Used in Model Selection**

The QTRSELECT procedure supports the following fit statistics that you can use as criteria for the CHOOSE=, SELECT=, and STOP= options in the SELECTION statement:

- **ADJR1** specifies the adjusted R1 statistic.
- **AIC** specifies Akaike’s information criterion (Akaike 1969; Koenker 2005).
- **AICC** specifies the corrected Akaike’s information criterion (Hurvich and Tsai 1989).
- **BIC | SBC** specifies the Schwarz Bayesian information criterion (Schwarz 1978; Koenker 2005).
- **R1** specifies the R1 statistic (Koenker and Machado 1999). The R1 statistic is not valid for the STOP= or CHOOSE= option.
Chapter 13: The QTRSELECT Procedure

SL specifies the significance level that is used to assess an effect’s contribution to the fit when it is added to or removed from a model. SL is not valid for the CHOOSE= option.

VALIDATE specifies the average check loss over the validation data.

Table 13.9 provides formulas and definitions for these fit statistics.

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Definition or Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>$n$</td>
<td>Number of observations</td>
</tr>
<tr>
<td>$p$</td>
<td>Number of parameters, including the intercept</td>
</tr>
<tr>
<td>$r_i(\tau)$</td>
<td>Residual for the $i$th observation; $r_i(\tau) = y_i - x_i^T \hat{\beta}(\tau)$</td>
</tr>
<tr>
<td>$D(\tau)$</td>
<td>Total sum of check losses; $D(\tau) = \sum_{i=1}^{n} \rho_\tau(r_i)$. $D(\tau)$ is labeled as Objective Function in the “Fit Statistics” table.</td>
</tr>
<tr>
<td>$D_0(\tau)$</td>
<td>Total sum of check losses for intercept-only model if the intercept is a forced-in effect; otherwise for empty model.</td>
</tr>
<tr>
<td>ACL(\tau)</td>
<td>Average check loss; $ACL(\tau) = \frac{D(\tau)}{n}$</td>
</tr>
<tr>
<td>R1(\tau)</td>
<td>Counterpart of linear regression R square for quantile regression; $R1(\tau) = 1 - \frac{D(\tau)}{D_0(\tau)}$ if intercept is a forced-in effect; otherwise $1 - \frac{D(\tau)}{nD_0(\tau)}$.</td>
</tr>
<tr>
<td>ADJR1(\tau)</td>
<td>Adjusted R1; $1 - \frac{(n-1)D(\tau)}{(n-p)D_0(\tau)}$ if intercept is a forced-in effect; otherwise $1 - \frac{nD(\tau)}{(n-p)D_0(\tau)}$.</td>
</tr>
<tr>
<td>AIC(\tau)</td>
<td>$2n \ln (ACL(\tau)) + 2p$</td>
</tr>
<tr>
<td>AICC(\tau)</td>
<td>$2n \ln (ACL(\tau)) + \frac{2pn}{n-p-1}$</td>
</tr>
<tr>
<td>SBC(\tau)</td>
<td>$2n \ln (ACL(\tau)) + p \ln(n)$</td>
</tr>
</tbody>
</table>

The ADJR1(\tau) criterion is equivalent to the generalized approximate cross validation (GACV) criterion for quantile regression (Yuan 2006). The GACV criterion is defined as

$$GACV(\tau) = \frac{D(\tau)}{(n-p)}$$

which is proportional to $1 - ADJR1(\tau)$.

Quasi-likelihood Information Criteria

Given the quantile level $\tau$, assume that the distribution of $Y_i$ conditional on $x_i$ follows the linear model

$$Y_i = x_i^T \beta + \epsilon_i$$

where $\epsilon_i$ for $i = 1, \ldots, n$ are iid in distribution $F$. Further assume that $F$ is an asymmetric Laplace distribution whose density function is

$$f_\tau(r) = \frac{\tau(1-\tau)}{\sigma} \exp\left(-\frac{\rho_\tau(r)}{\sigma}\right)$$
where $\sigma$ is the scale parameter. Then, the negative log-likelihood function is

$$l_\tau(\beta, \sigma) = n \log(\sigma) + \sigma^{-1} \sum_{i=1}^{n} \rho_\tau(y_i - x_i'\beta) - n \log(1 - \tau)$$

Under these settings, the maximum likelihood estimate (MLE) of $\beta$ is the same as the relevant level-$\tau$ quantile regression solution $\hat{\beta}(\tau)$, and the MLE for $\sigma$ is

$$\hat{\sigma}(\tau) = n^{-1} \sum_{i=1}^{n} \rho_\tau \left( y_i - x_i' \hat{\beta}(\tau) \right)$$

where $\hat{\sigma}(\tau)$ equals the level-$\tau$ average check loss $ACL(\tau)$ for the quantile regression solution.

Because the general form of Akaike’s information criterion (AIC) is $AIC = (-2l + 2p)$, the quasi-likelihood AIC for quantile regression is

$$AIC(\tau) = 2n \ln (ACL(\tau)) + 2p$$

where $p$ is the degrees of freedom for the fitted model.

Similarly, the quasi-likelihood AICC (corrected AIC) and SBC (Schwarz Bayesian information criterion) can be formulated as follows:

$$AICC(\tau) = 2n \ln (ACL(\tau)) + \frac{2pn}{n - p - 1}$$

$$SBC(\tau) = 2n \ln (ACL(\tau)) + p \ln(n)$$

In fact, the quasi-likelihood AIC, AICC, and SBC are fairly robust, and you can use them to select effects for data sets without the iid assumption in asymmetric Laplace distribution. For a simulation study that applies SBC for effect selection, see “Example 13.1: Simulation Study” on page 710. The study generates a data table by using a naive instrumental model (Chernozhukov and Hansen 2008).

**Statistical Tests for Significance Level**

The QTRSELECT procedure supports the significance level (SL) criterion for effect selection. Consider the general form of a quantile regression model:

$$Q_Y(\tau|x_1, x_2) = x_1'\beta_1(\tau) + x_2'\beta_2(\tau)$$

At each step of an effect-selection process, a candidate effect can be represented as $x_2$, and the significance level of the candidate effect can be calculated by testing the null hypothesis: $H_0 : \beta_2(\tau) = 0$.

The QTRSELECT procedure supports the Wald test for computing candidate significance levels. Let $\hat{\beta}(\tau) = \left(\hat{\beta}_1(\tau), \hat{\beta}_2(\tau)\right)'$ be the parameter estimates for the extended model, and denote the estimated covariance matrix of $\beta(\tau)$ as

$$\hat{\Sigma}(\tau) = \begin{bmatrix} \hat{\Sigma}_{11}(\tau) & \hat{\Sigma}_{12}(\tau) \\ \hat{\Sigma}_{21}(\tau) & \hat{\Sigma}_{22}(\tau) \end{bmatrix}$$

where $\hat{\Sigma}_{22}(\tau)$ is the covariance matrix for $\hat{\beta}_2(\tau)$. Then the Wald test score is defined as

$$\hat{\beta}_2(\tau) \hat{\Sigma}_{22}^{-1}(\tau) \hat{\beta}_2(\tau)$$
Under the null hypothesis that the reduced model is the true model, the Wald score follows a $\chi^2$ distribution with degrees of freedom $df = df_2 - df_1$, where $df_1$ and $df_2$ are the degrees of freedom for the reduced model and the extended model, respectively.

When you use SL as a criterion for effect selection, the algorithm for estimating sparsity function depends on whether an effect is being considered as an add or a drop candidate. For testing an add candidate effect, the sparsity values, $\hat{s}_i(\tau)$’s, are estimated by using the reduced model that does not include the add candidate effect. For testing a drop candidate effect, the sparsity values are estimated on the extended model that does not exclude the drop candidate effect. Then, these estimated sparsity function values are used to compute the covariance matrix of the parameter estimates for the extended model. However, for the model that is selected at each step, the sparsity function for estimating standard errors and confidence limits of the parameter estimates is estimated on that model itself, but not on the model that was selected at the preceding step.

Because the null hypotheses usually do not hold, the SLENTRY and SLSTAY values cannot reliably be viewed as probabilities. One way to address this difficulty is to replace hypothesis testing with a means of selecting a model with information criteria or out-of-sample prediction criteria.

### Diagnostic Statistics

This section gathers the formulas for the statistics available in the OUTPUT statement. All the statistics available in the OUTPUT statement are conditional on the selected model and do not take into account the variability that is introduced by doing model selection.

The model to be fit is $Q_Y(\tau|x) = x'\beta(\tau)$, and the parameter estimate $\hat{\beta}(\tau)$ is the solution that minimizes $\sum_{i=1}^n \rho_\tau(y_i - x'_i\beta)$. The subscript $i$ is for the $i$th observation. The subscript $j$ is for the $j$th quantile level of the specified QUANTILES levels in the MODEL statement. $\hat{\Sigma}(\tau)$ denotes the covariance estimation for $\hat{\beta}(\tau)$.

The ALPHA= option in the PROC QTRSELECT statement sets the $\alpha$ value for the confidence limit statistics. The degrees of freedom for $t_\alpha$ are $n - p$.

Table 13.10 contains the diagnostic statistics and their formulas. Each statistic is computed for each observation.

<table>
<thead>
<tr>
<th>MODEL Option or Statistic</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRED$j$</td>
<td>$\hat{y}_{ji} = x'_i\hat{\beta}(\tau_j)$</td>
</tr>
<tr>
<td>RES$j$</td>
<td>$y_i - \hat{y}_{ji}$</td>
</tr>
<tr>
<td>STDP$j$</td>
<td>$\sqrt{x'_i\hat{\Sigma}(\tau_j)x_i}$</td>
</tr>
<tr>
<td>LCLM$j$</td>
<td>$\hat{y}<em>{ji} - t</em>\alpha STDP_j$</td>
</tr>
<tr>
<td>UCLM$j$</td>
<td>$\hat{y}<em>{ji} + t</em>\alpha STDP_j$</td>
</tr>
</tbody>
</table>
Classification Variables and the SPLIT Option

PROC QTRSELECT supports the ability to split classification variables when you are doing model selection. You use the SPLIT option in the CLASS statement to specify that the columns of the design matrix that correspond to effects that contain a split classification variable can enter or leave a model independently of the other design columns of that effect. The following statements illustrate the use of the SPLIT option:

```plaintext
data mycas.splitExample;
  length c2 $6;
  drop i;
  do i=1 to 1000;
    c1 = 1 + mod(i,6);
    if i < 200 then c2 = 'low';
    else if i < 500 then c2 = 'medium';
    else c2 = 'high';
    x1 = ranuni(1);
    x2 = ranuni(1);
    y = x1+3*(c2 = 'low') + 10*(c1=3) +5*(c1=5) + rannor(1);
    output;
  end;
run;

proc qtrselect data=mycas.splitExample;
  class c1(split) c2(order=freq);
  model y = c1 c2 x1 x2;
  selection method=forward;
run;
```

The “Class Level Information” table shown in Figure 13.12 is produced by default whenever you specify a CLASS statement.

![Figure 13.12 Class Levels](image)

**The QTRSELECT Procedure**

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Class Levels</strong></td>
</tr>
<tr>
<td>c1</td>
</tr>
<tr>
<td>c2</td>
</tr>
</tbody>
</table>

The SPLIT option has been specified for the classification variable c1. This permits the parameters associated with the effect c1 to enter or leave the model individually. The “Parameter Estimates” table in Figure 13.13 shows that for this example the parameters that correspond only to levels 3 and 5 of c1 are in the selected model.
Chapter 13: The QTRSELECT Procedure

Figure 13.13 Parameter Estimates

| Parameter | DF | Estimate  | Standard Error | t Value | Pr > |t| |
|-----------|----|-----------|----------------|---------|-------|---|
| Intercept | 1  | 2.841327  | 0.11898        | 23.88   | <.001 |
| c1_3      | 1  | 10.153005 | 0.10121        | 100.31  | <.001 |
| c1_5      | 1  | 5.026833  | 0.09847        | 51.05   | <.001 |
| c2 high   | 1  | -3.106226 | 0.09550        | -32.52  | <.001 |
| c2 medium | 1  | -2.886239 | 0.11896        | -24.26  | <.001 |
| c2 low    | 0  | 0         | 0              | .       | .     |
| x1        | 1  | 1.239409  | 0.14059        | 8.82    | <.001 |

Using Validation and Test Data

When you have sufficient data, you can subdivide your data into three parts called the training, validation, and test data. The selection process fits models to the training data and uses the validation data to find the prediction errors for the models that are obtained in this way. This prediction error on the validation data can be used to decide when to terminate the selection process or to decide what effects to include as the selection process proceeds. Finally, after a selected model has been obtained, the test data can be used to assess how the selected model generalizes on data that played no role in selecting the model.

In some cases you might want to use only training and test data. For example, you might want to use an information criterion to decide what effects to include and when to terminate the selection process. In this case no validation data are required, but test data can still help you assess the predictive performance of the selected model. In other cases you might decide to use validation data during the selection process but forgo assessing the selected model on test data. Hastie, Tibshirani, and Friedman (2001) note that it is difficult to give a general rule for how many observations you should assign to each role. They state that a typical split might be 50% for training and 25% each for validation and testing.

You use a PARTITION statement to logically subdivide the DATA= data table into separate roles. You can name the fractions of the data that you want to reserve as test data and validation data. For example, the following statements randomly subdivide the mycas.inData data table, reserving 50% for training and 25% each for validation and testing:

```
proc qtrselect data=mycas.inData;
    partition fraction(test=0.25 validate=0.25);
    ...
run;
```

In some cases you might need to exercise more control over the partitioning of the input data table. You can do this by naming both a variable in the input data table and a formatted value of that variable that correspond to each role. For example, the following statements assign roles to the observations in the mycas.inData data table based on the value of the variable group in that data table. Observations in which the value of group is “group 1” are assigned to testing, and those whose value is “group 2” are assigned to training. All other observations are ignored.
proc qtrselect data=mycas.inData;
   partition roleVar=group(test='group 1' train='group 2')
   ...
run;

After you reserve observations for training, validation, and testing, a model fit of the training data is scored on the validation and test data, and the average check loss (ACL) is computed separately for each of these subsets. The ACL for each data role is the sum of check losses for observations in that role divided by the number of observations in that role.

The following statements illustrate the use of the ROLEVAR= option:

%let seed=321;
%let n=600;
%let p=10;

data mycas.roleExample;
   array x{&p} x1-x&p;
   length r $8;
   drop i j k;

   do i=1 to &n;
      do j=1 to &p;
         x{j} = ranuni(&seed);
      end;
   y = x1 + x2 + x3 + ranuni(&seed);
   k = mod(i,3);
   if k=0 then r = 'train';
   else if k=1 then r = 'validate';
   else if k=2 then r = 'test';
   output;
end;
run;

proc qtrselect data=mycas.roleExample;
   model y = x1-x&p;
   selection method=forward(select=validate stop=sbc);
   partition roleVar=r(train='train' validate='validate' test='test');
run;

The “Number of Observations” table shown in Figure 13.14 displays the number of observations used for training, validation, and testing.
Chapter 13: The QTRSELECT Procedure

Figure 13.14 Number of Observations

The QTRSELECT Procedure

<table>
<thead>
<tr>
<th>Selection Summary</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
<tr>
<td>Number of Observations Used for Training</td>
</tr>
<tr>
<td>Number of Observations Used for Validation</td>
</tr>
<tr>
<td>Number of Observations Used for Testing</td>
</tr>
</tbody>
</table>

The “Selection Summary” table shown in Figure 13.15 displays the validation ACL values for each step of the selection process.

Figure 13.15 Selection Summary

The QTRSELECT Procedure

Quantile Level = 0.5
Selection Details

<table>
<thead>
<tr>
<th>Selection Summary</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>SBC</th>
<th>Validation ACL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>0 Intercept</td>
<td>1</td>
<td>-588.4130</td>
<td>0.2150</td>
<td></td>
</tr>
<tr>
<td>1 x3</td>
<td>2</td>
<td>-645.5774</td>
<td>0.1826</td>
<td></td>
</tr>
<tr>
<td>2 x1</td>
<td>3</td>
<td>-730.3921</td>
<td>0.1478</td>
<td></td>
</tr>
<tr>
<td>3 x2</td>
<td>4</td>
<td>-831.1414*</td>
<td>0.1241</td>
<td></td>
</tr>
<tr>
<td>4 x4</td>
<td>5</td>
<td>-827.0261</td>
<td>0.1226*</td>
<td></td>
</tr>
<tr>
<td>5 x6</td>
<td>6</td>
<td>-821.8472</td>
<td>0.1227</td>
<td></td>
</tr>
<tr>
<td>6 x8</td>
<td>7</td>
<td>-816.8005</td>
<td>0.1229</td>
<td></td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

The “Fit Statistics” table shown in Figure 13.16 displays the training ACL, the validation ACL, and the testing ACL for the final model.

Figure 13.16 Fit Statistics

The QTRSELECT Procedure

Quantile Level = 0.5
Selected Model

<table>
<thead>
<tr>
<th>Objective Function</th>
<th>R1</th>
<th>Adj R1</th>
<th>AIC</th>
<th>AICC</th>
<th>SBC</th>
<th>ACL (Train)</th>
<th>ACL (Validate)</th>
<th>ACL (Test)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>23.74758</td>
<td>0.47615</td>
<td>0.46814</td>
<td>-844.33471</td>
<td>-844.12958</td>
<td>-831.14144</td>
<td>0.11874</td>
<td>0.12409</td>
</tr>
</tbody>
</table>
Using the Validation ACL as the SELECT= Criterion

If you provided observations for validation and specified a model selection method that uses the SELECT= criterion, then you can specify SELECT=VALIDATE as a suboption of the METHOD= option in the SELECTION statement. After each step, the selection process computes the validation ACL values for all the current candidate models. The candidate model that has the smallest validation ACL value usually serves as the model for the next selection step.

Using the Validation ACL as the STOP= Criterion

If you provided observations for validation, then you can specify STOP=VALIDATE as a suboption of the METHOD= option in the SELECTION statement. At step $k$ of the selection process, the best candidate effect to enter or leave the current model is determined. Here, “best candidate” means the effect that gives the best value of the SELECT= criterion; this criterion does not need to be based on the validation data. The validation ACL for the model with this candidate effect added or removed is computed. If this validation ACL is greater than the validation ACL for the model at step $k$, then the selection process terminates at step $k$.

Using the Validation ACL as the CHOOSE= Criterion

When you specify the CHOOSE=VALIDATE suboption of the METHOD= option in the SELECTION statement, the validation ACL is computed for the models at each step of the selection process. The smallest model at any step that yields the smallest validation ACL is selected.

Computational Method

Multithreading

The QTRSELECT procedure allocates data to different threads and calculates crossproduct matrices by accumulating the contributions from all threads. PROC QTRSELECT also uses multiple threads to compute matrix inverses and select candidates during model selection. For more information about how PROC QTRSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

Displayed Output

The following sections describe the output produced by PROC QTRSELECT. The output is organized into various tables, which are discussed in their order of appearance.

Selection Information

When you specify the SELECTION statement, the QTRSELECT procedure produces by default a series of tables that display information about the model selection. The “Selection Information” table informs you about the model selection method; select, stop, and choose criteria; and other parameters that govern the selection. You can suppress this table by specifying DETAILS=NONE in the SELECTION statement.
Number of Observations

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis. If you use a PARTITION statement, the table also displays the number of observations used for each data role.

Class Level Information

The “Class Level Information” table lists the levels of every variable that you specify in the CLASS statement. You should check this information to make sure that the data are correct. You can adjust the order of the CLASS variable levels by specifying the ORDER= option in the CLASS statement. You can suppress the “Class Level Information” table completely or partially by specifying the NOCLPRINT= option in the PROC QTRSELECT statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.

Dimensions

The “Dimensions” table displays the number of effects and the number of parameters from which the selected model is chosen. If you use split classification variables, then this table also displays the number of effects after splitting is taken into account.

Entry and Removal Candidates

When you specify the DETAILS=ALL or DETAILS=STEPS option in the SELECTION statement, the QTRSELECT procedure produces “Entry Candidates” and “Removal Candidates” tables that display the effect names and values of the criterion used to select entering or departing effects at each step of the selection process. The effects are displayed in sorted order from best to worst of the selection criterion.

Selection Summary

When you specify the SELECTION statement, the QTRSELECT procedure produces the “Selection Summary” table, which displays information about the sequence of steps of the selection process. For each step, the effect that was entered or dropped is displayed along with the statistics used to select the effect, stop the selection, and choose the selected model. For all criteria that you can use for model selection, the steps at which the optimal values of these criteria occur are also indicated.

You can suppress the display of the “Selection Summary” table by specifying DETAILS=NONE in the SELECTION statement.

Stop Reason

The “Stop Reason” table displays the reason why the selection stopped. To facilitate programmatic use of this table, an integer code is assigned to each reason and is included if you use an ODS OUTPUT statement or a DISPLAYOUT statement to output this table. The reasons and their associated codes follow:
<table>
<thead>
<tr>
<th>Code</th>
<th>Stop Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>All eligible effects are in the model.</td>
</tr>
<tr>
<td>2</td>
<td>All eligible effects have been removed.</td>
</tr>
<tr>
<td>3</td>
<td>Specified maximum number of steps done.</td>
</tr>
<tr>
<td>4</td>
<td>The model contains the specified maximum number of effects.</td>
</tr>
<tr>
<td>5</td>
<td>The model contains the specified minimum number of effects (for backward selection).</td>
</tr>
<tr>
<td>6</td>
<td>The stopping criterion is at a local optimum.</td>
</tr>
<tr>
<td>7</td>
<td>No suitable add or drop candidate could be found.</td>
</tr>
<tr>
<td>8</td>
<td>Adding or dropping any effect does not improve the selection criterion.</td>
</tr>
<tr>
<td>9</td>
<td>No candidate meets the appropriate SLE or SLS significance level.</td>
</tr>
<tr>
<td>10</td>
<td>Stepwise selection is cycling.</td>
</tr>
<tr>
<td>11</td>
<td>The model is an exact fit.</td>
</tr>
<tr>
<td>12</td>
<td>Dropping an effect would result in an empty model.</td>
</tr>
</tbody>
</table>

You can suppress the display of the “Stop Reason” table by specifying DETAILS=NONE in the SELECTION statement.

**Selection Reason**

When you specify the SELECTION statement, the QTRSELECT procedure produces a simple table that explains why the final model was selected.

You can suppress the display of the “Selection Reason” table by specifying DETAILS=NONE in the SELECTION statement.

**Selected Effects**

When you specify the SELECTION statement, the QTRSELECT procedure produces a simple table that lists which effects were selected for the final model.

**Fit Statistics**

The “Fit Statistics” table displays fit statistics for the selected model. The statistics include the following:

- Objective Function, total sum of check losses. Objective Function is denoted as $D(\tau)$ in Table 13.9.

- R1, a measure between 0 and 1 that indicates the portion of the (corrected) total check losses attributed to the fit rather than left to residuals. It is calculated as $1 - \frac{D(\tau)}{D_0(\tau)}$. It is the quantile regression counterpart of the linear regression R square.

- Adj R1, the adjusted R1, a version of R1 that has been adjusted for degrees of freedom. It is calculated as

  $$
  \text{Adj R1} = 1 - \frac{n - i}{n - p} (1 - \text{R1})
  $$

  where $i = 1$ if the intercept is forced in and $i = 0$ otherwise, $n$ is the number of observations used to fit the model, and $p$ is the number of parameters in the model.
• the fit criteria AIC, AICC, and SBC if they are used in the selection process. For the formulas to evaluate these criteria, see Table 13.9.

• the average check loss (ACL) on the training, validation, and test data

You can request the “Fit Statistics” tables for the model at each step of the selection process by specifying the DETAILS= option in the SELECTION statement.

Parameter Estimates

The “Parameter Estimates” table displays the parameters in the selected model and their estimates. The information displayed for each parameter in the selected model includes the following:

• the parameter label that includes the effect name and level information for effects that contain classification variables

• the degrees of freedom (DF) for the parameter. There is one degree of freedom unless the model is not full rank.

• the parameter estimate

• the standard error, which is the estimate of the standard deviation of the parameter estimate

• \( t \) Value, the \( t \) test that the parameter is 0. This is computed as the parameter estimate divided by the standard error.

• the \( \text{Pr} > |t| \), the probability that a \( t \) statistic would obtain a greater absolute value than that observed given that the true parameter is 0. This is the two-tailed significance probability.

When you do model selection, these \( p \)-values are usually liberal because they are not adjusted for the fact that the terms in the model have been selected.

You can request a “Parameter Estimates” table for the model at each step of the selection process by specifying the DETAILS= option in the SELECTION statement.

Timing

The “Timing” table displays the amount of time (in seconds) and the percentage of the time that PROC QTRSELECT required to perform different tasks in the analysis.

OutputCASTables

When you specify an OUTPUT statement or a DISPLAYOUT statement to create output tables on your CAS server, the “Output CAS Tables” table displays the names, the numbers of rows and columns, and the CAS libraries in which the table is created for every output table that you requested.

ODS Table Names

Each table that the QTRSELECT procedure creates has a name associated with it. You must use this name to refer to the table when you use ODS statements. These names are listed in Table 13.11.
Table 13.11  ODS Tables Produced by PROC QTRSELECT

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>Candidates</td>
<td>Swap candidates at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td>Default output</td>
</tr>
<tr>
<td>EntryCandidates</td>
<td>Candidates for entry at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default output</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>Default output</td>
</tr>
<tr>
<td>OutputCASTables</td>
<td>Library and name of the output data table, and number of rows and columns in the table</td>
<td>OUTPUT</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in the MODEL statement</td>
<td>Default output</td>
</tr>
<tr>
<td>RemovalCandidates</td>
<td>Candidates for removal at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
<tr>
<td>SelectedEffects</td>
<td>List of selected effects</td>
<td>SELECTION</td>
</tr>
<tr>
<td>SelectionInfo</td>
<td>Information about selection settings</td>
<td>Default output</td>
</tr>
<tr>
<td>SelectionReason</td>
<td>Reason for selecting the final model</td>
<td>SELECTION</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Summary information about the model selection steps</td>
<td>SELECTION</td>
</tr>
<tr>
<td>StopReason</td>
<td>Reason selection was terminated</td>
<td>SELECTION</td>
</tr>
<tr>
<td>Timing</td>
<td>Timing breakdown by task</td>
<td>SELECTION DETAILS</td>
</tr>
</tbody>
</table>

**ODS Graphics**

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in *SAS/STAT User’s Guide*.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.
When ODS Graphics is enabled, then the SELECTION statement can produce plots to help evaluate the selection process. For information about these plots, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

PROC QTRSELECT assigns a name to each graph that it creates using ODS. You can use these names to reference the graphs when using ODS. The names are listed in Table 13.12.

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CoefficientPanel</td>
<td>Coefficients and CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>ChooseCriterionPlot</td>
<td>CHOOSE= criterion by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CoefficientPlot</td>
<td>Coefficients by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CriterionPanel</td>
<td>Fit criteria by step</td>
<td>CRITERIA</td>
</tr>
<tr>
<td>AdjR1Plot</td>
<td>Adjusted R1 by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICCPPlot</td>
<td>Corrected Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICPlot</td>
<td>Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>SBCPlot</td>
<td>Schwarz Bayesian information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TEST_ACLPlot</td>
<td>Average check loss on testing data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TRAIN_ACLPlot</td>
<td>Average check loss on training data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>VAL_ACLPlot</td>
<td>Average check loss on validation data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>FitByRolePlot</td>
<td>Progression of average check loss by role</td>
<td>FITBYROLE</td>
</tr>
</tbody>
</table>

Examples: QTRSELECT Procedure

Example 13.1: Simulation Study

This example is based on the section “Simulation Study” (Examples: QUANTSELECT Procedure, SAS/STAT User’s Guide). This simulation study shows how you can use the forward selection method to select quantile regression models for single quantile levels. The following statements simulate a data set from a naive instrumental model (Chernozhukov and Hansen 2008):

```sas
%let seed=321;
%let p=20;
%let n=3000;
```
Example 13.1: Simulation Study

```plaintext
data analysisData;
   array x{&p} x1-x&p;
   do i=1 to &n;
      U = ranuni(&seed);
      x1 = ranuni(&seed);
      x2 = ranexp(&seed);
      x3 = abs(rannor(&seed));
      y = x1*(U-0.1) + x2*(U*U-0.25) + x3*(exp(U)-exp(0.9));
   do j=4 to &p;
      x{j} = ranuni(&seed);
   end;
   output;
   end;
run;
```

Variable U in the data set indicates the true quantile level of the response y conditional on \( x = (x_1, \ldots, x_p)' \).

Let \( Q_Y(\tau|x) = x'\beta(\tau) \) denote the underlying quantile regression model, where \( \beta(\tau) = (\beta_1(\tau), \ldots, \beta_p(\tau))' \).

Then, the true parameter functions are

\[
\begin{align*}
\beta_1(\tau) &= \tau - 0.1 \\
\beta_2(\tau) &= \tau^2 - 0.25 \\
\beta_3(\tau) &= \exp(\tau) - \exp(0.9) \\
\beta_4(\tau) &= \cdots = \beta_p(\tau) = 0
\end{align*}
\]

It is easy to see that, at \( \tau = 0.1 \), only \( \beta_2(0.1) = -0.24 \) and \( \beta_3(0.1) = \exp(0.1) - \exp(0.9) \approx -1.354432 \) are nonzero parameters. Therefore, an effective effect-selection method should select \( x_2 \) and \( x_3 \) and drop all the other effects in this data set at \( \tau = 0.1 \). By the same rationale, \( x_1 \) and \( x_3 \) should be selected at \( \tau = 0.5 \) with \( \beta_1(0.5) = 0.4 \) and \( \beta_3(0.5) \approx -0.810882 \), and \( x_1 \) and \( x_2 \) should be selected at \( \tau = 0.9 \) with \( \beta_1(0.9) = 0.8 \) and \( \beta_2(0.9) = 0.56 \).

The following statements load the analysisData data set into your CAS session by using the mycas engine libref:

```plaintext
data mycas.analysisData;
   set analysisData;
run;
```

The following statements use PROC QTRSELECT with the forward selection method. The STB option and the CLB option in the MODEL statement request the standardized parameter estimates and the confidence limits of parameter estimates, respectively.

```plaintext
proc qtrselect data=mycas.analysisData;
   model y= x1-x&p / quantile=0.1 0.5 0.9 clb;
   selection method=forward;
   output out=mycas.out p=pred;
run;
```

Output 13.1.1 shows that, by default, the CHOOSE= and STOP= options are both set to SBC.
Output 13.1.1 Model Information

The QTRSELECT Procedure

<table>
<thead>
<tr>
<th>Selection Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
</tbody>
</table>

Output 13.1.2, Output 13.1.3, and Output 13.1.4 display the selected effects and the parameter estimates for $\tau = 0.1$, $\tau = 0.5$, and $\tau = 0.9$, respectively. You can see that the forward selection method correctly selects active effects for all three quantile levels.

Output 13.1.2 Parameter Estimates at $\tau = 0.1$

**Selected Effects:** Intercept x2 x3

| Parameter | DF | Estimate | Standard Error | 95% Confidence Limits | t Value | Pr > |t| |
|-----------|----|----------|----------------|-----------------------|---------|------|---|
| Intercept | 1  | 0.011793 | 0.01192        | -0.01158 0.03516      | 0.99    | 0.3225|
| x2        | 1  | -0.228709| 0.00946        | -0.24725 -0.21017     | -24.19  | <.0001|
| x3        | 1  | -1.379907| 0.01556        | -1.41042 -1.34939     | -88.67  | <.0001|

Output 13.1.3 Parameter Estimates at $\tau = 0.5$

**Selected Effects:** Intercept x1 x3

| Parameter | DF | Estimate | Standard Error | 95% Confidence Limits | t Value | Pr > |t| |
|-----------|----|----------|----------------|-----------------------|---------|------|---|
| Intercept | 1  | 0.011778 | 0.03418        | -0.05524 0.07879      | 0.34    | 0.7304|
| x1        | 1  | 0.425843 | 0.06237        | 0.30355 0.54814       | 6.83    | <.0001|
| x3        | 1  | -0.863316| 0.04765        | -0.95674 -0.76989     | -18.12  | <.0001|

Output 13.1.4 Parameter Estimates at $\tau = 0.9$

**Selected Effects:** Intercept x1 x2

| Parameter | DF | Estimate | Standard Error | 95% Confidence Limits | t Value | Pr > |t| |
|-----------|----|----------|----------------|-----------------------|---------|------|---|
| Intercept | 1  | -0.007738| 0.03292        | -0.07228 0.05680      | -0.24   | 0.8142|
| x1        | 1  | 0.782942 | 0.05134        | 0.68228 0.88360       | 15.25   | <.0001|
| x2        | 1  | 0.576445 | 0.03422        | 0.50935 0.64354       | 16.85   | <.0001|
Example 13.2: Growth Charts for Body Mass Index

This example is modeled on an example in the section “Getting Started: QUANTREG Procedure” in the SAS/STAT User’s Guide. This example highlights the use of the QTRSELECT procedure for multiple-level quantile regression by creating growth charts for men’s body mass index (BMI).

BMI, which is defined as the ratio of weight (kg) to squared height (m²), is a standard measure for categorizing individuals as overweight or underweight. The percentiles of BMI for specified ages are of particular interest. This example draws smooth BMI quantile curves conditional on Age, which can serve as BMI growth charts in medical diagnoses to identify BMI percentiles for subjects.

The Sashelp.BMIMen data set records 1999–2000 and 2001–2002 survey results for men’s BMI. These survey results are published by the National Center for Health Statistics. The data set contains 3,264 observations for two variables, BMI and Age.

The following statements display the variables in the data set. Output 13.2.1 shows the results.

```sas
proc contents varnum data=sashelp.BMIMen;
   ods select position;
run;
```

**Output 13.2.1** Sashelp.BMIMen Data Set

<table>
<thead>
<tr>
<th>Variables in Creation Order</th>
<th># Variable</th>
<th>Type</th>
<th>Len</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 Age</td>
<td>Num</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>2 BMI</td>
<td>Num</td>
<td>8</td>
<td></td>
</tr>
</tbody>
</table>

The following statements load the Sashelp.BMIMen data set into your CAS session by using the mycas engine libref:

```sas
data mycas.BMIMen;
   set sashelp.BMIMen;
   SqrtAge = sqrt(Age);
   InveAge = 1/Age;
   LogBMI = log(BMI);
run;
```

The logarithm of BMI is used as the response. The following statements fit quantile regression models for the mycas.BMIMen data table at 10 quantile levels:

```sas
%let quantile=0.03 0.05 0.1 0.25 0.5 0.75 0.85 0.90 0.95 0.97;
%let nq=10;

proc qtrselect data=mycas.BMIMen;
   model logBMI = InveAge SqrtAge Age SqrtAge*Age Age*Age Age*Age
                  / quantile=&quantile;
   output out=mycas.BMIOut copyvars=(BMI Age) pred=P_LogBMI;
run;
```
The **OUTPUT** statement outputs the mean predicted quantiles for the 10 specified quantile levels. The **PRED=** option in the **OUTPUT** statement specifies the variable names for the quantile predictions. For example, **p1** is for quantile level 0.03, and **p2** is for quantile level 0.05.

The following statements define and apply a SAS macro function to create a quantile curves plot for the mycas.BMIOut data table:

```
%let BMIcolor=red olive orange blue brown gray violet black gold green;
%macro plotBMI;
  data BMIPred;
    set mycas.BMIOut;
    %do j=1 %to &nq;
      predBMI&j = exp(P_LogBMI&j);
    %end;
    label %do j=1 %to &nq;
      predBMI&j=%qscan(&quantile,&j,%str( ))
    %end;;
  run;

  proc sort data=BMIPred;
    by Age;
  run;

  proc sgplot data=BMIPred;
    %do j=1 %to &nq;
      series y=predBMI&j x=Age/lineattrs=(thickness=2 
        color=%qscan(&BMIcolor,&j,%str( )));
    %end;
    scatter y=BMI x=Age/markerattrs=(size=5);
  run;
%mend;
```

**Output 13.2.2** shows the BMI quantile curves, which can serve as BMI growth charts. For example, the percentiles of any observations (small blue circles) that are located between the top 0.95 quantile (gold) curve and the 0.97 quantile (green) curve are between the 95th percentile and the 97th percentile. By using this rule, you can measure the percentile range for any observations of interest.
Example 13.3: Pollution and Mortality

This example shows how you can produce the ODS graphical summary for the effect selection process, and how you can use the PARTITION statement and other options to control the effect selection process. The data for this example come from a study by McDonald and Schwing (1973). The data set contains 60 observations, 15 covariates, and one response variable. The response variable is the total age-adjusted mortality rate for Standard Metropolitan Statistical Areas in the United States in 1959–1961.

The following DATA step creates the Mortality data set:

```plaintext
data mortality;
  input index aap ajant ajult size65 nph nsch25 nfek ppsm snwp nowk nin3k
  hpi nopi sdpi datm DeathRate;
  label index="the index"
    aap="Average Annual Precipitation"
    ajant="Average January Temperature"
    ajult="Average July Temperature"
    size65="Size of Population Older Than 65"
    nph="Number of Members per Household";
```

---

**Output 13.2.2 Growth Chart for Body Mass Index**

![Growth Chart for Body Mass Index](chart.png)

---

**Example 13.3: Pollution and Mortality**

This example shows how you can produce the ODS graphical summary for the effect selection process, and how you can use the PARTITION statement and other options to control the effect selection process. The data for this example come from a study by McDonald and Schwing (1973). The data set contains 60 observations, 15 covariates, and one response variable. The response variable is the total age-adjusted mortality rate for Standard Metropolitan Statistical Areas in the United States in 1959–1961.

The following DATA step creates the Mortality data set:
nsch25="Number of Years of Schooling for Persons over 25"
nfek="Number of Households with Fully Equipped Kitchens"
ppsm="Population per Square Mile"
snwp="Size of the Nonwhite Population"
nowk="Number of Office Workers"
nin3k="Number of Families with an Income Less Than $3000"
hpi="Hydrocarbon Pollution Index"
nopi="Nitric Oxide Pollution Index"
sdpi="Sulfur Dioxide Pollution Index"
datm="Degree of Atmospheric Moisture"
DeathRate="Age-Adjusted Death Rate: Deaths per 100,000 Population"

The following statements load the mycas.Mortality data set into your CAS session. The DATA step assumes that your CAS engine libref is names mycas, but you can substitute any appropriately defined CAS engine libref.

```plaintext
data mycas.Mortality;
set Mortality;
run;
```

The following statements fit a median model for mortality rate conditional on a set of climate, demographic, and pollution covariates by using the forward selection method:

```plaintext
ods graphics on;
proc qtrselect data=mycas.Mortality;
partition fraction(validate=0.3 seed=8);
model DeathRate = aap aap*aap ajant ajant*ajant ajult
ajult*ajult size65 size65*size65 nph nph*nph nsch25
nsch25*nsch25 nfek nfek*nfek ppsm ppsm*ppsm snwp snwp*snwp
nowk nowk*nowk nin3k nin3k*nin3k hpi hpi*nopi
nopi*nopi sdpi sdpi*sdpi datm datm*datm
/ quantile=0.5;
selection method=forward(choose=validate) sh=8 hier=single
```
Because linear terms alone might not be sufficient to fit this model, quadratic terms are also added in the MODEL statement. The FRACTION option of the PARTITION statement requests that 30% of the observations be used for validation and the remaining 70% of the observations be used for training. The SEED suboption in the FRACTION option specifies the random seed for partitioning the data. The HIER=SINGLE option in the MODEL statement forces the effect selection process to ignore quadratic effect candidates if their corresponding main effects are not in the model. The OUTPUT statement creates a SAS data set named mycas.OutData, which contains the variable Role for observation roles and the variable Pred for median prediction conditional on final selected effects.

Output 13.3.1 shows the selection summary. You can see that the best model is at step 10 for validation ACL and step 14 for the SBC.

### Output 13.3.1  Selection Summary

#### The QTRSELECT Procedure

Quantile Level = 0.5
Selection Details

<table>
<thead>
<tr>
<th>Step</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>SBC</th>
<th>Validation ACL</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Intercept</td>
<td>1</td>
<td>261.3686</td>
<td>22.8437</td>
</tr>
<tr>
<td>1</td>
<td>aap</td>
<td>2</td>
<td>240.3825</td>
<td>24.9427</td>
</tr>
<tr>
<td>2</td>
<td>sdpi</td>
<td>3</td>
<td>228.1907</td>
<td>20.1780</td>
</tr>
<tr>
<td>3</td>
<td>snwp</td>
<td>4</td>
<td>220.3388</td>
<td>13.5864</td>
</tr>
<tr>
<td>4</td>
<td>nowk</td>
<td>5</td>
<td>218.4482</td>
<td>11.8243</td>
</tr>
<tr>
<td>5</td>
<td>ajult</td>
<td>6</td>
<td>218.2483</td>
<td>13.7236</td>
</tr>
<tr>
<td>6</td>
<td>snwp*snwp</td>
<td>7</td>
<td>217.6528</td>
<td>14.0458</td>
</tr>
<tr>
<td>7</td>
<td>ajant</td>
<td>8</td>
<td>219.0390</td>
<td>13.2277</td>
</tr>
<tr>
<td>8</td>
<td>ppsm</td>
<td>9</td>
<td>219.5677</td>
<td>14.0345</td>
</tr>
<tr>
<td>9</td>
<td>nin3k</td>
<td>10</td>
<td>217.7667</td>
<td>11.3952</td>
</tr>
<tr>
<td>10</td>
<td>sdp&amp;sdp</td>
<td>11</td>
<td>219.2240</td>
<td>11.2543*</td>
</tr>
<tr>
<td>11</td>
<td>nph</td>
<td>12</td>
<td>220.3916</td>
<td>15.8819</td>
</tr>
<tr>
<td>13</td>
<td>nfek</td>
<td>14</td>
<td>217.8975</td>
<td>24.3177</td>
</tr>
<tr>
<td>14</td>
<td>nsch25</td>
<td>15</td>
<td>211.1182*</td>
<td>22.1601</td>
</tr>
<tr>
<td>15</td>
<td>ajant*ajant</td>
<td>16</td>
<td>212.1622</td>
<td>24.7855</td>
</tr>
<tr>
<td>16</td>
<td>aap*aap</td>
<td>17</td>
<td>212.4622</td>
<td>22.3426</td>
</tr>
<tr>
<td>17</td>
<td>nfek*nfek</td>
<td>18</td>
<td>214.9810</td>
<td>21.4198</td>
</tr>
<tr>
<td>18</td>
<td>size65</td>
<td>19</td>
<td>217.9436</td>
<td>22.0706</td>
</tr>
<tr>
<td>19</td>
<td>nopi</td>
<td>20</td>
<td>219.4252</td>
<td>24.2372</td>
</tr>
<tr>
<td>20</td>
<td>datm</td>
<td>21</td>
<td>217.2521</td>
<td>27.5795</td>
</tr>
<tr>
<td>21</td>
<td>nowk*nowk</td>
<td>22</td>
<td>217.8324</td>
<td>31.1312</td>
</tr>
<tr>
<td>22</td>
<td>datm*datm</td>
<td>23</td>
<td>219.4309</td>
<td>32.3530</td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion
Output 13.3.2 shows the selected effects and the relevant estimates.

**Output 13.3.2 Parameter Estimates**

*Selected Effects:* Intercept aap ajult ajult ppsm snwp snwp*snwp nowk nin3k sdpi sdpi*sdpi

**The QTRSELECT Procedure**

**Quantile Level = 0.5**

**Selected Model**

<table>
<thead>
<tr>
<th>Objective Function</th>
<th>386.63080</th>
</tr>
</thead>
<tbody>
<tr>
<td>R1</td>
<td>0.63578</td>
</tr>
<tr>
<td>Adj R1</td>
<td>0.50570</td>
</tr>
<tr>
<td>AIC</td>
<td>200.92487</td>
</tr>
<tr>
<td>AICC</td>
<td>210.70265</td>
</tr>
<tr>
<td>SBC</td>
<td>219.22405</td>
</tr>
<tr>
<td>ACL (Train)</td>
<td>9.91361</td>
</tr>
<tr>
<td>ACL (Validate)</td>
<td>11.25432</td>
</tr>
</tbody>
</table>

**Parameter Estimates**

| Parameter       | DF | Estimate  | Standard Error | t Value | Pr > |t| |
|-----------------|----|-----------|----------------|---------|------|-----|
| Intercept       | 1  | 1002.739146 | 103.68721      | 9.67    | <.0001 |
| aap             | 1  | 2.887043    | 0.96214        | 3.00    | 0.0056 |
| ajult           | 1  | -1.908846   | 0.70846        | -2.69   | 0.0118 |
| ajult           | 1  | -4.060364   | 2.23017        | -1.82   | 0.0794 |
| ppsm            | 1  | 0.013711    | 0.00522        | 2.63    | 0.0138 |
| snwp            | 1  | 5.784638    | 2.15892        | 2.68    | 0.0122 |
| snwp * snwp     | 1  | -0.100740   | 0.06888        | -1.46   | 0.1547 |
| nowk            | 1  | 0.132541    | 1.35128        | 0.10    | 0.9226 |
| nin3k           | 1  | 6.159752    | 3.49428        | 1.76    | 0.0888 |
| sdpi            | 1  | -0.010327   | 0.59309        | -0.02   | 0.9862 |
| sdpi * sdpi     | 1  | 0.000836    | 0.00302        | 0.28    | 0.7840 |
Output 13.3.3 shows the progression of the standardized parameter estimates as the selection process proceeds.
Output 13.3.4 shows the progression of the average check losses for training data and validation data as the selection process proceeds.

**Output 13.3.4** Average Check Loss Plot

Proportion of ACL by Role for DeathRate
Quantile Level = 0.5

![Average Check Loss Plot](image)
Output 13.3.5 shows the progression of six effect selection criteria as the selection process proceeds.

**Output 13.3.5** Criterion Panel

### Fit Criteria for DeathRate
Quantile Level = 0.5

- **Adj R1**
- **AIC**
- **AICC**
- **SBC**
- **ACL (Train)**
- **ACL (Validate)**

**Effect Sequence**

[Star] Best Criterion Value  |  Selected Step
Output 13.3.6 shows the first 10 observations of the OUTPUT data set.

<table>
<thead>
<tr>
<th>Obs</th>
<th>Role</th>
<th>Pred</th>
<th>DeathRate</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
<td>934.43</td>
<td>921.87</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>942.04</td>
<td>997.88</td>
</tr>
<tr>
<td>3</td>
<td>2</td>
<td>919.09</td>
<td>962.35</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>991.17</td>
<td>982.29</td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>1044.15</td>
<td>1071.29</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>1030.38</td>
<td>1030.38</td>
</tr>
<tr>
<td>7</td>
<td>2</td>
<td>931.02</td>
<td>934.70</td>
</tr>
<tr>
<td>8</td>
<td>2</td>
<td>906.16</td>
<td>899.53</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>991.14</td>
<td>1001.90</td>
</tr>
<tr>
<td>10</td>
<td>1</td>
<td>941.66</td>
<td>912.35</td>
</tr>
</tbody>
</table>

References


Chapter 14

The REGSELECT Procedure

Contents

Overview: REGSELECT Procedure ................................................. 726
PROC REGSELECT Features .................................................... 726
PROC REGSELECT Compared with Other SAS Procedures .................. 727
Using CAS Sessions and CAS Engine Librefs ............................... 728
Getting Started: REGSELECT Procedure ................................... 729
Syntax: REGSELECT Procedure ............................................... 737
PROC REGSELECT Statement ................................................ 737
BY Statement ................................................................. 738
CLASS Statement ............................................................. 738
CODE Statement ............................................................... 739
DISPLAY Statement ........................................................... 739
DISPLAYOUT Statement ....................................................... 740
EFFECT Statement ............................................................. 741
FREQ Statement ............................................................... 742
MODEL Statement ............................................................... 743
OUTPUT Statement .............................................................. 745
PARTITION Statement .......................................................... 747
SELECTION Statement ........................................................... 748
WEIGHT Statement ............................................................. 749
Details: REGSELECT Procedure .............................................. 749
Criteria Used in Model Selection .............................................. 749
Diagnostic Statistics ............................................................. 751
Classification Variables and the SPLIT Option .............................. 752
Using Validation and Test Data ................................................. 753
Computational Method ......................................................... 754
Joint Tests and Type 3 Tests .................................................... 755
Displayed Output ............................................................... 755
ODS Table Names .............................................................. 759
ODS Graphics ................................................................. 760
Examples: REGSELECT Procedure .......................................... 761
Example 14.1: Model Selection with Validation ............................. 762
References ................................................................. 770
Overview: REGSELECT Procedure

The REGSELECT procedure fits and performs model selection for ordinary least squares regression models in SAS Viya.

The models that PROC REGSELECT supports can contain main effects that consist of both continuous and classification variables and interaction effects of these variables. The models can also include constructed effects such as splines. The procedure offers a number of effect-selection methods, including stepwise methods and modern LASSO methods. It also offers extensive capabilities for customizing the model selection by using a wide variety of selection and stopping criteria, from computationally efficient significance-level-based criteria to modern, computationally intensive validation-based criteria. PROC REGSELECT also provides a variety of regression diagnostics that are conditional on the selected model.

PROC REGSELECT Features

The main features of the REGSELECT procedure are as follows:

- **Model specification**
  - supports multiple parameterizations for classification effects
  - supports any degree of interaction (crossed effects) and nested effects
  - supports a hierarchy among effects
  - supports partitioning of data into training, validation, and testing roles
  - provides a FREQ statement for grouped analysis
  - provides a WEIGHT statement for weighted analysis

- **Selection control**
  - provides multiple effect-selection methods
  - offers selection of individual levels of classification effects
  - provides effect selection based on a variety of selection criteria
  - provides stopping rules based on a variety of model evaluation criteria
  - supports stopping and selection rules based on external validation and leave-one-out cross validation

- **Display and output**
  - produces output data tables that contain predicted values, residuals, studentized residuals, confidence limits, and influence statistics
  - uses ODS Graphics to create model selection plots as part of its output. For more information about ODS Graphics, see the section “ODS Graphics” on page 760.

The REGSELECT procedure supports the following effect-selection methods. For a more detailed description of these methods, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”
PROC REGSELECT Compared with Other SAS Procedures

- Forward selection starts with no effects in the model and adds effects.
- Backward elimination starts with all effects in the model and deletes effects.
- Stepwise regression is similar to forward selection, except that effects already in the model do not necessarily stay there.
- Forward-swap selection is an extension of the forward selection method. Before any addition step, PROC REGSELECT makes all pairwise swaps of one effect in the model and one effect out of the current model that improve the selection criterion. When the selection criterion is R square, this method is the same as the MAXR method in the REG procedure in SAS/STAT software.
- Least angle regression, like forward selection, starts with no effects in the model and adds effects. The parameter estimates at any step are “shrunk” when compared to the corresponding least squares estimates.
- LASSO adds and deletes parameters based on a version of ordinary least squares in which the sum of the absolute regression coefficients is constrained. PROC REGSELECT also supports adaptive LASSO selection, in which weights are applied to each of the parameters in forming the LASSO constraint.

Hybrid versions of the LAR and LASSO methods are also supported. They use LAR or LASSO to select the model, but they estimate the regression coefficients by ordinary weighted least squares.

Because the REGSELECT procedure runs on CAS, it also does the following:

- enables you to run on a cluster of machines that distribute the data and the computations
- enables you to run in single-machine mode on CAS
- exploits all the available cores and concurrent threads. For information about how PROC REGSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”

PROC REGSELECT Compared with Other SAS Procedures

The REGSELECT procedure provides regression modeling functionality that is comparable to that of the HPREG, GLMSELECT, and REG procedures in SAS/STAT software.

PROC REGSELECT Compared with the HPREG Procedure

The functionality of the REGSELECT procedure closely resembles that of the HPREG procedure, which is a high-performance procedure. The REGSELECT procedure is the next generation of the HPREG procedure, and it was developed specifically for SAS Viya. Both procedures are designed to run on a cluster of machines that distribute the data and the computations.

Both the REGSELECT and HPREG procedures fit and perform model selection for ordinary least squares regression models, which you can specify as general linear models that include classification variables. You request model selection by using the SELECTION statement.

The REGSELECT and HPREG procedures offer the same methods of effect selection, but the REGSELECT procedure also produces selection plots by using ODS Graphics. The REGSELECT and HPREG procedures
offer the same methods of customizing the model selection, and the same set of regression diagnostics. The main differences in functionality are that the REGSELECT procedure provides the ability to specify constructed effects with the EFFECT statement, and it computes Type 3 tests of effects.

**PROC REGSELECT Compared with the GLMSELECT Procedure**

The functionality of the REGSELECT procedure also closely resembles that of the GLMSELECT procedure. Both procedures fit and perform model selection for ordinary least squares regression models, which you can specify as general linear models that include classification variables. Both procedures offer the same methods of effect selection (including the LAR and LASSO methods), the ability to use external validation data and cross validation as selection criteria, and extensive options to customize the selection process. Both procedures provide the ability to specify constructed effects with the EFFECT statement.

Unlike the GLMSELECT procedure, the REGSELECT procedure does not perform model selection by default. If you request model selection by using the SELECTION statement, then the default selection method is stepwise selection based on the Schwarz Bayesian information criterion (SBC). This default matches the default method in PROC GLMSELECT.

With the REGSELECT procedure—but not with the GLMSELECT procedure—you can request observationwise residual and influence diagnostics in the OUTPUT statement and variance inflation and tolerance statistics for the parameter estimates. If the fitted model has been obtained by performing model selection, then these statistics are conditional on the selected model and do not take into account the variability introduced by the selection process.

**PROC REGSELECT Compared with the REG Procedure**

A major functional difference between the REGSELECT procedure and the REG procedure is that the REGSELECT procedure enables you to specify general linear models that include classification variables. In this respect it is similar to the GLM and GLMSELECT procedures in SAS/STAT.

Unlike the REG procedure, the REGSELECT procedure supports the LAR and LASSO methods, the ability to use external validation data and cross validation as selection criteria, and extensive options to customize the selection process. PROC REGSELECT does not support the all-subset-based methods that you find in PROC REG, nor does it support the MINR method.

Like the REG procedure, PROC REGSELECT does not perform model selection by default. If you request model selection by using the SELECTION statement in PROC REGSELECT, then the default selection method is stepwise selection based on the Schwarz Bayesian information criterion (SBC).

With the REGSELECT procedure, as with the REG procedure, you can request observationwise residual and influence diagnostics in the OUTPUT statement, and variance inflation and tolerance statistics for the parameter estimates. If the fitted model has been obtained by performing model selection, then these statistics are conditional on the selected model and do not take into account the variability introduced by the selection process.

---

**Using CAS Sessions and CAS Engine Librefs**

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator.
if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```latex
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```latex
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```latex
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

**Getting Started: REGSELECT Procedure**

The following example is closely modeled on the example in the section “Getting Started: GLMSELECT Procedure” in the *SAS/STAT User’s Guide*.

The Sashelp.Baseball data set contains salary and performance information for Major League Baseball players who played at least one game in both the 1986 and 1987 seasons, excluding pitchers. The salaries (*Sports Illustrated*, April 20, 1987) are from the 1987 season, and the performance measures are from 1986 (Collier Books, *The 1987 Baseball Encyclopedia Update*). The following step displays (in Figure 14.1) the variables in the data set:

```latex
proc contents varnum data=sashelp.baseball;
  ods select position;
run;
```
Chapter 14: The REGSELECT Procedure

Figure 14.1 Sashelp.Baseball Data Set

The CONTENTS Procedure

<table>
<thead>
<tr>
<th>Variables in Creation Order</th>
</tr>
</thead>
<tbody>
<tr>
<td>#</td>
</tr>
<tr>
<td>----</td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
<tr>
<td>6</td>
</tr>
<tr>
<td>7</td>
</tr>
<tr>
<td>8</td>
</tr>
<tr>
<td>9</td>
</tr>
<tr>
<td>10</td>
</tr>
<tr>
<td>11</td>
</tr>
<tr>
<td>12</td>
</tr>
<tr>
<td>13</td>
</tr>
<tr>
<td>14</td>
</tr>
<tr>
<td>15</td>
</tr>
<tr>
<td>16</td>
</tr>
<tr>
<td>17</td>
</tr>
<tr>
<td>18</td>
</tr>
<tr>
<td>19</td>
</tr>
<tr>
<td>20</td>
</tr>
<tr>
<td>21</td>
</tr>
<tr>
<td>22</td>
</tr>
<tr>
<td>23</td>
</tr>
<tr>
<td>24</td>
</tr>
</tbody>
</table>

Suppose you want to investigate whether you can model the players’ salaries from the 1987 season based on performance measures for the previous season. The aim is to obtain a parsimonious model that does not overfit these particular data, making the model useful for prediction. This example shows how you can use PROC REGSELECT as a starting point for such an analysis. Because the variation of salaries is much greater for the higher salaries, it is appropriate to apply a log transformation to the salaries before you do the model selection.

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

You can load the Sashelp.Baseball data set into your CAS session by using your CAS engine libref with the following DATA step:

```sas
   data mycas.baseball;
   set sashelp.baseball;
   run;
```

These statements assume that your CAS engine libref is named Mycas, as in the section “Using CAS Sessions and CAS Engine Librefs” on page 728, but you can substitute any appropriately defined CAS engine libref.
The following statements select a model by using the default settings for stepwise selection. ODS Graphics must be enabled before you can request plots. For more information about ODS Graphics, see the section “ODS Graphics” on page 760.

```plaintext
ods graphics on;

proc regselect data=mycas.baseball;
    class league division;
    model logSalary = nAtBat nHits nHome nRuns nRBI nBB
                     yrMajor crAtBat crHits crHome crRuns crRbi
                     crBB league division nOuts nAssts nError;
    selection method=stepwise plots=all;
run;
```

The output and graphics from this analysis are presented in Figure 14.2 through Figure 14.6.

**Figure 14.2** Selection Information, Number of Observations, Class Level Information, and Dimensions

<table>
<thead>
<tr>
<th>The REGSELECT Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Selection Information</strong></td>
</tr>
<tr>
<td>Selection Method</td>
</tr>
<tr>
<td>Select Criterion</td>
</tr>
<tr>
<td>Stop Criterion</td>
</tr>
<tr>
<td>Effect Hierarchy Enforced</td>
</tr>
<tr>
<td>Stop Horizon</td>
</tr>
<tr>
<td><strong>Number of Observations Read</strong></td>
</tr>
<tr>
<td><strong>Number of Observations Used</strong></td>
</tr>
<tr>
<td><strong>Class Level Information</strong></td>
</tr>
<tr>
<td>Class</td>
</tr>
<tr>
<td>League</td>
</tr>
<tr>
<td>Division</td>
</tr>
<tr>
<td><strong>Dimensions</strong></td>
</tr>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Number of Parameters</td>
</tr>
</tbody>
</table>

The “Selection Information” table provides details about the method and criteria used to perform the model selection. The requested selection method is a variant of the traditional stepwise selection in which the decisions about what effects to add or drop at any step and when to terminate the selection are both based on the Schwarz Bayesian information criterion (SBC). The effect in the current model whose removal yields the maximal decrease in the SBC value is dropped, provided that this lowers the SBC value. When no further decrease in the SBC value can be obtained by dropping an effect in the model, the effect whose addition to the model yields the lowest SBC value is added and the whole process is repeated. The method terminates when dropping or adding any effect increases the SBC value.
Figure 14.2 displays the “Number of Observations,” “Class Level Information,” and “Dimensions” tables. The “Number of Observations” table shows that of the 322 observations in the input data, only 263 observations are used in the analysis because there are observations that contain incomplete data. The “Class Level Information” table lists the levels of the classification variables division and league. When you specify effects that contain classification variables, the number of parameters is usually larger than the number of effects. The “Dimensions” table shows the number of effects and the number of parameters that are considered.

The “Stepwise Selection Summary” table in Figure 14.3 shows the effect that was added or dropped at each step of the selection process together with fit statistics for the model at each step. In this case, both selection and stopping are based on the SBC.

Figure 14.3 Selection Summary Table

The REGSELECT Procedure

Selection Details

<table>
<thead>
<tr>
<th>Step</th>
<th>Effect Entered</th>
<th>Effect Removed</th>
<th>Number Effects In</th>
<th>SBC</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Intercept</td>
<td></td>
<td>1</td>
<td>-57.2041</td>
</tr>
<tr>
<td>1</td>
<td>CrRuns</td>
<td>2</td>
<td>-194.3166</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>nHits</td>
<td>3</td>
<td>-252.5794</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>YrMajor</td>
<td>4</td>
<td>-262.7322</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>CrRuns</td>
<td>3</td>
<td>-262.8353</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>nBB</td>
<td>4</td>
<td>-269.7804*</td>
<td></td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

Figure 14.4 displays the “Stop Reason,” “Selection Reason,” and “Selected Effects” tables. Note that these tables are displayed without any titles. The “Stop Reason” table indicates that selection stopped because adding or removing any effect would worsen the SBC value that is used as the selection criterion. In this case, because no CHOOSE= criterion is specified in the SELECTION statement, the final model is the selected model; this is indicated in the “Selection Reason” table. The “Selected Effects” table lists the effects in the selected model.

Figure 14.4 Stopping and Selection Reasons

Stepwise selection stopped because adding or removing an effect does not improve the SBC criterion.

The model at step 5 is selected.

Selected Effects: Intercept nHits nBB YrMajor
The coefficient panel in Figure 14.5 enables you to visualize the selection process. In this plot, standardized coefficients of all the effects that are selected at some step of the stepwise method are plotted as a function of the step number. This enables you to assess the relative importance of the effects that are selected at any step of the selection process and to know when effects entered the model. The lower plot in the panel shows how the criterion that is used to choose the selected model changes as effects enter or leave the model.

**Figure 14.5 Coefficient Progression**

The criterion panel in Figure 14.6 provides a graphical view of the progression of the fit criteria as the selection process evolves.
Figure 14.6 Criterion Panel

Fit Criteria for logSalary

The “Analysis of Variance,” “Fit Statistics,” and “Parameter Estimates” tables shown in Figure 14.7 display details of the selected model.

Figure 14.7 Details of the Selected Model

The REGSELECT Procedure

<table>
<thead>
<tr>
<th>Selected Model</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Source</th>
<th>DF</th>
<th>Sum of Squares</th>
<th>Mean Square</th>
<th>F Value</th>
<th>Pr &gt; F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model</td>
<td>3</td>
<td>120.52553</td>
<td>40.17518</td>
<td>120.12</td>
<td>&lt;.0001</td>
</tr>
<tr>
<td>Error</td>
<td>259</td>
<td>86.62820</td>
<td>0.33447</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Corrected Total</td>
<td>262</td>
<td>207.15373</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Finally, a table is displayed that shows the amount of time (in seconds) that PROC REGSELECT required to perform the different tasks in the analysis.

**Figure 14.8 Procedure Timing**

<table>
<thead>
<tr>
<th>Task</th>
<th>Seconds</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>Setup and Parsing</td>
<td>0.03</td>
<td>41.84%</td>
</tr>
<tr>
<td>Levelization</td>
<td>0.03</td>
<td>40.14%</td>
</tr>
<tr>
<td>Model Initialization</td>
<td>0.00</td>
<td>0.44%</td>
</tr>
<tr>
<td>SSCP Computation</td>
<td>0.00</td>
<td>7.02%</td>
</tr>
<tr>
<td>Model Selection</td>
<td>0.00</td>
<td>1.59%</td>
</tr>
<tr>
<td>Cleanup</td>
<td>0.00</td>
<td>3.77%</td>
</tr>
<tr>
<td>Total</td>
<td>0.06</td>
<td>100.00%</td>
</tr>
</tbody>
</table>

You might want to examine regression diagnostics for the selected model to investigate whether collinearity among the selected parameters or the presence of outlying or high-leverage observations might be affecting the fit. The following statements include some options and statements to obtain these diagnostics:

```latex
proc regselect data=mycas.baseball;
  class league division;
  model logSalary = nAtBat nHits nHome nRuns nRBI nBB yrMajor crAtBat crHits crHome crRuns crRbi crBB league division nOuts nAssts nError / vif clb;
  selection method=stepwise;
  output out=mycas.baseballOut p=predictedLogSalary r h cookd rstudent copyvars=(name);
run;
```

The VIF and CLB options in the MODEL statement request variance inflation factors and 95% confidence limits, respectively, for the parameter estimates. Figure 14.9 shows the “Parameter Estimates” table, which displays these requested statistics. The variance inflation factors (VIF) measure the inflation in the variances of the parameter estimates due to collinearities that exist among the regressor (independent) variables.
Although there are no formal criteria for deciding whether a VIF is large enough to affect the predicted values, the VIF values for the selected effects in this example are small enough to indicate that there are no collinearity issues among the selected regressors.

**Figure 14.9** Parameter Estimates with Additional Statistics

### The REGSELECT Procedure

#### Selected Model

<table>
<thead>
<tr>
<th>Parameter</th>
<th>DF</th>
<th>Estimate</th>
<th>Standard Error</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>Variance Inflation</th>
<th>95% Confidence Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>1</td>
<td>4.013911</td>
<td>0.111290</td>
<td>36.07</td>
<td>&lt;.0001</td>
<td>0</td>
<td>3.79476 4.23306</td>
</tr>
<tr>
<td>nHits</td>
<td>1</td>
<td>0.007929</td>
<td>0.000994</td>
<td>7.98</td>
<td>&lt;.0001</td>
<td>1.49642</td>
<td>0.00597 0.00989</td>
</tr>
<tr>
<td>nBB</td>
<td>1</td>
<td>0.007280</td>
<td>0.002049</td>
<td>3.55</td>
<td>0.0005</td>
<td>1.52109</td>
<td>0.00325 0.01131</td>
</tr>
<tr>
<td>YrMajor</td>
<td>1</td>
<td>0.100663</td>
<td>0.007551</td>
<td>13.33</td>
<td>&lt;.0001</td>
<td>1.02488</td>
<td>0.08579 0.11553</td>
</tr>
</tbody>
</table>

By default, SAS Viya statistical procedures do not include all variables from the input data table in output data tables. The COPYVARS= option in the OUTPUT statement specifies that the variable name in the input data table be added as an identification variable in the `baseballOut` data table that is produced by the OUTPUT statement. In addition to this variable, the OUTPUT statement requests that predicted values, raw residuals, leverage values, Cook’s D statistics, and studentized residuals be added to the output data table. Note that default names are used for these statistics, except for the predicted values for which a specified name, `predictedLogSalary`, is supplied. The following statements use PROC PRINT to display five observations in this output data table:

```sas
proc print data=mycas.baseballOut(obs=5);
run;
```

**Figure 14.10** First 5 Observations of the baseballOut Data Set

<table>
<thead>
<tr>
<th>Obs</th>
<th>predictedLogSalary</th>
<th>Residual</th>
<th>COOKD</th>
<th>H</th>
<th>RSTUDENT</th>
<th>Name</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.73980</td>
<td>.</td>
<td>0.016087</td>
<td></td>
<td></td>
<td>Allanson, Andy</td>
</tr>
<tr>
<td>2</td>
<td>6.50852</td>
<td>-0.29392</td>
<td>0.000730178</td>
<td>0.011060</td>
<td>-0.51031</td>
<td>Dawson, Andre</td>
</tr>
<tr>
<td>3</td>
<td>4.66148</td>
<td>-0.41299</td>
<td>0.002516874</td>
<td>0.018999</td>
<td>-0.72031</td>
<td>Newman, Al</td>
</tr>
<tr>
<td>4</td>
<td>6.52518</td>
<td>0.47788</td>
<td>0.003069150</td>
<td>0.017361</td>
<td>0.83308</td>
<td>Thornton, Andre</td>
</tr>
<tr>
<td>5</td>
<td>5.65468</td>
<td>0.65524</td>
<td>0.002020832</td>
<td>0.006219</td>
<td>1.13715</td>
<td>Van Slyke, Andy</td>
</tr>
</tbody>
</table>
Syntax: REGSELECT Procedure

The following statements are available in the REGSELECT procedure:

```
PROC REGSELECT <options> ;
   BY variables ;
   CLASS variable <(options)> . . . < variable <(options)> > < global-options > ;
   CODE <options> ;
   DISPLAY < table-list > < options > ;
   DISPLAYOUT table-spec-list < options > ;
   EFFECT name=effect-type(variables < options >) ;
   FREQ variable ;
   MODEL dependent = < effects > < model-options > ;
   OUTPUT OUT=CAS-libref.data-table < keyword =<name>> . . . < keyword =<name>> < options > ;
   PARTITION partition-options ;
   SELECTION < METHOD=method <(method-options) > < options > ;
   WEIGHT variable ;
```

The PROC REGSELECT statement and a single MODEL statement are required. All other statements are optional. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the MODEL statement.

The rest of this section provides detailed syntax information about each of the preceding statements, beginning with the PROC REGSELECT statement. The remaining statements are described in alphabetical order.

PROC REGSELECT Statement

```
PROC REGSELECT <options> ;
```

The PROC REGSELECT statement invokes the procedure. Table 14.1 summarizes the options in the PROC REGSELECT statement by function.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Basic Options</td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data set</td>
</tr>
<tr>
<td>Other Options</td>
<td></td>
</tr>
<tr>
<td>NOCLPRINT</td>
<td>Limits or suppresses the display of class levels</td>
</tr>
<tr>
<td>ALPHA=</td>
<td>Sets the significance level to be used for the construction of confidence intervals</td>
</tr>
</tbody>
</table>

You can specify the following options:
**ALPHA=**number

sets the significance level to be used for the construction of confidence intervals. The value must be between 0 and 1; the default value of 0.05 results in 95% intervals. This option affects the keywords LCL, LCLM, UCL, and UCLM in the OUTPUT statement and the CLB option in the MODEL statement.

**DATA=**CAS-libref.data-table

names the input data table for PROC REGSELECT to use. The default is the most recently created data table. CAS-libref specifies the CAS library where the input data table resides, and data-table specifies the name of the input data table.

**NOCLPRINT<=**number

suppresses the display of the “Class Level Information” table if you do not specify number. If you specify number, the values of the classification variables are displayed for only those variables whose number of levels is less than number. Specifying number helps reduce the size of the “Class Level Information” table if some classification variables have a large number of levels.

---

### BY Statement

BY variables ;

You can specify a BY statement in PROC REGSELECT to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in *SAS Language Reference: Concepts*.

---

### CLASS Statement

CLASS variable <(options)> . . . <variable <(options)> > < / global-options> ;

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. You can list the response variable for binary models in the CLASS statement, but this is not required. Table 14.2 summarizes the values that you can use for either an option or a global-option. The options are fully documented in the section “CLASS Statement” on page 10 in Chapter 2, “Shared Concepts.”

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the sort order for the levels</td>
</tr>
<tr>
<td>PARAM=</td>
<td>Specifies the parameterization of the variable</td>
</tr>
<tr>
<td>REF=</td>
<td>Specifies the reference level of the variable</td>
</tr>
<tr>
<td>SPLIT</td>
<td>Allows design columns for a variable to enter or leave the model independently</td>
</tr>
</tbody>
</table>
**CODE Statement**

```sas
CODE < options > ;
```

The CODE statement writes SAS DATA step code for computing predicted values of the fitted model to a file, to a catalog entry, or to a CAS table. To score new data, you can then include the file or the catalog entry in a DATA step, or you can specify the CAS table in the `runCodeTable` action in the `dataStep` action set (for more information, see *SAS Viya: System Programming Guide*).

Table 14.3 summarizes the options available in the CODE statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COMMENT</td>
<td>Adds comments to the generated code</td>
</tr>
<tr>
<td>FILE=</td>
<td>Names the file in which to save the generated code</td>
</tr>
<tr>
<td>FORMATWIDTH=</td>
<td>Specifies the numeric format width for the regression coefficients</td>
</tr>
<tr>
<td>INDENTSIZE=</td>
<td>Specifies the number of spaces to indent the generated code</td>
</tr>
<tr>
<td>LABELID=</td>
<td>Specifies a number used to construct names and labels</td>
</tr>
<tr>
<td>LINESIZE=</td>
<td>Specifies the line size for the generated code</td>
</tr>
<tr>
<td>NOTRIM</td>
<td>Compares formatted values, including blank padding</td>
</tr>
<tr>
<td>OUT=</td>
<td>Names an output CAS table in which to save the generated code</td>
</tr>
</tbody>
</table>

For more information about the syntax of the CODE statement, see the section “CODE Statement” on page 14 in Chapter 2, “Shared Concepts.”

**DISPLAY Statement**

```sas
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions. The table names that you can specify are listed in the section “ODS Table Names” on page 759. A path is a table name that is prefixed with dot-separated grouping information. For example, a
SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

- **CASESENSITIVE**
  - performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  - displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  - suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  - displays the display table names, labels, and paths.

**DISPLAYOUT Statement**

```plaintext
DISPLAYOUT table-spec-list < / options > ;
```

The `DISPLAYOUT` statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- **key=value**
  - specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.

- **key**
  - specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the `DISPLAY` statement. The `DISPLAYOUT` statement does not support regular expressions.

You can specify the following `options` after a slash (/):
INCLUDEALL
creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

NOREPLACE
does not replace any existing CAS output table of the same name.

REPEATED
replicates all CAS output tables on all nodes.

**EFFECT Statement**

EFFECT name=effect-type (variables < / options> );

The EFFECT statement enables you to construct special collections of columns for design matrices. These collections are referred to as *constructed effects* to distinguish them from the usual model effects that are formed from continuous or classification variables, as discussed in the section “GLM Parameterization of Classification Variables and Effects” on page 52 in Chapter 2, “Shared Concepts.”

You can specify the following *effect-types*:

**COLLECTION**
specifies a collection effect that defines one or more variables as a single effect that has multiple degrees of freedom. The variables in a collection are considered as a unit for purposes of estimation and inference.

**MULTIMEMBER | MM**
specifies a multimember classification effect whose levels are determined by one or more variables that appear in a CLASS statement.

**POLYNOMIAL | POLY**
specifies a multivariate polynomial effect in the specified numeric variables.

**SPLINE**
specifies a regression spline effect whose columns are univariate spline expansions of one or more variables. A spline expansion replaces the original variable with an expanded or larger set of new variables.

Table 14.4 summarizes the *options* available in the EFFECT statement.

| **Table 14.4** EFFECT Statement Options |
|-----------------|---------------------------------|
| **Option**      | **Description**                  |
| **Collection Effects Options** | |
| DETAILS         | Displays the constituents of the collection effect |
| **Multimember Effects Options** | |
| DETAILS         | Displays the levels of the multimember effect |
| NOEFFECT        | Specifies that observations whose levels are all missing for the multimember variables should have 0 values in the corresponding design matrix columns |
| STDIZE          | Standardizes the design matrix entries so that each observation has a sum of 1 |
Table 14.4  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WEIGHT=</td>
<td>Specifies the weight variable for the contributions of each classification effect</td>
</tr>
</tbody>
</table>

**Polynomial Effects Options**

DEGREE= Specifies the degree of the polynomial
DETAILS Displays details of the specified polynomial
MDEGREE= Specifies the maximum degree of any variable in a term of the polynomial
NOSEPARATE Treats the polynomial as a single effect with multiple degrees of freedom
STANDARDIZE= Specifies centering and scaling suboptions for the variables that define the polynomial

**Spline Effects Options**

BASIS= Specifies the type of basis (B-spline basis or truncated power function basis) for the spline effect
DATABOUNDARY Uses the extremes of the data as boundary knots for a B-spline basis
DEGREE= Specifies the degree of the spline effect
DETAILS Displays the knots and locations for each spline basis function
KNOTMAX= Requests equally spaced right-side boundary knots starting at the variables’ maximum and ending at the KNOTMAX= value
KNOTMETHOD= Specifies how to construct the knots for the spline effect
KNOTMIN= Requests equally spaced left-side boundary knots starting at the KNOTMIN= value and ending at the variables’ minimum value
NATURALCUBIC Specifies a natural cubic spline basis for the spline effect
SEPARATE Treats the spline basis for each variable as a separate effect when multiple variables are specified
SPLIT Treats each design matrix column as a separate effect for selection methods

For more information about the syntax of these effect-types and how columns of constructed effects are computed, see the section “EFFECT Statement” on page 19 in Chapter 2, “Shared Concepts.”

**FREQ Statement**

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC REGSELECT treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.
**MODEL Statement**

MODEL dependent=<effects> / <model-options> ;

The MODEL statement names the dependent variable and the explanatory effects, including covariates, main effects, interactions, and nested effects. If you omit the explanatory effects, the procedure fits an intercept-only model.

After the keyword MODEL, the dependent (response) variable is specified, followed by an equal sign. The explanatory effects follow the equal sign.

For information about constructing the model effects, see the section “Specification and Parameterization of Model Effects” on page 49 in Chapter 2, “Shared Concepts.”

The *model-options* control other aspects of model formation and inference. Table 14.5 summarizes these options.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Model Options</strong></td>
<td></td>
</tr>
<tr>
<td>CLB</td>
<td>Requests confidence limits</td>
</tr>
<tr>
<td>INCLUDE=</td>
<td>Includes effects in all models for model selection</td>
</tr>
<tr>
<td>INFORMATIVE</td>
<td>Models missing values by using extra indicator variables</td>
</tr>
<tr>
<td>NOINT</td>
<td>Suppresses the intercept</td>
</tr>
<tr>
<td>SS3</td>
<td>Displays the Type 3 or joint tests of effects</td>
</tr>
<tr>
<td>START=</td>
<td>Includes effects in the initial model for model selection</td>
</tr>
<tr>
<td>STB</td>
<td>Displays standardized estimates</td>
</tr>
<tr>
<td>TOL</td>
<td>Displays tolerance values for the estimates</td>
</tr>
<tr>
<td>VIF</td>
<td>Displays variance inflation factors for the estimates</td>
</tr>
</tbody>
</table>

**Model Options**

You can specify the following *options* in the MODEL statement after a slash (/):

- CLB
  - requests the $100(1 - \alpha \%) \text{ upper and lower confidence limits for the parameter estimates.}$ By default, the $95\%$ limits are computed; you can use the ALPHA= option in the PROC REGSELECT statement to change the $\alpha$ level. The CLB option is not supported when you specify METHOD=LAR or METHOD=LASSO in the SELECTION statement.

- INCLUDE=n

- INCLUDE=single-effect

- INCLUDE=(effects)
  - forces effects to be included in all models. If you specify INCLUDE=n, then the first $n$ effects listed in the MODEL statement are included in all models. If you specify INCLUDE=single-effect or INCLUDE=(single-effect), then the specified effects are forced into all models. The INCLUDE=...
option is not available when you specify METHOD=LAR or METHOD=LASSO in the SELECTION statement.

INFORMATIVE
models missing values by using extra model effects. These effects consist of dummy variables that take the value 1 when the value of a continuous model variable involved in the effect is missing, and take the value 0 otherwise. The missing value in the original model effect is replaced by the average value of the effect for the nonmissing values. For continuous-by-class effects, such as A*x, where A is a classification variable and x is a continuous variable, informative missingness creates multiple dummy columns and substitutes the effect mean of x that corresponds to the respective level of A. Missing values for classification variables are treated as valid levels. For more information about informative missingness, see the section “Informative Missingness” on page 76 in Chapter 2, “Shared Concepts.”

NOINT
suppresses the intercept term that is otherwise included in the model.

SS3
displays a “Model Anova” table that contains tests computed with Type III sums of squares for each effect. For more information, see the section “Joint Tests and Type 3 Tests” on page 755.

START=n
START=single-effect
START=(effects)
is used to begin the selection process in the FORWARD, FORWARDSWAP, and STEPWISE selection methods from the initial model that you designate. If you specify START=n, then the starting model consists of the first n effects listed in the MODEL statement. If you specify START=single-effect or START=(single-effect), then the starting model consists of these specified effects. The START= option is not available when you specify METHOD=BACKWARD, METHOD=LAR, or METHOD=LASSO in the SELECTION statement.

STB
produces standardized regression coefficients. A standardized regression coefficient is computed by dividing a parameter estimate by the ratio of the sample standard deviation of the dependent variable to the sample standard deviation of the regressor.

TOL
produces tolerance values for the estimates. Tolerance for a parameter is defined as 1 – R², where R² is obtained from the regression of the parameter on all other parameters in the model. This option is not supported when you specify METHOD=LAR or METHOD=LASSO in the SELECTION statement.

VIF
produces variance inflation factors along with the parameter estimates. Variance inflation is the reciprocal of tolerance. The VIF option is not supported when you specify METHOD=LAR or METHOD=LASSO in the SELECTION statement.
OUTPUT Statement

```plaintext
OUTPUT OUT=CAS-libref.data-table
   < COPYVARS=(variables)>
   < keyword <=name>> . . . < keyword <=name>> ;
```

The OUTPUT statement creates a data table that contains observationwise statistics, which are computed after the model is fitted. The variables in the input data table are not included in the output data table, in order to avoid data duplication for large data tables; however, variables that you specify in the COPYVARS= option are included.

The output statistics are computed based on the parameter estimates for the selected model. For observations in which only the response variable is missing, predicted values are computed even though these observations do not affect the model fit. This enables, for example, predicted values to be computed for new observations.

You must specify the following option:

```
OUT=CAS-libref.data-table
```

names the output data table for PROC LOGSELECT to use. You must specify this option before any other options. **CAS-libref.data-table** is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about **CAS-libref**, see the section “Using CAS Sessions and CAS Engine Librefs” on page 728.

- **data-table** specifies the name of the output data table.

You can also specify the following syntax elements:

```
COPYVAR=variable
COPYVARS=(variables)
```

transfers one or more variables from the input data table to the output data table.

```
keyword <=name>
```

specifies the statistics to include in the output data table and optionally names the new variables that contain the statistics. Specify a keyword for each desired statistic (see the following list of keywords), followed optionally by an equal sign and a variable to contain the statistic.

If you specify `keyword=name`, the new variable that contains the requested statistic has the specified name. If you omit the optional `=name` after a `keyword`, then a default name is used.

You can specify the following values for `keyword` to request statistics that are available with all selection methods:

```
PREDICTED
PRED
P
```

requests predicted values for the response variable. The default is Pred.
requests the residual, calculated as ACTUAL – PREDICTED. The default is Residual.

ROLE requests a numeric variable that indicates the role played by each observation in fitting the model. The default is _ROLE_. For each observation, the interpretation of this variable is shown in Table 14.6.

Table 14.6 Role Interpretation

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by using a PARTITION statement, then the role variable value is 1 for observations used in fitting the model, and 0 for observations that have at least one missing or invalid value for the response, regressor, frequency, or weight variables.

In addition to the preceding statistics, you can also use the keywords listed in Table 14.7 in the OUTPUT statement to obtain additional statistics. These statistics are not available if you specify METHOD=LAR or METHOD=LASSO in the SELECTION statement. For computational formulas, see the section “Diagnostic Statistics” on page 751. All the statistics available in the OUTPUT statement are conditional on the selected model and do not take into account the variability introduced when you do model selection.

Table 14.7 Keywords for OUTPUT Statement

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>COOKD</td>
<td>Cook’s $D$ influence statistic</td>
</tr>
<tr>
<td>COVRATIO</td>
<td>Standard influence of observation on covariance of betas</td>
</tr>
<tr>
<td>DFFIT</td>
<td>Standard influence of observation on predicted value</td>
</tr>
<tr>
<td>H</td>
<td>Leverage, $x_i (X'X)^{-1} x_i'$</td>
</tr>
<tr>
<td>LCL</td>
<td>Lower bound of a 100(1 – $\alpha$)% confidence interval for an individual prediction. This includes the variance of the error and the variance of the parameter estimates.</td>
</tr>
<tr>
<td>LCLM</td>
<td>Lower bound of a 100(1 – $\alpha$)% confidence interval for the expected value (mean) of the dependent variable</td>
</tr>
<tr>
<td>LIKEDIST</td>
<td>Likelihood displacement, which measures the change in the error sum of squares when the current observation is deleted</td>
</tr>
<tr>
<td>PRESS</td>
<td>$i$th residual divided by $(1 – h)$, where $h$ is the leverage and where the model has been refit without the $i$th observation</td>
</tr>
</tbody>
</table>
Table 14.7  continued

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>RSTUDENT</td>
<td>A studentized residual with the current observation deleted</td>
</tr>
<tr>
<td>STDI</td>
<td>Standard error of the individual predicted value</td>
</tr>
<tr>
<td>STDP</td>
<td>Standard error of the mean predicted value</td>
</tr>
<tr>
<td>STDR</td>
<td>Standard error of the residual</td>
</tr>
<tr>
<td>STUDENT</td>
<td>Studentized residuals, which are the residuals divided by their standard errors</td>
</tr>
<tr>
<td>UCL</td>
<td>Upper bound of a $100(1 - \alpha)%$ confidence interval for an individual prediction</td>
</tr>
<tr>
<td>UCLM</td>
<td>Upper bound of a $100(1 - \alpha)%$ confidence interval for the expected value (mean) of the dependent variable</td>
</tr>
</tbody>
</table>

**PARTITION Statement**

The `PARTITION` statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following `partition-options`:

- **FRACTION**
  
  randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the `TEST=` and `VALIDATE=` suboptions. If you specify both the `TEST=` and `VALIDATE=` suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The `SEED=` option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify `SEED=number` or if `number` is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

- **ROLE**
  
  names the `variable` in the input data table whose values are used to assign roles to each observation. This `variable` cannot also appear as an analysis variable in other statements or options. The `TEST=`, `TRAIN=`, and `VALIDATE=` suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the `TRAIN=` suboption, then all observations whose role is not determined by the `TEST=` or `VALIDATE=` suboption are assigned to the training role.
Chapter 14: The REGSELECT Procedure

SELECTION Statement

**SELECTION <METHOD=**method**<(method-options)>** **>><options>** **;**

The SELECTION statement performs model selection by examining whether effects should be added to or removed from the model according to rules that are defined by model selection methods. The statement is fully documented in the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

The REGSELECT procedure supports the following values of the METHOD= option in the SELECTION statement:

- **BACKWARD** specifies the backward elimination method, which starts with all effects in the model and deletes effects.
- **FORWARD** specifies the forward selection method, which starts with no effects in the model and adds effects.
- **FORWARDSWAP** specifies forward-swap selection, which is an extension of the forward selection method. Before any addition step, PROC REGSELECT makes all pairwise swaps of one effect in the model and one effect out of the current model that improve the selection criterion. When the selection criterion is R square, this method is the same as the MAXR method in the REG procedure in SAS/STAT software.
- **LAR** specifies the least angle regression method. Like forward selection, this method starts with no effects in the model and adds effects. The parameter estimates at any step are “shrunk” when compared to the corresponding least squares estimates. If the model contains classification variables, then these classification variables are split. For more information about split classification variables, see Classification Variables and the SPLIT Option.
- **LASSO** specifies the LASSO method, which adds and deletes parameters based on a version of ordinary least squares in which the sum of the absolute regression coefficients is constrained. If the model contains classification variables, then these classification variables are split. For more information about split classification variables, see Classification Variables and the SPLIT Option.
- **NONE** specifies no model selection.
- **STEPWISE** specifies the stepwise regression method, which is similar to the forward selection method except that effects already in the model do not necessarily stay there.

By default, **METHOD=STEPWISE**.

The **DETAILS=ALL** and **DETAILS=STEPS** options produce the “ANOVA,” “Fit Statistics,” and “Parameter Estimates” tables, which provide information about the model that is selected at each step of the selection process.

If you specify the **PLOTS=CRITERIA** or **PLOTS=ALL** option, then a plot of the fit criteria by the selection step is created. The default fit criteria that are shown in this plot are the ADJRSQ, AIC, AICC, ASE, and SBC statistics. If you also specify a **PARTITION** statement, then the ASE statistics for all roles that are defined in the **PARTITION** statement are included. If you use the CP or PRESS statistic as the **SELECT=**, **STOP=**, or **CHOOSE=** criterion in the **SELECTION** statement, then these statistics are also added to the criterion panel.
If you specify the PLOTS=FITBYROLE or PLOTS=ALL option and a PARTITION statement, then a plot of
the ASE by the selection step for each role is created.

**WEIGHT Statement**

```
WEIGHT variable ;
```

The `variable` in the `WEIGHT` statement is used as a weight to perform a weighted analysis of the data.
Observations that have nonpositive or missing weights are not included in the analysis. If a `WEIGHT`
statement is not included, all observations that are used in the analysis are assigned a weight of 1.

---

**Details: REGSELECT Procedure**

---

**Criteria Used in Model Selection**

The REGSELECT procedure supports a variety of fit statistics that you can specify as criteria for the
`CHOOSE=`, `SELECT=`, and `STOP=` options in the `SELECTION` statement. The following statistics are
available:

- **ADJRSQ**: Adjusted R-square statistic (Darlington 1968; Judge et al. 1985)
- **AIC**: Akaike’s information criterion (Akaike 1969; Judge et al. 1985)
- **AICC**: Corrected Akaike’s information criterion (Hurvich and Tsai 1989)
- **BIC | SBC**: Schwarz Bayesian information criterion (Schwarz 1978; Judge et al. 1985)
- **CP**: Mallows’ $C_p$ statistic (Mallows 1973; Hocking 1976)
- **PRESS**: Predicted residual sum of squares statistic
- **RSQUARE**: R-square statistic (Darlington 1968; Judge et al. 1985)
- **SL**: Significance used to assess the contribution of an effect to the fit when it is added to or
  removed from a model
- **VALIDATE**: Average square error over the validation data

When you use SL as a criterion for effect selection, the definition depends on whether an effect is being
considered as a drop candidate or an add candidate. Assume that the current model has $p$ parameters,
excluding the intercept. If you denote its residual sum of squares by $\text{RSS}_p$, add an effect with $k$
degrees of freedom, and denote the residual sum of squares of the resulting model by $\text{RSS}_{p+k}$, then the $F$
statistic for entry with $k$ numerator degrees of freedom and $n - (p + k) - 1$ denominator degrees of freedom is given by

$$
F = \frac{\text{RSS}_p - \text{RSS}_{p+k}}{\text{RSS}_{p+k}/(n - (p + k) - 1)}
$$

where $n$ is number of observations used in the analysis. The significance level for adding an effect is the
$p$-value of this $F$ statistic, and the effect is deemed significant if it is smaller than the SLENTRY limit. (For
more information about the SLENTRY= option, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”) Among several such add candidates, the effect with the smallest \( p \)-value (most significant) is deemed best.

If you drop an effect that has \( k \) degrees of freedom and denote the residual sum of squares of the resulting model by \( \text{RSS}_{p-k} \), then the \( F \) statistic for removal with \( k \) numerator degrees of freedom and \( n - p - k \) denominator degrees of freedom is given by

\[
F = \frac{(\text{RSS}_{p-k} - \text{RSS}_p)/k}{\text{RSS}_p/(n - p - k)}
\]

where \( n \) is number of observations used in the analysis. The significance level for removal of an effect is the \( p \)-value of this \( F \) statistic, and the effect is deemed not significant if this \( p \)-value is larger than the SLSTAY limit. (For more information about the SLSTAY= option, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”) Among several such removal candidates, the effect with the largest \( p \)-value (least significant) is deemed the best removal candidate.

It is known that the “F-to-enter” and “F-to-delete” statistics do not follow an \( F \) distribution (Draper, Guttman, and Kanemasu 1971). Hence the SLENTRY and SLSTAY values cannot reliably be viewed as probabilities. One way to address this difficulty is to replace hypothesis testing as a means of selecting a model with information criteria or out-of-sample prediction criteria. Although Harrell (2001) points out that information criteria were developed for comparing only prespecified models, Burnham and Anderson (2002) note that AIC criteria have routinely been used for several decades to perform model selection in time series analysis.

Table 14.8 provides formulas and definitions for these fit statistics.

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Definition or Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>( n )</td>
<td>Number of observations</td>
</tr>
<tr>
<td>( p )</td>
<td>Number of parameters, including the intercept</td>
</tr>
<tr>
<td>( \hat{\sigma}^2 )</td>
<td>Estimate of pure error variance from fitting the full model</td>
</tr>
<tr>
<td>SST</td>
<td>Total sum of squares corrected for the mean for the dependent variable</td>
</tr>
<tr>
<td>SSE</td>
<td>Error sum of squares</td>
</tr>
<tr>
<td>ASE</td>
<td>( \frac{\text{SSE}}{n} )</td>
</tr>
<tr>
<td>MSE</td>
<td>( \frac{\text{SSE}}{n - p} )</td>
</tr>
<tr>
<td>( R^2 )</td>
<td>( 1 - \frac{\text{SSE}}{\text{SST}} )</td>
</tr>
<tr>
<td>ADJRSQ</td>
<td>( 1 - \frac{n - p}{(n - 1)(1 - R^2)} )</td>
</tr>
<tr>
<td>AIC</td>
<td>( n \ln \left( \frac{\text{SSE}}{n} \right) + 2p )</td>
</tr>
<tr>
<td>AICC</td>
<td>( 1 + \ln \left( \frac{\text{SSE}}{n} \right) + \frac{2(p + 1)}{n - p - 2} )</td>
</tr>
<tr>
<td>CP ( (C_p) )</td>
<td>( \frac{\text{SSE}}{\hat{\sigma}^2} + 2p - n )</td>
</tr>
</tbody>
</table>
Diagnostic Statistics

This section gathers the formulas for the statistics available in the OUTPUT statement. All the statistics available in the OUTPUT statement are conditional on the selected model and do not take into account the variability introduced by doing model selection.

The model to be fit is $Y = X\beta + \epsilon$, and the parameter estimate is denoted by $b = (X'X)^{-1}X'Y$. The subscript $i$ denotes values for the $i$th observation, and the parenthetical subscript $(i)$ means that the statistic is computed by using all observations except the $i$th observation.

The ALPHA= option in the PROC REGSELECT statement is used to set the $\alpha$ value for the confidence limit statistics.

Table 14.9 contains the diagnostic statistics and their formulas. Each statistic is computed for each observation.

### Table 14.8  continued

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Definition or Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRESS</td>
<td>$\sum_{i=1}^{n} \frac{r_i^2}{(1 - h_i)^2}$ where $r_i =$ residual at observation $i$ and $h_i =$ leverage of observation $i = x_i(X'X)^{-1}x'_i$</td>
</tr>
<tr>
<td>RMSE</td>
<td>$\sqrt{MSE}$</td>
</tr>
<tr>
<td>SBC</td>
<td>$n \ln \left( \frac{SSE}{n} \right) + p \ln(n)$</td>
</tr>
</tbody>
</table>

### Table 14.9  Formulas and Definitions for Diagnostic Statistics

<table>
<thead>
<tr>
<th>MODEL Option or Statistic</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRED ($\hat{Y}_i$)</td>
<td>$X_i b$</td>
</tr>
<tr>
<td>RES ($r_i$)</td>
<td>$Y_i - \hat{Y}_i$</td>
</tr>
<tr>
<td>H ($h_i$)</td>
<td>$x_i(X'X)^{-1}x'_i$</td>
</tr>
<tr>
<td>STDP</td>
<td>$\sqrt{h_i\hat{\sigma}^2}$</td>
</tr>
<tr>
<td>STDI</td>
<td>$\sqrt{(1 + h_i)\hat{\sigma}^2}$</td>
</tr>
<tr>
<td>STDR</td>
<td>$\sqrt{(1 - h_i)\hat{\sigma}^2}$</td>
</tr>
<tr>
<td>LCL</td>
<td>$\hat{Y}<em>i - t</em>{(\alpha/2)}STDI$</td>
</tr>
<tr>
<td>LCLM</td>
<td>$\hat{Y}<em>i - t</em>{(\alpha/2)}STDP$</td>
</tr>
<tr>
<td>UCL</td>
<td>$\hat{Y}<em>i + t</em>{(\alpha/2)}STDI$</td>
</tr>
<tr>
<td>UCLM</td>
<td>$\hat{Y}<em>i + t</em>{(\alpha/2)}STDP$</td>
</tr>
<tr>
<td>STUDENT</td>
<td>$\frac{STDR}{r_i}$</td>
</tr>
<tr>
<td>RSTUDENT</td>
<td>$\frac{STDR}{r_i} \sqrt{1 - h_i}$</td>
</tr>
</tbody>
</table>
### Table 14.9 continued

<table>
<thead>
<tr>
<th>MODEL Option or Statistic</th>
<th>Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>COOKD</td>
<td>$\frac{1}{p} \text{STUDENT}^2 \frac{\text{STDP}^2}{\text{STDR}^2}$</td>
</tr>
<tr>
<td>COVRATIO</td>
<td>$\frac{\det(\hat{\theta}(i)) (\mathbf{x}^T(i) \mathbf{x}(i))^{-1}}{\text{det}(\hat{\theta}^2(\mathbf{X} \mathbf{X})^{-1})}$</td>
</tr>
<tr>
<td>DFFITS</td>
<td>$\left(\frac{(\hat{\theta}(i) \sqrt{h_i})}{t_i}\right)$</td>
</tr>
<tr>
<td>PRESS(pred,i)</td>
<td>$\frac{1 - h_i}{1}$</td>
</tr>
</tbody>
</table>

### Classification Variables and the SPLIT Option

PROC REGSELECT supports the ability to split classification variables when you are doing model selection. You use the SPLIT option in the CLASS statement to specify that the columns of the design matrix that correspond to effects that contain a split classification variable can enter or leave a model independently of the other design columns of that effect. The following statements illustrate the use of the SPLIT option:

```plaintext
data mycas.splitExample;
  length c2 $6;
  drop i;
  do i=1 to 1000;
    c1 = 1 + mod(i,6);
    if i < 200 then c2 = 'low';
    else if i < 500 then c2 = 'medium';
    else c2 = 'high';
    x1 = ranuni(1);
    x2 = ranuni(1);
    y = x1+3*(c2 = 'low') + 10*(c1=3) +5*(c1=5) + rannor(1);
    output;
  end;
run;

proc regselect data=mycas.splitExample;
  class c1(split) c2(order=freq);
  model y = c1 c2 x1 x2;
  selection method=forward;
run;
```

The “Class Level Information” table shown in Figure 14.11 is produced by default whenever you specify a CLASS statement.
Figure 14.11 Class Levels

The REGSELECT Procedure

<table>
<thead>
<tr>
<th>Class Level Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Class Levels</td>
</tr>
<tr>
<td>c1</td>
</tr>
<tr>
<td>c2</td>
</tr>
</tbody>
</table>

The SPLIT option has been specified for the classification variable c1. This permits the parameters associated with the effect c1 to enter or leave the model individually. The “Parameter Estimates” table in Figure 14.12 shows that for this example the parameters that correspond only to levels 3 and 5 of c1 are in the selected model.

Figure 14.12 Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter Estimates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parameter</td>
</tr>
<tr>
<td>Intercept</td>
</tr>
<tr>
<td>c1_3</td>
</tr>
<tr>
<td>c1_5</td>
</tr>
<tr>
<td>c2 high</td>
</tr>
<tr>
<td>c2 medium</td>
</tr>
<tr>
<td>c2 low</td>
</tr>
<tr>
<td>x1</td>
</tr>
</tbody>
</table>

Using Validation and Test Data

When you have sufficient data, you can subdivide your data into three parts called the training, validation, and test data. The selection process fits models to the training data and uses the validation data to find the prediction errors for the models that are obtained in this way. This prediction error on the validation data can be used to decide when to terminate the selection process or to decide what effects to include as the selection process proceeds. Finally, after a selected model has been obtained, the test data can be used to assess how the selected model generalizes on data that played no role in selecting the model.

In some cases you might want to use only training and test data. For example, you might want to use an information criterion to decide what effects to include and when to terminate the selection process. In this case no validation data are required, but test data can still help you assess the predictive performance of the selected model. In other cases you might decide to use validation data during the selection process but forgo assessing the selected model on test data. Hastie, Tibshirani, and Friedman (2001) note that it is difficult to give a general rule for how many observations you should assign to each role. They state that a typical split might be 50% for training and 25% each for validation and testing.

You use a PARTITION statement to logically subdivide the DATA= data table into separate roles. You can name the fractions of the data that you want to reserve as test data and validation data. For example, the following statements randomly subdivide the inData data table, reserving 50% for training and 25% each for validation and testing:
In some cases you might need to exercise more control over the partitioning of the input data table. You can do this by naming both a variable in the input data table and a formatted value of that variable that correspond to each role. For example, the following statements assign roles to the observations in the inData data table based on the value of the variable group in that data table. Observations in which the value of group is “group 1” are assigned to testing, and those whose value is “group 2” are assigned to training. All other observations are ignored.

```r
proc regselect data=mycas.inData;
    partition roleVar=group(test='group 1' train='group 2')
    ...
run;
```

After you reserve observations for training, validation, and testing, a model fit of the training data is scored on the validation and test data, and the average squared error (ASE) is computed separately for each of these subsets. The ASE for each data role is the error sum of squares for observations in that role divided by the number of observations in that role.

**Using the Validation ASE as the STOP= Criterion**

If you have provided observations for validation, then you can specify STOP=VALIDATE as a suboption of the METHOD= option in the SELECTION statement. At step \( k \) of the selection process, the best candidate effect to enter or leave the current model is determined. Here, “best candidate” means the effect that gives the best value of the SELECT= criterion; this criterion does not need to be based on the validation data. The validation ASE for the model with this candidate effect added or removed is computed. If this validation ASE is greater than the validation ASE for the model at step \( k \), then the selection process terminates at step \( k \).

**Using the Validation ASE as the CHOOSE= Criterion**

When you specify the CHOOSE=VALIDATE suboption of the METHOD= option in the SELECTION statement, the validation ASE is computed for the models at each step of the selection process. The smallest model at any step that yields the smallest validation ASE is selected.

**Computational Method**

**Multithreading**

The REGSELECT procedure allocates data to different threads and calculates crossproduct matrices by accumulating the contributions from all threads. PROC REGSELECT also uses multiple threads to compute matrix inverses and select candidates during model selection. For more information about how PROC REGSELECT uses threads, see the section “Multithreading” on page 79 in Chapter 2, “Shared Concepts.”
Joint Tests and Type 3 Tests

Linear hypotheses for $\beta$ are expressed in matrix form as

$$H_0: L\beta = c$$

where $L$ is a matrix of coefficients for the linear hypotheses and $c$ is a vector of constants. The vector of regression coefficients $\hat{\beta}$ includes slope parameters and intercept parameters. The $F$ statistic for testing $H_0$ is computed as

$$F = (L\hat{\beta} - c)'[L\hat{\Sigma}(\hat{\beta})L']^{-1}(L\hat{\beta} - c)/r$$

where $\hat{\Sigma}(\hat{\beta}) = \hat{\sigma}^2(X'WX)^{-1}$ is the estimated covariance matrix of $\hat{\beta}$, with $\hat{\sigma}^2$ being the weighted residual sum of squares divided by the residual degrees of freedom $d$. Under $H_0$, $F$ has an asymptotic $F$ distribution with $r$ and $d$ degrees of freedom, where $r$ is the rank of $L$.

For models that use less-than-full-rank parameterization (as specified by the PARAM=GLM option in the CLASS statement), a Type 3 test of an effect of interest (main effect or interaction) is a test of the Type III estimable functions that are defined for that effect. When the model contains no missing cells, the Type 3 test of a main effect is equivalent to testing the hypothesis of equal marginal means. For more information about Type III estimable functions, see the chapter “The GLM Procedure” and the section “The Four Types of Estimable Functions” in SAS/STAT User’s Guide. Also see Littell, Freund, and Spector (1991).

For models that use full-rank parameterization, all parameters are estimable when there are no missing cells, so it is unnecessary to define estimable functions. The standard test of an effect of interest in this case is the joint test that the values of the parameters associated with that effect are 0. For a model that uses effects parameterization (as specified by the PARAM=EFFECT option in the CLASS statement), the joint test for a main effect is equivalent to testing the equality of marginal means. For a model that uses reference parameterization (as specified by the PARAM=REF option in the CLASS statement), the joint test is equivalent to testing the equality of cell means at the reference level of the other model effects. For more information about the coding scheme and the associated interpretation of results, see Muller and Fetterman (2002, Chapter 14).

If there is no interaction term, the Type 3 test of an effect for a model that uses GLM parameterization is the same as the joint test of the effect for the model that uses full-rank parameterization. In this situation, the joint test is also called the Type 3 test. For a model that contains an interaction term and no missing cells, the Type 3 test of a component main effect under GLM parameterization is the same as the joint test of the component main effect under effect parameterization. Both test the equality of cell means. But this Type 3 test differs from the joint test under reference parameterization, which tests the equality of cell means at the reference level of the other component main effect. If some cells are missing, you can obtain meaningful tests only by testing a Type III estimation function, so in this case you should use GLM parameterization.

The results of a Type 3 test or a joint test do not depend on the order in which you specify the terms in the MODEL statement.

Displayed Output

The following sections describe the output produced by PROC REGSELECT. The output is organized into various tables, which are discussed in their order of appearance.
Selection Information

When you specify the `SELECTION` statement, the REGSELECT procedure produces by default a series of tables that display information about the model selection. The “Selection Information” table informs you about the model selection method; select, stop, and choose criteria; and other parameters that govern the selection. You can suppress this table by specifying `DETAILS=NONE` in the `SELECTION` statement.

Number of Observations

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis. If you specify a `FREQ` statement, this table also displays the sum of frequencies read and used. If you use a `PARTITION` statement, the table also displays the number of observations used for each data role.

Class Level Information

The “Class Level Information” table lists the levels of every variable that you specify in the `CLASS` statement. You should check this information to make sure that the data are correct. You can adjust the order of the `CLASS` variable levels by specifying the `ORDER=` option in the `CLASS` statement. You can suppress the “Class Level Information” table completely or partially by specifying the `NOCLPRINT=` option in the `PROC REGSELECT` statement.

If the classification variables use a nonsingular parameterization, the “Class Level Information” table also displays the reference value for each variable.

Dimensions

The “Dimensions” table displays the number of effects and the number of parameters from which the selected model is chosen. If you use split classification variables, then this table also displays the number of effects after splitting is taken into account.

Entry and Removal Candidates

When you specify the `DETAILS=ALL` or `DETAILS=STEPS` option in the `SELECTION` statement, the REGSELECT procedure produces “Entry Candidates” and “Removal Candidates” tables that display the effect names and values of the criterion used to select entering or departing effects at each step of the selection process. The effects are displayed in sorted order from best to worst of the selection criterion.

Selection Summary

When you specify the `SELECTION` statement, the REGSELECT procedure produces the “Selection Summary” table, which displays information about the sequence of steps of the selection process. For each step, the effect that was entered or dropped is displayed along with the statistics used to select the effect, stop the selection, and choose the selected model. For all criteria that you can use for model selection, the steps at which the optimal values of these criteria occur are also indicated.

You can suppress the display of the “Selection Summary” table by specifying `DETAILS=NONE` in the `SELECTION` statement.
Stop Reason

The “Stop Reason” table displays the reason why the selection stopped. To facilitate programmatic use of this table, an integer code is assigned to each reason and is included if you use an ODS OUTPUT statement or a DISPLAYOUT statement to output this table. The reasons and their associated codes follow:

<table>
<thead>
<tr>
<th>Code</th>
<th>Stop Reason</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>All eligible effects are in the model.</td>
</tr>
<tr>
<td>2</td>
<td>All eligible effects have been removed.</td>
</tr>
<tr>
<td>3</td>
<td>Specified maximum number of steps done.</td>
</tr>
<tr>
<td>4</td>
<td>The model contains the specified maximum number of effects.</td>
</tr>
<tr>
<td>5</td>
<td>The model contains the specified minimum number of effects (for backward selection).</td>
</tr>
<tr>
<td>6</td>
<td>The stopping criterion is at a local optimum.</td>
</tr>
<tr>
<td>7</td>
<td>No suitable add or drop candidate could be found.</td>
</tr>
<tr>
<td>8</td>
<td>Adding or dropping any effect does not improve the selection criterion.</td>
</tr>
<tr>
<td>9</td>
<td>No candidate meets the appropriate SLE or SLS significance level.</td>
</tr>
<tr>
<td>10</td>
<td>Stepwise selection is cycling.</td>
</tr>
<tr>
<td>11</td>
<td>The model is an exact fit.</td>
</tr>
<tr>
<td>12</td>
<td>Dropping an effect would result in an empty model.</td>
</tr>
</tbody>
</table>

You can suppress the display of the “Stop Reason” table by specifying DETAILS=NONE in the SELECTION statement.

Selection Reason

When you specify the SELECTION statement, the REGSELECT procedure produces a simple table that explains why the final model was selected.

You can suppress the display of the “Selection Reason” table by specifying DETAILS=NONE in the SELECTION statement.

Selected Effects

When you specify the SELECTION statement, the REGSELECT procedure produces a simple table that lists which effects were selected for the final model.

ANOVA

The “ANOVA” table displays an analysis of variance for the selected model. This table includes the following:

- the Source of the variation, Model for the fitted regression, Error for the residual error, and C Total for the total variation after correcting for the mean. The Uncorrected Total Variation is produced when you specify the NOINT option.
- the degrees of freedom (DF) associated with the source
- the Sum of Squares for the term
• the Mean Square, which is the sum of squares divided by the degrees of freedom

• the *F* Value for testing the hypothesis that all parameters are 0 except for the intercept. This is formed by dividing the mean square for Model by the mean square for Error.

• the Prob>*F*, which is the probability of getting a greater *F* statistic than that observed if the hypothesis is true. When you do model selection, these *p*-values are usually liberal because they are not adjusted for the fact that the terms in the model have been selected.

You can request an “ANOVA” table for the model at each step of the selection process by specifying the DETAILS= option in the SELECTION statement.

**Fit Statistics**

The “Fit Statistics” table displays fit statistics for the selected model. The statistics include the following:

• Root MSE, an estimate of the standard deviation of the error term. It is calculated as the square root of the mean square error.

• R-square, a measure between 0 and 1 that indicates the portion of the (corrected) total variation attributed to the fit rather than left to residual error. It is calculated as SS(Model) divided by SS(Total) and is also called the *coefficient of determination*. It is the square of the multiple correlation—in other words, the square of the correlation between the dependent variable and the predicted values.

• Adj R-Sq, the adjusted R-square, which is a version of R-square that has been adjusted for degrees of freedom. It is calculated as

$$\hat{R}^2 = 1 - \frac{(n - i)(1 - R^2)}{n - p}$$

where *i* is equal to 1 if there is an intercept and 0 otherwise, *n* is the number of observations used to fit the model, and *p* is the number of parameters in the model.

• the fit criteria AIC, AICC, BIC, CP, and PRESS if they are used in the selection process. See Table 14.8 for the formulas to evaluate these criteria.

• the average square errors (ASE) on the training, validation, and test data

You can request a “Fit Statistics” table for the model at each step of the selection process by specifying the DETAILS= option in the SELECTION statement.

**Parameter Estimates**

The “Parameter Estimates” table displays the parameters in the selected model and their estimates. The information displayed for each parameter in the selected model includes the following:

• the parameter label that includes the effect name and level information for effects that contain classification variables
• the degrees of freedom (DF) for the parameter. There is one degree of freedom unless the model is not full rank.

• the parameter estimate

• the standard error, which is the estimate of the standard deviation of the parameter estimate

• t Value, the t test that the parameter is 0. This is computed as the parameter estimate divided by the standard error.

• the Pr > |t|, the probability that a t statistic would obtain a greater absolute value than that observed given that the true parameter is 0. This is the two-tailed significance probability.

When you do model selection, these p-values are usually liberal because they are not adjusted for the fact that the terms in the model have been selected.

You can request a “Parameter Estimates” table for the model at each step of the selection process by specifying the DETAILS= option in the SELECTION statement.

Model Analysis of Variance (Type III)

When you specify the SS3 option in the MODEL statement, the REGSELECT procedure produces the “Model Analysis of Variance (Type III)” table. This table displays tests that all parameters for a particular effect are equal to zero. These tests are computed by using a Type III sum of squares, which yields a balanced test of each effect, adjusted for every other effect. For more information, see the section “Joint Tests and Type 3 Tests” on page 755.

Timing

The “Timing” table displays the amount of time (in seconds) and the percentage of the time that PROC REGSELECT required to perform different tasks in the analysis.

OutputCASTables

When you specify an OUTPUT statement or a DISPLAYOUT statement to create output tables on your CAS server, the “Output CAS Tables” table displays the names, the numbers of rows and columns, and the CAS libraries in which the table is created for every output table that you requested.

ODS Table Names

Each table that the REGSELECT procedure creates has a name associated with it. You must use this name to refer to the table when you use ODS statements. These names are listed in Table 14.10.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ANOVA</td>
<td>Selected model ANOVA table</td>
<td>Default output</td>
</tr>
<tr>
<td>Candidates</td>
<td>Swap candidates at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
</tbody>
</table>
Table 14.10  continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Required Statement / Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ClassInfo</td>
<td>Level information from the CLASS statement</td>
<td>CLASS</td>
</tr>
<tr>
<td>Dimensions</td>
<td>Model dimensions</td>
<td>Default output</td>
</tr>
<tr>
<td>EntryCandidates</td>
<td>Candidates for entry at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
<tr>
<td>FitStatistics</td>
<td>Fit statistics</td>
<td>Default output</td>
</tr>
<tr>
<td>ModelAnova</td>
<td>Model analysis of variance (Type III)</td>
<td>MODEL SS3</td>
</tr>
<tr>
<td>NObs</td>
<td>Number of observations read and used</td>
<td>Default output</td>
</tr>
<tr>
<td>OutputCASTables</td>
<td>Library and name of the output data table, and number of rows and columns in the table</td>
<td>OUTPUT</td>
</tr>
<tr>
<td>ParameterEstimates</td>
<td>Solutions for the parameter estimates associated with effects in the MODEL statement</td>
<td>Default output</td>
</tr>
<tr>
<td>RemovalCandidates</td>
<td>Candidates for removal at step</td>
<td>SELECTION DETAILS=ALL</td>
</tr>
<tr>
<td>SelectedEffects</td>
<td>List of selected effects</td>
<td>SELECTION</td>
</tr>
<tr>
<td>SelectionInfo</td>
<td>Information about selection settings</td>
<td>Default output</td>
</tr>
<tr>
<td>SelectionReason</td>
<td>Reason for selecting the final model</td>
<td>SELECTION</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Summary information about the model selection steps</td>
<td>SELECTION</td>
</tr>
<tr>
<td>StopReason</td>
<td>Reason selection was terminated</td>
<td>SELECTION</td>
</tr>
<tr>
<td>Timing</td>
<td>Timing breakdown by task</td>
<td>SELECTION DETAILS</td>
</tr>
</tbody>
</table>

**ODS Graphics**

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in the “Statistical Graphics Using ODS” chapter in *SAS/STAT User’s Guide*.

Before you create graphs, ODS Graphics must be enabled (for example, with the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section “Enabling and Disabling ODS Graphics” in that chapter.

The overall appearance of graphs is controlled by ODS styles. Styles and other aspects of using ODS Graphics are discussed in the section “A Primer on ODS Statistical Graphics” in that chapter.
When ODS Graphics is enabled, the SELECTION statement can produce plots to help evaluate the selection process. For information about these plots, see the section “SELECTION Statement” on page 34 in Chapter 2, “Shared Concepts.”

PROC REGSELECT assigns a name to each graph that it creates using ODS. You can use these names to reference the graphs when using ODS. The names are listed in Table 14.11.

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CoefficientPanel</td>
<td>Coefficients and CHOOSE= criterion by step</td>
<td>COEFFICIENTS</td>
</tr>
<tr>
<td>ChooseCriterionPlot</td>
<td>CHOOSE= criterion by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CoefficientPlot</td>
<td>Coefficients by step</td>
<td>COEFFICIENTS(UNPACK)</td>
</tr>
<tr>
<td>CriterionPanel</td>
<td>Fit criteria by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AdjRSqPlot</td>
<td>Max-rescaled (adjusted) R-square by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICPlot</td>
<td>Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>AICCPlot</td>
<td>Corrected Akaike’s information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>CPPlot</td>
<td>Mallows’ $C_p$ statistic by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>PRESSPlot</td>
<td>PRESS criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>SBCPlot</td>
<td>Schwarz Bayesian information criterion by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TEST_ASEPlot</td>
<td>Average square error on testing data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>TRAIN_ASEPlot</td>
<td>Average square error on training data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>VAL_ASEPlot</td>
<td>Average square error on validation data by step</td>
<td>CRITERIA(UNPACK)</td>
</tr>
<tr>
<td>FitByRolePlot</td>
<td>Progression of average square error by role</td>
<td>FITBYROLE</td>
</tr>
</tbody>
</table>

**Examples: REGSELECT Procedure**

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
Example 14.1: Model Selection with Validation

This example is based on the example “Using Validation and Cross Validation” in the documentation for the GLMSELECT procedure in SAS/STAT software. The current example shows how you can use validation data to monitor and control variable selection. It also demonstrates the use of split classification variables.

The following DATA step produces analysis data that contain a variable that you can use to assign observations to the training, validation, and testing roles. In this case, each role has 5,000 observations.

```sas
data mycas.analysisData;
  drop i j c3Num;
  length c3$ 7;
  array x{20} x1-x20;
  do i=1 to 15000;
    do j=1 to 20;
      x{j} = ranuni(1);
    end;
    c1 = 1 + mod(i,8);
    c2 = ranbin(1,3,.6);
    if i < 50 then do; c3 = 'tiny'; c3Num=1;end;
    else if i < 250 then do; c3 = 'small'; c3Num=1;end;
    else if i < 600 then do; c3 = 'average'; c3Num=2;end;
    else if i < 1200 then do; c3 = 'big'; c3Num=3;end;
    else do; c3 = 'huge'; c3Num=5;end;
    yTrue = 10 + x1 + 2*x5 + 3*x10 + 4*x20 + 3*x1*x7 + 8*x6*x7 + 5*(c1=3)*c3Num + 8*(c1=7);
    error = 5*rannor(1);
    y = yTrue + error;
    if mod(i,3)=1 then Role = 'TRAIN';
    else if mod(i,3)=2 then Role = 'VAL';
    else Role = 'TEST';
    output;
  end;
run;
```

By construction, the true model consists of the main effects \(x1, x5, x10, x20\), and \(c1\) and the interaction effects \(x1\times7, x6\times7\), and \(c1\times c3\). Furthermore, you can see that only levels 3 and 7 of the classification variable \(c1\) are systematically related to the response.

Because the error term for each observation is five times a value drawn from a standard normal distribution, the expected error variance is 25. For the data in each role, you can compute an estimate of this error variance by forming the average square error (ASE) for the observations in the role. Output 14.1.1 shows the ASE for each role that you can compute with the following statements:
Example 14.1: Model Selection with Validation

![Example 14.1: Model Selection with Validation](image)

```
proc summary data=mycas.analysisData;
   class role;
   ways 1;
   var error;
   output out=ASE uss=uss n=n;
data ASE; set ASE;
   OracleASE = uss / n;
   label OracleASE = 'Oracle ASE';
   keep Role OracleASE;
proc print data=ASE label noobs;
run;
```

```
proc print data=ASE label noobs;
run;
```

**Output 14.1.1** Oracle ASE Values by Role

<table>
<thead>
<tr>
<th>Role</th>
<th>ASE</th>
</tr>
</thead>
<tbody>
<tr>
<td>TEST</td>
<td>25.5764</td>
</tr>
<tr>
<td>TRAIN</td>
<td>25.4008</td>
</tr>
<tr>
<td>VAL</td>
<td>25.8993</td>
</tr>
</tbody>
</table>

The ASE values shown Output 14.1.1 are labeled as “Oracle ASE” because you need to know the true underlying model if you want to compute these values from the response and underlying regressors. In a modeling context, a good predictive model produces values that are close to these oracle values. An overfit model produces a smaller ASE for the training data but higher values for the validation and test data. An underfit model exhibits higher values for all data roles.

Suppose you suspect that the dependent variable depends on both main effects and two-way interactions. You can use the following statements to select a model:

```
ods graphics on;

proc regselect data=mycas.analysisData;
   partition roleVar=role(train='TRAIN' validate='VAL' test='TEST');
   class c1 c2 c3;
   model y = c1|c2|c3|x1|x2|x3|x4|x5|x5|x6|x7|x8|x9|x10|x11|x12|x13|x14|x15|x16|x17|x18|x19|x20 @2 /stb;
   selection method = stepwise(select=sl sle=0.1 sls=0.15 choose=validate)
                   hierarchy=single details=steps plots(startstep=5)=all;
run;
```

A PARTITION statement assigns observations to training, validation, and testing roles based on the values of the input variable named role. The SELECTION statement requests stepwise selection based on significance level, where the SLE and SLS values are set to use the defaults of PROC REGSELECT. The CHOOSE=VALIDATE option selects the model that yields the smallest ASE value for the validation data.

The “Number of Observations” table in Output 14.1.2 confirms that there are 5,000 observations for each data role. The “Dimensions” table shows that the selection is from 278 effects with a total of 661 parameters.
Output 14.1.2  Number of Observations, Class Levels, and Dimensions

The REGSELECT Procedure

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
<td>15000</td>
</tr>
<tr>
<td>Number of Observations Used</td>
<td>15000</td>
</tr>
<tr>
<td>Number of Observations Used for Training</td>
<td>5000</td>
</tr>
<tr>
<td>Number of Observations Used for Validation</td>
<td>5000</td>
</tr>
<tr>
<td>Number of Observations Used for Testing</td>
<td>5000</td>
</tr>
</tbody>
</table>

Class Level Information

<table>
<thead>
<tr>
<th>Class</th>
<th>Levels</th>
<th>Values</th>
</tr>
</thead>
<tbody>
<tr>
<td>c1</td>
<td>8 1 2 3 4 5 6 7 8</td>
<td></td>
</tr>
<tr>
<td>c2</td>
<td>4 0 1 2 3</td>
<td></td>
</tr>
<tr>
<td>c3</td>
<td>5 average big huge small tiny</td>
<td></td>
</tr>
</tbody>
</table>

Dimensions

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Effects</td>
<td>278</td>
</tr>
<tr>
<td>Number of Parameters</td>
<td>661</td>
</tr>
</tbody>
</table>

Output 14.1.3 shows the “Selection Summary” table. You see that 18 steps are done, at which point all effects in the model are significant at the SLS value of 0.15 and all the remaining effects if added individually would not be significant at the SLE significance level of 0.1. However, because you specified the CHOOSE=VALIDATE option, the model at step 18 is not used as the selected model. Instead the model at step 10 (where the validation ASE achieves a local minimum value) is selected. The “Stop Reason,” “Selection Reason,” and “Selected Effects” in Output 14.1.4 tables provide this information.
Example 14.1: Model Selection with Validation

Output 14.1.3 Selection Summary

The REGSELECT Procedure

Selection Details

<table>
<thead>
<tr>
<th>Selection Summary</th>
<th>Effect Entered</th>
<th>Number Effects In</th>
<th>Validation ASE</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Step 0 Intercept</td>
<td>1</td>
<td>98.3895</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1 c1</td>
<td>2</td>
<td>34.8572</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>2 x7</td>
<td>3</td>
<td>32.5531</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>3 x6</td>
<td>4</td>
<td>31.0646</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>4 x20</td>
<td>5</td>
<td>29.7078</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>5 x6*x7</td>
<td>6</td>
<td>29.2210</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>6 x10</td>
<td>7</td>
<td>28.6683</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>7 x1</td>
<td>8</td>
<td>28.3250</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>8 x5</td>
<td>9</td>
<td>27.9766</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>9 c3</td>
<td>10</td>
<td>27.8288</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>10 c1*c3</td>
<td>11</td>
<td>25.9701*</td>
<td>&lt;.0001</td>
<td></td>
</tr>
<tr>
<td>11 x10*c1</td>
<td>12</td>
<td>26.0696</td>
<td>0.0109</td>
<td></td>
</tr>
<tr>
<td>12 x4</td>
<td>13</td>
<td>26.1594</td>
<td>0.0128</td>
<td></td>
</tr>
<tr>
<td>13 x4*x10</td>
<td>14</td>
<td>26.1814</td>
<td>0.0035</td>
<td></td>
</tr>
<tr>
<td>14 x20*c1</td>
<td>15</td>
<td>26.3294</td>
<td>0.0156</td>
<td></td>
</tr>
<tr>
<td>15 x1*c3</td>
<td>16</td>
<td>26.3945</td>
<td>0.0244</td>
<td></td>
</tr>
<tr>
<td>16 x1*x7</td>
<td>17</td>
<td>26.3632</td>
<td>0.0270</td>
<td></td>
</tr>
<tr>
<td>17 x7*x10</td>
<td>18</td>
<td>26.4120</td>
<td>0.0313</td>
<td></td>
</tr>
<tr>
<td>18 x1*x20</td>
<td>19</td>
<td>26.4330</td>
<td>0.0871</td>
<td></td>
</tr>
</tbody>
</table>

* Optimal Value Of Criterion

Output 14.1.4 Stopping and Selection Reasons

Selection stopped because all candidates for removal are significant at the 0.15 level and no candidate for entry is significant at the 0.1 level.

The model at step 10 is selected where Validation ASE is 25.9701.

Selected Effects: Intercept c1 c3 c1*c3 x1 x5 x6 x7 x6*x7 x10 x20

You can see that the selected effects include all the main effects in the true model and two of the three true interaction terms. Furthermore, the selected model does not include any variables that are not in the true model. Note that these statements are not true of the larger model at the final step of the selection process.

When you enable ODS Graphics, the PLOTS=ALL option in the SELECTION statement produces plots that illuminate the selection process. The STARTSTEP=5 suboption in the PLOTS= option requests that only steps 5 and beyond be displayed in the plots. This enables you to more easily assess how the fit criteria change near the selected step.

The upper plot in the coefficient panel in Output 14.1.5 shows how the standardized parameter estimates change with the selection step after step 5. The lower plot in the panel shows how the average square error on the validation data, which you specified as the CHOOSE= criterion, changes with the selection step.
The criterion panel in Output 14.1.6 shows how the various fit criteria change as the stepwise selection method proceeds. This plot shows that if you had used the SBC statistic as the CHOOSE= criterion, then the selected model would still be the model at step 10. However, the AIC or AICC statistic continues to decline for all steps of the selection process. If you had used either of these criteria as the CHOOSE= criterion, then the final model at step 18 would have been selected.
Output 14.1.6 Criterion Panel

Output 14.1.7 shows how the average square error compares for the training, test, and validation data. You see that the average square error on both the test and validation data starts to increase beyond the selected step. This indicates that the selected model does not overfit the training data.
Output 14.1.8 shows the fit statistics of the selected model. You can see that the ASE values for the training, validation, and test data are all similar, indicating a reasonable predictive model. In this case, where the true model is known, you can see that all three ASE values are close to the oracle values for the true model, as shown in Output 14.1.1.

Output 14.1.8 Fit Statistics for the Selected Model

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Root MSE</td>
<td>5.03976</td>
</tr>
<tr>
<td>R-Square</td>
<td>0.74483</td>
</tr>
<tr>
<td>Adj R-Sq</td>
<td>0.74246</td>
</tr>
<tr>
<td>AIC</td>
<td>21222</td>
</tr>
<tr>
<td>AICC</td>
<td>21223</td>
</tr>
<tr>
<td>SBC</td>
<td>16527</td>
</tr>
<tr>
<td>ASE (Train)</td>
<td>25.16041</td>
</tr>
<tr>
<td>ASE (Validate)</td>
<td>25.97010</td>
</tr>
<tr>
<td>ASE (Test)</td>
<td>25.83436</td>
</tr>
</tbody>
</table>

Because you specified the DETAILS=STEPS option in the SELECTION statement, you can see the fit statistics for the model at each step of the selection process. Output 14.1.9 shows these fit statistics for the
Example 14.1: Model Selection with Validation

The final model at step 18. You see that for this model, the ASE value for the training data is smaller than the ASE values for the validation and test data. This indicates an overfit model that might not generalize well to new data. You see that the ASE values for the validation and test data are now worse in comparison to the oracle values than the values for the selected model at step 10.

**Output 14.1.9** Fit Statistics for the Model at Step 18

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Root MSE</td>
<td>5.01386</td>
</tr>
<tr>
<td>R-Square</td>
<td>0.74862</td>
</tr>
<tr>
<td>Adj R-Sq</td>
<td>0.74510</td>
</tr>
<tr>
<td>AIC</td>
<td>21194</td>
</tr>
<tr>
<td>AICC</td>
<td>21196</td>
</tr>
<tr>
<td>SBC</td>
<td>16648</td>
</tr>
<tr>
<td>ASE (Train)</td>
<td>24.78688</td>
</tr>
<tr>
<td>ASE (Validate)</td>
<td>26.43304</td>
</tr>
<tr>
<td>ASE (Test)</td>
<td>26.07078</td>
</tr>
</tbody>
</table>

Output 14.1.10 shows part of the “Parameter Estimates” table for the selected model at step 10 that includes the estimates for the main effect c1. Because you specified the STB option in the MODEL statement, this table includes standardized estimates.

**Output 14.1.10** Part of the Parameter Estimates Table for the Selected Model

| Parameter | DF | Estimate | Standardized Estimate | Standard Error | t Value | Pr > |t| |
|-----------|----|----------|-----------------------|----------------|---------|------|--------|
| Intercept | 1  | 8.558686 | 0                     | 3.581926       | 2.39    | 0.0169|
| c1 1      | 1  | 13.177235 | 0.436872              | 5.043039       | 2.61    | 0.0090|
| c1 2      | 1  | -2.800921 | -0.093285             | 4.602421       | -0.61   | 0.5428|
| c1 3      | 1  | 9.669426  | 0.322709              | 5.043363       | 1.92    | 0.0548|
| c1 4      | 1  | 8.182340  | 0.272515              | 5.042136       | 1.62    | 0.1047|
| c1 5      | 1  | 3.097216  | 0.103154              | 5.041119       | 0.61    | 0.5390|
| c1 6      | 1  | 0.543642  | 0.018106              | 5.043466       | 0.11    | 0.9142|
| c1 7      | 1  | 11.857267 | 0.394910              | 5.042602       | 2.35    | 0.0187|
| c1 8      | 0  | 0        | 0                     | 0              | .       | .     |

The magnitudes of the standardized estimates and the t statistics of the parameters of the effect c1 reveal that only levels 3 and 7 of this effect contribute appreciably to the model. This suggests that you might obtain a more parsimonious model with similar or better predictive power if parameters that correspond to the levels of c1 can enter or leave the model independently. You request this by specifying the SPLIT option in the CLASS statement, as shown in the following statements:

```
proc regselect data=mycas.analysisData;
    partition roleVar=role(train='TRAIN' validate='VAL' test='TEST');
    class c1(split) c2 c3;
    model y = c1|c2|c3|x1|x2|x3|x4|x5|x6|x7|x8|x9|x10
            |x11|x12|x13|x14|x15|x16|x17|x18|x19|x20 /stb;
    selection method = stepwise(select=sl sle=0.1 sls=0.15 choose=validate) hierarchy=single details=steps;
run;
```
Output 14.1.11 shows the "Dimensions" table. You can see that because the columns in the design matrix that correspond to the levels of c1 are treated as separate effects, the selection is now from 439 effects, even though the number of parameters is unchanged.

**Output 14.1.11** Dimensions with c1 Split

<table>
<thead>
<tr>
<th>Dimensions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Effects</td>
</tr>
<tr>
<td>Number of Parameters</td>
</tr>
</tbody>
</table>

Output 14.1.12 shows the selected effects. You can see that, as anticipated, the selected model now depends on only levels 3 and 7 of c1.

**Output 14.1.12** Selected Effects with c1 Split

Selected Effects: intercept c1_3 c1_7 c1 c1_3*c3 x1 x5 x6 x7 x6*x7 x10 x20

Finally, the fit statistics for the selected model are shown in Output 14.1.13.

**Output 14.1.13** Fit Statistics for the Selected Model with c1 Split

<table>
<thead>
<tr>
<th>Statistics</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Root MSE</td>
<td>5.04060</td>
</tr>
<tr>
<td>R-Square</td>
<td>0.74325</td>
</tr>
<tr>
<td>Adj R-Sq</td>
<td>0.74238</td>
</tr>
<tr>
<td>AIC</td>
<td>21195</td>
</tr>
<tr>
<td>AICC</td>
<td>21195</td>
</tr>
<tr>
<td>SBC</td>
<td>16311</td>
</tr>
<tr>
<td>ASE (Train)</td>
<td>25.31622</td>
</tr>
<tr>
<td>ASE (Validate)</td>
<td>25.98055</td>
</tr>
<tr>
<td>ASE (Test)</td>
<td>25.76059</td>
</tr>
</tbody>
</table>

If you compare the ASE values for this model in Output 14.1.13 with the oracle values in Output 14.1.1 and the values for the model without splitting c1 in Output 14.1.8, you see that this more parsimonious model produces the best predictive performance for the test data of all the models considered in this example.

**References**


## Chapter 15
### The SPC Procedure

<table>
<thead>
<tr>
<th>Contents</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overview: SPC Procedure</td>
<td>774</td>
</tr>
<tr>
<td>Uses of Shewhart Charts</td>
<td>774</td>
</tr>
<tr>
<td>Characteristics of Shewhart Charts</td>
<td>775</td>
</tr>
<tr>
<td>Classification of Shewhart Charts</td>
<td>777</td>
</tr>
<tr>
<td>PROC SPC Compared with the SHEWHART Procedure</td>
<td>778</td>
</tr>
<tr>
<td>Using CAS Sessions and CAS Engine Librefs</td>
<td>778</td>
</tr>
<tr>
<td>Getting Started: SPC Procedure</td>
<td>779</td>
</tr>
<tr>
<td>Syntax: SPC Procedure</td>
<td>782</td>
</tr>
<tr>
<td>PROC SPC Statement</td>
<td>782</td>
</tr>
<tr>
<td>BY Statement</td>
<td>783</td>
</tr>
<tr>
<td>BOXCHART Statement</td>
<td>783</td>
</tr>
<tr>
<td>CCHART Statement</td>
<td>784</td>
</tr>
<tr>
<td>IRCHART Statement</td>
<td>785</td>
</tr>
<tr>
<td>MCHART Statement</td>
<td>785</td>
</tr>
<tr>
<td>MRCHART Statement</td>
<td>786</td>
</tr>
<tr>
<td>NPCHART Statement</td>
<td>787</td>
</tr>
<tr>
<td>PCHART Statement</td>
<td>788</td>
</tr>
<tr>
<td>RCHART Statement</td>
<td>788</td>
</tr>
<tr>
<td>SCHART Statement</td>
<td>789</td>
</tr>
<tr>
<td>UCHART Statement</td>
<td>790</td>
</tr>
<tr>
<td>XCHART Statement</td>
<td>790</td>
</tr>
<tr>
<td>XRCHART Statement</td>
<td>791</td>
</tr>
<tr>
<td>XSCHART Statement</td>
<td>792</td>
</tr>
<tr>
<td>Dictionary of Options</td>
<td>793</td>
</tr>
<tr>
<td>Details: SPC Procedure</td>
<td>798</td>
</tr>
<tr>
<td>Constructing Charts for Individual Measurements and Moving Ranges</td>
<td>798</td>
</tr>
<tr>
<td>Constructing Charts for Means</td>
<td>800</td>
</tr>
<tr>
<td>Constructing Charts for Medians</td>
<td>801</td>
</tr>
<tr>
<td>Constructing Charts for Ranges</td>
<td>802</td>
</tr>
<tr>
<td>Constructing Charts for Standard Deviations</td>
<td>804</td>
</tr>
<tr>
<td>Methods of Estimating the Standard Deviation</td>
<td>805</td>
</tr>
<tr>
<td>Percentile Definitions</td>
<td>808</td>
</tr>
<tr>
<td>Constructing Charts for Numbers of Nonconformities (c Charts)</td>
<td>809</td>
</tr>
<tr>
<td>Constructing Charts for Number Nonconforming (np Charts)</td>
<td>811</td>
</tr>
<tr>
<td>Constructing Charts for Proportion Nonconforming (p Charts)</td>
<td>813</td>
</tr>
<tr>
<td>Constructing Charts for Nonconformities per Unit (u Charts)</td>
<td>814</td>
</tr>
</tbody>
</table>
Overview: SPC Procedure

The SPC procedure performs Shewhart control chart analysis in SAS Viya.

The Shewhart control chart is a graphical and analytical tool for determining whether a process is in a state of statistical control. You can use the SPC procedure to compute many different types of control charts, including all commonly used charts for variables and attributes. In addition, you can use PROC SPC to do the following:

- analyze multiple process variables and produce a table that identifies processes that are out of statistical control
- adjust control limits to compensate for unequal subgroup sizes
- estimate control limits from the data, compute control limits from specified values for population parameters (known standards), or read limits from an input data table
- perform tests for special causes based on runs patterns (Western Electric rules)
- estimate the process standard deviation by using various methods (variable charts only)
- save chart statistics and control limits in output data tables that can be used as input for the SHEWHART procedure in SAS/QC software

Uses of Shewhart Charts

The Shewhart chart is named after Walter A. Shewhart (1891–1967), a physicist at Bell Telephone Laboratories, who introduced the method in 1924 and elaborated on it in his book *Economic Control of Quality of Manufactured Product* (1931). The concepts that underlie the control chart are that the natural variability in any process can be quantified by using a set of control limits and that variation exceeding these limits signals a change in the process. Although control charts were developed to improve manufacturing processes, they are used in many other fields, including finance and health care.

In industry, the Shewhart chart is the most commonly applied statistical quality control method of studying the variation in output from a manufacturing process. Shewhart charts are typically used to distinguish
variation due to *special causes* from variation due to *common causes*. Special causes, also referred to as *assignable causes*, are local, sporadic problems such as the failure of a particular machine or a mistakenly recorded measurement. Common causes are problems inherent in the system as a whole, such as inadequate product design, inherited defective material, and excessive humidity.

After the special causes have been identified and eliminated, the process is said to be in statistical control. When statistical control has been established, Shewhart charts can be used to monitor the process for the occurrence of future special causes and to measure and reduce the effects of common causes.

Deming (1982) emphasized that the improvement of a process can begin only after statistical control has been established. Deming also noted that control chart techniques are applicable to quality improvement in service industries as well as manufacturing industries.

---

**Characteristics of Shewhart Charts**

Figure 15.1 illustrates a typical Shewhart chart.
All Shewhart charts have the following characteristics:

- Each point represents a summary statistic that is computed from a sample of measurements of a quality characteristic. For example, the summary statistic might be the average value of a critical dimension of five items selected at random, or it might be the proportion of nonconforming items in a sample of 100 items.

- The samples from which the summary statistics are computed are referred to as rational subgroups or subgroup samples. The organization of the data into subgroups is critical to the interpretation of a Shewhart chart. Shewhart (1931) advocated selecting rational subgroups so that variation within subgroups is minimized and variation among subgroups is maximized; this makes the chart more sensitive to shifts in the process level. Various approaches to subgrouping are discussed by Grant and Leavenworth (1988), Montgomery (1996), and Kume (1985).

- The horizontal axis of a Shewhart chart identifies the subgroup samples. Frequently, the samples are indexed according to the order in which they were taken or the time at which they were taken. Subgroup samples can also be assigned labels that indicate some other type of classification (such as lot number).

- The central line on a Shewhart chart indicates the average (expected value) of the summary statistic when the process is in statistical control.

- The upper and lower control limits, labeled UCL and LCL, respectively, indicate the range of variation to be expected in the summary statistic when the process is in statistical control. The control limits are commonly computed as $3\sigma$ limits, which represent three standard errors of variation in the summary statistic above and below the central line. However, the limits can also be determined using a multiple of the standard error other than three.

The control limits are also determined by the subgroup sample size, because the standard error of the summary statistic is a function of sample size. If the sample size is constant across subgroups, the control limits are typically horizontal lines, as in Figure 15.1. However, if the sample size varies from subgroup to subgroup, the limits are usually adjusted to compensate for the effect of sample size, resulting in steplike boundaries.

Control limits can be estimated from the data that you are analyzing, or they can be standard, previously determined values. Estimated limits are often used when you are establishing statistical control, and standard limits are often used when you are maintaining statistical control.

- A point outside the control limits signals the presence of a special cause of variation. In addition, tests for special causes (also referred to as Western Electric rules and runs tests) can signal an out-of-control condition if a statistically unusual pattern of points is observed in the control chart. For example, one pattern that is commonly used to diagnose the existence of a trend is seven consecutive steadily increasing points.

When the process is in statistical control, a point can fall outside the control limits purely by chance, resulting in a false out-of-control signal. However, when the Shewhart chart correctly signals the presence of a special cause, you must take additional action to determine the nature of the problem and eliminate it.

---

1. In this context, $\sigma$ always stands for the standard error of the subgroup summary statistic that is plotted on the chart. Elsewhere in this section, $\sigma$ is also used to denote the standard deviation of a process, also referred to as the population standard deviation. This dual usage is standard practice.

2. The term standard deviation is also used by some authors to refer to this quantity; see, for example, Montgomery (1996). This section uses the term standard error for the dispersion of the distribution of a statistic and the term standard deviation for the dispersion of a distribution of individual measurements.
Classification of Shewhart Charts

Shewhart charts are broadly classified according to the type of data that you are analyzing:

- Shewhart charts for **variables** are used when you are measuring the quality characteristic of a process on a continuous scale.

- Shewhart charts for **attributes** are used when you are measuring the quality characteristic of a process by counting the number of nonconformities (defects) in an item or the number of nonconforming (defective) items in a sample.

Shewhart charts for variables are further classified according to the subgroup summary statistic that is plotted on the chart:

- $\bar{X}$ and $R$ charts display subgroup means (averages) and ranges. You usually present the two charts on the same page, aligning the $\bar{X}$ chart above the $R$ chart to facilitate the simultaneous analysis of the central tendency and variability of the process.

- $\bar{X}$ and $s$ charts display subgroup means (averages) and standard deviations. You usually present the two charts on the same page, aligning the $\bar{X}$ chart above the $s$ chart.

- Median and range charts display subgroup medians and ranges. You usually present the two charts on the same page, aligning the median chart above the $R$ chart.

- Charts for individual measurements and moving ranges display individual measurements and moving ranges of two or more successive measurements. In this case the subgroup sample consists of a single observation.

- Box charts display a box plot (box-and-whisker plot) for each subgroup and control limits for the subgroup means. This type of chart facilitates detailed analysis of the subgroup distributions and is applicable to large subgroup sample sizes (10 or more).

Likewise, Shewhart charts for attributes are classified according to the subgroup summary statistic that is plotted on the chart:

- A $p$ chart displays the proportion of nonconforming (defective) items in a subgroup sample.

- An $np$ chart displays the number of nonconforming (defective) items in a subgroup sample.

- A $u$ chart displays the number of nonconformities (defects) per unit in a subgroup sample that consists of an arbitrary number of units.

- A $c$ chart displays the number of nonconformities (defects) in a unit (here, a subgroup sample typically consists of one unit).

You can produce all the preceding types of Shewhart charts by using the SPC procedure.
Chapter 15: The SPC Procedure

PROC SPC Compared with the SHEWHART Procedure

The SPC procedure performs univariate control chart analysis that is comparable to that of the SHEWHART procedure in SAS/QC. Whereas PROC SHEWHART produces graphical control charts, PROC SPC produces tables that summarize signals of process instability. PROC SPC also produces output data tables that you can read into SAS data sets and use as input to PROC SHEWHART.

PROC SPC is intended to perform control chart analysis on many process variables in parallel. Its input data format and syntax are more conducive to processing large numbers of processes than those of PROC SHEWHART. You can use PROC SPC to produce concise summaries of process health for a large number of processes. After you identify potential problems, you can use PROC SHEWHART to produce control chart graphs of selected processes.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
Getting Started: SPC Procedure

A brewery monitors its bottling process to ensure that each bottle is filled with the proper amount of beer. The following statements create a SAS data set named Beer that contains the amount of beer, recorded in fluid ounces, for 23 sample batches:

```sas
data Beer;
  input Batch size @;
  do i=1 to size;
    input Amount @@;
    output;
  end;
  drop i size;
  label Batch = 'Batch Number';
datalines;
  1 5 12.01 11.97 11.93 11.98 12.00
  2 5 11.88 11.98 11.93 12.03 11.92
  3 5 11.93 11.99 12.00 12.03 11.95
  4 5 11.98 11.94 12.02 11.90 11.97
  5 5 12.02 12.02 11.98 12.04 11.90
  6 4 11.98 11.98 12.00 11.93
  7 5 11.93 11.95 12.02 11.91 12.03
  8 5 12.00 11.98 12.02 11.89 12.01
  9 5 11.98 11.93 11.99 12.02 11.91
 10 5 11.97 12.02 12.05 12.01 11.97
 11 5 12.02 12.01 11.97 12.02 11.94
 12 5 11.93 11.83 11.99 12.02 12.01
 13 5 12.01 11.98 11.94 12.04 12.01
 14 5 11.98 11.96 12.02 12.00 12.00
 15 5 11.97 11.99 12.03 11.95 11.96
 16 5 11.99 11.95 11.96 12.03 12.01
 17 4 11.99 11.97 12.03 12.01
 18 5 11.94 11.96 11.98 12.03 11.97
 19 5 11.97 11.87 11.90 12.01 11.95
 20 5 11.96 11.94 11.96 11.98 12.05
 21 3 12.06 12.07 11.98
 22 5 12.01 11.98 11.96 11.97 12.00
 23 5 12.00 12.02 12.03 11.99 11.96;
```

The format of the Beer data set makes it suitable for analysis by PROC SHEWHART. The process variable is Amount, and the subgroup variable is Batch. Figure 15.2 shows a partial listing of the data set.
Chapter 15: The SPC Procedure

Figure 15.2 Data Set Beer (PROC SHEWHART Format)

<table>
<thead>
<tr>
<th>Batch</th>
<th>Amount</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>12.01</td>
</tr>
<tr>
<td>1</td>
<td>11.97</td>
</tr>
<tr>
<td>1</td>
<td>11.93</td>
</tr>
<tr>
<td>1</td>
<td>11.98</td>
</tr>
<tr>
<td>1</td>
<td>12.00</td>
</tr>
<tr>
<td>2</td>
<td>11.88</td>
</tr>
<tr>
<td>2</td>
<td>11.98</td>
</tr>
<tr>
<td>2</td>
<td>11.93</td>
</tr>
<tr>
<td>2</td>
<td>12.03</td>
</tr>
<tr>
<td>3</td>
<td>11.92</td>
</tr>
<tr>
<td>3</td>
<td>11.93</td>
</tr>
<tr>
<td>3</td>
<td>11.99</td>
</tr>
<tr>
<td>3</td>
<td>12.00</td>
</tr>
<tr>
<td>3</td>
<td>12.03</td>
</tr>
<tr>
<td>3</td>
<td>11.95</td>
</tr>
</tbody>
</table>

The following DATA step modifies Beer so that it is suitable for analysis by PROC SPC:

```plaintext
data Beer;
  length processname $16 subgroupname $8;
  processname='Amount';
  subgroupname='Batch';
  set Beer(rename=(Amount=process Batch=subgroup));
run;
```

The modified data set is show in Figure 15.3.

Figure 15.3 Data Set Beer (PROC SPC Format)

<table>
<thead>
<tr>
<th>processname</th>
<th>subgroupname</th>
<th>subgroup</th>
<th>process</th>
</tr>
</thead>
<tbody>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>1</td>
<td>12.01</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>1</td>
<td>11.97</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>1</td>
<td>11.93</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>1</td>
<td>11.98</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>1</td>
<td>12.00</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>2</td>
<td>11.88</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>2</td>
<td>11.98</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>2</td>
<td>11.93</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>2</td>
<td>12.03</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>2</td>
<td>11.92</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>11.93</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>11.99</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>12.00</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>12.03</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>11.95</td>
</tr>
</tbody>
</table>

The PROC SPC data format is more conducive than the PROC SHEWHART format to analyzing many processes at once. Because process names are recorded in the process name variable, you do not have to list the processes to be analyzed in the procedure syntax.
The following statements create a data table called mycas.AllProcesses that contains the beer bottle data along with data from seven other data sets (not shown here) that appear in “The SHEWHART Procedure” chapter of SAS/QC User’s Guide. These statements assume that the CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

```sas
data mycas.AllProcesses;
  set Beer Detergent Disks Partgaps Times Turbine Wafers Wire;
  format subgroup;
run;
```

The following statements use PROC SPC to perform a means and ranges chart analysis of the eight processes:

```sas
proc spc data=mycas.AllProcesses;
  xchart;
run;
```

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The XRCHART statement performs an $\bar{X}$ and $R$ chart analysis on the process data, calculating control charts for subgroup means and subgroup ranges. By default, control limits are calculated from the data. Figure 15.4 shows the resulting output.

![Figure 15.4 PROC SPC Output](image)

The default output from PROC SPC is an exceptions summary table. For each process, the table shows the number of subgroups that were analyzed and the number of subgroup summary statistics that fell outside the control limits of each chart.

The table in Figure 15.3 shows signals of unusual variation in process Delay (from the Times data set) and process Diameter (from the Wafers data set). When unusual variation is signaled in a process, you should investigate to find and correct any special causes of variation.
Chapter 15: The SPC Procedure

Syntax: SPC Procedure

```
PROC SPC < options > ;
   BY variables ;
   BOXCHART < / options > ;
   CCHART < / options > ;
   IRCHART < / options > ;
   MCHART < / options > ;
   MRCHART < / options > ;
   NPCHART < / options > ;
   PCHART < / options > ;
   RCHART < / options > ;
   SCHART < / options > ;
   UCHART < / options > ;
   XCHART < / options > ;
   XRCHART < / options > ;
   XSCHART < / options > ;
```

The PROC SPC statement invokes the procedure.

You use the chart statements to perform control chart analysis. You can specify a BY statement to obtain separate analyses for each BY group.

PROC SPC Statement

```
PROC SPC < options > ;
```

The PROC SPC statement is required in order to invoke the SPC procedure. By itself, it does not perform any statistical process control analysis.

You can specify the following options in the PROC SPC statement:

**DATA=** `CAS-libref.data-table`

specifies the input data table that contains process information for PROC SPC to analyze. `CAS-libref` specifies the CAS library where the input data table resides, and `data-table` specifies the name of the input data table. For more information, see the section “DATA= Data Table” on page 822.

**LIMITS=** `CAS-libref.data-table`

names an input data table that contains preestablished control limits or the parameters from which control limits can be computed. Each observation in a LIMITS= data table provides control limit information for a process. You can create this data table as an OUTLIMITS= data table in a previous run of PROC SPC. For more information, see the section “LIMITS= Data Table” on page 822.

**NTHREADS=** `n`

specifies the number of threads per node to be used to perform the analysis. You can specify a number between 1 and 64, inclusive. By default, `n` is the maximum number of threads available on each node.
PROCESSNAME=variable
specifies the variable in the input data table that contains the names of processes to be analyzed. Each unique combination of process name and subgroup name in the input data table identifies the data for one control chart. By default, PROC SPC looks for a variable named ProcessName that contains the process names.

PROCESSVALUE=variable
specifies the variable in the input data table that contains the process measurements to be analyzed. By default, PROC SPC looks for a variable named Process that contains the process measurements.

SUBGROUPNAME=variable
specifies the variable in the input data table that contains the names of subgroup variables. Each unique combination of process name and subgroup name in the input data table identifies the data for one control chart. By default, PROC SPC looks for a variable named SubgroupName that contains the subgroup variable names.

SUBGROUPVALUE=variable
specifies the variable in the input data table that contains the subgroup values. Subgroup values identify rational subgroups for control chart analysis. By default, PROC SPC looks for a variable named Subgroup that contains the subgroup values.

**BY Statement**

BY variables;

You can specify a BY statement in PROC SPC to obtain separate analyses of observations in groups that are defined by the values of the BY variables. If you specify more than one BY statement, only the last one specified is used. For more information, see the discussion of BY-group processing in *SAS Language Reference: Concepts*.

**BOXCHART Statement**

BOXCHART < / options > ;

The BOXCHART statement produces control charts for subgroup means or medians, along with statistics that describe the distribution of data within each subgroup. Table 15.1 lists the options that you can specify in a BOXCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>CONTROLSTAT=</td>
<td>Specifies whether control limits are computed for subgroup means or subgroup medians</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
</tbody>
</table>
### Table 15.1 (continued)

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>MEDCENTRAL=</td>
<td>Specifies the method of estimating the process mean $\mu$</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than $3\sigma$ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>PCTLDEF=</td>
<td>Specifies the percentile definition for box-and-whisker computation</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation $\sigma$</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the box chart</td>
</tr>
</tbody>
</table>

### CCHART Statement

**CCHART**< /options>;

The CCHART statement produces $c$ charts for the numbers of nonconformities (defects) in subgroup samples. Table 15.2 lists the options that you can specify in a CCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

### Table 15.2  CCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than $3\sigma$ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SUBGROUPN=</td>
<td>Specifies a variable in the input data table that contains subgroup sample sizes</td>
</tr>
</tbody>
</table>
### Table 15.2 continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the c chart</td>
</tr>
</tbody>
</table>

---

**IRCHART Statement**

```plaintext
IRCHART < / options> ;
```

The IRCHART statement produces control charts for individual measurements and moving ranges. Table 15.3 lists the options that you can specify in an IRCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

### Table 15.3 IRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation σ</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the individual measurements chart</td>
</tr>
</tbody>
</table>

---

**MCHART Statement**

```plaintext
MCHART < / options> ;
```

The MCHART statement produces control charts for subgroup medians. Table 15.4 lists the options that you can specify in an MCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.
Table 15.4  MCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>MEDCENTRAL=</td>
<td>Specifies the method of estimating the process mean $\mu$</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than $3\sigma$ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation $\sigma$</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the median chart</td>
</tr>
</tbody>
</table>

MRCHART Statement

MRCHART < / options > ;

The MRCHART statement produces control charts for subgroup medians and ranges. Table 15.5 lists the options that you can specify in an MRCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.5  MRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>MEDCENTRAL=</td>
<td>Specifies the method of estimating the process mean $\mu$</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than $3\sigma$ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
</tbody>
</table>
NPCHART Statement

NPCHART < /options> ;

The NPCHART statement produces control charts for the **numbers of nonconforming items** in subgroup samples. Table 15.6 lists the options that you can specify in an NPCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SUBGROUPN=</td>
<td>Specifies a variable in the input data table that contains subgroup sample sizes</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the median chart</td>
</tr>
<tr>
<td>TESTS2=</td>
<td>Requests tests for special causes for the R chart</td>
</tr>
</tbody>
</table>
PCHART Statement

PCHART < / options> ;

The PCHART statement produces control charts for the proportions of nonconforming items in subgroup samples. Table 15.7 lists the options that you can specify in a PCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.7 PCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHEX</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SUBGROUPN=</td>
<td>Specifies a variable in the input data table that contains subgroup sample sizes</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the p chart</td>
</tr>
</tbody>
</table>

RCHART Statement

RCHART < / options> ;

The RCHART statement produces control charts for subgroup ranges. Table 15.8 lists the options that you can specify in an RCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.8 RCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
</tbody>
</table>
### Table 15.8  
*continued*

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTFTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation σ</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS2=</td>
<td>Requests tests for special causes for the $R$ chart</td>
</tr>
</tbody>
</table>

### SCHART Statement

**SCHART** < /options> ;

The SCHART statement produces control charts for subgroup standard deviations. Table 15.9 lists the options that you can specify in an SCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

### Table 15.9  
SCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTFTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation σ</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS2=</td>
<td>Requests tests for special causes for the $s$ chart</td>
</tr>
</tbody>
</table>
**UCHART Statement**

`UCHART < / options > ;`

The UCHART statement produces control charts for the numbers of nonconformities per inspection unit in subgroup samples. Table 15.10 lists the options that you can specify in a UCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3σ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SUBGROUPN=</td>
<td>Specifies a variable in the input data table that contains subgroup sample sizes</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the $u$ chart</td>
</tr>
</tbody>
</table>

**XCHART Statement**

`XCHART < / options > ;`

The XCHART statement produces control charts for subgroup means. Table 15.11 lists the options that you can specify in an XCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.
Table 15.11  XRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3(\sigma) limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation (\sigma)</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the (\bar{X}) chart</td>
</tr>
</tbody>
</table>

XRCHART Statement

XRCHART < /options> ;

The XRCHART statement produces control charts for subgroup means and ranges. Table 15.12 lists the options that you can specify in an XRCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.12  XRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3(\sigma) limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation (\sigma)</td>
</tr>
</tbody>
</table>

XRCHART Statement

XRCHART < /options> ;

The XRCHART statement produces control charts for subgroup means and ranges. Table 15.12 lists the options that you can specify in an XRCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.12  XRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3(\sigma) limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation (\sigma)</td>
</tr>
</tbody>
</table>

XRCHART Statement

XRCHART < /options> ;

The XRCHART statement produces control charts for subgroup means and ranges. Table 15.12 lists the options that you can specify in an XRCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.12  XRCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than 3(\sigma) limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation (\sigma)</td>
</tr>
</tbody>
</table>
Table 15.12  continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the $\bar{X}$ chart</td>
</tr>
<tr>
<td>TESTS2=</td>
<td>Requests tests for special causes for the $R$ chart</td>
</tr>
</tbody>
</table>

**XSCHART Statement**

XSCHART < / options>; 

The XSCHART statement produces control charts for subgroup means and standard deviations. Table 15.13 lists the options that you can specify in an XSCHART statement. For detailed descriptions of these options, see the section “Dictionary of Options” on page 793.

Table 15.13  XSCHART Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALLN</td>
<td>Includes all subgroups in the analysis, regardless of sample size</td>
</tr>
<tr>
<td>EXCHART</td>
<td>Produces results only for charts in which exceptions occur</td>
</tr>
<tr>
<td>LIMITN=</td>
<td>Specifies the nominal sample size for fixed control limits</td>
</tr>
<tr>
<td>NO3SIGMACHECK</td>
<td>Applies tests for special causes when control limits other than $3\sigma$ limits are in effect</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>OUTLIMITS=</td>
<td>Creates an output data table that contains control limits</td>
</tr>
<tr>
<td>OUTTABLE=</td>
<td>Creates an output data table that contains subgroup summary statistics and control limits</td>
</tr>
<tr>
<td>SIGMAS=</td>
<td>Specifies the width of the control limits in terms of a multiple of the standard error of the subgroup summary statistic</td>
</tr>
<tr>
<td>SMETHOD=</td>
<td>Specifies the method of estimating the process standard deviation $\sigma$</td>
</tr>
<tr>
<td>TEST2RUN=</td>
<td>Specifies the length of the pattern for Test 2</td>
</tr>
<tr>
<td>TEST3RUN=</td>
<td>Specifies the length of the pattern for Test 3</td>
</tr>
<tr>
<td>TESTNSTD</td>
<td>Applies tests for special causes to standardized chart statistics</td>
</tr>
<tr>
<td>TESTOVERLAP</td>
<td>Performs tests for special causes on overlapping patterns of points</td>
</tr>
<tr>
<td>TESTS=</td>
<td>Requests tests for special causes for the $\bar{X}$ chart</td>
</tr>
<tr>
<td>TESTS2=</td>
<td>Requests tests for special causes for the $R$ chart</td>
</tr>
</tbody>
</table>
Dictionary of Options

The following entries provide detailed descriptions of options that are available in the chart statements: BOXCHART, CCHART, IRCHART, MCHART, MRCHART, NPCHART, PCHART, RCHART, SCHART, UCHART, XCHART, XRCHART, and XSCHART.

**ALLN**

includes all subgroups in the analysis, regardless of whether the subgroup sample size equals the nominal control limit sample size \( n \) that you specify in the LIMITN= option or the variable _LIMITN_ in the LIMITS= data table. Use the ALLN option in conjunction with the LIMITN= option or the variable _LIMITN_.

**CONTROLSTAT=MEAN | MEDIAN**

specifies whether the control limits that are displayed in a box chart are computed for subgroup means or for subgroup medians. By default, CONTROLSTAT=MEAN. This option is available only in the BOXCHART statement.

**EXCHART**

includes a control chart in the results only when exceptions occur—specifically, when the control limits are exceeded or when any tests that you request by using the TESTS= or TESTS2= option are positive.

**LIMITN=\( n \)**

specifies a nominal sample size for the control limits.

If you specify LIMITN=\( n \), the control limits are computed for the fixed value \( n \), and they do not vary with the subgroup sample sizes. Moreover, only those subgroups whose sample size is equal to \( n \) are included in the analysis. You can specify ALLN in conjunction with LIMITN=\( n \) to force all subgroups to be included, regardless of subgroup sample size.

If you do not specify LIMITN=\( n \) and the subgroup sample sizes are constant, the default value of \( n \) is the constant subgroup sample size.

Depending on which chart statement you use, there are restrictions on the value of \( n \) that you can specify in the LIMITN= option. For the MRCHART, RCHART, and XRCHART statements, \( 2 \leq n \leq 25 \). For the SCHART and XSCHART statements, \( n \geq 2 \). For the BOXCHART, MCHART, and XCHART statements, \( n \geq 1 \). If the estimate of the process standard deviation is based on subgroup ranges (see the SMETHOD= option and the section “Methods of Estimating the Standard Deviation” on page 805), \( n < 26 \). For the CCHART and UCHART statements, \( n > 0 \), and \( n \) can assume fractional values (for all other chart statements, \( n \) must be a whole number). For the PCHART and NPCHART statements, \( n \geq 1 \).

Note the difference between the LIMITN= option and the SUBGROUPN= option that is available in the CCHART, NPCHART, PCHART, and UCHART statements. The LIMITN= option specifies a nominal sample size for the control limits, whereas the SUBGROUPN= option provides the sample sizes for the data.

**NOTE:** As an alternative to specifying the LIMITN= option, you can read the nominal control limit sample size from the variable _LIMITN_ in a LIMITS= data table.
Chapter 15: The SPC Procedure

**MEDCENTRAL=AVGMEAN | AVGMED | MEDMED**

identifies a method of estimating the process mean \( \mu \), which is represented by the central line on a median chart. The method that corresponds to each keyword is shown in Table 15.14.

**Table 15.14  Methods of Estimating the Process Mean**

<table>
<thead>
<tr>
<th>Keyword</th>
<th>Method</th>
</tr>
</thead>
<tbody>
<tr>
<td>AVGMEAN</td>
<td>Average of subgroup means</td>
</tr>
<tr>
<td>AVGMED</td>
<td>Average of subgroup medians</td>
</tr>
<tr>
<td>MEDMED</td>
<td>Median of subgroup medians</td>
</tr>
</tbody>
</table>

By default, MEDCENTRAL=AVGMED. This option is available only in the MCHART and MRCHART statements, and in the BOXCHART statement when you specify the CONTROL-STAT=MEDIAN option.

**NO3SIGMACHECK**

suppresses the check for 3\( \sigma \) limits when you request tests for special causes. This enables tests for special causes to be applied when you use SIGMAS= option to specify control limits other than the default 3\( \sigma \) limits. You should not use the NO3SIGMACHECK option for standard control chart applications, because the standard tests for special causes assume 3\( \sigma \) limits.

**NOPRINT**

suppresses the display of ODS output.

**OUTLIMITS=**CAS-libref.data-table

creates an output data table that saves the control limits. You can use an OUTLIMITS= data table as an input LIMITS= data table in a subsequent run of the procedure. **CAS-libref.data-table** is a two-level name, where **CAS-libref** refers to the caslib and session identifier, and **data-table** specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 778.

For more information about OUTLIMITS= data tables, see the section “OUTLIMITS= Data Table” on page 823.

**OUTTABLE=**CAS-libref.data-table

creates an output SAS data table that saves the information plotted on the chart, including the subgroup variable values and their corresponding summary statistics and control limits. **CAS-libref.data-table** is a two-level name, where **CAS-libref** refers to the caslib and session identifier, and **data-table** specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 778.

For more information about OUTTABLE= data tables, see the section “OUTTABLE= Data Table” on page 828.

**PCTLDEF=**index

specifies one of five definitions that are used to calculate percentiles in the construction of box-and-whisker plots that you request in the BOXCHART statement. The **index** can be 1, 2, 3, 4, or 5. The five corresponding percentile definitions are discussed in the section “Percentile Definitions” on page 808. By default, PCTLDEF=5. This option is available only in the BOXCHART statement.
**SIGMAS=k**

specifies the width of the control limits in terms of the multiple $k$ of the standard error of the subgroup summary statistic. The value of $k$ must be positive. By default, $k = 3$, and the control limits are $3\sigma$ limits.

**SMETHOD=MAD | MMR< (n) > | MVGRANGE< (n) > | RMSDF | RMVLUE | RNOWEIGHT | SMVLUE | SNOWEIGHT**

specifies the method of estimating the process standard deviation, $\sigma$, as summarized in Table 15.15.

<table>
<thead>
<tr>
<th>Table 15.15</th>
<th>Methods of Estimating the Process Standard Deviation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Keyword</strong></td>
<td><strong>Method</strong></td>
</tr>
<tr>
<td>MAD</td>
<td>Calculates a median absolute deviation estimate of $\sigma$</td>
</tr>
<tr>
<td>MMR</td>
<td>Calculates a median moving range estimate of $\sigma$</td>
</tr>
<tr>
<td>MVGRANGE</td>
<td>Estimates $\sigma$ based on a moving range of $n$ subgroup means</td>
</tr>
<tr>
<td>RMSDF</td>
<td>Calculates a root mean square estimate of $\sigma$</td>
</tr>
<tr>
<td>RMVLUE</td>
<td>Calculates a minimum variance linear unbiased estimate of $\sigma$ based on subgroup ranges</td>
</tr>
<tr>
<td>RNOWEIGHT</td>
<td>Estimates $\sigma$ as an unweighted average of unbiased subgroup estimates of $\sigma$ based on subgroup ranges</td>
</tr>
<tr>
<td>SMVLUE</td>
<td>Calculates a minimum variance linear unbiased estimate of $\sigma$ based on subgroup standard deviations</td>
</tr>
<tr>
<td>SNOWEIGHT</td>
<td>Estimates $\sigma$ as an unweighted average of unbiased subgroup estimates of $\sigma$ based on subgroup standard deviations</td>
</tr>
</tbody>
</table>

Table 15.16 lists the SMETHOD= option values that are valid for each chart statement. The default value for each statement is shown in bold.

<table>
<thead>
<tr>
<th>Table 15.16</th>
<th>Valid SMETHOD= Values by Chart Statement</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Chart Statement</strong></td>
<td><strong>Methods</strong></td>
</tr>
<tr>
<td>BOXCHART</td>
<td>RMSDF, RMVLUE, RNOWEIGHT, SMVLUE, SNOWEIGHT</td>
</tr>
<tr>
<td>IRCHART</td>
<td>MAD, MMR, MVGRANGE</td>
</tr>
<tr>
<td>MCHART</td>
<td>RMSDF, RMVLUE, RNOWEIGHT, SMVLUE, SNOWEIGHT</td>
</tr>
<tr>
<td>MRCHART</td>
<td>RMVLUE, RNOWEIGHT</td>
</tr>
<tr>
<td>RCHART</td>
<td>RMVLUE, RNOWEIGHT</td>
</tr>
<tr>
<td>SCHART</td>
<td>RMSDF, SMVLUE, SNOWEIGHT</td>
</tr>
<tr>
<td>XCHART</td>
<td>RMSDF, RMVLUE, RNOWEIGHT, SMVLUE, SNOWEIGHT</td>
</tr>
<tr>
<td>XRCHART</td>
<td>MVGRANGE, RMVLUE, RNOWEIGHT</td>
</tr>
<tr>
<td>XSCHART</td>
<td>MVGRANGE, RMSDF, SMVLUE, SNOWEIGHT</td>
</tr>
</tbody>
</table>

When you use the MMR or MVGRANGE method, you can specify the number $n$ of consecutive subgroup summary statistics from which moving ranges are computed by appending the number in parentheses to the keyword. For example, you can specify SMETHOD=MVGRANGE(4) to use moving ranges of four subgroup statistics. Values in the range $2 \leq n \leq 25$ are valid. By default, $n = 2$. 
For more information about the different methods of estimating the process standard deviation, see the section “Methods of Estimating the Standard Deviation” on page 805.

**SUBGROUPN=variable**
specifies a variable in the input data table whose values specify the subgroup sample sizes. This option is available only in the CCHART, NPCHART, PCHART, and UCHART statements. You must specify this option in the NPCHART, PCHART, and UCHART statements. For the CCHART statement, the default subgroup sample size is 1.

**TEST2RUN=run-length**
specifies the length of the pattern for Test 2 that you request in the TESTS= and TESTS2= options. The run-length values that you can specify are 7, 8, 9, 11, 14, and 20. The form of the test for each run-length value is shown in the following table. By default, TEST2RUN=9. For more information, see the section “Tests for Special Causes” on page 816.

<table>
<thead>
<tr>
<th>run-length</th>
<th>Number of Points on One Side of the Central Line</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>7 in a row</td>
</tr>
<tr>
<td>8</td>
<td>8 in a row</td>
</tr>
<tr>
<td>9</td>
<td>9 in a row</td>
</tr>
<tr>
<td>11</td>
<td>At least 10 out of 11 in a row</td>
</tr>
<tr>
<td>14</td>
<td>At least 12 out of 14 in a row</td>
</tr>
<tr>
<td>20</td>
<td>At least 16 out of 20 in a row</td>
</tr>
</tbody>
</table>

**TEST3RUN=run-length**
specifies the length of the pattern for Test 3 that you request in the TESTS= and TESTS2= options. Test 3 searches for a pattern of steadily increasing or decreasing values, where the length of the pattern is at least the value of run-length. The values that you can specify for run-length are 6, 7, and 8. By default, TEST3RUN=6. For more information, see the section “Tests for Special Causes” on page 816.

**TESTNSTD**
applies the tests for special causes that you request in the TESTS= and TESTS2= options to standardized test statistics when the subgroup sample sizes are not constant. This method was suggested by Nelson (1994). For more information, see the section “Tests for Special Causes” on page 816. By default, the tests are not applied to data that have varying subgroup sample sizes.

**TESTOVERLAP**
applies tests for special causes (which you request in the TESTS= or TESTS2= option) to overlapping patterns of points.

This option modifies the way in which the search for a subsequent pattern is done when a pattern is encountered. If you omit this option, the search begins with the first subgroup after the current pattern ends. If you specify this option, the search begins with the second subgroup in the current pattern.

The following statements request Test 3, which detects six subgroup means in a row that steadily increase or decrease:

```plaintext
proc spc;
   xchart / test=3;
   xchart / test=3 testoverlap;
run;
```
Suppose that the subgroup means are steadily increasing for subgroups 5, 6, 7, 8, 9, 10, and 11. The first XRCHART statement signals that Test 3 is positive at subgroup 10 but not at subgroup 11, because the search for the next pattern begins with subgroup 11. The second XRCHART statement signals that Test 3 is positive at subgroup 10 and subgroup 11, because the search for the next pattern begins with subgroup 6 and thus finds a second pattern that ends with subgroup 11. For more information, see the section “Tests for Special Causes” on page 816.

**CAUTION:** Specifying TESTOVERLAP affects the interpretation of the standard tests for special causes, because a particular point can contribute to more than one positive test. Typically, you should not use this option.

**TESTS=**\textit{index-list}
requests one or more tests for special causes, which are also known as \textit{runs tests}, \textit{pattern tests}, and \textit{Western Electric rules}. These tests detect particular nonrandom patterns in the points that are plotted on the primary control chart. The occurrence of a pattern, referred to as a \textit{signal}, suggests the presence of a special cause of variation.

Each pattern is defined in terms of Zones A, B, and C, which are constructed by dividing the interval between the control limits into six equally spaced subintervals. Zone A is the union of the subintervals immediately below the upper control limit and immediately above the lower control limit. Zone C is the union of the subintervals immediately above and below the central line. Zone B is the union of the subintervals between Zones A and C. For an illustration of test zones, see Figure 15.9.

Table 15.17 lists the standard tests that you can request by specifying this option. The tests are indexed according to the sequence used by Nelson (1984, 1985).

<table>
<thead>
<tr>
<th>Index</th>
<th>Pattern Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>One point beyond Zone A (outside the control limits)</td>
</tr>
<tr>
<td>2</td>
<td>Nine points in a row in Zone C or beyond on one side of the central line (see the TEST2RUN= option)</td>
</tr>
<tr>
<td>3</td>
<td>Six points in a row that steadily increase or decrease (see the TEST3RUN= option)</td>
</tr>
<tr>
<td>4</td>
<td>Fourteen points in a row that alternate up and down</td>
</tr>
<tr>
<td>5</td>
<td>Two out of three points in a row in Zone A or beyond</td>
</tr>
<tr>
<td>6</td>
<td>Four out of five points in a row in Zone B or beyond</td>
</tr>
<tr>
<td>7</td>
<td>Fifteen points in a row in Zone C on either or both sides of the central line</td>
</tr>
<tr>
<td>8</td>
<td>Eight points in a row on either or both sides of the central line, with no points in Zone C</td>
</tr>
</tbody>
</table>

You can specify any combination of the eight \textit{indexes} by using an explicit list or an implicit list, as in the following example:

```sas
proc spc;
   xchart / tests=1 2 3 4;
   xchart / tests=1 to 4;
run;
```
The TESTS= option is available in all chart statements except the RCHART and SCHART statements. Use only tests 1, 2, 3, and 4 in the CCHART, NPCHART, PCHART, and UCHART statements. By default, the TESTS= option is not applied in any chart statement unless the control limits are $3\sigma$ limits. You can use the NO3SIGMACHECK option to request tests for special causes when you use the SIGMAS= option to specify control limits other than $3\sigma$ limits.

For more information about the TESTS= option, see the section “Tests for Special Causes” on page 816. Related options include TEST2RUN=, TEST3RUN=, TESTNSTD, TESTOVERLAP, and TESTS2=.

TESTS2=index-list

requests one or more tests for special causes for $R$ charts or $s$ charts. The syntax for the TESTS2= option is identical to the syntax for the TESTS= option. The TESTS2= option is available in the MRCHART, RCHART, SCHART, XRCHART, and XSCHART statements. For more information about the TESTS2= option, see the section “Tests for Special Causes” on page 816. Related options include TEST2RUN=, TEST3RUN=, TESTNSTD, TESTOVERLAP, and TESTS=.

Details: SPC Procedure

Constructing Charts for Individual Measurements and Moving Ranges

You produce control charts for individual measurements and moving ranges by using the IRCHART statement. The following notation is used in this section:

- $\mu$: Process mean (expected value of the population of measurements)
- $\sigma$: Process standard deviation (standard deviation of the population of measurements)
- $X_i$: The $i$th individual measurement
- $\bar{X}$: Mean of the individual measurements, computed as $(X_1 + \cdots + X_N)/N$, where $N$ is the number of individual measurements
- $n$: Number of consecutive measurements that are used to calculate the moving ranges (by default, $n = 2$)
- $R_i$: Moving range that is computed for the $i$th subgroup (corresponding to the $i$th individual measurement). If $i < n$, then $R_i$ is assigned a missing value. Otherwise,

$$R_i = \max(X_i, X_{i-1}, \ldots, X_{i-n+1}) - \min(X_i, X_{i-1}, \ldots, X_{i-n+1})$$

This formula assumes that $X_i, X_{i-1}, \ldots, X_{i-n+1}$ are nonmissing.

- $\bar{R}$: Average of the nonmissing moving ranges, computed as

$$\frac{R_n + R_{n+1} + \cdots + R_N}{N + 1 - n}$$

- $d_2(n)$: Expected value of the range of $n$ independent normally distributed variables with unit standard deviation
- $d_3(n)$: Standard error of the range of $n$ independent observations from a normal population with unit standard deviation
Subgroup Summary Statistics

Each point on an individual measurements chart indicates the value of a measurement \( (X_i) \).

Each point on a moving range chart indicates the value of a moving range \( (R_i) \). For \( n = 2 \), for example, if the first three measurements are 3.4, 3.7, and 3.6, then the first moving range is \( |3.7 - 3.4| = 0.3 \), and the third moving range is \( |3.6 - 3.7| = 0.1 \).

Central Lines

By default, the central line on an individual measurements chart indicates an estimate for \( \mu \), which is computed as \( \bar{X} \). If you specify a known value \( (\mu_0) \) for \( \mu \), the central line indicates the value of \( \mu_0 \).

The central line on a moving range chart indicates an estimate for the expected moving range, which is computed as \( d_2(n)\hat{\sigma} \), where \( \hat{\sigma} = R/d_2(n) \). If you specify a known value \( (\sigma_0) \) for \( \sigma \), the central line indicates the value of \( d_2(n)\sigma_0 \).

Control Limits

The control limits are computed as a specified multiple \( (k) \) of the standard errors of \( X_i \) and \( R_i \) above and below the central line. The default limits are computed using \( k = 3 \) (these are referred to as \( 3\sigma \) limits).

Table 15.19 provides the formulas for the limits.

**Table 15.19  Limits for Individual Measurements and Moving Range Charts**

<table>
<thead>
<tr>
<th>Individual Measurements Chart</th>
<th>Moving Range Chart</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCL = lower control limit = ( \bar{X} - k\hat{\sigma} )</td>
<td>LCL = lower control limit = ( \max(d_2(n)\hat{\sigma} - k d_3(n)\hat{\sigma}, 0) )</td>
</tr>
<tr>
<td>UCL = upper control limit = ( \bar{X} + k\hat{\sigma} )</td>
<td>UCL = upper control limit = ( d_2(n)\hat{\sigma} + k d_3(n)\hat{\sigma} )</td>
</tr>
</tbody>
</table>

The formulas assume that the measurements are normally distributed. If the standard values \( \mu_0 \) and \( \sigma_0 \) are available for \( \mu \) and \( \sigma \), replace \( \bar{X} \) with \( \mu_0 \) and \( \hat{\sigma} \) with \( \sigma_0 \) in Table 15.19.

You can specify parameters for the limits as follows:

- Specify \( k \) by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify \( n \) by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify \( \mu_0 \) by using the variable _MEAN_ in the LIMITS= data table.
- Specify \( \sigma_0 \) by using the variable _STDDEV_ in the LIMITS= data table.
Constructing Charts for Means

You produce control charts for means by using the BOXCHART, XCHART, XRCHART, or XSCHART statement. The following notation is used in this section:

<table>
<thead>
<tr>
<th>Symbol</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \mu )</td>
<td>Process mean (expected value of the population of measurements)</td>
</tr>
<tr>
<td>( \sigma )</td>
<td>Process standard deviation (standard deviation of the population of measurements)</td>
</tr>
<tr>
<td>( \bar{X}_i )</td>
<td>Mean of measurements in ( i )th subgroup</td>
</tr>
<tr>
<td>( n_i )</td>
<td>Sample size of ( i )th subgroup</td>
</tr>
<tr>
<td>( R_i )</td>
<td>Range of measurements in ( i )th subgroup</td>
</tr>
<tr>
<td>( n )</td>
<td>Number of subgroups</td>
</tr>
<tr>
<td>( \bar{X} )</td>
<td>Weighted average of subgroup means</td>
</tr>
</tbody>
</table>

Subgroup Summary Statistic

Each point on an \( \bar{X} \) chart indicates the value of a subgroup mean (\( \bar{X}_i \)). For example, if the 10th subgroup contains the values 12, 15, 19, 16, and 14, the subgroup summary statistic is

\[
\bar{X}_{10} = \frac{12 + 15 + 19 + 16 + 14}{5} = 15.2
\]

Central Line

By default, the central line on an \( \bar{X} \) chart indicates an estimate for \( \mu \), which is computed as

\[
\hat{\mu} = \frac{n_1 \bar{X}_1 + \cdots + n_N \bar{X}_N}{n_1 + \cdots + n_N}
\]

If you specify a known value (\( \mu_0 \)) for \( \mu \), the central line indicates the value of \( \mu_0 \).

Control Limits

The limits are computed as a specified multiple (\( k \)) of the standard error of \( \bar{X}_i \) above and below the central line. The default limits are computed using \( k = 3 \) (these are referred to as 3\( \sigma \) limits).

Table 15.21 provides the formulas for the limits.

<table>
<thead>
<tr>
<th>Table 15.21 Limits for ( \bar{X} ) Charts</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCL = lower limit = ( \bar{X} - k\hat{\sigma} \sqrt{n_i} )</td>
</tr>
<tr>
<td>UCL = upper limit = ( \bar{X} + k\hat{\sigma} \sqrt{n_i} )</td>
</tr>
</tbody>
</table>

Note that the limits vary with \( n_i \). If the standard values \( \mu_0 \) and \( \sigma_0 \) are available for \( \mu \) and \( \sigma \), respectively, replace \( \bar{X} \) with \( \mu_0 \) and \( \hat{\sigma} \) with \( \sigma_0 \) in Table 15.21.

You can specify parameters for the limits as follows:
Constructing Charts for Medians

You produce control charts for medians by using the MCHART or MRCHART statement, and by using the BOXCHART statement when you specify CONTROLSTAT=MEDIAN. The following notation is used in this section:

- **\( \mu \)**: Process mean (expected value of the population of measurements)
- **\( \sigma \)**: Process standard deviation (standard deviation of the population of measurements)
- **\( \bar{X}_i \)**: Mean of measurements in \( i \)th subgroup
- **\( n_i \)**: Sample size of \( i \)th subgroup
- **\( N \)**: Number of subgroups
- **\( x_{ij} \)**: \( j \)th measurement in the \( i \)th subgroup, \( j = 1, 2, 3, \ldots, n_i \)
- **\( x_{i(j)} \)**: \( j \)th-largest measurement in the \( i \)th subgroup. Then

\[
x_{i(1)} \leq x_{i(2)} \leq \cdots \leq x_{i(n_i)}
\]

- **\( \overline{X} \)**: Weighted average of subgroup means
- **\( M_i \)**: Median of the measurements in the \( i \)th subgroup:

\[
M_i = \begin{cases} 
\frac{x_{i((n_i+1)/2)}}{2} & \text{if } n_i \text{ is odd} \\
\frac{(x_{i(n_i/2)} + x_{i((n_i/2)+1)})}{2} & \text{if } n_i \text{ is even}
\end{cases}
\]

- **\( \bar{M} \)**: Average of the subgroup medians:

\[
\bar{M} = \frac{(n_1 M_1 + \cdots + n_N M_N)}{(n_1 + \cdots + n_N)}
\]

- **\( \tilde{M} \)**: Median of the subgroup medians. Denote the \( j \)th-largest median by \( M_{(j)} \) so that

\[
M_{(1)} \leq M_{(2)} \leq \cdots \leq M_{(N)}.
\]

Then

\[
\tilde{M} = \begin{cases} 
\frac{M_{((N+1)/2)}}{2} & \text{if } N \text{ is odd} \\
\frac{(M_{(N/2)} + M_{(N/2)+1})}{2} & \text{if } N \text{ is even}
\end{cases}
\]

- **\( e_M(n) \)**: Standard error of the median of \( n \) independent, normally distributed variables with unit standard deviation (the value of \( e_M(n) \) can be calculated using the STDMED function in a DATA step)
Subgroup Summary Statistics

Each point on a median chart indicates the value of a subgroup median ($M_i$). For example, if the 10th contains the values 12, 15, 19, 16, and 14, the subgroup summary statistic is $M_{10} = 15$.

Central Line

The value of the central line indicates an estimate of $\mu$, which is computed as follows:

- $\bar{M}$ by default
- $\bar{X}$ when you specify MEDCENTRAL=AVGMEAN
- $\bar{M}$ when you specify MEDCENTRAL=MEDMED

Control Limits

The control limits are computed as a specified multiple ($k$) of the standard error of $M_i$ above and below the central line. The default limits are computed using $k = 3$ (these are referred to as $3\sigma$ limits).

Table 15.23 provides the formulas for the limits.

<table>
<thead>
<tr>
<th>Table 15.23</th>
<th>Limits for Median Charts</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCLM = lower limit = $\bar{M} - k\hat{\sigma}_M(n_i)$</td>
<td></td>
</tr>
<tr>
<td>UCLM = upper limit = $\bar{M} + k\hat{\sigma}_M(n_i)$</td>
<td></td>
</tr>
</tbody>
</table>

Note that the limits vary with $n_i$. In Table 15.23, replace $\bar{M}$ with $\bar{X}$ if you specify MEDCENTRAL=AVGMEAN, and replace $\bar{M}$ with $\bar{M}$ if you specify MEDCENTRAL=MEDMED. The formulas assume that the data are normally distributed.

You can specify parameters for the limits as follows:

- Specify $k$ by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify a constant nominal sample size $n_i \equiv n$ for the control limits by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify $\mu_0$ by using the variable _MEAN_ in the LIMITS= data table.
- Specify $\sigma_0$ by using the variable _STDDEV_ in the LIMITS= data table.

Constructing Charts for Ranges

You produce control charts for ranges by using the MRCHART, RCHART, or XRCHART statement. The following notation is used in this section:
Constructing Charts for Ranges

Subgroup Summary Statistics

Each point on an $R$ chart indicates the value of a subgroup range ($R_i$). For example, if the 10th subgroup contains the values 12, 15, 19, 16, and 14, the subgroup summary statistic is $R_{10} = 19 - 12 = 7$.

Central Line

By default, the central line for the $i$th subgroup indicates an estimate of the expected value of $R_i$, which is computed as $d_2(n_i)\hat{\sigma}$, where $\hat{\sigma}$ is an estimate of $\sigma$. If you specify a known value ($\sigma_0$) for $\sigma$, the central line indicates the value of $d_2(n_i)\sigma_0$. Note that the central line varies with $n_i$.

Control Limits

The control limits are computed as a specified multiple ($k$) of the standard error of $R_i$ above and below the central line. The default limits are computed using $k = 3$ (these are referred to as $3\sigma$ limits).

Table 15.25 provides the formulas for the limits.

<table>
<thead>
<tr>
<th>Formula</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>LCL = $\max(d_2(n_i)\hat{\sigma} - kd_3(n_i)\hat{\sigma}, 0)$</td>
<td>Lower limit</td>
</tr>
<tr>
<td>UCL = $d_2(n_i)\hat{\sigma} + kd_3(n_i)\hat{\sigma}$</td>
<td>Upper limit</td>
</tr>
</tbody>
</table>

The formulas assume that the data are normally distributed. Note that the control limits vary with $n_i$. If a standard value $\sigma_0$ is available for $\sigma$, replace $\hat{\sigma}$ with $\sigma_0$ in Table 15.25.

You can specify parameters for the limits as follows:

- Specify $k$ by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify a constant nominal sample size $n_i = n$ for the control limits by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify $\sigma_0$ by using the variable _STDDEV_ in a LIMITS= data table.
Constructing Charts for Standard Deviations

You produce control charts for standard deviations by using the SCHART or XSCHART statement. The following notation is used in this section:

- $\sigma$: Process standard deviation (standard deviation of the population of measurements)
- $s_i$: Standard deviation of measurements in $i$th subgroup
  \[ s_i = \sqrt{\frac{1}{n_i - 1} [(x_{i1} - \bar{X}_i)^2 + \cdots + (x_{in_i} - \bar{X}_i)^2]} \]
- $n_i$: Sample size of $i$th subgroup
- $c_4(n)$: Expected value of the standard deviation of $n$ independent normally distributed variables with unit standard deviation
- $c_5(n)$: Standard error of the standard deviation of $n$ independent observations from a normal population with unit standard deviation

Subgroup Summary Statistics

Each point on an $s$ chart indicates the value of a subgroup standard deviation ($s_i$). For example, if the 10th subgroup contains the values 12, 15, 19, 16, and 13, the subgroup summary statistic is

\[ s_{10} = \sqrt{\frac{1}{(12 - 15)^2 + (15 - 15)^2 + (19 - 15)^2 + (16 - 15)^2 + (13 - 15)^2}} = 2.739 \]

Central Line

By default, the central line for the $i$th subgroup indicates an estimate for the expected value of $s_i$, which is computed as $c_4(n_i)\hat{\sigma}$, where $\hat{\sigma}$ is an estimate of $\sigma$. If you specify a known value ($\sigma_0$) for $\sigma$, the central line indicates the value of $c_4(n_i)\sigma_0$. Note that the central line varies with $n_i$.

Control Limits

The control limits are computed as a specified multiple ($k$) of the standard error of $s_i$ above and below the central line. The default limits are computed using $k = 3$ (these are referred to as $3\sigma$ limits).

Table 15.27 provides the formulas for the limits.

<table>
<thead>
<tr>
<th>LCL = lower limit</th>
<th>UCL = upper limit</th>
</tr>
</thead>
<tbody>
<tr>
<td>$c_4(n_i)\hat{\sigma} - k c_5(n_i)\hat{\sigma}, 0$</td>
<td>$c_4(n_i)\hat{\sigma} + k c_5(n_i)\hat{\sigma}$</td>
</tr>
</tbody>
</table>

The formulas assume that the data are normally distributed. If a standard value $\sigma_0$ is available for $\sigma$, replace $\hat{\sigma}$ with $\sigma_0$ in Table 15.27. Note that the upper and lower limits vary with $n_i$.

You can specify parameters for the limits as follows:
Methods of Estimating the Standard Deviation

You can specify the **SMETHOD=** option to choose among several methods of estimating the process standard deviation for control charts for variables. The following sections describe the methods in detail.

**MAD Method**

If you specify **SMETHOD=MAD**, a median absolute deviation estimator is computed for \( \sigma \). This method is described by Boyles (1997) and computed as

\[
\hat{\sigma} = \text{median}\{|X_i - \bar{X}|, 1 \leq i \leq N\}/0.6745
\]

where \( \bar{X} \) is the sample median.

The MAD method is available only in the IRCHART statement.

**MMR Method**

If you specify **SMETHOD=MMR**, a median moving range estimator is computed for \( \sigma \). This estimator is described by Boyles (1997) and computed as

\[
\hat{\sigma} = \tilde{R}/0.954
\]

where \( \tilde{R} \) is the median of the nonmissing moving ranges.

The MMR method is available only in the IRCHART statement.

**MVGRANGE Method**

If you specify **SMETHOD=MVGRANGE**, \( \sigma \) is estimated by using a moving range of subgroup averages (or individual measurements in an IRCHART statement). The estimate of \( \sigma \) is

\[
\hat{\sigma} = \bar{R}/d_2(n)
\]

where \( \bar{R} \) is the average of the moving ranges; \( n \) is the number of consecutive subgroup averages that are used to compute each moving range; and the unbiasing factor \( d_2(n) \) is defined so that if the subgroup averages are normally distributed, the expected value of \( R_i \) is

\[
E(R_i) = d_2(n_i)\sigma
\]

This method is described by the American Society for Testing and Materials (1976).

The method is appropriate for constructing the three-way control chart that Wheeler (1995) advocated for this situation. A three-way control chart is useful when sampling *(within-group)* variation is not the only source
of variation. A three-way control chart contains a chart of subgroup means, a moving range chart of the subgroup means, and a chart of subgroup ranges. When you specify the SMETHOD=MVGRANGE option, the XRCHART statement produces the appropriate charts of subgroup means and subgroup ranges, and the XSCHART statement produces the appropriate charts of subgroup means and subgroup standard deviations.

The MVGRANGE method is available in the ICHART, XRCHART, and XSCHART statements. It is the default in the ICHART statement.

**RMSDF Method**

If you specify SMETHOD=RMSDF, a weighted root mean square estimate is computed for \( \sigma \),

\[
\hat{\sigma} = \sqrt{\frac{(n_1 - 1)s_1^2 + \cdots + (n_N - 1)s_N^2}{c_4(n)\sqrt{n_1 + \cdots + n_N - N}}}
\]

where \( n = n_1 + \cdots + n_N - (N - 1) \). The weights are the degrees of freedom \( n_i - 1 \). A subgroup standard deviation \( s_i \) is included in the calculation only if \( n_i \geq 2 \), and \( N \) is the number of subgroups for which \( n_i \geq 2 \).

If the unknown standard deviation \( \sigma \) is constant across subgroups, the root mean square estimate is more efficient than the minimum variance linear unbiased estimate (MVLUE). However, in process control applications, it is generally not assumed that \( \sigma \) is constant, and if \( \sigma \) varies across subgroups, the root mean square estimate tends to be more inflated than the MVLUE.

The RMSDF method is available in the BOXCHART, MCHART, SCHART, XCHART, and XSCHART statements.

**RMVLUE Method**

If you specify SMETHOD=RMVLUE, a minimum variance linear unbiased estimate (MVLUE) is computed for \( \sigma \); see Burr (1969, 1976) and Nelson (1989, 1994). The MVLUE is a weighted average of \( N \) unbiased estimates of \( \sigma \) of the form \( R_i/d_2(n_i) \), and it is computed as

\[
\hat{\sigma} = \frac{f_1R_1/d_2(n_1) + \cdots + f_NR_N/d_2(n_N)}{f_1 + \cdots + f_N}
\]

where

\[
f_i = \frac{[d_2(n_i)]^2}{[d_3(n_i)]^2}
\]

A subgroup range \( R_i \) is included in the calculation only if \( n_i \geq 2 \), and \( N \) is the number of subgroups for which \( n_i \geq 2 \). The unbiasing factor \( d_3(n_i) \) is defined so that, if the observations are normally distributed, the expected value of \( \sigma R_i/d_2(n_i) \) is \( d_3(n_i)\sigma \). The MVLUE assigns greater weight to estimates of \( \sigma \) from subgroups that have larger sample sizes, and it is intended for situations where the subgroup sample sizes vary. If the subgroup sample sizes are constant, the RMVLUE estimate reduces to the RNOWEIGHT estimate.

The RMVLUE method is available in the BOXCHART, MCHART, MRCHART, RCHART, XCHART, and XRCHART statements.
Methods of Estimating the Standard Deviation

**RNOWEIGHT Method**

If you specify SMETHOD=RNOWEIGHT, the estimate of $\sigma$ is

$$\hat{\sigma} = \frac{R_1/d_2(n_1) + \cdots + R_N/d_2(n_N)}{N}$$

where $N$ is the number of subgroups for which $n_i \geq 2$, and $R_i$ is the sample range of the observations $x_{i1}, \ldots, x_{in_i}$ in the $i$th subgroup:

$$R_i = \max_{1 \leq j \leq n_i} (x_{ij}) - \min_{1 \leq j \leq n_i} (x_{ij})$$

A subgroup range $R_i$ is included in the calculation only if $n_i \geq 2$. The unbiasing factor $d_2(n_i)$ is defined so that, if the observations are normally distributed, the expected value of $R_i$ is $d_2(n_i)\sigma$. Thus, $\hat{\sigma}$ is the unweighted average of $N$ unbiased estimates of $\sigma$. This method is described by the American Society for Testing and Materials (1976).

The RNOWEIGHT method is available in the BOXCHART, MCHART, MRCHART, RCHART, XCHART, and XRCHART statements. It is the default in the MCHART, MRCHART, RCHART, XCHART, and XRCHART statements.

**SMVLUE Method**

If you specify SMETHOD=SMVLUE, a minimum variance linear unbiased estimate (MVLUE) is computed for $\sigma$; see Burr (1969, 1976) and Nelson (1989, 1994). This estimate is a weighted average of $N$ unbiased estimates of $\sigma$ of the form $s_i/c_4(n_i)$, and it is computed as

$$\hat{\sigma} = \frac{h_1s_1/c_4(n_1) + \cdots + h_Ns_N/c_4(n_N)}{h_1 + \cdots + h_N}$$

where

$$h_i = \frac{[c_4(n_i)]^2}{1 - [c_4(n_i)]^2}$$

A subgroup standard deviation $s_i$ is included in the calculation only if $n_i \geq 2$, and $N$ is the number of subgroups for which $n_i \geq 2$. The MVLUE assigns greater weight to estimates of $\sigma$ from subgroups with larger sample sizes, and it is intended for situations where the subgroup sample sizes vary. If the subgroup sample sizes are constant, the SMVLUE estimate reduces to the SNOWEIGHT estimate.

The SMVLUE method is available in the BOXCHART, MCHART, SCHART, XCHART, and XSCHART statements.

**SNOWEIGHT Method**

If you specify SMETHOD=SNOWEIGHT, the estimate for $\sigma$ is

$$\hat{\sigma} = \frac{s_1/c_4(n_1) + \cdots + s_N/c_4(n_N)}{N}$$

where $N$ is the number of subgroups for which $n_i \geq 2$, $s_i$ is the sample standard deviation of the $i$th subgroup,

$$s_i = \sqrt{\frac{1}{n_i - 1} \sum_{j=1}^{n_i} (x_{ij} - \bar{X}_i)^2}$$
and
\[ c_4(n_i) = \frac{\Gamma(n_i/2) \sqrt{2/(n_i - 1)}}{\Gamma((n_i - 1)/2)} \]

Here \( \Gamma(\cdot) \) denotes the gamma function, and \( \bar{X}_i \) denotes the \( i \)th subgroup mean. A subgroup standard deviation \( s_i \) is included in the calculation only if \( n_i \geq 2 \). If the observations are normally distributed, the expected value of \( s_i \) is \( c_4(n_i) \sigma \). Thus, \( \hat{\sigma} \) is the unweighted average of \( N \) unbiased estimates of \( \sigma \). This method is described by the American Society for Testing and Materials (1976).

The SNOWEIGHT method is available in the BOXCHART, MCHART, SCHART, XCHART, and XSCHART statements. It is the default in the BOXCHART, SCHART, and XSCHART statements.

**Percentile Definitions**

You can use the PCTLDEF= option in the BOXCHART statement to specify one of five definitions for computing quantile statistics (percentiles). Let \( n \) equal the number of nonmissing values for a variable, and let \( x_1, x_2, \ldots, x_n \) represent the ordered values of the process variable. For the \( t \)th percentile, set \( p = t/100 \), and express \( np \) as
\[ np = j + g \]
where \( j \) is the integer part of \( np \), and \( g \) is the fractional part of \( np \).

The \( t \)th percentile (call it \( y \)) can be defined in five ways, as described in the next five sections.

**PCTLDEF=1**

This definition uses the weighted average at \( x_{np} \),
\[ y = (1 - g)x_j + gx_{j+1} \]
where \( x_0 \) is taken to be \( x_1 \).

**PCTLDEF=2**

This definition uses the observation numbered closest to \( np \),
\[ y = x_i \]
where \( i \) is the integer part of \( np + 1/2 \).

**PCTLDEF=3**

This definition uses the empirical distribution function:
\[
\begin{align*}
  y &= x_j & \text{if } g = 0 \\
  y &= x_{j+1} & \text{if } g > 0
\end{align*}
\]
Constructing Charts for Numbers of Nonconformities (c Charts)

You produce control charts for numbers of nonconformities by using the CCHART statement.

The following notation is used in this section:

- $u$: Expected number of nonconformities per unit that the process produces.
- $u_i$: Number of nonconformities per unit in the $i$th subgroup.
- $c_i$: Total number of nonconformities in the $i$th subgroup.
- $n_i$: Number of inspection units in the $i$th subgroup. Typically, $n_i = 1$ and $u_i = c_i$ for $c$ charts. In general, $u_i = c_i/n_i$.
- $\bar{u}$: Average number of nonconformities per unit taken across subgroups. The quantity $\bar{u}$ is computed as a weighted average:

$$\bar{u} = \frac{n_1 u_1 + \cdots + n_N u_N}{n_1 + \cdots + n_N} = \frac{c_1 + \cdots + c_N}{n_1 + \cdots + n_N}$$

- $N$: Number of subgroups.

Subgroup Summary Statistics

Each point on a $c$ chart represents the total number of nonconformities ($c_i$) in a subgroup. For example, Figure 15.5 displays three sections of pipeline that are inspected for defective welds (indicated by an X). Each section represents a subgroup that consists of a number of inspection units, which are 1,000-foot sections. The number of units in the $i$th subgroup is denoted by $n_i$, which is the subgroup sample size. The value of $n_i$ can be fractional; Figure 15.5 shows $n_3 = 2.5$ units in the third subgroup.
The number of nonconformities in the $i$th subgroup is denoted by $c_i$. The number of nonconformities per unit in the $i$th subgroup is denoted by $u_i = c_i/n_i$. In Figure 15.5, the number of welds per inspection unit in the third subgroup is $u_3 = 2/2.5 = 0.8$.

A $u$ chart that is created by the UCHART statement plots the quantity $u_i$ for the $i$th subgroup (see the section “Constructing Charts for Nonconformities per Unit ($u$ Charts)” on page 814). An advantage of a $u$ chart is that the value of the central line at the $i$th subgroup does not depend on $n_i$. This is not the case for a $c$ chart, so a $u$ chart is often preferred when the number of units $n_i$ is not constant across subgroups.

### Central Line

On a $c$ chart, the central line indicates an estimate for $n_i\hat{u}$, which is computed as $n_i\bar{u}$. If you specify a known value ($u_0$) for $u$, the central line indicates the value of $n_iu_0$.

Note that the central line varies with subgroup sample size $n_i$. When $n_i = 1$ for all subgroups, the central line has the constant value $\hat{c} = (c_1 + \cdots + c_N)/N$.

### Control Limits

The control limits are computed as a specified multiple ($k$) of the standard error of $c_i$ above and below the central line. The default limits are computed using $k = 3$ (these are referred to as $3\sigma$ limits).

The lower and upper control limits, LCLC and UCLC, respectively, are given by

\[
\text{LCLC} = \max\left(n_i\bar{u} - k\sqrt{n_i\bar{u}} \, , \, 0\right) \\
\text{UCLC} = n_i\bar{u} + k\sqrt{n_i\bar{u}}
\]
The lower and upper control limits vary with the number of inspection units per subgroup \( n_i \). If \( n_i = 1 \) for all subgroups, the control limits have constant values, as follows:

\[
\begin{align*}
LCLC &= \max \left( \bar{c} - k \sqrt{\bar{c}} , 0 \right) \\
UCLC &= \bar{c} + k \sqrt{\bar{c}}
\end{align*}
\]

If a standard value \( u_0 \) is available for \( u \), replace \( \bar{u} \) with \( u_0 \) in the formulas for the control limits. You can specify parameters for the limits as follows:

- Specify \( k \) by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify a constant nominal sample size \( n_i \equiv n \) for the control limits by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify \( u_0 \) by using the variable _U_ in a LIMITS= data table.

---

**Constructing Charts for Number Nonconforming (np Charts)**

You produce control charts for number nonconforming by using the NPCHART statement.

The following notation is used in this section:

- \( p \) Expected proportion of nonconforming items that the process produces
- \( p_i \) Proportion of nonconforming items in the \( i \)th subgroup
- \( X_i \) Number of nonconforming items in the \( i \)th subgroup
- \( n_i \) Number of items in the \( i \)th subgroup
- \( \bar{p} \) Average proportion of nonconforming items taken across subgroups:
  \[
  \bar{p} = \frac{n_1 p_1 + \cdots + n_N p_N}{n_1 + \cdots + n_N} = \frac{X_1 + \cdots + X_N}{n_1 + \cdots + n_N}
  \]
- \( N \) Number of subgroups

**Subgroup Summary Statistics**

Each point on an \( np \) chart represents the observed number (\( X_i \)) of nonconforming items in a subgroup. For example, in Figure 15.6 the first subgroup contains 12 items, of which 3 are nonconforming. The summary statistic for the first subgroup is \( X_1 = 3 \).
Note that a \( p \) chart displays the proportion of nonconforming items \( p_i \). You can use the PCHART statement to create \( p \) charts; for more information, see the section “Constructing Charts for Proportion Nonconforming (\( p \) Charts)” on page 813.

**Central Line**

By default, the central line on an \( np \) chart indicates an estimate for \( n_i p \), which is computed as \( n_i \bar{p} \). If you specify a known value (\( p_0 \)) for \( p \), the central line indicates the value of \( n_i p_0 \). Note that the central line varies with \( n_i \).

**Control Limits**

The control limits are computed as a specified multiple \( (k) \) of the standard error of \( X_i \) above and below the central line. The default limits are computed using \( k = 3 \) (these are referred to as 3\( \sigma \) limits).

The lower and upper control limits, LCL and UCL, respectively, are computed as

\[
\begin{align*}
\text{LCL} &= \max \left( n_i \bar{p} - k \sqrt{n_i \bar{p}(1 - \bar{p})} , 0 \right) \\
\text{UCL} &= \min \left( n_i \bar{p} + k \sqrt{n_i \bar{p}(1 - \bar{p})} , n_i \right)
\end{align*}
\]

You can specify parameters for the limits as follows:

- Specify \( k \) by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify a constant nominal sample size \( n_i \equiv n \) for the control limits by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify \( p_0 \) by using the variable _P_ in the LIMITS= data table.
Constructing Charts for Proportion Nonconforming (p Charts)

You produce control charts for proportion nonconforming by using the PCHART statement.

The following notation is used in this section:

- $p$: Expected proportion of nonconforming items that the process produces
- $p_i$: Proportion of nonconforming items in the $i$th subgroup
- $X_i$: Number of nonconforming items in the $i$th subgroup
- $n_i$: Number of items in the $i$th subgroup
- $\bar{p}$: Average proportion of nonconforming items taken across subgroups:
  \[
  \bar{p} = \frac{n_1 p_1 + \cdots + n_N p_N}{n_1 + \cdots + n_N} = \frac{X_1 + \cdots + X_N}{n_1 + \cdots + n_N}
  \]
- $N$: Number of subgroups

Subgroup Summary Statistics

Each point on a $p$ chart represents the observed proportion ($p_i = X_i/n_i$) of nonconforming items in a subgroup. For example, in Figure 15.7 the second subgroup contains 16 items, of which 2 are nonconforming. The summary statistic for the second subgroup is $p_2 = 2/16 = 0.125$.

Figure 15.7 Proportions versus Counts

Note that an $np$ chart displays the number (count) of nonconforming items $X_i$. You can use the NPCHART statement to create $np$ charts; for more information, see the section “Constructing Charts for Number Nonconforming (np Charts)” on page 811.
Central Line

By default, the central line on a \( p \) chart indicates an estimate of \( p \) that is computed as \( \hat{p} \). If you specify a known value (\( p_0 \)) for \( p \), the central line indicates the value of \( p_0 \).

Control Limits

The control limits are computed as a specified multiple (\( k \)) of the standard error of \( p_i \) above and below the central line. The default limits are computed using \( k = 3 \) (these are referred to as \( 3\sigma \) limits).

The lower and upper control limits, LCL and UCL, respectively, are computed as

\[
\begin{align*}
\text{LCL} & = \max \left( \hat{p} - k \sqrt{\hat{p}(1 - \hat{p})/n_i}, 0 \right) \\
\text{UCL} & = \min \left( \hat{p} + k \sqrt{\hat{p}(1 - \hat{p})/n_i}, 1 \right)
\end{align*}
\]

You can specify parameters for the limits as follows:

- Specify \( k \) by using the \texttt{SIGMAS=} option or the variable \texttt{_SIGMAS_} in a \texttt{LIMITS=} data table.
- Specify a constant nominal sample size \( n_i \equiv n \) for the control limits by using the \texttt{LIMITN=} option or the variable \texttt{_LIMITN_} in a \texttt{LIMITS=} data table.
- Specify \( p_0 \) by using the variable \texttt{_P_} in a \texttt{LIMITS=} data table.

Constructing Charts for Nonconformities per Unit (\( u \) Charts)

You produce control charts for nonconformities per unit by using the \texttt{UCHART} statement.

The following notation is used in this section:

\[
\begin{align*}
\bar{u} & \quad \text{Expected number of nonconformities per unit that the process produces} \\
\bar{u}_i & \quad \text{Number of nonconformities per unit in the } i\text{th subgroup. In general, } u_i = c_i/n_i. \\
c_i & \quad \text{Total number of nonconformities in the } i\text{th subgroup} \\
n_i & \quad \text{Number of inspection units in the } i\text{th subgroup} \\
\bar{u} & \quad \text{Average number of nonconformities per unit taken across subgroups. The quantity } \bar{u} \text{ is computed as a weighted average:} \\
\bar{u} & = \frac{n_1u_1 + \cdots + n_Nu_N}{n_1 + \cdots + n_N} = \frac{c_1 + \cdots + c_N}{n_1 + \cdots + n_N} \\
N & \quad \text{Number of subgroups}
\end{align*}
\]
Subgroup Summary Statistics

Each point on a $u$ chart indicates the number of nonconformities per unit ($u_i$) in a subgroup. For example, Figure 15.8 displays three sections of pipeline that are inspected for defective welds (indicated by an X). Each section represents a subgroup that consists of a number of inspection units, which are 1,000-foot sections. The number of units in the $i$th subgroup is denoted by $n_i$, which is the subgroup sample size.

The number of nonconformities in the $i$th subgroup is denoted by $c_i$. The number of nonconformities per unit in the $i$th subgroup is denoted by $u_i = c_i / n_i$. In Figure 15.8, the number of defective welds per unit in the third subgroup is $u_3 = 2/2.5 = 0.8$.

A $u$ chart plots the quantity $u_i$ for the $i$th subgroup. A $c$ chart plots the quantity $c_i$ for the $i$th subgroup (for more information, see the section “Constructing Charts for Numbers of Nonconformities ($c$ Charts)” on page 809). An advantage of a $u$ chart is that the value of the central line at the $i$th subgroup does not depend on $n_i$. This is not the case for a $c$ chart, so a $u$ chart is often preferred when the number of units $n_i$ is not constant across subgroups.

Central Line

On a $u$ chart, the central line indicates an estimate of $u$, which is computed as $\bar{u}$ by default. If you specify a known value ($u_0$) for $u$, the central line indicates the value of $u_0$.

Control Limits

The control limits are computed as a specified multiple ($k$) of the standard error of $u_i$ above and below the central line. The default limits are computed using $k = 3$ (these are referred to as $3\sigma$ limits).
The lower and upper control limits, LCLU and UCLU, respectively, are given by

\[
\begin{align*}
LCLU & = \max \left( \bar{u} - k \sqrt{\bar{u}/n_i} , 0 \right) \\
UCLU & = \bar{u} + k \sqrt{\bar{u}/n_i}
\end{align*}
\]

The limits vary with \( n_i \).

You can specify parameters for the limits as follows:

- Specify \( k \) by using the SIGMAS= option or the variable _SIGMAS_ in a LIMITS= data table.
- Specify a constant nominal sample size \( n_i \equiv n \) for the control limits by using the LIMITN= option or the variable _LIMITN_ in a LIMITS= data table.
- Specify \( u_0 \) by using the variable _U_ in a LIMITS= data table.

---

**Tests for Special Causes**

This section provides details about tests for special causes that you can apply by using the SPC procedure.

The SPC procedure provides eight standard tests for special causes, also referred to as rules for lack of control, supplementary rules, runs tests, runs rules, pattern tests, and Western Electric rules. These tests improve the sensitivity of the Shewhart chart to small changes in the process. You can also improve the sensitivity of the chart by increasing the rate of sampling, increasing the subgroup sample size, and using control limits that represent less than three standard errors of variation from the central line. However, increasing the sampling rate and sample size is often impractical, and tightening the control limits increases the chances of falsely signaling an out-of-control condition. By detecting particular nonrandom patterns in the subgroup summary statistics, the tests can provide greater sensitivity and useful diagnostic information while incurring a reasonable probability of a false signal.

The patterns that the eight standard tests detect are defined in Table 15.32 and Table 15.33 and illustrated in Figure 15.9 and Figure 15.10. All eight tests were developed for use with fixed 3\( \sigma \) limits. The tests are indexed according to the numbering sequence used by Nelson (1984, 1985). You can request any combination of the eight tests by specifying the test indexes in the TESTS= option in the BOXCHART, CCHART, IRCHART, MCHART, MRCHART, NPCHART, PCHART, UCHART, XCHART, XRCHART, and XSCHART statements.
The following restrictions apply to the tests:

- Only Tests 1, 2, 3, and 4 are recommended for \( c \) charts, \( np \) charts, \( p \) charts, and \( u \) charts that you create using the CCHART, NPCHART, PCHART, and UCHART statements, respectively. In these four cases, you should not use Test 2 unless the process distribution is symmetric or nearly symmetric.

- By default, the TESTS= option is not applied when the control limits are not 3\( \sigma \) limits or vary with subgroup sample size. You can use the NO3SIGMACHECK option to request tests for special causes when the SIGMAS= option specifies control limits other than 3\( \sigma \) limits. This is not recommended for standard control chart applications, because the standard tests for special causes are based on 3\( \sigma \) limits. You can apply tests for special causes when control limits vary with subgroup sample size by using the LIMITN= or TESTNSTD option (for more information, see the section “Applying Tests with Varying Subgroup Sample Sizes” on page 821).

**Table 15.32** Definitions of Tests 1 to 4

<table>
<thead>
<tr>
<th>Test Index</th>
<th>Pattern Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>One point beyond Zone A (outside the control limits)</td>
</tr>
<tr>
<td>2</td>
<td>Nine points in a row in Zone C or beyond on one side of the central line (see Note 1 after Figure 15.9)</td>
</tr>
<tr>
<td>3</td>
<td>Six points in a row that steadily increase or steadily decrease (see Note 2 after Figure 15.9)</td>
</tr>
<tr>
<td>4</td>
<td>Fourteen points in a row that alternate up and down</td>
</tr>
</tbody>
</table>
Figure 15.9 Examples of Tests 1 to 4

Notes:

1. You can specify the number of points in Test 2 as 7, 8, 9, 11, 14, or 20 in the TEST2RUN= option.

2. You can specify the number of points in Test 3 as 6, 7, or 8 in the TEST3RUN= option.
Table 15.33  Definitions of Tests 5 to 8

<table>
<thead>
<tr>
<th>Test Index</th>
<th>Pattern Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>Two out of three points in a row in Zone A or beyond</td>
</tr>
<tr>
<td>6</td>
<td>Four out of five points in a row in Zone B or beyond</td>
</tr>
<tr>
<td>7</td>
<td>Fifteen points in a row in Zone C on either or both sides of the central line</td>
</tr>
<tr>
<td>8</td>
<td>Eight points in a row on either or both sides of the central line, with no points in Zone C</td>
</tr>
</tbody>
</table>

Figure 15.10  Examples of Tests 5 to 8
Interpreting Tests for Special Causes

Nelson (1984, 1985) makes the following comments about interpreting the tests for special causes:

- When a process is in statistical control, the chance of a false signal for each test is less than 5 in 1,000.
- Test 1 is positive if there is a shift in the process mean, if there is an increase in the process standard deviation, or if there is a “single aberration in the process such as a mistake in calculation, an error in measurement, bad raw material, a breakdown of equipment, and so on” (Nelson 1985).
- Test 2 signals a shift in the process mean. The use of nine points (rather than seven, as in Grant and Leavenworth 1988 for the pattern that defines Test 2 makes the chance of a false signal comparable to that of Test 1. (To control the number of points for the pattern in test 2, use the TEST2RUN= option in the chart statement.)
- Test 3 signals a drift in the process mean. Nelson (1985) states that causes can include “tool wear, depletion of chemical baths, deteriorating maintenance, improvement in skill, and so on.”
- Test 4 signals “a systematic effect such as produced by two machines, spindles, operators or vendors used alternately” (Nelson 1985).
- Tests 1, 2, 3, and 4 should be applied routinely; the combined chance of a false signal from one or more of these tests is less than 1 in 100. Nelson (1985) describes these tests as “a good set that will react to many commonly occurring special causes.”
- In the case of charts for variables, the first four tests should be augmented by Tests 5 and 6 when earlier warning is desired. The chance of a false signal increases to 2 in 100.
- Tests 7 and 8 indicate stratification (observations in a subgroup have multiple sources with different means). Test 7 is positive when the observations in the subgroup always have multiple sources. Test 8 is positive when the subgroups are taken from one source at a time.

Nelson (1985) also comments that “the probabilities quoted for getting false signals should not be considered to be very accurate” because the probabilities are based on assumptions of normality and independence that might not be satisfied. Consequently, he recommends that the tests “should be viewed as simply practical rules for action rather than tests having specific probabilities associated with them.” Nelson cautions that “it is possible, though unlikely, for a process to be out of control yet not show any signals from these eight tests.”

Modifying Standard Tests for Special Causes

Some textbooks and references present slightly different versions of Tests 2 and 3. You can use the following options to request these modifications:

- TEST2RUN=run-length specifies the length of the pattern for Test 2. The form of the test for each run-length is shown in the following table. The default run-length is 9.
Tests for Special Causes

<table>
<thead>
<tr>
<th>run-length</th>
<th>Number of Points on One Side of the Central Line</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>7 in a row</td>
</tr>
<tr>
<td>8</td>
<td>8 in a row</td>
</tr>
<tr>
<td>9</td>
<td>9 in a row</td>
</tr>
<tr>
<td>11</td>
<td>At least 10 out of 11 in a row</td>
</tr>
<tr>
<td>14</td>
<td>At least 12 out of 14 in a row</td>
</tr>
<tr>
<td>20</td>
<td>At least 16 out of 20 in a row</td>
</tr>
</tbody>
</table>

• TEST3RUN=run-length specifies the length of the pattern for Test 3. The run-length values that you can specify are 6, 7, and 8. The default run-length is 6.

The Western Electric Company (now AT&T) Statistical Quality Control Handbook (1956) and Montgomery (1996) discuss a test that is signaled by eight points in a row in Zone C or beyond (on one side of the central line). You can request this test by specifying TESTS=2 and TEST2RUN=8. The Handbook also discusses tests that correspond to Tests 1, 5, 6, 7, and 8. Kume (1985) recommends a number of tests for special causes that can be regarded as modifications of Tests 2 and 3:

• seven points in a row on one side of the central line. Specify TESTS=2 and TEST2RUN=7.

• at least 10 out of 11 points in a row on one side of the central line. Specify TESTS=2 and TEST2RUN=11.

• at least 12 out of 14 points in a row on one side of the central line. Specify TESTS=2 and TEST2RUN=14.

• at least 16 out of 20 points in a row on one side of the central line. Specify TESTS=2 and TEST2RUN=20.

• seven points in a row that steadily increase or decrease. Specify TESTS=3 and TEST3RUN=7.

Applying Tests with Varying Subgroup Sample Sizes

Nelson (1989, 1994) describes the use of standardization to apply the tests for special causes to data that involve varying subgroup samples. This approach applies the tests to the standardized subgroup statistics, setting the control limits at ±3 and the zone boundaries at ±1 and ±2. For example, for an $\bar{X}$ chart with subgroup means $\bar{X}_i$ and varying subgroup sample sizes $n_i$, the tests are applied to the standardized values $z_i = (\overline{X}_i - \overline{X})/(s/\sqrt{n_i})$, where $\overline{X}$ estimates the process mean and $s$ estimates the process standard deviation. You can request this method by using the TESTNSTD option.

Alternatively, you can handle varying subgroup sample sizes by specifying a nominal sample size in the LIMITN= option. If you specify LIMITN=n, the control limits are computed for the fixed value n, and they do not vary with the subgroup sample sizes. Moreover, subgroup summary statistics are computed only for those subgroups whose sample size is equal to n; only those subgroups are included in the results. You can specify the ALLN option in conjunction with the LIMITN= option to force subgroup summary statistics to be computed for all subgroups, regardless of subgroup sample size.
Input Data Tables

**DATA= Data Table**

The SPC procedure accepts a primary input data table that you specify in the DATA= option in the PROC SPC statement. This data table contains measurements of one or more process quality characteristics. Data to be analyzed by using the CCHART, IRCHART, NPCHART, PCHART, or UCHART statement should contain one observation per subgroup. Data to be analyzed by using other chart statements usually contain multiple observations per subgroup.

The DATA= data table must contain the following variables:

- the process name variable, which contains the names of the process variables. You specify it in the PROCESSNAME= option in the PROC SPC statement.
- the process value variable, which contains the process measurements. You specify it in the PROCESSVALUE= option in the PROC SPC statement.
- the subgroup name variables, which contains the names of the subgroup variables. You specify it in the SUBGROUPNAME= option in the PROC SPC statement.
- the subgroup value variable, which contains the subgroup values. You specify it in the SUBGROUPVALUE= option in the PROC SPC statement.

An input data table that contains attribute data (see the section “Classification of Shewhart Charts” on page 777) can also include a variable that contains the number of inspection units per subgroup. You specify this variable in the SUBGROUPN= option in the chart statement. It is required in the NPCHART, PCHART, and UCHART statements and optional in the CCHART statement.

The DATA= data table can also contain BY variables (see the section “BY Statement” on page 783).

**LIMITS= Data Table**

You can read preestablished control limits or parameters from which the control limits can be calculated from a LIMITS= data table that you specify by using the LIMITS= option in the PROC SPC statement. The LIMITS= data table can be an OUTLIMITS= data table that was created in a previous run of the SPC procedure. Such data tables always contain the variables that a LIMITS= data table requires. For more information about the variables that are included in an OUTLIMITS= data table, see the section “OUTLIMITS= Data Table” on page 823.

The LIMITS= data table must contain the following variables:

- the process name variable, which contains the names of the process variables. You specify it in the PROCESSNAME= option in the PROC SPC statement.
- the subgroup name variable, which contains the names of the subgroup variables. You specify it in the SUBGROUPNAME= option in the PROC SPC statement.

For each control chart type, Table 15.34 lists the variables that are required to specify parameters from which control limits are calculated and the variables that contain preestablished control limits.
Table 15.34 Variables in the LIMITS= Data Table

<table>
<thead>
<tr>
<th>Chart Type</th>
<th>Parameters</th>
<th>Limits</th>
</tr>
</thead>
<tbody>
<tr>
<td>c</td>
<td><em>U</em></td>
<td><em>LCLC</em> , <em>C</em> , <em>UCLC</em></td>
</tr>
<tr>
<td>Individual</td>
<td><em>MEAN</em> , <em>STDDEV</em></td>
<td><em>LCLI</em> , <em>MEAN</em> , <em>UCLI</em></td>
</tr>
<tr>
<td>Moving range</td>
<td><em>STDDEV</em></td>
<td><em>LCLR</em> , <em>R</em> , <em>UCLR</em></td>
</tr>
<tr>
<td>Medians</td>
<td><em>MEAN</em> , <em>STDDEV</em></td>
<td><em>LCLM</em> , <em>MEAN</em> , <em>UCLM</em></td>
</tr>
<tr>
<td>np</td>
<td><em>P</em></td>
<td><em>LCLNP</em> , <em>NP</em> , <em>UCLNP</em></td>
</tr>
<tr>
<td>p</td>
<td><em>P</em></td>
<td><em>LCLP</em> , <em>P</em> , <em>UCLP</em></td>
</tr>
<tr>
<td>R</td>
<td><em>STDDEV</em></td>
<td><em>LCLR</em> , <em>R</em> , <em>UCLR</em></td>
</tr>
<tr>
<td>s</td>
<td><em>STDDEV</em></td>
<td><em>LCLS</em> , <em>S</em> , <em>UCLS</em></td>
</tr>
<tr>
<td>u</td>
<td><em>U</em></td>
<td><em>LCLU</em> , <em>U</em> , <em>UCLU</em></td>
</tr>
<tr>
<td>( \bar{X} )</td>
<td><em>MEAN</em> , <em>STDDEV</em></td>
<td><em>LCLX</em> , <em>MEAN</em> , <em>UCLX</em></td>
</tr>
</tbody>
</table>

Notes:

1. You can include the variable _LIMITN_, with or without parameters and limits variables, to specify different nominal subgroup sizes for different processes.

2. The variables _SIGMAS_ and _TYPE_ are optional, but they are recommended to maintain a complete set of control limit information. The variable _TYPE_ must be a character variable of length 8; valid values are ‘ESTIMATE’, ‘STANDARD’, ‘STDMU’, and ‘STDSIGMA’.

3. If you specify a BY statement, the LIMITS= data table must also contain the specified BY variables.

Output Data Tables

OUTLIMITS= Data Table

An OUTLIMITS= data table contains control limits and control limit parameters. It contains one observation for each process. The following variables are always included in an OUTLIMITS= data table:

- the process name variable, which contains the names of the process variables. You specify it in the PROCESSNAME= option in the PROC SPC statement.

- the subgroup name variable, which contains the names of the subgroup variables. You specify it in the SUBGROUPNAME= option in the PROC SPC statement.

In addition, if you specify any BY variables, they are included in the OUTLIMITS= data table.

The other variables that are included in an OUTLIMITS= data table depend on which chart statement produced that data table. Table 15.35 lists the variables that are included in OUTLIMITS= data tables for the different chart statements.
### Table 15.35 Variables in the OUTLIMITS= Data Table

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>BOXCHART Statement</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>LCLM</em></td>
<td>✓</td>
<td>Lower control limit for subgroup median</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>✓</td>
<td>Lower control limit for subgroup range</td>
</tr>
<tr>
<td><em>LCLS</em></td>
<td>✓</td>
<td>Lower control limit for subgroup standard deviation</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>✓</td>
<td>Lower control limit for subgroup mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>✓</td>
<td>Process mean (value of central line on box chart)</td>
</tr>
<tr>
<td><em>R</em></td>
<td>✓</td>
<td>Value of central line on R chart</td>
</tr>
<tr>
<td><em>S</em></td>
<td>✓</td>
<td>Value of central line on s chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple (k) of standard error of $\bar{X}_i$ or $M_i$</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLM</em></td>
<td>✓</td>
<td>Upper control limit for subgroup median</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>✓</td>
<td>Upper control limit for subgroup range</td>
</tr>
<tr>
<td><em>UCLS</em></td>
<td>✓</td>
<td>Upper control limit for subgroup standard deviation</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>✓</td>
<td>Upper control limit for subgroup mean</td>
</tr>
<tr>
<td><strong>CCHART Statement</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C</em></td>
<td>✓</td>
<td>Value of central line on c chart ($n_i \bar{u}$ or $n_i u_0$)</td>
</tr>
<tr>
<td><em>LCLC</em></td>
<td>✓</td>
<td>Lower control limit for number of nonconformities</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Sample size associated with the control limits</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple (k) of standard error of $c_i$</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>U</em></td>
</tr>
<tr>
<td><em>U</em></td>
<td></td>
<td>Average number of nonconformities per unit ($\bar{u}$ or $u_0$)</td>
</tr>
<tr>
<td><em>UCLC</em></td>
<td>✓</td>
<td>Upper control limit for number of nonconformities</td>
</tr>
<tr>
<td><strong>IRCHART Statement</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>LCLI</em></td>
<td></td>
<td>Lower control limit for individual measurements</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td></td>
<td>Lower control limit for moving ranges</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td></td>
<td>Number of consecutive measurements that are used to compute moving ranges</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td></td>
<td>Process mean</td>
</tr>
<tr>
<td><em>R</em></td>
<td></td>
<td>Value of central line on moving range chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple (k) of standard error of individual measurement or moving range</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLI</em></td>
<td></td>
<td>Upper control limit for individual measurements</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td></td>
<td>Upper control limit for moving ranges</td>
</tr>
<tr>
<td><strong>MCHART Statement</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>LCLM</em></td>
<td>✓</td>
<td>Lower control limit for subgroup median</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>✓</td>
<td>Lower control limit for subgroup range</td>
</tr>
<tr>
<td><em>LCLS</em></td>
<td>✓</td>
<td>Lower control limit for subgroup standard deviation</td>
</tr>
</tbody>
</table>
**Table 15.35  continued**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td></td>
<td>Value of central line on median chart ($\bar{M}$, $\tilde{M}$, $\bar{X}$, or $\mu_0$)</td>
</tr>
<tr>
<td><em>R</em></td>
<td>✓</td>
<td>Value of central line on $R$ chart</td>
</tr>
<tr>
<td><em>S</em></td>
<td>✓</td>
<td>Value of central line on $s$ chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $M_i$</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLM</em></td>
<td>✓</td>
<td>Upper control limit for subgroup median</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>✓</td>
<td>Upper control limit for subgroup range</td>
</tr>
<tr>
<td><em>UCLS</em></td>
<td>✓</td>
<td>Upper control limit for subgroup standard deviation</td>
</tr>
</tbody>
</table>

**MRCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LCLM</em></td>
<td>✓</td>
<td>Lower control limit for subgroup median</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>✓</td>
<td>Lower control limit for subgroup range</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td></td>
<td>Estimate of process mean ($\bar{M}$, $\tilde{M}$, $\bar{X}$, or $\mu_0$)</td>
</tr>
<tr>
<td><em>R</em></td>
<td>✓</td>
<td>Value of central line on range chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $M_i$ or $R_i$</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLM</em></td>
<td>✓</td>
<td>Upper control limit for subgroup median</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>✓</td>
<td>Upper control limit for subgroup range</td>
</tr>
</tbody>
</table>

**NPCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LCLNP</em></td>
<td>✓</td>
<td>Lower control limit for number of nonconforming items</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Sample size associated with the control limits</td>
</tr>
<tr>
<td><em>NP</em></td>
<td>✓</td>
<td>Average number of nonconforming items ($n_i \bar{p}$ or $n_i p_0$)</td>
</tr>
<tr>
<td><em>P</em></td>
<td></td>
<td>Average proportion of nonconforming items ($\bar{p}$ or $p_0$)</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $X_i$</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (standard or estimate) of <em>NP</em></td>
</tr>
<tr>
<td><em>UCLNP</em></td>
<td>✓</td>
<td>Upper control limit for number of nonconforming items</td>
</tr>
</tbody>
</table>

**PCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LCLP</em></td>
<td>✓</td>
<td>Lower control limit for proportion of nonconforming items</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>P</em></td>
<td></td>
<td>Average proportion of nonconforming items ($\bar{p}$ or $p_0$)</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $p_i$</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (standard or estimate) of <em>P</em></td>
</tr>
<tr>
<td><em>UCLP</em></td>
<td>✓</td>
<td>Upper control limit for proportion of nonconforming items</td>
</tr>
</tbody>
</table>

**RCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LCLR</em></td>
<td>✓</td>
<td>Lower control limit for subgroup range</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>✓</td>
<td>Lower control limit for subgroup mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Sample size associated with the control limits</td>
</tr>
</tbody>
</table>
**Table 15.35 continued**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>MEAN</em></td>
<td></td>
<td>Process mean ($\overline{X}$)</td>
</tr>
<tr>
<td><em>R</em></td>
<td>✓</td>
<td>Value of central line on $R$ chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $R_i$</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td></td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>✓</td>
<td>Upper control limit for subgroup range</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>✓</td>
<td>Upper control limit for subgroup mean</td>
</tr>
</tbody>
</table>

**SCHART Statement**

| _LCLS_  | ✓       | Lower control limit for subgroup standard deviation |
| _LCLX_  | ✓       | Lower control limit for subgroup mean |
| _LIMITN_ | ✓       | Sample size associated with the control limits |
| _MEAN_  |         | Process mean ($\overline{X}$ or $\mu_0$) |
| _S_     | ✓       | Value of central line on $s$ chart |
| _SIGMAS_ |         | Multiple ($k$) of standard error of $\overline{X}_i$ or $s_i$ |
| _STDDEV_ |         | Process standard deviation |
| _TYPE_  |         | Type (estimate or standard value) of _MEAN_ and _STDDEV_ |
| _UCLS_  | ✓       | Upper control limit for subgroup standard deviation |
| _UCLX_  | ✓       | Upper control limit for subgroup mean |

**UCHART Statement**

| _CLU_   | ✓       | Lower control limit for number of nonconformities per unit |
| _LIMITN_ | ✓       | Sample size associated with the control limits |
| _SIGMAS_ |         | Multiple ($k$) of standard error of $u_i$ |
| _TYPE_  |         | Type (estimate or standard value) of _U_ |
| _U_     |         | Value of central line of $u$ chart ($\bar{u}$ or $u_0$) |
| _UCLU_  | ✓       | Upper control limit for number of nonconformities per unit |

**XCHART Statement**

| _LCLR_  | ✓       | Lower control limit for subgroup range |
| _LCLS_  | ✓       | Lower control limit for subgroup standard deviation |
| _LCLX_  | ✓       | Lower control limit for subgroup mean |
| _LIMITN_ | ✓       | Sample size associated with the control limits |
| _MEAN_  |         | Process mean ($\overline{X}$ or $\mu_0$) |
| _R_     | ✓       | Value of central line on $R$ chart |
| _S_     | ✓       | Value of central line on $s$ chart |
| _SIGMAS_ |         | Multiple ($k$) of standard error of $\overline{X}_i$ |
| _STDDEV_ |         | Process standard deviation |
| _TYPE_  |         | Type (estimate or standard value) of _MEAN_ and _STDDEV_ |
| _UCLR_  | ✓       | Upper control limit for subgroup range |
| _UCLS_  | ✓       | Upper control limit for subgroup standard deviation |
| _UCLX_  | ✓       | Upper control limit for subgroup mean |
### Table 15.35  continued

<table>
<thead>
<tr>
<th>Variable</th>
<th>Varying</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>XRCHART Statement</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>✓</td>
<td>Lower control limit for subgroup range</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>✓</td>
<td>Lower control limit for subgroup mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>✓</td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td></td>
<td>Process mean ($\bar{X}$ or $\mu_0$)</td>
</tr>
<tr>
<td><em>R</em></td>
<td>✓</td>
<td>Value of central line on $R$ chart</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td></td>
<td>Multiple ($k$) of standard error of $\bar{X}_i$ or $R_i$</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td></td>
<td>Process standard deviation</td>
</tr>
<tr>
<td><em>TYPE</em></td>
<td>✓</td>
<td>Type (estimate or standard value) of <em>MEAN</em> and <em>STDDEV</em></td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>✓</td>
<td>Upper control limit for subgroup range</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>✓</td>
<td>Upper control limit for subgroup mean</td>
</tr>
</tbody>
</table>

| **XSCHART Statement** |         |                                                  |
| _LCLS_    | ✓       | Lower control limit for subgroup standard deviation |
| _CLX_     | ✓       | Lower control limit for subgroup mean           |
| _LIMITN_  | ✓       | Nominal sample size associated with the control limits |
| _MEAN_    |         | Process mean ($\bar{X}$ or $\mu_0$)            |
| _S_       | ✓       | Value of central line on $s$ chart              |
| _SIGMAS_  |         | Multiple ($k$) of standard error of $\bar{X}_i$ or $s_i$ |
| _STDDEV_  |         | Process standard deviation                      |
| _TYPE_    | ✓       | Type (estimate or standard value) of _MEAN_ and _STDDEV_ |
| _UCLS_    | ✓       | Upper control limit for subgroup standard deviation |
| _UCLX_    | ✓       | Upper control limit for subgroup mean           |

**Notes:**

1. If the control limits vary with subgroup sample size, the special missing value $V$ is assigned to the variables that are indicated by a check mark (✓) in the Varying column of Table 15.35.

2. For all charts for variables, the OUTLIMITS= data table includes control limits for means or medians and for ranges or standard deviations. This enables you to use the OUTLIMITS= data table as a LIMITS= data table for different charts for variables.

3. For the BOXCHART statement, the variables _LCLM_ and _UCLM_ are included if you specify CONTROLSTAT=MEDIAN; otherwise, the variables _LCLX_ and _UCLX_ are included. The variables _LCLR_, _R_, and _UCLR_ are included if you specify SMETHOD=RMVLUE or RNOWEIGHT; otherwise, the variables _LCLS_, _S_, and _UCLS_ are included.

4. For the MCHART and XCHART statements, the variables _LCLS_, _S_, and _UCLS_ are included if you specify SMETHOD=RMSDF, SMVLUE, or SNOWEIGHT; otherwise, the variables _LCLR_, _R_, and _UCLR_ are included.
OUTTABLE= Data Table

An OUTTABLE= data table contains subgroup summary statistics, control limits, and related information. The following variables are always included in an OUTTABLE= data table:

- `_VAR_`, which contains the process variable name
- the subgroup name variable, which contains subgroup variable names. You specify the name of the subgroup name variable in the `SUBGROUPNAME=` option in the PROC statement.
- the subgroup variable, which contains subgroup variable values. You specify the name of the subgroup variable in the `SUBGROUPVALUE=` option in the PROC statement.

In addition, if you specify any BY variables, they are included in the OUTTABLE= data table.

The other variables that are included in an OUTTABLE= data table depend on which chart statement produced that data table. Table 15.36 lists the variables that are included in OUTTABLE= data tables for the different chart statements.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>BOXCHART Statement</strong></td>
<td></td>
</tr>
<tr>
<td><code>_EXLIM_</code></td>
<td>Control limit exceeded on box chart</td>
</tr>
<tr>
<td><code>_LCLM_</code></td>
<td>Lower control limit for median</td>
</tr>
<tr>
<td><code>_LCLX_</code></td>
<td>Lower control limit for mean</td>
</tr>
<tr>
<td><code>_LIMITN_</code></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><code>_MEAN_</code></td>
<td>Process mean</td>
</tr>
<tr>
<td><code>_SIGMAS_</code></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><code>_STDDEV_</code></td>
<td>Process standard deviation ($\hat{\sigma}$ or $\sigma_0$)</td>
</tr>
<tr>
<td><code>_SUBMAX_</code></td>
<td>Subgroup maximum</td>
</tr>
<tr>
<td><code>_SUBMED_</code></td>
<td>Subgroup median</td>
</tr>
<tr>
<td><code>_SUBMIN_</code></td>
<td>Subgroup minimum</td>
</tr>
<tr>
<td><code>_SUBN_</code></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><code>_SUBQ1_</code></td>
<td>Subgroup first quartile (25th percentile)</td>
</tr>
<tr>
<td><code>_SUBQ3_</code></td>
<td>Subgroup third quartile (75th percentile)</td>
</tr>
<tr>
<td><code>_SUBX_</code></td>
<td>Subgroup mean</td>
</tr>
<tr>
<td><code>_TESTS_</code></td>
<td>Tests for special causes signaled on box chart</td>
</tr>
<tr>
<td><code>_UCLM_</code></td>
<td>Upper control limit for median</td>
</tr>
<tr>
<td><code>_UCLX_</code></td>
<td>Upper control limit for mean</td>
</tr>
</tbody>
</table>

<p>| <strong>CCHART Statement</strong> | |
| <code>_C_</code> | Average number of nonconformities |
| <code>_EXLIM_</code> | Control limit exceeded on $c$ chart |
| <code>_LCLC_</code> | Lower control limit for number of nonconformities |
| <code>_LIMITN_</code> | Nominal sample size associated with the control limits |
| <code>_SIGMAS_</code> | Multiple ($k$) of the standard error associated with the control limits |
| <code>_SUBC_</code> | Subgroup number of nonconformities |
| <code>_SUBN_</code> | Subgroup sample size |</p>
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on c chart</td>
</tr>
<tr>
<td><em>UCLC</em></td>
<td>Upper control limit for number of nonconformities</td>
</tr>
</tbody>
</table>

**IRCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on individual measurements chart</td>
</tr>
<tr>
<td><em>EXLIMR</em></td>
<td>Control limit exceeded on moving range chart</td>
</tr>
<tr>
<td><em>LCLI</em></td>
<td>Lower control limit for individual measurements</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>Lower control limit for moving range</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Number of consecutive measurements that are used to compute moving ranges</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Process mean</td>
</tr>
<tr>
<td><em>R</em></td>
<td>Average range</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple (k) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation (( \hat{\sigma} ) or ( \sigma_0 ))</td>
</tr>
<tr>
<td><em>SUBI</em></td>
<td>Individual measurement</td>
</tr>
<tr>
<td><em>SUBR</em></td>
<td>Moving range</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on individual measurements chart</td>
</tr>
<tr>
<td><em>UCLI</em></td>
<td>Upper control limit for individual measurements</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>Upper control limit for moving range</td>
</tr>
</tbody>
</table>

**MCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on median chart</td>
</tr>
<tr>
<td><em>LCLM</em></td>
<td>Lower control limit for median</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Estimate of process mean (( \bar{M}, \bar{M}, \bar{X}, ) or ( \mu_0 ))</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple (k) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation (( \hat{\sigma} ) or ( \sigma_0 ))</td>
</tr>
<tr>
<td><em>SUBMED</em></td>
<td>Subgroup median</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on median chart</td>
</tr>
<tr>
<td><em>UCLM</em></td>
<td>Upper control limit for median</td>
</tr>
</tbody>
</table>

**MRCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on median chart</td>
</tr>
<tr>
<td><em>EXLIMR</em></td>
<td>Control limit exceeded on range chart</td>
</tr>
<tr>
<td><em>LCLM</em></td>
<td>Lower control limit for median</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>Lower control limit for range</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Estimate of process mean (( \bar{M}, \bar{M}, \bar{X}, ) or ( \mu_0 ))</td>
</tr>
<tr>
<td><em>R</em></td>
<td>Average range</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple (k) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation (( \hat{\sigma} ) or ( \sigma_0 ))</td>
</tr>
<tr>
<td><em>SUBM</em></td>
<td>Subgroup median</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
</tbody>
</table>
### Table 15.36  
**continued**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>SUBR</em></td>
<td>Subgroup range</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on median chart</td>
</tr>
<tr>
<td><em>TESTS2</em></td>
<td>Tests for special causes signaled on range chart</td>
</tr>
<tr>
<td><em>UCLM</em></td>
<td>Upper control limit for mean</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>Upper control limit for range</td>
</tr>
</tbody>
</table>

**NPCHART Statement**

| _EXLIM_    | Control limit exceeded on \( np \) chart                                    |
| _LCLNP_    | Lower control limit for number of nonconforming items                       |
| _LIMITN_   | Nominal sample size associated with the control limits                       |
| _NP_       | Average number of nonconforming items                                       |
| _SIGMAS_   | Multiple (\( k \)) of the standard error of \( X_i \) associated with the control limits |
| _SUBNP_    | Subgroup number of nonconforming items                                     |
| _SUBN_     | Subgroup sample size                                                        |
| _TESTS_    | Tests for special causes signaled on \( np \) chart                         |
| _UCLNP_    | Upper control limit for number of nonconforming items                       |

**PCHART Statement**

| _EXLIM_    | Control limit exceeded on \( p \) chart                                    |
| _LCLP_     | Lower control limit for proportion of nonconforming items                  |
| _LIMITN_   | Nominal sample size associated with the control limits                      |
| _P_        | Average proportion of nonconforming items                                   |
| _SIGMAS_   | Multiple (\( k \)) of the standard error of \( p_i \) associated with the control limits |
| _SUBP_     | Subgroup proportion of nonconforming items                                 |
| _SUBN_     | Subgroup sample size                                                        |
| _TESTS_    | Tests for special causes signaled on \( p \) chart                         |
| _UCLP_     | Upper control limit for proportion of nonconforming items                  |

**RCHART Statement**

| _EXLIM_    | Control limit exceeded on \( R \) chart                                    |
| _LCLR_     | Lower control limit for range                                               |
| _LIMITN_   | Nominal sample size associated with the control limits                      |
| _R_        | Average range                                                               |
| _SIGMAS_   | Multiple (\( k \)) of the standard error associated with the control limits |
| _STDDEV_   | Process standard deviation (\( \hat{\sigma} \) or \( \sigma_0 \))           |
| _SUBN_     | Subgroup sample sizes                                                       |
| _SUBR_     | Subgroup range                                                              |
| _TESTS2_   | Tests for special causes signaled on \( R \) chart                         |
| _UCLR_     | Upper control limit for range                                               |

**SCHART Statement**

<p>| <em>EXLIM</em>    | Control limit exceeded on ( s ) chart                                    |</p>
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>LCLS</em></td>
<td>Lower control limit for standard deviation</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>S</em></td>
<td>Average standard deviation</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation ($\hat{\sigma}$ or $\sigma_0$)</td>
</tr>
<tr>
<td><em>SUBU</em></td>
<td>Subgroup number of nonconformities per unit</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on $s$ chart</td>
</tr>
<tr>
<td><em>UCLS</em></td>
<td>Upper control limit for standard deviation</td>
</tr>
</tbody>
</table>

**UCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on $u$ chart</td>
</tr>
<tr>
<td><em>LCLU</em></td>
<td>Lower control limit for number of nonconformities per unit</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>SUBU</em></td>
<td>Subgroup number of nonconformities per unit</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on $u$ chart</td>
</tr>
<tr>
<td><em>U</em></td>
<td>Average number of nonconformities per unit</td>
</tr>
<tr>
<td><em>UCLU</em></td>
<td>Upper control limit for number of nonconformities per unit</td>
</tr>
</tbody>
</table>

**XCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>Lower control limit for mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Process mean</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation ($\hat{\sigma}$ or $\sigma_0$)</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>SUBX</em></td>
<td>Subgroup mean</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>Upper control limit for mean</td>
</tr>
</tbody>
</table>

**XRCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>EXLIMR</em></td>
<td>Control limit exceeded on $R$ chart</td>
</tr>
<tr>
<td><em>LCLR</em></td>
<td>Lower control limit for range</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>Lower control limit for mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Process mean</td>
</tr>
<tr>
<td><em>R</em></td>
<td>Average range</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation ($\hat{\sigma}$ or $\sigma_0$)</td>
</tr>
</tbody>
</table>
### Table 15.36  continued

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>SUBR</em></td>
<td>Subgroup range</td>
</tr>
<tr>
<td><em>SUBX</em></td>
<td>Subgroup mean</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>TESTS2</em></td>
<td>Tests for special causes signaled on $R$ chart</td>
</tr>
<tr>
<td><em>UCLR</em></td>
<td>Upper control limit for range</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>Upper control limit for mean</td>
</tr>
</tbody>
</table>

**XSCHART Statement**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>EXLIM</em></td>
<td>Control limit exceeded on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>EXLIMS</em></td>
<td>Control limit exceeded on $s$ chart</td>
</tr>
<tr>
<td><em>LCLS</em></td>
<td>Lower control limit for standard deviation</td>
</tr>
<tr>
<td><em>LCLX</em></td>
<td>Lower control limit for mean</td>
</tr>
<tr>
<td><em>LIMITN</em></td>
<td>Nominal sample size associated with the control limits</td>
</tr>
<tr>
<td><em>MEAN</em></td>
<td>Process mean</td>
</tr>
<tr>
<td><em>S</em></td>
<td>Average standard deviation</td>
</tr>
<tr>
<td><em>SIGMAS</em></td>
<td>Multiple ($k$) of the standard error associated with the control limits</td>
</tr>
<tr>
<td><em>STDDEV</em></td>
<td>Process standard deviation ($\hat{\sigma}$ or $\sigma_0$)</td>
</tr>
<tr>
<td><em>SUBN</em></td>
<td>Subgroup sample size</td>
</tr>
<tr>
<td><em>SUBS</em></td>
<td>Subgroup standard deviation</td>
</tr>
<tr>
<td><em>SUBX</em></td>
<td>Subgroup mean</td>
</tr>
<tr>
<td><em>TESTS</em></td>
<td>Tests for special causes signaled on $\bar{X}$ chart</td>
</tr>
<tr>
<td><em>TESTS2</em></td>
<td>Tests for special causes signaled on $s$ chart</td>
</tr>
<tr>
<td><em>UCLS</em></td>
<td>Upper control limit for standard deviation</td>
</tr>
<tr>
<td><em>UCLX</em></td>
<td>Upper control limit for mean</td>
</tr>
</tbody>
</table>

**Notes:**

1. The variable _TESTS_ is saved if you specify the TESTS= option. The $k$th character of a value of _TESTS_ is $k$ if Test $k$ is positive at that subgroup. For example, if you request all eight tests and Tests 2 and 8 are positive for a given subgroup, the value of _TESTS_ has a 2 for the second character, an 8 for the eighth character, and blanks for the other six characters.

2. The variable _TESTS2_ is saved if you specify the TESTS2= option.

3. The variables _EXLIM_, _EXLIMS_, _TESTS_, and _TESTS2_ are character variables of length 8. All other variables are numeric.
ODS Table Names

Each table that the SPC procedure creates has a name associated with it. You must use this name to refer to the table when you use ODS statements. The name of this table and a short description of its contents are listed in Table 15.37.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ExceptionSummary</td>
<td>Summary of exceptions</td>
<td>All chart statements</td>
<td>Default output</td>
</tr>
</tbody>
</table>

Examples: SPC Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

Example 15.1: Creating Output Data Tables

The following statements do $\bar{X}$ and R chart analysis on the data set mycas.AllProcesses that was created in the section “Getting Started: SPC Procedure” on page 779. They perform $\bar{X}$ and R chart analyses of the data and save the results in OUTTABLE= and OUTLIMITS= data tables.

```sas
proc spc data=mycas.AllProcesses;
  xrchart / noprint
  outtable = mycas.AllTable
  outlimits = mycas.AllLimits;
run;
```

Output 15.1.1 shows a partial listing of the mycas.AllTable data table.
Output 15.1.1 Partial Listing of the mycas.AllTable Data Table

<table>
<thead>
<tr>
<th><em>VAR</em></th>
<th>subgroupname</th>
<th>Subgroup</th>
<th><em>SIGMAS</em></th>
<th><em>LIMITN</em></th>
<th><em>SUBN</em></th>
<th><em>LCLX</em></th>
<th><em>SUBX</em></th>
<th><em>MEAN</em></th>
<th><em>UCLX</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>1</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>2</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>3</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>4</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>5</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>6</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>7</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>8</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>9</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>10</td>
<td>3</td>
<td>5</td>
<td>5</td>
<td>34.906</td>
<td>34.932</td>
<td>34.993</td>
<td>35.006</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><em>STDDEV</em></th>
<th><em>EXLIM</em></th>
<th><em>LCLR</em></th>
<th><em>SUBR</em></th>
<th><em>R</em></th>
<th><em>UCLR</em></th>
<th><em>EXLIMR</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.02</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.03</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.01</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.02</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.02</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.01</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.03</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.02</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.03</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
<tr>
<td>0.009554128</td>
<td>0</td>
<td>0.02</td>
<td>0.022222</td>
<td>0.046989</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Output 15.1.2 displays the mycas.AllLimits data table.

Output 15.1.2 mycas.AllLimits Data Table

<table>
<thead>
<tr>
<th><em>processname</em></th>
<th>subgroupname</th>
<th><em>SIGMAS</em></th>
<th><em>LIMITN</em></th>
<th><em>LCLX</em></th>
<th><em>MEAN</em></th>
<th><em>UCLX</em></th>
<th><em>STDDEV</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Diameter</td>
<td>Batch</td>
<td>3</td>
<td>5</td>
<td>34.98</td>
<td>34.99</td>
<td>35.00</td>
<td>0.008</td>
</tr>
<tr>
<td>Partgap</td>
<td>Sample</td>
<td>3</td>
<td>5</td>
<td>241.94</td>
<td>260.00</td>
<td>278.05</td>
<td>13.454</td>
</tr>
<tr>
<td>Time</td>
<td>Lot</td>
<td>3</td>
<td>6</td>
<td>7.94</td>
<td>8.00</td>
<td>8.06</td>
<td>0.049</td>
</tr>
<tr>
<td>Amount</td>
<td>Batch</td>
<td>3</td>
<td>V</td>
<td>V</td>
<td>11.98</td>
<td>V</td>
<td>0.044</td>
</tr>
<tr>
<td>Breakstrength</td>
<td>Sample</td>
<td>3</td>
<td>V</td>
<td>V</td>
<td>59.98</td>
<td>V</td>
<td>2.111</td>
</tr>
<tr>
<td>Delay</td>
<td>Day</td>
<td>3</td>
<td>V</td>
<td>V</td>
<td>9.53</td>
<td>V</td>
<td>8.512</td>
</tr>
<tr>
<td>KWatts</td>
<td>Day</td>
<td>3</td>
<td>20</td>
<td>3362.10</td>
<td>3497.56</td>
<td>3633.02</td>
<td>201.937</td>
</tr>
<tr>
<td>Weight</td>
<td>Lot</td>
<td>3</td>
<td>5</td>
<td>21.49</td>
<td>24.61</td>
<td>27.74</td>
<td>2.330</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><em>LCLR</em></th>
<th><em>R</em></th>
<th><em>UCLR</em></th>
<th><em>TYPE</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>0.000</td>
<td>0.022</td>
<td>0.05</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>0.000</td>
<td>31.293</td>
<td>66.17</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>0.000</td>
<td>0.124</td>
<td>0.25</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>V</td>
<td>V</td>
<td>V</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>V</td>
<td>V</td>
<td>V</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>V</td>
<td>V</td>
<td>V</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>312.779</td>
<td>754.225</td>
<td>1195.67</td>
<td>ESTIMATE</td>
</tr>
<tr>
<td>0.000</td>
<td>5.420</td>
<td>11.46</td>
<td>ESTIMATE</td>
</tr>
</tbody>
</table>
Note that limits variables for three of the processes have the special missing value $V$, because the data for those processes have varying subgroup sample sizes.

The mycas.AllLimits data table has the same format as a LIMITS= data table, so it could provide limits for these processes in a later run of PROC SPC.

Example 15.2: Applying Tests for Special Causes

The following statements produce a data table for 100 simulated process measurements, called Process1 through Process100:

```sas
data mycas.Random;
  length processname $16 subgroupname $16;
  do i = 1 to 100;
    processname = 'Process' || left( put( i, 8. ) );
    subgroupname = 'Subgroup' || left( put( i, 8. ) );
    do subgroup = 1 to 30;
      do j = 1 to 5;
        process = rannor(123);
        output;
      end;
    end;
  end;
drop i j;
run;
```

The following statements use PROC SPC to do an $\bar{X}$ chart analysis of the simulated data and apply the first through fourth tests for special causes:

```sas
proc spc data=mycas.Random;
  xchart / exchart
    tests = 1 to 4
    outtable = mycas.RandomTests;
run;
```

The EXCHART option includes only processes for which an exception is flagged in the output. Output 15.2 shows the resulting exceptions summary table.
Nineteen of the 100 processes are flagged for at least one exception: a subgroup mean outside the control limits or a positive test result. Because these data were simulated from a normal distribution, they represent processes that are in statistical control. Therefore, you should regard all these exceptions as false positives.

The combined chance of a false signal when Tests 1–4 are applied together is less than 1 in 100 (see the section “Interpreting Tests for Special Causes” on page 820). Therefore, finding 21 exceptions in an analysis of 3,000 total subgroups is not unexpected.

Example 15.3: Producing Charts with PROC SHEWHART

The exceptions summary table that is displayed in Output 15.2.1 shows that the process variable Process47 had two signals of Test 3, indicating a drift in the process mean. The following statements extract the data for Process47 from the mycas.RandomTests data table into a SAS data set, and run PROC SHEWHART on the data set to produce an $\bar{X}$ chart of the Process47 data:

```sas
data Process47Tests;
   set mycas.RandomTests(where=(VAR_ eq 'Process47'));
run;

proc shewhart table=Process47Tests;
   xchart Process47 * Subgroup /
      tests = 1 to 4
      markers;
run;
```
The $\bar{X}$ chart for Process47 is shown in Output 15.3.1.

**Output 15.3.1** $\bar{X}$ Chart for Process47 Data

The sawtooth pattern of points in Output 15.3.1 indicates an alternating instability in the process. However, it is known that the simulated data are stable, and therefore this must be a random effect. Control chart analysis detects unusual variation in a process measurement, but if you analyze enough data, you will find unusual variation even in a stable process.
References


Overview: TREESPLIT Procedure

The TREESPLIT procedure builds tree-based statistical models for classification and regression in SAS Viya. The procedure produces a classification tree, which models a categorical response, or a regression tree, which models a continuous response. Both types of trees are called decision trees, because the model is expressed as a series of if-then statements. For each type of tree, you specify a response variable (also called a target variable), whose values you want PROC TREESPLIT to predict, and one or more input variables (called predictor variables), whose values the procedure uses to predict the values of the target variable.

The predictor variables for tree models can be categorical or continuous. The set of all possible combinations of the predictor variables is called the predictor space. The model is based on partitioning the predictor space into nonoverlapping segments, which correspond to the terminal nodes (called leaves) of the tree. Partitioning is done repeatedly, starting with the root node, which contains all the data, and continuing until a stopping criterion is met. At each step, the parent node is split into child nodes by selecting a predictor variable and a split value for that variable that minimize the variability, according to a specified measure (or the default measure), in the response variable across the child nodes. Various measures, such as the Gini index, entropy, and residual sum of squares, can be used to assess candidate splits for each node. The selected predictor variable and its split value are called the primary splitting rule.

Tree models are built from training data for which the response values are known, and these models are subsequently used to score (classify or predict) response values for new data. For classification trees, the most frequent response level of the training observations in a leaf is used to classify observations in that leaf. For regression trees, the average response of the training observations in a leaf is used to predict the response for observations in that leaf. The splitting rules that define the leaves provide the information that is needed to score new data; these rules consist of the primary splitting rules, surrogate rules, and default rules for each node.

The process of building a decision tree begins with growing a large, full tree. The full tree can overfit the training data, resulting in a model that does not adequately generalize to new data. To prevent overfitting, the full tree is often pruned back to a smaller subtree that balances the goals of fitting training data and predicting new data. Two commonly applied approaches for finding the best subtree are cost-complexity pruning (Breiman et al. 1984) and C4.5 pruning (Quinlan 1993). For more information, see the section “Building a Decision Tree” on page 869.

Compared with other regression and classification methods, tree models have the advantage that they are easy to interpret and visualize, especially when the tree is small. Tree-based methods scale well to large data, and they offer various methods of handling missing values, including surrogate splits.

However, tree models have limitations. Regression tree models fit response surfaces that are constant over rectangular regions of the predictor space, so they often lack the flexibility needed to capture smooth relationships between the predictor variables and the response. Another limitation of tree models is that small changes in the data can lead to very different splits, and this undermines the interpretability of the model (Hastie, Tibshirani, and Friedman 2009; Kuhn and Johnson 2013).

PROC TREESPLIT Features

The main features of the TREESPLIT procedure are as follows:
provides a computationally efficient strategy for generating candidate splits
provides the cost-complexity, C4.5, and reduced-error methods of pruning trees
supports the use of validation data for selecting the best subtree during pruning
supports the use of $k$-fold cross validation for cost-complexity pruning when validation data are not present
provides various methods of handling missing values, including surrogate rules
creates tree diagrams and plots for pruning analysis
computes statistics for assessing model fit
computes measures of variable importance
produces a file that contains SAS DATA step code for scoring new data
provides an output data table that contains leaf assignments and predicted values for observations

The TREESPLIT procedure uses ODS Graphics to create plots as part of its output. For information about the statistical graphics available with the TREESPLIT procedure, see the PLOTS options in the PROC TREESPLIT statement and the section “ODS Graphics” on page 891.

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:
cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: TRESPLIT Procedure

NOTE: Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

This example explains basic features of the TRESPLIT procedure for building a classification tree. The data contain measurements of 13 chemical attributes for 178 samples of wine. Each wine is derived from one of three cultivars that are grown in the same area of Italy, and the goal of the analysis is a model that classifies samples into cultivar groups. The data are available from the UCI Irvine Machine Learning Repository (Lichman 2013).

The following statements create a data set named Wine that contains the measurements:

data Wine;
  %let url = http://archive.ics.uci.edu/ml/machine-learning-databases;
  infile "&url/wine/wine.data" url delimiter=',';
  input Cultivar Alcohol Malic Ash Alkan Mg TotPhen Flav NFPhen Cyanins Color Hue ODRatio Proline;
  label Cultivar = "Cultivar"
      Alcohol = "Alcohol"
      Malic = "Malic Acid"
      Ash = "Ash"
      Alkan = "Alkalinity of Ash"
      Mg = "Magnesium"
      TotPhen = "Total Phenols"
      Flav = "Flavonoids"
      NFPhen = "Nonflavonoid Phenols"
      Cyanins = "Proanthocyanins"
      Color = "Color Intensity"
      Hue = "Hue"
      ODRatio = "OD280/OD315 of Diluted Wines"
      Proline = "Proline";
run;

The following DATA step loads the mycas.Wine data into your CAS session. This DATA step assumes that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

1Disclaimer: SAS may reference other websites or content or resources for use at Customer’s sole discretion. SAS has no control over any websites or resources that are provided by companies or persons other than SAS. Customer acknowledges and agrees that SAS is not responsible for the availability or use of any such external sites or resources, and does not endorse any advertising, products, or other materials on or available from such websites or resources. Customer acknowledges and agrees that SAS is not liable for any loss or damage that may be incurred by Customer or its end users as a result of the availability or use of those external sites or resources, or as a result of any reliance placed by Customer or its end users on the completeness, accuracy, or existence of any advertising, products, or other materials on, or available from, such websites or resources.
The variable Cultivar is a nominal categorical variable that has levels 1, 2, and 3, and the 13 attribute variables are continuous.

The following statements use the TREESPLIT procedure to create a classification tree:

```
ods graphics on;
proc treesplit data=mycas.Wine seed=54321;
   class Cultivar;
   model Cultivar = Alcohol Malic Ash Alkan Mg TotPhen Flav NFPhen Cyanins Color Hue ODRatio Proline;
   grow entropy;
   prune costcomplexity(leaves=SE);
run;
```

The MODEL statement specifies Cultivar as the response variable and the variables to the right of the equal sign as the predictor variables. The inclusion of Cultivar in the CLASS statement designates it as a categorical response variable and requests a classification tree. All the predictor variables are treated as continuous variables because none are included in the CLASS statement.

The GROW and PRUNE statements control two fundamental aspects of building classification and regression trees: growing and pruning. You use the GROW statement to specify the criterion for recursively splitting parent nodes into child nodes as the tree is grown. For classification trees, the default criterion is entropy; for more information, see the section “Splitting Criteria” on page 872.

By default, the growth process continues until the tree reaches a maximum depth of 10 (you can specify a different limit by using the MAXDEPTH= option). The result is often a large tree that overfits the data and is likely to perform poorly in predicting future data. A recommended strategy for avoiding this problem is to prune the tree to a smaller subtree that minimizes prediction error. You can use the PRUNE statement to specify the method of pruning. The default method is cost complexity.
The default output includes several informational tables, which are shown in Figure 16.2 through Figure 16.7. The “Model Information” table in Figure 16.2 provides information about the model and the methods that are used to grow and prune the tree.

**Figure 16.2  Model Information**

<table>
<thead>
<tr>
<th>Model Information</th>
</tr>
</thead>
<tbody>
<tr>
<td>Split Criterion</td>
</tr>
<tr>
<td>Pruning Method</td>
</tr>
<tr>
<td>Max Branches per Node</td>
</tr>
<tr>
<td>Max Tree Depth</td>
</tr>
<tr>
<td>Tree Depth Before Pruning</td>
</tr>
<tr>
<td>Tree Depth After Pruning</td>
</tr>
<tr>
<td>Number of Leaves Before Pruning</td>
</tr>
<tr>
<td>Number of Leaves After Pruning</td>
</tr>
</tbody>
</table>

The “Observation Information” table in Figure 16.3 provides the numbers of observations that are read and used. These numbers are the same in this example because there are no missing values in the predictor variables and the ASSIGNMISSING= option is not set to NONE.

**Figure 16.3  Observation Information**

<table>
<thead>
<tr>
<th>Training</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Read</td>
</tr>
<tr>
<td>Number of Observations Used</td>
</tr>
</tbody>
</table>

The plot in Figure 16.4 is a tool for selecting the tuning parameter for cost-complexity pruning. The parameter (indicated on the lower horizontal axis) indexes a sequence of progressively smaller subtrees that are nested within the large tree. The parameter value 0 corresponds to the fully grown tree, and positive values control the trade-off between complexity (number of leaves) and fit to the training data, as measured by average misclassification rate.
Figure 16.4 shows that the minimum average misclassification rate, which is obtained by 10-fold cross validation, is 0.0844. On the plot, this value is indicated by a filled-in circle. Information about the 1-SE misclassification rate is also included because the LEAVES=SE suboption was specified.

Breiman’s 1-SE rule chooses the parameter that corresponds to the smallest subtree for which the misclassification rate is less than one standard error above the minimum misclassification rate (Breiman et al. 1984). The parameter value that corresponds to the 1-SE rule is indicated by a star. The value 0.143 corresponds to a tree that only has three leaves. The dotted vertical line in Figure 16.4 indicates the chosen tree.

The tree diagram in Figure 16.5, which is produced by default when ODS Graphics is enabled, provides an overview of the tree as a classifier.
The tree is constructed starting with all the observations in the root node (labeled 0). This node is split into one internal node and one leaf node (1 and 2, respectively), and node 1 is further split into leaf nodes (3 and 4).

The color of the bar in each leaf node indicates the most frequent level of Cultivar among the observations in that node; this is also the classification level that is assigned to all observations in that node. The height of the bar indicates the proportion of observations in the node that have the most frequent level. The width of the link between parent and child nodes is proportional to the number of observations in the child node.

The diagram in Figure 16.6 provides more detail about the nodes and splits.
The detailed tree diagram displays a box for each node; the box contains six lines of information, separated by a horizontal line. The proportion of each level of the predictor variable is shown below the horizontal line, and the level that has the highest proportion is also displayed above the horizontal line. Also displayed above the horizontal line are the node identifier and the number of observations that are assigned to the node.

The root node (node 0) contains 178 samples. Because no MAXBRANCH= option is specified in the preceding statements, PROC TREESPLIT divides each node into two child nodes (MAXBRANCH=2 by default). At node 0, PROC TREESPLIT determines that the impurity of the root node is maximally decreased (as measured by the entropy criterion, which is the default) by splitting the 178 observations such that all samples for which $\text{ODRatio} \geq 2.4985$ are assigned to node 1 and all samples for which $\text{ODRatio} < 2.4985$ are assigned to node 2. This is the primary splitting rule for node 0. In this training phase, 109 samples are assigned to node 1 and 69 samples are assigned to node 2.

Figure 16.6 also indicates that node 1 contains 0 samples with level 2. The legend shows that level 2 corresponds to Cultivar=3, so node 1 contains no samples of the third cultivar. Similarly, the diagram indicates...
that node 2 contains 0 samples with level 1, and the legend shows that level 1 corresponds to \texttt{Cultivar}=1, so node 2 contains no samples of the first cultivar.

The primary splitting rule for node 1 consists of the variable \texttt{Alcohol} and the split value 12.74. All samples for which \texttt{Alcohol} $\geq$ 12.74 are assigned to node 3 (which then contains 64 samples), and all samples for which \texttt{Alcohol} $<$ 12.74 are assigned to node 4 (which then contains 45 samples).

The resulting classification tree yields simple rules for predicting the cultivar. For example, a sample for which \texttt{ODRatio} $\geq$ 2.4985 and \texttt{Alcohol} $<$ 12.74 is predicted to be from the second cultivar (node 4 indicates that level 3 has the highest proportion of observations, and the legend shows that level 3 corresponds to \texttt{Cultivar}=2).

Figure 16.6 displays the entire tree that begins with the root node and has a depth of three levels. You can use the PLOTS=ZOOMEDTREE option in the PROC TREESPLIT statement to request diagrams that begin with other nodes and have specified depths.

The table in Figure 16.7 displays fit statistics for the tree model.

\begin{table}[h]
\centering
\begin{tabular}{ccc}
\hline
\textbf{Fit Statistics for Selected Tree} & \\
\hline
\textbf{Number} & \textbf{Misclassification Rate} & \\
\textbf{of Leaves} & \\
\hline
\texttt{Training} & 3 & 0.1461 \\
\hline
\end{tabular}
\caption{Fit Statistics}
\end{table}

The misclassification rate is the total proportion of the 178 wine samples that were misclassified. The following numbers of samples were misclassified in the terminal nodes:

- node 2: 21
- node 3: 5
- node 4: 0

So the total misclassification rate is $(21 + 5 + 0)/178 \approx 0.1461$. 
Syntax: TREESPLIT Procedure

The following statements and options are available in the TREESPLIT procedure:

```
PROC TREESPLIT < options > ;
   AUTOTUNE < options > ;
   CLASS variables ;
   CODE FILE=filename ;
   FREQ variable ;
   GROW criterion < options > ;
   MODEL response = variable . . . ;
   OUTPUT OUT=CAS-libref.data-table output-options ;
   PARTITION < partition-options > ;
   PRUNE prune-method < (prune-options) > ;
   WEIGHT variable ;
```

The PROC TREESPLIT statement and the MODEL statement are required. If any variables are character or are to be treated as categorical, at least one CLASS statement is required. Variables that appear after the equal sign (=) in the MODEL statement are predictor variables that model the response variable. By default, all variables that appear in the MODEL statement are treated as continuous variables. A CLASS statement causes a variable to be treated as categorical. Specifying a variable in a CLASS statement but not in a MODEL statement causes the variable to be implicitly added to the MODEL statement.

The following sections describe the PROC TREESPLIT statement and then describe the other statements in alphabetical order.

**PROC TREESPLIT Statement**

```
PROC TREESPLIT < options > ;
```

The PROC TREESPLIT statement invokes the procedure. Table 16.1 summarizes the options in the PROC TREESPLIT statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>BINMETHOD=</td>
<td>Specifies how to bin interval inputs prior to training</td>
</tr>
<tr>
<td>CVCC</td>
<td>Requests a table of the results of the cost-complexity pruning based on cross validation</td>
</tr>
<tr>
<td>NUMBIN=</td>
<td>Specifies the number of bins to use for continuous variables</td>
</tr>
<tr>
<td>NOPRINT</td>
<td>Suppresses ODS output</td>
</tr>
<tr>
<td>NSURROGATES=</td>
<td>Specifies the number of surrogate rules to create</td>
</tr>
<tr>
<td>OUTMODEL=</td>
<td>Specifies the data table to which the decision tree model is to be saved</td>
</tr>
<tr>
<td>PLOTS=</td>
<td>Specifies options for plots</td>
</tr>
<tr>
<td>PRINTTARGET</td>
<td>Create tables that contain information about columns in the output</td>
</tr>
</tbody>
</table>
Table 16.1 continued

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>PRUNINGTABLE</td>
<td>Creates a table that contains the pruning information</td>
</tr>
<tr>
<td>RBAIMP</td>
<td>Creates a variable importance table by using random branch assignment</td>
</tr>
<tr>
<td>SEED=</td>
<td>Specifies the random number seed to use for autotuning or k-fold cross validation</td>
</tr>
<tr>
<td>VII=</td>
<td>Calculates the variable interaction importance for a specified number of interactions</td>
</tr>
</tbody>
</table>

Splitting Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ASSIGNMISSING=</td>
<td>Specifies how to handle missing values in a predictor variable</td>
</tr>
<tr>
<td>MAXBRANCH=</td>
<td>Specifies the maximum number of child nodes per parent node</td>
</tr>
<tr>
<td>MAXDEPTH=</td>
<td>Specifies the maximum tree depth</td>
</tr>
<tr>
<td>MINLEAFSIZE=</td>
<td>Specifies the minimum number of observations per child node</td>
</tr>
<tr>
<td>MINUSEINSEARCH=</td>
<td>Specifies the minimum number of observations to use with the USEINSEARCH policy for handling missing values</td>
</tr>
<tr>
<td>SPLITONCE</td>
<td>Specifies that a variable can be used to split only once per branch</td>
</tr>
</tbody>
</table>

You can specify the following options:

ASSIGNMISSING=BRANCH | NONE | MACSMALL | POPULAR | SIMILAR | USEINSEARCH

specifies how to handle missing values of predictor variables during training and how to handle missing values and unknown levels of predictor variables after all surrogate rules have been applied during scoring. An unknown level of a categorical predictor variable is a level that does not exist in the training data but is encountered during scoring. During scoring, unknown levels are treated as missing values.

Both this option and the NSURROGATES= option affect how missing values are handled in model training and scoring. For more information about how these rules are applied, see the section “Primary and Surrogate Splitting Rules” on page 874.

You can specify one of the following values:

BRANCH during the training phase, assigns any observation that has a missing value for the predictor variable to a specially created child node (branch). If all observations have nonmissing values for a predictor variable, then no branch is created to contain observations with missing values. In the scoring phase, if an observation has a missing value for a predictor variable and no special branch was created to contain observations with missing values, or if an observation has an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

NONE during the training phase, excludes any observation that has a missing value for any predictor variable. In the scoring phase, if an observation has a missing value or an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

MACSMALL during the training phase, treats a missing value in a categorical predictor variable as a separate, legitimate value. If all observations have nonmissing values for a
categorical predictor variable, then no branch is selected to contain observations with missing values. In the scoring phase, if an observation has a missing value for a categorical predictor variable and no branch is selected to contain observations with missing values, or if an observation has an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

In both the training and the scoring phases, missing values in continuous predictor variables are treated as the smallest possible value.

**POPULAR** during the training phase, assigns any observation that has a missing value in the predictor variable to the child node that has the most training observations. In the scoring phase, if an observation has a missing value or an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

**SIMILAR** during the training phase, assigns any observation that has a missing value in the predictor variable to the child node whose observations are most similar to it. This similarity is determined using the chi-square criterion for categorical responses or the $F$-test criterion for continuous responses. If all observations have nonmissing values for a predictor variable, then no branch is selected to contain observations with missing values. In the scoring phase, if an observation has a missing value for a predictor variable and no branch is selected to contain observations with missing values, or if an observation has an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

**USEINSEARCH** during the training phase, treats a missing value in a predictor variable as a separate, legitimate value. If all observations have nonmissing values for a predictor variable, then no branch is selected to contain observations with missing values. In the scoring phase, if an observation has a missing value for a predictor variable and no branch is selected to contain observations with missing values, or if an observation has an unknown level for a predictor variable, then the observation is assigned to the child node that contains the most training observations.

By default, ASSIGNMISSING=USEINSEARCH.

**BINMETHOD=BUCKET | QUANTILE** specifies how to bin interval input variables prior to growing the decision tree. The number of bins that are created is determined by the NUMBIN= option.

You can specify one of the following values:

**BUCKET** bins interval input variables into fixed-width bins. The width of each bin for a particular variable is calculated by subtracting the smallest value among all observations from the largest value among all observations, and then dividing that result by the number of bins.

**QUANTILE** bins interval input variables into bins according to their quantile. The width of the bins for a particular variable is not fixed, but the number of observations in each bin is approximately equal.

By default, BINMETHOD=BUCKET.
CVCC

CVCOSTCOMPLEXITY

requests a table of the results of cost-complexity pruning based on cross validation. For each penalty parameter in the cross validation, the table provides the penalty parameter, the minimum, the maximum, and the average error. The error is the misclassification rate when the response variable is categorical and is the average square error (ASE) when the response variable is continuous. You can use the PLOTS=CVCC option to request a plot of the information in this table.

DATA=CAS-libref.data-table

names the input data table for PROC TREESPLIT to use. CAS-libref.data-table is a two-level name, where

CAS-libref refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS-libref, see the section “Using CAS Sessions and CAS Engine Librefs” on page 841.

data-table specifies the name of the input data table.

MAXBRANCH=b

specifies the maximum number of child nodes per parent node in the tree. PROC TREESPLIT tries to create this number of children unless it is impossible (for example, if a split variable does not have enough levels).

By default, MAXBRANCH=2.

MAXDEPTH=number

specifies the maximum depth of the tree to be grown. The number of levels in a tree is equal to the depth plus one. The default is calculated by the following equation, where b is the value of the MAXBRANCH= option in the PROC TREESPLIT statement:

$$\text{MaxDepth} = \left\lceil \frac{10}{\log_2 (b)} \right\rceil$$

This value can be tuned with the AUTOTUNE statement.

MINLEAFSIZE=number

specifies the minimum number of observations in the training data that each child of a split must contain in order for the split to be considered.

By default, MINLEAFSIZE=5.

MINUSEINSEARCH=number

specifies a threshold for using missing values in the split search when ASSIGNMISSING=USEINSEARCH as the missing value policy. If the number of observations that have missing values for the splitting variable is greater than or equal to number, then PROC TREESPLIT uses the USEINSEARCH policy for missing values.

By default, MINUSERINSEARCH=1.
NOPRINT

suppresses the generation of ODS output.

NUMBIN=number

specifies the number of bins to use for binning interval predictor variables. PROC TREESPLIT bins continuous predictors to a fixed bin size. This option controls the number of bins and thereby also the size of the bins.

By default, NUMBIN=20. This value can be tuned with the AUTOTUNE statement.

NSURROGATES=number

specifies the number of surrogate rules to create for each splitting rule, where number is an integer greater than 0. Surrogate rules are backup splitting rules that are used when the variable that corresponds to the primary splitting rule is missing.

Both this option and the ASSIGNMISSING= affect training and scoring. For more information, see the section “Primary and Surrogate Splitting Rules” on page 874.

By default, NSURROGATES=0.

OUTMODEL=CAS-libref.data-table

names the output data table to which to save the decision tree model. CAS-libref.data-table is a two-level name, where

CAS-libref refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS Sessions and CAS Engine Librefs” on page 841.

data-table specifies the name of the input data table.

The data table that results from this option contains information about each node in the decision tree, including the splitting variables, the child nodes, the number of observations at each node, and the predicted response at each node.

PLOTS < (global-plot-option) > <= plot-request < (options) >>
PLOTS < (global-plot-option) > <= plot-request < (options) > <= … plot-request < (options) >> >

controls the plots that are produced through ODS Graphics. When you specify only one plot-request, you can omit the parentheses around it.

You can specify the following global-plot-option:

ONLY

suppresses the default plots. Only plots that you specifically request are displayed.

You can specify the following plot-requests:

ALL

produces all appropriate plots.

CVCC

produces a plot that is used to determine the tuning parameter for cost-complexity pruning when k-fold cross validation is used. This plot displays the average misclassification rate when the response variable is a classification variable and displays the average square error (ASE) when the response variable is a continuous variable.
NONE
suppresses the default plots. Only plots that you specifically request are displayed.

PRUNEUNTIL
plots the metric that is used to select the final subtree.

This option is enabled by default except when you specify the OFF option in the PRUNE statement (which turns off pruning completely). Specifying the PRUNEUNTIL option has no effect if you also specify the OFF option in the prune statement.

WHOLETREE < (whole-tree-options) >
produces a plot to visualize the entire finished (grown and pruned) tree. This option is enabled by default.

You can specify the following values:

LINKSTYLE=CURVED | ORTHOGONAL | STRAIGHT
specifies the style of links between nodes and leaves in the tree. You can specify the following link-styles:

CURVED requests curved links between the nodes and their children.

ORTHOGONAL requests that links go straight down partway from a node to its children, create a horizontal line at the base of the vertical line, and then go straight down from that line to each child.

STRAIGHT requests that links go straight from the nodes to their children.

By default, LINKSTYLE=CURVED.

LINKWIDTH=CONSTANT | PROPORTIONAL
specifies the width of links between nodes and leaves in the tree. You can specify the following values:

CONSTANT requests that all links have the same thickness.

PROPORTIONAL requests that links have a thickness proportional to the total number of observations that go between the node and each child.

By default, LINKWIDTH=PROPORTIONAL.

NOLEGEND
turns off the legend.

ZOOMEDTREE < (zoomed-tree-options) >
produces a plot to visualize a portion of the finished (grown and pruned) tree. This option is enabled by default.
You can specify the following values:

**DEPTH=depth**
creates a plot down to depth for each node-id specified in the NODES= option.

By default, DEPTH=2.

**LINKSTYLE=CURVED | ORTHOGONAL | STRAIGHT**
specifies the style of links between nodes and leaves in the tree. You can specify the following values:

- **CURVED** requests curved links between the nodes and their children.
- **ORTHOGONAL** requests that links go straight down partway from a node to its children, create a horizontal line at the base of the vertical line, and then go straight down from that line to each child.
- **STRAIGHT** requests that links go straight from the nodes to their children.

By default, LINKSTYLE=CURVED.

**LINKWIDTH=CONSTANT | PROPORTIONAL**
specifies the width of links between nodes and leaves in the tree. You can specify the following values:

- **CONSTANT** requests that all links have the same thickness.
- **PROPORTIONAL** requests that links have a thickness proportional to the total number of observations that go between the node and each child.

By default, LINKWIDTH=PROPORTIONAL.

**NODES=(node-id < node-id < . . . > >)** requests a plot for a subtree that is rooted at each node specified by a node-id. The values of node-id are alphanumeric strings that are displayed within the nodes in the plot that is created by the WHOLETREE option. PROC TREESPLIT creates one plot for each node-id that you specify. The default node ID is “0,” the root of the entire tree.

**NOLEGEND** suppresses the display of the legend

**PRINTTARGET**
outputs tables that indicate generated columns in the OUT= table from the OUTPUT statement. For a continuous response, PROC TREESPLIT generates an output table named PredName, which indicates the name of the predicted value column. For a categorical response, PROC TREESPLIT generates an output table named PredIntoName, which indicates the name of the predicted value column, and also an output table named PredProbName, which indicates the names of the predicted probability columns.

**PRUNINGTABLE**
outputs a table of the pruning results.
Chapter 16: The TREESPLIT Procedure

**RBAIMP**
creates a variable importance table by using random branch assignment (RBA). This table is created in addition to the normal variable importance table that is calculated using the residual sum of squares (RSS) error. For more information about RBA and RSS variable importance, see the section “Variable Importance” on page 881.

**SEED=number**
specifies the initial seed for random number generation for autotuning (when the AUTOTUNE statement is specified) or k-fold cross validation (when the COSTCOMPLEXITY and KFOLD options are specified, or used by default, in the PRUNE statement). The value of *number* must be an integer. By default, the seed is generated by reading the time of day from the computer’s clock.

**SPLITONCE**
splits predictor variables only once on a branch. When you specify this option, a variable cannot be split more than once on the path from the root to any particular terminal node. However, a variable can be used more than once across branches.

**VII=2 | 3 (Experimental )**

**INTERACTIONIMP=2 | 3**
calculates the variable interaction importance, which is described in the section “Variable Interaction Importance (Experimental)” on page 883. You can specify the following values:

2 calculates all two-way variable importance interactions.
3 calculates all three-way and all two-way variable importance interactions.

If you do not specify this option, then the variable interaction importance is not calculated.

---

**AUTOTUNE Statement**

```
AUTOTUNE < options > ;
```

The AUTOTUNE statement searches for the best combination of values of the MAXDEPTH= and NUMBIN= options in the PROC TREESPLIT statement and the criterion in the GROW statement. If you specify the AUTOTUNE statement, then you cannot also specify k-fold cross validation with cost-complexity pruning.

Table 16.2 summarizes the options you can specify in the AUTOTUNE statement.
# Table 16.2  AUTOTUNE Statement Options

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>EVALHISTORY=</td>
<td>Specifies how to report the evaluation history of the tuner</td>
</tr>
<tr>
<td>FRACTION=</td>
<td>Specifies the fraction of observations to use for validation</td>
</tr>
<tr>
<td>KFOLD=</td>
<td>Specifies the number of folds for ( k )-fold cross validation</td>
</tr>
<tr>
<td>MAXEVALS=</td>
<td>Specifies the maximum number of evaluations</td>
</tr>
<tr>
<td>MAXITER=</td>
<td>Specifies the maximum number of iterations when ( \text{SEARCHMETHOD}=\text{GA} ) or ( \text{SEARCHMETHOD}=\text{BAYESIAN} )</td>
</tr>
<tr>
<td>MAXTIME=</td>
<td>Specifies the maximum time for all iterations</td>
</tr>
<tr>
<td>NPARALLEL=</td>
<td>Specifies the number of parallel sessions</td>
</tr>
<tr>
<td>NSUBSESSIONWORKERS=</td>
<td>Specifies the number of workers in parallel sessions</td>
</tr>
<tr>
<td>OBJECTIVE=</td>
<td>Specifies the objective function</td>
</tr>
<tr>
<td>POPSIZE=</td>
<td>Specifies the population size when ( \text{SEARCHMETHOD}=\text{GA} ) or ( \text{SEARCHMETHOD}=\text{BAYESIAN} )</td>
</tr>
<tr>
<td>SAMPLESIZE=</td>
<td>Specifies the sample size when ( \text{SEARCHMETHOD}=\text{LHS} ) or ( \text{SEARCHMETHOD}=\text{RANDOM} )</td>
</tr>
<tr>
<td>SEARCHMETHOD=</td>
<td>Specifies the search method that the optimizer uses</td>
</tr>
<tr>
<td>TARGETEVENT=</td>
<td>Specifies the target event for ROC-based calculations</td>
</tr>
<tr>
<td>TUNINGPARAMETERS=</td>
<td>Specifies the custom tuning parameters</td>
</tr>
<tr>
<td>USEPARAMETERS=</td>
<td>Specifies how to handle the TUNINGPARAMETERS= option</td>
</tr>
</tbody>
</table>

**EVALHISTORY=ALL | LOG | NONE | TABLE**

specifies how to report the evaluation history of the tuner.

You can specify one of the following values:

- **ALL** reports each evaluation in the log and creates the EvaluationHistory ODS table.
- **LOG** prints the following information to the log for each evaluation: evaluation number, objective value, best objective value up to that point, evaluation time, and elapsed time since the beginning of the tuning process.
- **NONE** suppresses reporting of evaluations in the log and does not create the EvaluationHistory ODS table.
- **TABLE** creates the EvaluationHistory ODS table, which contains all evaluated points. The table contains columns for the evaluation number, all tuning parameters, and the objective function value.

By default, EVALHISTORY=TABLE

**FRACTION=number**

specifies the fraction of all data to be used for validation, where \( \text{number} \) must be between 0.01 and 0.99, inclusive. If you specify this option, the tuner uses a single-partition validation for finding the objective value (validation error estimate). This option might not be advisable for small or unbalanced data tables where the random assignment of the validation subset might not provide a good estimate of error. For large, balanced data tables, a single-partition validation is usually sufficient for estimating error; a single partition is more efficient than cross validation in terms of the total execution time.
If a PARTITION statement is specified, the validation partition defined in that statement is used, and this option is ignored. You cannot specify this option in combination with the KFOLD= option.

By default, FRACTION=0.3.

**KFOLD=**\textit{number}

specifies the number of folds (partitions) in the cross validation process, where \textit{number} must be between 2 and 20, inclusive. If you specify this option, the tuner uses cross validation to find the objective value. In cross validation, each model evaluation requires \textit{number} of training executions (on \textit{number}−1 data folds) and \textit{number} of scoring executions (on one hold-out fold). Thus, the evaluation time is increased by approximately a factor of \textit{number}. For small to medium data tables or for unbalanced data tables, cross validation provides on average a better representation of error across the entire data table (a better generalization error).

If you do not specify either this option or the FRACTION= option, then the default of FRACTION=0.3 is used. If a PARTITION statement is specified, the validation partition defined in that statement is used, and this option is ignored. You cannot specify this option in combination with the FRACTION= option.

**MAXEVALS=**\textit{number}

specifies the maximum number of configuration evaluations allowed for the tuner, where \textit{number} must be an integer greater than or equal to 3. When the \textit{number} of evaluations is reached, the tuner terminates the search and returns the results. To produce a single objective function value (validation error estimate), each configuration evaluation requires either a single model training and scoring execution on a validation partition, or a number of training and scoring executions equal to the value of the KFOLD= option for cross validation. The MAXEVALS= option might lead to termination before the value of the MAXITER= option or the MAXTIME= option is reached.

By default, MAXEVALS=50.

**MAXITER=**\textit{number}

specifies the maximum number of iterations of the optimization tuner, where \textit{number} must be greater than or equal to 1. Each iteration normally involves a number of objective evaluations up to the value of the POPSIZE= option. The MAXITER= option is used only when SEARCHMETHOD=GA or SEARCHMETHOD=BAYESIAN; it is ignored when SEARCHMETHOD=RANDOM or SEARCHMETHOD=LHS. The MAXITER= option might lead to termination before the value of the MAXEVALS= option or the MAXTIME= option is reached.

By default, MAXITER=5.

**MAXTIME=**\textit{number}

specifies the maximum time (in seconds) allowed for the tuner, where \textit{number} must be greater than or equal to 1. When this value is reached, the tuner terminates the search and returns results. The actual run time for optimization might be longer because it includes the remaining time needed to finish the current evaluation. For long-running model training (large data tables), the actual run time might significantly exceed \textit{number}. The MAXTIME= option might lead to termination before the value of the MAXEVALS= option or the MAXITER= option is reached.

By default, MAXTIME=36000.
**NPARALLEL=number**  
specifies the number of evaluations to be performed in parallel, where number must be greater than or equal to 0.  

By default, NPARALLEL=0, which indicates that the value of number is determined as follows:  
- If SEARCHMETHOD=GA or SEARCHMETHOD=BAYESIAN, then the number of parallel evaluations is equal to the value of the POPSIZE= option minus 1.  
- If SEARCHMETHOD=LHS or SEARCHMETHOD=RANDOM, then the number of parallel evaluations is equal to the value of the SAMPLESIZE= option, with a maximum value of 32.

**NSUBSESSIONWORKERS=number**  
specifies the number of workers to use in parallel subsessions. When alternative configurations are evaluated in parallel, a number of subsessions is created by the tuner, with each using multiple workers. By default, the number of workers that are used in a parallel subsession is determined as described in the section “Determining the Number of Parallel Evaluations” on page 886.

**OBJECTIVE=function**  
specifies which measure of model performance the tuner uses as the objective function.  
You can specify one of the following values for function. Some values can be specified only when the target variable is of a particular type, as shown in parentheses.

- **ASE** uses average squared error as the objective function.  
- **AUC** uses area under the curve as the objective function (nominal type only).  
- **F05** uses the F0.5 coefficient as the objective function (nominal type only).  
- **F1** uses the F1 coefficient as the objective function (nominal type only).  
- **GAMMA** uses the gamma coefficient as the objective function (nominal type only).  
- **GINI** uses the Gini coefficient as the objective function (nominal type only).  
- **KS** uses the Kolmogorov-Smirnov coefficient as the objective function (nominal type only).  
- **MAE** uses the mean absolute error as the objective function (interval type only).  
- **MCE** uses the misclassification rate as the objective function (nominal type only).  
- **MCLL** uses the multiclass log loss as the objective function (nominal type only).  
- **MISC** uses the misclassification error percentage as the objective function (nominal type only).  
- **MSE** uses the mean squared error as the objective function (interval type only).  
- **MSLE** uses the mean squared logarithmic error as the objective function (interval type only).  
- **RASE** uses the root average squared error as the objective function.  
- **RMAE** uses the root mean absolute error as the objective function (interval type only).  
- **RMSLE** uses the root mean squared logarithmic error as the objective function (interval type only).  
- **TAU** uses the tau coefficient as the objective function (nominal type only).

By default, OBJECTIVE=MISC for nominal targets, and OBJECTIVE=MSE for interval targets.
POPSIZE=number
specifies the maximum population size, where population is the number of configuration evaluations in one iteration (population). The number must be greater than or equal to 1. In some cases, the tuner algorithm might generate a number of new configurations that is smaller than number. The POPSIZE= option is used only when SEARCHMETHOD=GA or SEARCHMETHOD=BAYESIAN; it is ignored when SEARCHMETHOD=RANDOM or SEARCHMETHOD=LHS.

By default, POPSIZE=10.

SAMPLESIZE=number
specifies the total number of evaluations, where number must be greater than or equal to 1. This option is only used when SEARCHMETHOD=RANDOM or SEARCHMETHOD=LHS; it is ignored when SEARCHMETHOD=GA or SEARCHMETHOD=BAYESIAN.

By default, SAMPLESIZE=50.

SEARCHMETHOD=BAYESIAN | GA | LHS | RANDOM
specifies the search method to use for tuning. You can specify the following values:

BAYESIAN builds a kriging surrogate model to approximate the objective value and uses this surrogate model to generate new alternative configurations at each iteration. The kriging model is continuously updated during the search process.

GA uses an initial Latin hypercube sample that seeds a genetic algorithm to generate a new population of alternative configurations at each iteration.

LHS uses a Latin hypercube to generate a single sample of configurations that is uniform in each tuning parameter, but random in combinations.

RANDOM generates a single sample of purely random configurations.

By default, SEARCHMETHOD = GA.

TARGETEVENT=string
specifies the target event to use for calculating the selected objective function. This option is ignored when the value of the OBJECTIVE= option is not AUC, F1, F05, GINI, GAMMA, TAU, or KS.

If you do not specify the TARGETEVENT= option, the tuner selects one of the target levels and uses it for calculating the specified objective function.

TUNINGPARAMETERS=(suboption | ... | < suboption>)
TUNEPARMS=(suboption | ... | < suboption>)
specifies which parameters to tune and which ranges to tune over. If USEPARAMETERS=STANDARD, this option is ignored.

You can specify one or more of the following suboptions:

CRITERION (VALUES=value-list INIT=value EXCLUDE)
specifies information about the splitting criteria to use for tuning the decision tree. For more information about the criteria, see the GROW statement.

You can specify the following additional suboptions:
VALUES=value-list
specifies a list of splitting criteria to consider during tuning, where value-list is a space
separated list that can include one or more of the following values: CHAID, CHISQUARE,
FTEST, GAIN, GINI, and VARIANCE.

INIT=value
specifies the initial splitting criterion for the tuner to use. You can specify the following
values: CHAID, CHISQUARE, FTEST, GAIN, GINI, IGR, RSS, or VARIANCE.

By default, INIT=IGR for nominal targets and INIT=VARIANCE for interval targets.

EXCLUDE
excludes the splitting criterion from the tuning process.

MAXDEPTH (LB=number UB=number VALUES=value-list INIT=number EXCLUDE)
specifies information about the maximum depth to grow the decision tree to use for tuning the
decision tree. For more information, see the MAXDEPTH= option.

You can specify the following additional suboptions:

LB=number
specifies the minimum depth to consider during tuning. If you specify this suboption, you
cannot specify the VALUES= suboption.

By default, LB=1.

UB=number
specifies the maximum depth to consider during tuning. If you specify this suboption, you
cannot specify the VALUES= suboption.

By default, UB=19.

VALUES=value-list
specifies a list of depth values to consider during tuning, where value-list is a space-separated
list of positive integers. If you specify this suboption, you cannot specify either the LB= or
UB= suboption.

INIT=number
specifies the initial depth for the tuner to use.

By default, INIT=10.

EXCLUDE
excludes depth from the tuning process.

NUMBIN (LB=number UB=number VALUES=value-list INIT=number EXCLUDE)
specifies information about the number of bins in which to bin the interval inputs while tuning
the decision tree. For more information, see the NUMBIN= option.

You can specify the following additional suboptions:
**LB=**`number`
specifies the minimum number of bins to consider during tuning. If you specify this suboption, you cannot specify the VALUES= suboption.

By default, LB=20.

**UB=**`number`
specifies the maximum number of bins to consider during tuning. If you specify this suboption, you cannot specify the VALUES= suboption.

By default, UB=200.

**VALUES=**`value-list`
specifies a list of numbers of bins to consider during tuning, where `value-list` is a space-separated list of positive integers. If you specify this suboption, you cannot specify either the LB= or UB= suboption.

**INIT=**`number`
specifies the initial number of bins for the tuner to use.

By default, INIT=20.

**EXCLUDE**
excludes the number of bins from the tuning process.

**USEPARAMETERS=**`tuning-parameter-option`
specifies which set of parameters to tune.

You can specify the following `tuning-parameter-options`:

- **STANDARD** tunes using the default bounds and initial values for all parameters.
- **CUSTOM** tunes only the parameters that are specified in the TUNINGPARAMETERS= option.
- **COMBINED** tunes the parameters that are specified in the TUNINGPARAMETERS= option and uses default bounds and initial values to tune all other parameters.

---

**CLASS Statement**

```plaintext
CLASS variables;
```

The CLASS statement causes the specified `variables` to be treated as categorical variables in the analysis. These variables enter the analysis not through their values but through levels to which the unique values are mapped. For more information about these mappings, see the section “Levelization of Classification Variables” on page 47.

You can specify only one CLASS statement.

**NOTE:** All classification levels are padded or truncated to 32 characters.
CODE Statement

```
CODE FILE=filename ;
```

The CODE statement converts the final tree to SAS DATA step code that you can use for scoring. You must specify the following option:

```
FILE=filename
```

specifies the name of the file to write the SAS score code to.

If you do not specify this statement, no SAS DATA step code is output.

FREQ Statement

```
FREQ variable ;
```

The `variable` in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC TREESPLIT treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ `variable` for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

GROW Statement

```
GROW criterion <(options)> ;
```

The GROW statement specifies the `criterion` by which to split a parent node into child nodes. As it grows the tree, PROC TREESPLIT calculates the specified `criterion` for each predictor variable and then splits on the predictor variable that optimizes the specified `criterion`.

For categorical responses, the available `criteria` are CHAID, CHISQUARE, ENTROPY, GINI, and IGR; the default is IGR. For continuous responses, the available `criteria` are CHAID, FTEST, and RSS; the default is RSS.

For either categorical or continuous responses, you can specify the following `criterion`:

**CHAID**

```
CHAID <(options)>
```

for categorical predictor variables, CHAID uses the value (as specified in the ALPHA= option) of a chi-square statistic (for a classification tree) or an \( F \) statistic (for a regression tree) to merge similar levels of the predictor variable until the number of children in the proposed split reaches the number that you specify in the MAXBRANCH= option. The \( p \)-values for the final split determine the variable on which to split.

For continuous predictor variables, CHAID chooses the best single split until the number of children in the proposed split reaches the value that you specify in the MAXBRANCH= option.

You can specify the following `options`:
ALPHA=value
specifies the maximum p-value for a split to be considered.
By default, ALPHA=0.3.

BONFERRONI
requests a Bonferroni adjustment to the p-value for a variable after the split has been determined.
By default, no adjustment is made.

For categorical responses only, you can specify the following criteria:

CHISQUARE < (options) >
uses a chi-square statistic to split each variable and then uses the p-values that correspond to the resulting splits to determine the splitting variable.
You can specify the following options:

ALPHA=value
specifies the maximum p-value for a split to be considered.
By default, ALPHA=0.3.

BONFERRONI
requests a Bonferroni adjustment to the p-value for a variable after the split has been determined.
By default, no adjustment is made.

ENTROPY < option >
GAIN < option >
uses the gain in information (decrease in entropy) to split each variable and then to determine the split.
You can specify the following option:

MINENTROPY=number
MINGAIN=number
specifies the minimum gain value to validate a split.

GINI
uses the decrease in the Gini index to split each variable and then to determine the split.

IGR
uses the entropy metric to split each variable and then uses the information gain ratio to determine the split.

The default criterion for categorical responses is IGR.

For continuous responses only, you can specify the following criteria:

FTEST < (options) >
uses an F statistic to split each variable and then uses the resulting p-value to determine the split variable.
You can specify the following options:
**MODEL Statement**

**MODEL** response = variable;

The MODEL statement causes PROC TREESPLIT to create a tree model by using *response* as the response variable and one or more *variables* as predictors. By default, *variables* are treated as a continuous predictors if they are numeric variables, or as categorical variables if they also appear in a CLASS statement.

**NOTE:** Specifying a character variable in a MODEL statement without previously declaring it in a CLASS statement results in an error.

**OUTPUT Statement**

**OUTPUT OUT=CAS-libref.data-table < option> ;**

The OUTPUT statement creates an output data table that contains the results of PROC TREESPLIT.

You must specify the following argument:

**OUT=CAS-libref.data-table**

names the output data table for PROC TREESPLIT to use. You must specify this option before any other options. *CAS-libref.data-table* is a two-level name, where

*CAS-libref* refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about *CAS-libref*, see the section “Using CAS Sessions and CAS Engine Librefs” on page 841.

*data-table* specifies the name of the output data table.

You can also specify the following *options*:
COPYVAR=variable
COPYVARS=(variables)
lists one or more variables from the input data table to be transferred to the output data table.

ROLE=<name>
generates a numeric variable that indicates the role played by each observation in fitting the model. By default, the variable is named _ROLE_. You can add an optional =name to change the name of this generated variable. For each observation, the interpretation of this variable is shown in Table 16.3.

Table 16.3  Role Interpretation

<table>
<thead>
<tr>
<th>Value</th>
<th>Observation Role</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>Not used</td>
</tr>
<tr>
<td>1</td>
<td>Training</td>
</tr>
<tr>
<td>2</td>
<td>Validation</td>
</tr>
<tr>
<td>3</td>
<td>Testing</td>
</tr>
</tbody>
</table>

If you do not partition the input data by using a PARTITION statement, then the value of the role variable is 1 for all observations.

PARTITION Statement

PARTITION partition-option ;

The PARTITION statement specifies how observations in the input data set are logically partitioned into disjoint subsets for model training, validation, and testing. For more information, see the section “Using Validation and Test Data” on page 78 in Chapter 2, “Shared Concepts.” Either you can designate a variable in the input data table and a set of formatted values of that variable to determine the role of each observation, or you can specify proportions to use for randomly assigning observations to each role.

You must specify exactly one of the following partition-options:

FRACTION(< TEST=fraction > < VALIDATE=fraction > < SEED=number >)
randomly assigns specified proportions of the observations in the input data table to the roles. You specify the proportions for testing and validation by using the TEST= and VALIDATE= suboptions. If you specify both the TEST= and VALIDATE= suboptions, then the sum of the specified fractions must be less than 1 and the remaining fraction of the observations are assigned to the training role. The SEED= option specifies an integer that is used to start the pseudorandom number generator for random partitioning of data for training, testing, and validation. If you do not specify SEED=number or if number is less than or equal to 0, the seed is generated by reading the time of day from the computer’s clock.

ROLE=variable (< TEST='value' > < TRAIN='value' > < VALIDATE='value' >)
ROLEVAR=variable (< TEST='value' > < TRAIN='value' > < VALIDATE='value' >)
names the variable in the input data table whose values are used to assign roles to each observation. This variable cannot also appear as an analysis variable in other statements or options. The TEST=,
TRAIN=, and VALIDATE= suboptions specify the formatted values of this variable that are used to assign observation roles. If you do not specify the TRAIN= suboption, then all observations whose role is not determined by the TEST= or VALIDATE= suboption are assigned to the training role.

**PRUNE Statement**

```plaintext
PRUNE <prune-method><(prune-options)> ;
```

The PRUNE statement specifies the pruning method and related options.

You can specify the following `prune-methods`. The default `prune-method` is COSTCOMPLEXITY.

**C45** `<(CONFIDENCE=confidence-level)>` requests C4.5 pruning (Quinlan 1993), which is based on the upper confidence limit for the error rate. For more information, see the section “Pruning” on page 875. This pruning method is available only for classification trees (which have a categorical response). PROC TREESPLIT uses the error rate from the training data only.

You can specify the following `prune-option`:

**CONFIDENCE=** `confidence-level` specifies the pruning confidence level, which must be a positive number in the range of [0, 1]. The default confidence level is 0.25.

**COSTCOMPLEXITY** `<(prune-options)>` requests cost-complexity pruning (Breiman et al. 1984; Quinlan 1987; Zhang and Singer 2010). You can specify this pruning method both for classification trees (which have a categorical response) and for regression trees (which have a continuous response).

By default, cost-complexity pruning uses k-fold cross validation. If you specify a validation data set by using the PARTITION statement, PROC TREESPLIT uses the validation data for subtree selection and does not perform k-fold cross validation.

You can specify one the following `prune-options`:

**ALPHA=number** selects the subtree whose cost-complexity value $\alpha$ is equal to `number` instead of using k-fold cross validation. You cannot specify this option with either the KFOLD= or the LEAVES= options.

**KFOLD=number** specifies the `number` of folds for k-fold cross validation. This option is ignored if you specify the PARTITION statement. You can specify this option and the LEAVES=SE value at the same time.

By default, KFOLD=10.

**LEAVES=number | ALL | SE** selects the subtree according to one of the following values:
**Chapter 16: The TREESPLIT Procedure**

- **number** selects the subtree that has the number of leaves, or the subtree whose number of leaves is less than and closest to number if no subtree with exactly number of leaves exists, instead of using k-fold cross validation.

- **ALL** selects the largest tree instead of using k-fold cross validation.

- **SE** selects the subtree by performing k-fold cross validation and using the Breiman’s 1-SE rule instead of the minimum error rate. You can specify this value and the KFOLD= option at the same time.

**OFF**

**NONE**

turns off pruning completely. No pruning is performed, and no pruning plots are generated.

**REDUCEDERROR < (prune-options) >**

**REP < (prune-options) >**

requests reduced-error pruning (Quinlan 1986). Reduced-error pruning has two stages: subtree sequence generation and subtree selection. The validation data are used for both stages. The PARTITION statement is required. For more information, see the section “Pruning” on page 875.

PROC TREESPLIT generates a pruning plot that shows the requested error metric as a function of the number of leaves in the subtree.

You can specify the following prune-options:

**LEAVES=number | ALL**

selects the subtree that has the requested number of leaves, or if no subtree with exactly that number of leaves is available, selects the subtree whose number of leaves is less than and closest to number. When LEAVES=ALL, the largest tree is selected.

By default, PRUNE=COSTCOMPLEXITY.

---

**WEIGHT Statement**

**WEIGHT variable ;**

The variable in the WEIGHT statement is used as a weight to perform a weighted analysis of the data. Observations that have nonpositive or missing weights are not included in the analysis. If a WEIGHT statement is not included, all observations that are used in the analysis are assigned a weight of 1.
Details: TREESPLIT Procedure

Building a Decision Tree

Algorithms for building a decision tree use the training data to split the predictor space (the set of all possible combinations of values of the predictor variables) into nonoverlapping regions. These regions correspond to the terminal nodes of the tree, which are also known as leaves.

The splitting is done by recursive partitioning, starting with all the observations, which are represented by the node at the top of the tree. The algorithm splits this parent node into two or more child nodes in such a way that the values (or levels) of the response variable within each child region are as similar as possible. The splitting process is then repeated for each of the child nodes, and the recursion continues until a stopping criterion is satisfied. At that point, the tree is considered to be fully built (grown).

At each step, the split is determined by finding the best predictor variable and the best split value (or possibly a set of split values when the value of the MAXBRANCH= option is greater than 2) that optimize a specified criterion in the response variable across the child nodes to which the parent node is split. For more information about the splitting methods available in the TREESPLIT procedure, see the section “Splitting Criteria” on page 872.

The best predictor variable and split value (or set of split values) is called the primary splitting rule. You can also request one or more surrogate splitting rules, which are determined in a fashion similar to the primary splitting rule and are applied when the primary splitting rule’s variable is missing. Each nonterminal node has a primary splitting rule and zero or more surrogate splitting rules. For more information about surrogate splitting rules, see the section “Primary and Surrogate Splitting Rules” on page 874.

Each region, which corresponds to a terminal node, is described by a set of primary and surrogate splitting rules that determine the observations that are assigned to the region. During scoring these rules are applied to determine the predicted values for new observations. For classification trees, the predicted value for a scored observation is the level of the response variable that is most common in the region in which the scored observation exists. For regression trees, the predicted value for a scored observation is the mean of the response variable across training observations values in the region in which the scored observation exists.

Figure 16.8, Figure 16.9, and Figure 16.10 illustrate this process. Figure 16.8 shows a classification tree of depth 2.
Figure 16.8 First Two Splits for the mycas.hmeq Data Table
All 4,172 observations in the data are initially assigned to node 0 at the top of the tree, which represents the entire predictor space. PROC TREESPLIT splits this space into two nonoverlapping regions, represented by node 1 and node 2. PROC TREESPLIT determines that the predictor variable and its split value that optimize the growing criterion across the child nodes are Debtinc and 43.77156, respectively. This split variable and split value constitute the primary splitting rule for node 0. Observations in which Debtinc < 43.77156 are assigned to node 2, and observations in which Debtinc ≥ 43.77156 are assigned to node 1.

Figure 16.9 presents a scatter plot of the predictor space for the primary splitting rule for node 0. The split of the variable Debtinc divides the predictor space into node 1 and node 2; these nodes are represented by the two rectangular regions, which have different ratios of events to nonevents for the response variable.

**Figure 16.9** Scatter Plot of the Predictor Space for the First Split

Next, the algorithm determines the primary splitting rule for node 2 and splits the region that is represented by node 2 into two nonoverlapping regions, represented by node 3 and node 4. PROC TREESPLIT chooses the variable Delinq and its values to optimize the growing criterion. Observations in which values of the categorical predictor variable Delinq are equal to 0, 1, 2, 3, or 4 are assigned to node 3, and observations in which the values of Delinq are equal to 5, 6, 7, 8, or 10 are assigned to node 4.

Figure 16.10 presents a scatter plot of the predictor space for the primary splitting rule of node 2. The split of the variable Delinq further divides the predictor space of node 2 into two regions: node 3 and node 4, which have different ratios of events to nonevents for the response variable.

Node 3 has a very high proportion of observations for which Bad is equal to 0. In contrast, Bad is equal to 1 for almost all the observations in node 4.

Note that several observations have the same values for Debtinc or Delinq, so the scatter plot gives the perception of fewer observations than there actually are.
This example illustrates recursive binary splitting, in which each parent node is split into two child nodes. By default, the TREESPLIT procedure creates at most two child nodes per split. You can use the MAXBRANCH= option to specify the maximum possible number of child nodes you want per split of a parent node. Based on the splitting criterion you specify, PROC TREESPLIT determines the best number of child nodes up to the value of the MAXBRANCH= option.

**Splitting Criteria**

The goal of recursive partitioning, as described in the section “Building a Decision Tree” on page 869, is to subdivide the predictor space in such a way that the values of the response variable for the observations within a terminal node are similar as possible. The TREESPLIT procedure provides two types of criteria for splitting a parent node: criteria that maximize a decrease in node impurity, as defined by an impurity function, and criteria that are defined by a statistical test. You can specify the criterion in the GROW statement. If you do not specify a criterion in the GROW statement, the entropy criterion is used for classification trees and the RSS criterion is used for regression trees.

**Criteria Based on Impurity**

The entropy, Gini index, and RSS criteria decrease impurity. The impurity of a parent node $\tau$ is defined as $i(\tau)$, a nonnegative number that is equal to zero for a pure node (a node in which all the observations have the same value of the response variable). Nodes in which the observations have very different values of the response variable have a large impurity.
The TREESPLIT procedure selects the best split variable and the best split value to produce the highest reduction in impurity,

$$\Delta i(s, \tau) = i(\tau) - \sum_{b=1}^{B} p(\tau_b|\tau)i(\tau_b)$$

where $$\tau_b$$ denotes the $$b$$th child node, $$p(\tau_b|\tau)$$ is the proportion of observations in $$\tau$$ that are assigned to $$\tau_b$$, and $$B$$ is the number of branches after splitting $$\tau$$.

**Impurity Reduction Criteria for Classification Trees**

The following impurity reduction criteria available for classification trees are based on different impurity functions $$i(\tau)$$:

- Entropy criterion: The entropy impurity of node $$\tau$$ is defined as
  $$i(\tau) = - \sum_{j=1}^{J} p_j \log_2 p_j$$
  where $$p_j$$ is the proportion of observations that have the $$j$$th response value.

- Gini index criterion: This criterion defines $$i(\tau)$$ as the Gini index that corresponds to the ASE of a class response and is given by
  $$i(\tau) = - \sum_{j=1}^{J} p_j^2$$

  For more information, see Hastie, Tibshirani, and Friedman (2009).

**Impurity Reduction Criterion for Regression Trees**

Only one impurity reduction criterion, the RSS criterion, is available for regression trees. This criterion, also called the ANOVA criterion, defines $$i(\tau)$$ as the residual sum of squares,

$$i(\tau) = \frac{1}{N(\tau)} \sum_{i=1}^{N(\tau)} (Y_i - \bar{Y})^2$$

where $$N(\tau)$$ is the number of observations in $$\tau$$, $$Y_i$$ is the response value of observation $$i$$, and $$\bar{Y}$$ is the average response of the observations in $$\tau$$.

**Criteria Based on Statistical Test**

The chi-square, $$F$$ test, and CHAID criteria are defined by statistical tests. These criteria calculate the worth of a split by testing for a significant difference in the response variable across the branches that are defined by a split. The worth is defined as $$- \log(p)$$, where $$p$$ is the $$p$$-value of the test. You can adjust the $$p$$-values for these criteria by specifying the BONFERRONI option in the GROW statement.
**Statistical Criterion for Classification Trees**
In the chi-square criterion for categorical response variables, the worth is based on the \( p \)-value for the Pearson chi-square test, which compares the frequencies of the levels of the response across the child nodes.

**Statistical Criterion for Regression Trees**
In the \( F \)-test criterion for continuous response variables, the worth is based on the \( F \) test for the null hypothesis that the means of the response values are identical across the child nodes. The test statistic is

\[
F = \frac{SS_{\text{between}}/(B - 1)}{SS_{\text{within}}/(N(\tau) - B)}
\]

where

\[
SS_{\text{between}} = \sum_{b=1}^{B} N(\tau_b)(\bar{Y}(\tau_b) - \bar{Y}(\tau))^2
\]

\[
SS_{\text{within}} = \sum_{b=1}^{B} \sum_{i=1}^{N(\tau_b)} (Y_{bi} - \bar{Y}(\tau_b))^2
\]

**Statistical Criterion for Both Classification and Regression Trees**
Available for both categorical and continuous response variables, CHAID, first described by Kass (1980), is an approach that regards every possible split as representing a test. CHAID tests the hypothesis of no association between the values of the response (target) variable and the branches of a node. The Bonferroni adjusted probability is defined as \( ma \), where \( \alpha \) is the significance level of a test and \( m \) is the number of independent tests.

**Primary and Surrogate Splitting Rules**
During training, PROC TREESPLIT creates a primary splitting rule for each nonterminal node by examining all the node’s observations’ variables and their values and calculating which variable and which of its values to split on such that the observations within each resulting child node are as similar as possible. If you specify a value, \( x \), for the NSURROGATES= option, then PROC TREESPLIT creates \( x \) surrogate rules in a similar fashion, each time using a different variable that has a similar predictive ability. The TREESPLIT procedure uses the method of Breiman et al. (1984) to determine surrogate rules. Surrogate rules are ordered by agreement, which is measured by the proportion of observations that have a nonmissing value in the rule’s predictor variable that two rules assign to the same branch. For example, if the primary splitting rule assigns 100 observations to a child node, surrogate rule A assigns 40 observations to the same child node, and surrogate rule B assigns 50 observations to the same child node, then surrogate rule B is applied before surrogate rule A. Surrogate rules enable you to make better use of the data.
During scoring, the primary and surrogate splitting rules are applied as follows:

1. The primary splitting rule is applied if the primary rule’s variable is not missing; otherwise,
2. The surrogate rule that has the highest agreement with the primary rule is applied if the first surrogate rule’s variable is not missing; otherwise,
3. Each subsequent splitting rule (ordered by agreement) is applied if the preceding rule has a missing value.
4. If all of the surrogate rules’ variables are missing, then the default splitting rule (as specified in the ASSIGNMISSING= option) is used. The default splitting rule enables all data to be scored even if the primary rule and all surrogate rules cannot be used on a particular observation.

Table 16.4 shows an example set of rules for a particular node in a decision tree where X, Y, and Z are three continuous predictors.

<table>
<thead>
<tr>
<th>Rule</th>
<th>Assign to Branch 1</th>
<th>Assign to Branch 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Primary</td>
<td>X ≥ 1</td>
<td>X &lt; 1</td>
</tr>
<tr>
<td>Surrogate 1</td>
<td>X is missing, Y &lt; 0</td>
<td>X is missing, Y ≥ 0</td>
</tr>
<tr>
<td>Surrogate 2</td>
<td>X and Y are missing, Z ≥ 100</td>
<td>X and Y are missing, Z &lt; 100</td>
</tr>
<tr>
<td>Default</td>
<td>None</td>
<td>X, Y, and Z are missing</td>
</tr>
</tbody>
</table>

By default, NSURROGATES=0. If a variable is used as a surrogate, you can see exactly how it is used in the SAS DATA step code that is generated when you specify the CODE statement.

Pruning

The TREESPLIT procedure creates a classification or regression tree by first growing a tree as described in the section “Splitting Criteria” on page 872. This usually results in a large tree that provides a good fit to the training data. The problem with this tree is its potential for overfitting the data: the tree can be tailored too specifically to the training data and not generalize well to new data. The solution is to find a smaller subtree that results in a low error rate on the validation data.

It is often prohibitively expensive to evaluate the error on all possible subtrees of the full tree. A more practical strategy is to focus on a sequence of nested trees that are obtained by successively pruning leaves from the tree. Figure 16.11 shows an example of pruning in which node 3’s leaves (terminal nodes 4 and 5) are removed to create a nested subtree of the full tree. In the nested subtree, node 3 is now a leaf that contains all the observations that were previously in nodes 4 and 5. This process is repeated until only the root node remains.
Many different methods have been proposed for pruning in this manner. These methods address both how to select which nodes to prune to create the sequence of subtrees and how then to select the optimal subtree from this sequence as the final tree. You can use the `PRUNE` statement in PROC TREESPLIT to specify which pruning method to apply and related options. Several well-known pruning methods, described in this section, are available, and you can override the final selected tree based on your preferences or domain knowledge.

**Cost-Complexity Pruning**

Cost-complexity pruning is a widely used pruning method that was originally proposed by Breiman et al. (1984). You can request cost-complexity pruning for either a categorical or continuous response variable by specifying the following statement:

```r
prune costcomplexity;
```

The cost-complexity pruning method helps prevent overfitting by making a trade-off between the complexity (size) of a tree and the error rate. Thus large trees with a low error rate are penalized in favor of smaller trees. The cost complexity of a tree $T$ is defined as

$$CC(T) = R(T) + \alpha|T|$$

where $R(T)$ represents $T$’s error rate, $|T|$ represents the number of leaves on $T$, and the complexity parameter $\alpha$ represents the cost of each leaf. For a categorical response variable, the misclassification rate is used for the error rate, $R(T)$; for a continuous response variable, the residual sum of squares (RSS), also called the sum of square errors (SSE), is used for the error rate. Only the training data are used to evaluate cost complexity. Breiman et al. (1984) show that for each value of $\alpha$, there is a subtree of $T$ that minimizes cost complexity. When $\alpha = 0$, this is the full tree, $T_0$. As $\alpha$ increases, the corresponding subtree becomes progressively smaller, and the subtrees are in fact nested. Then, at some value of $\alpha$, the root node has the minimal cost complexity for any $\alpha$ greater than or equal to that value. Because there are a finite number of
possible subtrees, each subtree corresponds to an interval of values of $\alpha$; that is,

$$[0, \alpha_1) = \text{interval where } T_0 \text{ (the full tree) has minimal cost complexity}$$

$$[\alpha_1, \alpha_2) = \text{interval where } T_1 \text{ has minimal cost complexity}$$

$$\vdots$$

$$[\alpha_m, \infty) = \text{interval where } T_m \text{ (the root node) has minimal cost complexity}$$

PROC TREESPLIT uses weakest-link pruning, as described by Breiman et al. (1984), to create the sequence of $\alpha_1, \ldots, \alpha_m$ values and the corresponding sequence of nested subtrees, $T_1, \ldots, T_m$.

Finding the optimal subtree from this sequence is then a question of determining the optimal value of the complexity parameter $\alpha$. This is performed either by using the validation partition (when you use the PARTITION statement to reserve a validation holdout sample) or by using cross validation. In the first case, the subtree in the pruning sequence that has the lowest validation error rate is selected as the final tree. When there is no validation partition, $k$-fold cross validation can be applied to cost-complexity pruning to select a subtree that generalizes well and does not overfit the training data (Breiman et al. 1984; Zhang and Singer 2010). The algorithm proceeds as follows after creating the sequence of subtrees and $\alpha$ values by using the entire set of training data as described earlier:

1. Randomly divide the training observations into $k$ approximately equal-sized parts, or folds.

2. Define a sequence of $\beta$ values as the geometric mean of the endpoints of the $[\alpha_i, \alpha_{i+1})$ intervals (that is, $\beta_i = \sqrt{\alpha_i \times \alpha_{i+1}}$) to represent the intervals.

3. For each of the $k$ folds, hold out the current fold for validation and use the remaining $k - 1$ folds for the training data in the following steps:
   a) Grow a tree as is done using the full training data set with the same splitting criterion.
   b) Using the $\beta_1, \ldots, \beta_m$ values that are calculated in step 2, create a sequence of subtrees for each $\beta_i$ as described in the pruning steps given earlier, but now using $\beta_i$ as a fixed value for $\alpha$ and minimizing the cost complexity, $CC(T)$, to select a subtree at each pruning step.
   c) For each $\beta_i$, set $T_{ij}$ to be the subtree that has the minimum cost complexity from the sequence for the $j$th fold.
   d) Calculate the error for each $T_{ij}$ by using the current ($j$th) fold (the one omitted from the training).

4. Now the error rate can be averaged across folds, and the $\beta_i$ that has the smallest average error is selected. The tree $T_i$ from pruning the complete training data that corresponds to the selected $\beta_i$ is the final selected subtree.

Because the $k$-fold cross validation is done sequentially, the process can take a long time for deep trees or for large amounts of data. Consider using the PARTITION statement for pruning large amounts of data.

The TREESPLIT procedure provides two plots that you can use to tune and evaluate the pruning process: the cost-complexity analysis plot and the cost-complexity pruning plot.

When performing cost-complexity pruning with cross validation (that is, no PARTITION statement is specified), it is recommended that you examine the cost-complexity analysis plot that is created by default. This plot displays the error as a function of the complexity parameters $\beta_i$, and it uses a vertical reference line
to indicate the $\beta_i$ that minimizes the error. You can use this plot to examine alternative choices for $\beta_i$. For example, you might prefer to select a smaller tree that has only a slightly higher error rate. You can specify LEAVES=SE to use the 1-SE rule developed by Breiman et al. (1984).

When you specify validation data by using the PARTITION statement, the cost-complexity pruning plot displays the error rate $R(T)$ as a function of the number of leaves $|T|$ for both the training and validation data. This plot indicates the final selected tree, the tree with the minimum $R(T)$ for the validation data, by using a vertical reference line. Like the cost-complexity analysis plot that is produced when you perform cross validation, this plot can help you identify a smaller tree that has only a slightly higher validation error rate. For an example of this plot, see Output 16.1.5 in “Example 16.1: Creating a Binary Classification Tree with Validation Data” on page 893.

You can use the LEAVES= option in the PRUNE statement to select a tree that has a specified number of leaves. Alternatively, you can use the ALPHA= option in the PRUNE statement to select a tree that has a specified value of the cost-complexity value $\alpha$.

### C4.5 Pruning

Quinlan (1987) first introduced pessimistic pruning as a method of pruning classification trees. In this method, the estimate of the true error rate is increased by using a statistical correction in order to prevent overfitting. C4.5 pruning (Quinlan 1993) evolved from pessimistic pruning to employ an even more pessimistic (that is, higher) estimate of the true error rate. An advantage of methods such as pessimistic and C4.5 pruning is that they enable you to use all the data for training instead of requiring a holdout sample. In C4.5 pruning, the upper confidence limit of the true error rate based on the binomial distribution is used to estimate the error rate. PROC TREESPLIT implements a C4.5 algorithm variant that uses the beta distribution in place of the binomial distribution to estimate the upper confidence limit. This pruning method is available only for categorical response variables and it uses only training data for tree pruning. It is implemented by the following statement:

```
prune C45;
```

The C4.5 pruning method follows these steps:

1. Grow a tree from the training data table, and call this full, unpruned tree $T_0$.

2. Set $i = 0$, and do the following until $T_i$ is only the root node:

   a) For each leaf (terminal node) in the tree $T_i$, solve the following equation for $p_l$ (which is the adjusted prediction error rate for leaf $l$):

   $$
   \alpha = 1 - \frac{\Gamma (N_l + 1)}{\Gamma (F_l + 1) \Gamma (N_l - F_l)} \int_0^{p_l} v^{F_l} (1 - v)^{N_l - F_l + 1} \, dv
   $$

   Here the confidence level $\alpha$ is the value of the CONFIDENCE= option in the PRUNE statement, $F_l$ is the number of failures (misclassified observations) at leaf $l$, $N_l$ is the number of observations at leaf $l$, and the function $\Gamma(x)$ is defined as

   $$
   \Gamma(x) = \int_0^\infty v^{x-1} e^{-v} \, dv
   $$
Pruning

Let the leaves be numbered as in the following search process:

b) Given these values of \( p_l \), use the following formula for the prediction error \( E_i \) of tree \( T_i \):

\[
E_i = \sum_{l \in T_i} N_l p_l
\]

c) For each node in tree \( T_i \) that has only leaves as children, create a candidate subtree by pruning those leaves.

d) For each candidate subtree, use the equations from steps 2 and 3 to calculate its prediction error. Then select the candidate subtree that has the largest decrease (or smallest increase) in prediction error, \( E_i \). Let this be the next subtree in the sequence, \( T_{i+1} \).

e) Set \( i = i + 1 \)

3. Calculate the change in error between each pair of consecutive subtrees, \( \Delta_i = E_i - E_{i-1} \) for each \( i = 1, \ldots, m \).

4. Find the smallest integer \( j \) such that \( \Delta_j > 0 \).

5. Select the subtree \( T_{j-1} \) as the final subtree.

**Reduced-Error Pruning**

Quinlan’s reduced-error pruning (1987) performs pruning and subtree selection based on minimizing the error rate in the validation partition at each pruning step and then in the overall subtree sequence. The error rate is based on the misclassification rate for a categorical response variable and on the ASE for a continuous response. The following PRUNE statement implements reduced-error pruning:

```
prune reducederror;
```

Reduced-error pruning creates a sequence of subtrees from the largest tree, \( T_0 \), to the root node, \( T_m \). The subtree that has the smallest validation error is then selected as the final subtree. Pruning could be stopped as soon as the error begins to increase in the validation data as originally described by Quinlan; continuing to prune to create a subtree sequence back to the root node enables you to select a smaller tree that still has an acceptable error rate, as discussed in the next section.

**User Specification of Subtree**

You might want to select a different tree from the one selected by default when you use cost-complexity or reduced-error pruning to create the sequence of subtrees. For example, you might have a subtree that has a slightly larger error but is smaller, and thus simpler, than the subtree that has the minimum error according to reduced-error pruning. You can override the selected subtree and instead select the subtree that has \( n \) leaves and was created by cost-complexity or reduced-error pruning, where \( n \) is specified in the LEAVES= option in the PRUNE statement. In addition, if you are using cost-complexity pruning, you can override the selected subtree by using the ALPHA= option in the PRUNE statement.

Alternatively, you might want to select the largest tree that is created in one of the following ways:

- Specify LEAVES=ALL in the PRUNE statement to still see the statistics for the sequence of subtrees that are created according to the specified pruning error measure, even though the largest (unpruned) tree is selected as the final subtree.
- Specify the following statement to select the largest tree with no pruning performed:
Statistics are not calculated and plots are not created for a sequence of subtrees.

**Scoring**

After you create a tree model, you can apply it to training or test data for model assessment or to new data for making predictions. The process of applying a model to a data table is called *scoring*. You can score data as described in the following sections.

**Scoring the Input Data Table**

Usually, the purpose of scoring training data is to diagnose the model. The training data table is the data table that you specify with the DATA= option. To score the training data, use the OUTPUT statement to create an output data table that contains one observation for each observation in the training data. You can specify the output data table by using the OUT= option in the OUTPUT statement.

In the following example, the input data table (mycas.hmeq) is scored after the tree model has been created:

```sas
proc treesplit data=mycas.hmeq;
   class Bad Delinq Derog Job Ninq Reason;
   model Bad = Delinq Derog Job Ninq Reason;
   output out=mycas.scored;
run;
```

For classification trees, the scored data table also contains one new variable for each level of the response variable. These new variables have the prefix “P_”; for all observations in the same leaf, these new variables represent the proportion of the training observations in that leaf that have that particular response level. For example, if the name of the categorical response variable is Color and it has two levels, 'Blue' and 'Green', then the scored data table contains the variable P_ColorBlue (which provides the proportion of training data in this leaf that have the response level 'Blue') and the variable P_ColorGreen (which provides the proportion of training data in this leaf that have the response level 'Green').

For regression trees, the scored data table contains exactly one new variable with the prefix “P_”, which represents the average value of the response variable for all observations in the same leaf. For example, if the name of the continuous response variable is logSalary, then the scored data table contains one new variable, P_logSalary, which represents the average value of the response variable logSalary in the training data for observations in the same leaf.

**Scoring Using DATA Step Code**

You can use the CODE statement to generate SAS DATA step code that you can use to score new data. The following example uses PROC TREESPLIT to produce SAS DATA step code:

```sas
proc treesplit data=mycas.hmeq;
   class Bad Delinq Derog Job Ninq Reason;
   model Bad = Delinq Derog Job Ninq Reason;
   code file="treesplit_data_step.sas";
run;
```
Measures of Model Fit

The TREESPLIT procedure measures model fit based on the misclassification rate for classification trees or the average square error for regression trees, as follows:

- The misclassification rate is calculated from the number of incorrectly predicted observations:

\[
\text{Misc} = \frac{1}{N_0} \sum \begin{cases} 
0 & \text{if prediction is correct} \\
1 & \text{otherwise} 
\end{cases}
\]

- The average square error (ASE) for regression trees is defined as

\[
\text{ASE} = \frac{\text{RSS}}{N_0}
\]

Variable Importance

A training data table can contain a large number of predictor variables, some of which are useful for predicting the response variable, and others of which are not. You can use the TREESPLIT procedure to select the most useful predictor variables based on variable importance. (See “Example 16.3: Assessing Variable Importance” on page 902.) Variable importance is an indication of which predictor variables are the most useful for predicting the response variable.

The most important variables might not be the ones near the top of the tree. The TREESPLIT procedure implements several methods for computing variable importance, which are described in the following subsections. By default, PROC TREESPLIT calculates the variable importance by the count-based, change in the residual sum of square errors, and relative importance methods, and outputs these in one table. You can request that the TREESPLIT procedure also calculate the variable importance by random branch assignment (RBA), by specifying the RBAIMP option.

Count-Based Importance Method

PROC TREESPLIT calculates two count-based variable importance methods:

- Count-based variable importance simply counts the number of times in the tree that a particular variable is used in a split.

- If the NSURROGATES= option is used, then the surrogate-count-based variable importance also counts the number of times that a variable is used in a surrogate splitting rule.
Chapter 16: The TREESPLIT Procedure

Residual Sum of Squares (RSS) Importance Method

This method measures variable importance based on the change of RSS when a split is found at a node. The change for variable \( v \) is

\[
\Delta_d^v = \text{RSS}_d - \sum_i \text{RSS}_{i}^d
\]

where

- \( d \) denotes the node
- \( i \) denotes the index of a child that this node includes
- \( \text{RSS}_d \) is the RSS if the node is treated as a leaf
- \( \text{RSS}_{i}^d \) is the RSS of the node after it has been split

If the change in RSS is negative (which is possible when you measure the validation set), then the change is set to 0.

The residual sum of squares for regression trees is defined as

\[
\text{RSS} = \sum_{\lambda} \sum_{i \in \lambda} (y_i - \hat{y}_\lambda^T)^2
\]

where

- \( i \) is an observation on leaf \( \lambda \)
- \( y_i \) is the predicted value of the response variable of observation \( i \)
- \( \hat{y}_\lambda^T \) is the actual value of the response variable on leaf \( \lambda \)

The residual sum of squares for classification trees is defined as

\[
\text{RSS} = \sum_{\lambda} \sum_{\Phi} N_{\Phi}^\lambda \left[ \sum_{\tau \neq \Phi} \left( P_{i\tau}^\lambda \right)^2 + \left( 1 - P_{i\Phi}^\lambda \right)^2 \right]
\]

where

- \( \Phi \) is the actual response level
- \( N_{\Phi}^\lambda \) is the number of observations on leaf \( \lambda \) that have response level \( \Phi \)
- \( P_{i\tau}^\lambda \) is the posterior probability for the response level \( \tau \) on leaf \( \lambda \)
- \( P_{i\Phi}^\lambda \) is the posterior probability for the actual response level \( \Phi \) on leaf \( \lambda \)
If surrogate rules are in effect, they are also credited with a portion of the change in RSS. The credit is proportional to the agreement between the primary and surrogate splitting rules at the node. The agreement at node $d$ (denoted by $\kappa_d$) is defined as

$$\kappa_d = \sum_i \frac{N_i}{N_d}$$

where $N_d$ is the number of nonmissing observations and $N_i$ is the number of observations that were assigned to $i$ by both the primary and surrogate rules.

The change in RSS from the surrogate rules for variable $v$ is defined as

$$\Delta^v_d = \kappa_d \left( \text{RSS}_d - \sum_i \text{RSS}_i^d \right)$$

The RSS-based importance for a single variable, $v$, is then defined as

$$\sum_{d=1}^D \Delta^v_d$$

where $D$ is the total number of nodes in which $v$ was used as the splitting variable.

**Relative Variable Importance Method**

The relative variable importance metric is a number between 0 and 1, which is calculated in two steps:

1. PROC TREESPLIT finds the maximum RSS-based variable importance.
2. For each variable, PROC TREESPLIT calculates the relative variable importance as the RSS-based importance of this variable divided by the maximum RSS-based importance among all the variables.

The RSS and relative importance are calculated from the validation data. If no validation data exist, they are calculated instead from the training data.

**Variable Interaction Importance (Experimental)**

In some cases, interactions of variables are of more interest than a single variable. When you specify the VII= option in the PROC TREESPLIT statement, the procedure computes variable interaction importance as follows.

The two-way interaction importance for variables $v$ and $w$ is

$$\sum_{d,e} \frac{\Delta^v_d + \Delta^w_e}{\Delta^v_d}$$

where

- $d$ and $e$ denote nodes, with node $d$ being the parent of node $e$
- $v$ and $w$ are variables, with $v$ being the splitting variable for node $d$ and $w$ being the splitting variable for node $e$
This summation is across all parent-child node combinations with respect to the variables \( v \) and \( w \).

The three-way interaction importance for variables \( v \), \( w \), and \( x \) is

\[
\sum_{d,e,f} \frac{\Delta^v_d + \Delta^w_e + \Delta^x_f}{\Delta^v_d + \Delta^w_e}
\]

where

- \( d \), \( e \), and \( f \) denote nodes, with node \( d \) being the parent of node \( e \), which is the parent of node \( f \)
- \( v \), \( w \), and \( x \) are variables, with \( v \) being the splitting variable for node \( d \), \( w \) being the splitting variable for node \( e \), and \( x \) being the splitting variable for node \( f \)

This summation is across all parent-child-grandchild node combinations with respect to the variables \( v \), \( w \), and \( x \).

When comparing variable importance values, you should only compare a two-way interaction with another two-way interaction, or a three-way interaction with another three-way interaction. Comparing a two-way interaction to a three-way interaction is not meaningful, because the values for the importance are not on the same scale.

**Random Branch Assignment Importance Method**

The random branch assignment (RBA) method computes the importance of an input variable \( v \) by comparing how well the data fit the predictions before and after they are modified. Neville and Tan (2014) motivate and introduce the RBA method of variable importance. To modify the predictions, the TREESPLIT procedure replaces all splitting rules that use variable \( v \) by a rule that randomly assigns an observation to a branch. The probability of assigning an observation to a branch is proportional to the number of observations that are assigned to the branch in the current data. The current data are the training data when RBA is computed during training. Otherwise, the current data are those being scored on an existing model.

The RBA importance can be expressed mathematically as

\[
I_{\text{RBA}}(v) \propto \sum_{i=1}^{n} \text{Loss}(y_i, \hat{y}_i) - \sum_{i=1}^{n} \text{Loss}(y_i, \hat{y}_i)
\]

where \( \hat{y}_i \) is the modified prediction for observation \( i \) and \( \hat{y}_i \) is the standard prediction.

For a continuous response, PROC TREESPLIT computes the RBA importance of squared error loss. For a categorical response, PROC TREESPLIT uses the misclassification rate as the loss function.

Neville and Tan (2014) motivate and introduce the RBA method of variable importance.

**Hyperparameter Tuning**

The quality of the predictive model that a machine learning algorithm creates depends on the values for various options that govern the training process; these options are called hyperparameters. The default values of these hyperparameters might not be suitable for all applications. In order to reduce the manual effort in
adjusting these hyperparameters, you can use the AUTOTUNE statement to identify the best settings for them.

To tune hyperparameters, the AUTOTUNE statement directs the procedure to engage a search method (tuner) that searches for the best possible combination of values of these hyperparameters while trying to minimize or maximize an objective function. The objective function is a validation error or accuracy estimate—for example, MISC (misclassification error) for nominal targets or ASE (average square error) for interval targets. The tuning process involves multiple evaluations of the objective function (one for each model hyperparameter configuration it evaluates) and might include multiple iterations, depending on the specified search method. The tuning process also requires data partitioning in order to avoid overfitting to training data; models are trained on a training partition and validated on a validation partition to obtain the objective function value for each chosen hyperparameter configuration. The options for data partitioning are described in the next section, followed by descriptions of the default hyperparameter tuning process and determination of sizing for parallel tuning.

Data Partitioning

Each evaluation of the objective function can consist of one or several training and scoring (validation) executions, depending on whether single-partition validation or k-fold cross validation is used. In both cases, the tuner partitions the data unless the PARTITION statement is used (in this case, the tuner does not partition the training data, but instead uses the data roles that are specified in the PARTITION statement for training and validation).

Single-Partition Validation

By default, the tuner uses single-partition validation. In this process, the tuner partitions all the data into two subsets: one subset for model training and one subset for model validation. For each newly generated configuration of hyperparameters, a new model is trained on the training subset and then the validation subset is scored using the trained model to find the resulting objective function value.

The AUTOTUNE statement calls the sampling action set, which creates the training and validation partitions. The stratified action in the sampling action set is used for a target of nominal type (if all target levels can be included in both the training and validation partitions), and the srs action in the sampling action set is used for a target of interval type and for cases in which stratified sampling is not possible. By default, a validation partition of 30% is used and the remaining 70% is used for model training. The validation partition size can be adjusted by specifying the FRACTION= option in the AUTOTUNE statement. For more information about the sampling action set, see Chapter 12, “Sampling and Partitioning Action Set” (SAS Visual Statistics: Programming Guide).

Cross Validation

If k-fold cross validation is specified, the tuner partitions all the data into k subsets (folds). For each fold, a new model is trained on all folds except the selected (holdout) fold (that is, it is trained on k–1 folds) and then validated using the selected (holdout) fold. The objective function value is averaged over the set of fold validation executions to obtain a single error estimate value. Cross validation is specified using theKFOLD= option in the AUTOTUNE statement.

For efficiency, the cross validation process might be terminated before all k folds are evaluated. Cross validation is terminated under the following conditions: the validation score is 2 times worse than the current best score after the first fold, the validation score is 1.75 times worse than the current best score after two folds, or the validation score is 1.5 times worse than the current best score after three or more folds.
Hyperparameter Tuning Process

By default, the tuner chooses the model hyperparameter configurations to evaluate by using a hybrid optimization strategy that is based on a genetic algorithm (GA), which applies principles of natural selection and evolution to find an improved configuration. The tuner performs the following steps:

1. A default model configuration (default values of select model hyperparameters) is evaluated first and designated as Iteration 0. The objective function value is obtained by using either single-partition validation or $k$-fold cross validation and then recorded for comparison.

2. An initial set of hyperparameter configurations, also called a “population,” is generated using a technique called Latin hypercube sampling (LHS). Each configuration of hyperparameters in the Latin hypercube sample is evaluated, and the objective function value for each is again recorded for comparison. This set becomes Iteration 1. All or a portion of the sample configurations can be evaluated in parallel, as described in the section “Determining the Number of Parallel Evaluations” on page 886.

3. The best model configurations from the Iteration 1 are used to generate the next population of model configurations, Iteration 2, which are then evaluated, in parallel when possible (see the section “Determining the Number of Parallel Evaluations” on page 886). This process is repeated for the remaining iterations, as long as the maximum number of evaluations or the maximum time has not been reached. The default number of iterations is 5, and the default maximum time is 36,000 seconds (10 hours).

4. The best model configuration (the one that minimizes or maximizes the objective function) is reevaluated by executing a single model training and scoring, and information about the model training and scoring for this configuration is returned.

5. All evaluated model configurations are ranked, and the hyperparameter and objective function values of the top 10 configurations are returned in the TunerResults table.

Alternate search methods can be specified: Bayesian, random, and LHS. If the search method is random or LHS, step 3 is eliminated; a single sample of candidate configurations is generated (either randomly or using a Latin hypercube sample) and evaluated as step 2.

If the tuner had partitioned the data for training and scoring (if the PARTITION statement is not specified), then the final (best) model configuration is trained on all the data and scored on all the data; as a result the final model that is returned and its reported validation score might not match the value that is observed during tuning, when the model was trained to a portion of the data and validated on the remaining validation partition.

Determining the Number of Parallel Evaluations

By default, the number of possible parallel evaluations during step 2 and step 3 (if performed) in the section “Hyperparameter Tuning Process” on page 886 is determined by the population size for GA or Bayesian search methods or by the sample size for random or LHS sampling. The maximum number of parallel evaluations is limited by the total number of worker nodes that are connected to the server divided by the number of worker nodes that are used by the parallel sessions that are created. For example, if the server is configured with 100 worker nodes and four workers are used in the sessions, at most 25 parallel evaluations are performed by
default. This limit can be overridden by a factor of 2, resulting in up to 50 parallel evaluations in this example scenario.

Specifically, the number of parallel evaluations is determined as follows:

1. If you do not specify the number of workers to use in parallel subsessions by using the NSUBSESSIONWORKERS= option in the AUTOTUNE statement, the number of workers is determined using the size of the data table: NSUBSESSIONWORKERS = 1 + nDataRows * nDataColumns * 2E–8. If determined based on the data table size, the number of workers in each subsession is fairly aggressively set at one node per 50 million values. The efficiency benefits of tuning in parallel generally outweigh the time savings from distributed training if the data can be managed on fewer nodes. For example, if training a single model on four workers takes 1 minute versus 2 minutes on one worker, then training four models in parallel on one worker each requires only 2 minutes, whereas training four sequential models each on four workers would require 4 minutes.

2. The number of possible parallel evaluations is then determined either as one less than the population size for GA or Bayesian search methods, or as the sampling size for the random or LHS search methods.

3. The number of parallel evaluations is then limited by the server configuration:
   - In single-machine mode, if the number of possible parallel evaluations is greater than 4 and not specified in the NPARALLEL= option in the AUTOTUNE statement, it is limited to 4. This limit can be overridden up to a value of 32 by specifying the NPARALLEL= option (the value of the NPARALLEL= option is reduced if it is greater than 32).
   - In distributed mode, the upper limit for the number of parallel evaluations is calculated as $W/n$, where $W$ is the number of workers connected to the server and $n$ is the number of workers in the parallel subsessions. This limit can be overridden by a factor of 2 by specifying the NPARALLEL= option; the new limit is $2W/n$ (the value of the NPARALLEL= option is reduced if it is greater than $2W/n$).

You can use the AUTOTUNE statement to tune the following options in the PROC TREESPLIT statement:

- the value of the NUMBIN= option for the number of bins for continuous predictors
- the value of the MAXDEPTH= option for the maximum depth of the decision tree
- the criterion on the GROW statement for how the nodes are split

### Displayed Output

The following sections describe the output that PROC TREESPLIT produces. The output is organized into various tables, which are discussed in the order of appearance.
Model Information

The “Model Information” table contains the settings of the training parameters. This table also contains some basic information about the resulting decision tree. This table is produced by default.

Number of Observations

The “Number of Observations” table contains the number of observations that are read from the input data table and the number of observations that are used in the analysis. When you specify the PARTITION statement, the table also indicates the number of observations that are used in each partition. This table is produced by default.

CV Statistics

The “CV Statistics” table contains information about $k$-fold cross validated cost complexity pruning, such as the alpha values, the corresponding size of the tree, and the corresponding minimum, average, and maximum error. The table is generated when you specify the CVCC option in the PROC TREESPLIT statement, and you are also using $k$-fold cross validated cost complexity pruning.

Tree Performance

The “Tree Performance” table contains statistics that measure the model’s goodness of fit. If you specify the PARTITION statement, the table also indicates these statistics on all partitions of the data.

Variable Importance

The “Variable Importance” table displays variable importance based on residual sum of square errors, which is explained in the section “Residual Sum of Squares (RSS) Importance Method” on page 882. This table is produced by default.

RBA Variable Importance

The “RBA Variable Importance” table displays variable importance based on the random branch assignment (RBA) method, which is explained in the section “Random Branch Assignment Importance Method” on page 884. This table is produced by the RBAIMP option in the PROC TREESPLIT statement.

Reduced Error

The “Reduced Error” table contains the pruning results of reduced error pruning that uses validation data. This is the table of the data shown in the PruningPlot. This table is generated when you specify the PRUNINGTABLE option and are using reduced error pruning in the PRUNE statement with validation data.

Cost Complexity

The “Cost Complexity” table contains the pruning results of cost complexity pruning that uses validation data. This is the table of the data shown in the PruningPlot. This table is generated when you specify the PRUNINGTABLE option and are using cost complexity pruning in the PRUNE statement with validation data.
Output CAS Tables

When you specify the OUTPUT statement or the OUTMODEL= option in the PROC TREESPLIT statement to create output tables on your CAS server, the TREESPLIT procedure produces the output data table along with a table that lists the CAS library, the data table name, and the number of rows and columns in that data table.

Tuner Information

The “Tuner Information” table displays the setup values that the tuner uses. This table is produced by the AUTOTUNE statement.

Tuner Summary

The “Tuner Summary” table displays statistics about the tuning process. This table is produced by the AUTOTUNE statement.

Tuner Timing

The “Tuner Timing” table displays the total time spent on different tasks while tuning. This table is produced by the AUTOTUNE statement.

Best Configuration

The “Best Configuration” table displays the hyperparameters and objective function values for the best configuration. This table is produced by the AUTOTUNE statement.

Tuner Results

The “Tuner Results” table displays the values of the hyperparameters, the objective function for the default configuration (Iteration 0), and up to 10 best found configurations. This table is produced by the AUTOTUNE statement.

Evaluation History

The “Evaluation History” tables displays the values of the hyperparameters and the objective function for all configurations. This table is produced by the AUTOTUNE statement, either by default or when EVALHISTORY=ALL.

Predicted Probability Names

The “Predicted Probability Names” table indicates the names of the created variables in either the score code or the data table that is specified in the OUT= option in the OUTPUT statement. This table is produced when you specify the PRINTTARGET option in the PROC TREESPLIT statement.
Chapter 16: The TREESPLIT Procedure

ODS Table Names

PROC TREESPLIT assigns a name to each table it creates. You can use these names to refer to the table when you use the Output Delivery System (ODS) to select tables and create output data tables. Table 16.5 lists these names.

Table 16.5 ODS Tables Produced by PROC TREESPLIT

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>BestConfiguration</td>
<td>Hyperparameters and objective function values for the best configuration</td>
<td>AUTOTUNE</td>
<td>Default</td>
</tr>
<tr>
<td>CostComplexity</td>
<td>Information about the number of leaves and the error for cost-complexity pruning when validation data are used</td>
<td>PROC TREESPLIT</td>
<td>PRUNINGTABLE</td>
</tr>
<tr>
<td>CrossValidationValues</td>
<td>Results for cost-complexity pruning based on cross validation</td>
<td>PROC TREESPLIT</td>
<td>CVCC</td>
</tr>
<tr>
<td>EvaluationHistory</td>
<td>Values of the hyperparameters and the objective function for all configurations</td>
<td>AUTOTUNE</td>
<td>Default / EvalHistory=ALL</td>
</tr>
<tr>
<td>ModelInfo</td>
<td>Information about the modeling environment</td>
<td>PROC TREESPLIT</td>
<td>Default</td>
</tr>
<tr>
<td>NObs</td>
<td>Observation information</td>
<td>PROC TREESPLIT</td>
<td>Default</td>
</tr>
<tr>
<td>PredName</td>
<td>Predicted name information for interval targets</td>
<td>PROC TREESPLIT</td>
<td>PRINTTARGET</td>
</tr>
<tr>
<td>PredProbName</td>
<td>Predicted probability name information for nominal targets</td>
<td>PROC TREESPLIT</td>
<td>PRINTTARGET</td>
</tr>
<tr>
<td>PredIntoName</td>
<td>Predicted name information for nominal targets</td>
<td>PROC TREESPLIT</td>
<td>PRINTTARGET</td>
</tr>
<tr>
<td>RBAImportance</td>
<td>Random branch assignment variable importance</td>
<td>PROC TREESPLIT</td>
<td>RBAIMP</td>
</tr>
<tr>
<td>ReducedError</td>
<td>Information about the number of leaves and the error for reduced-error pruning when validation data are used</td>
<td>PROC TREESPLIT</td>
<td>PRUNINGTABLE</td>
</tr>
<tr>
<td>TreePerformance</td>
<td>Fit statistics for the selected tree</td>
<td>PROC TREESPLIT</td>
<td>Default</td>
</tr>
<tr>
<td>TunerInfo</td>
<td>Setup values used by the tuner</td>
<td>AUTOTUNE</td>
<td>Default</td>
</tr>
<tr>
<td>TunerResults</td>
<td>Values of the hyperparameters and the objective function for the default configuration (Iteration 0) and up to 10 best configurations found</td>
<td>AUTOTUNE</td>
<td>Default</td>
</tr>
<tr>
<td>TunerSummary</td>
<td>Statistics about the tuning process</td>
<td>AUTOTUNE</td>
<td>Default</td>
</tr>
</tbody>
</table>
Table 16.5  continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>TunerTiming</td>
<td>Total time spent on different tasks while tuning</td>
<td>AUTOTUNE</td>
<td>Default</td>
</tr>
<tr>
<td>VariableImportance</td>
<td>Variable importance</td>
<td>PROC TREESPLIT</td>
<td>Default</td>
</tr>
</tbody>
</table>

**ODS Graphics**

You can refer to every graph that is produced through ODS Graphics by name. The names of the graphs that PROC TREESPLIT generates are listed in Table 16.6, along with the relevant PLOTS= options.

Table 16.6  Graphs Produced by PROC TREESPLIT

<table>
<thead>
<tr>
<th>ODS Graph Name</th>
<th>Plot Description</th>
<th>PLOTS= Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>CrossValidationASEPlot</td>
<td>Cross validation cost-complexity ASE plot when the response is continuous</td>
<td>CVCC</td>
</tr>
<tr>
<td>CrossValidationMisclassPlot</td>
<td>Cross validation cost-complexity misclassification plot when the response is categorical</td>
<td>CVCC</td>
</tr>
<tr>
<td>PruningPlot</td>
<td>Plot of the error sum of squares, misclassification rate, or cost complexity when it is used for final tree selection</td>
<td>PRUNEUNTIL</td>
</tr>
<tr>
<td>WholeTreePlot</td>
<td>Overview plot of final tree</td>
<td>WHOLETREE</td>
</tr>
<tr>
<td>ZoomedTreePlot</td>
<td>Detailed plot of portion of final tree</td>
<td>ZOOMEDTREE</td>
</tr>
</tbody>
</table>

**INPUT and TARGET Statement Syntax**

In addition to the syntax that is described in the CLASS and MODEL statement sections, PROC TREESPLIT supports INPUT/TARGET syntax that you might be familiar with from other procedures. The INPUT/TARGET syntax cannot be used together with the CLASS/MODEL syntax.

This syntax requires one TARGET statement and one or more INPUT statements. If you use this syntax, then the PROC TREESPLIT statement, the TARGET statement, and the INPUT statement are required. Depending on the options in those statements, specified variables can be interval or nominal. By default, numeric INPUT variables are treated as interval (or continuous) predictors, and character INPUT variables are treated as nominal (or categorical) predictors.
Chapter 16: The TREESPLIT Procedure

**INPUT Statement**

```plaintext
INPUT variables < / option > ;
```

**TARGET Statement**

```plaintext
TARGET variable < / option > ;
```

The INPUT statement specifies predictor `variables` for the decision tree or regression tree. The value of `variable` can be a range such as “var_1–var_1000” or the special “_ALL_” value to include all variables in the data tables. As with CLASS variables, all nominal INPUT variables are padded or truncated to 32 characters.

You cannot use an INPUT statement with a MODEL or CLASS statement.

You can specify the following option:

**LEVEL=INTERVAL | NOMINAL**

specifies whether the specified predictor `variables` are interval or nominal. You can specify the following values:

- **INTERVAL**
  - treats all numeric `variables` as interval predictors.
- **NOMINAL**
  - treats all `variables` as nominal predictors.

By default, numeric `variables` are treated as interval predictors, and character `variables` are treated as nominal predictors. Specifying LEVEL=NOMINAL forces all `variables` in that statement to be treated as nominal. You cannot specify LEVEL=INTERVAL for character variables.

The TARGET statement names the `variable` whose values PROC TREESPLIT predicts. Missing values in the target are ignored except during scoring.

You cannot use a TARGET statement with a MODEL or CLASS statement.

You can specify the following option:

**LEVEL=INTERVAL | NOMINAL**

specifies whether the specified response `variable` is interval or nominal. You can specify the following values:

- **INTERVAL**
  - treats the response as an interval variable and creates a regression tree.
- **NOMINAL**
  - treats the response as a nominal variable and creates a decision tree.

By default, LEVEL=INTERVAL for numeric variables and LEVEL=NOMINAL for categorical variables.
Examples: TREETREE Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

---

**Example 16.1: Creating a Binary Classification Tree with Validation Data**

A common use of classification trees is to predict whether a mortgage applicant will default on a loan. The data table Hmeq, which is in the Sampsio library that SAS provides, contains observations for 5,960 mortgage applicants. A variable named Bad indicates whether the applicant, after being approved for a loan, paid off or defaulted on the loan.

This example uses Hmeq to build a tree model that is used to score the data and can be used to score data about new applicants. Table 16.7 describes the variables in Hmeq.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Role</th>
<th>Level</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bad</td>
<td>Response</td>
<td>Binary</td>
<td>1 = applicant defaulted on the loan or is seriously delinquent</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>0 = applicant paid off the loan</td>
</tr>
<tr>
<td>CLAge</td>
<td>Predictor</td>
<td>Interval</td>
<td>Age of oldest credit line in months</td>
</tr>
<tr>
<td>CLNo</td>
<td>Predictor</td>
<td>Interval</td>
<td>Number of credit lines</td>
</tr>
<tr>
<td>DebtInc</td>
<td>Predictor</td>
<td>Interval</td>
<td>Debt-to-income ratio</td>
</tr>
<tr>
<td>Delinq</td>
<td>Predictor</td>
<td>Interval</td>
<td>Number of delinquent credit lines</td>
</tr>
<tr>
<td>Derog</td>
<td>Predictor</td>
<td>Interval</td>
<td>Number of major derogatory reports</td>
</tr>
<tr>
<td>Job</td>
<td>Predictor</td>
<td>Nominal</td>
<td>Occupational category</td>
</tr>
<tr>
<td>Loan</td>
<td>Predictor</td>
<td>Interval</td>
<td>Requested loan amount</td>
</tr>
<tr>
<td>MortDue</td>
<td>Predictor</td>
<td>Interval</td>
<td>Amount due on mortgage</td>
</tr>
<tr>
<td>nInq</td>
<td>Predictor</td>
<td>Interval</td>
<td>Number of recent credit inquiries</td>
</tr>
<tr>
<td>Reason</td>
<td>Predictor</td>
<td>Binary</td>
<td>'DebtCon' = debt consolidation</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>'HomeImp' = home improvement</td>
</tr>
<tr>
<td>Value</td>
<td>Predictor</td>
<td>Interval</td>
<td>Value of property</td>
</tr>
<tr>
<td>YoJ</td>
<td>Predictor</td>
<td>Interval</td>
<td>Years at present job</td>
</tr>
</tbody>
</table>

The response variable for the tree model is Bad, a classification variable that has two values (0 for payment of loan and 1 for default). The other variables are predictor variables for the model. The following statements load mycas.hmeq data into your CAS session and display the first 10 observations of the data table. For this example, the statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

---
Chapter 16: The TREESPLIT Procedure

/* Convert variable names to mixed case */
data mycas.hmeq;
  length Bad Loan MortDue Value 8 Reason Job $7 YoJ Derog Delinq CLAge nInq CLNo DebtInc 8;
set sampsio.hmeq;
run;

proc print data=mycas.hmeq(obs=10); run;

Output 16.1.1 shows the first 10 observations of mycas.hmeq.

Output 16.1.1 Partial Listing of the mycas.hmeq Data

<table>
<thead>
<tr>
<th>Obs</th>
<th>Bad</th>
<th>Loan</th>
<th>MortDue</th>
<th>Value</th>
<th>Reason</th>
<th>Job</th>
<th>YoJ</th>
<th>Derog</th>
<th>Delinq</th>
<th>CLAge</th>
<th>nInq</th>
<th>CLNo</th>
<th>DebtInc</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1100</td>
<td>25860</td>
<td>39025</td>
<td>HomeImpt</td>
<td>Other</td>
<td>10.5</td>
<td>0</td>
<td>0</td>
<td>94.367</td>
<td>1</td>
<td>9</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1500</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1800</td>
<td>48649</td>
<td>57037</td>
<td>HomeImpt</td>
<td>Other</td>
<td>5</td>
<td>3</td>
<td>2</td>
<td>77.100</td>
<td>1</td>
<td>17</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>2000</td>
<td>62250</td>
<td>40150</td>
<td>HomeImpt</td>
<td>Sales</td>
<td>16</td>
<td>0</td>
<td>0</td>
<td>115.800</td>
<td>0</td>
<td>13</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>1</td>
<td>2000</td>
<td>45000</td>
<td>55000</td>
<td>HomeImpt</td>
<td>Other</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>86.067</td>
<td>2</td>
<td>25</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>2200</td>
<td>24280</td>
<td>34687</td>
<td>HomeImpt</td>
<td>Other</td>
<td>.</td>
<td>0</td>
<td>1</td>
<td>300.867</td>
<td>0</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>2300</td>
<td>28192</td>
<td>40150</td>
<td>HomeImpt</td>
<td>Other</td>
<td>4.5</td>
<td>0</td>
<td>0</td>
<td>54.600</td>
<td>1</td>
<td>16</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>2400</td>
<td>50000</td>
<td>73395</td>
<td>HomeImpt</td>
<td>ProfExe</td>
<td>5.0</td>
<td>1</td>
<td>0</td>
<td>.</td>
<td>1</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>2400</td>
<td>17180</td>
<td>.</td>
<td>HomeImpt</td>
<td>Other</td>
<td>.</td>
<td>0</td>
<td>0</td>
<td>14.567</td>
<td>3</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>1</td>
<td>2500</td>
<td>15000</td>
<td>20200</td>
<td>HomeImpt</td>
<td></td>
<td>18</td>
<td>0</td>
<td>0</td>
<td>136.067</td>
<td>1</td>
<td>19</td>
<td></td>
</tr>
</tbody>
</table>

The following statements use the TREESPLIT procedure to create a classification tree:

ods graphics on;

proc treesplit data=mycas.hmeq maxdepth=5;
  class Bad Delinq Derog Job nInq Reason;
  model Bad = Delinq Derog Job nInq Reason CLAge CLNo DebtInc Loan MortDue Value YoJ;
  prune costcomplexity;
  partition fraction(validate=0.3 seed=123);
  code file='treesplexc.sas';
run;

The MAXDEPTH= option specifies that the maximum depth of the tree to be grown is 5.

Specifying Bad to the left of the equal sign in the MODEL statement indicates that it is the response variable. Because no GROW statement is included, PROC TREESPLIT defaults to using the entropy metric, which calculates the gain to grow the tree. The PRUNE statement requests cost-complexity pruning.

The PARTITION statement requests that the observations in Hmeq be partitioned into disjoint subsets for model training and validation. Observations are randomly selected for the validation subset with probability 0.3; the remaining observations are selected for the training subset.

The FILE= option in the CODE statement requests that SAS DATA step score code be saved to a file named treesplexc.sas.
The tree diagram in Output 16.1.2 provides an overview of the full tree.

**Output 16.1.2** Overview Diagram of Final Tree

The observations in terminal nodes 9, C, D, F, and I are assigned a prediction of Bad=0, and those in terminal nodes 3, 8, A, G, and H are assigned a prediction of Bad=1. Node C contains the most observations, as indicated by the thickness of the link from its parent node.

The tree diagram in Output 16.1.3 is a detailed view of the top portion of the tree. You can use the PLOTS= option in the PROC TREESPLIT statement to control which nodes are displayed.
By default, this view provides detailed splitting information about the first three levels of the tree, including the root level. The splitting rule above each node shows the splitting variable and splitting value; the rule determines which observations from the parent node are included in the node. The first row of the table inside the node provides the node identifier. The second row provides the number of training observations. The third row shows the predicted response for observations in that node if classification occurs at that point, along with the proportion of training observations with that observed response. Note that the legend shows what actual value of the response variable is represented by the value shown in the node. For example, in node 6, 93.39% of the 3,208 observations in the training data have an observed response value of Bad=0, as indicated by the value 2.
Output 16.1.4 displays the fit statistics for the final tree.

<table>
<thead>
<tr>
<th>Number of Leaves</th>
<th>Missclassification Rate</th>
</tr>
</thead>
<tbody>
<tr>
<td>Training</td>
<td>6</td>
</tr>
<tr>
<td>Validation</td>
<td>6</td>
</tr>
</tbody>
</table>

Output 16.1.5 displays the pruning plot.

This plot displays the misclassification rates for the training and validation data as the tree is pruned. The tree with 10 leaves is selected as the final tree because it has the lowest misclassification rate for the validation data.

Creating Score Code and Scoring New Data

In addition to seeing information about the tree model, you might be interested in applying the model to predict the response variable in other data tables where the response is unknown. You can use the score code file `treesplexc.sas` (which was created by the FILE= option in the CODE statement) to score new data anywhere that you can run SAS DATA step code. The following is an example of using the score code file `treesplexc.sas` to score the data in `Hmeq` and save the results in a SAS data table named `Scored`.
data scored;
   set sampsio.hmeq;
   %include 'treesplexc.sas';
run;

Output 16.1.6 shows a partial listing of Scored.

Output 16.1.6  Partial Listing of the Scored Hmeq Data

<table>
<thead>
<tr>
<th>Obs</th>
<th>BAD</th>
<th>LOAN</th>
<th>MORTDUE</th>
<th>VALUE</th>
<th>REASON</th>
<th>JOB</th>
<th>YOJ</th>
<th>DEROG</th>
<th>DELinq</th>
<th>CLAGE</th>
<th>NINQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1100</td>
<td>25860</td>
<td>39025</td>
<td>Homelmp</td>
<td>Other</td>
<td>10.5</td>
<td>0</td>
<td>0</td>
<td>94.367</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1300</td>
<td>70053</td>
<td>68400</td>
<td>Homelmp</td>
<td>Other</td>
<td>7.0</td>
<td>0</td>
<td>2</td>
<td>121.833</td>
<td>0</td>
</tr>
<tr>
<td>3</td>
<td>1</td>
<td>1500</td>
<td>13500</td>
<td>16700</td>
<td>Homelmp</td>
<td>Other</td>
<td>4.0</td>
<td>0</td>
<td>0</td>
<td>149.467</td>
<td>1</td>
</tr>
<tr>
<td>4</td>
<td>1</td>
<td>1500</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>5</td>
<td>0</td>
<td>1700</td>
<td>97800</td>
<td>112000</td>
<td>Homelmp</td>
<td>Office</td>
<td>3.0</td>
<td>0</td>
<td>0</td>
<td>93.333</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>1</td>
<td>1700</td>
<td>30548</td>
<td>40320</td>
<td>Homelmp</td>
<td>Other</td>
<td>9.0</td>
<td>0</td>
<td>0</td>
<td>101.466</td>
<td>1</td>
</tr>
<tr>
<td>7</td>
<td>1</td>
<td>1800</td>
<td>48649</td>
<td>57037</td>
<td>Homelmp</td>
<td>Other</td>
<td>5.0</td>
<td>3</td>
<td>2</td>
<td>77.100</td>
<td>1</td>
</tr>
<tr>
<td>8</td>
<td>1</td>
<td>1800</td>
<td>28502</td>
<td>43034</td>
<td>Homelmp</td>
<td>Other</td>
<td>11.0</td>
<td>0</td>
<td>0</td>
<td>88.766</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>1</td>
<td>2000</td>
<td>32700</td>
<td>46740</td>
<td>Homelmp</td>
<td>Other</td>
<td>3.0</td>
<td>0</td>
<td>2</td>
<td>216.933</td>
<td>1</td>
</tr>
<tr>
<td>10</td>
<td>1</td>
<td>2000</td>
<td>.</td>
<td>62250</td>
<td>Homelmp</td>
<td>Sales</td>
<td>16.0</td>
<td>0</td>
<td>0</td>
<td>115.800</td>
<td>0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Obs</th>
<th>CLNO</th>
<th>DEBTINC</th>
<th><em>leaf_id</em></th>
<th><em>Bad</em></th>
<th>P_Bad1</th>
<th>P_Bad0</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>9</td>
<td></td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>14</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>10</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>.</td>
<td>.</td>
<td>5 1</td>
<td>0.93421</td>
<td>0.06579</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>14</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>8</td>
<td>37.1136</td>
<td>10 0</td>
<td>0.06568</td>
<td>0.93432</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>17</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>8</td>
<td>36.8849</td>
<td>10 0</td>
<td>0.06568</td>
<td>0.93432</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>12</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>13</td>
<td>.</td>
<td>9 1</td>
<td>0.58906</td>
<td>0.41094</td>
<td></td>
</tr>
</tbody>
</table>

The data table contains the 13 original variables and 4 new variables that are created by the score code. The variable P_BAD1 is the proportion of training observations in this leaf for which BAD=1; this variable can be interpreted as the probability of default. The variable I_BAD indicates the predicted value of BAD for the observation.

You can use the preceding statements to score new data by including the new data table in place of Hmeq in the SET statement. The new data table must contain the same variables as the data that are used to build the tree model, but not the unknown response variable that you now want to predict.
Example 16.2: Creating a Regression Tree

This example performs an analysis in which a linear regression model is fit. You can alternatively fit a regression tree to predict the salaries of Major League Baseball players based on their performance measures from the previous season by using almost identical code. Regression trees are piecewise constant models that, for relatively small data tables such as Sashelp.Baseball, provide succinct summaries of how the predictor variables determine the predictions. These models are usually easier to interpret than linear regression models. The Sashelp.Baseball data table contains salary and performance information for Major League Baseball players (excluding pitchers) who played at least one game in both the 1986 and 1987 seasons (Time Inc. 1987). You can load the Sashelp.Baseball data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```plaintext
data mycas.baseball;
  set sashelp.baseball;
run;
```

The following statements create a regression tree model:

```plaintext
ods graphics on;

proc treesplit data=mycas.baseball maxdepth=3;
  class league division;
  model logSalary = nAtBat nHits nHome nRuns nRBI nBB
                   yrMajor crAtBat crHits crHome crRuns crRbi
                   crBB league division nOuts nAssts nError;
  output out=mycas.treesplout;
  prune none;
run;
```

Because no GROW statement is specified, the tree is grown using the RSS criterion by default. Because no PRUNE statement is included, no pruning is performed. The OUTPUT statement requests generation of the data table mycas.treesplout, which contains the predicted salary from the tree model for each observation.

Much of the output for a regression tree is identical to the output for a classification tree. Where there are differences, tables and plots are displayed and discussed on the following pages.

Output 16.2.1 displays the full regression tree.
The final selected tree has eight leaves. In a regression tree, the shade of the leaves represents the predicted response value, which is the average observed logSalary for the observations in that leaf. Node E has the lowest predicted response value, indicated by the lightest shade of blue, and node 7 has the highest, indicated by the dark shade.

Output 16.2.2 shows details of the first three levels of the tree, including the root node.
Output 16.2.2 Detailed Diagram of Regression Tree

As in Output 16.1.3, this diagram displays split variables and split values for the nodes, along with the exact predicted response value, which is the average observed response, in each node.

Output 16.2.3 displays the fit statistic for the final regression tree (the only fit statistic provided for a regression tree is the ASE).

Output 16.2.3 Regression Tree Performance

**The TREESPLIT Procedure**

<table>
<thead>
<tr>
<th>Fit Statistics for Selected Tree</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Number of Leaves</strong></td>
</tr>
<tr>
<td>----------------------</td>
</tr>
<tr>
<td>Training</td>
</tr>
</tbody>
</table>
Output 16.2.4 is a partial display of the mycas.treesplout data table that is created when you specify the OUTPUT statement.

```
Output 16.2.4 Scored Predictor Data Table

<table>
<thead>
<tr>
<th>Obs</th>
<th>P_logSalary</th>
<th>DT_PredStd</th>
<th>_LeafID</th>
<th>_Residual</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>4.6555457426</td>
<td>0.3064936468</td>
<td>14</td>
<td>.</td>
</tr>
<tr>
<td>2</td>
<td>6.8573201516</td>
<td>0.4410266912</td>
<td>7</td>
<td>0.6427120531</td>
</tr>
<tr>
<td>3</td>
<td>4.6555457426</td>
<td>0.3064936468</td>
<td>14</td>
<td>0.4070505006</td>
</tr>
<tr>
<td>4</td>
<td>6.8573201516</td>
<td>0.4410266912</td>
<td>7</td>
<td>-0.145745307</td>
</tr>
<tr>
<td>5</td>
<td>5.7477251685</td>
<td>0.3269101703</td>
<td>11</td>
<td>-0.56219311</td>
</tr>
<tr>
<td>6</td>
<td>4.6555457426</td>
<td>0.3064936468</td>
<td>14</td>
<td>.</td>
</tr>
<tr>
<td>7</td>
<td>6.8573201516</td>
<td>0.4410266912</td>
<td>7</td>
<td>.</td>
</tr>
<tr>
<td>8</td>
<td>4.6555457426</td>
<td>0.3064936468</td>
<td>14</td>
<td>-0.089386386</td>
</tr>
<tr>
<td>9</td>
<td>6.8573201516</td>
<td>0.4410266912</td>
<td>7</td>
<td>0.2023084645</td>
</tr>
<tr>
<td>10</td>
<td>6.35986721</td>
<td>0.5351772705</td>
<td>8</td>
<td>-0.260205997</td>
</tr>
</tbody>
</table>
```

The variable \( P\_\log\text{Salary} \) contains the predicted salaries on the log scale. Note that all observations in the same leaf have the same predicted response. The OUT= data table can contain additional variables from the DATA= data table if you specify them by using the COPYVARS= option.

### Example 16.3: Assessing Variable Importance

This example creates a classification tree model to determine important variables (parameters) during the manufacture of a semiconductor device. Some of the variables that are involved in the manufacturing process are: gTemp, the growth temperature of substrate; aTemp, the annealing temperature; Rot, rotation speed; Dopant, the atom used during device growth; and Usable, which indicates whether the device is usable.

The following statements create a data table named mycas.MBE_Data, which contains measurements for 20 devices:

```plaintext
data mycas.MBE_Data;
  label gTemp = 'Growth Temperature of Substrate';
  label aTemp = 'Anneal Temperature';
  label Rot = 'Rotation Speed';
  label Dopant = 'Dopant Atom';
  label Usable = 'Experiment Could Be Performed';
  input gTemp aTemp Rot Dopant $ 39-40 Usable $ 47-54;
datalines;
  384.614 633.172 1.01933 C Unusable
  363.874 512.942 0.72057 C Unusable
  397.395 671.179 0.90419 C Unusable
  389.962 653.940 1.01417 C Unusable
  387.763 612.545 1.00417 C Unusable
  394.206 617.021 1.07188 Si Usable
  387.135 616.035 0.94740 Si Usable
  428.783 745.345 0.99087 Si Unusable
  399.365 600.932 1.23307 Si Unusable
  455.502 648.821 1.01703 Si Unusable
```

The following statements create the tree model:

```plaintext
proc treesplit data=mycas.MBE_Data maxdepth=6;
class Usable Dopant;
model Usable = gTemp aTemp Rot Dopant;
prune none;
run;
```

Output 16.3.1 shows the “Variable Importance” table.

Output 16.3.1  Variable Importance

<table>
<thead>
<tr>
<th>Variable</th>
<th>Std Dev Importance</th>
<th>Relative Importance</th>
<th>Count</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dopant</td>
<td>2.7000</td>
<td>1.0000</td>
<td>1</td>
</tr>
<tr>
<td>aTemp</td>
<td>1.0500</td>
<td>0.3889</td>
<td>1</td>
</tr>
</tbody>
</table>

This table shows that the predictor gTemp has the largest importance value. This means that the growth temperature of the substrate is the most important consideration in determining the usability of the sample. The column Count indicates how many times the variable was used in for splits within the decision tree.

References


Part III

Utility
Chapter 17
The ASSESS Procedure

Overview: ASSESS Procedure

The ASSESS procedure assesses and compares supervised learning models in SAS Viya. For a supervised learning model that has a nominal target, the ASSESS procedure produces lift information and receiver operating characteristic (ROC) information. For a regression model, the ASSESS procedure performs a quantile binning of the predictions and then returns the summary statistics of the response variable for each bin. PROC ASSESS also calculates fit statistics such as average square error, mean square logarithmic error, mean absolute error, mean consequential error, and multiclass log loss.

The expected input to the ASSESS procedure is score data from supervised learning models.
PROC ASSESS Features

The ASSESS procedure can be used to select a champion model from several models or to evaluate a certain model during the model assessment phase. The following list summarizes some basic features of PROC ASSESS:

- executes analysis in parallel on multiple machines
- is highly multithreaded
- calculates lift and gain in each bucket based on percentile
- calculates ROC information based on cut size
- calculates popular fit statistics for regression and classification models
- performs analysis for each partition

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the `CASHOST` and `CASPORT` of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:
cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: ASSESS Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

This example demonstrates how to use the ASSESS procedure to compute lift regression information and fit statistics.

The following SAS DATA step creates the SAS data table `mycas.score`, which is similar to score data from a linear regression, and loads the table into your CAS session:

```sas
data mycas.score;
  input _PartInd_ good p_good;
datalines;
0 0.8224 0.7590
0 0.6538 0.4632
0 0.7693 0.7069
0 0.7491 0.7087
0 0.7779 0.7209
1 0.7161 0.8389
1 0.6779 0.6209
1 0.6392 0.6077
1 0.8090 0.9096
1 0.6064 0.7355
;
```

These statements assume that your CAS engine libref is named `mycas`, but you can substitute any appropriately defined CAS engine libref.

In this data table, the variable `good` is the ground truth and the variable `p_good` is the prediction from modeling. The variable `_PartInd_` assigns each observation to one of two partitions for the analysis.

The following statements call the ASSESS procedure to compute lift regression information and fit statistics.

```sas
proc assess data=mycas.score nbins=2;
  var p_good;
  target good;
  by _PartInd_;
run;
```

The **VAR** statement specifies that the variable `p_good` should be analyzed in the model assessment. The **TARGET** statement specifies that the variable `good` is the response variable. The **BY** statement specifies that PROC ASSESS should perform the analysis separately for each value of `_PartInd_`.

Figure 17.1 shows the minimum, maximum, and mean of the actual and predicted values for `_PartInd_`=0.
Figure 17.1  Lift Regression Information for the First Partition

The ASSESS Procedure

_PartInd_=0

<table>
<thead>
<tr>
<th>Variable</th>
<th>Depth</th>
<th>Number of Observations</th>
<th>Predicted</th>
<th>Actual</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Minimum</td>
<td>Maximum</td>
</tr>
<tr>
<td>p_good</td>
<td>0</td>
<td>0</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>3</td>
<td>0.708700</td>
<td>0.759000</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>2</td>
<td>0.463200</td>
<td>0.706900</td>
</tr>
</tbody>
</table>

Figure 17.2 shows the error metrics of the interval target for _PartInd_=0.

Figure 17.2  Fit Statistics for the First Partition

_PartInd_=0

<table>
<thead>
<tr>
<th>Number of Observations</th>
<th>Divisor of Average</th>
<th>Squared Error</th>
<th>Absolute Error</th>
<th>Squared Logarithmic Error</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Average</td>
<td>Root Average</td>
<td>Root Mean</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Mean</td>
<td>Mean</td>
<td>Mean</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>5</td>
<td>0.009825</td>
<td>0.099119</td>
</tr>
</tbody>
</table>

Figure 17.3 shows the minimum, maximum, and mean of the actual and predicted values for _PartInd_=1.

Figure 17.3  Lift Regression Information for the Second Partition

The ASSESS Procedure

_PartInd_=1

<table>
<thead>
<tr>
<th>Variable</th>
<th>Depth</th>
<th>Number of Observations</th>
<th>Predicted</th>
<th>Actual</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>Minimum</td>
<td>Maximum</td>
</tr>
<tr>
<td>p_good</td>
<td>0</td>
<td>0</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td></td>
<td>50</td>
<td>3</td>
<td>0.735500</td>
<td>0.909600</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>2</td>
<td>0.607700</td>
<td>0.620900</td>
</tr>
</tbody>
</table>

Figure 17.4 shows the error metrics for the interval target for _PartInd_=1.
The following statements are available in the ASSESS procedure:

```
PROC ASSESS < options > ;
    INPUT variable ;
    TARGET variables < /options > ;
    FITSTAT PVAR=variables / PEVENT="event-list" < DLM="character" > ;
    FREQ variable ;
    BY variable ;
```

The PROC ASSESS, INPUT, and TARGET statements are required.

The following sections describe the PROC ASSESS statement and then describe the other statements in alphabetical order.

### PROC ASSESS Statement

```
PROC ASSESS < options > ;
```

The PROC ASSESS statement invokes the ASSESS procedure.

You can specify the following `options`:

- **DATA=** `CAS-libref.data-table`
  
  names the input data table for PROC ASSESS to use. The default is the most recently created data table. `CAS-libref.data-table` is a two-level name, where

  - `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 908.

  - `data-table` specifies the name of the input data table.
**FITSTATOUT=**`CAS-libref.data-table`

specifies the name of the fit statistics results table. *CAS-libref.data-table* is a two-level name, where *CAS-libref* refers to the caslib and session identifier, and *data-table* specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 908.

If you specify this option, all ODS tables are suppressed. This option is valid only if you also include a FITSTAT statement.

**LIFTOUT=**`CAS-libref.data-table`

specifies the name of the lift results table. *CAS-libref.data-table* is a two-level name, where *CAS-libref* refers to the caslib and session identifier, and *data-table* specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 908.

If you specify this option, all ODS tables are suppressed.

**MAXITER=**`integer`

specifies the maximum number of iterations for the percentile algorithm, where *integer* must be an integer greater than or equal to 1. By default, MAXITER=5 times the value of the NBINS= option.

**NBINS=**`integer`

specifies the number of bins to be used in the lift calculation, where *integer* must be an integer greater than or equal to 2.

By default, NBINS=20.

**NCUTS=**`integer`

specifies the number of cuts to be used in the ROC calculation, where *integer* must be an integer greater than or equal to 2. The inverse of *integer* represents the step size of the quantile. For example, NCUTS=10 generates 10 intervals for ROC analysis, with each step size 0.1. You cannot specify this option when the response variable that is specified in the TARGET statement is interval.

By default, NCUTS=100.

**NTHREADS=**`number`

specifies the number of threads that are used in the computation, where *number* must be an integer between 1 and 64, inclusive. The default value is the number of CPUs available in the machine.

**ROCOUT=**`CAS-libref.data-table`

specifies the name of the ROC results table. *CAS-libref.data-table* is a two-level name, where *CAS-libref* refers to the caslib and session identifier, and *data-table* specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 908.

If you specify this option, all ODS tables are suppressed. This option is valid only for a nominal target (LEVEL=NOMINAL in the TARGET statement).

**BY Statement**

```
BY variable;
```

The BY statement specifies one partition *variable* to be used in the predictive model. If you specify the BY statement, PROC ASSESS performs the analysis separately for each value of the BY variable. If you do not specify the BY statement, PROC ASSESS treats the entire input data as one group for analysis.
FITSTAT Statement

FITSTAT PVAR=variables / PEVENT="event-list" <DLM="character"> ;

The FITSTAT statement reports the following error metrics for a nominal target: average square error, divisor of average square error, root average square error, mean consequential error, and multiclass log loss. (For an interval target, the following metrics are created without specifying the FITSTAT statement: average square error, divisor of average square error, root average square error, mean absolute error, root mean absolute error, mean square logarithmic error, and root mean square logarithmic error.)

You must specify the following arguments:

PVAR=variables
   specifies the posterior probability for each level in model prediction except the variable specified in the INPUT statement. Duplicate variables are not allowed. If you specify the variable that is specified in the INPUT statement, it is ignored.

PEVENT="event-list"
   specifies the events that correspond to each variable in the PVAR= option. The “event-list” cannot include the event that corresponds to the variable in the TARGET statement. You must specify the PEVENT= and PVAR= options one-to-one in the same order. The maximal length allowed of PEVENT is 5000 characters.

You can also specify the following option:

DELIMITER="character"
DLM="character"
   specifies the delimiter that is used to separate events that are specified in the PEVENT= option. A delimiter is used when event names contain embedded spaces (for example, “Fuel Oil”) or special characters (for example, “;” or “*”). You must specify the quotation marks around character. You can specify only one delimiter; combinations of delimiters are not supported. The valid values of the DELIMITER= option are “ “ (space), “;” (semicolon), “*” (asterisk), “.” (period), and “,” (comma).

By default, DELIMITER=” “ (space).
If a delimiter other than “ “ is specified, PROC ASSESS treats any spaces (including empty spaces) to be valid characters. You are responsible for mapping events correctly in order to obtain correct results.

FREQ Statement

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC ASSESS treats each observation as if it appears f times, where f is the value of the FREQ variable for the observation. If f is not an integer, it is truncated to an integer. If f is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.
Chapter 17: The ASSESS Procedure

**INPUT Statement**

```plaintext
INPUT variable ;
VAR variable ;
```

The INPUT statement specifies the name of one `variable` to be analyzed in model assessment. When the variable specified in the TARGET statement is nominal, `variable` is the posterior probability of the event to be analyzed; when the variable specified in the TARGET statement is interval, `variable` is the predicted value.

**TARGET Statement**

```plaintext
TARGET variable < /options> ;
```

The TARGET statement specifies the response `variable` in supervised learning. You can specify the following `options`:

- `LEVEL=INTERVAL | NOMINAL` specifies the `variable` type.
  - By default, `LEVEL=INTERVAL`.
- `EVENT="string"` specifies the formatted value of response `variable` that represents the event. For an interval target (LEVEL=INTERVAL), the EVENT= option is ignored. For a nominal target (LEVEL=NOMINAL), the EVENT= option is required.

**Details: ASSESS Procedure**

**Lift Information**

In the lift information table, the number of events are first allocated to each bin based on a percentile analysis of the probability of the event. In distributed mode, the percentile analysis is based on a heuristic, so it is an estimation of the precise percentile cutoff points that are used for binning. Consequently, the resulting cutoff points might be different from the cutoff points that are based on sorting the whole data set. This difference is more likely to happen when the data set is small.

Events are allocated to bins in two ways in order to perform the analysis. One way is the baseline case, which allocates events evenly to bins with the assumption that no analytic models are applied. The second way is...
the predicted case, which allocates events to each bin based on probabilities from modeling. In each case, the following metrics are calculated independently:

- captured response percentage, which is the number of events in each bin divided by the total number of events
- cumulative captured response percentage, which accumulates the captured response percentages over bins
- response percentage, which is the number of events divided by the number of observations in each bin
- cumulative response percentage, which accumulates the response percentages over bins

Lift is defined as the ratio of the captured response percentage from the predicted case to the captured response percentage from the baseline case. Gain is defined as the ratio of the cumulative response percentage from the predicted case to the cumulative response percentage from the baseline case, minus one.

---

**ROC Information**

In the receiver operating characteristic (ROC) information table, the confusion matrix is calculated based on the event in each cutoff point. More terminology and the derivation of a confusion matrix is available in Fawcett (2006), Powers (2011), and Derby (2013).

The following notation is necessary for discussion of ROC information:

- $m$ is the total cutoff points
- $n$ is the number of observations
- $N$ is the sum of observation frequencies in the data
- $w_i$ are the observation frequencies, so

$$N = \sum_{i=1}^{n} w_i$$

- $a_k$ is true positive at cutoff point $k$, $k \in [0, m - 1]$
- $b_k$ is false positive at cutoff point $k$, $k \in [0, m - 1]$
- $c_k$ is false negative at cutoff point $k$, $k \in [0, m - 1]$

The definitions of $C$ (area under the curve), Gini, gamma, and tau are as follows:

$$C = \frac{\mu + \theta}{\rho}$$
Gini = \frac{\mu - \omega}{\rho}

gamma = \frac{\mu - \omega}{\mu + \omega}

tau = \frac{\mu - \omega}{\frac{N}{2}(N - 1)}

where:

\[ \theta = \sum_{k=1}^{m} ((a_{k-1} - a_k)(b_{k-1} - b_k)) \]

\[ \mu = \sum_{k=2}^{m} \left( (a_{k-1} - a_k) \sum_{j=1}^{k} (b_{j-1} - b_j) \right) \]

\[ \omega = \sum_{k=1}^{m} \left( (a_{k-1} - a_k) \sum_{j=k+1}^{m} (b_{j-1} - b_j) \right) \]

\[ \rho = a_0b_0, a_m = 0 \text{ and } b_m = 0 \]

The F0.5 score at cutoff point \( k \) is extended from F1 and is defined as follows:

\[ (1 + \beta^2) \frac{pr}{\beta^2p + r} \]

where \( p = \frac{a_k}{a_k + c_k}, r = \frac{a_k}{a_k + c_k}, \) and \( \beta = 0.5 \). For more information about F0.5, see Kaggle Inc. (2015).

The Kolmogorov-Smirnov chart and other metrics are available in Derby (2013).

**Fit Statistics**

The following notation is necessary for discussion of fit statistics:

- \( n \) is the number of observations
- \( r \) is the number of levels for a nominal target
- $N$ is the sum of observation frequencies in the data
- $w_i$ is the frequency of observation $i$, so
  \[ N = \sum_{i=1}^{n} w_i \]
- $y_i$ is the actual target value of observation $i$
- $\hat{y}_i$ is the predicted target value of observation $i$
- $t_i$ is the level from the target in observation $i$
- $\hat{t}_i$ is the predicted level from the target in observation $i$
- $y_{i,j}$ is 1 if observation $i$ is assigned to target level $j$, otherwise is 0
- $p_{i,j}$ is the predicted probability that observation $i$ is assigned to target level $j$

For interval targets, PROC ASSESS calculates the following metrics:

- average square error
  \[ ASE = \frac{1}{N} \sum_{i=1}^{n} (y_i - \hat{y}_i)^2 w_i \]
- root average square error
  \[ RASE = \sqrt{ASE} \]
- mean square logarithmic error
  \[ MSLE = \frac{1}{N} \sum_{i=1}^{n} \left( \log(\hat{y}_i + 1) - \log(y_i + 1) \right)^2 w_i \]
- mean absolute error
  \[ MAE = \frac{1}{N} \sum_{i=1}^{n} |y_i - \hat{y}_i| w_i \]

For nominal targets, PROC ASSESS calculates the following metrics:

- average square error
  \[ ASE = \frac{1}{rN} \sum_{i=1}^{n} \sum_{j=1}^{m} (y_{i,j} - p_{i,j})^2 w_i \]
- root average square error
  \[ RASE = \sqrt{ASE} \]
• mean consequential error (misclassification)

\[ MCE = \frac{1}{N} \sum_{t_i \neq \hat{t}_i} w_i \]

• multi-class log loss

\[ \text{logloss} = -\frac{1}{N} \sum_{i=1}^{n} \sum_{j=1}^{m} y_{i,j} \log(p_{i,j}) w_i \]

Displayed Output

The following sections describe the output that PROC ASSESS produces. The output is organized into various tables, which are discussed in the order of their appearance.

Fit Statistics

The “Fit Statistics” table contains the following error metrics for a nominal target if you specify the FITSTAT statement: average square error, divisor of average square error, root average square error, mean consequential error, and multiclass log loss.

For an interval target, the following metrics are created without specifying the FITSTAT statement: average square error, divisor of average square error, root average square error, mean absolute error, root mean absolute error, mean square logarithmic error, and root mean square logarithmic error.

Lift Information

The “Lift Information” table contains information about the lift and gain of each partition for a nominal target.

ROC Information

The “ROC Information” table contains information about the receiver operating characteristic (ROC) of each partition for a nominal target.

Lift Regression Information

The “Lift Regression Information” table contains information about lift regression for each partition for an interval target.

ODS Table Names

Each table created by the ASSESS procedure has a name associated with it, and you must use this name to refer to the table when you use ODS statements. The names of each table and a short description of the contents are listed in Table 17.1.
Table 17.1  ODS Tables Produced by PROC ASSESS

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>FitStat</td>
<td>Fit statistics</td>
<td>FITSTAT</td>
<td>PVAR= and PEVENT= for a nominal target; default for interval target</td>
</tr>
<tr>
<td>LIFTInfo</td>
<td>Lift information</td>
<td>PROC</td>
<td>Default for nominal target</td>
</tr>
<tr>
<td>LIFTRegInfo</td>
<td>Lift regression information</td>
<td>PROC</td>
<td>Default for interval target</td>
</tr>
<tr>
<td>ROCInfo</td>
<td>ROC information</td>
<td>PROC</td>
<td>Default for nominal target</td>
</tr>
</tbody>
</table>

Examples: ASSESS Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

Example 17.1: Assess a Model That Has a Binary Target

The following example demonstrates how to use the ASSESS procedure to compute ROC information, lift information, and fit statistics for a model that has a nominal target.

The following DATA step creates a score data table from a previously trained model. For example, the model could be a tree-based model, a neural network, or a support vector machine.

```sas
   data mycas.score2;
      length good_bad $4;
      input _PartInd_ good_bad p_good p_bad;
   datalines;
   0  good  0.6675  0.3325
   0  good  0.5189  0.4811
   0  good  0.6852  0.3148
   0  bad   0.0615  0.9385
   0  bad   0.3053  0.6947
   0  bad   0.6684  0.3316
   0  good  0.6422  0.3578
   0  good  0.6752  0.3248
   0  good  0.5396  0.4604
   0  good  0.4983  0.5017
```
The following PROC ASSESS call uses five bins to do lift analysis and uses 0.2 as the incremental step size for ROC analysis:

```latex
proc assess data=mycas.score2 ncuts=5 nbins=5;
  var p_good;
  target good_bad / event="good" level=nominal;
  fitstat pvar=p_bad / pevent="bad" ;
  by _PartInd_; 
run;
```

Output 17.1.1 shows the lift and gain for each bin in the first partition.

**Output 17.1.1** Lift Regression Information for the First Partition

**The ASSESS Procedure**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Event Depth</th>
<th>Observations</th>
<th>Number of Events</th>
<th>Captured Response Percent</th>
<th>Lift</th>
<th>Response Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>p_good</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
<td></td>
<td>0.00</td>
</tr>
<tr>
<td></td>
<td>20</td>
<td>3</td>
<td>3</td>
<td>27.27</td>
<td>1.363636</td>
<td>100.00</td>
</tr>
<tr>
<td></td>
<td>40</td>
<td>3</td>
<td>2</td>
<td>18.18</td>
<td>0.909091</td>
<td>66.67</td>
</tr>
<tr>
<td></td>
<td>60</td>
<td>3</td>
<td>3</td>
<td>27.27</td>
<td>1.363636</td>
<td>100.00</td>
</tr>
<tr>
<td></td>
<td>80</td>
<td>3</td>
<td>3</td>
<td>27.27</td>
<td>1.363636</td>
<td>125.00</td>
</tr>
<tr>
<td></td>
<td>100</td>
<td>3</td>
<td>0</td>
<td>0.00</td>
<td>1.250000</td>
<td>100.00</td>
</tr>
</tbody>
</table>

**Gain**

- 0.363636
- 0.136364
- 0.212121
- 0.250000

0
Output 17.1.2 shows the ROC information, including the confusion matrix and its derivations, for each bin in the first partition.

**Output 17.1.2  ROC Information for the First Partition**

| Variable | Event | Cutoff | TP  | FP  | FN  | TN  | FPR  | FDR  | TPR  | TNR  | ACC  | KS   | Youden Index | F1 Score | F0.5 Score |
|----------|-------|--------|-----|-----|-----|-----|------|------|------|------|------|-----|-----|-------------|---------|-----------|
| p_good   | good  | 0.2000 | 11  | 2   | 0   | 0   | 0.5000 | 0.5000 | 0.6667 | 0.6667 | 0.7333 | 0.8667 | 0.0.846154 | 0.774648 |
|          |       | 0.4000 | 11  | 1   | 0   | 3   | 0.5000 | 0.5000 | 0.6667 | 0.6667 | 0.7333 | 0.8667 | 0.916667 | 0.873016 |
|          |       | 0.6000 | 11  | 1   | 0   | 3   | 0.5000 | 0.5000 | 0.6667 | 0.6667 | 0.7333 | 0.8667 | 0.916667 | 0.873016 |
|          |       | 0.8000 | 11  | 1   | 0   | 3   | 0.5000 | 0.5000 | 0.6667 | 0.6667 | 0.7333 | 0.8667 | 0.916667 | 0.873016 |

Output 17.1.3 shows the error metrics of the nominal target in the first partition.

**Output 17.1.3  Fit Statistics for the First Partition**

<table>
<thead>
<tr>
<th>AUC</th>
<th>Gini</th>
<th>Gamma</th>
<th>Tau</th>
<th>Misclassification (Event)</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.266667</td>
</tr>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.133333</td>
</tr>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.066667</td>
</tr>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.466667</td>
</tr>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.733333</td>
</tr>
<tr>
<td>0.806818</td>
<td>0.613636</td>
<td>0.692308</td>
<td>0.257143</td>
<td>0.733333</td>
</tr>
</tbody>
</table>

**Fit Statistics**

<table>
<thead>
<tr>
<th>Squared Error</th>
<th>Number of Observations</th>
<th>Divisor of Average</th>
<th>Root Average</th>
<th>Mean Consequential Error</th>
<th>Mean Multiclass Log Loss</th>
</tr>
</thead>
<tbody>
<tr>
<td>15</td>
<td>15</td>
<td>0.169127</td>
<td>0.411250</td>
<td>0.266667</td>
<td>0.514728</td>
</tr>
</tbody>
</table>
Output 17.1.4 shows the lift and gain for each bin in the second partition.

**Output 17.1.4** Lift Regression Information for the Second Partition

---

**The ASSESS Procedure**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Event</th>
<th>Depth</th>
<th>Number of Observations</th>
<th>Number of Events</th>
<th>Lift Information</th>
<th>Response Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>p_good</td>
<td>good</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>20</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>3</td>
<td>27.27</td>
<td>27.27</td>
</tr>
<tr>
<td>40</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>3</td>
<td>27.27</td>
<td>54.55</td>
</tr>
<tr>
<td>60</td>
<td>3</td>
<td>3</td>
<td>0</td>
<td>3</td>
<td>27.27</td>
<td>81.82</td>
</tr>
<tr>
<td>80</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.00</td>
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<td>100.00</td>
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</tbody>
</table>

---

**Gain**

- 0.363636
- 0.363636
- 0.363636
- 0.022727
- 0

Output 17.1.5 shows the ROC information, including the confusion matrix and its derivations, for each bin in the second partition.
**Chapter 17: The ASSESS Procedure**

### Output 17.1.5 ROC Information for the Second Partition

<table>
<thead>
<tr>
<th>Variable</th>
<th>Event</th>
<th>Cutoff</th>
<th>TP</th>
<th>FP</th>
<th>FN</th>
<th>TN</th>
<th>FPR</th>
<th>FDR</th>
<th>TPR</th>
<th>TNR</th>
<th>ACC</th>
<th>KS</th>
<th>Youden Index</th>
<th>F1 Score</th>
<th>F0.5 Score</th>
</tr>
</thead>
<tbody>
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<td><code>p_good</code></td>
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<td>1</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0.214286</td>
<td>1</td>
<td>0</td>
<td>0.785714</td>
<td>0</td>
<td>0</td>
<td>0.880000</td>
<td>0.820896</td>
</tr>
<tr>
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<td>1</td>
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<td>0.909091</td>
<td>0</td>
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<td>0</td>
<td>-0.09091</td>
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<td>0.793651</td>
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<td>2</td>
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<td>1</td>
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<td>0.818182</td>
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<td>0</td>
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<td>0.454545</td>
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<td>0.806452</td>
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<td>0.272727</td>
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<td>0.652174</td>
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</tr>
<tr>
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<td></td>
<td>1</td>
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<td>.</td>
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<td>0</td>
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<td>0</td>
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<td></td>
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</table>

<table>
<thead>
<tr>
<th>Variable</th>
<th>Event</th>
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<th>Gini</th>
<th>Gamma</th>
<th>Tau</th>
<th>Misclassification (Event)</th>
</tr>
</thead>
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<tr>
<td></td>
<td></td>
<td>0.636364</td>
<td>0.272727</td>
<td>0.428571</td>
<td>0.098901</td>
<td>0.214286</td>
</tr>
<tr>
<td></td>
<td></td>
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<td>0.272727</td>
<td>0.428571</td>
<td>0.098901</td>
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<td>0.098901</td>
<td>0.428571</td>
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<td>0.272727</td>
<td>0.428571</td>
<td>0.098901</td>
<td>0.571429</td>
</tr>
<tr>
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<td></td>
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<td>0.272727</td>
<td>0.428571</td>
<td>0.098901</td>
<td>0.785714</td>
</tr>
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</table>
Output 17.1.6 shows the error metrics of the nominal target in the second partition.

### Output 17.1.6

**Fit Statistics for the Second Partition**

<table>
<thead>
<tr>
<th>PartInd_=1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Squared Error</td>
</tr>
<tr>
<td>Number of Observations</td>
</tr>
<tr>
<td>Divisor Average</td>
</tr>
<tr>
<td>Root Average Consequential Error</td>
</tr>
<tr>
<td>Mean Log Loss</td>
</tr>
<tr>
<td>Multiclass Log Loss</td>
</tr>
<tr>
<td>Log Loss</td>
</tr>
</tbody>
</table>

---

**References**


Chapter 18
The BINNING Procedure

Contents

Overview: BINNING Procedure .................................................. 928
   Bucket Binning ................................................................. 928
   Winsorized Binning .......................................................... 928
   Quantile Binning ............................................................... 928
   Cutpoint Binning ............................................................. 928
   Tree-Based Binning ........................................................... 928
   PROC BINNING Features .................................................... 929
   Using CAS Sessions and CAS Engine Librefs .......................... 929
Getting Started: BINNING Procedure ....................................... 930
   Bucket Binning ................................................................. 930
Syntax: BINNING Procedure .................................................... 932
   PROC BINNING Statement ............................................... 932
   CODE Statement ............................................................. 935
   FREQ Statement ............................................................. 935
   INPUT Statement ............................................................ 935
   OUTPUT Statement .......................................................... 936
   TARGET Statement .......................................................... 937
Details: BINNING Procedure ................................................... 937
   Binning Computation and Formulas .................................... 937
   Tree-Based Binning .......................................................... 939
   Computing the Weight of Evidence and Information Value ....... 939
   Displayed Output ............................................................. 940
   ODS Table Names ........................................................... 941
Examples: BINNING Procedure ............................................... 942
   Example 18.1: Quantile Binning ......................................... 942
   Example 18.2: Winsorized Binning ....................................... 944
   Example 18.3: Bucket Binning and Weight-of-Evidence Computation .......... 946
   Example 18.4: Cutpoint Binning ......................................... 948
   Example 18.5: Tree-Based Binning ....................................... 949
Overview: BINNING Procedure

The BINNING procedure performs binning in SAS Viya. Binning is a common step in the data preparation stage of the model-building process. You can use binning to classify missing variables, reduce the impact of outliers, and generate multiple effects. The generated effects are useful and contain certain nonlinear information about the original interval variables.

The BINNING procedure supports several binning methods, which are described in the following subsections. The BINNING procedure can also calculate the weight of evidence (WOE) and information value (IV) based on binning results.

Bucket Binning

Bucket binning creates equal-length bins and assigns the data to one of these bins. You can choose the number of bins during the binning; the default number of bins (the binning level) is 16.

Winsorized Binning

Winsorized binning is similar to bucket binning except that both tails are cut off to obtain a smooth binning result. This technique is often used to remove outliers during the data preparation stage.

Quantile Binning

PROC BINNING calculates the quantile (or percentile) cutpoints and uses them as the lower bound and upper bound in creating bins. As a result, each bin should have a similar number of observations. Because PROC BINNING always assigns observations that have the same value to the same bin, quantile binning might create unbalanced bins if any variable has tied values. For more information, see the section “Binning Computation and Formulas” on page 937.

Cutpoint Binning

The cutpoint binning method enables you to create bins by specifying the bin upper bound.

Tree-Based Binning

The tree-based binning method enables you to create bins by creating decision trees or regression trees. This technique requires you to specify a target variable. If the target variable is nominal, PROC BINNING creates decision trees; if the target variable is interval, PROC BINNING creates regression trees.
PROC BINNING Features

The BINNING procedure has the following features:

- provides a bucket (equal-length) binning method
- provides a Winsorized binning method and Winsorized statistics
- provides a quantile binning method
- provides a cutpoints binning method
- provides a tree-based binning method
- calculates the weight of evidence (WOE) and information value (IV) based on binning results

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”
Getting Started: BINNING Procedure

Bucket Binning

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The following DATA step creates the data table mycas.bucket, which consists of 1,000 observations of an ID variable (id) and three continuous variables (x1–x3), in your CAS session:

```sas
data mycas.bucket;
    length id 8;
    do id=1 to 1000;
        x1 = ranuni(101);
        x2 = 10*ranuni(201);
        x3 = 100*ranuni(301);
        output;
    end;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements show how you can use the BINNING procedure to perform bucket binning:

```sas
proc binning data=mycas.bucket numbin=10 method=bucket;
    input x1-x3;
    output out=mycas.out;
run;
```

The DATA= option specifies the input data table. The NUMBIN= option requests that 10 bins be created for all binning variables. The METHOD= option requests that the bucket binning method be used. The INPUT statement names three continuous variables (x1–x3) as input variables for binning. The OUTPUT statement creates an OUTPUT data table to contain the results of PROC BINNING.

Figure 18.1 displays the “Binning Details” table. This table shows the binning variable, bin ID, bin lower bound, bin upper bound, bin width, number of observations in that bin, and some statistics of that bin (such as mean, standard deviation, minimum, and maximum).
### Figure 18.1 Binning Details

#### The BINNING Procedure

<table>
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<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
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<td>x1</td>
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<td>0.1002</td>
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<td>90.078</td>
<td>99.898</td>
</tr>
</tbody>
</table>
Syntax: BINNING Procedure

The following statements are available in the BINNING procedure:

```plaintext
PROC BINNING <options>;
    CODE FILE=filename;
    FREQ variable;
    INPUT variables </option>;
    OUTPUT OUT=CAS-libref.data-table </option>;
    TARGET variable / EVENT="category";
```

The PROC BINNING statement and at least one INPUT statement are required. You can specify multiple INPUT statements. The TARGET statement is required to calculate the weight of evidence (WOE) and information value (IV).

The following sections describe the PROC BINNING statement and then describe the other statements in alphabetical order.

PROC BINNING Statement

```plaintext
PROC BINNING <options>;
```

The PROC BINNING statement invokes the procedure. Table 18.1 summarizes important options in the PROC BINNING statement by function.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
<tr>
<td><strong>Binning Level Options</strong></td>
<td></td>
</tr>
<tr>
<td>NUMBIN=</td>
<td>Specifies the global number of bins for all binning variables</td>
</tr>
<tr>
<td><strong>Binning Method Options</strong></td>
<td></td>
</tr>
<tr>
<td>METHOD=</td>
<td>Specifies which binning method to use</td>
</tr>
<tr>
<td><strong>Weight-of-Evidence Options</strong></td>
<td></td>
</tr>
<tr>
<td>WOE(WOEADJUST=)</td>
<td>Computes the weight of evidence and information values</td>
</tr>
</tbody>
</table>
You can specify the following **options**: 

**DATA=** `CAS-libref.data-table`

names the input data table for PROC BINNING to use. The default is the most recently created data table. `CAS-libref.data-table` is a two-level name, where

- `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 929.

- `data-table` specifies the name of the input data table.

**METHOD=** `BUCKET | QUANTILE | WINSOR(RATE=) | CUTPTS(numlist) | TREE <options>`

specifies which binning method to use.

You can specify one of the following methods:

**BUCKET**

specifies the bucket binning method.

**QUANTILE**

specifies the quantile binning method.

**WINSOR(RATE=** `rate`)**

specifies the Winsorized binning method and the `rate` that it uses. You must specify a `rate` between 0 and 0.5, exclusive.

**CUTPTS(numlist)**

specifies the cutpoints binning method and the lower and upper bounds of the bin.

**TREE <options>**

specifies the tree-based binning method. You can specify the following **options**:

**INITBIN=** `integer`

specifies the initial number of bins for interval input variables to start the tree-based binning process. The final number of bins created by PROC BINNING might be different than the number you specify. The value of `integer` can be any integer between 1 and 10,000, inclusive. By default, INITBIN=100.

**INITMETHOD=** `BUCKET | QUANTILE`

specifies the method to initialize the tree-based binning for interval input variables. You can specify either of the following values:

**BUCKET** uses the bucket binning method.

**QUANTILE** uses the quantile binning method.

By default, the bucket binning method is used.
LEAFSIZE=integer

MINNOBSINBIN=integer
specifies the allowed minimum number of observations per leaf for tree-based binning. The value of integer can be any integer between 1 and 30,000, inclusive. There is no default.

MAXNBINS=integer
specifies the desired maximum number of bins for all variables. The value of integer can be any integer between 2 and 10,000, inclusive. If this option is specified, PROC BINNING tries to make sure that the final number of bins for all variables is no more than the specified integer. By default, MAXNBINS=5.

MINNBINS=integer
specifies the desired minimum number of bins for all variables. The value of integer can be any integer between 1 and 10,000, inclusive. If this option is specified, PROC BINNING tries to make sure that the final number of bins for all variables is no less than the specified integer. By default, MINNBINS=1.

CRITERIA <options>
specifies the criteria for growing the tree for the tree-based binning method. You can specify the following options:

GAIN

ENTROPY
uses the gain in information (decrease in entropy) as the tree-growing criterion. This criterion is available only for a nominal target.

GAINRATIO

ENTROPYRATIO
uses the gain ratio in information (decrease in entropy ratio) as the tree-growing criterion. This criterion is available only for a nominal target. This is the default criterion for a nominal target.

GINI
uses the Gini statistic as the tree-growing criterion. This criterion is available only for a nominal target.

SSE
uses the sum of squared error as the tree-growing criterion. This criterion is available only for an interval target. This is the default criterion for an interval target.

NUMBIN=integer
specifies the global number of binning levels for all binning variables. The value of integer can be any integer between 2 and 1,000, inclusive.

By default, NUMBIN=16.

In tree-based binning, this option is ignored.
WOE(WOEADJUST=number) enables computation of the weight of evidence and information values. You can specify the following suboption:

WOEADJUST=number
 specifies the adjustment factor for the weight-of-evidence calculation, where number is between 0 and 1, inclusive.

By default, WOEADJUST=0.5.

CODE Statement

CODE FILE=filename ;

The CODE statement generates score code and stores it in a file that can be used for scoring purposes. Only one CODE statement is processed. If you specify multiple CODE statements, only the first one is used.

You must specify the following option:

FILE=filename
 specifies the filename of the file to write the SAS score code to.

FREQ Statement

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC BINNING treats each observation as if it appears f times, where f is the value of the FREQ variable for the observation. If f is not an integer, it is truncated to an integer. If f is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

INPUT Statement

INPUT variables < / options > ;

The INPUT statement names one or more variables as input variables for binning. The specified variables must be interval variables. If classification variables are provided, PROC BINNING stops and returns an error message. PROC BINNING does not support duplicate variables. If the INPUT statement contains a duplicate variable, PROC BINNING takes only the first variable and provides a warning message.

You must specify the following options after a slash (/):

NUMBIN=int
 specifies the number of binning levels for all binning variables in the current INPUT statement. The value of int can be any integer between 2 and 1,000, inclusive.
The number of binning levels that you specify in an INPUT statement overwrites the global number of binning levels, which is specified in the NUMBIN= option in the PROC BINNING statement (or is 16 by default).

In tree-based binning, this option is ignored.

**LEVEL=**<options>

specifies whether to treat the specified variables as interval or nominal. You can specify the following options:

- **INTERVAL**
- **INT**
  - treats all numeric variables that are specified in this INPUT statement as interval.

- **NOMINAL**
- **NOM**
  - treats all variables are specified in this INPUT statement as nominal.

---

**OUTPUT Statement**

```plaintext
OUTPUT OUT=CAS-libref.data-table < option > ;
```

The OUTPUT statement enables you to write an output table back to the CAS server by creating an output data table that contains the results of PROC BINNING. If you do not specify the OUTPUT statement, the write-back process is skipped. This is useful when you want only the ODS output. By default, the output table contains the new binned variables. If you specify the COPYVARS= option, the output table contains the “copied variables” and the “binned variables.”

**NOTE:** If an input variable value is missing, then the binning output level value is 0.

You must specify the following option:

- **OUT=**<CAS-libref.data-table>
  - names the output data table for PROC BINNING to use. You must specify this option before any other options. `<CAS-libref.data-table>` is a two-level name, where

  - **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `<CAS-libref>`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 929.

  - **data-table** specifies the name of the output data table.

The output data table contains the scored data.

You can also specify the following option:
COPYVAR=variable
COPYVARS=(variables)
lists one or more variables from the input data table to be transferred to the output data table.

**TARGET Statement**

TARGET variable / EVENT="category";

The TARGET statement names the variable that PROC BINNING uses to calculate the weight of evidence and information value.

You must specify the following options after a slash (/):

**EVENT=** "category"

specifies the target event category that PROC BINNING uses to calculate the weight of evidence and information value in a quoted string of characters.

**LEVEL=** <options>

specifies whether to treat the target variable as interval or nominal. You can specify the following options:

**INTERVAL**

INT

treats the target variable as interval.

**NOMINAL**

NOM

treats the target variable as nominal.

**Details: BINNING Procedure**

**Binning Computation and Formulas**

For variable x, assume that the data are represented by \( \{x_i\} \), where \( i = 1, 2, \ldots, n \). Let \( \min(x) = \min_{i \in \{1, \ldots, n\}} \{x_i\} \), and let \( \max(x) = \max_{i \in \{1, \ldots, n\}} \{x_i\} \). The range of the variable is \( \text{range}(x) = \max(x) - \min(x) \).

The computations for the various binning methods are as follows, where numbin is the value of the NUMBIN= option in the PROC BINNING statement:

- For bucket binning, the length of the bucket is

\[
L = \frac{\max(x) - \min(x)}{n}
\]
The split points are

\[ s_k = \min(x) + L \times k \]

where \( k = 1, 2, \ldots, \text{numbin} - 1 \).

When the data are evenly distributed on the cloud, the time complexity for bucket binning is \( O(n)/(\text{nodes} \times \text{nThreads}) \), where \( n \) is the number of observations, \( \text{nodes} \) is the number of computer nodes in the cloud, and \( \text{nThreads} \) is the number of CPUs on each node.

- For quantile binning, PROC BINNING calculates a quantile table \( P \). Let \( P = \{p_k\} \), where \( k = 1, 2, \ldots, \text{numbin} \). Then \( p_k \) is described as

\[
p_k = \begin{cases} 
1.0/\text{numbin} + p_{k-1} & \text{if } 0 < k < \text{numbin} \\
1.0 & \text{if } k = \text{numbin}
\end{cases}
\]

Quantile binning often requires data to be sorted in a particular way, and the sorting process usually consumes a significant amount of CPU time and memory. When the input data table is larger than the available memory, the sorting algorithm becomes more complicated. In distributed computing, data communications overhead also increases the sorting challenge. To avoid the time-consuming sorting process, the BINNING procedure uses an iterative projection method for quantile binning, which runs much faster than the sorting-based quantile binning method in most cases.

After calculating the quantile table, PROC BINNING uses an iterative projection method to compute quantiles (percentiles) and uses these quantiles to create bins.

Quantile binning aims to assign the same number of observations to each bin. As a result, each bin should have a similar number of observations. Because PROC BINNING always assigns observations that have the same value to the same bin, quantile binning might create unbalanced bins if any variable has tied values. For example, if an observation whose value is \( x \) is assigned to bin \( k \), then every observation whose value is \( x \) is assigned to bin \( k \) for this variable, and no observation whose value is \( x \) is assigned to the next bin, bin \( k + 1 \). Therefore, bin \( k \) might have more observations than bin \( k + 1 \), because the tied values at the boundaries between bin \( k \) and bin \( k + 1 \) are all assigned to bin \( k \). That is, tied values at the boundaries between two bins are always assigned to the lower-numbered bin.

- Winsorized binning applies bucket binning to the Winsorized data table. Winsorization involves replacing lower and upper outliers (which are defined according to the RATE= suboption in the METHOD=WINSOR option in the PROC BINNING statement) by the lower and upper thresholds. For variable \( x \), PROC BINNING uses a simple bucket sorting method to obtain the basic information. Let \( N \) be the number of buckets. For each bucket \( B_i, i = 1, 2, \ldots, N \), PROC BINNING keeps following information:

  - \( c_i \): count of \( x \) in \( B_i \)
  - \( \text{min}_i \): minimum value of \( x \) in \( B_i \)
  - \( \text{max}_i \): maximum value of \( x \) in \( B_i \)
  - \( \sum x_i \): sum of \( x \) in \( B_i \)
  - \( \sum x_i^2 \): sum of \( x^2 \) in \( B_i \)

The Winsorized statistics are computed first. After the minimum and maximum have been found, the bin lower and upper bounds are calculated the same way as in bucket binning.

Let the tail count, \( wc \), be \( \text{ceil}(\text{Rate} \times n) \), and find the smallest \( I \) such that \( \sum_{i=1}^{I} c_i \geq wc \). Then the left tail count is \( \text{lwc} = \sum_{i=1}^{I} c_i \). Find the next \( I \) such that \( \sum_{i=1}^{I} c_i > \text{lwc} \). Therefore, the minimum
value is $\text{WinsorMin} = \min_{I_r}$. Similarly, find the largest $I$ such that $\sum_{i=1}^{N} c_i \geq wc$. The right tail count is $rwc = \sum_{i=1}^{N} c_i$. Find the next $I_r$ such that $\sum_{i=I_r}^{N} c_i > rwc$. Then the maximum value is $\text{WinsorMax} = \max_{I_r}$. The mean is calculated by the formula

$$\text{WinsorMean} = \frac{lwc \times \text{WinsorMin} + \sum_{i=I_l}^{I_r} x_i + rwc \times \text{WinsorMax}}{n}$$

The trimmed mean is calculated by the formula

$$\text{TrimmedMean} = \frac{\sum_{i=I_l}^{I_r} x_i}{n - lwc - rwc}$$

**NOTE:** PROC BINNING reserves bin 0 for missing values.

**NOTE:** Whenever possible, PROC BINNING always tries to generate the specified number of bins. In some cases, some bins might have no observations in them.

---

**Tree-Based Binning**

Tree-based binning is different from other binning methods. The basic idea of tree-based binning is to bin (group) input variables by growing a one-level decision tree (or regression tree, when the target variable is not nominal) for each input variable. In the literature, the difference between a decision tree and a regression tree is often ignored (with some exceptions). This chapter uses the term decision tree in the following way. To grow a decision tree, PROC BINNING uses a training data set to split the target variable space into nonoverlapping regions. These regions correspond to the terminal nodes of the tree, which are also known as leaves.

The tree growing is done by splitting; the splitting starts with all the observations, which are represented by the node at the top of the tree. The algorithm splits this parent node into child nodes in such a way that the values (levels) of the target variable within each child region are as similar as possible. The split is determined by finding the best split value that optimizes a specified criterion across the child nodes for each input variable. The goal of maximizing similarity is achieved by minimizing node impurity. For an interval target, the default and only available growing criterion is SSE (sum of squared error), which aims to minimize node impurity. For a nominal target, the default growing criterion is GAINRATIO (or ENTROPYRATIO as the alias), which measures the gain ratio in information (decrease in entropy ratio) with the goal of minimizing node impurity. For a nominal target, the other supported growing criteria are GAIN (or ENTROPY as the alias) and GINI, which measure the gain in information (decrease in entropy) and the Gini statistic with the goal to minimize node impurity.

---

**Computing the Weight of Evidence and Information Value**

PROC BINNING can compute the weight of evidence and the information value.

Weight of evidence (WOE) is a measure of how much the evidence supports or undermines a hypothesis. WOE measures the relative risk of an attribute of binning level. The value depends on whether the value of the target variable is a nonevent or an event. An attribute’s WOE is defined as follows:
\[
\text{WOE}_{\text{attribute}} = \ln \frac{p_{\text{attr} \text{(nonevent)}}}{p_{\text{attr} \text{(event)}}} = \ln \frac{N_{\text{attr} \text{(nonevent)}}/N_{\text{tot} \text{(nonevent)}}}{N_{\text{attr} \text{(event)}}/N_{\text{tot} \text{(event)}}}
\]

The definitions of the quantities in the preceding formula are as follows:

- \(N_{\text{attr} \text{(nonevent)}}\): the number of nonevent records that exhibit the attribute
- \(N_{\text{tot} \text{(nonevent)}}\): the total number of nonevent records
- \(N_{\text{attr} \text{(event)}}\): the number of event records that exhibit the attribute
- \(N_{\text{tot} \text{(event)}}\): the total number of event records

To avoid an undefined WOE, an adjustment factor, \(x\), is used:

\[
\text{WOE}_{\text{attribute}} = \ln \frac{(N_{\text{attr} \text{(nonevent)}} + x)/N_{\text{tot} \text{(nonevent)}}}{(N_{\text{attr} \text{(event)}} + x)/N_{\text{tot} \text{(event)}}}
\]

You can use the WOEADJUST= option to specify a value between [0, 1] for \(x\). By default, \(x\) is 0.5.

The information value (IV) is a weighted sum of the WOE of the characteristic’s attributes. The weight is the difference between the conditional probability of an attribute for an event and the conditional probability of that attribute for a nonevent. In the following formula of IV, \(m\) is the number of bins of a variable:

\[
\text{IV} = \sum_{i=1}^{m} \left( \frac{N_{\text{attr} \text{(nonevent)}}}{N_{\text{tot} \text{(nonevent)}}} - \frac{N_{\text{attr} \text{(event)}}}{N_{\text{tot} \text{(event)}}} \right) \times \text{WOE}_i
\]

An information value can be any real number. Generally speaking, the higher the information value, the more predictive an attribute is likely to be.

### Displayed Output

The following sections describe the output that PROC BINNING produces. The output is organized into various tables.

### Bin Details

The “Bin Details” table displays some parameters and data information, which includes the binning variable, bin ID, bin lower bound, bin upper bound, bin width, number of observations in that bin, and some statistics of that bin (such as mean, standard deviation, minimum, and maximum). If you specify the WOE= option, this table also includes the target event count, weight of evidence, and information value of that bin.
Trimmed Statistics

The “Trimmed Statistics” table displays the binning variable, trimmed minimum, maximum, mean, standard error mean, left tail, left tail percentage, right tail, and right tail percentage. PROC BINNING generates this table if you specify the METHOD=WINSOR option in the PROC BINNING statement.

Winsorized Statistics

The “Winsorized Statistics” table displays the binning variable, Winsorized minimum, maximum, mean, standard error mean, left tail, left tail percentage, right tail, and right tail percentage. PROC BINNING generates this table if you specify the METHOD=WINSOR option in the PROC BINNING statement.

Variable Information Value

The “Variable Information Value (IV)” table displays the information value for each variable. PROC BINNING generates this table if you specify the WOE option in the PROC BINNING statement.

Variable Transformation Information

The “Variable Transformation Information” table displays the transformation information for each variable, in tree-based binning. PROC BINNING generates this table if you specify the METHOD=TREE option in the PROC BINNING statement.

ODS Table Names

Each table created by the BINNING procedure has a name associated with it, and you must use this name to refer to the table when you use ODS statements. The names of each table and a short description of the contents are listed in Table 18.2.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>BinDetails</td>
<td>Basic binning information and parameters</td>
<td>PROC BINNING</td>
<td>Default</td>
</tr>
<tr>
<td>InfoValue</td>
<td>Information value for each variable</td>
<td>PROC BINNING</td>
<td>WOE</td>
</tr>
<tr>
<td>Trim</td>
<td>Trimmed statistics for the given variables</td>
<td>PROC BINNING</td>
<td>METHOD=WINSOR</td>
</tr>
<tr>
<td>Winsor</td>
<td>Winsor statistics for the given variables</td>
<td>PROC BINNING</td>
<td>METHOD=WINSOR</td>
</tr>
<tr>
<td>VarTransInfo</td>
<td>Transformation information for the specified variables</td>
<td>PROC BINNING</td>
<td>METHOD=TREE</td>
</tr>
</tbody>
</table>
Examples: BINNING Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

---

**Example 18.1: Quantile Binning**

The following DATA step generates 1,000,000 observations of an ID variable (id) and two continuous variables (x1–x2). The mycas CAS library reference enables your client machine to communicate with the CAS session. These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

```sas
data mycas.ex1;
  length id 8;
  do id=1 to 1000000;
    x1 = ranuni(101);
    x2 = 10*ranuni(201);
    output;
  end;
run;
```

The following statements demonstrate how to use PROC BINNING to perform the quantile binning:

```sas
proc binning data=mycas.ex1 numbin=10 method=quantile;
  input x1-x2;
  output out=mycas.out1;
run;
```

The DATA= option specifies the input data table. The NUMBIN= option requests that 10 bins be created for all binning variables. The METHOD= option requests that the quantile binning method be used. The INPUT statement names two continuous variables (x1–x2) as input variables for binning. The OUTPUT statement creates an OUTPUT data table to contain the results of PROC BINNING.

The “Binning Details” table in Output 18.1 shows the binning variable, bin ID, bin lower bound, bin upper bound, bin width, number of observations in that bin, and some statistics of that bin (such as mean, standard deviation, minimum, and maximum). When the binning method is quantile, PROC BINNING assigns the same number of observations to each bin for the input variables if possible.
### Output 18.1.1  Binning Details

#### The BINNING Procedure

<table>
<thead>
<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>Missing</td>
<td>0</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>-Infy</td>
<td>0.0999</td>
<td></td>
<td>99999</td>
<td>0.0288</td>
<td>224E-9</td>
<td>0.0999</td>
<td></td>
</tr>
<tr>
<td></td>
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<td>0.0999</td>
<td>0.1994</td>
<td>0.0996</td>
<td>100000</td>
<td>0.0287</td>
<td>0.0999</td>
<td>0.1994</td>
<td></td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>0.1994</td>
<td>0.2992</td>
<td>0.0998</td>
<td>100000</td>
<td>0.0288</td>
<td>0.1994</td>
<td>0.2992</td>
<td>0.3995</td>
</tr>
<tr>
<td></td>
<td>4</td>
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<td>99999</td>
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<td></td>
</tr>
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<td></td>
<td>5</td>
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<td>100001</td>
<td>0.0291</td>
<td>0.3995</td>
<td>0.4999</td>
<td></td>
</tr>
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<td></td>
<td>6</td>
<td>0.4999</td>
<td>0.5997</td>
<td>0.0998</td>
<td>100000</td>
<td>0.0288</td>
<td>0.4999</td>
<td>0.5997</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>0.5997</td>
<td>0.7004</td>
<td>0.1006</td>
<td>100000</td>
<td>0.0291</td>
<td>0.5997</td>
<td>0.7004</td>
<td></td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>0.7004</td>
<td>0.8002</td>
<td>0.0999</td>
<td>100000</td>
<td>0.0288</td>
<td>0.7004</td>
<td>0.8002</td>
<td></td>
</tr>
<tr>
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<td></td>
<td>10</td>
<td>0.9002</td>
<td>Infy</td>
<td></td>
<td>100001</td>
<td>0.0288</td>
<td>0.9002</td>
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<tr>
<td>x2</td>
<td>Missing</td>
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<td></td>
<td></td>
<td></td>
<td></td>
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</tr>
<tr>
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<td>-Infy</td>
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<td></td>
<td>99999</td>
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<td>0.9969</td>
<td>1.9947</td>
<td></td>
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<td>0.9990</td>
<td>100000</td>
<td>0.2887</td>
<td>1.9947</td>
<td>2.9937</td>
<td></td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>2.9937</td>
<td>3.9946</td>
<td>1.0009</td>
<td>100000</td>
<td>0.2889</td>
<td>2.9937</td>
<td>3.9946</td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>3.9946</td>
<td>4.9985</td>
<td>1.0039</td>
<td>100000</td>
<td>0.2901</td>
<td>3.9946</td>
<td>4.9985</td>
<td></td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>4.9985</td>
<td>5.9970</td>
<td>0.9985</td>
<td>100000</td>
<td>0.2881</td>
<td>4.9985</td>
<td>5.9970</td>
<td></td>
</tr>
<tr>
<td></td>
<td>7</td>
<td>5.9970</td>
<td>6.9927</td>
<td>0.9956</td>
<td>100000</td>
<td>0.2876</td>
<td>5.9970</td>
<td>6.9927</td>
<td></td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>6.9927</td>
<td>7.9985</td>
<td>1.0059</td>
<td>99999</td>
<td>0.2895</td>
<td>6.9927</td>
<td>7.9985</td>
<td></td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>7.9985</td>
<td>8.9994</td>
<td>1.0008</td>
<td>100000</td>
<td>0.2890</td>
<td>7.9985</td>
<td>8.9994</td>
<td></td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>8.9994</td>
<td>Infy</td>
<td></td>
<td>100002</td>
<td>0.2895</td>
<td>8.9994</td>
<td>10.000</td>
<td></td>
</tr>
</tbody>
</table>
Example 18.2: Winsorized Binning

The following DATA step generates 10,000 observations of an ID variable (id) and three continuous variables (x1–x3). The mycas CAS library reference enables your client machine to communicate with the CAS session.

```sas
data mycas.ex2;
  length id 8;
  do id=1 to 10000;
    x1 = ranuni(101);
    x2 = 10*ranuni(201);
    x3 = 100*ranuni(301);
    output;
  end;
run;
```

For Winsorized binning, PROC BINNING provides bucket binning and basic Winsorized statistical information for the input data.

The following statements include the WINSOR(RATE=0.05) option and generate tables for Winsorized and trimmed statistics:

```sas
proc binning data=mycas.ex2 numbin=10 method=winsor(rate=0.05);
  input x1-x3;
  output out=mycas.out2;
run;
```

The preceding statements generate Output 18.2.1 through Output 18.2.3.
### Example 18.2: Winsorized Binning

#### The BINNING Procedure

#### Output 18.2.1 Binning Details

<table>
<thead>
<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>Missing</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>-Infy</td>
<td>0.1377</td>
<td></td>
<td></td>
<td>1405</td>
<td>0.0767</td>
<td>0.0304</td>
<td>0.0475</td>
<td>0.1376</td>
</tr>
<tr>
<td>2</td>
<td>0.1377</td>
<td>0.2278</td>
<td>0.0902</td>
<td></td>
<td>849</td>
<td>0.1832</td>
<td>0.0259</td>
<td>0.1380</td>
<td>0.2276</td>
</tr>
<tr>
<td>3</td>
<td>0.2278</td>
<td>0.3180</td>
<td>0.0902</td>
<td></td>
<td>897</td>
<td>0.2726</td>
<td>0.0263</td>
<td>0.2279</td>
<td>0.3180</td>
</tr>
<tr>
<td>4</td>
<td>0.3180</td>
<td>0.4082</td>
<td>0.0902</td>
<td></td>
<td>864</td>
<td>0.3625</td>
<td>0.0258</td>
<td>0.3181</td>
<td>0.4081</td>
</tr>
<tr>
<td>5</td>
<td>0.4082</td>
<td>0.4983</td>
<td>0.0902</td>
<td></td>
<td>906</td>
<td>0.4519</td>
<td>0.0258</td>
<td>0.4082</td>
<td>0.4982</td>
</tr>
<tr>
<td>6</td>
<td>0.4983</td>
<td>0.5885</td>
<td>0.0902</td>
<td></td>
<td>899</td>
<td>0.5430</td>
<td>0.0269</td>
<td>0.4984</td>
<td>0.5884</td>
</tr>
<tr>
<td>7</td>
<td>0.5885</td>
<td>0.6786</td>
<td>0.0902</td>
<td></td>
<td>936</td>
<td>0.6341</td>
<td>0.0268</td>
<td>0.5886</td>
<td>0.6786</td>
</tr>
<tr>
<td>8</td>
<td>0.6786</td>
<td>0.7688</td>
<td>0.0902</td>
<td></td>
<td>900</td>
<td>0.7248</td>
<td>0.0258</td>
<td>0.6786</td>
<td>0.7686</td>
</tr>
<tr>
<td>9</td>
<td>0.7688</td>
<td>0.8589</td>
<td>0.0902</td>
<td></td>
<td>950</td>
<td>0.8124</td>
<td>0.0263</td>
<td>0.7690</td>
<td>0.8589</td>
</tr>
<tr>
<td>10</td>
<td>0.8589</td>
<td>Infy</td>
<td></td>
<td></td>
<td>1394</td>
<td>0.9192</td>
<td>0.0307</td>
<td>0.8589</td>
<td>0.9491</td>
</tr>
</tbody>
</table>

| x2       | Missing |              |             |           |                        | 0    |                   |         |         |
| 1        | -Infy  | 1.3978       |             |           | 1385                   | 0.7827 | 0.2989            | 0.4948  | 1.3958  |
| 2        | 1.3978 | 2.3008       | 0.9030      |           | 941                    | 1.8522 | 0.2597            | 1.3997  | 2.2997  |
| 3        | 2.3008 | 3.2038       | 0.9030      |           | 888                    | 2.7546 | 0.2623            | 2.3027  | 3.2037  |
| 4        | 3.2038 | 4.1069       | 0.9030      |           | 855                    | 3.6590 | 0.2597            | 3.2060  | 4.1065  |
| 5        | 4.1069 | 5.0099       | 0.9030      |           | 905                    | 4.5591 | 0.2567            | 4.1072  | 5.0091  |
| 6        | 5.0099 | 5.9129       | 0.9030      |           | 864                    | 5.4573 | 0.2571            | 5.0105  | 5.9106  |
| 7        | 5.9129 | 6.8159       | 0.9030      |           | 908                    | 6.3697 | 0.2596            | 5.9137  | 6.8156  |
| 8        | 6.8159 | 7.7189       | 0.9030      |           | 909                    | 7.2777 | 0.2550            | 6.8161  | 7.7163  |
| 9        | 7.7189 | 8.6220       | 0.9030      |           | 935                    | 8.1767 | 0.2593            | 7.7201  | 8.6218  |
| 10       | 8.6220 | Infy         |             |           | 1410                   | 9.2308 | 0.3049            | 8.6222  | 9.5250  |

| x3       | Missing |              |             |           |                        | 0    |                   |         |         |
| 1        | -Infy  | 14.323       |             |           | 1443                   | 8.2442 | 2.9877            | 5.3640  | 14.310  |
| 3        | 23.282 | 32.241       | 8.9589      |           | 902                    | 27.757 | 2.6725            | 23.305  | 32.227  |
| 4        | 32.241 | 41.200       | 8.9589      |           | 898                    | 36.908 | 2.5926            | 32.242  | 41.184  |
| 5        | 41.200 | 50.158       | 8.9589      |           | 906                    | 45.582 | 2.5960            | 41.246  | 50.135  |
| 6        | 50.158 | 59.117       | 8.9589      |           | 901                    | 54.656 | 2.5158            | 50.165  | 59.108  |
| 7        | 59.117 | 68.076       | 8.9589      |           | 898                    | 63.534 | 2.5844            | 59.121  | 68.065  |
| 8        | 68.076 | 77.035       | 8.9589      |           | 877                    | 72.557 | 2.5229            | 68.090  | 77.026  |
| 9        | 77.035 | 85.994       | 8.9589      |           | 870                    | 81.437 | 2.5739            | 77.039  | 85.980  |
| 10       | 85.994 | Infy         |             |           | 1398                   | 92.050 | 3.0000            | 86.001  | 94.953  |
Chapter 18: The BINNING Procedure

Output 18.2.2 \ Winsorized Statistics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>N Left Tail</th>
<th>Percent</th>
<th>N Right Tail</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>0.0475</td>
<td>0.9491</td>
<td>0.5018</td>
<td>0.2848</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
<tr>
<td>x2</td>
<td>0.4948</td>
<td>9.5250</td>
<td>5.0302</td>
<td>2.8663</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
<tr>
<td>x3</td>
<td>5.3640</td>
<td>94.953</td>
<td>49.793</td>
<td>28.373</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
</tbody>
</table>

Output 18.2.3 \ Trimmed Statistics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>N Left Tail</th>
<th>Percent</th>
<th>N Right Tail</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>0.0475</td>
<td>0.9491</td>
<td>0.5021</td>
<td>0.2599</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
<tr>
<td>x2</td>
<td>0.4948</td>
<td>9.5250</td>
<td>5.0320</td>
<td>2.6201</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
<tr>
<td>x3</td>
<td>5.3640</td>
<td>94.953</td>
<td>49.748</td>
<td>25.916</td>
<td>499</td>
<td>4.99</td>
<td>500</td>
<td>5.00</td>
</tr>
</tbody>
</table>

Example 18.3: Bucket Binning and Weight-of-Evidence Computation

The following DATA step generates a data table that contains 10 observations of a target variable (y), three continuous variables (x0–x2), and some other variables. The mycas CAS library reference enables your client machine to communicate with the CAS session.

```latex
data mycas.ex3;
  input cl1 $ x0 x1 x2 y $ freq id;
  datalines;
  a 2 . 7 n 2 1
  a 2 2 6 . 3 2
  a 3 0 1 o 0 3
  c 2 3 7 y . 4
  c 2 . 4 n -5 5
  a 3 6 7 n 3 6
  b 1 4 4 y 4 7
  b 2 5 6 y 3 8
  b 1 6 4 o 1 9
  b 2 3 2 n 3 10
;
```

The following statements show how you can use the BINNING procedure to perform bucket binning and compute the WOE and the information value (IV):

```latex
proc binning data=mycas.ex3 numbin=5 woe;
  input x1/numbin=4;
  input x2;
  target y/event="y";
  output out=mycas.out3;
run;
```

The DATA= option specifies the input data table. The WOE option enables computation of the weight of evidence and information values with WOEADJUST=0.5 by default. The first INPUT statement names one continuous variable (x1) as the first input variable for binning with four bins. The second INPUT statement
names another continuous variable \((x_2)\) as the second input variable for binning with five bins, as specified in the NUMBIN= global option. The TARGET statement names the variable \((y)\) that PROC BINNING uses to calculate the weight of evidence, and the EVENT= option specifies the target event category in a quoted string. The OUTPUT statement creates an OUTPUT data table to contain the results of PROC BINNING.

The preceding statements generate Output 18.3.1 through Output 18.3.2.

**Output 18.3.1** Binning Details

**The BINNING Procedure**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Event Count</th>
<th>Weight of Evidence</th>
<th>Information Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>Missing</td>
<td>-Inf</td>
<td>1.5000</td>
<td>1.5000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.8109</td>
<td>0.2027</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1 1.5000</td>
<td>3</td>
<td>1.5000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.8109</td>
<td>0.2027</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3 3.333</td>
<td>4.5000</td>
<td>1.5000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.4087</td>
<td>0.0676</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4 4.5000</td>
<td>Infty</td>
<td>3</td>
<td>5.6667</td>
<td>0.5774</td>
<td>5</td>
<td>6</td>
<td>1</td>
<td>0.4055</td>
<td>0.0676</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>x2</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
<th>Event Count</th>
<th>Weight of Evidence</th>
<th>Information Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Missing</td>
<td>-Inf</td>
<td>2.0000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0.3054</td>
<td>0.3054</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1 2.2000</td>
<td>3.4000</td>
<td>1.2000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>3 3.4000</td>
<td>4.6000</td>
<td>1.2000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4 4.6000</td>
<td>5.8000</td>
<td>1.2000</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>5 5.8000</td>
<td>Infty</td>
<td>5</td>
<td>6.6000</td>
<td>0.5477</td>
<td>6</td>
<td>7</td>
<td>2</td>
<td>-0.288</td>
<td>0.0479</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

**Output 18.3.2** Variable Information Value

<table>
<thead>
<tr>
<th>Variable</th>
<th>Information Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>x1</td>
<td>0.8817</td>
</tr>
<tr>
<td>x2</td>
<td>0.3534</td>
</tr>
</tbody>
</table>
Example 18.4: Cutpoint Binning

The following DATA step generates a data table that contains 10 observations of a target variable (y), two continuous variables (x1, x2), and some other variables:

```plaintext
data mycas.ex4;
  input cl1 $ cl2 x1 x2 y freq id;
datalines;
  a 2 3 7 9 2 1
  a 2 2 6 8 3 2
  a 3 0 1 5 0 3
  c 2 3 7 4 . 4
  c 2 . 4 8 -5 5
  a 3 6 7 5 3 6
  b 1 4 4 8 4 7
  b 2 5 6 3 3 8
  b 1 6 4 8 1 9
  b 2 3 2 6 3 10;
;
```

The following statements show how you can use the BINNING procedure to perform cutpoint binning:

```plaintext
proc binning data=mycas.ex4 numbin=4 method=cutpts(2, 2.3, 4.5, 3.1, 5);
  input x2;
  input x1/numbin=3;
run;
```

The DATA= option specifies the input data table. The first INPUT statement names one continuous variable x2 as the first input variable for binning with 4 bins specified by the NUMBIN= global option. The second INPUT statement names another continuous variable x1 as the second input variable for binning with 3 bins. The METHOD= option specifies that cutpoint binning method will be used. For the first input variable x2, 2, 2.3, 4.5 (and infinity) will be used as the upper bounds for its 4 bins. For the second input variable x1, 3.1, 5 (and infinity) will be used as the upper bounds for its 3 bins.

Output 18.4.1 shows the “Binning Details” table.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>x2</td>
<td>Missing</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>0</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>-Infy</td>
<td>2</td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>2.3000</td>
<td>4.5000</td>
<td>2.2000</td>
<td></td>
<td>3</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>4.5000</td>
<td>Infy</td>
<td></td>
<td></td>
<td>5</td>
<td>6.0000</td>
<td>0.5477</td>
<td>6</td>
</tr>
<tr>
<td>x1</td>
<td>Missing</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>-Infy</td>
<td>3.1000</td>
<td></td>
<td></td>
<td>5</td>
<td>2.2000</td>
<td>1.3038</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>3.1000</td>
<td>5</td>
<td>1.9000</td>
<td></td>
<td>1</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td></td>
<td>Infy</td>
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<td></td>
<td>3</td>
<td>5.6667</td>
<td>0.5774</td>
<td>5</td>
</tr>
</tbody>
</table>
Example 18.5: Tree-Based Binning

The following statements show how you can use the BINNING procedure to perform tree-based binning:

```plaintext
data mycas.hmeq;
    set sampsio.hmeq;
run;

proc binning data=mycas.hmeq method=tree;
    target bad/level=int;
    input mortdue/level = int;
    input job/ level = nom;
run;
```

The DATA= option specifies the input data table. The METHOD= option requests that tree-based binning method be used. The TARGET statement specifies bad as the target variable and requests that it be treated as an interval variable. The first INPUT statement names one variable, mortdue, and requests that it be treated as interval. The second INPUT statement names one variable, job, and requests that it be treated as nominal.

Output 18.5.1 shows the “Binning Details” table.

**Output 18.5.1 Binning Details**

<table>
<thead>
<tr>
<th>Variable</th>
<th>Bin ID</th>
<th>Lower Bound</th>
<th>Upper Bound</th>
<th>Bin Width</th>
<th>N Levels</th>
<th>Number of Observations</th>
<th>Mean</th>
<th>Standard Deviation</th>
<th>Minimum</th>
<th>Maximum</th>
</tr>
</thead>
<tbody>
<tr>
<td>MORTDUE</td>
<td>Missing</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>518</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td>-Infy</td>
<td>37837</td>
<td></td>
<td></td>
<td>933</td>
<td>23701</td>
<td>9087.0</td>
<td>2063</td>
<td>37750</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>37837</td>
<td>73611</td>
<td>35774</td>
<td></td>
<td>2309</td>
<td>56416</td>
<td>9712.4</td>
<td>37843</td>
<td>73600</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>73611</td>
<td>105410</td>
<td>31799</td>
<td></td>
<td>1283</td>
<td>87448</td>
<td>9032.3</td>
<td>73624</td>
<td>105328</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>105410</td>
<td>145158</td>
<td>39749</td>
<td></td>
<td>575</td>
<td>124127</td>
<td>11706</td>
<td>105422</td>
<td>145127</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>145158</td>
<td>Infy</td>
<td></td>
<td></td>
<td>342</td>
<td>191406</td>
<td>48765</td>
<td>145324</td>
<td>399550</td>
</tr>
<tr>
<td>JOB</td>
<td>Missing</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>279</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>109</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>193</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>2</td>
<td>3155</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1276</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>948</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Output 18.5.2 shows the “Transformation Information” table.

**Output 18.5.2 Transformation Information**

<table>
<thead>
<tr>
<th>Variable</th>
<th>N</th>
<th>N Miss</th>
<th>N Bins</th>
<th>Importance</th>
<th>Relative Importance</th>
</tr>
</thead>
<tbody>
<tr>
<td>MORTDUE</td>
<td>5442</td>
<td>518</td>
<td>6</td>
<td>8.6977</td>
<td>0.5006</td>
</tr>
<tr>
<td>JOB</td>
<td>5681</td>
<td>279</td>
<td>6</td>
<td>17.375</td>
<td>1</td>
</tr>
</tbody>
</table>
Chapter 19
The CARDINALITY Procedure

Contents

Overview: CARDINALITY Procedure .......................................................... 951
PROC CARDINALITY Features ................................................................. 952
PROC CARDINALITY Compared to Other SAS Procedures .................. 952
Using CAS Sessions and CAS Engine Librefs ............................... 952
Getting Started: CARDINALITY Procedure ........................................... 953
Syntax: CARDINALITY Procedure ......................................................... 956
PROC CARDINALITY Statement .............................................................. 956
FREQ Statement ................................................................................... 957
VAR Statement ...................................................................................... 957
Details: CARDINALITY Procedure .......................................................... 958
Displayed Output ................................................................................... 958
Examples: CARDINALITY Procedure ....................................................... 960
Example 19.1: Limited Cardinality of the Species Variable ................. 960
Example 19.2: Limited Cardinality of the Sepal Length Variable ......... 961
Example 19.3: More Levels of the Sepal Length Variable ................. 963
Example 19.4: A Variable with a User-Defined Format ...................... 965
Example 19.5: Forcing Another Order on the engineSize Variable ...... 967
References ................................................................................................. 968

Overview: CARDINALITY Procedure

The CARDINALITY procedure determines a variable’s cardinality or limited cardinality in SAS Viya. The cardinality of a variable is the number of its distinct values, and the limited cardinality of a variable is the number of its distinct values that do not exceed a specified threshold.

In order to decide whether to include a variable in a subsequent SAS analysis as a classification or interval variable, it is sufficient to compute only the limited cardinality (and not the full cardinality) because both tend to yield the same decision. The limited cardinality is computationally less expensive than the full cardinality, especially for big data.

The CARDINALITY procedure creates the following:

- a cardinality data table, which contains summary information for each variable and some additional statistics about numeric variables
- a details data table, which contains the levels of each variable
PROC CARDINALITY Features

The CARDINALITY procedure has the following features:

- treats all variables as classification variables and attempts to determine the highest levels of each variable not to exceed a specified limit
- performs a single pass to determine the limited cardinality of each variable
- runs with all the input variables in the data table or with a specified list of variables
- can be run multiple times with a WHERE clause to reveal more levels. The results are not affected by the number of units doing the work (distributed or threaded or both) because PROC CARDINALITY produces the highest levels of each variable without exceeding the specified limit.
- recommends a level (CLASS, INTERVAL, or ID) for each variable. You can override these recommended levels in subsequent steps.
- can be run multiple times to extract subsequent segments of the full histogram of any variable
- builds the levelization in an ascending or descending order with or without formats

PROC CARDINALITY Compared to Other SAS Procedures

Other SAS procedures, such as the SUMMARY procedure, can calculate the cardinality of variables, but some are expensive to compute and result in a huge data set, and others yield nondeterministic results (that is, the results depend on the number of working units).

Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:
cas mysess;
libname mycas cas sessref=mysess;

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

### Getting Started: CARDINALITY Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

This example uses the Iris data set as input to demonstrate how to use PROC CARDINALITY. The Iris data published by Fisher (1936) include the species of iris and the sepal length, sepal width, petal length, and petal width (which are measured in millimeters) on 50 iris specimens from each of three species: *Iris setosa, I. versicolor, and I. virginica*.

You can load the sashelp.iris data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

data mycas.iris;
   set sashelp.iris;
run;

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements show the basic usage:

```
proc cardinality data=mycas.iris outcard=mycas.card
   outdetails=mycas.details maxlevels=10;
run;
```

The DATA= option names mycas.iris as the input data table. Two output data tables are requested: the required OUTCARD= option requests that cardinality and summary information be stored in the mycas.card data table, and the OUTDETAILS= option requests that the levels found for each variable be stored in the mycas.details data table. The MAXLEVELS= option specifies 10 as the maximum number of levels to report.
The following statements produce the “Cardinality Output Data” table, shown in Figure 19.1. This table contains one row for each variable in the input data table. If you do not want to display all the variables in the input data table, you can use the VAR statement to specify which variables you want to display.

```
proc print data=mycas.card;
    var _varname_ _type_ _cardinality_ _more_;
run;
```

![Figure 19.1](image)

Table 19.1 explains the columns in the “Cardinality Output Data Table.” This example works with a simple subset of the variables in both the cardinality and details data tables.

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>VARNAME</em></th>
<th><em>TYPE</em></th>
<th><em>CARDINALITY</em></th>
<th><em>MORE</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Species</td>
<td>C</td>
<td>3</td>
<td>N</td>
</tr>
<tr>
<td>2</td>
<td>SepalLength</td>
<td>N</td>
<td>10</td>
<td>Y</td>
</tr>
<tr>
<td>3</td>
<td>SepalWidth</td>
<td>N</td>
<td>10</td>
<td>Y</td>
</tr>
<tr>
<td>4</td>
<td>PetalLength</td>
<td>N</td>
<td>10</td>
<td>Y</td>
</tr>
<tr>
<td>5</td>
<td>PetalWidth</td>
<td>N</td>
<td>10</td>
<td>Y</td>
</tr>
</tbody>
</table>

Table 19.1 shows that the `Species` variable has `_TYPE_ = C`, indicating that it is a character variable; its `_CARDINALITY_` value is 3, indicating that three levels (values) are reported in the details data; and `_MORE_ = N`, indicating that there are no unreported levels.

Figure 19.1 shows that the `SepalLength` variable is a numeric variable (`_TYPE_ = N`); its `_CARDINALITY_` value is 10, indicating that 10 different values are reported; and `_MORE_ = Y`, indicating that there are still more levels that can be explored.

The following statements produce the details output data table, as shown in Figure 19.2:

```
data details;
    set mycas.details;
    where _varname_ in ('Species', 'SepalLength');
run;

proc print data=details;
    var _VARNAME_ _INDEX_ _FREQ_ _RAWNUM_ _RAWCHAR_;
run;
```
Table 19.2 explains the columns in the details output data table.

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>VARNAME</em></td>
<td>Variable name</td>
</tr>
<tr>
<td><em>INDEX</em></td>
<td>Index of the level</td>
</tr>
<tr>
<td><em>FREQ</em></td>
<td>Frequency of the level</td>
</tr>
<tr>
<td><em>RAWNUM</em></td>
<td>Raw level of the variable if numeric</td>
</tr>
<tr>
<td><em>RAWCHAR</em></td>
<td>Raw level of the variable if character</td>
</tr>
</tbody>
</table>

The Species variable has three rows in the details data table, one row for each of the reported levels (the _CARDINALITY_ variable in the “Cardinality Output Data Table” has the value 3). Each of these rows has _FREQ_ = 50, and the _RAWCHAR_ values are reported for each level. There are no more unreported levels for the variable Species (_MORE_ = N); thus, no row has a missing value (.) in the _INDEX_ column for the Species variable.

The “Details Output Data Table” reports the top 10 levels of the SepalLength variable and shows that there are still as many as 105 unreported levels that are greater than 52. (For the SepalLength variable, _CARDINALITY_ = 10 and _MORE_ = Y in the “Cardinality Output Data Table.”) Therefore, SepalLength occupies 11 rows in the details data table (10 reported levels and one additional level that describes the group of all unreported levels.) The _INDEX_ of the unreported group of levels for the SepalLength variable is missing, reminding you that many levels make up this group. Essentially, the last row lumps all the other SepalLength rows into one level that has a missing _INDEX_ value. So you see 10 levels in addition to the levels greater than 52, a total of 11 rows for the SepalLength variable. The last row, which includes a missing _INDEX_ value, contains enough information to run the procedure again with a WHERE clause to obtain the next set of details.
Syntax: CARDINALITY Procedure

The following statements are available in the CARDINALITY procedure:

```
PROC CARDINALITY OUTCARD=CAS-libref.data-table < options > ;
    FREQ variable ;
    VAR variables < / options > ;
```

The PROC CARDINALITY statement is required.

PROC CARDINALITY Statement

```
PROC CARDINALITY OUTCARD=CAS-libref.data-table < options > ;
```

The PROC CARDINALITY statement invokes the procedure. Table 19.3 summarizes the options available in the PROC CARDINALITY statement.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Input and Output Data Sets</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
<tr>
<td>OUTCARD=</td>
<td>Names the cardinality data table to contain the summary information for each variable</td>
</tr>
<tr>
<td>OUTDETAILS=</td>
<td>Names an optional data table to contain the detailed levels of all the variables</td>
</tr>
<tr>
<td><strong>Cardinality Options</strong></td>
<td></td>
</tr>
<tr>
<td>MAXLEVELS=</td>
<td>Specifies the maximum number of levels to consider</td>
</tr>
<tr>
<td>ORDER=</td>
<td>Specifies the order to be applied to all variables that have an unspecified order</td>
</tr>
</tbody>
</table>

You must specify the following option:

**OUTCARD=** _CAS-libref.data-table_

specifies the output data table to contain the cardinality and summary information for each variable. _CAS-libref.data-table_ is a two-level name, where _CAS-libref_ refers to the caslib and session identifier, and _data-table_ specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 952.

You can also specify the following _options_:

**DATA=** _CAS-libref.data-table_

names the input data table for PROC CARDINALITY to use. _CAS-libref.data-table_ is a two-level name, where

_CAS-libref_ refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME
FREQ Statement

**FREQ**: 
variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC CARDINALITY treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

Except for the minimum and the maximum values, the statistics for each variable are affected by the value of variable. Missing and nonpositive values do not contribute to the other statistics.

VAR Statement

**VAR**: 
variables <./ options> ;

The VAR statement enables you to specify a subset of variables in the input data table (which is specified in the DATA= option in the PROC CARDINALITY statement) and specify how to order them.

You can specify one or more VAR statements for each type of ordering that you want. You cannot specify a variable more than once in all the VAR statements.
requests a specific method of levelization. You can specify the following values:

- **ASC** orders the specified variables in unformatted ascending order.
- **DESC** orders the specified variables in unformatted descending order.
- **ASCFMT** orders the specified variables in formatted ascending order.
- **DESFMT** orders the specified variables in formatted descending order.

By default, the value of the ORDER= option in the PROC CARDINALITY statement is used. If the ORDER= option is not specified in the PROC CARDINALITY statement, ORDER=ASC by default if the variable is unformatted or ORDER=ASCFMT by default if the variable is unformatted.

---

**Details: CARDINALITY Procedure**

**Displayed Output**

The output data tables have fixed variable names and labels. Each variable occupies one row in the cardinality data table; the number of rows that it can occupy in the details data table is less than or equal to the value of the MAXLEVELS= option plus 1. The following statements run PROC CARDINALITY and then PROC CONTENTS to examine contents of the CARD table:

```plaintext
proc cardinality data=mycas.iris outcard=mycas.card
   outdetails=mycas.details maxlevels=10;
run;

data card;
   set mycas.card;
run;

proc contents data=card order=varnum;
run;
```
### Figure 19.3 Contents of the Cardinality Output Data Table

#### The CONTENTS Procedure

<table>
<thead>
<tr>
<th>#</th>
<th>Variable</th>
<th>Type</th>
<th>Len</th>
<th>Format</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><em>VARNAME</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Variable name</td>
</tr>
<tr>
<td>2</td>
<td><em>FMTWIDTH</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Width of the variable formatted value</td>
</tr>
<tr>
<td>3</td>
<td><em>TYPE</em></td>
<td>Char</td>
<td>1</td>
<td>$</td>
<td>Type of the raw values</td>
</tr>
<tr>
<td>4</td>
<td><em>RLEVEL</em></td>
<td>Char</td>
<td>10</td>
<td>$</td>
<td>Recommended level for analytics</td>
</tr>
<tr>
<td>5</td>
<td><em>ORDER</em></td>
<td>Char</td>
<td>8</td>
<td>$</td>
<td>Variable sort order</td>
</tr>
<tr>
<td>6</td>
<td><em>MORE</em></td>
<td>Char</td>
<td>1</td>
<td>$</td>
<td>Have more unreported levels</td>
</tr>
<tr>
<td>7</td>
<td><em>CARDINALITY</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Number of levels</td>
</tr>
<tr>
<td>8</td>
<td><em>NOBS</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Number of observations</td>
</tr>
<tr>
<td>9</td>
<td><em>SUMFREQS</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Total summation of frequencies</td>
</tr>
<tr>
<td>10</td>
<td><em>NMISS</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Number of missing values</td>
</tr>
<tr>
<td>11</td>
<td><em>MISSFMT</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Format of the missing value</td>
</tr>
<tr>
<td>12</td>
<td><em>VISIBLE</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Percentage of the visible part of the report</td>
</tr>
<tr>
<td>13</td>
<td><em>MIN</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Minimum numeric value</td>
</tr>
<tr>
<td>14</td>
<td><em>MAX</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Maximum numeric value</td>
</tr>
<tr>
<td>15</td>
<td><em>MEAN</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Mean</td>
</tr>
<tr>
<td>16</td>
<td><em>STDDEV</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Standard deviation</td>
</tr>
<tr>
<td>17</td>
<td><em>SKEWNESS</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Skewness</td>
</tr>
<tr>
<td>18</td>
<td><em>KURTOSIS</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Kurtosis</td>
</tr>
<tr>
<td>19</td>
<td><em>M_FREQ</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Maximum frequency</td>
</tr>
<tr>
<td>20</td>
<td><em>M_FREQFNDLEVEL</em></td>
<td>Char</td>
<td>1</td>
<td>$</td>
<td>Found maximum frequency in the visible part of the report</td>
</tr>
<tr>
<td>21</td>
<td><em>M_FREQNUM</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Numeric level with the maximum frequency</td>
</tr>
<tr>
<td>22</td>
<td><em>M_FREQCHR</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Character level with the maximum frequency</td>
</tr>
<tr>
<td>23</td>
<td><em>M_FREQCFMT</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Formatted level with the maximum frequency</td>
</tr>
<tr>
<td>24</td>
<td><em>LASTNUM</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Last raw numeric value (cutoff)</td>
</tr>
<tr>
<td>25</td>
<td><em>LASTCHR</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Last raw character value (cutoff)</td>
</tr>
<tr>
<td>26</td>
<td><em>LASTCFMT</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Last formatted value (cutoff)</td>
</tr>
</tbody>
</table>

Note that even though the numbers of columns is fixed, the width of some of the columns in both data tables (for example, _RAWCHAR_ and _CFMT_) is related to the raw and formatted data values of each input variable. The width of these two variables is set to the maximum width over all the variables in the reports.

### Figure 19.4 Contents of the Details Output Data Table

#### The CONTENTS Procedure

<table>
<thead>
<tr>
<th>#</th>
<th>Variable</th>
<th>Type</th>
<th>Len</th>
<th>Format</th>
<th>Label</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td><em>VARNAME</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Variable name</td>
</tr>
<tr>
<td>2</td>
<td><em>INDEX</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Level index</td>
</tr>
<tr>
<td>3</td>
<td><em>FREQ</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Level frequency</td>
</tr>
<tr>
<td>4</td>
<td><em>FREQPERCENT</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Percentage of the frequency of current level</td>
</tr>
<tr>
<td>5</td>
<td><em>NMISSPERCENT</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Percentage of non missing values</td>
</tr>
<tr>
<td>6</td>
<td><em>RAWNUM</em></td>
<td>Num</td>
<td>8</td>
<td>BEST.</td>
<td>Raw numeric value</td>
</tr>
<tr>
<td>7</td>
<td><em>RAWCHAR</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Raw character value</td>
</tr>
<tr>
<td>8</td>
<td><em>CFMT</em></td>
<td>Char</td>
<td>32</td>
<td>$</td>
<td>Formatted value of a variable</td>
</tr>
</tbody>
</table>
Examples: CARDINALITY Procedure

NOTE: Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

Example 19.1: Limited Cardinality of the Species Variable

This example illustrates how you can use PROC CARDINALITY to determine the limited cardinality of a variable. It uses the same input data table as is used in the section “Getting Started: CARDINALITY Procedure” on page 953.

You can load the sashelp.iris data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sas
data mycas.iris;
  set sashelp.iris;
run;
```

The following statements run PROC CARDINALITY and plot the levels from the details data set for the variable Species:

```sas
proc cardinality data=mycas.iris outcard=mycas.card
   outdetails=mycas.details maxlevels=5;
run;
```

```sas
data sp;
  set mycas.details( where=( _varname_='Species' ));
  label _cfmt_='Formatted value of the variable Species';
  if _index_ = . then do;
    _cfmt_=cats(">",left(_cfmt_));
  end;
  _cfmt_=left(_cfmt_);
run;
```

```sas
proc sgplot data=sp;
  vbar _cfmt_ / freq=_freq_; 
run;
```

Output 19.1.1 shows that the variable Species has only three levels in the details data.
Whether MAXLEVELS=100 or 5, the Species variable remains fully visible with a _CARDINALITY_ value of 3.

Example 19.2: Limited Cardinality of the Sepal Length Variable

This example demonstrates how to use PROC CARDINALITY with more levels; it uses the same data table as is used in the section “Getting Started: CARDINALITY Procedure” on page 953.

You can load the sashelp.iris data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```plaintext
data mycas.iris;
  set sashelp.iris;
run;
```

The following statements run PROC CARDINALITY and display some of the contents of the cardinality data set:

```plaintext
proc cardinality data=mycas.iris outcard=mycas.card
   outdetails=mycas.details maxlevels=100;
run;
```

```plaintext
proc print data=mycas.card;
  var _varname_ _type_ _cardinality_ _more_ _visible_ _min_ _max_
run;
```

Output 19.2.1 shows that all the variables have a _VISIBILITY_ value of 100%.
Output 19.2.1 Visibility of the Variables

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>VARNAME</em></th>
<th><em>TYPE</em></th>
<th><em>CARDINALITY</em></th>
<th><em>MORE</em></th>
<th><em>VISIBLE</em></th>
<th><em>MIN</em></th>
<th><em>MAX</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Species</td>
<td>C</td>
<td>3</td>
<td>N</td>
<td>100</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>2</td>
<td>SepalLength</td>
<td>N</td>
<td>35</td>
<td>N</td>
<td>100</td>
<td>43</td>
<td>79</td>
</tr>
<tr>
<td>3</td>
<td>SepalWidth</td>
<td>N</td>
<td>23</td>
<td>N</td>
<td>100</td>
<td>20</td>
<td>44</td>
</tr>
<tr>
<td>4</td>
<td>PetalLength</td>
<td>N</td>
<td>43</td>
<td>N</td>
<td>100</td>
<td>10</td>
<td>69</td>
</tr>
<tr>
<td>5</td>
<td>PetalWidth</td>
<td>N</td>
<td>22</td>
<td>N</td>
<td>100</td>
<td>1</td>
<td>25</td>
</tr>
</tbody>
</table>

The following statements extract and display the levels of the variable SepalLength:

```plaintext
data sp;
   label _cfmt_='Formatted Value of the Variable SepalLength';
   set mycas.details( where=(_varname_='SepalLength'));
   if _index_ = . then do;
      _cfmt_=cats(">",left(_cfmt_));
   end;
   _cfmt_=left(_cfmt_);
run;

proc sgplot data=sp;
   vbar _cfmt_ / freq=_freq_;
run;
```

Output 19.2.2 shows the histogram.

Output 19.2.2 Full Histogram of the SepalLength Variable

The following statements specify MAXLEVELS=5, so only the leftmost five levels of the full histogram are displayed. All the other levels are combined into one level, which is reported in the details data table with a missing value in the _INDEX_ column.

```plaintext
proc cardinality data=mycas.iris outcard=mycas.card
   outdetails=mycas.details maxlevels=5;
run;

data sp;
```
Example 19.3: More Levels of the Sepal Length Variable

You can load the sashelp.iris data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```plaintext
data mycas.iris;
  set sashelp.iris;
run;
```

You can dig deeper by requesting a subsequent segment of the histogram of any variable. This example further examines the SepalLength variable. The cutoff reported from Example 19.2 was 47, which means that all levels less than or equal to 47 have been reported. So you might want to run PROC CARDINALITY again in order to report levels greater than 47, as shown in the following statements:

```plaintext
proc cardinality data=mycas.iris (where=(SepalLength > 47))
  outcard=mycas.card outdetails=mycas.details maxlevels=5;
  var SepalLength;
run;

data sp;
  set mycas.details;
```
Chapter 19: The CARDINALITY Procedure

```
label _cfmt_ = 'Formatted Value of the Variable SepalLength > 47';
if _index_ = . then do;
  _cfmt_ = cats('>', left(_cfmt_));
end;
_cfmt_ = left(_cfmt_);
run;

proc sgplot data=sp;
  vbar _cfmt_ / freq=_freq_; run;
```

Output 19.3.1 Histogram for SepalLength Levels Greater Than 47

The union of the detailed levels from Example 19.2 and this example cover 10 levels of the SepalLength variable.

Table 19.4 lists the variables that are related to the maximum frequency in the histogram.

<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>MFREQ</em></td>
<td>Maximum frequency</td>
</tr>
<tr>
<td><em>MFREQFOUNDLEVEL</em></td>
<td>Maximum frequency found in the visible part of the report</td>
</tr>
<tr>
<td><em>MFREQNUM</em></td>
<td>Numeric level that has the maximum frequency</td>
</tr>
<tr>
<td><em>MFREQCHR</em></td>
<td>Character level that has the maximum frequency</td>
</tr>
<tr>
<td><em>MFREQFMT</em></td>
<td>Formatted level that has the maximum frequency</td>
</tr>
</tbody>
</table>

The maximum frequency can be attained in the visible part of the histogram, or it can be hidden with the others. If the level that has the maximum frequency is in the visible part, the _MFREQFOUNDLEVEL_ variable is set to Y (Yes); otherwise it is set to N (No). This information is reported here because it is useful for subsequent analysis.

The following statements illustrate the variables that pertain to the maximum frequency of each variable.
Example 19.4: A Variable with a User-Defined Format

This example demonstrates how PROC CARDINALITY determines how to order variables that have user-defined formats. User-defined formats are considered to be prior knowledge about the variable and are used by default. (You can override this behavior by requesting a specific order in the ORDER= option.)

You can load the sashelp.cars data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```r
    data mycas.cars;
    set sashelp.cars;
    run;
```

The following statements create the format on the variable engineSize, run the procedure, and examine some of the variables in the cardinality data set:

```r
    proc format casfmtlib='myfmtlib';
    value engsize
      low - <3 = 'toys'
      3 - <6 = 'granny'
      6 -high='usable';
    run;

    data mycas.cars;
    format engineSize engsize.;
```

For the Species variable, the value of _MFREQ_ is 50. Because the Species variable has a limited cardinality of 3, _MFREQFOUNDLEVEL_ = Y. Also note that both _MFREQCHR_ and its formatted value in _MFREQCFMT_ are Setosa.

For the SepalLength variable, _MFREQ_ is 139 (which occurs for the value _MFREQNUM_ = .), and _MFREQFOUNDLEVEL_ = N (which means that the visible part of the histogram does not contain the level that has the maximum frequency).
set mycas.cars;
run;

proc cardinality data=mycas.cars outcard=mycas.card outdetails=mycas.details maxlevels=5;
   var engineSize;
run;

title 'Cars data with a user-defined format';
proc print data=mycas.card;
   var _varname_ _order_ _more_ _cardinality_; 
run;

Output 19.4.1 Summary of the Variable engineSize

Cars data with a user-defined format

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>VARNAME</em></th>
<th><em>ORDER</em></th>
<th><em>MORE</em></th>
<th><em>CARDINALITY</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>engineSize</td>
<td>ASCFMT</td>
<td>N</td>
<td>3</td>
</tr>
</tbody>
</table>

The order that is used for the engineSize variable is ascending formatted (ASCFMT), because engineSize has a user-defined format (engsize7). Three levels were found (_CARDINALITY_ = 3). There are no more levels to report (_MORE_ = N). The full histogram is displayed. The following statements produce Output 19.4.2:

proc print data=mycas.details;
   var _varname_ _index_ _freq_ _cfmt_;
run;

Output 19.4.2 Details Data with a User-Defined Format for the Variable engineSize

Cars data with a user-defined format

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>VARNAME</em></th>
<th><em>INDEX</em></th>
<th><em>FREQ</em></th>
<th><em>CFMT</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>engineSize</td>
<td>1</td>
<td>242</td>
<td>granny</td>
</tr>
<tr>
<td>2</td>
<td>engineSize</td>
<td>2</td>
<td>178</td>
<td>toys</td>
</tr>
<tr>
<td>3</td>
<td>engineSize</td>
<td>3</td>
<td>8</td>
<td>usable</td>
</tr>
</tbody>
</table>

The order that is used for the engineSize variable is ascending formatted (ASCFMT), because engineSize has a user-defined format engsize7. All the levels are reported. There is no missing values in the _INDEX_ column for the engineSize variable.
Example 19.5: Forcing Another Order on the engineSize Variable

You can load the sashelp.cars data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sas
data mycas.cars;
    set sashelp.cars;
run;
```

The following statements specify the ORDER= option in the VAR statement in order to use a different levelization order:

```sas
title 'Cars data with a user-defined format with an ASC order';
proc cardinality data=mycas.cars outcard=mycas.card
    outdetails=mycas.details maxlevels=5;
    var engineSize /order=asc;
run;
```

The order that is used in the engineSize variable is ascending unformatted, as requested by the ORDER=ASC option in the VAR statement. The reported levels are based on the numeric raw values of the engineSize variable. The format engsize7. is ignored. The raw values are more than 5 (the value of the MAXLEVEL= option). The details data table contains six rows: five for reported known levels and one for all the remaining unreported levels. The cardinality data table reports _MORE_ = Y (Yes) and _CARDINALITY_ = 5 for the engineSize variable. The details of the variable engineSize are discussed next, starting with the details data set produced in the previous step:

```
data details(drop=_rawchar_);
    set mycas.details;
    if _index_ = . then do;
        _cfmt_ = cats(">", put(_rawnum_,best12.));
        _rawnum_ = .;
    end;
    _cfmt_ = left(_cfmt_);
run;
```

```
proc print data=details;
run;
```
Output 19.5.2 Details of the engineSize Variable without a Format

Cars data with a user-defined format with an ASC order

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>VARNAME</em></th>
<th><em>INDEX</em></th>
<th><em>FREQ</em></th>
<th>FREQPERCENT</th>
<th>NMISSPERCENT</th>
<th><em>RAWNUM</em></th>
<th><em>CFMT</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>EngineSize</td>
<td>1</td>
<td>2</td>
<td>0.4672897196</td>
<td>0.4672897196</td>
<td>1.3</td>
<td>1.3</td>
</tr>
<tr>
<td>2</td>
<td>EngineSize</td>
<td>2</td>
<td>1</td>
<td>0.2336448598</td>
<td>0.2336448598</td>
<td>1.4</td>
<td>1.4</td>
</tr>
<tr>
<td>3</td>
<td>EngineSize</td>
<td>3</td>
<td>6</td>
<td>1.4018691589</td>
<td>1.4018691589</td>
<td>1.5</td>
<td>1.5</td>
</tr>
<tr>
<td>4</td>
<td>EngineSize</td>
<td>4</td>
<td>10</td>
<td>2.3364485981</td>
<td>2.3364485981</td>
<td>1.6</td>
<td>1.6</td>
</tr>
<tr>
<td>5</td>
<td>EngineSize</td>
<td>5</td>
<td>4</td>
<td>0.9345794393</td>
<td>0.9345794393</td>
<td>1.7</td>
<td>1.7</td>
</tr>
<tr>
<td>6</td>
<td>EngineSize</td>
<td>.</td>
<td>405</td>
<td>94.626168224</td>
<td>94.626168224</td>
<td>. &gt;1.7</td>
<td></td>
</tr>
</tbody>
</table>

The order that is used in the engineSize variable is ascending unformatted, as requested by the ORDER=ASC option in the VAR statement. The reported levels are based on the numeric raw value of the engineSize variable in ascending order. The format engsize7. is ignored. Five raw values are displayed with one additional level, indicating that the histogram of the variable is partial and not full. The observation for which _INDEX_ = . indicates that there are still unreported levels in the raw values. A second pass with a WHERE clause can reveal the details of the levels.

References

Chapter 20
The PARTITION Procedure

Overview: PARTITION Procedure
The PARTITION procedure performs sampling in SAS Viya. It performs simple random sampling, stratified sampling, and oversampling to produce a table that contains a subset of the observations or that contains partitioned observations.

The PARTITION procedure creates the following:

- one output data table, which contains the subset or partitioned data table
- one summary table, which contains the numbers of observations and variables in the data table
- one frequency table, which contains the frequency information for the population and sample
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```sas
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```sas
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```sas
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: PARTITION Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
This example performs stratified partitioning of 5,960 fictitious mortgages, with the BY variable `bad` used as the stratum. The input data table `mycas.hmeq` includes information about the fictitious mortgages. Each observation represents an applicant for a home equity loan, and all applicants have an existing mortgage.

You can load the `sampsio.hmeq` data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sql
data mycas.hmeq;
    set sampsio.hmeq;
run;
```

The following statements perform the partitioning:

```sql
proc partition data=mycas.hmeq samppct=10 samppct2=20 seed=1234 partind;
    by bad;
    output out=mycas.out1 copyvars=(bad loan derog mortdue value yoj delinq clage ninq clno debtinc);
run;
```

The SAMPPCT=10 option requests that 10% of the input data be included in the training partition, and the SAMPPCT2=20 option requests that 20% of the input data be included in the testing partition. The SEED= option specifies 1234 as the random seed to be used in the partitioning process. The PARTIND option requests that the output data table, `mycas.out1`, include an indicator that shows whether each observation is selected to a partition (1 for training or 2 for testing) or not (0). The binary BY variable `bad` indicates whether an applicant eventually defaulted or was ever seriously delinquent. The BY statement triggers stratified sampling, which enables you to sample each subpopulation in the BY variable (stratum) independently. The OUTPUT statement creates a new data table to contain the variables from the input data table that are listed in the COPYVARS= option and the partition indicator. The displayed output includes a frequency table (Figure 20.1) that shows the frequency of observations in each level of `bad`.

**Figure 20.1** Frequency Information Table

<table>
<thead>
<tr>
<th>Stratified Sampling Frequency</th>
<th>Data</th>
<th>Sample</th>
<th>Sample</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number Index</td>
<td>BAD of Obs</td>
<td>Size 1</td>
<td>Size 2</td>
</tr>
<tr>
<td>0 0</td>
<td>4771</td>
<td>477</td>
<td>954</td>
</tr>
<tr>
<td>1 1</td>
<td>1189</td>
<td>119</td>
<td>238</td>
</tr>
</tbody>
</table>
Syntax: PARTITION Procedure

The following statements are available in the PARTITION procedure:

```
PROC PARTITION <options> ;
   BY variable < variable . . . variable > ;
   OUTPUT OUT=CAS-libref.data-table <options> ;
   DISPLAY <table-list> </options> ;
   DISPLAYOUT table-spec-list </options> ;
```

The BY statement is required for stratified sampling and oversampling. The OUTPUT statement is required for all sampling methods.

PROC PARTITION statement

```
PROC PARTITION <options> ;
```

The PROC PARTITION statement invokes the procedure.

You can specify the following options for all types of sampling:

- `DATA=CAS-libref.data-table`
  names the input data table for PROC PARTITION to use. `CAS-libref.data-table` is a two-level name, where

  - `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 970.

  - `data-table` specifies the name of the input data table.

- `NTHREADS=number-of-threads`
  specifies the number of threads to be used. The default is the CPU count on each node.

- `PARTIND`
  adds to the output data table a partition indicator, _PartInd_, which indicates whether an observation is selected to a partition (1 or 2) or not (0).

- `SEED=random-seed`
  specifies an integer that is used to start the pseudorandom number generator. If you do not specify a seed or you specify a value less than or equal to 0, the seed is generated from reading the time of day from the computer’s clock. The SEED= option enables you to reproduce the same sample output.

You can specify the following options only for simple random sampling and stratified sampling:
SAMPPCT=sample-percentage

specifies what percentage of the data is to be sampled, where sample-percentage is a positive number less than or equal to 100. For example, SAMPPCT=50.5 samples 50.5% of data. When you specify this option along with the PARTIND option, the percentage of the sample whose _PartInd_ is 1 is specified in sample-percentage, and the percentage of the sample whose _PartInd_ is 0 is 100 minus sample-percentage.

SAMPPCT2=sample-percentage-2

partitions the input data into three parts when specified along with the SAMPPCT= and PARTIND options. The percentage of the sample whose _PartInd_ is 1 is specified in the SAMPPCT= option, the percentage of the sample whose _PartInd_ is 2 is specified in the SAMPPCT2= option, and the percentage of the sample whose _PartInd_ is 0 is 100 minus the sum of the values of the SAMPPCT= and SAMPPCT2= options. The sum of the sample-percentages specified in the SAMPPCT= and SAMPPCT2= options must be a positive number less than or equal to 100.

The following formulas are used to calculate sample sizes for partitions:

\[
\begin{align*}
n &= \text{round}((\text{sample-percentage} + \text{sample-percentage-2}) \times N) \\
n_1 &= \text{round}((\text{sample-percentage}/(\text{sample-percentage} + \text{sample-percentage-2})) \times n) \\
n_2 &= n - n_1
\end{align*}
\]

where \(N\) is the number of observations in the input data, \(n\) is the total number of observations in the partitions, \(n_1\) is the number of observations in the first sample, and \(n_2\) is the number of observations in the second sample.

You can specify the following options only for oversampling:

EVENT=“rare-event-level”

specifies the level (category) that corresponds to a rare event of the variable that is specified in the BY statement. If you have a format applied to the variable, you should specify the formatted event level in this option. If you specify this option, PROC PARTITION uses an oversampling technique to adjust the class distribution of the data, and the following two options are required.

EVENTPROP=event-proportion

specifies the proportion of rare events that you want in the sample, where event-proportion is a positive number less than or equal to 1. For example, EVENTPROP=0.3 specifies that 30% of the sample are rare events and 70% are not rare.

SAMPPCTEVT=sample-event-percentage

specifies the sample percentage from the rare event level, where sample-event-percentage is a positive number less than or equal to 100. For example, SAMPPCTEVT=50.5 specifies that you want to sample 50.5% of the rare events.

---

**BY Statement**

BY variable < variable ... variable> ;

The BY statement specifies classification variables to be used for stratification. There is no limit on the BY variables for stratified sampling, but only one BY variable is allowed for oversampling.
**DISPLAY Statement**

```plaintext
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 977. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying “/tions/” selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying “!/tions/” selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

- **CASESENSITIVE**
  performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  suppresses display of all tables. This option takes precedence over the other options.

- **TRACE**
  displays the display table names, labels, and paths.
**DISPLAYOUT Statement**

```
DISPLAYOUT table-spec-list </ options> ;
```

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The `table-spec-list` specifies a list of CAS output tables to create. Each entry in the list has either a `key=value` format or a `key` format:

- `key=value` specifies `key` as the ODS table name, path, or partial pathname, and specifies `value` as the CAS output table name.
- `key` specifies `key` as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following `options` after a slash (`/`):

- **INCLUDEALL** creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the `table-spec-list` specification is ignored.
- **NOREPLACE** does not replace any existing CAS output table of the same name.
- **REPEATED** replicates all CAS output tables on all nodes.

---

**OUTPUT Statement**

```
OUTPUT OUT=CAS-libref.data-table < options > ;
```

The OUTPUT statement creates a data table to contain the sampled observations and stratification information for the sample.

You must specify the following option:

- **OUT=**`CAS-libref.data-table` names the output data table for PROC PARTITION to use. You must specify this option before any other options. `CAS-libref.data-table` is a two-level name, where

  - `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the `caslib`, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 970.
data-table specifies the name of the output data table.

This table includes variables that are specified in the COPYVARS= option. If you also specify the PARTIND option in the PROC PARTITION statement, the output includes one more column, _PartInd_. In the oversampling case, an additional column, _Freq_, is provided. It is calculated as the ratio of target level’s proportion in the population to its proportion in the sample. _PartInd_ and _Freq_ are reserved names. If they exist in the input data table and you specify them in the COPYVARS= option, you need to use the PARTINDNAME= and FREQNAME= options to change the generated columns’ names.

You can also specify the following options:

COPYVAR=variable
COPYVARS=(variables)
  lists one or more variables from the input data table to be transferred to the output data table.
  If the COPYVARS= option is not specified, all the variables in the input data table are transferred to the output data table.

FREQNAME=freq-name
  renames the output data table’s _Freq_ column (which is generated in the oversampling case) to the specified freq-name.

PARTINDNAME=partition-indicator-name
  renames the generated partition indicator, _PartInd_, in the output data table to the specified partition-indicator-name.

### Details: PARTITION Procedure

#### Training, Validation, and Test Data

You can use the PARTITION procedure to partition the input data table into disjoint subsets for model training, validation, and testing. When you specify the percentages for training and testing partitions in the SAMPPCT= and SAMPPCT2= options, the _PartInd_ indicator shows whether each observation is selected to the training partition (1) or the testing partition (2), respectively. The remaining observations are assigned 0 for _PartInd_ and belong to the validation partition.

#### Classification Level

For classification variables, a classification level is an observed value that is distinct after beginning and ending white space have been removed. For example, the values “MyLevel” and “MYLEVEL” are treated as different levels in the data table. But, “a” and “a” are treated as the same level.
Displayed Output

The following sections describe the output that PROC PARTITION produces. The output is organized into various tables, which are discussed in the order of their appearance.

Frequency Information Table

For simple random sampling, the “Simple Random Sampling Frequency” table lists the number of observations in the input data table and in the sample output data table.

For stratified sampling, the “Stratified Sampling Frequency” table lists the respective frequency in each stratum for the input data and the sample. If one BY variable is specified, each level of the BY variable represents a stratum; if two BY variables are specified, a combination of the levels of two BY variables represents a stratum.

For oversampling, the “Oversampling Frequency” table lists the number of observations in each stratum for the input data and the sample.

Output CAS Tables

When you specify the OUTPUT statement, the PARTITION procedure produces the output data table along with a table that lists the CAS library, the data table name, and the number of rows and columns in that data table.

ODS Table Names

Each table that the PARTITION procedure creates has a name associated with it. You must use this name to refer to the table when you use the DISPLAY statement or ODS statements. These names are listed in Table 20.1.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>OutputCASTables</td>
<td>Contains the name of the CAS library, name of the output data table, and number of rows and columns in the output data table</td>
<td>OUTPUT</td>
<td>OUT=</td>
</tr>
<tr>
<td>OVERFreq</td>
<td>Frequency table of input data size and sample size in different levels of the BY variable for the oversampling level of the BY variable (this table is produced for oversampling)</td>
<td>PROC PARTITION</td>
<td>Default</td>
</tr>
</tbody>
</table>
Table 20.1 continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SRSFreq</td>
<td>Frequency table of input data size and sample size (this table is produced for simple random sampling)</td>
<td>PROC PARTITION</td>
<td>Default</td>
</tr>
<tr>
<td>STRAFreq</td>
<td>Frequency table of input data size and sample size in different stratification levels that are defined by BY variables (this table is produced for stratified sampling)</td>
<td>PROC PARTITION</td>
<td>Default</td>
</tr>
</tbody>
</table>

Examples: PARTITION Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

Example 20.1: Simple Random Sampling

This example demonstrates how to use PROC PARTITION to perform simple random sampling on the mycas.hmeq data table.

You can load the sampsio.hmeq data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sas
data mycas.hmeq;
  set sampsio.hmeq;
run;
```

The following statements perform the sampling:

```sas
proc partition data=mycas.hmeq samppct=10 seed=10 nthreads=1;
  output out=mycas.out2 copyvars=(job reason loan value delinq derog);
  display 'SRSFreq';
run;
```

```sas
proc print data=mycas.out2(obs=20);
run;
```

The SAMPPCT=10 option requests that 10% of the input data be sampled. The OUTPUT statement requests that the sampled data be stored in a table named mycas.out2, and the COPYVARS= option lists the variables
to be copied from mycas.hmeq to mycas.out2. The DISPLAY statement requests that the SRSFreq ODS table be displayed.

**Output 20.1.1** shows the number of observations in the mycas.hmeq data table and the number of samples.

**Output 20.1.1** Frequency Information Table

<table>
<thead>
<tr>
<th>Simple Random Sampling</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Obs</td>
<td>Number of Samples</td>
</tr>
<tr>
<td>5960</td>
<td>596</td>
</tr>
</tbody>
</table>

**Output 20.1.2** shows the sample data, which are stored in the mycas.out2 data table.

**Output 20.1.2** Sample Data

<table>
<thead>
<tr>
<th>Obs</th>
<th>JOB</th>
<th>REASON</th>
<th>LOAN</th>
<th>VALUE</th>
<th>DELinq</th>
<th>DERog</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Sales</td>
<td>Debtcn</td>
<td>4300</td>
<td>78698</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>ProfEx</td>
<td>Homeim</td>
<td>4500</td>
<td>146870</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>Self</td>
<td>Homeim</td>
<td>5000</td>
<td>53448</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>4</td>
<td>Other</td>
<td>Debtcn</td>
<td>5100</td>
<td>97064</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>5</td>
<td>Office</td>
<td>Homeim</td>
<td>5500</td>
<td>65054</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>Other</td>
<td>Homeim</td>
<td>5700</td>
<td>85753</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>Other</td>
<td>Homeim</td>
<td>5800</td>
<td>58191</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>8</td>
<td>Mgr</td>
<td>Debtcn</td>
<td>5900</td>
<td>.</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>Mgr</td>
<td>Homeim</td>
<td>6000</td>
<td>95500</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>10</td>
<td>Other</td>
<td>Homeim</td>
<td>6100</td>
<td>35250</td>
<td>.</td>
<td>.</td>
</tr>
<tr>
<td>11</td>
<td>ProfEx</td>
<td>Debtcn</td>
<td>6300</td>
<td>69000</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>12</td>
<td>ProfEx</td>
<td>Homeim</td>
<td>6800</td>
<td>160063</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>13</td>
<td>Other</td>
<td>Homeim</td>
<td>7000</td>
<td>99149</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>14</td>
<td>Other</td>
<td>Debtcn</td>
<td>7100</td>
<td>180104</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>15</td>
<td>Other</td>
<td>Debtcn</td>
<td>7500</td>
<td>50125</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>16</td>
<td>Mgr</td>
<td>Homeim</td>
<td>7500</td>
<td>71799</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>17</td>
<td>Office</td>
<td>Debtcn</td>
<td>7600</td>
<td>62357</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>18</td>
<td>Other</td>
<td>Homeim</td>
<td>7900</td>
<td>75189</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>19</td>
<td>Office</td>
<td>Debtcn</td>
<td>8000</td>
<td>86900</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>20</td>
<td>Other</td>
<td>Homeim</td>
<td>8200</td>
<td>50061</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

---

**Example 20.2: Stratified Sampling**

This example demonstrates how to use PROC PARTITION to perform stratified sampling to partition the data; it uses the same data table as is used in Example 20.1.

You can load the sampio.hmeq data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:
data mycas.hmeq;
   set sampsio.hmeq;
run;

The following statements perform the partitioning:

   proc partition data=mycas.hmeq samppct=10 samppct2=20 seed=10 partind nthreads=3;
      by bad;
      output out=mycas.out3 copyvars=(job reason loan value delinq derog);
   run;

   proc print data=mycas.out3(obs=20);
   run;

The SAMPPCT=10 option requests that 10% of the input data be included in the training partition, and the SAMPPCT2=20 option requests that 20% of the input data be included in the testing partition. The SEED= option specifies 10 as the random seed to be used in the partitioning process. The PARTIND option requests that the output data table, mycas.out3, include an indicator that shows whether each observation is selected to a partition (1 for training or 2 for testing) or not (0). The OUTPUT statement requests that the sampled data be stored in a table named mycas.out3, and the COPYVARS= option lists the variables to be copied from mycas.hmeq to mycas.out3.

Output 20.2.1 shows the frequency information for each level of BY variable bad in the mycas.hmeq data table.

Output 20.2.1  Frequency Information Table

<table>
<thead>
<tr>
<th>Stratified Sampling Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Index BAD</td>
</tr>
<tr>
<td>-----------</td>
</tr>
<tr>
<td>0 0</td>
</tr>
<tr>
<td>1 1</td>
</tr>
</tbody>
</table>

Output 20.2.2 shows the first 20 output sample observations in mycas.out3; the _PartInd_ column shows which partition the observation is selected for (1 for training or 2 for testing) or none (0).
### Output 20.2.2 Sample Output with Partition Indicator

<table>
<thead>
<tr>
<th>Obs</th>
<th>JOB</th>
<th>REASON</th>
<th>LOAN</th>
<th>VALUE</th>
<th>DELINQ</th>
<th>DEROG</th>
<th>PartInd</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Other</td>
<td>HomeImp</td>
<td>1100</td>
<td>39025</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1500</td>
<td></td>
<td>.</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>Other</td>
<td>HomeImp</td>
<td>1800</td>
<td>57037</td>
<td>2</td>
<td>3</td>
<td>2</td>
</tr>
<tr>
<td>4</td>
<td>Sales</td>
<td>HomeImp</td>
<td>2000</td>
<td>62250</td>
<td>0</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>5</td>
<td>Other</td>
<td>HomeImp</td>
<td>2000</td>
<td>55000</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>6</td>
<td>Other</td>
<td>HomeImp</td>
<td>2200</td>
<td>34687</td>
<td>1</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>Other</td>
<td>HomeImp</td>
<td>2300</td>
<td>40150</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>8</td>
<td>ProfExe</td>
<td>HomeImp</td>
<td>2400</td>
<td>73395</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>9</td>
<td>Other</td>
<td>HomeImp</td>
<td>2400</td>
<td>17180</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>10</td>
<td>HomeImp</td>
<td>2500</td>
<td>20200</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>ProfExe</td>
<td>HomeImp</td>
<td>2500</td>
<td>78600</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>12</td>
<td>ProfExe</td>
<td>DebtCon</td>
<td>2900</td>
<td>113000</td>
<td>0</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>13</td>
<td>Other</td>
<td>HomeImp</td>
<td>2900</td>
<td>67996</td>
<td>0</td>
<td>3</td>
<td>0</td>
</tr>
<tr>
<td>14</td>
<td>Other</td>
<td>HomeImp</td>
<td>3000</td>
<td>20300</td>
<td>0</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>15</td>
<td>Other</td>
<td>HomeImp</td>
<td>3000</td>
<td>193500</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>16</td>
<td>Other</td>
<td>HomeImp</td>
<td>3000</td>
<td>14100</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>17</td>
<td>Mgr</td>
<td>HomeImp</td>
<td>3000</td>
<td>71500</td>
<td>2</td>
<td>.</td>
<td>2</td>
</tr>
<tr>
<td>18</td>
<td>3100</td>
<td>70400</td>
<td>.</td>
<td>.</td>
<td>.</td>
<td></td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>Other</td>
<td>HomeImp</td>
<td>3200</td>
<td>40834</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>20</td>
<td>Mgr</td>
<td>HomeImp</td>
<td>3200</td>
<td>.</td>
<td>2</td>
<td>.</td>
<td>0</td>
</tr>
</tbody>
</table>
Example 20.3: Oversampling

This example demonstrates how to use PROC PARTITION to perform oversampling; it uses the same data table as in Example 20.1.

You can load the sampsio.hmeq data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sql
data mycas.hmeq;
  set sampsio.hmeq;
run;
```

The following statements perform oversampling:

```sql
proc partition data=mycas.hmeq samppctevt=90 eventprop=0.5
  event="1" seed=10 nthreads=1;
  by bad;
  ods output OVERFREQ=outFreq;
  output out=mycas.out4 copyvars=(job loan value delinqu derog)
    freqname=_Freq2_;
run;
```

```sql
proc print data=mycas.out4(obs=20);
run;
```

The EVENTPROP=0.5 option specifies that 50% of the sample are rare events. The SAMPPCTEVT=90 option requests that 90% of the rare events be sampled. The EVENT="1" option specifies that the second level of the variable BAD corresponds to a rare event. The OUTPUT statement requests that the sampled data be stored in a table named mycas.out4, specifies the variables to be transferred from the input data table, requests that the _Freq_ column be renamed to _Freq2_.

Output 20.3.1 shows the number of observations in the sample and in each level of the BY variable bad in the mycas.hmeq data table.

**Output 20.3.1 Frequency Information Table**

<table>
<thead>
<tr>
<th>Oversampling Frequency</th>
<th>The PARTITION Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td>Index</td>
<td>BAD</td>
</tr>
<tr>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

Output 20.3.2 shows the first 20 output sample observations in the mycas.out4 data table; the _Freq2_ column shows the ratio of target level’s proportion in the population to its proportion in the sample.
### Output 20.3.2  Output Data Table

<table>
<thead>
<tr>
<th>Obs</th>
<th>JOB</th>
<th>LOAN</th>
<th>VALUE</th>
<th>DELinq</th>
<th>DEROG</th>
<th><em>Freq2</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Other</td>
<td>1100</td>
<td>39025</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>2</td>
<td></td>
<td>1500</td>
<td></td>
<td></td>
<td></td>
<td>0.39899</td>
</tr>
<tr>
<td>3</td>
<td>Other</td>
<td>1800</td>
<td>57037</td>
<td>2</td>
<td>3</td>
<td>0.39899</td>
</tr>
<tr>
<td>4</td>
<td>Sales</td>
<td>2000</td>
<td>62250</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>5</td>
<td>Other</td>
<td>2000</td>
<td>55000</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>6</td>
<td>Other</td>
<td>2200</td>
<td>34687</td>
<td>1</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>7</td>
<td>Other</td>
<td>2300</td>
<td>40150</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>8</td>
<td>ProfExe</td>
<td>2400</td>
<td>73395</td>
<td>0</td>
<td>1</td>
<td>0.39899</td>
</tr>
<tr>
<td>9</td>
<td>Other</td>
<td>2400</td>
<td>17180</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>10</td>
<td></td>
<td>2500</td>
<td>20200</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>11</td>
<td>ProfExe</td>
<td>2900</td>
<td>113000</td>
<td>0</td>
<td>1</td>
<td>0.39899</td>
</tr>
<tr>
<td>12</td>
<td>Other</td>
<td>2900</td>
<td>67996</td>
<td>0</td>
<td>3</td>
<td>0.39899</td>
</tr>
<tr>
<td>13</td>
<td>Other</td>
<td>3000</td>
<td>20300</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>14</td>
<td>Other</td>
<td>3000</td>
<td>193500</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>15</td>
<td>Other</td>
<td>3000</td>
<td>14100</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>16</td>
<td>Mgr</td>
<td>3000</td>
<td>71500</td>
<td>2</td>
<td></td>
<td>1.60101</td>
</tr>
<tr>
<td>17</td>
<td>Other</td>
<td>3200</td>
<td>40834</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>18</td>
<td>Mgr</td>
<td>3200</td>
<td></td>
<td>2</td>
<td></td>
<td>0.39899</td>
</tr>
<tr>
<td>19</td>
<td>Office</td>
<td>3400</td>
<td>52000</td>
<td>1</td>
<td>0</td>
<td>0.39899</td>
</tr>
<tr>
<td>20</td>
<td>Other</td>
<td>3900</td>
<td>45960</td>
<td>0</td>
<td>0</td>
<td>0.39899</td>
</tr>
</tbody>
</table>
Overview: VARIMPUTE Procedure

The VARIMPUTE procedure performs variable imputation in SAS Viya. Imputation is a common step in data preparation.

The VARIMPUTE procedure can replace numeric missing values with a specified value, with the mean or median of the nonmissing values, or with some random value between the minimum value and the maximum value of the nonmissing values.

The VARIMPUTE procedure can replace nominal missing values with a specified value and with the nonmissing value which has the most frequent appearance for that variable.

The VARIMPUTE procedure also supports formatted values including user defined formats.

When PROC VARIMPUTE calculates the mean, median, mode, or a random value, it ignores any observation that has a value that is less than or equal to 0 for any variable that is named in the FREQ statement.
Using CAS Sessions and CAS Engine Librefs

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:

```
proc options option=(CASHOST CASPORT);
run;
```

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

```
cas mysess;
libname mycas cas sessref=mysess;
```

The CAS statement creates the CAS session named `mysess`, and the LIBNAME statement creates the `mycas` CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the `mysess` session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

```
cas mysess terminate;
```

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

Getting Started: VARIMPUTE Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

The VARIMPUTE procedure can use any or all of six methods to impute numeric missing values. This example uses all six imputation methods to manipulate a data table. The input data table `mycas.hmeq` includes information about fictitious mortgages. Each observation represents an applicant for a home equity loan, and all applicants have an existing mortgage.

You can load the `sampsio.hmeq` data table into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:
data mycas.hmeq;
  set sampsio.hmeq;
run;

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements perform the imputation:

```sas
proc varimpute data=mycas.hmeq seed=18000;
  input clage /ctech=mean;
  input delinq/ctech=median;
  input ninq/ctech=random;
  input reason/ntech=mode;
  input job/ntech=value valuescharacter=Office;
  input debtinc yoj/ctech=value cvalues=50,100;
  output out=mycas.out;
run;
```

The SEED= option specifies 18,000 as the random seed to be used in the random imputation process. The first INPUT statement (which includes the CTECH=MEAN option) requests that mean imputation be used for the variable clage. The second INPUT statement (which includes the CTECH=MEDIAN option) requests that median imputation be used for the variable delinq. The third INPUT statement (which includes the CTECH=RANDOM option) requests that random imputation be used for the variable ninq. The fourth INPUT statement (which includes the NTECH=MODE option) requests that mode imputation be used for the variable reason. The fifth INPUT statement (which includes the NTECH=VALUE option) requests that Office be imputed as the value of the variable job. The sixth INPUT statement (which includes the CTECH=VALUE option) requests that 50 be imputed as the value of variable debtinc and 100 be imputed as the value of variable yoj. The OUTPUT statement creates a new data table to contain the imputed values; it is shown in Output 21.1 and Output 21.2. The Variable column shows the original variable names from the input data table. The Imputation Method column shows the types of imputation methods: value (for character or numeric variables), median, random (between the minimum value and the maximum value of the nonmissing values), mean, and mode. For random imputation, the last column does not show any number, because the imputation is done by using a random seed. For other imputation methods, the last column shows the imputation values that are used to replace missing values. The Result Variable column shows the new variable names in the output data table.

**Figure 21.1** Imputed Values for Interval Variables

<table>
<thead>
<tr>
<th>Variable</th>
<th>Imputation Method</th>
<th>Result Variable</th>
<th>N</th>
<th>Number of Missing Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>CLAGE</td>
<td>Mean</td>
<td>IM_CLAGE</td>
<td>5652</td>
<td>308 179.766</td>
</tr>
<tr>
<td>DELINQ</td>
<td>Median</td>
<td>IM_DELINQ</td>
<td>5380</td>
<td>580 0</td>
</tr>
<tr>
<td>NINQ</td>
<td>Random</td>
<td>IM_NINQ</td>
<td>5450</td>
<td>510</td>
</tr>
<tr>
<td>DEBTINC</td>
<td>Value</td>
<td>IM_DEBTINC</td>
<td>4693</td>
<td>1267 50</td>
</tr>
<tr>
<td>YOJ</td>
<td>Value</td>
<td>IM_YOJ</td>
<td>5445</td>
<td>515 100</td>
</tr>
</tbody>
</table>
Syntax: VARIMPUTE Procedure

The following statements are available in the VARIMPUTE procedure:

```plaintext
PROC VARIMPUTE DATA=CAS-libref.data-table < options > ;
  CODE FILE=filename ;
  FREQ variable ;
  INPUT variables </options > ;
  OUTPUT OUT=CAS-libref.data-table < option > ;
```

The PROC VARIMPUTE and INPUT statements are required. The INPUT statement can appear multiple times. If the same variable is specified in more than one INPUT statement, the imputation method specified in the first INPUT statement (or the default imputation method if the first statement does not specify a method) is applied.

PROC VARIMPUTE Statement

```plaintext
PROC VARIMPUTE DATA=CAS-libref.data-table < options > ;
```

The PROC VARIMPUTE statement invokes the procedure.

You can specify the following `options`:

**DATA=CAS-libref.data-table**

names the input data table for PROC VARIMPUTE to use. The default is the most recently created data table. `CAS-libref.data-table` is a two-level name, where

- `CAS-libref` refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about `CAS-libref`, see the section “Using CAS Sessions and CAS Engine Librefs” on page 986.

- `data-table` specifies the name of the input data table.

**NTHREADS=number-of-threads**

specifies the number of threads to be used. The default is the CPU count on each node.
**SEED=**random-seed

specifies an integer that is used to start the pseudorandom number generator. If you do not specify a seed or you specify a value less than or equal to 0, the seed is generated from reading the time of day from the computer’s clock. If your specified seed is out of the range of an integer, the computer’s clock time is used as the seed. The SEED= option enables you to reproduce the same sample output.

---

**CODE Statement**

**CODE FILE=**filename;

The CODE statement generates SAS DATA step code that mimics the computations that are performed. Only one CODE statement is processed. If you specify multiple CODE statements, only the first one is used.

You can specify the following option:

**FILE=**filename

specifies the name of the file to write the SAS score code to.

---

**FREQ Statement**

**FREQ** variable;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC VARIMPUTE treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.

---

**INPUT Statement**

**INPUT** variables < /options>;

The INPUT statement names one or more input variables and specifies the method that is used to impute missing values.

You can specify the following options:

**CONTINUOUSTECH=**imputation-method

**CTECH=**imputation-method

specifies the imputation method for interval variables.

You can choose from the following methods:

**MEAN**

specifies that missing values of each variable are replaced by the algebraic mean of the nonmissing values of that variable.

**MEDIAN**

specifies that missing values of each variable are replaced by the algebraic median of the nonmissing values of that variable.
Chapter 21: The VARIMPUTE Procedure

RANDOM specifies that missing values of each variable are replaced by a random value that is drawn between the minimum value and the maximum values of the nonmissing values of that variable.

VALUE CVALUES=value-list specifies that missing values for each numeric input variable are replaced by the corresponding numeric value in the value-list.

By default, CONTINUOUSTECH=MEAN.

NOMINALTECH=imputation-method
NTECH=imputation-method
specifies the imputation method for nominal variables.

You can choose from the following imputation-methods:

MODE replaces missing values of each variable by the nonmissing value that appears most frequently for that variable.

VALUE VALUESNUMERIC=value-list replaces missing values for each numeric input variable by the corresponding numeric value in the value-list.

VALUE VALUESCHARACTER=value-list replaces missing values for each character input variable by the corresponding character value in the value-list.

By default, NOMINALTECH=MODE.

OUTPUT Statement

OUTPUT OUT=CAS-libref.data-table < option > ;

The OUTPUT statement creates an output data table to contain the results of PROC VARIMPUTE.

You must specify the following option:

OUT=CAS-libref.data-table

names the output data table for PROC VARIMPUTE to use. You must specify this option before any other options. CAS-libref.data-table is a two-level name, where

CAS-libref refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to where the data table is to be stored, and a session identifier, which defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS-libref, see the section “Using CAS Sessions and CAS Engine Librefs” on page 986.

data-table specifies the name of the output data table.

The output data table contains the scored data.

You can also specify the following option:
COPYVAR=variable
COPYVARS=(variables)

lists one or more variables from the input data table to be transferred to the output data table.

Details: VARIMPUTE Procedure

Obtaining the Statistics for Imputation

PROC VARIMPUTE first computes the imputation value and then imputes with that value. The statistics mean, median, mode, minimum, and maximum are computed precisely. To compute the median, PROC VARIMPUTE uses the empirical distribution function. Let \( n \) be the number of nonmissing values for a variable, and let \( x_1, x_2, \ldots, x_n \) represent the ordered values of the variable. Let the 50th percentile be \( y \), \( p = 0.5 \), and \( np = j + g \) where \( j \) is the integer part of \( np \) and \( g \) is the fractional part of \( np \). Then, the median \( y \) is

\[
y = \begin{cases} x_j & \text{if } g = 0 \\ x_{j+1} & \text{if } g > 0 \end{cases}
\]

Random Imputation

If you specify CONTINUOUSTECH=RANDOM in the INPUT statement, PROC VARIMPUTE replaces missing values with a random value that is drawn between the minimum and maximum of the variable. For variable \( x \), assume that the input data table is \( \{ x_i \} \), where \( i = 1, 2, \ldots, n \). Let \( \min(x) = \min_{i \in \{1, \ldots, n\}} \{ x_i \} \), and let \( \max(x) = \max_{i \in \{1, \ldots, n\}} \{ x_i \} \). The random value is calculated as

\[
R = \min(x) + (\max(x) - \min(x)) \times \text{rand('uniform')},
\]

where \( \text{rand('uniform')} \) is a function that takes a seed as input and returns a random value from a uniform distribution between 0 and 1. You can specify the seed as a nonnegative integer in the SEED= option in the PROC VARIMPUTE statement. If you do not specify the SEED= option, the seed is generated from reading the time of day from the computer’s clock.

Displayed Output

The following sections describe the output that PROC VARIMPUTE produces. The output is organized into various tables, which are discussed in their order of appearance.

Imputation Requests

The first table displayed lists the imputation method, the number of variables that are imputed, and the seed value for the random imputation.
Imputed Values for Interval Variables

The “Imputed Values for Interval Variables” table lists the names of the interval variables, the imputation method, the numbers of nonmissing and missing values for each variable, and the imputation values that replace missing values for interval variables.

Imputed Values for Nominal Variables

The “Imputed Values for Nominal Variables” table lists the names of the nominal variables, the imputation method, the numbers of nonmissing and missing values for each variable, and the imputation values that replace missing values for nominal variables.

ODS Table Names

Each table that the VARIMPUTE procedure creates has a name associated with it. You must use this name to refer to the table when you use ODS statements. The name of each table and a short description of the contents are listed in Table 21.1.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>ImputeInfo</td>
<td>Imputation method, number of variables that are imputed, and seed for the pseudorandom number generator</td>
<td>PROC VARIMPUTE</td>
<td>Default</td>
</tr>
<tr>
<td>VarImputeInfo (Interval Variables)</td>
<td>Variables, imputation method, number of nonmissing values, number of missing values, and imputation values</td>
<td>PROC VARIMPUTE</td>
<td>Default</td>
</tr>
<tr>
<td>VarImputeInfo (Nominal Variables)</td>
<td>Variables, imputation method, number of nonmissing values, number of missing values, and imputation values</td>
<td>PROC VARIMPUTE</td>
<td>Default</td>
</tr>
</tbody>
</table>

Examples: VARIMPUTE Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”
Example 21.1: Imputation of Missing Values for HMEQ Data Table

This example demonstrates how to use PROC VARIMPUTE to perform imputation; it uses the same data table as in the section “Getting Started: VARIMPUTE Procedure” on page 986.

You can load the sampsi.o.hmeq data table into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

``` SAS
data mycas.hmeq;
  set sampsi.o.hmeq;
  id = _N_;
run;
```

The following statements perform the imputation:

``` SAS
proc varimpute data=mycas.hmeq seed=12345;
  input derog c/no/ctech=value cvalues=5,20;
  input value /ctech=mean;
  input job/ntech=mode;
  input mortdue /ctech=median;
  input ninq /ctech=random;
  input reason/ntech=value values=character=unknown;
  output out=mycas.out1 copyvar=(id);
run;
```

``` SAS
data out2; set mycas.out1; run;
proc sort data=out2; by id; run;
proc print data=out2(firstobs=110 obs=124);
run;
```

Output 21.1.1 shows the number of variables for which the missing observations are imputed and the random seed value for the random imputation method.

**Output 21.1.1** Imputation Requests

<table>
<thead>
<tr>
<th>The VARIMPUTE Procedure</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Imputation Method</strong></td>
</tr>
<tr>
<td>Mean</td>
</tr>
<tr>
<td>Random</td>
</tr>
<tr>
<td>Median</td>
</tr>
<tr>
<td>Numeric Value</td>
</tr>
<tr>
<td>Mode</td>
</tr>
<tr>
<td>Character Value</td>
</tr>
</tbody>
</table>

Output 21.1.2 shows the imputation results with interval variables.
Chapter 21: The VARIMPUTE Procedure

Output 21.1.2 Imputed Values for Interval Variables

<table>
<thead>
<tr>
<th>Variable</th>
<th>Imputation Method</th>
<th>Result Variable</th>
<th>N</th>
<th>Number of Missing Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>VALUE</td>
<td>Mean</td>
<td>IM_VALUE</td>
<td>5848</td>
<td>112 101776</td>
</tr>
<tr>
<td>MORTDUE</td>
<td>Median</td>
<td>IM_MORTDUE</td>
<td>5442</td>
<td>518 65017</td>
</tr>
<tr>
<td>NINQ</td>
<td>Random</td>
<td>IM_NINQ</td>
<td>5450</td>
<td>510</td>
</tr>
<tr>
<td>DEROG</td>
<td>Value</td>
<td>IMDEROG</td>
<td>5252</td>
<td>708 5</td>
</tr>
<tr>
<td>CLNO</td>
<td>Value</td>
<td>IM_CLNO</td>
<td>5738</td>
<td>222 20</td>
</tr>
</tbody>
</table>

Output 21.1.3 shows the imputation results for nominal variables.

Output 21.1.3 Imputed Values for Nominal Variables

<table>
<thead>
<tr>
<th>Variable</th>
<th>Imputation Method</th>
<th>Result Variable</th>
<th>N</th>
<th>Number of Missing Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>JOB</td>
<td>Mode</td>
<td>IM_JOB</td>
<td>5681</td>
<td>279 Other</td>
</tr>
<tr>
<td>REASON</td>
<td>Value</td>
<td>IM_REASON</td>
<td>5708</td>
<td>252 UNKNOWN</td>
</tr>
</tbody>
</table>

Output 21.1.4 shows 15 output observations with the new imputed values for those input variable values that were missing.

Output 21.1.4 Output data table

<table>
<thead>
<tr>
<th>Obs</th>
<th>id</th>
<th>IM_VALUE</th>
<th>IM_MORTDUE</th>
<th>IM_NINQ</th>
<th>IM_DEROG</th>
<th>IM_CLNO</th>
<th>IM_JOB</th>
<th>IM_REASON</th>
</tr>
</thead>
<tbody>
<tr>
<td>110</td>
<td>110</td>
<td>79852.00</td>
<td>68815</td>
<td>0.0000</td>
<td>0</td>
<td>14</td>
<td>Other</td>
<td>Homelmp</td>
</tr>
<tr>
<td>111</td>
<td>111</td>
<td>80027.00</td>
<td>72021</td>
<td>0.0000</td>
<td>2</td>
<td>5</td>
<td>Other</td>
<td>Homelmp</td>
</tr>
<tr>
<td>112</td>
<td>112</td>
<td>63869.00</td>
<td>53969</td>
<td>0.0000</td>
<td>0</td>
<td>30</td>
<td>ProfEx</td>
<td>DebtCon</td>
</tr>
<tr>
<td>113</td>
<td>113</td>
<td>60250.00</td>
<td>65017</td>
<td>10.9178</td>
<td>5</td>
<td>20</td>
<td>Other</td>
<td>UNKNOWN</td>
</tr>
<tr>
<td>114</td>
<td>114</td>
<td>64074.00</td>
<td>53091</td>
<td>0.0000</td>
<td>1</td>
<td>17</td>
<td>Office</td>
<td>DebtCon</td>
</tr>
<tr>
<td>115</td>
<td>115</td>
<td>79087.00</td>
<td>66127</td>
<td>0.0000</td>
<td>1</td>
<td>15</td>
<td>Other</td>
<td>Homelmp</td>
</tr>
<tr>
<td>116</td>
<td>116</td>
<td>77182.00</td>
<td>65017</td>
<td>13.8192</td>
<td>5</td>
<td>20</td>
<td>Other</td>
<td>UNKNOWN</td>
</tr>
<tr>
<td>117</td>
<td>117</td>
<td>66000.00</td>
<td>39000</td>
<td>1.0000</td>
<td>0</td>
<td>19</td>
<td>Other</td>
<td>Homelmp</td>
</tr>
<tr>
<td>118</td>
<td>118</td>
<td>79247.00</td>
<td>71082</td>
<td>0.0000</td>
<td>0</td>
<td>14</td>
<td>Other</td>
<td>Homelmp</td>
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Chapter 22
The VARREDUCE Procedure

Contents

Overview: VARREDUCE Procedure .................................................. 996
  PROC VARREDUCE Features ......................................................... 996
  PROC VARREDUCE Compared to Other SAS Procedures ..................... 997
  Using CAS Sessions and CAS Engine Librefs ................................ 997

Getting Started: VARREDUCE Procedure ...................................... 998
  Unsupervised Variable Selection ............................................... 1000
  Supervised Variable Selection .................................................. 1002

Syntax: VARREDUCE Procedure ..................................................... 1003
  PROC VARREDUCE Statement ..................................................... 1003
  CLASS Statement ........................................................................ 1005
  DISPLAY Statement .................................................................... 1006
  DISPLAYOUT Statement .............................................................. 1007
  FREQ Statement ........................................................................ 1007
  REDUCE Statement ..................................................................... 1008

Details: VARREDUCE Procedure ..................................................... 1009
  Missing Values ........................................................................... 1009
  Unsupervised Variable Selection ............................................... 1010
  Supervised Variable Selection ................................................... 1010
  Variable Selection for Regression .............................................. 1010
  Variable Selection for Classification ......................................... 1011
  Criteria Used in Model Selection ............................................... 1011
  Computational Method ............................................................... 1012
  GLM Parameterization of Classification Variables and Effects ........ 1013
    Intercept .................................................................................. 1014
    Regression Effects ................................................................... 1014
    Main Effects ............................................................................ 1014
    Interaction Effects .................................................................... 1015
    Nested Effects .......................................................................... 1016
    Continuous-Nesting-Class Effects ............................................ 1016
    Continuous-by-Class Effects .................................................... 1017
    General Effects ........................................................................ 1017
  Displayed Output ....................................................................... 1018
    Number of Observations ........................................................... 1018
    Selection Summary .................................................................... 1018
    Selected Variables .................................................................... 1018
  ODS Table Names ....................................................................... 1018
Overview: VARREDUCE Procedure

The VARREDUCE procedure performs both supervised and unsupervised variable selection in SAS Viya. You can use the VARREDUCE procedure to read data in distributed form and perform variable selection in parallel.

The VARREDUCE procedure performs unsupervised variable selection by identifying a set of variables that jointly explain the maximum amount of data variance. Unlike principal component analysis (PCA), which reduces dimensionality by generating a set of new variables (variable extraction), the VARREDUCE procedure reduces dimensionality by selecting a subset of the original variables (variable selection). Thus, this technique preserves model interpretation.

The VARREDUCE procedure performs supervised variable selection by identifying a set of variables that jointly explain the maximum amount of variance contained in the response variables. The VARREDUCE procedure supports variable selection in both the regression setting and the classification (categorization) setting.

PROC VARREDUCE Features

The VARREDUCE procedure analyzes variance and reduces dimensionality by selecting the variables that contribute the most to the overall variance of the data in unsupervised variable selection (or to the overall variance of the response variables in supervised variable selection). The following list summarizes the basic features of the VARREDUCE procedure:

- Variable selection is based on covariance analysis.
- Input data can be read in parallel.
- Computation of the Pearson correlation, covariance, or sums of squares and crossproducts matrix is distributed.
- Computation of the variable selection steps is distributed.
- All phases of analytic execution use of high degree of multithreading.
- Both supervised and unsupervised variable selection are supported.
- Multiple response variables are supported in variable selection for regression.
- The CLASS statement supports categorical inputs.
• The `REDUCE` statement supports main and interaction effects.

• The `OUTCP` option supports outputting a CORR, COV, or SSCP matrix.

---

**PROC VARREDUCE Compared to Other SAS Procedures**

This section compares the VARREDUCE procedure with the PCA and GENSELECT procedures in SAS Visual Statistics and with the FACTOR, PRINCOMP, GLMSELECT, and DISCRIM procedures in SAS/STAT software.

When PROC VARREDUCE performs unsupervised variable selection, it analyzes variance and reduces dimensionality by forward selection of the variables that contribute the most to the overall data variance. The output lists the variables in order of their contribution to data variance; the output can be used directly for reporting or for selecting variables for procedures that build models. In contrast, principal component analysis analyzes the variance and then projects the data space onto an orthogonal set of axes by a linear combination of the original variables. These new principal components best explain the data variance and can be used as input to procedures that build models. Principal component analysis can be done through the FACTOR, PRINCOMP, and PCA procedures, which reduce the number of inputs from the original set. The primary difference between principal component analysis (PCA) and PROC VARREDUCE is that PCA generates new variables, whereas PROC VARREDUCE reduces data dimensionality by selecting a subset of the original variables. This feature of PROC VARREDUCE is beneficial in applications where retaining the original variables is important for model exploration and interpretation.

When PROC VARREDUCE performs supervised variable selection, it analyzes the variance and reduces dimensionality by forward selection of the variables that contribute the most to explaining the overall variance of the response variables (targets). The output lists the variables in order of their contribution to explaining the response variance. The output can be used directly for reporting or for selecting variables for procedures that build models. When PROC VARREDUCE is used to perform supervised variable selection, it most resembles the GLMSELECT and GENSELECT procedures. However, PROC VARREDUCE allows multiple response variables, whereas PROC GLMSELECT and PROC GENSELECT do not. When the response variable is a classification variable and its levelization is done in a special format, PROC VARREDUCE analyzes the variance in the same way that linear discriminant analysis (LDA) does. LDA can be done through the DISCRIM procedure in SAS/STAT. Like principal component analysis, LDA generates new variables by linearly combining all original variables, whereas PROC VARREDUCE reduces data dimensionality by selecting a subset of the original variables.

---

**Using CAS Sessions and CAS Engine Librefs**

SAS Cloud Analytic Services (CAS) is the analytic server and associated cloud services in SAS Viya. This section describes how to create a CAS session and set up a CAS engine libref that you can use to connect to the CAS session. It assumes that you have a CAS server already available; contact your system administrator if you need help starting and terminating a server. This CAS server is identified by specifying the host on which it runs and the port on which it listens for communications. To simplify your interactions with this CAS server, the host information and port information for the server are stored as SAS option values that are retrieved automatically whenever this CAS server needs to be accessed. You can examine the host and port values for the server at your site by using the following statements:
proc options option=(CASHOST CASPORT);
run;

In addition to starting a CAS server, your system administrator might also have created a CAS session and a CAS engine libref for your use. You can define your own sessions and CAS engine librefs that connect to the CAS server as shown in the following statements:

    cas mysess;
    libname mycas cas sessref=mysess;

The CAS statement creates the CAS session named mysess, and the LIBNAME statement creates the mycas CAS engine libref that you use to connect to this session. It is not necessary to explicitly name the CASHOST and CASPORT of the CAS server in the CAS statement, because these values are retrieved from the corresponding SAS option values.

If you have created the mysess session, you can terminate it by using the TERMINATE option in the CAS statement as follows:

    cas mysess terminate;

For more information about the CAS and LIBNAME statements, see the section “Introduction to Shared Concepts” on page 8 in Chapter 2, “Shared Concepts.”

---

**Getting Started: VARREDUCE Procedure**

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

This example uses a data table which contains 100 observations that contain one character variable (C), one classification variable (y), and 10 continuous variables (x1–x10). This data table is used for both of the getting-started examples in the following sections.

The following DATA step stores the variables in the mycas.getStarted data table and loads the table into your CAS session:

```sas
data mycas.getStarted;
  input C$ y x1-x10;
  datalines;
  D 0 10.2 6 1.6 38 15 2.4 20 0.8 8.5 3.9
  F 1 12.2 6 2.6 42 61 1.5 10 0.6 8.5 0.7
  D 1 7.7 1 2.1 38 61 1 90 0.6 7.5 5.2
  J 1 10.9 7 3.5 46 42 0.3 0 0.2 6 3.6
  E 0 17.3 6 3.8 26 47 0.9 10 0.4 1.5 4.7
  A 0 18.7 4 1.8 2 34 1.7 80 1 9.5 2.2
  B 0 7.2 1 0.3 48 61 1.1 10 0.8 3.5 4
  D 0 0.1 3 2.4 0 65 1.6 70 0.8 3.5 0.7
  H 1 2.4 4 0.7 38 22 0.2 20 0 3 4.2
  J 0 15.6 7 1.4 0 98 0.3 0 1 5 5.2
  J 0 11.1 3 2.4 42 55 2.2 60 0.6 4.5 0.7
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<td>31</td>
<td>2.4</td>
<td>10</td>
<td>0.2</td>
<td>7</td>
<td>1.6</td>
</tr>
<tr>
<td>J</td>
<td>0</td>
<td>13</td>
<td>1</td>
<td>1.8</td>
<td>14</td>
<td>11</td>
<td>2.3</td>
<td>50</td>
<td>0.6</td>
<td>5.5</td>
<td>2.6</td>
</tr>
<tr>
<td>A</td>
<td>0</td>
<td>17.9</td>
<td>4</td>
<td>3.1</td>
<td>46</td>
<td>58</td>
<td>2.6</td>
<td>90</td>
<td>0.6</td>
<td>1.5</td>
<td>3.2</td>
</tr>
<tr>
<td>D</td>
<td>1</td>
<td>19.4</td>
<td>6</td>
<td>3</td>
<td>20</td>
<td>50</td>
<td>2.8</td>
<td>100</td>
<td>0.2</td>
<td>9</td>
<td>1.2</td>
</tr>
<tr>
<td>I</td>
<td>0</td>
<td>19.6</td>
<td>3</td>
<td>3.6</td>
<td>22</td>
<td>19</td>
<td>1.2</td>
<td>0</td>
<td>0.6</td>
<td>5</td>
<td>4.1</td>
</tr>
<tr>
<td>I</td>
<td>1</td>
<td>6.2</td>
<td>1</td>
<td>1.5</td>
<td>30</td>
<td>30</td>
<td>2.2</td>
<td>20</td>
<td>0.4</td>
<td>8.5</td>
<td>5.3</td>
</tr>
<tr>
<td>G</td>
<td>0</td>
<td>13.8</td>
<td>1</td>
<td>2.7</td>
<td>0</td>
<td>52</td>
<td>2.4</td>
<td>20</td>
<td>0.8</td>
<td>6</td>
<td>2</td>
</tr>
<tr>
<td>B</td>
<td>0</td>
<td>14.3</td>
<td>4</td>
<td>2.9</td>
<td>30</td>
<td>11</td>
<td>0.6</td>
<td>90</td>
<td>0.6</td>
<td>0.5</td>
<td>4.9</td>
</tr>
<tr>
<td>E</td>
<td>0</td>
<td>15.6</td>
<td>0</td>
<td>0.4</td>
<td>38</td>
<td>79</td>
<td>0.4</td>
<td>80</td>
<td>0.4</td>
<td>1</td>
<td>3.3</td>
</tr>
<tr>
<td>D</td>
<td>0</td>
<td>14</td>
<td>2</td>
<td>1</td>
<td>22</td>
<td>61</td>
<td>3</td>
<td>90</td>
<td>0.6</td>
<td>2</td>
<td>0.1</td>
</tr>
<tr>
<td>C</td>
<td>1</td>
<td>9.4</td>
<td>5</td>
<td>0.4</td>
<td>12</td>
<td>53</td>
<td>1.7</td>
<td>40</td>
<td>0</td>
<td>3</td>
<td>1.1</td>
</tr>
<tr>
<td>H</td>
<td>0</td>
<td>13.2</td>
<td>1</td>
<td>1.6</td>
<td>40</td>
<td>15</td>
<td>0.7</td>
<td>40</td>
<td>0.2</td>
<td>9</td>
<td>5.5</td>
</tr>
<tr>
<td>A</td>
<td>0</td>
<td>13.5</td>
<td>5</td>
<td>2.4</td>
<td>18</td>
<td>89</td>
<td>1.6</td>
<td>20</td>
<td>0.4</td>
<td>9.5</td>
<td>4.7</td>
</tr>
<tr>
<td>E</td>
<td>0</td>
<td>2.6</td>
<td>4</td>
<td>2.3</td>
<td>38</td>
<td>6</td>
<td>0.8</td>
<td>20</td>
<td>0.4</td>
<td>5</td>
<td>5.3</td>
</tr>
<tr>
<td>E</td>
<td>0</td>
<td>12.4</td>
<td>3</td>
<td>1.3</td>
<td>26</td>
<td>8</td>
<td>2.8</td>
<td>10</td>
<td>0.8</td>
<td>6</td>
<td>5.8</td>
</tr>
</tbody>
</table>
Unsupervised Variable Selection

The following statements use PROC VARREDUCE for unsupervised variable selection:

```
proc varreduce data=mycas.getStarted technique=VarianceAnalysis;
   class C;
   reduce unsupervised C x1-x10 / maxeffects=5 varexp=0.99;
run;
```

The TECHNIQUE= option in the PROC VARREDUCE statement specifies variance analysis as the technique to be used for variable selection. In the REDUCE statement, the MAXEFFECTS= option specifies 5 as the maximum number of variables to select, and the VAREXP= option specifies 99% as the maximum percentage of the total variance to explain. The procedure stops when either of these two conditions is satisfied.

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.
The output from this analysis is presented in Figure 22.1 through Figure 22.3. Figure 22.1 displays the “Number of Observations” tables. This table shows that all 100 observations in the data table are used in the analysis.

**Figure 22.1** Number of Observations

The VARREDUCE Procedure

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>100</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Used</td>
<td>100</td>
</tr>
</tbody>
</table>

Figure 22.2 and Figure 22.3 show the “Selection Summary” and “Selected Effects” tables. The “Selection Summary” table shows which variable (or level for CLASS variables) is selected in each step, in addition to showing the total variance that is explained by the variables selected so far. The “Selected Effects” table presents all the selected variables and their corresponding variable types.

**Figure 22.2** Selection Summary

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Parameter</th>
<th>Proportion of Variance Explained</th>
<th>SSE</th>
<th>MSE</th>
<th>AIC</th>
<th>AICC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>x3</td>
<td>0.068102</td>
<td>18.637953</td>
<td>0.188262</td>
<td>7.105200</td>
<td>27.216339</td>
<td>2.971252</td>
</tr>
<tr>
<td>2</td>
<td>x7</td>
<td>0.132579</td>
<td>17.348424</td>
<td>0.177025</td>
<td>6.993502</td>
<td>26.094008</td>
<td>2.945605</td>
</tr>
<tr>
<td>3</td>
<td>x10</td>
<td>0.193293</td>
<td>16.134131</td>
<td>0.166331</td>
<td>6.860937</td>
<td>24.945494</td>
<td>2.919092</td>
</tr>
<tr>
<td>4</td>
<td>C I</td>
<td>0.252883</td>
<td>14.942348</td>
<td>0.155649</td>
<td>6.704199</td>
<td>23.767490</td>
<td>2.888406</td>
</tr>
<tr>
<td>5</td>
<td>C F</td>
<td>0.311964</td>
<td>13.760728</td>
<td>0.144850</td>
<td>6.521819</td>
<td>22.558528</td>
<td>2.852077</td>
</tr>
<tr>
<td>6</td>
<td>C J</td>
<td>0.368951</td>
<td>12.620982</td>
<td>0.134266</td>
<td>6.315361</td>
<td>21.320171</td>
<td>2.811671</td>
</tr>
<tr>
<td>7</td>
<td>C B</td>
<td>0.425720</td>
<td>11.485609</td>
<td>0.123501</td>
<td>6.081095</td>
<td>20.048690</td>
<td>2.763457</td>
</tr>
<tr>
<td>8</td>
<td>C G</td>
<td>0.481257</td>
<td>10.374861</td>
<td>0.112770</td>
<td>5.819386</td>
<td>18.744449</td>
<td>2.707799</td>
</tr>
<tr>
<td>9</td>
<td>C D</td>
<td>0.535098</td>
<td>9.298037</td>
<td>0.102176</td>
<td>5.529803</td>
<td>17.407018</td>
<td>2.644269</td>
</tr>
<tr>
<td>10</td>
<td>C H</td>
<td>0.588910</td>
<td>8.221792</td>
<td>0.091353</td>
<td>5.206788</td>
<td>16.030839</td>
<td>2.567305</td>
</tr>
<tr>
<td>11</td>
<td>C A</td>
<td>0.640665</td>
<td>7.186698</td>
<td>0.080749</td>
<td>4.852232</td>
<td>14.617801</td>
<td>2.478801</td>
</tr>
<tr>
<td>12</td>
<td>x5</td>
<td>0.691609</td>
<td>6.167815</td>
<td>0.070089</td>
<td>4.459345</td>
<td>13.161117</td>
<td>2.371965</td>
</tr>
</tbody>
</table>

**Figure 22.3** Selected Effects

<table>
<thead>
<tr>
<th>Selected Effects</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Selected Number</strong></td>
</tr>
<tr>
<td>1</td>
</tr>
<tr>
<td>2</td>
</tr>
<tr>
<td>3</td>
</tr>
<tr>
<td>4</td>
</tr>
<tr>
<td>5</td>
</tr>
</tbody>
</table>
### Supervised Variable Selection

The following statements use PROC VARREDUCE for supervised variable selection. The CLASS statement specifies that `y` is a categorical response variable. The TECHNIQUE= option specifies discriminant analysis as the technique to be used for variable selection. The MAXEFFECTS= option in the REDUCE statement specifies 5 as the maximum number of variables to select.

```plaintext
proc varreduce data=mycas.getStarted technique=DiscriminantAnalysis;
   class C y;
   reduce supervised y = C x1-x10 / maxeffects=5;
run;
```

The output from this analysis is presented in Figure 22.4 through Figure 22.6.

Figure 22.4 shows that all 100 observations in the data table are used in the analysis.

**Figure 22.4** Number of Observations

The **VARREDUCE Procedure**

<table>
<thead>
<tr>
<th>Number of Observations Read</th>
<th>100</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of Observations Used</td>
<td>100</td>
</tr>
</tbody>
</table>

Figure 22.5 and Figure 22.6 show the “Selection Summary” and “Selected Effects” tables. The “Selection Summary” table shows which variable (or level for CLASS variables) is selected in each step, in addition to showing the total variance that is explained by the variables selected so far. The “Selected Effects” table presents all the selected variables and their corresponding variable types.

**Figure 22.5** Selection Summary

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Parameter</th>
<th>Proportion of Variance Explained</th>
<th>SSE</th>
<th>MSE</th>
<th>AIC</th>
<th>ACC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>C J</td>
<td>0.081099 0.918901</td>
<td>0.009282</td>
<td>0.015424</td>
<td>2.019590</td>
<td>-0.038525</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>x8</td>
<td>0.132303 0.867697</td>
<td>0.008854</td>
<td>-0.001913</td>
<td>2.005456</td>
<td>-0.049809</td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>x2</td>
<td>0.168747 0.831253</td>
<td>0.008570</td>
<td>-0.004821</td>
<td>2.006669</td>
<td>-0.046665</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>C C</td>
<td>0.199152 0.800848</td>
<td>0.008342</td>
<td>-0.002084</td>
<td>2.014475</td>
<td>-0.037877</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>x4</td>
<td>0.218366 0.781634</td>
<td>0.008228</td>
<td>0.013631</td>
<td>2.036240</td>
<td>0.016110</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>x9</td>
<td>0.236688 0.763132</td>
<td>0.008118</td>
<td>0.029676</td>
<td>2.059346</td>
<td>0.005986</td>
<td></td>
</tr>
</tbody>
</table>

**Figure 22.6** Selected Effects

<table>
<thead>
<tr>
<th>Selected Effects Number</th>
<th>Selected Variable</th>
<th>Variable Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>C</td>
<td>CLASS</td>
</tr>
<tr>
<td>2</td>
<td>x8</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>3</td>
<td>x2</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>4</td>
<td>x4</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>5</td>
<td>x9</td>
<td>INTERVAL</td>
</tr>
</tbody>
</table>
PROC VARREDUCE Statement

The following statements are available in the VARREDUCE procedure:

```plaintext
PROC VARREDUCE < options > ;
   CLASS variable < (options) > . . . variable < (options) > ;
   DISPLAY < table-list > < /options > ;
   DISPLAYOUT table-spec-list < /options > ;
   REDUCE UNSUPERVISED effects < / reduce-options > ;
   REDUCE SUPERVISED response . . . < response > = effects < / reduce-options > ;
   FREQ variable ;
```

The PROC VARREDUCE statement and one REDUCE statement are required. The CLASS statement can appear multiple times. If a CLASS statement is specified, it must precede the REDUCE statement.

### PROC VARREDUCE Statement

**PROC VARREDUCE < options > ;**

The PROC VARREDUCE statement invokes the procedure. Table 22.1 summarizes the important options in the PROC VARREDUCE statement by function. The options are then described fully in alphabetical order.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Basic Options</strong></td>
<td></td>
</tr>
<tr>
<td>DATA=</td>
<td>Specifies the input data table</td>
</tr>
</tbody>
</table>

#### Options Related to Variable Selection

- **NOPRINT** suppresses ODS output
- **MATRIX=** specifies the matrix to use to select variables
- **TECHNIQUE=** selects the variable selection technique
- **OUTCP=** outputs the CORR, COV, or SSCP matrix, which is specified in the MATRIX= option

#### Options for Multithreads

You can specify the following *options*:

**DATA=** *CAS-libref.data-table*

names the input data table for PROC VARREDUCE to use. The default is the most recently created data table. *CAS-libref.data-table* is a two-level name, where

- **CAS-libref** refers to a collection of information that is defined in the LIBNAME statement and includes the caslib, which includes a path to the data, and a session identifier, which
Chapter 22: The VARREDUCE Procedure

defaults to the active session but which can be explicitly defined in the LIBNAME statement. For more information about CAS-libref, see the section “Using CAS Sessions and CAS Engine Librefs” on page 997.

data-table specifies the name of the input data table.

`MATRIX=CORR | COV | SSCP`

specifies which matrix to use to select variables.

You can specify the following values:

CORR selects variables based on the Pearson correlation matrix. Assuming that $X$ and $Y$ are two variables, the correlation between $X$ and $Y$ is computed by

$$\text{Corr}(X, Y) = \frac{E((X - E(X))(Y - E(Y)))}{\sqrt{E((X - E(X))^2)} \sqrt{E((Y - E(Y))^2)}}$$

COV selects variables based on the covariance matrix. Assuming that $X$ and $Y$ are two variables, the covariance between $X$ and $Y$ is computed by

$$\text{Cov}(X, Y) = E((X - E(X))(Y - E(Y)))$$

SSCP selects variables based on the sums of squares and crossproducts matrix. Assuming that $X$ and $Y$ are two variables and that $x$ and $y$ are their corresponding variable vectors, the SSCP between $X$ and $Y$ is computed by

$$\text{SSCP}(X, Y) = x^T y$$

By default, `MATRIX=CORR`.

`NOPRINT` suppresses the generation of ODS output.

`OUTCP=CAS-libref.data-table < / LIST < EPS = number >>`

creates a data table that contains a symmetric matrix that depicts the relationships among variables and also creates a set of statistics about the input data table and variables. `CAS-libref.data-table` is a two-level name, where `CAS-libref` refers to the caslib and session identifier, and `data-table` specifies the name of the output data table. For more information about this two-level name, see the DATA= option and the section “Using CAS Sessions and CAS Engine Librefs” on page 997. Depending on the value of the `MATRIX=` option, the symmetric matrix can be a correlation (CORR) matrix, a covariance (COV) matrix, or a sums of squares and crossproducts (SSCP) matrix.

When you specify the LIST option, the symmetric matrix is output in the list-of-list (LIL) format. In this format, the matrix is represented as a set of tuples $(i, j, x)$, where $x$ is an entry in the matrix and $i$ and $j$ denote its row and column indices, respectively. LIL format can be used when the output contains too many columns to fit in a data table. For example, in most database systems, the maximum number of columns in a table is usually limited to several thousand. If an output matrix contains more columns than the limit, you must use the LIST option to avoid errors that would arise from writing too many columns to the table. When LIL format is used, all 0 entries in the matrix are ignored in the output.

When you specify EPS= `number` in the LIST suboption, matrix entries whose absolute value is smaller than `number` are ignored in the output. This feature helps omit unreliable estimations and generate a compact representation of the matrix. When you do not specify the EPS= option, only the 0 entries in the matrix are ignored in the output.
TECHNIQUE=keyword

specifies the variable selection technique.

You can specify the following keywords:

VARIANCEANALYSIS | VAR performs variance analysis for variable selection.

DISCRIMINANTANALYSIS | DSC performs discriminant analysis for variable selection.

By default, TECHNIQUE=VAR.

You can use variance analysis for both supervised and unsupervised variable selection. You can use discriminant analysis only for supervised variable selection that uses one classification variable as the response. For more information, see the section “Variable Selection for Classification” on page 1011.

CLASS Statement

CLASS variable < (options)> . . . < variable < (options)> > </ global-options> ;

The CLASS statement names the classification variables to be used as explanatory variables in the analysis. The CLASS statement must precede the REDUCE statement.

The VARREDUCE procedure supports the GLM method of CLASS variable parameterization; for more information, see the section “GLM Parameterization of Classification Variables and Effects” on page 1013.

You can specify options either as individual variable options, by enclosing the options in parentheses after the variable name, or as global-options, by placing them after a slash (/). Global-options are applied to all variables that are specified in the CLASS statement. If you specify more than one CLASS statement, the global-options that are specified in any one CLASS statement apply to all CLASS statements. However, individual CLASS variable options override the global-options.

Table 22.2 summarizes the values you can use for either an option or a global-option. The options are described in detail in the list that follows Table 22.2.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>DESCENDING</td>
<td>Reverses the sort order</td>
</tr>
<tr>
<td>MISSING</td>
<td>Treats missing values as valid levels</td>
</tr>
</tbody>
</table>

DESCENDING

DESC

reverses the sort order of the classification variable.

MISSING

treats missing values (".", ".A", . . . , ".Z" for numeric variables and blanks for character variables) as valid values for the CLASS variable.
If you do not specify the MISSING option, observations that have missing values for CLASS variables are removed from the analysis.

---

**DISPLAY Statement**

```plaintext
DISPLAY < table-list > < / options > ;
```

The DISPLAY statement enables you to specify a list of display tables to display or exclude. This statement is similar to the ODS SELECT, ODS EXCLUDE, and ODS TRACE statements. However, the DISPLAY statement can improve performance when a large number of tables could be generated (such as in BY-group processing). The procedure processes the DISPLAY statement on a CAS server and thus sends only a subset of ODS tables to the SAS client. Because ODS statements are processed on a SAS client, first all the generated display tables are sent to the client, and then the client creates a subset.

If you use both DISPLAY and ODS statements together, the DISPLAY statement takes precedence over the ODS statements. Note that the ODS EXCLUDE statement processes tables that are sent to the client after they have been filtered by the DISPLAY statement. In some cases, it might appear that the ODS EXCLUDE statement is taking precedence because it can further filter the tables. For more information about ODS, see *SAS Output Delivery System: Procedures Guide*.

You can specify the `table-list` as a list of table names, paths, partial pathnames, and regular expressions.

The table names that you can specify are listed in the section “ODS Table Names” on page 1018. A path is a table name that is prefixed with dot-separated grouping information. For example, a SelectionSummary table that a procedure produces during a selection routine might have the path `Bygroup1.Summary.SelectionSummary`. A partial pathname does not include all groups; for example, `SelectionSummary` and `Summary.SelectionSummary` are partial pathnames for `Bygroup1.Summary.SelectionSummary`.

When you specify a table name or partial pathname, all display tables whose paths end in the specified name are selected for display or exclusion. For example, both `SelectionSummary` and `Summary.SelectionSummary` select `Bygroup1.Summary.SelectionSummary`.

A regular expression is enclosed in forward slashes (/). For example, specifying `/*tions/` selects all pathnames that contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is selected. Specifying `!/tions/` selects all pathnames that do not contain the substring “tions”; in particular, the `Bygroup1.Summary.SelectionSummary` table is not selected.

You can specify the following `options` after a slash (/):

- **CASESENSITIVE**
  - performs a case-sensitive comparison of table names in the `table-list` to display table names when tables are subsetted for display. To preserve case, you must enclose table names in the `table-list` in quotation marks.

- **EXCLUDE**
  - displays all display tables except those that you specify in the `table-list`.

- **EXCLUDEALL**
  - suppresses display of all tables. This option takes precedence over the other options.
TRACE
  displays the display table names, labels, and paths.

DISPLAYOUT Statement

DISPLAYOUT table-spec-list < / options > ;

The DISPLAYOUT statement enables you to create CAS output tables from your displayed output. This statement is similar to the ODS OUTPUT statement. For more information about ODS, see SAS Output Delivery System: Procedures Guide.

The table-spec-list specifies a list of CAS output tables to create. Each entry in the list has either a key=value format or a key format:

- key=value specifies key as the ODS table name, path, or partial pathname, and specifies value as the CAS output table name.
- key specifies key as the ODS table name and also as the CAS output table name.

Table names and partial pathnames are discussed under the DISPLAY statement. The DISPLAYOUT statement does not support regular expressions.

You can specify the following options after a slash (/):

- INCLUDEALL
  creates output CAS tables for all display tables. The name of the created output CAS table is the same as the corresponding display table name. If you specify this option, the table-spec-list specification is ignored.

- NOREPLACE
  does not replace any existing CAS output table of the same name.

- REPEATED
  replicates all CAS output tables on all nodes.

FREQ Statement

FREQ variable ;

The variable in the FREQ statement identifies a numeric variable in the data set that contains the frequency of occurrence of each observation. PROC VARREDUCE treats each observation as if it appears \( f \) times, where \( f \) is the value of the FREQ variable for the observation. If \( f \) is not an integer, it is truncated to an integer. If \( f \) is less than 1 or missing, the observation is not used in the analysis. When the FREQ statement is not specified, each observation is assigned a frequency of 1.
Chapter 22: The VARREDUCE Procedure

REDUCE Statement

**REDUCE UNSUPERVISED** effects < / reduce-options > ;

**REDUCE SUPERVISED** response-variable < response-variable > . . . = effects < / reduce-options > ;

PROC VARREDUCE can be used for either of the following types of variable selection:

- For unsupervised variable selection, you specify the **effects** to be considered in the variable selection process. An **effect** can be an original variable in the input data table or a variable that is constructed from the original variables.

- For supervised variable selection, you specify both the **effects** and one or more **response-variables**. A **response-variable** can be an original variable in the input data table or a variable that is constructed from the original variables. PROC VARREDUCE supports variable selection both in a classification (categorization) context, in which you specify one **response-variable**, and in a regression context, in which you can specify more than one **response-variable**.

Table 22.3 summarizes the **reduce-options**, which control the number of variables to be selected.

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIC</td>
<td>Uses Akaike’s information criterion to perform model selection</td>
</tr>
<tr>
<td>AICC</td>
<td>Uses the corrected Akaike’s information criterion to perform model selection</td>
</tr>
<tr>
<td>BIC</td>
<td>Uses Schwarz Bayesian information criterion to perform model selection</td>
</tr>
<tr>
<td>MAXITER</td>
<td>MAXSTEPS=</td>
</tr>
<tr>
<td>MAXEFFECTS=</td>
<td>Specifies the number of effects to select; the number must be greater than or equal to 1.</td>
</tr>
<tr>
<td>VARIANCEEXPLAINED</td>
<td>VAREXP=</td>
</tr>
<tr>
<td>MINVARIANCEINCREMENT</td>
<td>VARINC=</td>
</tr>
</tbody>
</table>

The **reduce-options** determine the number of variables to be selected. You can specify the following **reduce-options** as stopping criteria for the VARREDUCE procedure. When you specify more than one option, PROC VARREDUCE stops whenever one of the specified options is satisfied, or when the explained variance equals the total variance. In the latter case, the procedure prints the following message in the log: “Early stop: the proportion of the explained variance to the total variance equals 1.”

You can specify the following **reduce-options** only for supervised variable selection:
AIC
stops PROC VARREDUCE if the Akaike’s information criterion (AIC) value fails to decrease in three contiguous steps.

AICC
stops PROC VARREDUCE if the corrected Akaike’s information (AICC) value fails to decrease in three contiguous steps.

BIC
stops PROC VARREDUCE if the Schwarz Bayesian information criterion (BIC) value fails to decrease in three contiguous steps.

You can specify the following reduce-options for both supervised and unsupervised variable selection:

MAXITER=n
MAXSTEPS=n
stops PROC VARREDUCE after it runs n steps.

MAXEFFECTS=n
stops PROC VARREDUCE after n effects have been selected. Because individual levels of one classification variable can be selected in different steps of the variable selection process, selecting n effects might require more steps than are specified by the value of MAXITER= option.

VARIANCEEXPLAINED=fraction
VAREXP=fraction
stops PROC VARREDUCE when the fraction of the total variance can be explained by the selected variables.

MINVARIANCEINCREMENT=fraction
VARINC=fraction
stops PROC VARREDUCE when the minimum increment of the explained variance is less than fraction of the total variance.

Details: VARREDUCE Procedure
The performance of a learning model usually decreases in terms of accuracy and efficiency when the dimensionality of the input data is high. The problem is known as the “curse of dimensionality.” Variable selection techniques can reduce the dimensionality of data by removing irrelevant and redundant variables (Liu and Motoda 1998).

The VARREDUCE procedure performs both supervised and unsupervised variable selection. It selects variables by identifying a set of variables that can jointly explain the maximum amount of data variance.

Missing Values
Any observation that has missing values for the responses, frequency, or effects is excluded from the analysis; however, missing values are valid for responses and effects if the MISSING option is specified in the CLASS statement. Observations that have a frequency less than 1 are also excluded.
Unsupervised Variable Selection

When no response variable is specified, PROC VAREDUCTE conducts unsupervised variable selection. Assume that \( k \) variables need to be selected. Let \( X \in \mathbb{R}^{n \times m} \) be a data table that contains \( n \) samples and \( m \) variables; let \( X = (X_1, X_2) \), where \( X_1 \in \mathbb{R}^{n \times k} \) contains the \( k \) selected variables and \( X_2 \in \mathbb{R}^{n \times (m-k)} \) contains the remaining \( m-k \) variables. PROC VAREDUCTE selects the variables by minimizing the following equation:

\[
\min \text{Trace} \left( X_2^T \left( I - X_1 \left( X_1^T X_1 \right)^{-1} X_1^T \right) X_2 \right)
\]

\( \left( I - X_1 \left( X_1^T X_1 \right)^{-1} X_1^T \right)^{1/2} \) projects \( X_2 \) to the null space of \( X_1 \). Therefore, the preceding equation measures the data variance that resides in the null space of \( X_1 \), which is the data variance that cannot be explained by the variables in \( X_1 \). Minimizing this equation leads to the selection of the variables that jointly explain the maximum amount of the variance in the original data.

Let \( C_{11} = X_1^T X_1 \), \( C_{12} = X_1^T X_2 \), and \( C_{21} = X_2^T X_1 \). The following equations hold:

\[
C = X^T X = \begin{pmatrix} C_{11} & C_{12} \\ C_{21} & C_{22} \end{pmatrix}
\]

\[
X_2^T \left( I - X_1 \left( X_1^T X_1 \right)^{-1} X_1^T \right) X_2 = C_{22} - C_{21} C_{11}^{-1} C_{12}
\]

When all the variables are centralized to have a zero mean, \( C \) is the covariance matrix. This corresponds to specifying MATRIX=COV in the PROC VAREDUCTE statement, which requests that the covariance matrix be used for variable selection. Similarly, if variables need to be both centralized and normalized to have unit length, you should specify MATRIX=CORR in the PROC VAREDUCTE statement, which requests that the correlation matrix be used for variable selection. If neither centralization nor normalization should be applied, specify MATRIX=SSCP in the PROC VAREDUCTE statement.

Principal component analysis (PCA) (Jolliffe 2002) also reduces dimensionality by preserving data variance. The key difference between PCA and PROC VAREDUCTE is that PCA generates a small set of new variables (variable extraction) by linearly combining the original variables, whereas PROC VAREDUCTE selects a small set of the original variables (variable selection). The variables returned by PROC VAREDUCTE are the original variables. This feature is very important in applications where retaining the original variables is important for model exploration or interpretation (for example, genetic analysis and text mining).

Supervised Variable Selection

When response variables are specified in a REDUCE statement, PROC VAREDUCTE conducts supervised variable selection, either in a regression context or in a classification (categorization) context.

Variable Selection for Regression

In a regression context, all response variables should be numerical. When the response is a classification variable, it needs to be levelized to multiple dummy variables, where each dummy variable corresponds to a
level of the classification variable. You can achieve this levelization by adding this variable to the variable list in the CLASS statement.

Let $Y \in \mathbb{R}^{n \times t}$ be the response data that contain $t$ response variables. Assume that $k$ variables need to be selected. Let $X \in \mathbb{R}^{n \times m}$ be a data table that contains $n$ samples and $m$ variables; let $X = (X_1, X_2)$, where $X_1 \in \mathbb{R}^{n \times k}$ contains the $k$ selected variables and $X_2 \in \mathbb{R}^{n \times (m-k)}$ contains the remaining $m-k$ variables. PROC VARREDUCE selects the variables by minimizing the following equation:

$$
\min \text{Trace} \left( Y^T \left( I - X_1 \left( X_1^T X_1 \right)^{-1} X_1^T \right) Y \right)
$$

$\left( I - X_1 \left( X_1^T X_1 \right)^{-1} X_1^T \right)^{1/2} Y$ projects $Y$ onto the null space of $X_1$. Therefore, the equation measures the response variance that resides in the null space of $X_1$, which is the variance of the response variables that cannot be explained by the variables in $X_1$. Minimizing the equation leads to the selection of the variables that jointly explain the maximum amount of the variance of the response variables.

### Variable Selection for Classification

In a classification context, one classification variable is specified as the response, and each of its levels corresponds to a category of the classification problem. Let the classification variable be $y$ with $c$ levels $\{1, \ldots, c\}$. Then $y$ can be levelized in a special way to generate response data $Y \in \mathbb{R}^{n \times c}$ as:

$$
Y_{i,j} = \begin{cases}
\frac{1}{\sqrt{n}} \left( \sqrt{\frac{n}{n_j}} - \sqrt{\frac{n}{n}} \right), & y_i = j \\
-\frac{1}{\sqrt{n}} \sqrt{\frac{n_j}{n}}, & y_i \neq j
\end{cases}
$$

By using this $Y$ in the variance analysis, PROC VARREDUCE selects variables by using the discriminant criterion that is specified in linear discriminant analysis (LDA) (Fisher 1936; Cooley and Lohnes 1971). LDA also reduces dimensionality. The key difference between LDA and PROC VARREDUCE is that LDA generates a small set of new variables (variable extraction) by linearly combining the original variables, whereas PROC VARREDUCE selects a small set of the original variables (variable selection).

### Criteria Used in Model Selection

The VARREDUCE procedure supports the following three fit statistics that you can specify as stopping criteria in the REDUCE statement. These statistics are produced only for the supervised variable selection:

- **AIC** Akaike’s information criterion (Akaike 1969; Judge et al. 1985)
- **AICC** Corrected Akaike’s information criterion (Hurvich and Tsai 1989)
- **BIC** Schwarz Bayesian information criterion (Schwarz 1978; Judge et al. 1985)

The VARREDUCE procedure supports multiple response variables; therefore, it computes the AIC, AICC, and BIC that are defined for multivariate regression. Besides the three criteria, it also computes the error sum of squares (SSE) and residual mean square error (MSE).

Table 22.4 provides formulas and definitions for these fit statistics.
### Table 22.4  Formulas and Definitions for Model Fit Summary Statistics

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Definition or Formula</th>
</tr>
</thead>
<tbody>
<tr>
<td>( n )</td>
<td>Number of observations</td>
</tr>
<tr>
<td>( p )</td>
<td>Number of parameters</td>
</tr>
<tr>
<td>( t )</td>
<td>Number of response variables in supervised selection; number of unselected variables in unsupervised selection</td>
</tr>
<tr>
<td>SSE</td>
<td>Error sum of squares</td>
</tr>
<tr>
<td>MSE</td>
<td>( \frac{SSE}{n-p} )</td>
</tr>
<tr>
<td>AIC</td>
<td>( \ln (SSE) + \frac{2pt + t(t + 1)}{n} )</td>
</tr>
<tr>
<td>AICC</td>
<td>( \ln (SSE) + \frac{(n + p)t}{n - p - t - 1} )</td>
</tr>
<tr>
<td>BIC</td>
<td>( \ln (SSE) + \frac{p \ln(n)}{n} )</td>
</tr>
</tbody>
</table>

### Computational Method

Given \( m \) variables, finding the \( k \) variables that minimize the proposed equations is a combinatorial problem, which is NP-hard (nondeterministic polynomial-time hard). To select \( k \) variables, PROC VARREDUCE applies \( k \) steps of a greedy search to generate a suboptimal solution for the problem.

Assume that \( q \) features have been selected, that \( X_1 \) contains the \( q \) selected variables, and that \( X_2 \) contains the remaining variables. PROC VARREDUCE selects the \( q + 1 \) variable, \( F \), by minimizing the equation

\[
\arg \min_F \text{Trace}
\left[
\hat{X}_2^T \left(I - \hat{X}_1 \left(\hat{X}_1^T \hat{X}_1\right)^{-1} \hat{X}_1^T\right) \hat{X}_2\right]
\]

where \( \hat{X}_1 \) is the data table that contains the feature \( F \) and the \( q \) selected variables, and \( \hat{X}_2 \) is the data table that contains the remaining variables. Minimizing the preceding problem is equivalent to maximizing the following problem:

\[
\left\| X_2^T \left(I - X_1 \left(X_1^T X_1\right)^{-1} X_1^T\right) f \right\|_2^2
\]

\[
\left\| \left(I - X_1 \left(X_1^T X_1\right)^{-1} X_1^T\right)^{\frac{1}{2}} f \right\|_2^2
\]

In the preceding equation, \( \left\| X_2^T \left(I - X_1 \left(X_1^T X_1\right)^{-1} X_1^T\right) f \right\|_2^2 \) is the summation of the squares of the covariance between the variable \( f \) and all the unselected variables in the null space of \( X_1 \). And \( \left\| \left(I - X_1 \left(X_1^T X_1\right)^{-1} X_1^T\right)^{\frac{1}{2}} f \right\|_2^2 \) is the square of the variance of \( f \) in the null space of \( X_1 \), which is used as a normalization factor.
This problem can be solved efficiently. Assuming that \( m \gg k \), the time complexity for solving it is

\[
O \left( m^2 (n + k^2) \right)
\]

where \( m \) is the number of variables, \( n \) is the number of samples, and \( k \) is the number of selected variables. In the equation, \( m^2 n \) corresponds to the time for computing the covariance (or correlation or SSCP) matrix. And \( m^2 k^2 \) corresponds to the time for selecting \( k \) variables out of \( m \).

Similar analysis also applies to supervised variable selection with PROC VAREDUCE. The following problem is maximized for supervised variable selection:

\[
\left\| Y^\top \left( I - X_1 (X_1^\top X_1)^{-1} X_1^\top \right) f \right\|_2^2 \\
\left\| \left( I - X_1 (X_1^\top X_1)^{-1} X_1^\top \right)^{1/2} f \right\|_2^2
\]

Here, \( Y \) is the response data table. Let \( c \) be the number of columns in \( Y \). The time complexity for selecting \( k \) variables by solving the preceding problem is

\[
O \left( k^2 (c + k) m + m^2 n \right)
\]

Note that for most data of very high dimensionality, \( c + k \ll m \).

PROC VAREDUCE is fully threaded and distributed. When there are \( p \) machines used for computing, the time complexity for unsupervised variable selection is

\[
\text{CPU} \left( \frac{m^2 (n + k^2)}{p} + m^2 \log p \right) + \text{NET} \left( m^2 \log p \right)
\]

and the time complexity for supervised variable selection is

\[
\text{CPU} \left( \frac{k^2 (c + k) m + m^2 n}{p} + m^2 \log p \right) + \text{NET} \left( m^2 \log p \right)
\]

where CPU corresponds to the time used for computing and NET corresponds to the time used for communication among computers.

### Table 22.5 Available Types of Effects

<table>
<thead>
<tr>
<th>Effect</th>
<th>Example</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>Default</td>
<td>Intercept (unless the NOINT option is specified)</td>
</tr>
<tr>
<td>Regression</td>
<td>X Z</td>
<td>Continuous variables</td>
</tr>
<tr>
<td>Polynomial</td>
<td>X*Z</td>
<td>Interaction of continuous variables</td>
</tr>
</tbody>
</table>
Chapter 22: The VARREDUCE Procedure

<table>
<thead>
<tr>
<th>Effect</th>
<th>Example</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Main</td>
<td>A B</td>
<td>CLASS variables</td>
</tr>
<tr>
<td>Interaction</td>
<td>A*B</td>
<td>Crossing of CLASS variables</td>
</tr>
<tr>
<td>Nested</td>
<td>A(B)</td>
<td>Main effect A nested within CLASS effect B</td>
</tr>
<tr>
<td>Continuous-by-class</td>
<td>X*A</td>
<td>Crossing of continuous and CLASS variables</td>
</tr>
<tr>
<td>Continuous-nesting-class</td>
<td>X(A)</td>
<td>Continuous variable X1 nested within CLASS variable A</td>
</tr>
<tr>
<td>General</td>
<td>X<em>Z</em>A(B)</td>
<td>Combinations of different types of effects</td>
</tr>
</tbody>
</table>

Table 22.6 shows some examples of MODEL statements that use various types of effects.

<table>
<thead>
<tr>
<th>Specification</th>
<th>Type of Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>model Y=X;</td>
<td>Simple regression</td>
</tr>
<tr>
<td>model Y=X Z;</td>
<td>Multiple regression</td>
</tr>
<tr>
<td>model Y=X X*X;</td>
<td>Polynomial regression</td>
</tr>
<tr>
<td>model Y=A;</td>
<td>One-way analysis of variance (ANOVA)</td>
</tr>
<tr>
<td>model Y=A B C;</td>
<td>Main-effects ANOVA</td>
</tr>
<tr>
<td>model Y=A B A*B;</td>
<td>Factorial ANOVA with interaction</td>
</tr>
<tr>
<td>model y=A B(A) C(B A);</td>
<td>Nested ANOVA</td>
</tr>
<tr>
<td>model Y=A X;</td>
<td>Analysis of covariance (ANCOVA)</td>
</tr>
<tr>
<td>model Y=A X(A);</td>
<td>Separate-slopes regression</td>
</tr>
<tr>
<td>model Y=A X X*A;</td>
<td>Homogeneity-of-slopes regression</td>
</tr>
</tbody>
</table>

**Intercept**

By default, linear models that are created by the VARREDUCE procedure automatically include a column of 1s in X. This column corresponds to an intercept parameter. In many procedures, you can use the NOINT option in the MODEL statement to suppress this intercept. For example, the NOINT option is useful when the MODEL statement contains a classification effect and you want the parameter estimates to be in terms of the mean response for each level of that effect.

**Regression Effects**

Numeric variables or polynomial terms that involve them can be included in the model as regression effects (covariates). The actual values of such terms are included as columns of the relevant model matrices. You can use the bar operator along with a regression effect to generate polynomial effects. For example, X | X | X expands to X X*X X*X*X, which is a cubic model.

**Main Effects**

If a classification variable has m levels, the GLM parameterization generates m columns for its main effect in the model matrix. Each column is an indicator variable for a particular level. The order of the columns is the sort order of the values of their levels and can be controlled by the ORDER= option in the CLASS statement.
Table 22.7 is an example where $\beta_0$ denotes the intercept and A and B are classification variables that have two and three levels, respectively.

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>B</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>B</td>
<td>$\beta_0$</td>
<td>A1</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

There are usually more columns for these effects than there are degrees of freedom to estimate them. In other words, the GLM parameterization of main effects is *singular*.

**Interaction Effects**

Often a model includes interaction (crossed) effects to account for how the effect of a variable changes along with the values of other variables. With an interaction, the terms are first reordered to correspond to the order of the variables in the `CLASS` statement. Thus, B*A becomes A*B if A precedes B in the `CLASS` statement. Then, the GLM parameterization generates columns for all combinations of levels that occur in the data. The order of the columns is such that the rightmost variables in the interaction change faster than the leftmost variables (Table 22.8).

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>B</th>
<th>A*B</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
</tbody>
</table>

In the preceding matrix, main-effects columns are not linearly independent of crossed-effects columns. In fact, the column space for the crossed effects contains the space of the main effect.

When your model contains many interaction effects, you might be able to code them more parsimoniously by using the bar operator (|). The bar operator generates all possible interaction effects. For example, A|B|C expands to A B A*B C A*C B*C A*B*C. To eliminate higher-order interaction effects, use the at sign (@) in conjunction with the bar operator. For example, A|B|C|D@2 expands to A B A*B C A*C B*C D A*D B*D C*D.
**Nested Effects**

Nested effects are generated in the same manner as crossed effects. Hence, the design columns that are generated by the following two statements are the same (but the ordering of the columns is different):

```
model Y=A B(A);
model Y=A A*B;
```

The nesting operator in the VARREDUCE procedure is more of a notational convenience than an operation that is distinct from crossing. Nested effects are typically characterized by the property that the nested variables do not appear as main effects. The order of the variables within nesting parentheses is made to correspond to the order of these variables in the `CLASS` statement. The order of the columns is such that variables outside the parentheses index faster than those inside the parentheses, and the rightmost nested variables index faster than the leftmost variables (Table 22.9).

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>A1</td>
<td>A2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
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</tr>
<tr>
<td>1</td>
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<tr>
<td>2</td>
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</tr>
<tr>
<td>2</td>
<td>2</td>
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<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>2</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

**Continuous-Nesting-Class Effects**

When a continuous variable nests or crosses with a classification variable, the design columns are constructed by multiplying the continuous values into the design columns for the classification effect (Table 22.10).

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>A</th>
<th>β₀</th>
<th>A1</th>
<th>A2</th>
<th>X(A1)</th>
<th>X(A2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>21</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>21</td>
<td>0</td>
</tr>
<tr>
<td>24</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>24</td>
<td>0</td>
</tr>
<tr>
<td>22</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>22</td>
<td>0</td>
</tr>
<tr>
<td>28</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>28</td>
<td></td>
</tr>
<tr>
<td>19</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td>23</td>
<td>2</td>
<td>1</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>23</td>
<td></td>
</tr>
</tbody>
</table>

This model estimates a separate intercept and a separate slope for X within each level of A.
Continuous-by-Class Effects

Continuous-by-class effects generate the same design columns as continuous-nesting-class effects. Table 22.11 shows the construction of the $X*A$ effect. The two columns for this effect are the same as the columns for the $X(A)$ effect in Table 22.10.

<table>
<thead>
<tr>
<th>Data</th>
<th>I</th>
<th>X</th>
<th>A</th>
<th>X*A</th>
<th>X*A1</th>
<th>X*A2</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>A</td>
<td>β₀</td>
<td>X</td>
<td>A1</td>
<td>A2</td>
<td>X*A1</td>
</tr>
<tr>
<td>21</td>
<td>1</td>
<td>21</td>
<td>1</td>
<td>0</td>
<td>21</td>
<td>0</td>
</tr>
<tr>
<td>24</td>
<td>1</td>
<td>24</td>
<td>1</td>
<td>0</td>
<td>24</td>
<td>0</td>
</tr>
<tr>
<td>22</td>
<td>1</td>
<td>22</td>
<td>1</td>
<td>0</td>
<td>22</td>
<td>0</td>
</tr>
<tr>
<td>28</td>
<td>2</td>
<td>28</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>28</td>
</tr>
<tr>
<td>19</td>
<td>2</td>
<td>19</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>19</td>
</tr>
<tr>
<td>23</td>
<td>2</td>
<td>23</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>23</td>
</tr>
</tbody>
</table>

You can use continuous-by-class effects together with pure continuous effects to test for homogeneity of slopes.

General Effects

An example that combines all the effects is $X1*X2*A*B*(D E)$. The continuous list comes first, followed by the crossed list, followed by the nested list in parentheses.

Effects might be renamed by the procedure to correspond to ordering rules. For example, $B*A*(E D)$ might be renamed $A*B*(D E)$ to satisfy the following:

- Classification variables that occur outside parentheses (crossed effects) are sorted in the order in which they appear in the CLASS statement.
- Variables within parentheses (nested effects) are sorted in the order in which they appear in the CLASS statement.

The sequencing of the parameters that are generated by an effect is determined by the variables whose levels are indexed faster:

- Variables in the crossed list index faster than variables in the nested list.
- Within a crossed or nested list, variables to the right index faster than variables to the left.

For example, suppose that a model includes four effects—A, B, C, and D—each having two levels, 1 and 2, and that the CLASS statement is as follows:

```plaintext
class A B C D;
```
Then the order of the parameters for the effect $B*A(C\ D)$, which is renamed $A*B(C\ D)$, is as follows:

$$
A_1B_1C_1D_1 \rightarrow A_1B_2C_1D_1 \rightarrow A_2B_1C_1D_1 \rightarrow A_2B_2C_1D_1 \\
A_1B_1C_1D_2 \rightarrow A_1B_2C_1D_2 \rightarrow A_2B_1C_1D_2 \rightarrow A_2B_2C_1D_2 \\
A_1B_1C_2D_1 \rightarrow A_1B_2C_2D_1 \rightarrow A_2B_1C_2D_1 \rightarrow A_2B_2C_2D_1 \\
A_1B_1C_2D_2 \rightarrow A_1B_2C_2D_2 \rightarrow A_2B_1C_2D_2 \rightarrow A_2B_2C_2D_2
$$

Note that first the crossed effects $B$ and $A$ are sorted in the order in which they appear in the `CLASS` statement so that $A$ precedes $B$ in the parameter list. Then, for each combination of the nested effects in turn, combinations of $A$ and $B$ appear. The $B$ effect changes fastest because it is rightmost in the cross list. Then $A$ changes next fastest, and $D$ changes next fastest. The $C$ effect changes most slowly because it is leftmost in the nested list.

## Displayed Output

The following sections describe the output that PROC VARREDUCE produces by default. The output is organized into various tables, which are discussed in the order of appearance.

### Number of Observations

The “Number of Observations” table displays the number of observations read from the input data table and the number of observations used in the analysis.

### Selection Summary

The “Selection Summary” table displays for each iteration the name of the selected effect, the name of the selected level, and the total variance explained after the iteration.

### Selected Variables

The “Selected Variables” table summarizes which variables were selected in the selection process. It also provides information about the variable type of each selected variable.

## ODS Table Names

Each table that the VARREDUCE procedure creates has a name associated with it. You must use this name to refer to the table when you use ODS statements. The name of each table and a short description of the contents are listed in Table 22.12.

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>NObs</td>
<td>Number of observations read and used; number of events and trials, if applicable</td>
<td>PROC VARREDUCE</td>
<td>Default</td>
</tr>
</tbody>
</table>
Table 22.12  continued

<table>
<thead>
<tr>
<th>Table Name</th>
<th>Description</th>
<th>Statement</th>
<th>Option</th>
</tr>
</thead>
<tbody>
<tr>
<td>SelectedEffects</td>
<td>Summary of selected variables</td>
<td>PROC VARREDUCE</td>
<td>Default</td>
</tr>
<tr>
<td>SelectionSummary</td>
<td>Selection summary</td>
<td>PROC VARREDUCE</td>
<td>Default</td>
</tr>
</tbody>
</table>

Examples: VARREDUCE Procedure

**NOTE:** Input data must be in a CAS table that is accessible in your CAS session. You must refer to this table by using a two-level name. The first level must be a CAS engine libref, and the second level must be the table name. For more information, see the sections “Using CAS Sessions and CAS Engine Librefs” on page 8 and “Loading a SAS Data Set onto a CAS Server” on page 9 in Chapter 2, “Shared Concepts.”

Example 22.1: Analyzing Framingham Heart Study Data

This example analyzes the data from the Framingham Heart Study for feature selection, which are available in a data set named Heart in the Sashelp library.

You can load the Sashelp.Heart data set into your CAS session by naming your CAS engine libref in the first statement of the following DATA step:

```sas
data mycas.heart;
  set sashelp.heart;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements invoke the VARREDUCE procedure:

```sas
proc varreduce data=mycas.heart matrix=COV tech=DSC;
  ods output SelectionSummary=Summary;
  class Status Sex Chol_Status BP_Status Weight_Status Smoking_Status;
  reduce supervised Status = Sex AgeAtStart Height Weight Diastolic Systolic MRW Smoking Cholesterol Chol_Status BP_Status Weight_Status Smoking_Status/ maxiter=15 BIC;
  display 'SelectionSummary' 'SelectedEffects';
run;

proc sgplot data=Summary;
  series x=Iteration y=BIC;
run;
```

The TECH=DSC option in the PROC VARREDUCE statement requests a discriminant analysis of the Heart data table for feature selection. The ODS OUTPUT statement stores the “Selection Summary” table as a
local file named *Summary*. The MATRIX=COV option in the PROC VARREDUCE statement requests that selections be done based on the covariance matrix. The BIC option specifies the stop criterion, and the MAXITER= option specifies 15 as the maximum number of iterations. The selection process terminates when the BIC statistic increases in the last three consecutive steps.

Output 22.1.1 and Output 22.1.2 display the selection summary from each iteration and the selected effects.

**Output 22.1.1 Selection Summary**

<table>
<thead>
<tr>
<th>Iteration</th>
<th>Parameter</th>
<th>Proportion of Variance Explained</th>
<th>SSE</th>
<th>MSE</th>
<th>AIC</th>
<th>AICC</th>
<th>BIC</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>AgeAtStart</td>
<td>0.191310</td>
<td>0.808690</td>
<td>0.00016052</td>
<td>-0.210355</td>
<td>1.789647</td>
<td>-0.210648</td>
</tr>
<tr>
<td>2</td>
<td>Smoking</td>
<td>0.220923</td>
<td>0.779077</td>
<td>0.00015467</td>
<td>-0.246867</td>
<td>1.753136</td>
<td>-0.246262</td>
</tr>
<tr>
<td>3</td>
<td>Systolic</td>
<td>0.245405</td>
<td>0.754505</td>
<td>0.00014984</td>
<td>-0.278002</td>
<td>1.722002</td>
<td>-0.276499</td>
</tr>
<tr>
<td>4</td>
<td>Sex Female</td>
<td>0.255479</td>
<td>0.744521</td>
<td>0.00014787</td>
<td>-0.290648</td>
<td>1.709358</td>
<td>-0.288247</td>
</tr>
<tr>
<td>5</td>
<td>Weight_Status Underweight</td>
<td>0.256772</td>
<td>0.743228</td>
<td>0.00014764</td>
<td>-0.291593</td>
<td>1.708415</td>
<td>-0.288294</td>
</tr>
<tr>
<td>6</td>
<td>BP_Status Normal</td>
<td>0.257880</td>
<td>0.742120</td>
<td>0.00014745</td>
<td>-0.292291</td>
<td>1.707720</td>
<td>-0.288093</td>
</tr>
<tr>
<td>7</td>
<td>Smoking_Status Non-smoker</td>
<td>0.258962</td>
<td>0.741038</td>
<td>0.00014727</td>
<td>-0.292957</td>
<td>1.707057</td>
<td>-0.287861</td>
</tr>
<tr>
<td>8</td>
<td>Chol_Status Borderline</td>
<td>0.259547</td>
<td>0.740453</td>
<td>0.00014718</td>
<td>-0.292952</td>
<td>1.707065</td>
<td>-0.286958</td>
</tr>
</tbody>
</table>

**Output 22.1.2 Selected Effects**

<table>
<thead>
<tr>
<th>Number</th>
<th>Selected Variable</th>
<th>Variable Type</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>AgeAtStart</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>2</td>
<td>Smoking</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>3</td>
<td>Systolic</td>
<td>INTERVAL</td>
</tr>
<tr>
<td>4</td>
<td>Sex</td>
<td>CLASS</td>
</tr>
<tr>
<td>5</td>
<td>Weight_Status</td>
<td>CLASS</td>
</tr>
<tr>
<td>6</td>
<td>BP_Status</td>
<td>CLASS</td>
</tr>
<tr>
<td>7</td>
<td>Smoking_Status</td>
<td>CLASS</td>
</tr>
<tr>
<td>8</td>
<td>Chol_Status</td>
<td>CLASS</td>
</tr>
</tbody>
</table>

Output 22.1.3 shows the BIC curve change throughout iterations.
Example 22.2: Output a Correlation Matrix to a SAS Data File

This example shows how to output a correlation matrix to a SAS data file. The OUTCP= option creates an output data table named mycas.corr.

The following DATA step generates a data table that has 2,000 observations and contains both interval variables (x1–x2) and CLASS variables (a, c1, and c2):

```sas
data mycas.data1;
  array x{2};
  array c{2};
  do i=1 to 2000;
    a=int(ranuni(1)*2);
    do j=1 to 2;
      x{j}=ranuni(1);
      c{j}=int(ranuni(1)*2);
    end;
    output;
  end;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements invoke the VARREDUCE procedure:

```sas
title "Output the Correlation Matrix";

proc varreduce data=mycas.data1 matrix=corr outcp=mycas.corr;
  class a;
  reduce unsupervised a x1-x2 /maxsteps=4;
run;

proc print data=mycas.corr;
run;
```
Output 22.2.1 shows the content of the data file that PROC VARREDUCE generates.

Output 22.2.1  Output the Correlation Matrix

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>ID</em></th>
<th>TYPE</th>
<th><em>VAR</em></th>
<th>v1</th>
<th>v2</th>
<th>v3</th>
<th>v4</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>1</td>
<td>MEAN/FREQ</td>
<td></td>
<td>1015.00</td>
<td>985.00</td>
<td>0.50</td>
<td>0.50</td>
</tr>
<tr>
<td>2</td>
<td>2</td>
<td>N</td>
<td></td>
<td>2000.00</td>
<td>2000.00</td>
<td>2000.00</td>
<td>2000.00</td>
</tr>
<tr>
<td>3</td>
<td>3</td>
<td>CORR</td>
<td>a 0</td>
<td>1.00</td>
<td>-1.00</td>
<td>-0.00</td>
<td>-0.02</td>
</tr>
<tr>
<td>4</td>
<td>4</td>
<td>CORR</td>
<td>a 1</td>
<td>v2</td>
<td>-1.00</td>
<td>1.00</td>
<td>0.00</td>
</tr>
<tr>
<td>5</td>
<td>5</td>
<td>CORR</td>
<td>x1</td>
<td>v3</td>
<td>-0.00</td>
<td>0.00</td>
<td>1.00</td>
</tr>
<tr>
<td>6</td>
<td>6</td>
<td>CORR</td>
<td>x2</td>
<td>v4</td>
<td>-0.02</td>
<td>0.02</td>
<td>-0.01</td>
</tr>
</tbody>
</table>

The _VAR_ column displays the names of all variables and the levels of the CLASS variables. Assuming that you have \( n \) effects (the total number of interval variables and the levels of CLASS variables), the _vID_ column contains \( n \) markers, v1 to vn, where vi denotes the ith effect. The column _TYPE_ defines the role of each row. When the _TYPE_ column displays MEAN/FREQ, the corresponding row contains either the mean for an interval variable or the frequency for a level of a CLASS variable. When the _TYPE_ column displays N, the corresponding row contains the number of samples. And when the _TYPE_ column displays CORR, COV, or SSCP, the corresponding row contains a row of the CORR, COV, or SSCP matrix. In this example, the CORR matrix is \( 4 \times 4 \), and it resides in the table in rows 3–6 and columns 7–10.

Example 22.3: Output the Correlation Matrix in LIL Format

This example shows how to output a correlation matrix in list-of-list (LIL) format. The OUTCP= option creates an output data table named mycas.corr_lil.

The following DATA step generates a data table that has 2,000 observations and contains both interval variables (x1–x2) and a CLASS variable (a):

```plaintext
data mycas.data2;
  array x{2};
  do i=1 to 2000;
    a=int(ranuni(1)*2);
    do j=1 to 2;
      x{j}=ranuni(1);
    end;
    output;
  end;
run;
```

These statements assume that your CAS engine libref is named mycas, but you can substitute any appropriately defined CAS engine libref.

The following statements invoke the VARREDUCE procedure:
Example 22.3: Output the Correlation Matrix in LIL Format

```sas
title "Output the Correlation Matrix in LIL Format";

proc varreduce data=mycas.data2 matrix=corr outcp=mycas.corr_lil/list eps=0.01;
  class a;
  reduce unsupervised a x1-x2 /maxsteps=4;
run;

proc print data=mycas.corr_lil;
run;
```

Output 22.3.1 shows the correlation matrix in LIL format.

### Output 22.3.1 Output the Correlation Matrix in LIL Format

<table>
<thead>
<tr>
<th>Obs</th>
<th><em>TYPE</em></th>
<th><em>ID</em></th>
<th><em>NAME1</em></th>
<th><em>NAME2</em></th>
<th><em>VAL</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>S</td>
<td>1</td>
<td>samples</td>
<td></td>
<td>2000.00</td>
</tr>
<tr>
<td>2</td>
<td>S</td>
<td>2</td>
<td>nVar</td>
<td></td>
<td>3.00</td>
</tr>
<tr>
<td>3</td>
<td>S</td>
<td>3</td>
<td>nEff</td>
<td></td>
<td>4.00</td>
</tr>
<tr>
<td>4</td>
<td>F</td>
<td>1</td>
<td>a 0</td>
<td>979.00</td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>2</td>
<td>a 1</td>
<td>1021.00</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>M</td>
<td>3</td>
<td>x1</td>
<td>0.49</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>M</td>
<td>4</td>
<td>x2</td>
<td>0.50</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>R</td>
<td>1</td>
<td>1</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>R</td>
<td>2</td>
<td>1</td>
<td>-1.00</td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>R</td>
<td>3</td>
<td>2</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>R</td>
<td>4</td>
<td>1</td>
<td>0.03</td>
<td></td>
</tr>
<tr>
<td>12</td>
<td>R</td>
<td>5</td>
<td>2</td>
<td>-0.03</td>
<td></td>
</tr>
<tr>
<td>13</td>
<td>R</td>
<td>6</td>
<td>3</td>
<td>1.00</td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>R</td>
<td>10</td>
<td>4</td>
<td>1.00</td>
<td></td>
</tr>
</tbody>
</table>

The column _TYPE_ defines the type of each row:

- When the _TYPE_ column displays S, the corresponding row contains the statistics of the data table. More specifically, when the _TYPE_ column displays S and the _NAME1_ column displays samples, the _VAL_ column in the corresponding row contains the number of samples in the data table. Similarly, when the _TYPE_ column displays S and the _NAME1_ column displays nVar, the _VAL_ column contains the number of variables. And when the _TYPE_ column displays S and the _NAME1_ column displays nEff, the _VAL_ column in the corresponding row contains the number of effects.

- When the _TYPE_ column displays F, the row contains the frequency of a level of a CLASS variable. In this case, the _NAME1_ column contains the name and level of the CLASS variable.

- When the _TYPE_ column displays M, the row contains the mean of an interval variable. In this case, the _NAME1_ column contains the name of the variable and the _NAME2_ column is empty.

- When the _TYPE_ column displays R, the row contains an entry in the correlation matrix. In this case, the _NAME1_ column contains the row ID, the _NAME2_ column contains the column ID, and the _VAL_ column contains the value.
• When the _TYPE_ column displays V or P, the corresponding row contains an entry of a COV matrix or an SSCP matrix, respectively.

Only entries in the lower triangle of the correlation matrix are written to the file, because the correlation matrix is symmetric. Also, any entry of the matrix whose value is smaller than 0.01 is ignored in the output (EPS = 0.01); this saves storage space.

References


Subject Index

ABC parameters
  KCLUS procedure, 442

ABC statistics
  KCLUS procedure, 442

AC1 agreement coefficient
  FREQTAB procedure, 255

adaptive LASSO selection
  Shared Concepts, 67

adjusted odds ratio
  FREQTAB procedure, 260

adjusted relative risks
  FREQTAB procedure, 261

agreement, measures of
  FREQTAB procedure, 249

Agresti-Caffo confidence limits
  risk difference (FREQTAB), 224

Agresti-Coull confidence limits
  proportions (FREQTAB), 215

ANCOVA effects
  Shared Concepts, 53

ANOVA (row mean scores) statistic
  Mantel-Haenszel (FREQTAB), 258

ANCOVA effects
  Shared Concepts, 52

ANOVA table
  REGSELECT procedure, 757

ASSESS procedure, 907
  B-spline basis, 31
  computational method, 79, 80
  convergence criterion, 42–44, 46
  displayed output, 918
  fit statistics, 916, 918
  function-based convergence criteria, 42, 43
  gradient-based convergence criteria, 42, 44
  input data tables, 911
  input variables, 914
  lift information, 914, 918
  lift regression information, 918
  multithreading, 79
  natural cubic spline basis, 33
  ODS table names, 33, 918
  optimization techniques, 46, 80
  parameter-based convergence criteria, 42, 46
  ROC information, 915, 918
  splines and spline bases, 29
  target variables, 914

test data, 78
truncated power function (TPF) basis, 30
validation, 78

association, measures of
  FREQTAB procedure, 204

at sign (@) operator
  Shared Concepts, 51, 54, 1015

B-spline
  spline basis (Shared Concepts), 31

B-spline basis
  ASSESS procedure, 31
  BINNING procedure, 31
  CARDINALITY procedure, 31
  CORRELATION procedure, 31
  GAMMOD procedure, 31
  GENSELECT procedure, 31
  KCLUS procedure, 31
  LOGSELECT procedure, 31
  NLSELECT procedure, 31
  NLMOD procedure, 31
  PARTITION procedure, 31
  PCA procedure, 31
  PHSELECT procedure, 31
  PLSMOD procedure, 31
  QTRSELECT procedure, 31
  REGSELECT procedure, 31
  TREESPLIT procedure, 31
  VARIMPUTE procedure, 31
  VARREDUCE procedure, 31

backward elimination
  Shared Concepts, 62

bar (l) operator
  Shared Concepts, 50, 53, 54, 1015
  VARREDUCE procedure, 1014

bar charts
  FREQTAB procedure, 180

Barnard’s test
  FREQTAB procedure, 232

Bernoulli distribution
  NLMOD procedure, 532

best configuration
  TREESPLIT procedure, 889

bin details
  BINNING procedure, 940

binary distribution
  NLMOD procedure, 531

BINNING procedure
  B-spline basis, 31
bin details, 940
computation, 937
computational method, 79, 80
convergence criterion, 42–44, 46
displayed output, 940
formula, 937
function-based convergence criteria, 42, 43
gradient-based convergence criteria, 42, 44
information value, 939
input data tables, 933
multithreading, 79
natural cubic spline basis, 33
ODS table names, 33, 941
optimization techniques, 46, 80
output data tables, 936
parameter-based convergence criteria, 42, 46
splines and spline bases, 29
test data, 78
tree-based binning, 939
trimmed statistics, 941
truncated power function (TPF) basis, 30
validation, 78
variable information value (IV) table, 941
variable transformation information table, 941
Winsorized statistics, 941
binomial distribution
NLMOD procedure, 531
binomial proportions
Clopper-Pearson test (FREQTAB), 218
certainty limits (FREQTAB), 214
equivalence tests (FREQTAB), 220
exact test (FREQTAB), 218
FREQTAB procedure, 214
noninferiority tests (FREQTAB), 219
superiority tests (FREQTAB), 220
tests (FREQTAB), 217
TOST (FREQTAB), 220
Blacker confidence limits proportions (FREQTAB), 216
boundary constraints, 528
bounds
NLMOD procedure, 528
Bowker’s symmetry test
FREQTAB procedure, 249, 250
Breslow method
likelihood (PHSELECT), 612
Breslow-Day test
FREQTAB procedure, 262
Tarone’s adjustment (FREQTAB), 262
C charts
central line, 810
time limit equations, 810, 811
time limit parameters, 811
C4.5 pruning
TREESPLIT procedure, 867, 878
candidates for addition or removal
GENSELECT procedure, 406
LOGSELECT procedure, 498
PHSELECT procedure, 619
QTRSELECT procedure, 706
REGSELECT procedure, 756
CARDINALITY procedure, 951
B-spline basis, 31
computational method, 79, 80
convergence criterion, 42–44, 46
displayed output, 958
function-based convergence criteria, 42, 43
gradient-based convergence criteria, 42, 44
input data tables, 956
multithreading, 79
natural cubic spline basis, 33
ODS table names, 33
optimization techniques, 46, 80
parameter-based convergence criteria, 42, 46
splines and spline bases, 29
test data, 78
truncated power function (TPF) basis, 30
validation, 78
variable information value (IV) table, 941
variable transformation information table, 941
case-control studies
odds ratio (FREQTAB), 236
categorical data analysis
FREQTAB procedure, 112
cell count data
FREQTAB procedure, 194
centering and scaling information
PCA procedure, 574
PLSMOD procedure, 662
chi-square goodness-of-fit test
FREQTAB procedure, 199
chi-square tests
FREQTAB procedure, 199
Cicchetti-Allison weights
kappa coefficient (FREQTAB), 254
class level
GAMMOD procedure, 307, 333
GENSELECT procedure, 366, 405
LOGSELECT procedure, 468, 497
PHSELECT procedure, 597, 618
PLSMOD procedure, 647, 662
QTRSELECT procedure, 684, 706
REGSELECT procedure, 738, 756
CLASS statement
Shared Concepts, 47
syntax (Shared Concepts), 10, 47
classification level
PARTITION procedure, 976
classification trees, see decision trees
classification variables
Shared Concepts, 47
Clopper-Pearson confidence limits
proportions (FREQTAB), 215
cluster summary
KCLUS procedure, 439
cluster summary for mixed variables
KCLUS procedure, 441
cluster summary for nominal variables
KCLUS procedure, 441
Cochran’s Q test
FREQTAB procedure, 249, 256
Cochran-Armitage test for trend
FREQTAB procedure, 246
Cochran-Mantel-Haenszel statistics
FREQTAB procedure, 256
CODE statement
syntax (Shared Concepts), 14
cohort studies
relative risks (FREQTAB), 240
colon (:) operator
Shared Concepts, 51
common odds ratio
exact confidence limits (FREQTAB), 263
exact test (FREQTAB), 263
logit (FREQTAB), 260
Mantel-Haenszel (FREQTAB), 260
common relative risks
logit (FREQTAB), 261
Mantel-Haenszel (FREQTAB), 261
complete separation
GENSELECT procedure, 397
LOGSELECT procedure, 488
components
PLSMOD procedure, 632
computation
BINNING procedure, 937
computational method
ASSESS procedure, 79, 80
BINNING procedure, 79, 80
CARDINALITY procedure, 79, 80
CORRELATION procedure, 79, 80
GAMMOD procedure, 79, 80
GENSELECT procedure, 79, 80
KCLUS procedure, 79, 80
LOGSELECT procedure, 79, 80
NLMOD procedure, 79, 80
PARTITION procedure, 79, 80
PCA procedure, 79, 80
PHSELECT procedure, 79, 80
PLSMOD procedure, 79, 80
QTRSELECT procedure, 79, 80
REGSELECT procedure, 79, 80, 754
TREESPLIT procedure, 79, 80
VARIMPUTE procedure, 79, 80
VARREDUCE procedure, 79, 80, 1012
concordant observations
FREQTAB procedure, 204
confidence limits
exact (FREQTAB), 124
measures of association (FREQTAB), 205
model parameters (GENSELECT), 374, 376
model parameters (LOGSELECT), 476
model parameters (PHSELECT), 605
model parameters (QTRSELECT), 690
model parameters (REGSELECT), 744
proportions (FREQTAB), 214
continuity-adjusted chi-square test
FREQTAB procedure, 202
continuity-adjusted chi-square test
FREQTAB procedure, 202
continuous-by-class effects
Shared Concepts, 55
VARREDUCE procedure, 1017
continuous-nesting-class effects
Shared Concepts, 55
VARREDUCE procedure, 1016
correction criterion
ASSESS procedure, 42–44, 46
BINNING procedure, 42–44, 46
CARDINALITY procedure, 42–44, 46
CORRELATION procedure, 42–44, 46
GAMMOD procedure, 42–44, 46, 307
GENSELECT procedure, 42–44, 46, 365
KCLUS procedure, 42–44, 46
LOGSELECT procedure, 42–44, 46, 467
NLMOD procedure, 42–44, 46
PARTITION procedure, 42–44, 46
PCA procedure, 42–44, 46
PHSELECT procedure, 42–44, 46, 596
PLSMOD procedure, 42–44, 46
QTRSELECT procedure, 42–44, 46
REGSELECT procedure, 42–44, 46
Shared Concepts, 42–44, 46
TREESPLIT procedure, 42–44, 46
VARIMPUTE procedure, 42–44, 46
VARREDUCE procedure, 42–44, 46
corrected sums of squares and crossproducts, 93
correlation
PCA procedure, 574
principal components, 572, 574
correlation coefficients
limited combinations of, 97
printing, for each variable, 93
suppressing probabilities, 93
correlation matrix
GENSELECT procedure, 365, 408
LOGSELECT procedure, 467, 499
PHSELECT procedure, 596, 620
CORRELATION procedure, 87
B-spline basis, 31
computational method, 79, 80
convergence criterion, 42–44, 46
details, 98
examples, 102
function-based convergence criteria, 42, 43
gradient-based convergence criteria, 42, 44
input data tables, 93
multithreading, 79
natural cubic spline basis, 33
ODS table names, 33, 102
optimization techniques, 46, 80
OUTP= data table, 100
parameter-based convergence criteria, 42, 46
splines and spline bases, 29
syntax, 92
task tables, 92
test data, 78
truncated power function (TPF) basis, 30
validation, 78
correlation statistic
Mantel-Haenszel (FREQTAB), 258
cost complexity
TREESPLIT procedure, 888
cost-complexity pruning
TREESPLIT procedure, 867, 876
covariance
PCA procedure, 574
principal components, 572, 574
covariance matrix
GENSELECT procedure, 366, 407
LOGSELECT procedure, 467, 499
PHSELECT procedure, 597, 620
covariances, 93
Cramér’s V statistic
FREQTABLE procedure, 204
Cronbach’s coefficient alpha, 99
calculating and printing, 93
test example, 105
cross validation
TREESPLIT procedure, 877
crossed effects
Shared Concepts, 54
VARREDUCE procedure, 1015
crosstabulation tables
FREQTABLE procedure, 112, 145, 275
cv statistics
TREESPLIT procedure, 888
dash (-) operator
Shared Concepts, 51
decision trees
TREESPLIT procedure, 840, 869
degrees of freedom
GAMMOD procedure, 329
descriptive statistics
KCLUS procedure, 440
diagnostic statistics
QTRSELECT procedure, 700
REGSELECT procedure, 751
dimensions
GENSELECT procedure, 407
LOGSELECT procedure, 498
PHSELECT procedure, 620
PLSMOD procedure, 662
QTRSELECT procedure, 706
REGSELECT procedure, 756
discordant observations
FREQTABLE procedure, 204
dispersion parameter
GAMMOD procedure, 330
DISPLAY statement
test syntax (Shared Concepts), 17
displayed output
ASSESS procedure, 918
BINNING procedure, 940
CARDINALITY procedure, 958
GAMMOD procedure, 332
GENSELECT procedure, 405
KCLUS procedure, 439
LOGSELECT procedure, 496
PLSMOD procedure, 540
PARTITION procedure, 977
PCA procedure, 573
PHSELECT procedure, 617
PLSMOD procedure, 662
QTRSELECT procedure, 705
REGSELECT procedure, 755
TREESPLIT procedure, 887
VARIMPUTE procedure, 991
VARREDUCE procedure, 1018
DISPLAYOUT statement
test syntax (Shared Concepts), 18
distribution function
GAMMOD procedure, 318
GENSELECT procedure, 374
distribution functions
<table>
<thead>
<tr>
<th>Subject</th>
<th>Documentation</th>
</tr>
</thead>
<tbody>
<tr>
<td>NLMOD procedure</td>
<td>538</td>
</tr>
<tr>
<td>dot plots</td>
<td></td>
</tr>
<tr>
<td>FREQTAB procedure</td>
<td>180</td>
</tr>
<tr>
<td>double dash (- -) operator</td>
<td></td>
</tr>
<tr>
<td>Shared Concepts</td>
<td>52</td>
</tr>
<tr>
<td>dummy parameterization</td>
<td></td>
</tr>
<tr>
<td>Shared Concepts</td>
<td>52</td>
</tr>
<tr>
<td>VARREDUCE procedure</td>
<td>1013</td>
</tr>
<tr>
<td>effect parameterization</td>
<td></td>
</tr>
<tr>
<td>Shared Concepts</td>
<td>57</td>
</tr>
<tr>
<td>EFFECT statement</td>
<td></td>
</tr>
<tr>
<td>collection effect (Shared Concepts), 21</td>
<td></td>
</tr>
<tr>
<td>multimember effect (Shared Concepts), 21</td>
<td></td>
</tr>
<tr>
<td>polynomial effect (Shared Concepts), 23</td>
<td></td>
</tr>
<tr>
<td>spline effect (Shared Concepts), 26</td>
<td></td>
</tr>
<tr>
<td>syntax (Shared Concepts), 19</td>
<td></td>
</tr>
<tr>
<td>eigenvalue decomposition method</td>
<td></td>
</tr>
<tr>
<td>PCA procedure, 551, 569</td>
<td></td>
</tr>
<tr>
<td>eigenvalues</td>
<td></td>
</tr>
<tr>
<td>PCA procedure, 574</td>
<td></td>
</tr>
<tr>
<td>eigenvalues and eigenvectors</td>
<td></td>
</tr>
<tr>
<td>PCA procedure, 569, 572, 574</td>
<td></td>
</tr>
<tr>
<td>eigenvectors</td>
<td></td>
</tr>
<tr>
<td>PCA procedure, 574</td>
<td></td>
</tr>
<tr>
<td>empirical Bayes estimate</td>
<td></td>
</tr>
<tr>
<td>NLMOD procedure, 534</td>
<td></td>
</tr>
<tr>
<td>equivalence tests</td>
<td></td>
</tr>
<tr>
<td>binomial proportions, 220</td>
<td></td>
</tr>
<tr>
<td>relative risk (FREQTAB), 244</td>
<td></td>
</tr>
<tr>
<td>risk difference (FREQTAB), 231</td>
<td></td>
</tr>
<tr>
<td>estimated number of clusters</td>
<td></td>
</tr>
<tr>
<td>KCLUS procedure, 442</td>
<td></td>
</tr>
<tr>
<td>estimates for smoothing components</td>
<td></td>
</tr>
<tr>
<td>GAMMOD procedure, 335</td>
<td></td>
</tr>
<tr>
<td>evaluation history</td>
<td></td>
</tr>
<tr>
<td>TREESPLIT procedure, 889</td>
<td></td>
</tr>
<tr>
<td>exact confidence limits</td>
<td></td>
</tr>
<tr>
<td>odds ratio (FREQTAB), 238</td>
<td></td>
</tr>
<tr>
<td>proportion difference (FREQTAB), 226</td>
<td></td>
</tr>
<tr>
<td>proportions (FREQTAB), 215</td>
<td></td>
</tr>
<tr>
<td>ratio of proportions (FREQTAB), 242</td>
<td></td>
</tr>
<tr>
<td>relative risks (FREQTAB), 242</td>
<td></td>
</tr>
<tr>
<td>risk difference (FREQTAB), 226</td>
<td></td>
</tr>
<tr>
<td>exact p-values</td>
<td></td>
</tr>
<tr>
<td>FREQTAB procedure, 267</td>
<td></td>
</tr>
<tr>
<td>exact tests</td>
<td></td>
</tr>
<tr>
<td>computational algorithms (FREQTAB), 266</td>
<td></td>
</tr>
<tr>
<td>computational resources (FREQTAB), 268</td>
<td></td>
</tr>
<tr>
<td>FREQTABLE procedure, 124, 265</td>
<td></td>
</tr>
<tr>
<td>Monte Carlo estimation (FREQTAB), 132</td>
<td></td>
</tr>
<tr>
<td>network algorithm (FREQTAB), 266</td>
<td></td>
</tr>
<tr>
<td>examples, ASSESS</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, BINNING</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, CARDINALITY</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, CORRELATION</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, GAMMOD</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, GENSELECT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, KCLUS</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, LOGSELECT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, NLMOD</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, NLMOD procedure</td>
<td></td>
</tr>
<tr>
<td>boundary specification, 528</td>
<td></td>
</tr>
<tr>
<td>conditional model expression, 545</td>
<td></td>
</tr>
<tr>
<td>enzyme data, 522</td>
<td></td>
</tr>
<tr>
<td>gamma distribution, 539</td>
<td></td>
</tr>
<tr>
<td>join point, 545</td>
<td></td>
</tr>
<tr>
<td>plateau model, 545</td>
<td></td>
</tr>
<tr>
<td>predicted values, 545</td>
<td></td>
</tr>
<tr>
<td>segmented model, 545</td>
<td></td>
</tr>
<tr>
<td>starting values, data table, 533</td>
<td></td>
</tr>
<tr>
<td>starting values, grid, 532</td>
<td></td>
</tr>
<tr>
<td>examples, PARTITION</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, PCA</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, PHSELECT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, PLSMOD</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, QTRSELECT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, REGSELECT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, TREESPLIT</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, VARIMPUTE</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>examples, VARREDUCE</td>
<td></td>
</tr>
<tr>
<td>multimember effect, 22</td>
<td></td>
</tr>
<tr>
<td>explained variation of variables</td>
<td></td>
</tr>
<tr>
<td>PCA procedure, 574</td>
<td></td>
</tr>
<tr>
<td>factors</td>
<td></td>
</tr>
<tr>
<td>PLSMOD procedure, 632</td>
<td></td>
</tr>
<tr>
<td>Farrington-Manning test</td>
<td></td>
</tr>
<tr>
<td>risk difference (FREQTAB), 230</td>
<td></td>
</tr>
<tr>
<td>finding the number of clusters</td>
<td></td>
</tr>
<tr>
<td>KCLUS procedure, 435</td>
<td></td>
</tr>
</tbody>
</table>

**Subject Index ★ 1029**
Fisher’s exact test
- FREQTAB procedure, 203

fit criteria
- QTRSELECT procedure, 697
- REGSELECT procedure, 749
- VARREDUCE procedure, 1011

fit statistics
- ASSESS procedure, 916, 918
- GAMMOD procedure, 334
- GENSELECT procedure, 407
- LOGSELECT procedure, 499
- PHSELECT procedure, 620
- QTRSELECT procedure, 707
- REGSELECT procedure, 758

fitting algorithms
- GAMMOD procedure, 327

Fleiss-Cohen weights
- kappa coefficient (FREQTAB), 254

formula
- BINNING procedure, 937

forward selection
- Shared Concepts, 60

forward swap selection
- Shared Concepts, 65

Freeman-Halton test
- FREQTAB procedure, 203

FREQTAB procedure, 112
- AC1 agreement coefficient, 255
- adjusted odds ratio (Mantel-Haenszel), 260
- adjusted relative risks (Mantel-Haenszel), 261
- Agresti-Caffo confidence limits, 224
- Agresti-Coull confidence limits, 215
- ANOVA (row mean scores) statistic, 258
- bar charts, 180
- Barnard’s test, 232
- binomial proportions, 214
- Blaker confidence limits, 216
- Bowker’s symmetry test, 249, 250
- Breslow-Day test, 262
- cell count data, 194
- chi-square goodness-of-fit test, 199
- chi-square tests, 199
- Clopper-Pearson confidence limits, 215
- Cochran’s Q test, 249, 256
- Cochran-Armitage test for trend, 246
- common odds ratio, 263
- computational resources (exact tests), 268
- contingency coefficient, 204
- continuity-adjusted chi-square test, 202
- correlation statistic, 258
- Cramér’s V statistic, 204
- crosstabulation tables, 275
- default tables, 145
- displayed output, 273
- dot plots, 180
- equivalence tests, 220
- equivalence tests (relative risk), 244
- equivalence tests (risk difference), 231
- exact confidence limits, 124
- exact p-values, 267
- exact tests, 124, 265
- exact unconditional confidence limits, 226
- Farrington-Manning test, 230
- Fisher’s exact test, 203
- Freeman-Halton test, 203
- Gail-Simon test, 265
- gamma statistic, 204, 206
- general association statistic, 259
- Hauck-Anderson confidence limits, 224
- input data sets, 194
- input data tables, 122
- Jeffreys confidence limits, 216
- Jonckheere-Terpstra test, 248
- kappa coefficient, 249, 251
- Kendall’s tau-b statistic, 204, 206
- lambda asymmetric, 204, 212
- lambda symmetric, 204, 212
- likelihood ratio chi-square test, 202
- Likelihood ratio confidence limits, 216
- Logit confidence limits, 216
- Mantel-Fleiss criterion, 259
- Mantel-Haenszel chi-square test, 202
- Mantel-Haenszel statistics, 256
- maximum time (exact tests), 132
- McNemar’s test, 249
- measures of agreement, 249
- measures of association, 204
- Mid-p confidence limits, 217, 239
- Miettinen-Nurminen confidence limits, 224
- missing values, 195
- Monte Carlo estimation (exact tests), 124, 132, 269
- mosaic plots, 173
- multiway tables, 274
- network algorithm, 266
- Newcombe confidence limits, 225, 230
- noninferiority tests, 219
- noninferiority tests (relative risk), 243
- noninferiority tests (risk difference), 228
- odds ratio, 236
- ODS graph names, 286
- ODS table names, 282
- one-way frequency tables, 273
- ordering of levels, 123
- output data sets, 134, 270
- overall kappa coefficient, 255
- Pearson chi-square test, 200
- Pearson correlation coefficient, 204, 208
phi coefficient, 204
polychoric correlation coefficient, 204, 211
prevalence-adjusted bias-adjusted kappa, 254
relative risks, 240
risk difference, 222
score confidence limits, 224, 241
scores, 198
simple kappa coefficient, 251
Somers’ D statistics, 204, 208
Spearman rank correlation coefficient, 204, 209
standardized residuals, 200
Stuart’s tau-c statistic, 204, 207
superiority tests, 220
superiority tests (relative risk), 244
superiority tests (risk difference), 230
tetrachoric correlation coefficient, 211
uncertainty coefficients, 204, 213, 214
Wald confidence limits (risk difference), 226
weighted kappa coefficient, 249, 252
Wilson confidence limits, 217
Yule’s Q statistic, 206
Zelen’s exact test, 262
calculated
frequencies and descriptive statistics for nominal
variables
KCLUS procedure, 441
frequency information table
PARTITION procedure, 977
frequency tables
FREQTAB procedure, 112, 145
one-way (FREQTAB), 273
function-based convergence criteria
ASSESS procedure, 42, 43
BINNING procedure, 42, 43
CARDINALITY procedure, 42, 43
CORRELATION procedure, 42, 43
GAMMOD procedure, 42, 43
GENSELECT procedure, 42, 43
KCLUS procedure, 42, 43
LOGSELECT procedure, 42, 43
NLMOD procedure, 42, 43
PARTITION procedure, 42, 43
PCA procedure, 42, 43
PHESELECT procedure, 42, 43
PLSMOD procedure, 42, 43
QTRSELECT procedure, 42, 43
REGSELECT procedure, 42, 43
Shared Concepts, 42, 43
TREESPLIT procedure, 42, 43
VARMUPTTE procedure, 42, 43
VARREDUCE procedure, 42, 43
Gail-Simon test
FREQTAB procedure, 265
gamma distribution
NLMOD procedure, 531
gamma statistic
FREQTAB procedure, 204, 206
GAMMOD procedure, 295
B-spline basis, 31
class level, 307, 333
computational method, 79, 80
convergence criterion, 42–44, 46, 307
convergence status, 334
degrees of freedom, 329
dispersion parameter, 330
displayed output, 332
distribution function, 318
estimates for smoothing components, 335
fit statistics, 334
fitting algorithms, 327
function-based convergence criteria, 42, 43
generalized additive models, 325
generalized linear models, 325
gradient-based convergence criteria, 42, 44
input data tables, 307
iteration history, 333
link function, 319
low-rank approximation, 324
model evaluation criteria, 327
model inference, 330
model information, 333
model options summary, 313
multithreading, 79, 332
natural cubic spline basis, 33
number of observations, 333
ODS Graphics, 336
ODS table names, 33, 335
optimization algorithms, 332
optimization techniques, 46, 80
outer iteration, 328
output CAS tables, 335
output data tables, 321
parameter estimates, 335
parameter-based convergence criteria, 42, 46
penalized likelihood estimation, 326
performance iteration, 329
response level ordering, 314
response profile, 333
response variable options, 314
spline details, 333
splines and spline bases, 29
test data, 78
tests for smoothing components, 331, 335
thin-plate regression splines, 322
thin-plate smoothing splines, 323
truncated power function (TPF) basis, 30
validation, 78
weighting, 322
Gaussian distribution
   NLMOD procedure, 531
general association statistic
   Mantel-Haenszel (FREQTAB), 259
general distribution
   NLMOD procedure, 531
general effects
   Shared Concepts, 56
   VARREDUCE procedure, 1017
generalized additive models
   GAMMOD procedure, 325
generalized linear models
   GAMMOD procedure, 325
GENSELECT procedure, 356, 376
   B-spline basis, 31
   candidates for addition or removal, 406
   class level, 366, 405
   complete separation, 397
   computational method, 79, 80
   confidence limits, 374
   convergence criterion, 42–44, 46, 365
   convergence status, 406
   correlation matrix, 365, 408
   covariance matrix, 366, 407
   dimensions, 407
   displayed output, 405
   distribution function, 374
   existence of MLEs, 397
   fit statistics, 407
   function-based convergence criteria, 42, 43
   gradient-based convergence criteria, 42, 44
   infinite parameter estimates, 397
   input data tables, 366
   iteration history, 406
   LASSO method, 398
   LASSO selection, 398
   link function, 376
   maximum likelihood estimates, 397
   model information, 405
   model options summary, 372
   multithreading, 79, 404
   natural cubic spline basis, 33
   number of observations, 405
   ODS graph names, 409
   ODS table names, 33, 408
   optimization algorithms, 404
   optimization techniques, 46, 80
   output CAS tables, 408
   output data tables, 379
   parameter estimates, 407
   parameter-based convergence criteria, 42, 46
   quasi-complete separation, 397
   response level ordering, 373
   response profile, 405
response variable options, 372
   selected effects, 407
   selection information, 406
   selection reason, 407
   selection summary, 406
   separation, 397
   splines and spline bases, 29
   stop reason, 407
   test data, 78
   truncated power function (TPF) basis, 30
   validation, 78
GLM parameterization
   Shared Concepts, 52, 1013
   global test
   LOGSELECT procedure, 499
gradient-based convergence criteria
   ASSESS procedure, 42, 44
   BINNING procedure, 42, 44
   CARDINALITY procedure, 42, 44
   CORRELATION procedure, 42, 44
   GAMMOD procedure, 42, 44
   GENSELECT procedure, 42, 44
   KCLUS procedure, 42, 44
   LOGSELECT procedure, 42, 44
   NLMOD procedure, 42, 44
   PARTITION procedure, 42, 44
   PCA procedure, 42, 44
   PHSELECT procedure, 42, 44
   PLSMOD procedure, 42, 44
   QTRSELECT procedure, 42, 44
   REGSELECT procedure, 42, 44
   Shared Concepts, 42, 44
   TREESPLIT procedure, 42, 44
   VARIMPUTE procedure, 42, 44
   VARREDUCE procedure, 42, 44
   group LASSO selection
   Shared Concepts, 67
Hauk-Anderson confidence limits
   risk difference (FREQTAB), 224
Hessian
   PHSELECT procedure, 597
hyperparameter tuning
   TREESPLIT procedure, 884
hypothesis tests
   exact (FREQTAB), 124
imputation information table
   VARIMPUTE procedure, 992
imputation requests table
   VARIMPUTE procedure, 991
individual measurement and moving range charts
   central line, 799
   control limit equations, 799
notation, 798
subgroup summary statistics, 799
infinite parameter estimates
  GENSELECT procedure, 397
  LOGSELECT procedure, 488
information criteria
  QTRSELECT procedure, 698
information value
  BINNING procedure, 939
initial values
  NLMOD procedure, 531
input variables
  ASSESS procedure, 914
interaction effects
  Shared Concepts, 54
  VARREDUCE procedure, 1015
intercept
  Shared Concepts, 53
  VARREDUCE procedure, 1014
iteration history
  GAMMOD procedure, 333
  GENSELECT procedure, 406
  KCLUS procedure, 440
  LOGSELECT procedure, 497
  PHSELECT procedure, 618
ITERGS method
  PCA procedure, 551, 570
Jeffreys confidence limits
  proportions (FREQTAB), 216
Jonckheere-Terpstra test
  FREQTAB procedure, 248
kappa coefficient
  FREQTAB procedure, 249, 251
  weights (FREQTAB), 254
KCLUS procedure, 420
  ABC parameters, 442
  ABC statistics, 442
  B-spline basis, 31
  cluster centroid output data tables, 429
  cluster summary, 439
  cluster summary for mixed variables, 441
  cluster summary for nominal variables, 441
  computational method, 79, 80
  convergence criterion, 42–44, 46
  descriptive statistics, 440
  displayed output, 439
  estimated number of clusters, 442
  finding the number of clusters, 435
  frequencies and descriptive statistics for nominal variables, 441
  function-based convergence criteria, 42, 43
  gradient-based convergence criteria, 42, 44
input data tables, 426
iteration history, 440
missing values, 434
model information, 440
multithreading, 79
natural cubic spline basis, 33
number of observations, 439
ODS table names, 33, 443
optimization techniques, 46, 80
output CAS tables, 443
output data tables, 433
parameter-based convergence criteria, 42, 46
splines and spline bases, 29
standardization, 442
test data, 78
truncated power function (TPF) basis, 30
validation, 78
within-cluster statistics, 440
Kendall’s tau-\(b\) statistic
  FREQTAB procedure, 204, 206
lag functionality
  NLMOD procedure, 536
lambda asymmetric
  FREQTAB procedure, 204, 212
lambda symmetric
  FREQTAB procedure, 204, 212
LAR selection
  Shared Concepts, 65
LASSO method
  GENSELECT procedure, 398
LASSO selection
  GENSELECT procedure, 398
  LOGSELECT procedure, 489
  PHSELECT procedure, 612
  Shared Concepts, 66
latent variables
  PLSMOD procedure, 632
latent vectors
  PLSMOD procedure, 632
LD statistic
  PHSELECT procedure, 615
least squares
  NLMOD procedure, 537
least squares distribution
  NLMOD procedure, 531
left-truncation variable
  model parameters (PHSELECT), 605
levelization
  Shared Concepts, 47
lift information
  ASSESS procedure, 914, 918
lift regression information
  ASSESS procedure, 918
likelihood displacement
PHSELECT procedure, 615
likelihood ratio chi-square test
FREQTAB procedure, 202
Likelihood ratio confidence limits
proportions (FREQTAB), 216
link function
GAMMOD procedure, 319
GENSELECT procedure, 376
LOGSELECT procedure, 476
listwise deletion, 100
loadings
PCA procedure, 570, 575
local influence
score residuals (PHSELECT), 615
log-likelihood functions
NLMOD procedure, 538
Logit confidence limits
proportions (FREQTAB), 216
LOGSELECT procedure, 456, 476
B-spline basis, 31
candidates for addition or removal, 498
class level, 468, 497
complete separation, 488
computational method, 79, 80
confidence limits, 476
convergence criterion, 42–44, 46, 467
convergence status, 497
correlation matrix, 467, 499
covariance matrix, 467, 499
dimensions, 498
displayed output, 496
existence of MLEs, 488
fit statistics, 499
function-based convergence criteria, 42, 43
global test, 499
gradient-based convergence criteria, 42, 44
infinite parameter estimates, 488
input data tables, 467
iteration history, 497
LASSO selection, 489
link function, 476
maximum likelihood estimates, 488
model information, 496
model options summary, 474
multithreading, 79, 495
natural cubic spline basis, 33
number of observations, 496
ODS graph names, 501
ODS table names, 33, 500
optimization algorithms, 495
optimization techniques, 46, 80
output CAS tables, 500
output data tables, 478, 745
parameter estimates, 499
parameter-based convergence criteria, 42, 46
quasi-complete separation, 488
response level ordering, 475
response profile, 497
response variable options, 474
selected effects, 498
selection information, 497
selection reason, 498
selection summary, 498
separation, 488
splines and spline bases, 29
stop reason, 498
test data, 78
truncated power function (TPF) basis, 30
Type III tables, 499
validation, 78
low-rank approximation
GAMMOD procedure, 324
main effects
Shared Concepts, 53
VARREDUCE procedure, 1014
Mantel-Fleiss criterion
FREQTAB procedure, 259
Mantel-Haenszel chi-square test
FREQTAB procedure, 202
Mantel-Haenszel statistics
ANOVA (row mean scores) statistic (FREQTAB), 258
correlation statistic (FREQTAB), 258
FREQTAB procedure, 256
general association statistic (FREQTAB), 259
Mantel-Fleiss criterion (FREQTAB), 259
maximum likelihood estimates
GENSELECT procedure, 397
LOGSELECT procedure, 488
McNemar’s test
FREQTAB procedure, 249
measures of association
exact tests (FREQTAB), 206
tests (FREQTAB), 205
median charts
central line, 802
control limit equations, 802
notation, 801
subgroup summary statistics, 802
Mehta-Patel network algorithm
exact tests (FREQTAB), 266
Mid-p confidence limits
odds ratio (FREQTAB), 239
Mid-p confidence limits
proportions (FREQTAB), 217
Miettinen-Nurminen confidence limits
risk difference (FREQTAB), 224
missing values
  CORRELATION procedure, 100
  FREQTAB procedure, 195
  KCLUS procedure, 434
  PCA procedure, 571
  PLSMOD procedure, 661
  VARREDUCE procedure, 1009
model
  information (GENSELECT), 405
model details
  PLSMOD procedure, 663
model evaluation criteria
  GAMMOD procedure, 327
model inference
  GAMMOD procedure, 330
model information
  GAMMOD procedure, 333
  KCLUS procedure, 439
  LOGSELECT procedure, 496
  PCA procedure, 573
  PHSELECHT procedure, 618
  PLSMOD procedure, 662
  TREESELECHT procedure, 888
model specification
  NLMOD procedure, 530
modified ridit scores
  FREQTAB procedure, 198
Monte Carlo estimation
  exact tests (FREQTAB), 124, 132, 269
mosaic plots
  FREQTAB procedure, 173
multithreading
  ASSESS procedure, 79
  BINNING procedure, 79
  CARDINALITY procedure, 79
  CORRELATION procedure, 79
  GAMMOD procedure, 79, 332
  GENSELECHT procedure, 79, 404
  KCLUS procedure, 79
  LOGSELECT procedure, 79, 495
  NLMOD procedure, 79, 540
  PARTITION procedure, 79
  PCA procedure, 79
  PHSELECHT procedure, 79, 617
  PLSMOD procedure, 79
  QTRSELECT procedure, 79, 705
  REGSELECT procedure, 79, 754
  TREESELECHT procedure, 79
  VARIMPUTE procedure, 79
  VARREDUCE procedure, 79
multiway tables
  FREQTAB procedure, 112, 145, 274
natural cubic spline basis
  ASSESS procedure, 33
  BINNING procedure, 33
  CARDINALITY procedure, 33
  CORRELATION procedure, 33
  GAMMOD procedure, 33
  GENSELECHT procedure, 33
  KCLUS procedure, 33
  LOGSELECT procedure, 33
  NLMOD procedure, 33
  PARTITION procedure, 33
  PCA procedure, 33
  PHSELECHT procedure, 33
  PLSMOD procedure, 33
  QTRSELECT procedure, 33
  REGSELECT procedure, 33
  Shared Concepts, 33
  TREESELECHT procedure, 33
  VARIMPUTE procedure, 33
  VARREDUCE procedure, 33
negative binomial distribution
  NLMOD procedure, 531
nested effects
  Shared Concepts, 54
  VARREDUCE procedure, 1016
nested versus crossed effects
  Shared Concepts, 54
  VARREDUCE procedure, 1016
network algorithm
  exact tests (FREQTAB), 266
Newcombe confidence limits
  risk difference (FREQTAB), 225, 230
NIPALS method
  PCA procedure, 551, 570
NLMOD procedure, 519
  additional estimates, 530, 542
  additional estimates correlation, 543
  additional estimates covariance, 543
  ANOVA, 542
  B-spline basis, 31
  Bernoulli distribution, 531
  binary distribution, 531
  binomial distribution, 531
  bounds, 528
  computational method, 79, 80
  convergence criterion, 42–44, 46
  convergence status, 541
  correlation, 542
  covariance, 542
  dimensions, 541
  displayed output, 540
  distribution functions, 538
  empirical Bayes estimate, 534
  fit statistics, 542
function-based convergence criteria, 42, 43
gamma distribution, 531
Gaussian distribution, 531
general distribution, 531
gradient-based convergence criteria, 42, 44
initial values, 531
input data tables, 527
iteration history, 541
lag functionality, 536
least squares, 537
least squares distribution, 531
linear constraints, 541
log-likelihood functions, 538
multithreading, 79, 540
natural cubic spline basis, 33
negative binomial distribution, 531
normal distribution, 531
number of observations, 541
ODS table names, 33, 543
optimization algorithms, 540
optimization techniques, 46, 80
output data tables, 527
parameter estimates, 542
parameter-based convergence criteria, 42, 46
parameters, 541
Poisson distribution, 531
prediction, 534
procedure task timing, 543
programming statements, 535
residual distribution, 531
restrictions, 534
segmented model example, 544
specifications, 540
splines and spline bases, 29
starting values, 531
test data, 78
truncted power function (TPF) basis, 30
validation, 78
noninferiority tests
binomial proportions, 219
relative risk (FREQTAB), 243
risk difference (FREQTAB), 228
nonsingular parameterization
Shared Concepts, 56
normal distribution
NLMOD procedure, 531
np charts
central line, 812
control limit equations, 812
control limit parameters, 812
notation, 811
subgroup summary statistics, 811
null model log likelihood
PHSELECT procedure, 618
number of observations
GAMMOD procedure, 333
GENSELECT procedure, 405
KCLUS procedure, 439
LOGSELECT procedure, 496
PCA procedure, 573
PHSELECT procedure, 618
PLSMOD procedure, 662
QTRSELECT procedure, 706
REGSELECT procedure, 756
TREESPLIT procedure, 888
VARREDUCE procedure, 1018
number of variables
PCA procedure, 573
odds ratio
Breslow-Day test (FREQTAB), 262
case-control studies (FREQTAB), 236
certainty limits (FREQTAB), 237, 240
exact confidence limits (FREQTAB), 238
FREQTAB procedure, 236
likelihood ratio confidence limits (FREQTAB), 238
logit adjusted (FREQTAB), 260
Mantel-Haenszel adjusted (FREQTAB), 260
mid-p confidence limits (FREQTAB), 239
score confidence limits (FREQTAB), 237
Wald (log) confidence limits (FREQTAB), 237
Zelen’s exact test (FREQTAB), 262
ODS (Output Delivery System)
CORRELATION procedure and, 102
ODS graph names
FREQTAB procedure, 286
GENSELECT procedure, 409
LOGSELECT procedure, 501
PCA procedure, 576
PHSELECT procedure, 622
QTRSELECT procedure, 709
REGSELECT procedure, 760
TREESPLIT procedure, 891
ODS Graphics
GAMMOD procedure, 336
ODS table names
ASSESS procedure, 33
BINNING procedure, 33
CARDINALITY procedure, 33
CORRELATION procedure, 33
GAMMOD procedure, 33, 335
GENSELECT procedure, 33
KCLUS procedure, 33
LOGSELECT procedure, 33
NLMOD procedure, 33
PARTITION procedure, 33
PCA procedure, 33, 575
PHSELECT procedure, 33
PLSMOD procedure, 33, 663
QTRSELECT procedure, 33
REGSELECT procedure, 33
TREESPLIT procedure, 33, 890
VARIMPUTE procedure, 33
VARREDUCE procedure, 33
optimization algorithms
GAMMOD procedure, 332
GENSELECT procedure, 404
LOGSELECT procedure, 495
NLMOD procedure, 540
PHSELECT procedure, 617
optimization techniques
ASSESS procedure, 46, 80
BINNING procedure, 46, 80
CARDINALITY procedure, 46, 80
CORRELATION procedure, 46, 80
GAMMOD procedure, 46, 80
GENSELECT procedure, 46, 80
KCLUS procedure, 46, 80
LOGSELECT procedure, 46, 80
NLMOD procedure, 46, 80
PARTITION procedure, 46, 80
PCA procedure, 46, 80
PHSELECT procedure, 46, 80
PLSMOD procedure, 46, 80
QTRSELECT procedure, 46, 80
REGSELECT procedure, 46, 80
Shared Concepts, 46
TREESPLIT procedure, 46, 80
VARIMPUTE procedure, 46, 80
VARREDUCE procedure, 46, 80
options summary
CLASS statement, 11, 1005
EFFECT statement, 20, 370, 472, 602, 650, 688, 741
PROC BINNING statement, 932
PROC CARDINALITY statement, 956
PROC GAMMOD statement, 306
PROC GENSELECT statement, 364
PROC KCLUS statement, 425
PROC LOGSELECT statement, 466
PROC NLMOD statement, 526
PROC PHSELECT statement, 595
PROC QTRSELECT statement, 683
PROC REGSELECT statement, 737
PROC TREESPLIT statement, 849
PROC VARREDUCE statement, 1003
ordering
of class levels (Shared Concepts), 48
ordinal parameterization
Shared Concepts, 57
ORTHEFFECT parameterization
Shared Concepts, 58
ORTHORDINAL parameterization
Shared Concepts, 58
ORTHOTHERM parameterization
Shared Concepts, 58
ORTHPOLY parameterization
Shared Concepts, 58
ORTHREF parameterization
Shared Concepts, 59
outer iteration
GAMMOD procedure, 328
OUTP= data table
CORRELATION procedure, 100
output CAS tables
GAMMOD procedure, 335
GENSELECT procedure, 408
KCLUS procedure, 443
LOGSELECT procedure, 500
PARTITION procedure, 977
PHSELECT procedure, 620
QTRSELECT procedure, 708
REGSELECT procedure, 759
output data tables
PCA procedure, 566
PLSMOD procedure, 651
saving correlations in, 108
output table
TREESPLIT procedure, 889
OUTSTAT= data table
PCA procedure, 571
p charts
central line, 814
control limit equations, 814
control limit parameters, 814
notation, 813
subgroup summary statistics, 813
pairwise deletion, 100
parameter estimates
GAMMOD procedure, 335
GENSELECT procedure, 407
LOGSELECT procedure, 499
PHSELECT procedure, 620
PLSMOD procedure, 663
QTRSELECT procedure, 708
REGSELECT procedure, 758
parameter-based convergence criteria
ASSESS procedure, 42, 46
BINNING procedure, 42, 46
CARDINALITY procedure, 42, 46
CORRELATION procedure, 42, 46
GAMMOD procedure, 42, 46
GENSELECT procedure, 42, 46
KCLUS procedure, 42, 46
LOGSELECT procedure, 42, 46
NLMOD procedure, 42, 46
PARTITION procedure, 42, 46
PCA procedure, 42, 46
PHSELECT procedure, 42, 46
PLSMOD procedure, 42, 46
QTRSELECT procedure, 42, 46
REGSELECT procedure, 42, 46
Shared Concepts, 42, 46
TREESPLIT procedure, 42, 46
VARIMPUTE procedure, 42, 46
VARREDUCE procedure, 42, 46

parameterization
dummy (Shared Concepts), 52
dummy (VARREDUCE procedure), 1013
effect (Shared Concepts), 57
GLM (Shared Concepts), 52, 1013
nonsingular (Shared Concepts), 56
ordinal (Shared Concepts), 57
ORTHEFFECT (Shared Concepts), 58
ORTHORDINAL (Shared Concepts), 58
ORTHOSTERM (Shared Concepts), 58
ORTHPOLY (Shared Concepts), 58
ORTHREF (Shared Concepts), 59
polynomial (Shared Concepts), 58
reference (Shared Concepts), 57
Shared Concepts, 49
thermometer (Shared Concepts), 57

partial correlation
PCA procedure, 574
principal components, 574

partial covariance
PCA procedure, 574
principal components, 574

partial least squares
PLSMOD procedure, 632, 633, 655

partial likelihood
PHSELECT procedure, 612
PARTITION procedure, 969

B-spline basis, 31
centering and scaling information, 574
computational method, 79, 80, 559
correction for means, 561
correlation, 574
covariance, 574
crime rate data, example, 554
displayed output, 573
eigenvalue decomposition method, 551, 569
eigenvalues, 574
eigenvalues and eigenvectors, 569, 572, 574
eigenvectors, 574
test data, 78
training, validation, and test data, 976
truncate power function (TPF) basis, 30
validation, 78

PARTITION statement
syntax (Shared Concepts), 34
pattern tests, see Shewhart charts, tests for special causes

PCA procedure, 550
B-spline basis, 31
centering and scaling information, 574
computational method, 79, 80, 559
correction for means, 561
correlation, 574
covariance, 574
crime rate data, example, 554
displayed output, 573
eigenvalue decomposition method, 551, 569
eigenvalues, 574
eigenvalues and eigenvectors, 569, 572, 574
eigenvectors, 574
examples, 576
explained variation of variables, 574
function-based convergence criteria, 42, 43
gradation-based convergence criteria, 42, 44
input data tables, 559
ITERGS method, 551, 570
loadings, 570, 575
model information, 573
multithreading, 79
natural cubic spline basis, 33
NIPALS method, 551, 570, 578
number of observations, 573
number of variables, 573
ODS graph names, 576
ODS table names, 33, 575
optimization techniques, 46, 80
output data tables, 561, 566, 571, 572
OUTSTAT= data table, 571
parameter-based convergence criteria, 42, 46
partial correlation, 574
partial covariance, 574
RANDOM method, 551, 570, 581
regression coefficients, 574
regression statistics, 574
simple statistics, 573
splines and spline bases, 29
test data, 78
timing, 575
total variance, 574
truncated power function (TPF) basis, 30
validation, 78
Pearson chi-square test
  FREQTAB procedure, 200
Pearson correlation coefficient
  FREQTAB procedure, 204, 208
Pearson correlation statistics
  Pearson product-moment correlation, 98
  probability values, 98
  suppressing, 93
penalized likelihood estimation
  GAMMOD procedure, 326
percentage of variation accounted for by extracted factors
  PLSMOD procedure, 663
performance iteration
  GAMMOD procedure, 329
phi coefficient
  FREQTAB procedure, 204
PHSELECT procedure, 587, 605
  B-spline basis, 31
  candidates for addition or removal, 619
  class level, 597, 618
  computational method, 79, 80
  confidence limits, 605
  convergence criterion, 42–44, 46, 596
  convergence status, 618
  correlation matrix, 596, 620
  covariance matrix, 597, 620
  dimensions, 620
  displayed output, 617
  fit statistics, 620
  function-based convergence criteria, 42, 43
  global influence, 615
  gradient-based convergence criteria, 42, 44
  Hessian, 597
  input data tables, 597
  iteration history, 618
  LASSO selection, 612
  left-truncation, 605
  likelihood displacement, 615
  model information, 618
  model options summary, 604
  multithreading, 79, 617
  natural cubic spline basis, 33
  null model log likelihood, 618
  number of observations, 618
  ODS graph names, 622
  ODS table names, 33, 621
  optimization algorithms, 617
  optimization techniques, 46, 80
  output CAS tables, 620
  output data tables, 606
  parameter estimates, 620
  parameter-based convergence criteria, 42, 46
  partial likelihood, 612
  residuals, 615
  selected effects, 619
  selection information, 618
  selection reason, 619
  selection summary, 619
  splines and spline bases, 29
  stop reason, 619
  test data, 78
  truncated power function (TPF) basis, 30
  Type III tables, 620
PLSMOD procedure, 632
  algorithms, 646
  B-spline basis, 31
  centering, 661
  centering and scaling information, 662
  class level, 647, 662
  compared with other procedures, 632
  components, 632
  computational method, 79, 80, 646
  convergence criterion, 42–44, 46
  dimensions, 662
  displayed output, 662
  examples, 665
  factors, 632
  factors, selecting the number of, 639
  function-based convergence criteria, 42, 43
  gradient-based convergence criteria, 42, 44
  input data tables, 645
  introductory example, 636
  latent variables, 632
  latent vectors, 632
  missing values, 661
  model details, 663
  model information, 662
  multithreading, 79
  natural cubic spline basis, 33
  number of observations, 662
  ODS table names, 33, 663
  optimization techniques, 46, 80
  output data tables, 651, 652
  parameter estimates, 663
  parameter-based convergence criteria, 42, 46
  reduced least squares regression, 632, 633, 655
  percentage of variation accounted for by extracted factors, 663
  predicting new observations, 643
  principal component regression, 633, 656
  reduced rank regression, 633, 656
  scaling, 661
  SIMPLS method, 656
  splines and spline bases, 29
  test data, 78
test set validation, 659, 663, 665
timing, 663
truncated power function (TPF) basis, 30
validation, 78
Poisson distribution
  NLMOD procedure, 531
polychoric correlation coefficient
  FREQTAB procedure, 204, 211
polynomial effects
  Shared Concepts, 53
  VARREDUCE procedure, 1014
polynomial parameterization
  Shared Concepts, 58
predicted probability names
  TREESPLIT procedure, 889
prediction
  NLMOD procedure, 534
prevalence-adjusted bias-adjusted kappa
  FREQTAB procedure, 254
principal component
  regression (PLSMOD), 633, 656
principal components
  interpreting eigenvalues, 556
  partialing out variables, 568
PROC BINNING, 927
PROC BINNING binning methods
  bucket, 928
  cutpoint, 928
  quantile, 928
  tree, 928
  Winsorized, 928
PROC BINNING features, 929
programming statements
  NLMOD procedure, 535
proportion difference
  FREQTAB procedure, 222
proportions, see binomial proportions
QTRSELECT procedure, 671, 690
  B-spline basis, 31
  candidates for addition or removal, 706
  class level, 684, 706
  computational method, 79, 80, 705
  convergence criterion, 42–44, 46
  diagnostic statistics, 700
  dimensions, 706
  displayed output, 705
  fit criteria, 697
  fit statistics, 707
  function-based convergence criteria, 42, 43
  gradient-based convergence criteria, 42, 44
  information criteria, 698
  input data tables, 684
  introductory example, 675
model options summary, 689
multithreading, 79, 705
natural cubic spline basis, 33
number of observations, 706
ODS graph names, 709
ODS table names, 33, 708
optimization techniques, 46, 80
output CAS tables, 708
output data tables, 691
parameter estimates, 708
parameter-based convergence criteria, 42, 46
quantile regression, 695
selected effects, 707
selection information, 705
selection reason, 707
selection summary, 706
significance level criteria, 699
spline regression, 695
stop reason, 706
test data, 78, 702
timing, 708
truncated power function (TPF) basis, 30
validation, 78, 702
quantile regression
  QTRSELECT procedure, 695
quasi-complete separation
  GENSELECT procedure, 397
  LOGSELECT procedure, 488
R charts
  central line, 803
  control limit equations, 803
  subgroup summary statistics, 803
RANDOM method
  PCA procedure, 551, 570
rank scores
  FREQTAB procedure, 198
reduce options
  VARREDUCE procedure, 198
reduce options summary
  VARREDUCE procedure, 1008
reduced error
  TREESPLIT procedure, 888
reduced rank regression, 633
  PLSMOD procedure, 656
reduced-error pruning
  TREESPLIT procedure, 868, 879
reference parameterization
  Shared Concepts, 57
regression
  partial least squares (PROC PLSMOD), 633, 655
  principal component (PROC PLSMOD), 633, 656
  reduced rank (PROC PLSMOD), 633, 656
regression coefficients
Subject Index

PCA procedure, 574
regression effects
Shared Concepts, 52, 53
VARREDUCE procedure, 1014
regression statistics
PCA procedure, 574
regression trees, see decision trees
REGSELECT procedure, 725, 744
ANOVA table, 757
B-spline basis, 31
candidates for addition or removal, 756
class level, 738, 756
computational method, 79, 80, 754
convergence criterion, 42–44, 46
diagnostic statistics, 751
dimensions, 756
displayed output, 755
fit criteria, 749
fit statistics, 758
function-based convergence criteria, 42, 43
gradient-based convergence criteria, 42, 44
input data tables, 738
introductory example, 729
model options summary, 743
multithreading, 79, 754
natural cubic spline basis, 33
number of observations, 756
ODS graph names, 760
ODS table names, 33, 759
optimization techniques, 46, 80
output CAS tables, 759
parameter estimates, 758
parameter-based convergence criteria, 42, 46
selected effects, 757
selection information, 756
selection reason, 757
selection summary, 756
splines and spline bases, 29
stop reason, 757
test data, 78, 753
timing, 759
truncated power function (TPF) basis, 30
Type III tables, 759
validation, 78, 753
relative risk
equivalence tests (FREQTAB), 244
likelihood ratio confidence limits (FREQTAB), 242
noninferiority tests (FREQTAB), 243
superiority tests (FREQTAB), 244
tests (FREQTAB), 243
Wald confidence limits (FREQTAB), 240
relative risks
cohort studies (FREQTAB), 240
exact confidence limits (FREQTAB), 242
FREQTAB procedure, 240
logit adjusted (FREQTAB), 261
Mantel-Haenszel adjusted (FREQTAB), 261
residual distribution
NLMOD procedure, 531
residuals
and partial correlation (PCA), 571
partial correlation (PCA), 568
Schoenfeld (PHSELECT), 615
score (PHSELECT), 615
weighted Schoenfeld (PHSELECT), 615
response level ordering
GAMMOD procedure, 314
GENSELECT procedure, 373
LOGSELECT procedure, 475
response profile
GAMMOD procedure, 333
GENSELECT procedure, 405
LOGSELECT procedure, 497
response variable options
GAMMOD procedure, 314
GENSELECT procedure, 372
LOGSELECT procedure, 474
restrictions
NLMOD procedure, 534
reverse response level ordering
GAMMOD procedure, 314
GENSELECT procedure, 373
ridit scores
FREQTAB procedure, 198
risk difference
certainty limits (FREQTAB), 224
equivalence tests (FREQTAB), 231
exact confidence limits (FREQTAB), 226
FREQTAB procedure, 222
noninferiority tests (FREQTAB), 228
superiority tests (FREQTAB), 230
tests (FREQTAB), 228
TOST (FREQTAB), 231, 245
risks, see also binomial proportions
FREQTAB procedure, 222
ROC information
ASSESS procedure, 915, 918
row mean scores statistic
Mantel-Haenszel (FREQTAB), 258
rules for lack of control, see Shewhart charts, tests for special causes
runs rules, see Shewhart charts, tests for special causes
runs tests, see Shewhart charts, tests for special causes
s charts
central line, 804
control limit equations, 804
notation, 804
subgroup summary statistics, 804
saving correlations
example, 108
Schoenfeld residuals
PHSELECT procedure, 615
score confidence limits
odds ratio (FREQTAB), 237
relative risk (FREQTAB), 241
risk difference (FREQTAB), 224
score residuals
PHSELECT procedure, 615
selected effects
GENSELECT procedure, 407
LOGSELECT procedure, 498
PHSELECT procedure, 619
QTRSELECT procedure, 707
REGSELECT procedure, 757
selected variable
VARREDUCE procedure, 1018
selection information
GENSELECT procedure, 406
LOGSELECT procedure, 497
PHSELECT procedure, 618
QTRSELECT procedure, 705
REGSELECT procedure, 756
selection plots
Shared Concepts, 69
selection reason
GENSELECT procedure, 407
LOGSELECT procedure, 498
PHSELECT procedure, 619
QTRSELECT procedure, 707
REGSELECT procedure, 757
SELECTION statement
syntax (Shared Concepts), 34
selection summary
GENSELECT procedure, 406
LOGSELECT procedure, 498
PHSELECT procedure, 619
QTRSELECT procedure, 706
REGSELECT procedure, 756
VARREDUCE procedure, 1018
separation
GENSELECT procedure, 397
LOGSELECT procedure, 488
Shared Concepts
ABSICONV option, 42
ABSFCONV option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
adaptive LASSO selection, 67
ANCOVA effects, 53
ANOVA effects, 52
at sign (@) operator, 51, 54, 1015
backward elimination, 62
bar (|) operator, 50, 53, 54, 1015
CLASS statement, 10, 47
classification variables, 47
CODE statement, 14
collection effect (EFFECT statement), 21
colon (:) operator, 51
continuous-by-class effects, 55
continuous-nesting-class effects, 55
crossed effects, 54
dash (-) operator, 51
DISPLAY statement, 17
DISPLAYOUT statement, 18
double dash (---) operator, 52
dummy parameterization, 52
effect parameterization, 57
EFFECT statement, 19
FCONV option, 43
FCONV2 option, 43
forward selection, 60
forward swap selection, 65
FTOL option, 43
FTOL2 option, 43
function-based convergence criteria, 42, 43
GCONV option, 44
GCONV2 option, 44
general effects, 56
GLM parameterization, 52, 1013
gradient-based convergence criteria, 42, 44
group LASSO selection, 67
GTOL option, 44
GTOL2 option, 44
interaction effects, 54
intercept, 53
LAR selection, 65
LASSO selection, 66
levelization, 47
main effects, 53
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
missing values, CLASS variables, 48
multimember effect (EFFECT statement), 21
nested effects, 54
nested versus crossed effects, 54
nonsingular parameterization, 56
NORMALIZE= option, 45

optimization techniques, 46
ORDER= option, 48
ordering of class levels, 48
ordinal parameterization, 57
ORTHEFFECT parameterization, 58
ORTHORDINAL parameterization, 58
ORTHOTHERM parameterization, 58
ORTHPOLY parameterization, 58
ORTHREF parameterization, 59
parameter-based convergence criteria, 42, 46
partition statement, 34
polynomial effect (EFFECT statement), 23
polynomial effects, 53
polynomial parameterization, 58
reference parameterization, 57
regression effects, 52, 53
selection plots, 69
SELECTION statement, 34
singular parameterization, 53
sort order of class levels, 48
spline basis, B-spline, 31
spline basis, natural cubic spline, 33
spline basis, truncated power function, 30
spline effect (EFFECT statement), 26
stepwise selection, 63
TECHNIQUE= option, 46
thermometer parameterization, 57
XCONV option, 46
XTOL option, 46
Shewhart charts, tests for special causes, 797
definitions, 817, 818
standard tests, 816–818, 820
standard tests, interpreting, 820
standard tests, modifying, 820
varying subgroup sample sizes, 821
significance level criteria
QTRSELECT procedure, 699
simple statistics
PCA procedure, 573
SIMPLS method
PLSMOD procedure, 656
singular parameterization
Shared Concepts, 53
VARREDUCE procedure, 1015
Somers’ D statistics
FREQTAB procedure, 204, 208
sort order
of class levels (Shared Concepts), 48
SPC procedure
details, 798
equalities, 833
reading preestablished control limits, 822
Spearman rank correlation coefficient
FREQTAB procedure, 204, 209
spline details
GAMMMOD procedure, 333
splines and spline bases
ASSESS procedure, 29
BINNING procedure, 29
CARDINALITY procedure, 29
CORRELATION procedure, 29
GAMMMOD procedure, 29
GENSELECT procedure, 29
KCLUS procedure, 29
LOGSELECT procedure, 29
PARTITION procedure, 29
PLSMOD procedure, 29
QTRSELECT procedure, 29
REGSELECT procedure, 29
TREESPLIT procedure, 29
VARIMPUTE procedure, 29
VARREDUCE procedure, 29
splitting criteria
TREESPLIT procedure, 863, 872
standard deviation, 93
standardization
KCLUS procedure, 442
standardized residuals
FREQTAB procedure, 200
starting values
NLMOD procedure, 531
stepwise selection
Shared Concepts, 63
stop reason
GENSELECT procedure, 407
LOGSELECT procedure, 498
PHSELECT procedure, 619
QTRSELECT procedure, 706
REGSELECT procedure, 757
stratified analysis
FREQTAB procedure, 112, 145
Stuart’s tau-c statistic
FREQTAB procedure, 204, 207
sums of squares and crossproducts, 93
superiority tests
binomial proportions, 220
relative risk (FREQTAB), 244
risk difference (FREQTAB), 230
supervised variable selection
VARREDUCE procedure, 1010
supplementary rules, see Shewhart charts, tests for
special causes
surrogate rules
TREESPLIT procedure, 853, 874
table scores
  FREQTAB procedure, 198
tables
  contingency (FREQTAB), 112
  crosstabulation (FREQTAB), 112, 275
  multiway (FREQTAB), 112, 274
  one-way frequency (FREQTAB), 112, 273
target variables
  ASSESS procedure, 914
  Tarone’s adjustment
  Breslow-Day test (FREQTAB), 262
test data
  ASSESS procedure, 78
  BINNING procedure, 78
  CARDINALITY procedure, 78
  CORRELATION procedure, 78
  GAMMOD procedure, 78
  GENESELECT procedure, 78
  KCLUS procedure, 78
  LOGSELECT procedure, 78
  NLMOD procedure, 78
  PARTITION procedure, 78
  PCA procedure, 78
  PHSELECT procedure, 78
  PLSMOD procedure, 78
  QTRSELECT procedure, 78, 702
  REGSELECT procedure, 78, 753
  TREESPLIT procedure, 78
  VARIMPUTE procedure, 78
  VARREDUCE procedure, 78
test set validation
  PLSMOD procedure, 659, 663
tests for smoothing components
  GAMMOD procedure, 331, 335
tetrachoric correlation coefficient
  FREQTAB procedure, 211
thermometer parameterization
  Shared Concepts, 57
thin-plate regression splines
  GAMMOD procedure, 322
thin-plate smoothing splines
  GAMMOD procedure, 323
timing
  PCA procedure, 575
  PLSMOD procedure, 663
  QTRSELECT procedure, 708
  REGSELECT procedure, 759
TOST
equivalence tests (FREQTAB), 220, 231, 245
total variance
  PCA procedure, 574
TPF basis, see truncated power function (TPF) basis
training, validation, and test data
  PARTITION procedure, 976
tree performance
  TREESPLIT procedure, 888
tree-based binning
  BINNING procedure, 939
  TREESPLIT procedure, 839
    B-spline basis, 31
    best configuration, 889
    C4.5 pruning, 867, 878
    computational method, 79, 80
    convergence criterion, 42–44, 46
    cost complexity, 888
    cost-complexity pruning, 867, 876
    cross validation, 877
    cv statistics, 888
    decision trees, 869
    displayed output, 887
    evaluation history, 889
    function-based convergence criteria, 42, 43
    gradient-based convergence criteria, 42, 44
    hyperparameter tuning, 884
    input data tables, 852
    model information, 888
    multithreading, 79
    natural cubic spline basis, 33
    number of observations, 888
    ODS graph names, 891
    ODS table names, 33, 890
    optimization techniques, 46, 80
    output data tables, 865
    output table, 889
    parameter-based convergence criteria, 42, 46
    predicted probability names, 889
    reduced error, 888
    reduced-error pruning, 868, 879
    splines and spline bases, 29
    splitting criteria, 863, 872
    surrogate rules, 853, 874
    test data, 78
    tree performance, 888
    truncated power function (TPF) basis, 30
    tuner information, 889
    tuner results, 889
    tuner summary, 889
    tuner timing, 889
    validation, 78
    variable importance, 888
trend test
  FREQTAB procedure, 246
trimmed statistics
  BINNING procedure, 941
truncated power function (TPF) basis
  ASSESS procedure, 30
  BINNING procedure, 30
  CARDINALITY procedure, 30
Subject Index

- CORRELATION procedure, 30
- GAMMOD procedure, 30
- GENSELECT procedure, 30
- KCLUS procedure, 30
- LOGSELECT procedure, 30
- NLMOD procedure, 30
- PARTITION procedure, 30
- PCA procedure, 30
- PHSELECT procedure, 30
- PLSMOD procedure, 30
- QTRSELECT procedure, 30
- REGSELECT procedure, 30
- Shared Concepts, 30
- TREESPLIT procedure, 30
- VARIMPUTE procedure, 30
- VARREDUCE procedure, 30

- tuner information
  - TREESPLIT procedure, 889
- tuner results
  - TREESPLIT procedure, 889
- tuner summary
  - TREESPLIT procedure, 889
- tuner timing
  - TREESPLIT procedure, 889

- Type III tables
  - LOGSELECT procedure, 499
  - PHSELECT procedure, 620
  - REGSELECT procedure, 759

- u charts
  - central line, 815
  - compared with c charts, 815
  - control limit equations, 815, 816
  - control limit parameters, 816
  - notation, 814
  - subgroup summary statistics, 815

- uncertainty coefficients
  - FREQTAB procedure, 204, 213, 214

- unsupervised variable selection
  - VARREDUCE procedure, 1010

- validation
  - ASSESS procedure, 78
  - BINNING procedure, 78
  - CARDINALITY procedure, 78
  - CORRELATION procedure, 78
  - GAMMOD procedure, 78
  - GENSELECT procedure, 78
  - KCLUS procedure, 78
  - LOGSELECT procedure, 78
  - NLMOD procedure, 78
  - PARTITION procedure, 78
  - PCA procedure, 78
  - PHSELECT procedure, 78
  - PLSMOD procedure, 78
  - QTRSELECT procedure, 78, 702
  - REGSELECT procedure, 78, 753
  - TREESPLIT procedure, 78
  - VARIMPUTE procedure, 78
  - VARREDUCE procedure, 78

- variable importance
  - TREESPLIT procedure, 888

- variable information value (IV) table
  - BINNING procedure, 941

- variable transformation information table
  - BINNING procedure, 941

- variances, 93

- VARIMPUTE procedure, 985
  - B-spline basis, 31
  - computational method, 79, 80
  - convergence criterion, 42–44, 46
  - displayed output, 991
  - function-based convergence criteria, 42, 43
  - gradient-based convergence criteria, 42, 44
  - imputation information table, 992
  - imputation requests table, 991
  - input data tables, 988
  - multithreading, 79
  - natural cubic spline basis, 33
  - ODS table names, 33, 992
  - optimization techniques, 46, 80
  - output data tables, 990
  - parameter-based convergence criteria, 42, 46
  - splines and spline bases, 29
  - test data, 78
  - truncated power function (TPF) basis, 30
  - validation, 78

- VARREDUCE procedure, 996
  - ANCOVA effects, 1014
  - ANOVA effects, 1014
  - B-spline basis, 31
  - bar (|) operator, 1014
  - computational method, 79, 80, 1012
  - continuous-by-class effects, 1017
  - continuous-nesting-class effects, 1016
  - convergence criterion, 42–44, 46
  - correlations, 1004
  - crossed effects, 1015
  - displayed output, 1018
  - dummy parameterization, 1013
  - fit criteria, 1011
  - function-based convergence criteria, 42, 43
  - general effects, 1017
  - gradient-based convergence criteria, 42, 44
  - input data tables, 1003
  - interaction effects, 1015
  - intercept, 1014
  - main effects, 1014
maximum effects, 1009
maximum steps, 1009
minimal explained variance increment, 1009
missing values, 1009
multithreading, 79
natural cubic spline basis, 33
nested effects, 1016
nested versus crossed effects, 1016
number of observations, 1018
ODS table names, 33, 1018
optimization techniques, 46, 80
parameter-based convergence criteria, 42, 46
polynomial effects, 1014
regression effects, 1014
selected variable, 1018
selection summary, 1018
singular parameterization, 1015
splines and spline bases, 29
supervised variable selection, 1010
test data, 78
truncated power function (TPF) basis, 30
unsupervised variable selection, 1010
validation, 78
variance explained, 1009

Wald confidence limits
risk difference (FREQTAB), 226
weighted kappa coefficient
FREQTAB procedure, 249, 252
weighted Schoenfeld residuals
PHSELECT procedure, 615
weighting
GAMMOD procedure, 322
Western Electric rules, see Shewhart charts, tests for special causes
Wilson confidence limits
proportions (FREQTAB), 217
Winsorized statistics
BINNING procedure, 941
within-cluster statistics
KCLUS procedure, 440

\( \bar{X} \) charts
central line, 800
control limit equations, 800
subgroup summary statistics, 800

Yule’s \( Q \) statistic
FREQTAB procedure, 206

Zelen’s test
equal odds ratios (FREQTAB), 262
zeros, structural and random
agreement statistics (FREQTAB), 256
Syntax Index

ABSCONV option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENSELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSFCONV option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENSELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSFGCONV option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENSELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSGCONV option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENSELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSFTOL option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENSELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSTOL option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENESELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ADAPTIVE option
SELECTION statement (ASSESS), 36
SELECTION statement (BINNING), 36
SELECTION statement (CARDINALITY), 36
SELECTION statement (CORRELATION), 36
SELECTION statement (GAMMOD), 36
SELECTION statement (GENSELECT), 36
SELECTION statement (KCLUS), 36
SELECTION statement (LOGSELECT), 36
SELECTION statement (NLMODE), 36
SELECTION statement (PARTITION), 36
SELECTION statement (PCA), 36
SELECTION statement (PHSELECT), 36
SELECTION statement (PLSMOD), 36
SELECTION statement (QTRSELECT), 36
SELECTION statement (REGSELECT), 36
SELECTION statement (TREESPLIT), 36
SELECTION statement (VARIMPUTE), 36
SELECTION statement (VARREDUCE), 36

ABSXCONV option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENESELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ABSXTOL option
PROC ASSESS statement, 42
PROC BINNING statement, 42
PROC CARDINALITY statement, 42
PROC CORRELATION statement, 42
PROC GAMMOD statement, 42
PROC GENESELECT statement, 42
PROC KCLUS statement, 42
PROC LOGSELECT statement, 42
PROC NLMOD statement, 42
PROC PARTITION statement, 42
PROC PCA statement, 42
PROC PHSELECT statement, 42
PROC PLSMOD statement, 42
PROC QTRSELECT statement, 42
PROC REGSELECT statement, 42
PROC TREESPLIT statement, 42
PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

PROC VARIMPUTE statement, 42
PROC VARREDUCE statement, 42

ADJUST option (PLCORR)
TABLES statement (FREQTAB), 168

AGREE option
EXACT statement (FREQTAB), 126
OUTPUT statement (FREQTAB), 137
TABLES statement (FREQTAB), 148
TEST statement (FREQTAB), 191

AIC option
REDUCE statement, 1009

AICCC option
REDUCE statement, 1009

AJCHI option
OUTPUT statement (FREQTAB), 137

ALGORITHM= option
PROC PLSMOD statement, METHOD=PLS option, 646

ALL option
OUTPUT statement (FREQTAB), 138
OUTPUT statement (GENSELECT), 379
OUTPUT statement (LOGSELECT), 478
TABLES statement (FREQTAB), 150

ALLN option
chart statements (SPC), 793

ALLOBS option
MODEL statement (SPC), 317

ALPHA option
PROC CORRELATION statement, 93

ALPHA= option
ESTIMATE statement (NLMODE), 530
EXACT statement (FREQTAB), 132
GROW statement (TREESPLIT), 864
OUTPUT statement (GAMMOD), 321
OUTPUT statement (GENSELECT), 379
OUTPUT statement (LOGSELECT), 478
PREDICT statement (NLMod), 534
PROC GAMMOD statement, 307
PROC GENSELECT statement, 365
PROC LOGSELECT statement, 467
PROC NLMod statement, 527
PROC PHSELECT statement, 596
PROC QTRSELECT statement, 684
PROC REGSELECT statement, 738
PRUNE statement (TREESPLIT), 867
TABLES statement (FREQTAB), 150
ASSESS procedure, BY statement, 912
ASSESS procedure, CLASS statement
  DESCENDING option, 11, 1005
  MISSING option, 11, 1005
  ORDER= option, 11
  PARAM= option, 12
  REF= option, 13
  SPLIT option, 13
ASSESS procedure, CODE statement
  COMMENT option, 15
  FILE= option, 15
  FORMATWIDTH= option, 15
  INDENTSIZE= option, 15
  LABELID= option, 16
  LINESIZE= option, 16
  NOTRIM option, 16
  OUT= option, 16
ASSESS procedure, DISPLAY statement
  CASESENSITIVE option, 18
  EXCLUDE option, 18
  EXCLUDEALL option, 18
  TRACE option, 18
ASSESS procedure, DISPLAYOUT statement
  INCLUDEALL option, 19
  NOREPLACE option, 19
  REPEATED option, 19
ASSESS procedure, EFFECT statement
  BASIS option (spline), 26
  DATABOUNDARY option (spline), 26
  DEGREE option (polynomial), 24
  DEGREE option (spline), 27
  DETAILS option (multimember), 23
  DETAILS option (polynomial), 24
  DETAILS option (spline), 27
  KNOTMAX= option (spline), 27
  KNOTMETHOD option (spline), 27
  KNOTMIN= option (spline), 28
  MDEGREE option (polynomial), 24
  NATURALCUBIC option (spline), 28
  NOEFFECT option (multimember), 23
  NOSEPARATE option (polynomial), 24
  SEPARATE option (spline), 28
  SPLIT option (spline), 29
ASSESS procedure, FITSTAT statement
  DELIMITER= option, 913
  DLM= option, 913
  PEVENT= option, 913
  PVAR= option, 913
ASSESS procedure, INPUT statement, 914
ASSESS procedure, PARTITION statement
  FRACTION option, 34
  ROLEVAR= option, 34
ASSESS procedure, PROC ASSESS statement, 911
  ABSCONV option, 42
  ABSFCOV option, 42
  ABSFTOL option, 42
  ABSSGCONV option, 42
  ABSSGTOL option, 42
  ABSTOL option, 42
  ABSXCONV option, 42
  ABSXTOL option, 42
  DATA= option, 911
  FCONV option, 43
  FCONV2 option, 43
  FITSTATOUT= option, 912
  FTOL option, 43
  FTOL2 option, 43
  GCONV option, 44
  GCONV2 option, 44
  GTOL option, 44
  GTOL2 option, 44
  LIFTOPTION, 912
  MAXFUNC= option, 45
  MAXITER= option, 45, 912
  MAXTIME= option, 45
  MINITER= option, 45
  NBINS= option, 912
  NCUTS= option, 912
  NORMALIZE= option, 45
  NTHREADS= option, 912
  ROCOUT= option, 912
  TECHNIQUE= option, 46
  XCONV option, 46
  XTOL option, 46
ASSESS procedure, SELECTION statement
  ADAPTIVE option, 36
  CHOOSE= option, 36
  COMPETITIVE option, 36
  CRITERION= option, 36
  DETAILS= option, 38, 39
  FAST option, 37
  HIERARCHY= option, 39
  LS_COEFS= option, 37
  MAXEFFECTS= option, 37
  MAXSTEPS= option, 37
  METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41
ASSESS procedure, syntax, 911
ASSESS procedure, TARGET statement, 914
ASSIGNMISSING= option
PROC TREESPLIT statement, 850
AUTOTUNE statement
TREESPLIT procedure, 856
BARNARD option
EXACT statement (FREQTAB), 127
BASIS option
EFFECT statement, spline (ASSESS), 26
EFFECT statement, spline (BINNING), 26
EFFECT statement, spline (CARDINALITY), 26
EFFECT statement, spline (CORRELATION), 26
EFFECT statement, spline (GAMMOD), 26
EFFECT statement, spline (GENSELECT), 26
EFFECT statement, spline (KCLUS), 26
EFFECT statement, spline (PARTITION), 26
EFFECT statement, spline (PCA), 26
EFFECT statement, spline (PHSELECT), 26
EFFECT statement, spline (PLSMOD), 26
EFFECT statement, spline (QTRSELECT), 26
EFFECT statement, spline (REGSELECT), 26
EFFECT statement, spline (TREESPLIT), 26
EFFECT statement, spline (VARIMPUTE), 26
EFFECT statement, spline (VARREDUCE), 26
BDCHI option
OUTPUT statement (FREQTAB), 138
BDT option (CMH)
TABLES statement (FREQTAB), 158
BEST= option
PROC CORRELATION statement, 93
BIC option
REDUCE statement, 1009
BINMETHOD = option
PROC TREESPLIT statement, 851
BINNING procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
BINNING procedure, CODE statement, 935
COMMENT option, 15
FILE= option, 15, 935
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
BINNING procedure, DISPLAY statement
CASESENSITIVE option, 18
EXCLUDE option, 18
EXCLUDEALL option, 18
TRACE option, 18
BINNING procedure, DISPLAYOUT statement
INCLUDEALL option, 19
NOREPLACE option, 19
REPEATED option, 19
BINNING procedure, EFFECT statement
BASIS option (spline), 26
DATABASEBOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
BINNING procedure, INPUT statement, 935
LEVEL= option, 936
NUMBIN= option, 935
BINNING procedure, OUTPUT statement, 936
COPYVARS= option, 937
OUT= option, 936
BINNING procedure, PARTITION statement
FRACTION option, 34
ROLEV AR= option, 34
BINNING procedure, PROC BINNING statement, 932
ABS_CONV option, 42
ABS_CONV option, 42
ABS_FCTOL option, 42
ABS_GCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
DATA= option, 933
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
METHOD= option, 933
MINITER= option, 45
NORMALIZE= option, 45
NUMBIN= option, 934
TECHNIQUE= option, 46
WOE(WOEADJUST=) option, 935
XCONV option, 46
XTOL option, 46
BONFERRONI option
GROW statement (TREESPLIT), 864
BOUNDS statement
NLMOD procedure, 528
BOWKER option
OUTPUT statement (FREQTAB), 145
BOXCHART statement
BOXCHART procedure, 783
BY statement
ASSESS procedure, 912
CORRELATION procedure, 95
FREQTAB procedure, 124
GAMMOD procedure, 309
GENSELECT procedure, 367
LOOSELECT procedure, 469
NLMOD procedure, 528
PARTITION procedure, 973
PCA procedure, 563
PHSELECT procedure, 598
PLSMOD procedure, 647
QTRSELECT procedure, 684
REGSELECT procedure, 738
SPC procedure, 783
C45 option
PRUNE statement (TREESPLIT), 867
CARDINALITY procedure
VAR statement, 957
CARDINALITY procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
CARDINALITY procedure, CODE statement
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
CARDINALITY procedure, DISPLAY statement
CASESENSITIVE option, 18
EXCLUDE option, 18
EXCLUDEALL option, 18
TRACE option, 18
CARDINALITY procedure, DISPLAYOUT statement
INCLUDEALL option, 19
NOREPLACE option, 19
REPEATED option, 19
CARDINALITY procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
CARDINALITY procedure, PARTITION statement
  FRACTION option, 34
  ROLEVAR= option, 34
CARDINALITY procedure, PROC CARDINALITY
  statement, 956
  ABSCONV option, 42
  ABSSFCONV option, 42
  ABSFTOL option, 42
  ABSGCONV option, 42
  ABSGTOL option, 42
  ABSTOL option, 42
  ABSXCONV option, 42
  ABSXTOL option, 42
  DATA= option, 956
  FCONV option, 43
  FCONV2 option, 43
  FTOL option, 43
  FTOL2 option, 43
  GCONV option, 44
  GCONV2 option, 44
  GTOL option, 44
  GTOL2 option, 44
  MAXFUNC= option, 45
  MAXITER= option, 45
  MAXLEVELS= option, 957
  MAXTIME= option, 45
  MINITER= option, 45
  NORMALIZE= option, 45
  ORDER= option, 957
  OUTCARD= option, 956
  OUTDETAILS= option, 957
  TECHNIQUE= option, 46
  XCONV option, 46
  XTOL option, 46
CARDINALITY procedure, SELECTION statement
  ADAPTIVE option, 36
  CHOOSE= option, 36
  COMPETITIVE option, 36
  CRITERION= option, 36
  DETAILS= option, 38, 39
  FAST option, 37
  HIERARCHY= option, 39
  LSCOREFS option, 37
  MAXEFFECTS= option, 37
  MAXSTEPS= option, 37
  METHOD= option, 35
  MINEFFECTS= option, 37
  ORDERSELECT option, 39
  SELECT= option, 37
  SELECTION= option, 41
  STOP= option, 38
  STOPHORIZON= option, 41
CARDINALITY procedure, syntax, 956
CARDINALITY procedure, VAR statement
  ORDER= option, 958
CASESENSITIVE option
  DISPLAY statement (ASSESS), 18
  DISPLAY statement (BINNING), 18
  DISPLAY statement (CARDINALITY), 18
  DISPLAY statement (CORRELATION), 18, 95
  DISPLAY statement (GAMMOD), 18, 311
  DISPLAY statement (GENSELECT), 18, 369
  DISPLAY statement (KCLUS), 18, 432
  DISPLAY statement (LOGSELECT), 18, 471
  DISPLAY statement (NLMOD), 18, 529
  DISPLAY statement (PARTITION), 18, 974
  DISPLAY statement (PCA), 18, 565
  DISPLAY statement (PHSELECT), 18, 601
  DISPLAY statement (PLSMOD), 18, 648
  DISPLAY statement (QTRSELECT), 18, 686
  DISPLAY statement (REGSELECT), 18, 740
  DISPLAY statement (TREESPLIT), 18
  DISPLAY statement (VARIMPUTE), 18
  DISPLAY statement (VARREDUCE), 18, 1006
CBAR= option
  OUTPUT statement (GENSELECT), 380
  OUTPUT statement (LOGSELECT), 480
CCHART statement
  CCHART procedure, 784
CELLCHI2 option
  TABLES statement (FREQTAB), 156
CENSCALE option
  MODEL statement (GENSELECT), 374
CHAID option
  GROW statement (TREESPLIT), 863
chart statements
  SPC procedure, 793
CHISQ option
  EXACT statement (FREQTAB), 127
  OUTPUT statement (FREQTAB), 138
  TABLES statement (FREQTAB), 156
CHISQUARE option
  GROW statement (TREESPLIT), 864
CHOOSE= option
  SELECTION statement (ASSESS), 36
  SELECTION statement (BINNING), 36
  SELECTION statement (CARDINALITY), 36
  SELECTION statement (CORRELATION), 36
  SELECTION statement (GAMMOD), 36
  SELECTION statement (GENSELECT), 36
  SELECTION statement (KCLUS), 36
  SELECTION statement (LOGSELECT), 36
  SELECTION statement (NLMOD), 36
  SELECTION statement (PARTITION), 36
  SELECTION statement (PCA), 36
  SELECTION statement (PHSELECT), 36
  SELECTION statement (PLSMOD), 36
  SELECTION statement (QTRSELECT), 36
  SELECTION statement (REGSELECT), 36
  SELECTION statement (TREESPLIT), 36
  SELECTION statement (VARIMPUTE), 36
  SELECTION statement (VARREDUCE), 36
CL option
  TABLES statement (FREQTAB), 158
CL= option (BINOMIAL)
  TABLES statement (FREQTAB), 152
CL= option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 159
CL= option (RELRISK)
  TABLES statement (FREQTAB), 182
CL= option (RISKDIFF)
  TABLES statement (FREQTAB), 185
CL=AGRESTICAFFO option (RISKDIFF)
  TABLES statement (FREQTAB), 186
CL=AGRESTICOULL option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=BLAKER option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=CLOPPERPEARSON option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=EXACT option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=EXACT option (RISKDIFF)
  TABLES statement (FREQTAB), 186
CL=HA option (RISKDIFF)
  TABLES statement (FREQTAB), 186
CL=JEFFREYS option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=LIKELIHOODRATIO option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=LOGIT option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=MH option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 153
CL=MIDP option (BINOMIAL)
  TABLES statement (FREQTAB), 160
CL=MR option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 153
CL=NEWCOMBE option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 160
CL=NEWCOMBE option (RISKDIFF)
  TABLES statement (FREQTAB), 186
CL=NEWCOMBEMR option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 160
CL=SCORE option (COMMONRISKDIFF)
  TABLES statement (FREQTAB), 160
CL=WALD option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CL=WALD option (RISKDIFF)
  TABLES statement (FREQTAB), 186
CL=WILSON option (BINOMIAL)
  TABLES statement (FREQTAB), 153
CLASS statement
  ASSESS procedure, 10, 47
  BINNING procedure, 10, 47
  CARDINALITY procedure, 10, 47
  CORRELATION procedure, 10, 47
  GAMMOD procedure, 10, 47, 310
  GENSELECT procedure, 10, 47, 367
  KCLUS procedure, 10, 47
  LOGSELECT procedure, 10, 47, 469
  NLMOD procedure, 10, 47
  PARTITION procedure, 10, 47
  PCA procedure, 10, 47
  PHSELECT procedure, 10, 47, 598
  PLSMOD procedure, 10, 47, 647
  QTRSELECT procedure, 10, 47, 684
  REGSELECT procedure, 10, 47, 738
  TREESPLIT procedure, 10, 47, 862
  VARIMPUTE procedure, 10, 47
  VARREDUCE procedure, 10, 47, 1005
CLB option
  MODEL statement (GENSELECT), 374
  MODEL statement (LOGSELECT), 476
  MODEL statement (PHSELECT), 605
  MODEL statement (QTRSELECT), 689
  MODEL statement (REGSELECT), 743
CMH option
  OUTPUT statement (FREQTAB), 138
  TABLES statement (FREQTAB), 158
CMH1 option
  OUTPUT statement (FREQTAB), 138
  TABLES statement (FREQTAB), 159
<table>
<thead>
<tr>
<th>Syntax Index</th>
</tr>
</thead>
<tbody>
<tr>
<td>CMH2 option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 159</td>
</tr>
<tr>
<td>CMHCOR option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>CMHG option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>CMHRMS option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>COCH option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>CODE statement</td>
</tr>
<tr>
<td>ASSESS procedure, 14</td>
</tr>
<tr>
<td>BINNING procedure, 14, 935</td>
</tr>
<tr>
<td>CARDINALITY procedure, 14</td>
</tr>
<tr>
<td>CORRELATION procedure, 14</td>
</tr>
<tr>
<td>GAMMOD procedure, 14</td>
</tr>
<tr>
<td>GENSELECT procedure, 14, 368</td>
</tr>
<tr>
<td>KCLUS procedure, 14, 431</td>
</tr>
<tr>
<td>LOGSELECT procedure, 14, 470</td>
</tr>
<tr>
<td>NLMOD procedure, 14</td>
</tr>
<tr>
<td>PARTITION procedure, 14</td>
</tr>
<tr>
<td>PCA procedure, 14, 563</td>
</tr>
<tr>
<td>PHSELECT procedure, 14, 598</td>
</tr>
<tr>
<td>PLSMOD procedure, 14</td>
</tr>
<tr>
<td>QTRSELECT procedure, 14, 685</td>
</tr>
<tr>
<td>REGSELECT procedure, 14, 739</td>
</tr>
<tr>
<td>TREESPLIT procedure, 14, 863</td>
</tr>
<tr>
<td>VARIMPUTE procedure, 14, 989</td>
</tr>
<tr>
<td>VARREDUCE procedure, 14</td>
</tr>
<tr>
<td>COLUMN= option (COMMONRISKDIFF)</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 160</td>
</tr>
<tr>
<td>COLUMN= option (RELRISK)</td>
</tr>
<tr>
<td>EXACT statement (FREQTAB), 130</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 182</td>
</tr>
<tr>
<td>COLUMN= option (RISKDIFF)</td>
</tr>
<tr>
<td>EXACT statement (FREQTAB), 130</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 186</td>
</tr>
<tr>
<td>COMMENT option</td>
</tr>
<tr>
<td>CODE statement (ASSESS), 15</td>
</tr>
<tr>
<td>CODE statement (BINNING), 15</td>
</tr>
<tr>
<td>CODE statement (CARDINALITY), 15</td>
</tr>
<tr>
<td>CODE statement (CORRELATION), 15</td>
</tr>
<tr>
<td>CODE statement (GAMMOD), 15</td>
</tr>
<tr>
<td>CODE statement (GENSELECT), 15</td>
</tr>
<tr>
<td>CODE statement (KCLUS), 15</td>
</tr>
<tr>
<td>CODE statement (LOGSELECT), 15</td>
</tr>
<tr>
<td>CODE statement (NLMOD), 15</td>
</tr>
<tr>
<td>CODE statement (PARTITION), 15</td>
</tr>
<tr>
<td>CODE statement (PCA), 15</td>
</tr>
<tr>
<td>CODE statement (PHSELECT), 15</td>
</tr>
<tr>
<td>CODE statement (PLSMOD), 15</td>
</tr>
<tr>
<td>CODE statement (QTRSELECT), 15</td>
</tr>
<tr>
<td>CODE statement (REGSELECT), 15</td>
</tr>
<tr>
<td>CODE statement (TREESPLIT), 15</td>
</tr>
<tr>
<td>CODE statement (VARIMPUTE), 15</td>
</tr>
<tr>
<td>CODE statement (VARREDUCE), 15</td>
</tr>
<tr>
<td>COMMON option (RISKDIFF)</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 187</td>
</tr>
<tr>
<td>COMMONRISKDIFF option</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 159</td>
</tr>
<tr>
<td>COMOR option</td>
</tr>
<tr>
<td>EXACT statement (FREQTAB), 127</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 141</td>
</tr>
<tr>
<td>COMPETITIVE option</td>
</tr>
<tr>
<td>SELECTION statement (ASSESS), 36</td>
</tr>
<tr>
<td>SELECTION statement (BINNING), 36</td>
</tr>
<tr>
<td>SELECTION statement (CARDINALITY), 36</td>
</tr>
<tr>
<td>SELECTION statement (CORRELATION), 36</td>
</tr>
<tr>
<td>SELECTION statement (GAMMOD), 36</td>
</tr>
<tr>
<td>SELECTION statement (GENSELECT), 36</td>
</tr>
<tr>
<td>SELECTION statement (KCLUS), 36</td>
</tr>
<tr>
<td>SELECTION statement (LOGSELECT), 36</td>
</tr>
<tr>
<td>SELECTION statement (NLMOD), 36</td>
</tr>
<tr>
<td>SELECTION statement (PARTITION), 36</td>
</tr>
<tr>
<td>SELECTION statement (PCA), 36</td>
</tr>
<tr>
<td>SELECTION statement (PHSELECT), 36</td>
</tr>
<tr>
<td>SELECTION statement (PLSMOD), 36</td>
</tr>
<tr>
<td>SELECTION statement (QTRSELECT), 36</td>
</tr>
<tr>
<td>SELECTION statement (REGSELECT), 36</td>
</tr>
<tr>
<td>SELECTION statement (TREESPLIT), 36</td>
</tr>
<tr>
<td>SELECTION statement (VARIMPUTE), 36</td>
</tr>
<tr>
<td>SELECTION statement (VARREDUCE), 36</td>
</tr>
<tr>
<td>COMPONENT option</td>
</tr>
<tr>
<td>OUTPUT statement (GAMMOD), 321</td>
</tr>
<tr>
<td>COMPRESS option</td>
</tr>
<tr>
<td>PROC FREQTAB statement, 122</td>
</tr>
<tr>
<td>CONFIDENCE= option</td>
</tr>
<tr>
<td>PRUNE statement (TREESPLIT), 867</td>
</tr>
<tr>
<td>CONTENTS= option</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 161</td>
</tr>
<tr>
<td>CONTGY option</td>
</tr>
<tr>
<td>OUTPUT statement (FREQTAB), 139</td>
</tr>
<tr>
<td>CONTROLSTAT= option</td>
</tr>
<tr>
<td>chart statements (SPC), 793</td>
</tr>
<tr>
<td>CONVERGE= option (PLCORR)</td>
</tr>
<tr>
<td>TABLES statement (FREQTAB), 168</td>
</tr>
<tr>
<td>COPYVAR= option</td>
</tr>
<tr>
<td>OUTPUT statement (GAMMOD), 321</td>
</tr>
<tr>
<td>OUTPUT statement (GENSELECT), 379</td>
</tr>
<tr>
<td>OUTPUT statement (LOGSELECT), 478</td>
</tr>
<tr>
<td>OUTPUT statement (PHSELECT), 606</td>
</tr>
<tr>
<td>OUTPUT statement (QTRSELECT), 691</td>
</tr>
<tr>
<td>OUTPUT statement (REGSELECT), 745</td>
</tr>
<tr>
<td>COPYVARS= option</td>
</tr>
<tr>
<td>OUTPUT statement, 434, 866, 937, 976, 991</td>
</tr>
<tr>
<td>OUTPUT statement (PCA), 566</td>
</tr>
<tr>
<td>OUTPUT statement (PLSMOD), 652</td>
</tr>
</tbody>
</table>
CORR option
   PROC NLMOD statement, 527
CORRB option
   PROC GENSELECT statement, 365
   PROC LOGSELECT statement, 467
   PROC PHSELECT statement, 596
CORRECT option (BINOMIAL)
   TABLES statement (FREQTAB), 154
CORRECT option (RISKDIFF)
   TABLES statement (FREQTAB), 187
CORRECT=NO option (COMMONRISKDIFF)
   TABLES statement (FREQTAB), 160
CORRELATION procedure
   syntax, 92
   CORRELATION procedure, CLASS statement
      DESCENDING option, 11, 1005
      MISSING option, 11, 1005
      ORDER= option, 11
      PARAM= option, 12
      REF= option, 13
      SPLIT option, 13
   CORRELATION procedure, CODE statement
      COMMENT option, 15
      FILE= option, 15
      FORMATWIDTH= option, 15
      INDENTSIZE= option, 15
      LABELID= option, 16
      LINESIZE= option, 16
      NOTRIM option, 16
      OUT= option, 16
   CORRELATION procedure, DISPLAY statement
      CASESENSITIVE option, 18, 95
      EXCLUDE option, 18, 96
      EXCLUDEALL option, 18, 96
      TRACE option, 18, 96
   CORRELATION procedure, DISPLAYOUT statement
      INCLUDEALL option, 19, 96
      NOREPLACE option, 19, 96
      REPEATED option, 19, 96
   CORRELATION procedure, EFFECT statement
      BASIS option (spline), 26
      DATABOUNDARY option (spline), 26
      DEGREE option (polynomial), 24
      DEGREE option (spline), 27
      DETAILS option (multimember), 23
      DETAILS option (polynomial), 24
      DETAILS option (spline), 27
      KNOTMAX= option (spline), 27
      KNOTMETHOD option (spline), 27
      KNOTMIN= option (spline), 28
      MDEGREE option (polynomial), 24
      NATURALCUBIC option (spline), 28
      NOEFFECT option (multimember), 23
      NOSEPARATE option (polynomial), 24
      SEPARATE option (spline), 28
      SPLIT option (spline), 29
      STANDARDIZE option (polynomial), 24
   CORRELATION procedure, PROC CORRELATION
      statement, 92
      ABSCONV option, 42
      ABSFCONV option, 42
      ABSFTOL option, 42
      ABSGCONV option, 42
      ABSGTOL option, 42
      ABSTOL option, 42
      ABSXTOL option, 42
      ALPHA option, 93
      BEST= option, 93
      COV option, 93
      CSSSCP option, 93
      DATA= option, 93
      EXCLNPWGHT option, 93
      FCONV option, 43
      FCONV2 option, 43
      FTOL option, 43
      FTOL2 option, 43
      GCONV option, 44
      GCONV2 option, 44
      GTOL option, 44
      GTOL2 option, 44
      MAXFUN= option, 45
      MAXITER= option, 45
      MAXTIME= option, 45
      MINITER= option, 45
      NOCORR option, 93
      NOMISS option, 93
      NOPROB option, 94
      NORMALIZE= option, 45
      NOSIMPLE option, 94
      OUT= option, 94
      OUTP= option, 94
      RANK option, 94
      SSCP option, 94
      TECHNIQUE= option, 46
      VARDEF= option, 94
      XCONV option, 46
      XTOL option, 46
   CORRELATION procedure, SELECTION statement
      ADAPTIVE option, 36
      CHOOSE= option, 36
      COMPETITIVE option, 36
      CRITERION= option, 36
      DETAILS= option, 38, 39
      FAST option, 37
      HIERARCHY= option, 39
      LSCEFFS option, 37
      MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

CORRELATION procedure, VAR statement, 97
CORRELATION procedure, WEIGHT statement, 97
CORRELATION procedure, WITH statement, 97

COSTCOMPLEXITY option
PRUNE statement (TREESPLIT), 867

COV option
PROC CORRELATION statement, 93
PROC NLMOD statement, 527
PROC PCA statement, 559

COV=SPARSITY option
PROC QTRSELECT statement, 684

COVARIANCE option
PROC PCA statement, 559

COVB option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 467
PROC PHSELECT statement, 597

CRAMV option
OUTPUT statement (FREQTAB), 139

CRITERION= option
MODEL statement (GAMMOD), 317
SELECTION statement (ASSESS), 36
SELECTION statement (BINNING), 36
SELECTION statement (CARDINALITY), 36
SELECTION statement (CORRELATION), 36
SELECTION statement (GAMMOD), 36
SELECTION statement (GENSELECT), 36
SELECTION statement (KCLUS), 36
SELECTION statement (LOGSELECT), 36
SELECTION statement (NLMOD), 36
SELECTION statement (PARTITION), 36
SELECTION statement (PCA), 36
SELECTION statement (PHSELECT), 36
SELECTION statement (PLSMOD), 36
SELECTION statement (QTRSELECT), 36
SELECTION statement (REGSELECT), 36
SELECTION statement (TREESPLIT), 36
SELECTION statement (VARIMPUTE), 36
SELECTION statement (VARREDUCE), 36

CROSSLIST option
TABLES statement (FREQTAB), 162

CSSCP option
PROC CORRELATION statement, 93

CUMCOL option
TABLES statement (FREQTAB), 162

CUMHAZ option
CODE statement (PHSELECT), 15, 599
OUTPUT statement (PHSELECT), 607

CVCC option
PROC TREESPLIT statement, 852

CVTEST option
PROC PLSMOD statement, 645

DATA= option
PROC ASSESS statement, 911
PROC BINNING statement, 933
PROC CARDINALITY statement, 956
PROC CORRELATION statement, 93
PROC FREQTAB statement, 122
PROC GAMMOD statement, 307
PROC GENSELECT statement, 366
PROC KCLUS statement, 426
PROC LOGSELECT statement, 467
PROC NLMOD statement, 527
PROC PARTITION statement, 972
PROC PCA statement, 559
PROC PHSELECT statement, 597
PROC PLSMOD statement, 645
PROC QTRSELECT statement, 684
PROC REGSELECT statement, 738
PROC SPC statement, 782, 822
PROC TREESPLIT statement, 852
PROC VARIMPUTE statement, 988
PROC VARREDUCE statement, 1003

DATABOUNDARY option
EFFECT statement, spline (ASSESS), 26
EFFECT statement, spline (BINNING), 26
EFFECT statement, spline (CARDINALITY), 26
EFFECT statement, spline (CORRELATION), 26
EFFECT statement, spline (GAMMOD), 26
EFFECT statement, spline (GENSELECT), 26
EFFECT statement, spline (KCLUS), 26
EFFECT statement, spline (LOGSELECT), 26
EFFECT statement, spline (NLMOD), 26
EFFECT statement, spline (PARTITION), 26
EFFECT statement, spline (PCA), 26
EFFECT statement, spline (PHSELECT), 26
EFFECT statement, spline (PLSMOD), 26
EFFECT statement, spline (QTRSELECT), 26
EFFECT statement, spline (REGSELECT), 26
EFFECT statement, spline (TREESPLIT), 26
EFFECT statement, spline (VARIMPUTE), 26
EFFECT statement, spline (VARREDUCE), 26

DEGREE option
EFFECT statement, polynomial (ASSESS), 24
EFFECT statement, polynomial (BINNING), 24
EFFECT statement, polynomial (CARDINALITY), 24
EFFECT statement, polynomial (CORRELATION), 24
EFFECT statement, polynomial (GAMMOD), 24
EFFECT statement, polynomial (GENSELECT), 24
EFFECT statement, polynomial (KCLUS), 24
EFFECT statement, polynomial (LOGSELECT), 24
EFFECT statement, polynomial (NLMOD), 24
EFFECT statement, polynomial (PARTITION), 24
EFFECT statement, polynomial (PCA), 24
EFFECT statement, polynomial (PHSELECT), 24
EFFECT statement, polynomial (PLSMOD), 24
EFFECT statement, polynomial (QTRSELECT), 24
EFFECT statement, polynomial (REGSELECT), 24
EFFECT statement, polynomial (TREESPLIT), 24
EFFECT statement, polynomial (VARIIMPUTE), 24
EFFECT statement, polynomial (VARIREDUCE), 24
EFFECT statement, spline (ASSESS), 27
EFFECT statement, spline (BINNING), 27
EFFECT statement, spline (CARDINALITY), 27
EFFECT statement, spline (CORRELATION), 27
EFFECT statement, spline (GAMMOD), 27
EFFECT statement, spline (GENSELECT), 27
EFFECT statement, spline (KCLUS), 27
EFFECT statement, spline (LOGSELECT), 27
EFFECT statement, spline (NLMOD), 27
EFFECT statement, spline (PARTITION), 27
EFFECT statement, spline (PCA), 27
EFFECT statement, spline (PHSELECT), 27
EFFECT statement, spline (PLSMOD), 27
EFFECT statement, spline (QTRSELECT), 27
EFFECT statement, spline (REGSELECT), 27
EFFECT statement, spline (TREESPLIT), 27
EFFECT statement, spline (VARIIMPUTE), 27
EFFECT statement, spline (VARIREDUCE), 27

DELIMITER= option
FITSTAT statement, 913

DESCENDING option
CLASS statement (ASSESS), 11, 1005
CLASS statement (BINNING), 11, 1005
CLASS statement (CARDINALITY), 11, 1005
CLASS statement (CORRELATION), 11, 1005
CLASS statement (GAMMOD), 11, 1005
CLASS statement (GENSELECT), 11, 1005
CLASS statement (KCLUS), 11, 1005
CLASS statement (LOGSELECT), 11, 1005
CLASS statement (NLMOOD), 11, 1005
CLASS statement (PARTITION), 11, 1005
CLASS statement (PCA), 11, 1005
CLASS statement (PHSELECT), 11, 1005
CLASS statement (PLSMOD), 11, 1005
CLASS statement (QTRSELECT), 11, 1005
CLASS statement (REGSELECT), 11, 1005
CLASS statement (TREESPLIT), 11, 1005
CLASS statement (VARIMPUTE), 11, 1005
CLASS statement (VARREDUCE), 11, 1005
MODEL statement (GAMMOD), 314
MODEL statement (GENSELECT), 373
MODEL statement (LOGSELECT), 475

DETAILS option
EFFECT statement, multimember (ASSESS), 23
EFFECT statement, multimember (BINNING), 23
EFFECT statement, multimember (CARDINALITY), 23
EFFECT statement, multimember (CORRELATION), 23
EFFECT statement, multimember (GAMMOD), 23
EFFECT statement, multimember (GENSELECT), 23
EFFECT statement, multimember (KCLUS), 23
EFFECT statement, multimember (LOGSELECT), 23
EFFECT statement, multimember (NLMOOD), 23
EFFECT statement, multimember (PARTITION), 23
EFFECT statement, multimember (PCA), 23
EFFECT statement, multimember (PHSELECT), 23
EFFECT statement, multimember (PLSMOD), 23
EFFECT statement, multimember (QTRSELECT), 23
EFFECT statement, multimember (REGSELECT), 23
EFFECT statement, multimember (TREESPLIT), 23
EFFECT statement, multimember (VARIMPUTE), 23
EFFECT statement, multimember (VARREDUCE), 23
EFFECT statement, polynomial (ASSESS), 24
EFFECT statement, polynomial (BINNING), 24
EFFECT statement, polynomial (CARDINALITY), 24
EFFECT statement, polynomial (CORRELATION), 24
EFFECT statement, polynomial (GAMMOD), 24
EFFECT statement, polynomial (GENSELECT), 24
EFFECT statement, polynomial (KCLUS), 24
EFFECT statement, polynomial (LOGSELECT), 24
EFFECT statement, polynomial (NLMOD), 24
EFFECT statement, polynomial (PARTITION), 24
EFFECT statement, polynomial (PCA), 24
EFFECT statement, polynomial (PHSELECT), 24
EFFECT statement, polynomial (PLSMOD), 24
EFFECT statement, polynomial (QTRSELECT), 24
EFFECT statement, polynomial (REGSELECT), 24
EFFECT statement, polynomial (TREESPLIT), 24
EFFECT statement, polynomial (VARIMPUTE), 24
EFFECT statement, polynomial (VARREDUCE), 24
EFFECT statement, spline (ASSESS), 27
EFFECT statement, spline (BINNING), 27
EFFECT statement, spline (CARDINALITY), 27
EFFECT statement, spline (CORRELATION), 27
EFFECT statement, spline (GAMMOD), 27
EFFECT statement, spline (GENSELECT), 27
EFFECT statement, spline (KCLUS), 27
EFFECT statement, spline (LOGSELECT), 27
EFFECT statement, spline (PCA), 27
EFFECT statement, spline (PHSELECT), 27
EFFECT statement, spline (PLSMOD), 27
EFFECT statement, spline (QTRSELECT), 27
EFFECT statement, spline (REGSELECT), 27
EFFECT statement, spline (TREESPLIT), 27
EFFECT statement, spline (VARIMPUTE), 27
EFFECT statement, spline (VARREDUCE), 27
MODEL statement (GAMMOD), 315
PROC PLSMOD statement, 646
DETAILS= option
SELECTION statement (ASSESS), 38, 39
SELECTION statement (BINNING), 38, 39
SELECTION statement (CARDINALITY), 38, 39
SELECTION statement (CORRELATION), 38, 39
SELECTION statement (GAMMOD), 38, 39
SELECTION statement (GENSELECT), 38, 39
SELECTION statement (KCLUS), 38, 39
SELECTION statement (LOGSELECT), 38, 39
SELECTION statement (NLMOD), 38, 39
SELECTION statement (PARTITION), 38, 39
SELECTION statement (PCA), 38, 39
SELECTION statement (PHSELECT), 38, 39
SELECTION statement (PLSMOD), 38, 39
SELECTION statement (QTRSELECT), 38, 39
SELECTION statement (REGSELECT), 38, 39
SELECTION statement (TREESPLIT), 38, 39
SELECTION statement (VARIMPUTE), 38, 39
SELECTION statement (VARREDUCE), 38, 39
DEViation option
TABLES statement (FREQTAB), 162
DF= option
ESTIMATE statement (NLMOD), 530
MODEL statement (GAMMOD), 315
PREDICT statement (NLMOD), 534
PROC NLMod statement, 527
DF= option (CHISQ)
TABLES statement (FREQTAB), 156
DFBETA option
OUTPUT statement (PHSELECT), 607
DIFCHISQ= option
OUTPUT statement (GENSELECT), 380
OUTPUT statement (LOGSELECT), 480
DIFDEV= option
OUTPUT statement (GENSELECT), 380
OUTPUT statement (LOGSELECT), 480
DISPERSION= option
MODEL statement (GAMMOD), 318
DISPLAY statement
ASSESS procedure, 17
BINNING procedure, 17
CARDINALITY procedure, 17
CORRELATION procedure, 17, 95
GAMMOD procedure, 17, 310
GENSELECT procedure, 17, 368
KCLUS procedure, 17, 431
LOGSELECT procedure, 17, 470
NLMod procedure, 17, 528
PARTITION procedure, 17, 974
PCA procedure, 17, 564
PHSELECT procedure, 17, 600
PLSMOD procedure, 17, 648
QTRSELECT procedure, 17, 686
REGSELECT procedure, 17, 739
TREESPLIT procedure, 17
VARIMPUTE procedure, 17
VARREDUCE procedure, 17, 1006
DISPLAYOUT statement
ASSESS procedure, 18
BINNING procedure, 18
CARDINALITY procedure, 18
CORRELATION procedure, 18, 96
GAMMOD procedure, 18, 311
GENSELECT procedure, 18, 369
KCLUS procedure, 18, 432
<table>
  <tr><td>LOGSELECT procedure</td><td>, 18, 471</td></tr>
  <tr><td>NLMOD procedure</td><td>, 18, 529</td></tr>
  <tr><td>PARTITION procedure</td><td>, 18, 975</td></tr>
  <tr><td>PCA procedure</td><td>, 18, 565</td></tr>
  <tr><td>PHSELECT procedure</td><td>, 18, 601</td></tr>
  <tr><td>PLSMOD procedure</td><td>, 18, 649</td></tr>
  <tr><td>QTRSELECT procedure</td><td>, 18, 687</td></tr>
  <tr><td>REGSELECT procedure</td><td>, 18, 740</td></tr>
  <tr><td>TREESPLIT procedure</td><td>, 18</td></tr>
  <tr><td>VARIMPUTE procedure</td><td>, 18</td></tr>
  <tr><td>VARREDUCE procedure</td><td>, 18, 1007</td></tr>
  <tr><td>DISTANCE= option</td><td>PROC KCLUS statement, 426</td></tr>
  <tr><td>DISTANCENOM= option</td><td>PROC KCLUS statement, 427</td></tr>
  <tr><td>DISTRIBUTION= option</td><td>MODEL statement (GAMMOD), 318</td></tr>
  <tr><td>MODEL statement (GENSELECT), 374</td></tr>
  <tr><td>DLM= option</td><td>FITSTAT statement, 913</td></tr>
  <tr><td>ECORR option</td><td>PROC NLMOD statement, 527</td></tr>
  <tr><td>ECOV option</td><td>PROC NLMOD statement, 527</td></tr>
  <tr><td>EFFECT statement</td><td></td></tr>
  <tr><td>ASSESS procedure, 19</td></tr>
  <tr><td>BINNING procedure, 19</td></tr>
  <tr><td>CARDINALITY procedure, 19</td></tr>
  <tr><td>collection effect, 21</td></tr>
  <tr><td>CORRELATION procedure, 19</td></tr>
  <tr><td>GAMMOD procedure, 19</td></tr>
  <tr><td>GENSELECT procedure, 19, 370</td></tr>
  <tr><td>KCLUS procedure, 19</td></tr>
  <tr><td>LOGSELECT procedure, 19, 472</td></tr>
  <tr><td>multimember effect, 21</td></tr>
  <tr><td>NLMOD procedure, 19</td></tr>
  <tr><td>PARTITION procedure, 19</td></tr>
  <tr><td>PCA procedure, 19</td></tr>
  <tr><td>PHSELECT procedure, 19, 602</td></tr>
  <tr><td>PLSMOD procedure, 19, 649</td></tr>
  <tr><td>polynomial effect, 23</td></tr>
  <tr><td>QTRSELECT procedure, 19, 687</td></tr>
  <tr><td>REGSELECT procedure, 19, 741</td></tr>
  <tr><td>spline effect, 26</td></tr>
  <tr><td>TREESPLIT procedure, 19</td></tr>
  <tr><td>VARIMPUTE procedure, 19</td></tr>
  <tr><td>VARREDUCE procedure, 19</td></tr>
  <tr><td>ENTROPY option</td><td></td></tr>
  <tr><td>GROW statement (TREESPLIT), 864</td></tr>
  <tr><td>ENTRY= option</td><td></td></tr>
  <tr><td>MODEL statement (PHSELECT), 605</td></tr>
  <tr><td>EPSILON= option</td><td>PROC PCA statement, METHOD=ITERGS option, 559</td></tr>
  <tr><td>PROC PCA statement, METHOD=NIPALS option, 560</td></tr>
  <tr><td>PROC PLSMOD statement, METHOD=PLS option, 646</td></tr>
  <tr><td>EQKAP option</td><td>OUTPUT statement (FREQQTAB), 139</td></tr>
  <tr><td>EQOR option</td><td>EXACT statement (FREQQTAB), 127</td></tr>
  <tr><td>EQUAL option (RELRISK)</td><td>TABLES statement (FREQQTAB), 183</td></tr>
  <tr><td>EQUAL option (RISKDIFF)</td><td>TABLES statement (FREQQTAB), 187</td></tr>
  <tr><td>EQUIVALENCE option (BINOMIAL)</td><td>TABLES statement (FREQQTAB), 154</td></tr>
  <tr><td>EQUIVALENCE option (RELRISK)</td><td>TABLES statement (FREQQTAB), 183</td></tr>
  <tr><td>EQUIVALENCE option (RISKDIFF)</td><td>TABLES statement (FREQQTAB), 187</td></tr>
  <tr><td>EQWKP option</td><td></td></tr>
  <tr><td>EXACT option</td><td>OUTPUT statement (FREQQTAB), 139</td></tr>
  <tr><td>ESTIMATE statement</td><td></td></tr>
  <tr><td>NLMOD procedure, 530</td></tr>
  <tr><td>EVALHISTORY= option</td><td>PROC PARTITION statement, 973</td></tr>
  <tr><td>EVENT= option</td><td>TARGET statement, 914, 937</td></tr>
  <tr><td>EVENTPROP= option</td><td>PROC PARTITION statement, 973</td></tr>
  <tr><td>EXCHART option</td><td></td></tr>
  <tr><td>chart statements (SPC), 793</td></tr>
  <tr><td>EXCLNPWGTT option</td><td>PROC CORRELATION statement, 93</td></tr>
  <tr><td>EXCLUDE option</td><td></td></tr>
  <tr><td>DISPLAY statement (ASSESS), 18</td></tr>
  <tr><td>DISPLAY statement (BINNING), 18</td></tr>
  <tr><td>DISPLAY statement (CARDINALITY), 18</td></tr>
  <tr><td>DISPLAY statement (CORRELATION), 18, 96</td></tr>
  <tr><td>DISPLAY statement (GAMMOD), 18, 311</td></tr>
  <tr><td>DISPLAY statement (GENSELECT), 18, 369</td></tr>
  <tr><td>DISPLAY statement (KCLUS), 18, 432</td></tr>
  <tr><td>DISPLAY statement (LOGSELECT), 18, 471</td></tr>
  <tr><td>DISPLAY statement (NLMOD), 18, 529</td></tr>
  <tr><td>DISPLAY statement (PARTITION), 18, 974</td></tr>
  <tr><td>DISPLAY statement (PCA), 18, 565</td></tr>
  <tr><td>DISPLAY statement (PHSELECT), 18, 601</td></tr>
</table>
DISPLAY statement (PLSMOD), 18, 649
DISPLAY statement (QTRSELECT), 18, 686
DISPLAY statement (REGSELECT), 18, 740
DISPLAY statement (TREESPLIT), 18
DISPLAY statement (VARIMPUTE), 18
DISPLAY statement (VARREDUCE), 18, 1006
EXCLUDEALL option
DISPLAY statement (ASSESS), 18
DISPLAY statement (BINNING), 18
DISPLAY statement (CARDINALITY), 18
DISPLAY statement (CORRELATION), 18, 96
DISPLAY statement (GAMMOD), 18, 311
DISPLAY statement (GENSELECT), 18, 369
DISPLAY statement (KCLUS), 18, 432
DISPLAY statement (LOGSELECT), 18, 529
DISPLAY statement (PARTITION), 18, 974
DISPLAY statement (PCA), 18, 565
DISPLAY statement (PHSELECT), 18, 601
DISPLAY statement (PLSMOD), 18, 649
DISPLAY statement (QTRSELECT), 18, 686
DISPLAY statement (REGSELECT), 18, 740
DISPLAY statement (TREESPLIT), 18
DISPLAY statement (VARIMPUTE), 18
DISPLAY statement (VARREDUCE), 18, 1006
EXPECTED option
    TABLES statement (FREQTAB), 163
FAST option
    SELECTION statement (ASSESS), 37
    SELECTION statement (BINNING), 37
    SELECTION statement (CARDINALITY), 37
    SELECTION statement (CORRELATION), 37
    SELECTION statement (GAMMOD), 37
    SELECTION statement (GENSELECT), 37
    SELECTION statement (KCLUS), 37
    SELECTION statement (LOGSELECT), 37
    SELECTION statement (NLMOD), 37
    SELECTION statement (PARTITION), 37
    SELECTION statement (PCA), 37
    SELECTION statement (PHSELECT), 37
    SELECTION statement (PLSMOD), 37
    SELECTION statement (QTRSELECT), 37
    SELECTION statement (REGSELECT), 37
    SELECTION statement (TREESPLIT), 37
    SELECTION statement (VARIMPUTE), 37
    SELECTION statement (VARREDUCE), 37
FCONV option
    PROC ASSESS statement, 43
    PROC BINNING statement, 43
    PROC CARDINALITY statement, 43
    PROC CORRELATION statement, 43
    PROC GAMMOD statement, 43
    PROC KCLUS statement, 43
    PROC LOGSELECT statement, 43
    PROC NLMOD statement, 43
    PROC PARTITION statement, 43
    PROC PCA statement, 43
    PROC PHSELECT statement, 43
    PROC PLSMOD statement, 43
    PROC QTRSELECT statement, 43
    PROC REGSELECT statement, 43
    PROC TREESPLIT statement, 43
    PROC VARIMPUTE statement, 43
    PROC VARREDUCE statement, 43
FCONV2 option
    PROC ASSESS statement, 43
    PROC BINNING statement, 43
    PROC CARDINALITY statement, 43
    PROC CORRELATION statement, 43
    PROC GAMMOD statement, 43
    PROC KCLUS statement, 43
    PROC LOGSELECT statement, 43
    PROC NLMOD statement, 43
    PROC PARTITION statement, 43
    PROC PCA statement, 43
    PROC PHSELECT statement, 43
    PROC PLSMOD statement, 43
    PROC QTRSELECT statement, 43
    PROC REGSELECT statement, 43
    PROC TREESPLIT statement, 43
    PROC VARIMPUTE statement, 43
    PROC VARREDUCE statement, 43
FDHESSIAN= option
    MODEL statement (GAMMOD), 319
FILE= option
    CODE statement, 431, 935, 989
    CODE statement (ASSESS), 15
    CODE statement (BINNING), 15
    CODE statement (CARDINALITY), 15
    CODE statement (CORRELATION), 15
    CODE statement (GAMMOD), 15
    CODE statement (GENSELECT), 15
    CODE statement (KCLUS), 15
    CODE statement (LOGSELECT), 15
    CODE statement (NLMOD), 15
    CODE statement (PARTITION), 15
    CODE statement (PCA), 15
    CODE statement (PHSELECT), 15
    CODE statement (PLSMOD), 15
    CODE statement (QTRSELECT), 15
    CODE statement (REGSELECT), 15
    CODE statement (TREESPLIT), 15
    CODE statement (VARIMPUTE), 15
    CODE statement (VARREDUCE), 15
FISHER option
    CODE statement (PHSELECT), 15, 599
    CODE statement (PLSMOD), 15
    CODE statement (QTRSELECT), 15
    CODE statement (REGSELECT), 15
    CODE statement (TREESPLIT), 15
    CODE statement (VARIMPUTE), 15
    CODE statement (VARREDUCE), 15
Syntax Index

- EXACT statement (FREQTAB), 127
- OUTPUT statement (FREQTAB), 140
- TABLES statement (FREQTAB), 163

FITSTAT statement
- ASSESS procedure, 913
- FITSTATOUT= option
- PROC ASSESS statement, 912
- FIXEDOFFSET= option
- OUTPUT statement (LOGSELECT), 479

FORMAT= option
- TABLES statement (FREQTAB), 163
- FORMATWIDTH= option
- CODE statement (ASSESS), 15
- CODE statement (BINNING), 15
- CODE statement (CARDINALITY), 15
- CODE statement (CORRELATION), 15
- CODE statement (GAMMOD), 15
- CODE statement (GENSELECT), 15
- CODE statement (KCLUS), 15
- CODE statement (LOGSELECT), 15
- CODE statement (NLIMOD), 15
- CODE statement (PARTITION), 15
- CODE statement (PCA), 15
- CODE statement (PHSELECT), 15
- CODE statement (PLSMOD), 15
- CODE statement (QTRSELECT), 15
- CODE statement (REGSELECT), 15
- CODE statement (TREESPLIT), 15
- CODE statement (VARIMPUTE), 15
- CODE statement (VARREDUCE), 15

FORMCHAR= option
- PROC FREQTAB statement, 122

FRACTION option
- PARTITION statement (ASSESS), 34
- PARTITION statement (BINNING), 34
- PARTITION statement (CARDINALITY), 34
- PARTITION statement (GENSELECT), 34, 383
- PARTITION statement (KCLUS), 34
- PARTITION statement (LOGSELECT), 34, 483
- PARTITION statement (NLIMOD), 34
- PARTITION statement (PARTITION), 34
- PARTITION statement (PHSELECT), 34, 609
- PARTITION statement (PLSMOD), 34
- PARTITION statement (QTRSELECT), 34, 693
- PARTITION statement (REGSELECT), 34, 747
- PARTITION statement (TREESPLIT), 34, 866
- PARTITION statement (VARIMPUTE), 34
- PARTITION statement (VARREDUCE), 34

FRACTION= option
- AUTOTUNE statement, 857

FREQ statement
- ASSESS procedure, 913
- BINNING procedure, 935
- CARDINALITY procedure, 957
- CORRELATION procedure, 957
- GAMMOD procedure, 312
- GENSELECT procedure, 371
- KCLUS procedure, 432
- LOGSELECT procedure, 473
- PCA procedure, 466
- PHSELECT procedure, 512
- REGSELECT procedure, 742
- TREESPLIT procedure, 863
- VARIMPUTE procedure, 989
- VARREDUCE procedure, 1007

FREQNAME= option
- OUTPUT statement, 976

FREQTAB procedure
- syntax, 121
- FREQTAB procedure, EXACT statement, 124
- AGREE option, 126
- ALPHA= option, 132
- BARNARD option, 127
- BINOMIAL option, 127
- CHISQ option, 127
- COLUMN= option (RELRISK), 130
- COLUMN= option (RISKDIFF), 130
- COMOR option, 127
- EQOR option, 127
- FISHER option, 127
- JT option, 128
- KAPPA option, 128
- KENTB option, 128
- LRCHI option, 128
- MAXTIME= option, 132
- Mc option, 132
- MCNEM option, 128
- MEASURES option, 128
- METHOD= option (RELRISK), 130
- METHOD= option (RISKDIFF), 131
- MHCHI option, 129
- MIDP option, 133
- N= option, 133
- OR option, 129
- PCHI option, 129
- PCORR option, 129
- PFFORMAT= option, 133
- POINT option, 133
- RELRISK option, 129
- RISKDIFF option, 130
- SCORR option, 131
- SEED= option, 134
- SMDCR option, 131
- SMDCRC option, 131
- STUTC option, 131
- SYMMETRY option, 132
- TREND option, 132
<table>
<thead>
<tr>
<th>Syntax Index</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>WTKAPPA option, 132</td>
<td>RISK1 option, 143</td>
</tr>
<tr>
<td>ZELEN option, 127</td>
<td>RISK11 option, 144</td>
</tr>
<tr>
<td>FREQTAB procedure, OUTPUT statement, 134</td>
<td>RISK12 option, 144</td>
</tr>
<tr>
<td>AGREE option, 137</td>
<td>RISK2 option, 144</td>
</tr>
<tr>
<td>AJCHI option, 137</td>
<td>RISK21 option, 144</td>
</tr>
<tr>
<td>ALL option, 138</td>
<td>RISK22 option, 144</td>
</tr>
<tr>
<td>BDCHI option, 138</td>
<td>RISKDIFF option, 143</td>
</tr>
<tr>
<td>BINOMIAL option, 138</td>
<td>RISKDIFF1 option, 143</td>
</tr>
<tr>
<td>BOWKER option, 145</td>
<td>RISKDIFF2 option, 143</td>
</tr>
<tr>
<td>CHISQ option, 138</td>
<td>RRC1 option, 143</td>
</tr>
<tr>
<td>CMH option, 138</td>
<td>RRC2 option, 143</td>
</tr>
<tr>
<td>CMH1 option, 138</td>
<td>SCORR option, 144</td>
</tr>
<tr>
<td>CMH2 option, 139</td>
<td>SMDCR option, 144</td>
</tr>
<tr>
<td>CMHCOR option, 139</td>
<td>SMDRC option, 144</td>
</tr>
<tr>
<td>CMHGA option, 139</td>
<td>STUTC option, 144</td>
</tr>
<tr>
<td>CMHRMS option, 139</td>
<td>TAUB option, 140</td>
</tr>
<tr>
<td>COCHQ option, 139</td>
<td>TAUC option, 144</td>
</tr>
<tr>
<td>COMOR option, 141</td>
<td>TREND option, 145</td>
</tr>
<tr>
<td>CONTGY option, 139</td>
<td>TSYMM option, 145</td>
</tr>
<tr>
<td>CRAMV option, 139</td>
<td>U option, 145</td>
</tr>
<tr>
<td>EKAP option, 139</td>
<td>UCR option, 145</td>
</tr>
<tr>
<td>EQOR option, 139</td>
<td>URC option, 145</td>
</tr>
<tr>
<td>EQWKP option, 139</td>
<td>WTKAPPA option, 145</td>
</tr>
<tr>
<td>EXACT option, 140</td>
<td>ZELEN option, 139</td>
</tr>
<tr>
<td>FISHER option, 140</td>
<td>FREQTAB procedure, PROC FREQTAB statement, 121</td>
</tr>
<tr>
<td>GAILSIMON option, 140</td>
<td>COMPRESS option, 122</td>
</tr>
<tr>
<td>GAMMA option, 140</td>
<td>DATA= option, 122</td>
</tr>
<tr>
<td>JT option, 140</td>
<td>FORMCHAR= option, 122</td>
</tr>
<tr>
<td>KAPPA option, 140</td>
<td>MISSING option, 123</td>
</tr>
<tr>
<td>KENTB option, 140</td>
<td>NLEVELS option, 123</td>
</tr>
<tr>
<td>LAMCR option, 140</td>
<td>NOPRINT option, 123</td>
</tr>
<tr>
<td>LAMDA option, 140</td>
<td>ORDER= option, 123</td>
</tr>
<tr>
<td>LMRC option, 140</td>
<td>PAGE option, 124</td>
</tr>
<tr>
<td>LGOR option, 141</td>
<td>FREQTAB procedure, TABLES statement, 145</td>
</tr>
<tr>
<td>LGRRC1 option, 141</td>
<td>ADJUST option (PLCORR), 168</td>
</tr>
<tr>
<td>LGRRC2 option, 141</td>
<td>AGREE option, 148</td>
</tr>
<tr>
<td>LRCHI option, 141</td>
<td>ALL option, 150</td>
</tr>
<tr>
<td>MCNEM option, 141</td>
<td>ALPHA= option, 150</td>
</tr>
<tr>
<td>MEASURES option, 141</td>
<td>BDT option (CMH), 158</td>
</tr>
<tr>
<td>MHCHI option, 141</td>
<td>BINOMIAL option, 151</td>
</tr>
<tr>
<td>MHOR option, 141</td>
<td>CELLCHI2 option, 156</td>
</tr>
<tr>
<td>MHRRC1 option, 142</td>
<td>CHISQ option, 156</td>
</tr>
<tr>
<td>MHRRC2 option, 142</td>
<td>CL option, 158</td>
</tr>
<tr>
<td>N option, 142</td>
<td>CL= option (BINOMIAL), 152</td>
</tr>
<tr>
<td>NMISS option, 142</td>
<td>CL= option (COMMONRISKDIFF), 159</td>
</tr>
<tr>
<td>OR option, 142</td>
<td>CL= option (RELRISK), 182</td>
</tr>
<tr>
<td>OUT= option, 134</td>
<td>CL= option (RISKDIFF), 185</td>
</tr>
<tr>
<td>output-options, 134</td>
<td>CL=AGRESTICAFFO option (RISKDIFF), 186</td>
</tr>
<tr>
<td>PCHI option, 142</td>
<td>CL=AGRESTICOLL option (BINOMIAL), 153</td>
</tr>
<tr>
<td>PCORR option, 142</td>
<td>CL=BLAKER option (BINOMIAL), 153</td>
</tr>
<tr>
<td>PLCORR option, 142</td>
<td>CL=CLOPPERPEARSON option (BINOMIAL), 153</td>
</tr>
<tr>
<td>RDIF1 option, 143</td>
<td>CL=EXACT option (BINOMIAL), 153</td>
</tr>
<tr>
<td>RDIF2 option, 143</td>
<td></td>
</tr>
<tr>
<td>Option</td>
<td>Page</td>
</tr>
<tr>
<td>--------------------------------</td>
<td>------</td>
</tr>
<tr>
<td>CL=EXACT option (RISKDIFF)</td>
<td>186</td>
</tr>
<tr>
<td>CL=HA option (RISKDIFF)</td>
<td>186</td>
</tr>
<tr>
<td>CL=JEFFREYS option (BINOMIAL)</td>
<td>153</td>
</tr>
<tr>
<td>CL=LIKELIHOODRATIO option</td>
<td>153</td>
</tr>
<tr>
<td>CL=LOGIT option (BINOMIAL)</td>
<td>153</td>
</tr>
<tr>
<td>CL=MH option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CL=MIDP option (BINOMIAL)</td>
<td>153</td>
</tr>
<tr>
<td>CL=MR option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CL=NEWCOMBE option</td>
<td></td>
</tr>
<tr>
<td>(COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CL=NEWCOMBE option (RISKDIFF)</td>
<td>186</td>
</tr>
<tr>
<td>CL=NEWCOMBEMR option</td>
<td></td>
</tr>
<tr>
<td>(COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CL=SCORE option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CL=WALD option (BINOMIAL)</td>
<td>153</td>
</tr>
<tr>
<td>CL=WALD option (RISKDIFF)</td>
<td>186</td>
</tr>
<tr>
<td>CL=WILSON option (BINOMIAL)</td>
<td>153</td>
</tr>
<tr>
<td>CMH option</td>
<td>158</td>
</tr>
<tr>
<td>CMH1 option</td>
<td>159</td>
</tr>
<tr>
<td>CMH2 option</td>
<td>159</td>
</tr>
<tr>
<td>COLUMN= option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>COLUMN= option (RELRISK)</td>
<td>182</td>
</tr>
<tr>
<td>COLUMN= option (RISKDIFF)</td>
<td>186</td>
</tr>
<tr>
<td>COMMON option (RISKDIFF)</td>
<td>187</td>
</tr>
<tr>
<td>COMMONRISKDIFF option</td>
<td>159</td>
</tr>
<tr>
<td>CONTENTS= option</td>
<td>161</td>
</tr>
<tr>
<td>CONVERGE= option (PLCORR)</td>
<td>168</td>
</tr>
<tr>
<td>CORRECT option (BINOMIAL)</td>
<td>154</td>
</tr>
<tr>
<td>CORRECT option (RISKDIFF)</td>
<td>187</td>
</tr>
<tr>
<td>CORRECT=NO option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>CROSSLIST option</td>
<td>161</td>
</tr>
<tr>
<td>CUMCOL option</td>
<td>162</td>
</tr>
<tr>
<td>DEVIATION option</td>
<td>162</td>
</tr>
<tr>
<td>DF= option (CHISQ)</td>
<td>156</td>
</tr>
<tr>
<td>EQUAL option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>EQUAL option (RISKDIFF)</td>
<td>187</td>
</tr>
<tr>
<td>EQUIVALENCE option (BINOMIAL)</td>
<td>154</td>
</tr>
<tr>
<td>EQUIVALENCE option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>EQUIVALENCE option (RISKDIFF)</td>
<td>187</td>
</tr>
<tr>
<td>EXACT option</td>
<td>163</td>
</tr>
<tr>
<td>EXPECTED option</td>
<td>163</td>
</tr>
<tr>
<td>FISHER option</td>
<td>163</td>
</tr>
<tr>
<td>FORMAT= option</td>
<td>163</td>
</tr>
<tr>
<td>GAILSIMON option</td>
<td>163</td>
</tr>
<tr>
<td>JT option</td>
<td>164</td>
</tr>
<tr>
<td>LEVEL= option (BINOMIAL)</td>
<td>154</td>
</tr>
<tr>
<td>LIST option</td>
<td>164</td>
</tr>
<tr>
<td>LRCHI option (CHISQ)</td>
<td>157</td>
</tr>
<tr>
<td>MANTELFLIESS option (CMH)</td>
<td>159</td>
</tr>
<tr>
<td>MARGIN= option (BINOMIAL)</td>
<td>154</td>
</tr>
<tr>
<td>MARGIN= option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>MARGIN= option (RISKDIFF)</td>
<td>187</td>
</tr>
<tr>
<td>MAXITER= option (PLCORR)</td>
<td>168</td>
</tr>
<tr>
<td>MAXLEVELS= option</td>
<td>164</td>
</tr>
<tr>
<td>MEASURES option</td>
<td>164</td>
</tr>
<tr>
<td>METHOD= option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>METHOD= option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>METHOD=FM option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>METHOD=FM option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>METHOD=HA option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>METHOD=LR option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>METHOD=NEWCOMBE option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>METHOD=WALD option (RELRISK)</td>
<td>183</td>
</tr>
<tr>
<td>METHOD=WALD option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>MISSPRINT option</td>
<td>123</td>
</tr>
<tr>
<td>NOCOL option</td>
<td>165</td>
</tr>
<tr>
<td>NOCUM option</td>
<td>165</td>
</tr>
<tr>
<td>NOFREQ option</td>
<td>165</td>
</tr>
<tr>
<td>NONINFERIORITY option (BINOMIAL)</td>
<td>155</td>
</tr>
<tr>
<td>NONINFERIORITY option (RELRISK)</td>
<td>184</td>
</tr>
<tr>
<td>NONINFERIORITY option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>NOPERCENT option</td>
<td>165</td>
</tr>
<tr>
<td>NOPRINT option</td>
<td>165</td>
</tr>
<tr>
<td>NORISKS option (RISKDIFF)</td>
<td>188</td>
</tr>
<tr>
<td>NOROW option</td>
<td>165</td>
</tr>
<tr>
<td>NOSPARSE option</td>
<td>165</td>
</tr>
<tr>
<td>NOWARN option</td>
<td>166</td>
</tr>
<tr>
<td>OR option</td>
<td>166</td>
</tr>
<tr>
<td>OUT= option</td>
<td>167</td>
</tr>
<tr>
<td>OUTCUM option</td>
<td>167</td>
</tr>
<tr>
<td>OUTEXPECT option</td>
<td>167</td>
</tr>
<tr>
<td>OUTLEVEL option (BINOMIAL)</td>
<td>155</td>
</tr>
<tr>
<td>OUTPCT option</td>
<td>167</td>
</tr>
<tr>
<td>P= option (BINOMIAL)</td>
<td>155</td>
</tr>
<tr>
<td>PEARMONRES option (CROSSLIST)</td>
<td>162</td>
</tr>
<tr>
<td>PLOCCOR option</td>
<td>167</td>
</tr>
<tr>
<td>PLOTS= option</td>
<td>168</td>
</tr>
<tr>
<td>PLOTS=AGREEPLOT option</td>
<td>170</td>
</tr>
<tr>
<td>PLOTS=CUMFREQPLOT option</td>
<td>170</td>
</tr>
<tr>
<td>PLOTS=DEVIATIONPLOT option</td>
<td>171</td>
</tr>
<tr>
<td>PLOTS=FreqPLOT option</td>
<td>171</td>
</tr>
<tr>
<td>PLOTS=KAPPAPLOT option</td>
<td>172</td>
</tr>
<tr>
<td>PLOTS=MOSAICPLOT option</td>
<td>173</td>
</tr>
<tr>
<td>PLOTS=NONE option</td>
<td>174</td>
</tr>
<tr>
<td>PLOTS=ODDSRATIOPLOT option</td>
<td>174</td>
</tr>
<tr>
<td>PLOTS=RELRISKPLOT option</td>
<td>174</td>
</tr>
<tr>
<td>PLOTS=RISKDIFFPLOT option</td>
<td>175</td>
</tr>
<tr>
<td>PLOTS=WTKAPPAPLOT</td>
<td>175</td>
</tr>
<tr>
<td>POLYCHORIC option</td>
<td>167</td>
</tr>
<tr>
<td>PRINTALL option (RELRISK)</td>
<td>184</td>
</tr>
<tr>
<td>PRINTKWTS option</td>
<td>150, 181</td>
</tr>
<tr>
<td>PRINTWTS option (COMMONRISKDIFF)</td>
<td>160</td>
</tr>
<tr>
<td>RELRISK option</td>
<td>181</td>
</tr>
</tbody>
</table>
RISKDIFF option, 184
SCORES= option, 189
SCOROUT option, 189
STDRES option (CROSSLIST), 162
SUPERIORITY option (BINOMIAL), 155
SUPERIORITY option (RELRISK), 184
SUPERIORITY option (RISKDIFF), 189
TEST option (COMMONRISKDIFF), 161
TEST=MH option (COMMONRISKDIFF), 161
TEST=MR option (COMMONRISKDIFF), 161
TEST=SCORE option (COMMONRISKDIFF),
    161
TESTF= option, 200
TESTF= option (CHISQ), 157
TESTP= option, 200
TESTP= option (CHISQ), 157
TOTPCT option, 189
TREND option, 190
VAR= option (BINOMIAL), 155
VAR= option (RISKDIFF), 189
WARN= option (CHISQ), 157
FREQTAB procedure, TEST statement, 190
    AGREE option, 191
    GAMMA option, 191
    KAPPA option, 191
    KENTB option, 192
    MEASURES option, 192
    PCORR option, 192
    PLCORR option, 192
    SCORR option, 192
    SMDCR option, 192
    SMDRC option, 193
    STUTC option, 193
    TAUB option, 192
    TAUC option, 193
    WTKAPPA option, 193
FREQTAB procedure, WEIGHT statement, 193
    ZEROs option, 194
FTEST option
    GROW statement (TREESPLIT), 864
FTOL option
    PROC ASSESS statement, 43
    PROC BINNING statement, 43
    PROC CARDINALITY statement, 43
    PROC CORRELATION statement, 43
    PROC GAMMOD statement, 43
    PROC GENSELECT statement, 43
    PROC KCLUS statement, 43
    PROC LOGSELECT statement, 43
    PROC PCA statement, 43
    PROC PHSELECT statement, 43
    PROC QTRSELECT statement, 43
    PROC REGSELECT statement, 43
    PROC TREESPLIT statement, 43
    PROC PLSMOD statement, 43
    PROC PHSELECT statement, 43
    PROC QTRSELECT statement, 43
    PROC REGSELECT statement, 43
    PROC VARIMPUTE statement, 43
    PROC VARREDUCE statement, 43
FTOL2 option
    PROC ASSESS statement, 43
    PROC BINNING statement, 43
    PROC CARDINALITY statement, 43
    PROC CORRELATION statement, 43
    PROC GAMMOD statement, 43
    PROC GENSELECT statement, 43
    PROC KCLUS statement, 43
    PROC LOGSELECT statement, 43
    PROC NLMOD statement, 43
    PROC PARTITION statement, 43
    PROC PCA statement, 43
    PROC PHSELECT statement, 43
    PROC QTRSELECT statement, 43
    PROC REGSELECT statement, 43
    PROC TREESPLIT statement, 43
    PROC VARIMPUTE statement, 43
    PROC VARREDUCE statement, 43
GAILSIMON option
    OUTPUT statement (FREQTAB), 140
    TABLES statement (FREQTAB), 163
GAMMA option
    OUTPUT statement (FREQTAB), 140
    TEST statement (FREQTAB), 191
GAMMOD procedure, 306
    MODEL statement, 312
    OUTPUT statement, 320
    PROC GAMMOD statement, 306
    syntax, 306
    WEIGHT statement, 322
GAMMOD procedure, CLASS statement, 310
    DESCENDING option, 11, 1005
    MISSING option, 11, 1005
    ORDER= option, 11
    PARAM= option, 12
    REFL= option, 13
    SPLIT option, 13
GAMMOD procedure, CODE statement
    COMMENT option, 15
    FILE= option, 15
    FORMATWIDTH= option, 15
    INDENTSIZE= option, 15
    LABELID= option, 16
    LINESIZE= option, 16
    NOTRIM option, 16
    OUT= option, 16
GAMMOD procedure, DISPLAY statement
CASESENSITIVE option, 18, 311
EXCLUDE option, 18, 311
EXCLUDEALL option, 18, 311
TRACE option, 18, 311

GAMMOD procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 311
NOREPLACE option, 19, 311
REPEATED option, 19, 312

GAMMOD procedure, EFFECT statement
BASIS option (spline), 26
DATABASEBOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24

GAMMOD procedure, MODEL statement, 312
ALLOBS option, 317
CRITERION= option, 317
DESCENDING option, 314
DETAILS option, 315
DF= option, 315
DISPERSION= option, 318
DISTRIBUTION= option, 318
FDHESSIAN option, 319
INITIALPHI= option, 319
INITSMOOTH= option, 315
KNOTS= option, 315
LINK= option, 319
M= option, 316
MAXDF= option, 316
MAXKNOTS= option, 317
MAXPHI= option, 319
MAXSMOOTH= option, 317
METHOD= option, 319
MINPHI= option, 320
MINSMOOTH= option, 317
NORMALIZE option, 320
OFFSET= option, 320
ORDER= option, 315
RIDGE= option, 320
SCALE= option, 320
SMOOTH= option, 317

GAMMOD procedure, OUTPUT statement, 320
ALPHA= option, 321
COMPONENT option, 321
COPYV AR= option, 321
keyword= option, 321
OUT= option, 321

GAMMOD procedure, PROC GAMMOD statement, 306
ABSCONV option, 42
ABSFCONV option, 42
ABSFTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
ALPHA= option, 307
DATA= option, 307
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
ITDETAILS option, 307
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NOCCLPRINT option, 307
NOPRINT option, 307
NORMALIZE= option, 45
PLIKEOPTIONS option, 307
plots(unpack) option, 308
PLOTS= option, 308
SEED= option, 308
SINGCHOL= option, 308
SINGULAR= option, 309
SMOOTHOPTIONS option, 309
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46

GAMMOD procedure, SELECTION statement
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

GAMMOD procedure, WEIGHT statement, 322
GCONV option
PROC ASSESS statement, 44
PROC BINNING statement, 44
PROC CARDINALITY statement, 44
PROC CORRELATION statement, 44
PROC GAMMOD statement, 44
PROC GENSELECT statement, 44
PROC KCLUS statement, 44
PROC LOGSELECT statement, 44
PROC NLMOD statement, 44
PROC PARTITION statement, 44
PROC PCA statement, 44
PROC PHSELECT statement, 44
PROC PLSMOD statement, 44
PROC QTRSELECT statement, 44
PROC REGSELECT statement, 44
PROC TREESPLIT statement, 44
PROC VARIMPUTE statement, 44
PROC VARREDUCE statement, 44

GCONV2 option
PROC ASSESS statement, 44
PROC BINNING statement, 44
PROC CARDINALITY statement, 44
PROC CORRELATION statement, 44
PROC GAMMOD statement, 44
PROC GENSELECT statement, 44
PROC KCLUS statement, 44
PROC LOGSELECT statement, 44
PROC NLMOD statement, 44
PROC PARTITION statement, 44
PROC PCA statement, 44
PROC PHSELECT statement, 44
PROC PLSMOD statement, 44
PROC QTRSELECT statement, 44
PROC REGSELECT statement, 44
PROC TREESPLIT statement, 44
PROC VARIMPUTE statement, 44
PROC VARREDUCE statement, 44

GENSELECT procedure, CLASS statement, 367
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

GENSELECT procedure, CODE statement, 368
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
IPROB option, 16
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
PCATALL option, 16

GENSELECT procedure, DISPLAY statement
CASESENSITIVE option, 18, 369
EXCLUDE option, 18, 369
EXCLUDEALL option, 18, 369
TRACE option, 18, 369

GENSELECT procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 370
NOREPLACE option, 19, 370
REPEATED option, 19, 370

GENSELECT procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24

GENSELECT procedure, MODEL statement, 372
CENTER option, 374
CLB option, 374
DESCENDING option, 373
DISTRIBUTION= option, 374
INCLUDE option, 376
INFORMATIVE option, 376
LINK= option, 376

GENSELECT procedure, MODEL statement, 372
MODEL statement, 372
PROC GENSELECT statement, 364
SELECTION statement, 384

syntax, 364
SYNTAX INDEX

NOCHECK option, 366
NOINT option, 378
OFFSET= option, 378
ORDER= option, 373
PHI= option, 378
START option, 378
TYPE3 option, 378

GENSELECT procedure, OUTPUT statement, 378
   ALL option, 379
   ALPHA= option, 379
   CBAR= option, 380
   COPYVAR= option, 379
   DIFCHISQ= option, 380
   DIFDEV= option, 380
   H= option, 380
   INDIVIDUAL= option, 381
   IPRED= option, 381
   keyword= option, 379
   LCL= option, 381
   LCLM= option, 381
   LINP= option, 383
   LOWER= option, 381
   LOWERXBETA= option, 381
   OBSCAT option, 379
   OUT= option, 379
   PREDICTED= option, 381
   RESCHI= option, 381
   RESDEV= option, 382
   RESIDUAL= option, 382
   RESLIK= option, 382
   RESRAW= option, 382
   RESWORK= option, 382
   ROLE= option, 382
   STDERR= option, 382
   STDRESCHI= option, 382
   STDRESDEV= option, 382
   STDXBETA = option, 382
   UCL= option, 383
   UCLM= option, 383
   UPPER= option, 383
   UPPERXBETA= option, 383
   XBETA= option, 383

GENSELECT procedure, SELECTION statement, 384
   ADAPTIVE option, 36
   CHOOSE= option, 36
   COMPETITIVE option, 36
   CRITERION= option, 36
   DETAILS= option, 38, 39
   FAST option, 37
   HIERARCHY= option, 39
   LSCOEFFS option, 37
   MAXEFFECTS= option, 37
   MAXSTEPS= option, 37
   METHOD= option, 35
   MINEFFECTS= option, 37
   ORDERSELECT option, 39
   SELECT= option, 37
   SELECTION= option, 41
   SLE= option, 37
   SLENTRY= option, 37
   SLS= option, 37
   SLSTAY= option, 37
   STOP= option, 38
   STOPHORIZON= option, 41

GENSELECT procedure, PARTITION statement
   FRACTION option, 34, 383
   ROLEVAR= option, 34, 383

GENSELECT procedure, PROC GENSELECT statement, 364
   ABS_CONV option, 42
   ABSFX_CONV option, 42
   ABSTOL option, 42
   ABSSG_CONV option, 42
   ABSSGTOL option, 42
   ABSTOL option, 42
   ABSX_CONV option, 42
   ABSXTOL option, 42
   ALPHA= option, 365
   CORRB option, 365
   COVB option, 366
   DATA= option, 366
   FCONV option, 43
   FCONV2 option, 43
   FTOL option, 43
   FTOL2 option, 43
   GCONV option, 44
   GCONV2 option, 44
   GTOL option, 44
   GTOL2 option, 44
   ITHIST option, 366
   LASSORHO= option, 366
   LASSOSTEPS= option, 366
   MAXTOL option, 366
   MAXITER= option, 45
   MAXOPTBATCH= option, 365
   MAXTIME= option, 45
   MINITER= option, 45
   NOCLPRINT option, 366
   NORMALIZE= option, 45
   NOSTDERR option, 366
   PARTFIT option, 366
   TECHNIQUE= option, 46
   XCONV option, 46
   XTOL option, 46

GINI option
   GROW statement (TREESPLIT), 864

GROW statement
   TREESPLIT procedure, 863
GTOL option
PROC ASSESS statement, 44
PROC BINNING statement, 44
PROC CARDINALITY statement, 44
PROC CORRELATION statement, 44
PROC GAMMOD statement, 44
PROC GENSELECT statement, 44
PROC KCLUS statement, 44
PROC LOGSELECT statement, 44
PROC NLMOD statement, 44
PROC PARTITION statement, 44
PROC PCA statement, 44
PROC PHSELECT statement, 44
PROC PLSMOD statement, 44
PROC QTRSELECT statement, 44
PROC REGSELECT statement, 44
PROC TREESPLIT statement, 44
PROC VARIMPUTE statement, 44
PROC VAREDUCE statement, 44

GTOL2 option
PROC ASSESS statement, 44
PROC BINNING statement, 44
PROC CARDINALITY statement, 44
PROC CORRELATION statement, 44
PROC GAMMOD statement, 44
PROC GENSELECT statement, 44
PROC KCLUS statement, 44
PROC LOGSELECT statement, 44
PROC NLMOD statement, 44
PROC PARTITION statement, 44
PROC PCA statement, 44
PROC PHSELECT statement, 44
PROC PLSMOD statement, 44
PROC QTRSELECT statement, 44
PROC REGSELECT statement, 44
PROC TREESPLIT statement, 44
PROC VARIMPUTE statement, 44
PROC VAREDUCE statement, 44

H= option
OUTPUT statement (GENSELECT), 380
OUTPUT statement (LOGSELECT), 480

HESSIAN option
PROC PHSELECT statement, 597

HIERARCHY= option
SELECTION statement (ASSESS), 39
SELECTION statement (BINNING), 39
SELECTION statement (CARDINALITY), 39
SELECTION statement (CORRELATION), 39
SELECTION statement (GAMMOD), 39
SELECTION statement (GENSELECT), 39
SELECTION statement (KCLUS), 39
SELECTION statement (LOGSELECT), 39
SELECTION statement (NLMOD), 39

ID statement
NLMOD procedure, 530

IGR option
GROW statement (TREESPLIT), 864

IMPUTE= option
PROC KCLUS statement, 427

IMPUTENOM= option
PROC KCLUS statement, 427

INCLUDE option
MODEL statement (GENSELECT), 376
MODEL statement (LOGSELECT), 476
MODEL statement (QTRSELECT), 689
MODEL statement (REGSELECT), 743

INCLUDE= option
MODEL statement (PHSELECT), 605

INCLUDEALL option
DISPLAYOUT statement (ASSESS), 19
DISPLAYOUT statement (BINNING), 19
DISPLAYOUT statement (CARDINALITY), 19
DISPLAYOUT statement (CORRELATION), 19, 96
DISPLAYOUT statement (GAMMOD), 19, 311
DISPLAYOUT statement (GENSELECT), 19, 370
DISPLAYOUT statement (KCLUS), 19, 432
DISPLAYOUT statement (LOGSELECT), 19, 472
DISPLAYOUT statement (NLMOD), 19, 529
DISPLAYOUT statement (PARTITION), 19, 975
DISPLAYOUT statement (PCA), 19, 565
DISPLAYOUT statement (PHSELECT), 19, 602
DISPLAYOUT statement (PLSMOD), 19, 649
DISPLAYOUT statement (QTRSELECT), 19, 687
DISPLAYOUT statement (REGSELECT), 19, 741
DISPLAYOUT statement (TREESPLIT), 19
DISPLAYOUT statement (VARIMPUTE), 19
DISPLAYOUT statement (VAREDUCE), 19, 1007

INDENTSIZE= option
CODE statement (ASSESS), 15
CODE statement (BINNING), 15
CODE statement (CARDINALITY), 15
CODE statement (CORRELATION), 15
CODE statement (GAMMOD), 15
CODE statement (GENSELECT), 15
CODE statement (KCLUS), 15
CODE statement (LOGSELECT), 15
CODE statement (NLMOD), 15
CODE statement (PARTITION), 15
CODE statement (PCA), 15
CODE statement (PHSELECT), 15
CODE statement (PLSMOD), 15
CODE statement (QTRSELECT), 15
CODE statement (REGSELECT), 15
CODE statement (TREESPLIT), 15
CODE statement (VARIMPUTE), 15
CODE statement (VARREDUCE), 15

INDIVIDUAL= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 480

INFORMATIVE option
MODEL statement (GENSELECT), 376
MODEL statement (LOGSELECT), 476
MODEL statement (PHSELECT), 605
MODEL statement (QTRSELECT), 690
MODEL statement (REGSELECT), 744

INIT= option
PROC KCLUS statement, 427

INITIALPHI= option
MODEL statement (GAMMOD), 319

INITSMOOTH= option
MODEL statement (GAMMOD), 315

INPUT statement
ASSESS procedure, 914
BINNING procedure, 935
KCLUS procedure, 433
TREESPLIT procedure, 892
VARIMPUTE procedure, 989

INTERCEPT option
MODEL statement (PLSMOD), 651

INTO= option
OUTPUT statement (LOGSELECT), 381, 480

IPRED= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 480

IPROB option
CODE statement (GENSELECT), 16
CODE statement (LOGSELECT), 16

IRCHART statement
IRCHART procedure, 785

ITDETAILS option
PROC GAMMOD statement, 307

ITHIST option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 468
PROC PHSELECT statement, 597

JT option
EXACT statement (FREQTAB), 128
OUTPUT statement (FREQTAB), 140
TABLES statement (FREQTAB), 164

KAPPA option
EXACT statement (FREQTAB), 128
OUTPUT statement (FREQTAB), 140
TEST statement (FREQTAB), 191

KCLUS procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

KCLUS procedure, CODE statement, 431
COMMENT option, 15
FILE= option, 15, 431
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16, 431
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16

KCLUS procedure, DISPLAY statement
CASESENSITIVE option, 18, 432
EXCLUDE option, 18, 432
EXCLUDEALL option, 18, 432
TRACE option, 18, 432

KCLUS procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 432
NOREPLACE option, 19, 432
REPEATED option, 19, 432

KCLUS procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (polynomial), 24
SEPARATE option (polynomial), 24
SPLIT option (polynomial), 29

KCLUS procedure, INPUT statement, 433
LEVEL= option, 433
KCLUS procedure, OUTPUT statement
COPYVARS= option, 434
OUT= option, 433
KCLUS procedure, PARTITION statement
FRACTION option, 34
ROLEVAR= option, 34
KCLUS procedure, PROC KCLUS statement, 425
ABSCONV option, 42
ABSFCONV option, 42
ABSFRTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXCTOL option, 42
DATA= option, 426
DISTANCE= option, 426
DISTANCENOM= option, 427
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
IMPUTE= option, 427
IMPUTENOM= option, 427
INIT= option, 427
KPROTOTYPEPARAMS= option, 430
MAXCLUSTERS= option, 428
MAXFMC= option, 45
MAXITER= option, 45, 428
MAXTIME= option, 45
MINITER= option, 45
NORMALIZE= option, 45
NTHREADS, 429
OUTSTAT= option, 429
PRINTALLDISTANCES option, 430
SEED= option, 429
STANDARDIZE= option, 429
STOPCRITERION= option, 428, 430
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46
KCLUS procedure, SCORE statement, 433
KCLUS procedure, SELECTION statement
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINFMD= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLE= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41
KCLUS procedure, syntax, 425
KENTB option
EXACT statement (FREQTAB), 128
OUTPUT statement (FREQTAB), 140
TEST statement (FREQTAB), 192
keyword option
OUTPUT statement (PLSMOD), 652
keyword= option
OUTPUT statement (GAMMOD), 321
OUTPUT statement (GENSELECT), 379
OUTPUT statement (QTRSELECT), 692
OUTPUT statement (REGSELECT), 745
KENTB= option
AUTOTUNE statement, 858
PRUNE statement (TREESPLIT), 867
KNOTMAX= option
EFFECT statement, spline (ASSESS), 27
EFFECT statement, spline (BNING), 27
EFFECT statement, spline (CARDINALITY), 27
EFFECT statement, spline (CORRELATION), 27
EFFECT statement, spline (GAMMOD), 27
EFFECT statement, spline (GENSELECT), 27
EFFECT statement, spline (KCLUS), 27
EFFECT statement, spline (LOGSELECT), 27
EFFECT statement, spline (NLMOD), 27
EFFECT statement, spline (PARTITION), 27
EFFECT statement, spline (PCA), 27
EFFECT statement, spline (PHSELECT), 27
EFFECT statement, spline (PLSMOD), 27
EFFECT statement, spline (QTRSELECT), 27
EFFECT statement, spline (REGSELECT), 27
EFFECT statement, spline (TREESPLIT), 27
EFFECT statement, spline (VARIMPUTE), 27
EFFECT statement, spline (VARREDUCE), 27
KNOTMETHOD option
EFFECT statement, spline (ASSESS), 27
EFFECT statement, spline (BNING), 27
EFFECT statement, spline (CARDINALITY), 27
EFFECT statement, spline (CORRELATION), 27
EFFECT statement, spline (GAMMOD), 27
EFFECT statement, spline (GENSELECT), 27
EFFECT statement, spline (KCLUS), 27
EFFECT statement, spline (LOGSELECT), 27
EFFECT statement, spline (NLMOD), 27
EFFECT statement, spline (PARTITION), 27
EFFECT statement, spline (PCA), 27
EFFECT statement, spline (PHSELECT), 27
EFFECT statement, spline (PLSMOD), 27
EFFECT statement, spline (QTRSESELECT), 27
EFFECT statement, spline (REGSELECT), 27
EFFECT statement, spline (TREESPLIT), 27
EFFECT statement, spline (VARIMPUTE), 27
EFFECT statement, spline (VARREDUCE), 27

KNOTMIN= option
EFFECT statement, spline (ASSESS), 28
EFFECT statement, spline (BINNING), 28
EFFECT statement, spline (CARDINALITY), 28
EFFECT statement, spline (CORRELATION), 28
EFFECT statement, spline (GAMMOD), 28
EFFECT statement, spline (GENSELECT), 28
EFFECT statement, spline (KCLUS), 28
EFFECT statement, spline (LOGSELECT), 28
EFFECT statement, spline (NLMOD), 28
EFFECT statement, spline (PARTITION), 28
EFFECT statement, spline (PCA), 28
EFFECT statement, spline (PHSELECT), 28
EFFECT statement, spline (PLSMOD), 28
EFFECT statement, spline (QTRSESELECT), 28
EFFECT statement, spline (REGSELECT), 28
EFFECT statement, spline (TREESPLIT), 28
EFFECT statement, spline (VARIMPUTE), 28
EFFECT statement, spline (VARREDUCE), 28

KNOTS= option
MODEL statement (GAMMOD), 315
KPROTOTYPEPARAMS= option
PROC KCLUS statement, 430

LABELID= option
CODE statement (ASSESS), 16
CODE statement (BINNING), 16
CODE statement (CARDINALITY), 16
CODE statement (CORRELATION), 16
CODE statement (GAMMOD), 16
CODE statement (GENSELECT), 16
CODE statement (KCLUS), 16
CODE statement (LOGSELECT), 16
CODE statement (NLMOD), 16
CODE statement (PARTITION), 16
CODE statement (PCA), 16
CODE statement (PHSELECT), 16
CODE statement (PLSMOD), 16
CODE statement (QTRSESELECT), 16
CODE statement (REGSELECT), 16

LAMCR option
OUTPUT statement (FREQTAB), 140

LAMDAS option
OUTPUT statement (FREQTAB), 140

LAMRC option
OUTPUT statement (FREQTAB), 140

LASSORHO= option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 468
PROC PHSELECT statement, 597

LASSOEPS= option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 468
PROC PHSELECT statement, 597

LASSOTOL= option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 468
PROC PHSELECT statement, 597

LCL= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 480

LCLM= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 481

LEAVES= option
PRUNE statement (TREESPLIT), 867, 868

LEVEL= option
INPUT statement, 433, 936
OUTPUT statement (LOGSELECT), 381, 481
TARGET statement, 914, 937

LEVEL= option (BINOMIAL)
TABLES statement (FREQTAB), 154

LGOR option
OUTPUT statement (FREQTAB), 141

LGRRC1 option
OUTPUT statement (FREQTAB), 141

LGRRC2 option
OUTPUT statement (FREQTAB), 141

LIFOUT= option
PROC ASSESS statement, 912

LIMITN= option
chart statements (SPC), 793

LINESIZE= option
CODE statement (ASSESS), 16
CODE statement (BINNING), 16
CODE statement (CARDINALITY), 16
CODE statement (CORRELATION), 16
CODE statement (GAMMOD), 16
CODE statement (GENSELECT), 16
CODE statement (KCLUS), 16
CODE statement (LOGSELECT), 16
CODE statement (NLMOD), 16
CODE statement (PARTITION), 16
CODE statement (PCA), 16
CODE statement (PHSELECT), 16
CODE statement (PLSMOD), 16
CODE statement (QTRSESELECT), 16
CODE statement (REGSELECT), 16

LABELID= option
CODE statement (ASSESS), 16
CODE statement (BINNING), 16
CODE statement (CARDINALITY), 16
CODE statement (CORRELATION), 16
CODE statement (GAMMOD), 16
CODE statement (GENSELECT), 16
CODE statement (KCLUS), 16
CODE statement (LOGSELECT), 16

CODE statement (NLMOD), 16
CODE statement (PARTITION), 16
CODE statement (PCA), 16
CODE statement (PHSELECT), 16
CODE statement (PLSMOD), 16
CODE statement (QTRSELECT), 16
CODE statement (REGSELECT), 16
CODE statement (TREESPLIT), 16
CODE statement (VARIIMPUTE), 16
CODE statement (VARREDUCE), 16

LINK= option
MODEL statement (GAMMOD), 319
MODEL statement (GENSELECT), 376
MODEL statement (LOGSELECT), 476

LINP= option
OUTPUT statement (GENSELECT), 383
OUTPUT statement (LOGSELECT), 482

LIST option
TABLES statement (FREQTAB), 164
LOGLIKENULL option
PROC PHSELECT statement, 597

LOGSELECT procedure, CLASS statement, 469
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

LOGSELECT procedure, CODE statement, 470
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
IPROB option, 16
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
PCATALL option, 16

LOGSELECT procedure, DISPLAY statement
CASESENSITIVE option, 18, 471
EXCLUDE option, 18, 471
EXCLUDEALL option, 18, 471
TRACE option, 18, 471

LOGSELECT procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 472
NOREPLACE option, 19, 472
REPEATED option, 19, 472

LOGSELECT procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23

LOGSELECT procedure, MODEL statement, 474
CLB option, 476
DESCENDING option, 475
INCLUDE option, 476
INFORMATIVE option, 476
LINK= option, 476
NOCHECK option, 468
NOINT option, 477
OFFSET= option, 477
ORDER= option, 475
START option, 477
TYPE3 option, 477

LOGSELECT procedure, OUTPUT statement, 477
ALL option, 478
ALPHA= option, 478
CBAR= option, 480
COPYVAR= option, 478
DIFCHISQ= option, 480
DIFDEV= option, 480
FIXEDOFFSET= option, 479
H= option, 480
INDIVIDUAL= option, 480
INTO= option, 381, 480
IPRED= option, 480
LCL= option, 480
LCLM= option, 481
LEVEL= option, 381, 481
LINP= option, 482
LOWER= option, 481
LOWERXBETA= option, 480
OBSCAT option, 479
OUT= option, 478, 745
PREDICTED= option, 481
PREDPROBS option, 379, 479
RESCHI= option, 481
RESDEV= option, 481
RESIDUAL= option, 481
RESLIK= option, 481
RESRAW= option, 481
RESWORK= option, 481
ROLE= option, 481
STDRESCHI= option, 482

LOGSELECT procedure, OUTPUT statement, 477

LOGSELECT procedure, OUTPUT statement, 477

LOGSELECT procedure, OUTPUT statement, 477

LOGSELECT procedure, OUTPUT statement, 477
STDRESDEV= option, 482
STDXBETA = option, 482
UCL= option, 482
UCLM= option, 482
UPPER= option, 482
UPPERXBETA= option, 482
XBETA= option, 482
LOGSELECT procedure, PARTITION statement
FRACTION option, 34, 483
ROLEVAR= option, 34, 483
LOGSELECT procedure, PROC GENSELECT
statement
STB option, 367
LOGSELECT procedure, PROC LOGSELECT
statement, 466
ABSCONV option, 42
ABSFCONV option, 42
ABSFXTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSTOL Conv option, 42
ABSXTOL option, 42
ALPHA= option, 467
CORRB option, 467
COVB option, 467
DATA= option, 467
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
ITHIST option, 468
LASSORHO= option, 468
LASSOSTEPS= option, 468
LASSOTOL= option, 468
MAXFNC= option, 45
MAXITER= option, 45
MAXOPTBATCH= option, 468
MAXTIME= option, 45
MINITER= option, 45
NOCCLPRINT option, 468
NORMALIZE= option, 45
NOSTDERR option, 468
PARTFIT option, 469
STB option, 469
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46
LOGSELECT procedure, SELECTION statement, 483
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41
LOGSELECT procedure, syntax, 466
LOWERM= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 481
PREDICT statement (NLMOD), 534
LOGSELECT procedure, syntax, 466
LOWERXBETA= option
OUTPUT statement (GENSELECT), 381
OUTPUT statement (LOGSELECT), 480
LRCHI option
EXACT statement (FREQTAB), 128
OUTPUT statement (FREQTAB), 141
LRCHI option (CHISQ)
TABLES statement (FREQTAB), 157
LSCOEFFS option
SELECTION statement (ASSESS), 37
SELECTION statement (Binning), 37
SELECTION statement (CARDINALITY), 37
SELECTION statement (CORRELATION), 37
SELECTION statement (GAMMOD), 37
SELECTION statement (GENSELECT), 37
SELECTION statement (KCLUS), 37
SELECTION statement (LOGSELECT), 37
SELECTION statement (NLMOD), 37
SELECTION statement (PARTITION), 37
SELECTION statement (PCA), 37
SELECTION statement (PHSELECT), 37
SELECTION statement (PLSMOD), 37
SELECTION statement (QTRSELECT), 37
SELECTION statement (REGSELECT), 37
SELECTION statement (TREESPLIT), 37
SELECTION statement (VARIMPUTE), 37
SELECTION statement (VARREDUCE), 37
M= option
SELECTION statement (KCLUS), 37
SELECTION statement (LOGSELECT), 37
SELECTION statement (NLMOD), 37
SELECTION statement (PARTITION), 37
SELECTION statement (PCA), 37
SELECTION statement (PHSELECT), 37
SELECTION statement (PLSMOD), 37
SELECTION statement (QTRSELECT), 37
SELECTION statement (REGSELECT), 37
SELECTION statement (TREESPLIT), 37
SELECTION statement (VARIMPUTE), 37
SELECTION statement (VARREDUCE), 37

MAXTIME= option
AUTOTUNE statement, 858
EXACT statement (FREQTAB), 132
PROC ASSESS statement, 45
PROC BINNING statement, 45
PROC CARDINALITY statement, 45
PROC CORRELATION statement, 45
PROC GAMMOD statement, 45
PROC GENSELECT statement, 45
PROC KCLUS statement, 45
PROC LOGSELECT statement, 45
PROC NLMOD statement, 45
PROC PARTITION statement, 45
PROC PCA statement, 45
PROC PHSELECT statement, 45
PROC PLSMOD statement, 45
PROC QTRSELECT statement, 45
PROC REGSELECT statement, 45
PROC TREESPLIT statement, 45
PROC VARIMPUTE statement, 45
PROC VARREDUCE statement, 45

MC option
EXACT statement (FREQTAB), 132
PROC ASSESS statement, 45
PROC BINNING statement, 45
PROC CARDINALITY statement, 45
PROC CORRELATION statement, 45
PROC GAMMOD statement, 45
PROC GENSELECT statement, 45
PROC KCLUS statement, 45
PROC LOGSELECT statement, 45
PROC NLMOD statement, 45
PROC PARTITION statement, 45
PROC PCA statement, 45
PROC PHSELECT statement, 45
PROC PLSMOD statement, 45
PROC QTRSELECT statement, 45
PROC REGSELECT statement, 45
PROC TREESPLIT statement, 45
PROC VARIMPUTE statement, 45
PROC VARREDUCE statement, 45

MEDCENTRAL= option
chart statements (SPC), 794

METHOD= option
MODEL statement (GAMMOD), 319
PROC BINNING statement, 933
PROC PCA statement, 559
PROC PLSMOD statement, 646
SELECTION statement (ASSESS), 35
SELECTION statement (BINNING), 35
SELECTION statement (CARDINALITY), 35
SELECTION statement (CORRELATION), 35
SELECTION statement (GAMMOD), 35
SELECTION statement (GENSELECT), 35
SELECTION statement (KCLUS), 35
SELECTION statement (LOGSELECT), 35
SELECTION statement (NLMOD), 35
SELECTION statement (PARTITION), 35
SELECTION statement (PCA), 35
SELECTION statement (PHSELECT), 35
SELECTION statement (PLSMOD), 35
SELECTION statement (QTRSELECT), 35
SELECTION statement (REGSELECT), 35
SELECTION statement (TREESPLIT), 35
SELECTION statement (VARIMPUTE), 35
SELECTION statement (VARREDUCE), 35

METHOD= option (RELRISK)
EXACT statement (FREQTAB), 130
TABLES statement (FREQTAB), 183

METHOD= option (RISKDIFF)
EXACT statement (FREQTAB), 131
TABLES statement (FREQTAB), 188
METHOD=FM option (RELRISK)
TABLES statement (FREQTAB), 183
METHOD=FM option (RISKDIFF)
TABLES statement (FREQTAB), 188
METHOD=HA option (RISKDIFF)
  TABLES statement (FREQTAB), 188
METHOD=LR option (RELRISK)
  TABLES statement (FREQTAB), 183
METHOD=NEWCOMBE option (RISKDIFF)
  TABLES statement (FREQTAB), 188
METHOD=WALD option (RELRISK)
  TABLES statement (FREQTAB), 183
METHOD=WALD option (RISKDIFF)
  TABLES statement (FREQTAB), 188
METHOD=WALDMODIFIED option (RELRISK)
  TABLES statement (FREQTAB), 184
MHCHI option
  EXACT statement (FREQTAB), 129
  OUTPUT statement (FREQTAB), 141
MHOR option
  OUTPUT statement (FREQTAB), 141
MHRRC1 option
  OUTPUT statement (FREQTAB), 142
MHRRC2 option
  OUTPUT statement (FREQTAB), 142
MIDP option
  EXACT statement (NPAR1WAY), 133
MINEFFECTS= option
  SELECTION statement (ASSESS), 37
  SELECTION statement (BINNING), 37
  SELECTION statement (CARDINALITY), 37
  SELECTION statement (CORRELATION), 37
  SELECTION statement (GAMMOD), 37
  SELECTION statement (GENSELECT), 37
  SELECTION statement (KCLUS), 37
  SELECTION statement (LOGSELECT), 37
  SELECTION statement (NLMOD), 37
  SELECTION statement (PARTITION), 37
  SELECTION statement (PCA), 37
  SELECTION statement (PHSELECT), 37
  SELECT statement (PLSMOD), 37
  SELECT statement (QTRSELECT), 37
  SELECT statement (REGSELECT), 37
  SELECT statement (TREESPLIT), 37
  SELECT statement (VARIMPUTE), 37
  SELECT statement (VARREDUCE), 37
MINITER= option
  PROC ASSESS statement, 45
  PROC BINNING statement, 45
PROC CARDINALITY statement, 45
PROC CORRELATION statement, 45
PROC GAMMOD statement, 45
PROC GENSELECT statement, 45
PROC KCLUS statement, 45
PROC LOGSELECT statement, 45
PROC NLMOD statement, 45
PROC PARTITION statement, 45
PROC PCA statement, 45
PROC PHSELECT statement, 45
PROC PLSMOD statement, 45
PROC QTRSELECT statement, 45
PROC REGSELECT statement, 45
PROC TREESPLIT statement, 45
PROC VARIMPUTE statement, 45
PROC VARREDUCE statement, 45
MINLEAFSIZE= option
  PROC TREESPLIT statement, 852
MINPHI= option
  MODEL statement (GAMMOD), 320
MINSMOOTH= option
  MODEL statement (GAMMOD), 317
MINUSEINSEARCH= option
  PROC TREESPLIT statement, 852
MINVARIANCEINCREMENT= option
  REDUCE statement, 1009
MISSING option
  CLASS statement (ASSESS), 11, 1005
  CLASS statement (BINNING), 11, 1005
  CLASS statement (CARDINALITY), 11, 1005
  CLASS statement (CORRELATION), 11, 1005
  CLASS statement (GAMMOD), 11, 1005
  CLASS statement (GENSELECT), 11, 1005
  CLASS statement (KCLUS), 11, 1005
  CLASS statement (LOGSELECT), 11, 1005
  CLASS statement (NLMOD), 11, 1005
  CLASS statement (PARTITION), 11, 1005
  CLASS statement (PCA), 11, 1005
  CLASS statement (PHSELECT), 11, 1005
  CLASS statement (PLSMOD), 11, 1005
  CLASS statement (QTRSELECT), 11, 1005
  CLASS statement (REGSELECT), 11, 1005
  CLASS statement (TREESPLIT), 11, 1005
  CLASS statement (VARIMPUTE), 11, 1005
  CLASS statement (VARREDUCE), 11, 1005
  PROC FREQTAB statement, 123
MISSPRINT option
  TABLES statement (FREQTAB), 123
MODEL statement
  GAMMOD procedure, 312
  GENSELECT procedure, 372
  LOGSELECT procedure, 474
  NLMOD procedure, 530
  PHSELECT procedure, 604
  PLSMOD procedure, 651
  QTRSELECT procedure, 689
  REGSELECT procedure, 743
  TREESPLIT procedure, 865
MRCHART statement
  MRCHART procedure, 786
N option
OUTPUT statement (FREQTAB), 142
N= option
EXACT statement (FREQTAB), 133
PROC PCA statement, 561
NATURALCUBIC option
EFFECT statement, spline (ASSESS), 28
EFFECT statement, spline (BINNING), 28
EFFECT statement, spline (CARDINALITY), 28
EFFECT statement, spline (CORRELATION), 28
EFFECT statement, spline (GAMMOD), 28
EFFECT statement, spline (GENSELECT), 28
EFFECT statement, spline (KCLUS), 28
EFFECT statement, spline (LOGSELECT), 28
EFFECT statement, spline (NLMOD), 28
EFFECT statement, spline (PARTITION), 28
EFFECT statement, spline (PCA), 28
EFFECT statement, spline (PHSELECT), 28
EFFECT statement, spline (PLSMOD), 28
EFFECT statement, spline (QTRSELECT), 28
EFFECT statement, spline (REGSELECT), 28
EFFECT statement, spline (TREESPLIT), 28
EFFECT statement, spline (VARIMPUTE), 28
EFFECT statement, spline (VAREDUCE), 28
NBINS= option
PROC ASSESS statement, 912
NCUTS= option
PROC ASSESS statement, 912
NFAC= option
PROC PLSMOD statement, 646
NITER= option
PROC PCA statement, METHOD=RANDOM option, 560
NLEVELS option
PROC FREQTAB statement, 123
NLMOD procedure, 525
PROC NLMOD statement, 526
syntax, 525
NLMOD procedure, BOUNDS statement, 528
NLMOD procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
NLMOD procedure, CODE statement
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
NLMOD procedure, DISPLAY statement
CASESENSITIVE option, 18, 529
EXCLUDE option, 18, 529
EXCLUDEALL option, 18, 529
TRACE option, 18, 529
NLMOD procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 529
NOREPLACE option, 19, 530
REPEATED option, 19, 530
NLMOD procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
NLMOD procedure, ESTIMATE statement, 530
ALPHA= option, 530
DF= option, 530
NLMOD procedure, MODEL statement, 530
NLMOD procedure, PARAMETERS statement, 531
NLMOD procedure, PARTITION statement
FRACTION option, 34
ROLEVAR= option, 34
NLMOD procedure, PREDICT statement, 534
ALPHA= option, 534
DF= option, 534
LOWER= option, 534
PRED= option, 534
PROBT= option, 534
STDERR= option, 534
TVALUE= option, 534
UPPER= option, 534
NLMOD procedure, PROC NLMOD statement, 526
ABSCONV option, 42
ABSFCNV option, 42
ABSFTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSTOL option, 42
ALPHA= option, 527
Syntax Index

CORR option, 527
COV option, 527
DATA= option, 527
DF= option, 527
ECORR option, 527
ECOV option, 527
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NOITPRINT option, 527
NOPRINT option, 527
NORMALIZE= option, 45
OUT= option, 527
SINGULAR= option, 527
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46

NLMOD procedure, RESTRICT statement, 535
NLMOD procedure, SELECTION statement

ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

NMISS option
OUTPUT statement (FREQTAB), 142
NO3SIGMACHECK option
chart statements (SPC), 794
NOCENTER option

PROC PCA statement, METHOD=ITERGS option, 560
PROC PCA statement, METHOD=NIPALS option, 560
PROC PCA statement, METHOD=RANDOM option, 560
PROC PLSMOD statement, 647

NOCLPRINT option
PROC GAMMOD statement, 307
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 468
PROC PHSELECT statement, 597
PROC PLSMOD statement, 647
PROC QTRSELECT statement, 684
PROC REGSELECT statement, 738

NOCOL option
TABLES statement (FREQTAB), 165

NOCORR option
PROC CORRELATION statement, 93

NOCUM option
TABLES statement (FREQTAB), 165

NOCVSTDIZE option
PROC PLSMOD statement, 647

NOEFFECT option
EFFECT statement, multimember (ASSESS), 23
EFFECT statement, multimember (BINNING), 23
EFFECT statement, multimember (CARDINALITY), 23
EFFECT statement, multimember (CORRELATION), 23
EFFECT statement, multimember (GENSELECT), 23
EFFECT statement, multimember (KCLUS), 23
EFFECT statement, multimember (LOGSELECT), 23
EFFECT statement, multimember (NLMOD), 23
EFFECT statement, multimember (PARTITION), 23
EFFECT statement, multimember (PCA), 23
EFFECT statement, multimember (PHSELECT), 23
EFFECT statement, multimember (PLSMOD), 23
EFFECT statement, multimember (QTRSELECT), 23
EFFECT statement, multimember (RESELECT), 23
EFFECT statement, multimember (TREESPLIT), 23
EFFECT statement, multimember (VARIMPUTE), 23
EFFECT statement, multimember
(VARREDUCE), 23

NOFREQ option
TABLES statement (FREQTAB), 165

NOINT option
MODEL statement (GENSELECT), 366, 378
MODEL statement (LOGSELECT), 468, 477
MODEL statement (QTRSELECT), 690
MODEL statement (REGSELECT), 744
PROC PCA statement, 561

NOITPRINT option
PROC NLMMOD statement, 527

NOMISS option
PROC CORRELATION statement, 93

NONINFERIORITY option (BINOMIAL)
TABLES statement (FREQTAB), 155

NONINFERIORITY option (RELRISK)
TABLES statement (FREQTAB), 184

NONINFERIORITY option (RISKDIFF)
TABLES statement (FREQTAB), 188

NOPERCENT option
TABLES statement (FREQTAB), 165

NOPRINT option
chart statements (SPC), 794
PROC FREQTAB statement, 123
PROC GAMMOD statement, 307
PROC NLMMOD statement, 527
PROC TREESPLIT statement, 853
PROC VARREDUCE statement, 1004
TABLES statement (FREQTAB), 165

NOPROB option
PROC CORRELATION statement, 94

NOREPLACE option
PROC NLMMOD statement, 527

NORMALIZE option
MODEL statement (GAMMOD), 320

NORMALIZE= option
PROC ASSESS statement, 45
PROC BINNING statement, 45
PROC CARDINALITY statement, 45
PROC CORRELATION statement, 45
PROC GAMMOD statement, 45
PROC GENSELECT statement, 45
PROC KCLUS statement, 45
PROC LOGSELECT statement, 45
PROC NLMMOD statement, 45
PROC PARTITION statement, 45
PROC PCA statement, 45
PROC PHSELECT statement, 45
PROC PLMMOD statement, 45
PROC QTRSELECT statement, 45
PROC REGSELECT statement, 45
PROC TREESPLIT statement, 45
PROC VARIMPUTE statement, 45
PROC VARREDUCE statement, 45

NOROW option
TABLES statement (FREQTAB), 165

NOSCALE option
PROC PCA statement, METHOD=ITERGS option, 560
PROC PCA statement, METHOD=NIPALS option, 560
PROC PCA statement, METHOD=RANDOM option, 560
PROC PLMMOD statement, 647

NOSEPARATE option
EFFECT statement, polynomial (ASSESS), 24
EFFECT statement, polynomial (BINNING), 24
EFFECT statement, polynomial (CARDINALITY), 24
EFFECT statement, polynomial (CORRELATION), 24
EFFECT statement, polynomial (GAMMOD), 24
EFFECT statement, polynomial (GENSELECT), 24
EFFECT statement, polynomial (KCLUS), 24
EFFECT statement, polynomial (LOGSELECT), 24
EFFECT statement, polynomial (PLMMOD), 24
EFFECT statement, polynomial (QTRSELECT), 24
EFFECT statement, polynomial (REGSELECT), 24
EFFECT statement, polynomial (TREESPLIT), 24
EFFECT statement, polynomial (PCA), 24
EFFECT statement, polynomial (PLSMOD), 24
EFFECT statement, polynomial (QTRSELECT), 24
EFFECT statement, polynomial (REGSELECT), 24
EFFECT statement, polynomial (TREESPLIT), 24
EFFECT statement, polynomial (VARIMPUTE), 24
EFFECT statement, polynomial (VARREDUCE), 24
NOSIMPLE option
  PROC CORRELATION statement, 94
NOSPARSE option
  TABLES statement (FREQTAB), 165
NOSTDERR option
  PROC GENSELECT statement, 366
  PROC LOGSELECT statement, 468
  PROC PHSELECT statement, 598
NOSURVIVAL option
  CODE statement (PHSELECT), 16, 599
NOTRIM option
  CODE statement (ASSESS), 16
  CODE statement (BINNING), 16
  CODE statement (CARDINALITY), 16
  CODE statement (CORRELATION), 16
  CODE statement (GAMMOD), 16
  CODE statement (GENSELECT), 16
  CODE statement (KCLUS), 16
  CODE statement (LOGSELECT), 16
  CODE statement (PARTITION), 16
  CODE statement (PCA), 16
  CODE statement (PHSELECT), 16
  CODE statement (PLSMOD), 16
  CODE statement (QTRSELECT), 16
  CODE statement (REGSELECT), 16
  CODE statement (TREESPLIT), 16
  CODE statement (VARIMPUTE), 16
  CODE statement (VARREDUCE), 16
NOWARN option
  TABLES statement (FREQTAB), 166
NPCHART statement
  NPCHART procedure, 787
NSAMP= option
  PROC PLSMOD statement, CVTEST option, 645
NSUBSESSIONWORKERS= option
  AUTOTUNE statement, 859
NSURROGATES= option
  PROC TREESPLIT statement, 853
NTAU option
  QUANTILES option (QTRSELECT), 690
NTHREADS
  PROC KCLUS statement, 429
NTHREADS= option
  PROC ASSESS statement, 912
  PROC PARTITION statement, 972
  PROC SPC statement, 782
  PROC VARIMPUTE statement, 988
NUMBIN= option
  INPUT statement, 935
  PROC BINNING statement, 934
  PROC TREESPLIT statement, 853
OBJECTIVE= option
  AUTOTUNE statement, 859
OBSCAT option
  OUTPUT statement (GENSELECT), 379
  OUTPUT statement (LOGSELECT), 479
OFF option
  PRUNE statement (TREESPLIT), 868
OFFSET= option
  MODEL statement (GAMMOD), 320
  MODEL statement (GENSELECT), 378
  MODEL statement (LOGSELECT), 477
  MODEL statement (PHSELECT), 605
OR option
  EXACT statement (FREQTAB), 129
  OUTPUT statement (FREQTAB), 142
  TABLES statement (FREQTAB), 166
ORDER= option
  CLASS statement (ASSESS), 11
  CLASS statement (BINNING), 11
  CLASS statement (CARDINALITY), 11
  CLASS statement (CORRELATION), 11
  CLASS statement (GAMMOD), 11
  CLASS statement (GENSELECT), 11
  CLASS statement (KCLUS), 11
  CLASS statement (LOGSELECT), 11
  CLASS statement (NLMOD), 11
  CLASS statement (PARTITION), 11
  CLASS statement (PCA), 11
  CLASS statement (PHSELECT), 11
  CLASS statement (PLSMOD), 11
  CLASS statement (QTRSELECT), 11
  CLASS statement (REGSELECT), 11
  CLASS statement (TREESPLIT), 11
  CLASS statement (VARIMPUTE), 11
  CLASS statement (VARREDUCE), 11
NOWARN option
  TABLES statement (FREQTAB), 166
NPCHART statement
  NPCHART procedure, 787
NSAMP= option
  PROC PLSMOD statement, CVTEST option, 645
NSUBSESSIONWORKERS= option
  AUTOTUNE statement, 859
NSURROGATES= option
  PROC TREESPLIT statement, 853
NTAU option
  QUANTILES option (QTRSELECT), 690
NTHREADS
  PROC KCLUS statement, 429
SELECT statement (CARDINALITY), 39
SELECT statement (CORRELATION), 39
SELECT statement (GAMMOD), 39
SELECT statement (GENSELECT), 39
SELECT statement (KCLUS), 39
SELECT statement (LOGSELEcT), 39
SELECT statement (NLMOD), 39
SELECT statement (PARTITION), 39
SELECT statement (PCA), 39
SELECT statement (PHSELECT), 39
SELECT statement (PLSMOD), 39
SELECT statement (QTRSELECT), 39
SELECT statement (REGSELEcT), 39
SELECT statement (TREESPLIT), 39
SELECT statement (VARIMPUTE), 39
SELECT statement (VARREDUCE), 39

OUT= option
CODE statement (ASSESS), 16
CODE statement (BINNING), 16
CODE statement (CARDINALITY), 16
CODE statement (CORRELATION), 16
CODE statement (GAMMOD), 16
CODE statement (GENSELECT), 16
CODE statement (KCLUS), 16
CODE statement (LOGSELEcT), 16
CODE statement (NLMOD), 16
CODE statement (PARTITION), 16
CODE statement (PCA), 16
CODE statement (PHSELECT), 16
CODE statement (PLSMOD), 16
CODE statement (QTRSELECT), 16
CODE statement (REGSELEcT), 16
CODE statement (TREESPLIT), 16
CODE statement (VARIMPUTE), 16

PROC VARREDUCE statement, 1004
OUTCUM option
TABLES statement (FREQQTAB), 167
OUTDETAILS= option
PROC CARDINALITY statement, 957
OUTEXPECT option
TABLES statement (FREQQTAB), 167
OUTLEVEL option (BINOMIAL)
TABLES statement (FREQQTAB), 155
OUTLIMITS= option
chart statements (SPC), 794
OUTMODEL option
PROC TREESPLIT statement, 853
OUTP= option
PROC CORRELATION statement, 94
OUTPCT option
TABLES statement (FREQQTAB), 167

OUTPUT option
BINNING procedure, 936
FREQQTAB procedure, 134
GAMMOD procedure, 320
GENSELECT procedure, 378
LOGSELECT procedure, 477
PARTITION procedure, 975
PCA procedure, 566
PHSELECT procedure, 605
PLSMOD procedure, 651
QTRSELECT procedure, 691
REGSELECT procedure, 745
TREESPLIT procedure, 865
VARIMPUTE procedure, 990

OUTSTAT= option
PROC KCLUS statement, 429
PROC PCA statement, 561
OUTTABLE= option
chart statements (SPC), 794

P= option (BINOMIAL)
TABLES statement (FREQQTAB), 155

PAGE option
PROC FREQQTAB statement, 124

PARAM= option
CLASS statement (ASSESS), 12
CLASS statement (BINNING), 12
CLASS statement (CARDINALITY), 12
CLASS statement (CORRELATION), 12
CLASS statement (GAMMOD), 12
CLASS statement (GENSELECT), 12
CLASS statement (KCLUS), 12
CLASS statement (LOGSELECT), 12
CLASS statement (NLMOD), 12
CLASS statement (PARTITION), 12
CLASS statement (PCA), 12
CLASS statement (PHSELECT), 12
CLASS statement (PLSMOD), 12
CLASS statement (QTRSELECT), 12
CLASS statement (REGSELECT), 12
CLASS statement (TREESPLIT), 12
CLASS statement (VARIMPUTE), 12
CLASS statement (VARREDUCE), 12

PARAMETERS statement
NLMOD procedure, 531
PARPREFIX= option
PROC PCA statement, 562

PARTFIT option
PROC GENSELECT statement, 366
PROC LOGSELECT statement, 469

PARTIAL statement
PCA procedure, 568
PARTIND option
PROC PARTITION statement, 972
PARTINDNAME= option
OUTPUT statement, 975

PARTITION procedure, BY statement, 973
PARTITION procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

PARTITION procedure, CODE statement
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16

PARTITION procedure, DISPLAY statement
CASESENSITIVE option, 18, 974
EXCLUDE option, 18, 974
EXCLUDEALL option, 18, 974
TRACE option, 18, 974

PARTITION procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 975
NOREPLACE option, 19, 975
REPEATED option, 19, 975

PARTITION procedure, EFFECT statement
BASIS option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27

KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 28
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24

PARTITION procedure, OUTPUT statement, 975
COPYVARS= option, 976
FREQNAME= option, 976
OUT= option, 975
PARTINDNAME= option, 976

PARTITION procedure, PARTITION statement
FRACTION option, 34
ROLEVAR= option, 34

PARTITION procedure, PROC PARTITION statement, 972
ABSCONV option, 42
ABSFCONV option, 42
ABSFTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOl option, 42
DATA= option, 972
EVENT= option, 973
EVENTPROP= option, 973
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NORMALIZE= option, 45
NTHREADS= option, 972
PARTIND option, 972
SAMPPCT2= option, 973
SAMPPCT= option, 973
SAMPPC TeVT= option, 973
SEED= option, 972
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46

PARTITION procedure, SELECTION statement
ADAPTIVE option, 36
CHOICE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLEENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

PARTITION procedure, syntax, 972

PARTITION statement
ASSESS procedure, 34
BINNING procedure, 34
CARDINALITY procedure, 34
GENSELECT procedure, 34, 383
KCLUS procedure, 34
LOGSELECT procedure, 34, 482
NLMOD procedure, 34
PARTITION procedure, 34
PHSELECT procedure, 34, 608
PLSMOD procedure, 34, 654
QTRSELECT procedure, 34, 693
REGSELECT procedure, 34, 747
TREESPLIT procedure, 34, 866
VARIMPUTE procedure, 34
VARREDUCE procedure, 34

PCA procedure
PROC PCA statement, 558
syntax, 558

PCA procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

PCA procedure, CODE statement, 563
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16

PCA procedure, DISPLAY statement
CASESENSITIVE option, 18, 565
EXCLUDE option, 18, 565
EXCLUDEALL option, 18, 565
TRACE option, 18, 565

PCA procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 565
NOREPLACE option, 19, 565
REPEATED option, 19, 565

PCA procedure, EFFECT statement
BASIS option (spline), 26
CASESENSITIVE option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
MDEGREE option (spline), 27
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24

PCA procedure, OUTPUT statement, 566
COPYVARS= option, 566
keyword option, 566
OUT= option, 566

PCA procedure, PARTIAL statement, 568

PCA procedure, PROC PCA statement, 558
ABS_CONV option, 42
ABS_F_CONV option, 42
ABS_FTOL option, 42
ABS_GC_CONV option, 42
ABS_GTOL option, 42
ABS_S_CONV option, 42
ABS_STOL option, 42
COV option, 559
COVARIANCE option, 559
DATA= option, 559
FC_CONV option, 43
FC_CONV2 option, 43
FO option, 43
FTOL option, 43
FTOL2 option, 43
GC_CONV option, 44
GC_CONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
METHOD= option, 559
MINITER= option, 45
N= option, 561
NOINT option, 561
NORMALIZE= option, 45
OUTSTAT= option, 561
PARPREFIX= option, 562
PLOTS= option, 561
PREFIX= option, 562
RPREFIX= option, 562
SING= option, 562
SINGULAR= option, 562
STANDARD option, 563
STD option, 563
TECHNIQUE= option, 46
VARDEF= option, 563
XCONV option, 46
XTOL option, 46

PCA procedure, PROC PCA statement,
METHOD=ITERGS option
EPSILON= option, 559
MAXITER= option, 559
NOCENTER option, 560
NOSCALE option, 560

PCA procedure, PROC PCA statement,
METHOD=NIPALS option
EPSILON= option, 560
MAXITER= option, 560
NOCENTER option, 560
NOSCALE option, 560

PCA procedure, PROC PCA statement,
METHOD=RANDOM option
NITER= option, 560
NOCENTER option, 560
NOSCALE option, 560
SEED= option, 560

PCA procedure, SELECTION statement
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 41
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

PCA procedure, VAR statement, 568
PCATALL option
CODE statement (GENSELECT), 16
CODE statement (LOGSELECT), 16
PCHART statement
PCHART procedure, 788
ACHI option
EXACT statement (FREQTAB), 129
OUTPUT statement (FREQTAB), 142
PCORR option
EXACT statement (FREQTAB), 129
OUTPUT statement (FREQTAB), 142
TEST statement (FREQTAB), 192
PCTLDEF= option
chart statements (SPC), 794
PEARSONRES option (CROSSLIST)
TABLES statement (FREQTAB), 162
PEVENT= option
FITSTAT statement, 913
PFORMAT= option
EXACT statement (FREQTAB), 133
PHI= option
MODEL statement (GENSELECT), 378
PHSELECT procedure, CLASS statement, 598
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
PHSELECT procedure, CODE statement, 598
COMMENT option, 15
CUMHAZ option, 15, 599
FILE= option, 15, 599
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOSURVIVAL option, 16, 599
NOTRIM option, 16
OUT= option, 16
SHOWTIME option, 16, 599
TIME= option, 599
TIMEPOINT= option, 16, 599
PHSELECT procedure, DISPLAY statement
CASESENSITIVE option, 18, 601
EXCLUDE option, 18, 601
EXCLUDEALL option, 18, 601
TRACE option, 18, 601
PHSELECT procedure, DISPLAYOUT statement
   INCLUDEALL option, 19, 602
   NOREPLACE option, 19, 602
   REPEATED option, 19, 602
PHSELECT procedure, EFFECT statement
   BASIS option (spline), 26
   DATABOUNDARY option (spline), 26
   DEGREE option (polynomial), 24
   DEGREE option (spline), 27
   DETAILS option (multimember), 23
   DETAILS option (polynomial), 24
   DETAILS option (spline), 27
   KNOTMAX= option (spline), 27
   KNOTMETHOD option (spline), 27
   KNOTMIN= option (spline), 28
   MDEGREE option (polynomial), 24
   NATURALCUBIC option (spline), 28
   NOEFFECT option (multimember), 23
   NOSEPARATE option (polynomial), 24
   SEPARATE option (spline), 28
   SPLIT option (spline), 29
   STANDARDIZE option (polynomial), 24
PHSELECT procedure, MODEL statement, 604
   CLB option, 605
   ENTRY= option, 605
   INCLUDE= option, 605
   INFORMATIVE option, 605
   OFFSET= option, 605
   START= option, 605
   TYPE3 option, 605
PHSELECT procedure, OUTPUT statement, 605
   COPYVAR= option, 606
   CUMHAZ option, 607
   DBETA option, 607
   LD option, 607
   OUT= option, 606
   RESDEV option, 607
   RESMART option, 607
   RESCH option, 607
   RESSCO option, 608
   ROLE option, 608
   STDXBETA option, 608
   SURVIVAL option, 608
   WRESSCH option, 608
   XBETA option, 608
PHSELECT procedure, PARTITION statement
   FRACTION option, 34, 609
   ROLEVAR= option, 34, 609
PHSELECT procedure, PROC PHSELECT statement, 595
   ABSCONV option, 42
ABSCONV option, 42
ABSFTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
ALPHA= option, 596
CORRB option, 596
COVB option, 597
DATA= option, 597
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
HESSIAN option, 597
ITHIST option, 597
LASSORHO= option, 597
LASSOSTEPS= option, 597
LASSOTOL= option, 597
LOGLIKENUM option, 597
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NOCLPRINT option, 597
NORMALIZE= option, 45
NOCLPRINT option, 597
NORMALIZE= option, 45
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46
PHSELECT procedure, SELECTION statement, 609
   ADAPTIVE option, 36
   CHOOSE= option, 36
   COMPETITIVE option, 36
   CRITERION= option, 36
   DETAILS= option, 38, 39
   FAST option, 37
   HIERARCHY= option, 39
   LSCOEFFS option, 37
   MAXEFFECTS= option, 37
   MAXSTEPS= option, 37
   METHOD= option, 35
   MINEFFECTS= option, 37
   ORDERSELECT option, 39
   SELECT= option, 37
   SELECTION= option, 41
   SLE= option, 37
   SENTRY= option, 37
   SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41
PHSELECT procedure, STRATA statement, 611
PHSELECT procedure, syntax, 595
PLCORR option
  OUTPUT statement (FREQTAB), 142
  TABLES statement (FREQTAB), 167
  TEST statement (FREQTAB), 192
PLIKEOPTIONS option
PROC GAMMOD statement, 307
PLOTS= option
  PROC GAMMOD statement, 308
  PROC PCA statement, 561
  PROC TREESPLIT statement, 853
  TABLES statement (FREQTAB), 168
PLOTS=AGREEPLOT option
  TABLES statement (FREQTAB), 170
PLOTS=CUMFREQPLOT option
  TABLES statement (FREQTAB), 170
PLOTS=DEVIATIONPLOT option
  TABLES statement (FREQTAB), 171
PLOTS=FREQPLOT option
  TABLES statement (FREQTAB), 171
PLOTS=KAPPAPLOT option
  TABLES statement (FREQTAB), 172
PLOTS=MOSAICPLOT option
  TABLES statement (FREQTAB), 173
PLOTS=NONE option
  TABLES statement (FREQTAB), 174
PLOTS=ODDSRATIOPLOT option
  TABLES statement (FREQTAB), 174
PLOTS=RELRISKPLOT option
  TABLES statement (FREQTAB), 174
PLOTS=RISKDIFFPLOT option
  TABLES statement (FREQTAB), 175
PLOTS=WTKAPPAPLOT option
  TABLES statement (FREQTAB), 175
PLSMOD procedure
  syntax, 644
PLSMOD procedure, CLASS statement, 647
  DESCENDING option, 11, 1005
  MISSING option, 11, 1005
  ORDER= option, 11
  PARAM= option, 12
  REF= option, 13
  SPLIT option, 13
PLSMOD procedure, CODE statement
  COMMENT option, 15
  FILE= option, 15
  FORMATWIDTH= option, 15
  INDENTSIZE= option, 15
  LABELID= option, 16
  LINESIZE= option, 16
  NOTRIM option, 16
  OUT= option, 16
PLSMOD procedure, DISPLAY statement
  CASESENSITIVE option, 18, 648
  EXCLUDE option, 18, 649
  EXCLUDEALL option, 18, 649
  TRACE option, 18, 649
PLSMOD procedure, DISPLAYOUT statement
  INCLUDEALL option, 19, 649
  NOREPLACE option, 19, 649
  REPEATED option, 19, 649
PLSMOD procedure, EFFECT statement
  BASIS option (spline), 26
  DATABOUNDARY option (spline), 26
  DEGREE option (polynomial), 24
  DEGREE option (spline), 27
  DETAILS option (multimember), 23
  DETAILS option (polynomial), 24
  DETAILS option (spline), 27
  KNOTMAX= option (spline), 27
  KNOTMETHOD option (spline), 27
  KNOTMIN= option (spline), 28
  MDEGREE option (polynomial), 24
  NATURALCUBIC option (spline), 28
  NOEFFECT option (multimember), 23
  NOSEPARATE option (polynomial), 24
  SEPARATE option (spline), 28
  SPLIT option (spline), 29
  STANDARDIZE option (polynomial), 24
PLSMOD procedure, MODEL statement, 651
  INTERCEPT option, 651
  SOLUTION option, 651
PLSMOD procedure, OUTPUT statement, 651
  COPYVARS= option, 652
  keyword option, 652
  OUT= option, 652
PLSMOD procedure, PARTITION statement, 654
  FRACTION option, 34, 654
  ROLEVAR= option, 34, 655
PLSMOD procedure, PROC PLSMOD statement, 644
  ABSCONV option, 42
  ABSFCNV option, 42
  ABSFTOL option, 42
  ABSGCONV option, 42
  ABSGTOL option, 42
  ABSTOL option, 42
  ABSXCONV option, 42
  ABSXTOL option, 42
  CENSSCALE option, 645
  CVTEST option, 645
  DATA= option, 645
  DETAILS option, 646
  FCONV option, 43
  FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
METHOD= option, 46
MINITER= option, 45
NFAC= option, 46
NOCENTER option, 46
NOCLPRINT option, 46
NORMALIZE= option, 46
NOCVSTDIZE option, 46
NORMALIZE= option, 46
VARSS option, 46
XCONV option, 46
XTOL option, 46
PLSMOD procedure, PROC PLSMOD statement,
   CVTEST option
   NSAMP= option, 46
   PVAL= option, 46
   SEED= option, 46
   STAT= option, 46
PLSMOD procedure, PROC PLSMOD statement,
   METHOD=PLS option
   ALGORITHM= option, 46
   EPSILON= option, 46
   MAXITER= option, 46
PLSMOD procedure, SELECTION statement
   ADAPTIVE option, 36
   CHOOSE= option, 36
   COMPETITIVE option, 36
   CRITERION= option, 36
   DETAILS= option, 38, 39
   FAST option, 37
   HIERARCHY= option, 39
   LSCOEFFS option, 37
   MAXEFFECTS= option, 37
   MAXSTEPS= option, 37
   METHOD= option, 35
   MINEFFECTS= option, 37
   ORDERSELECT option, 39
   SELECT= option, 37
   SELECTION= option, 41
   SLE= option, 37
   SLENTRY= option, 37
   SLS= option, 37
   SLSTAY= option, 37
   STOP= option, 38
   STOPHORIZON= option, 41
POINT option
   EXACT statement (FREQTAB), 133
POLychoric option
   TABLES statement (FREQTAB), 167
POPsize= option
   AUTOTUNE statement, 859, 860
PPREFIX= option
   PROC PCA statement, 562
PRED= option
   PREDICT statement (NLMod), 534
PREDICT statement
   NLMod procedure, 534
PREDICTED= option
   OUTPUT statement (GENSELECT), 381
   OUTPUT statement (LOGSELECT), 481
PREDPROBS option
   OUTPUT statement (LOGSELECT), 379, 479
PREFIX= option
   PROC PCA statement, 562
PRINTALL option (RELRIk)
   TABLES statement (FREQTAB), 184
PRINTALLDISTANCES option
   PROC KCLUS statement, 430
PRINTKwts option
   TABLES statement (FREQTAB), 150, 181
PRINTTARGET option
   PROC TREESPLIT statement, 855
PRINTWTS option (COMMONRISKDIFF)
   TABLES statement (FREQTAB), 160
PROB= option
   PREDICT statement (NLMod), 534
PROC ASSESS statement, see ASSESS procedure
PROC BINNING statement, see BINNING procedure
PROC CARDINALITY statement, see
   CARDINALITY procedure
PROC CORRELATION statement, 92, see
   CORRELATION procedure
   CORRELATION procedure, 92
PROC FREQTAB statement, see FREQTAB procedure
PROC GAMMOD statement, see GAMMOD procedure
PROC GENSELECT statement, see GENSELECT procedure
PROC KCLUS statement, see KCLUS procedure
PROC LOGSELECT statement, see LOGSELECT procedure
PROC NLMOD statement, see NLMOD procedure
   NLMod procedure, 526
PROC PARTITION statement, see PARTITION procedure
PROC PCA statement, see PCA procedure
   PCA procedure, 558
PROC PHSELECT statement, see PHSELECT procedure
PROC PLSMOD statement, *see* PLSMOD procedure
PLSMOD procedure, 644
PROC QTRSELECT statement, *see* QTRSELECT procedure
QTRSELECT procedure, 683
PROC REGSELECT statement, *see* REGSELECT procedure
REGSELECT procedure, 737
PROC SPC statement, 782, *see* SPC procedure
PROC TREESPLIT statement, *see* TREESPLIT procedure
TREESPLIT procedure, 849
PROC VARIMPUTE statement, *see* VARIMPUTE procedure
PROC VARREDUCE statement, *see* VARREDUCE procedure
PROCESSNAME= option
PROC SPC statement, 783
PROCESSVALUE= option
PROC SPC statement, 783
PRUNE statement
TREESPLIT procedure, 867
PRUNINGTABLE option
PROC TREESPLIT statement, 855
PVAL= option
PROC PLSMOD statement, CVTEST option, 645
PVAR= option
FITSTAT statement, 913
QTRSELECT procedure
MODEL statement, 689
OUTPUT statement, 691
PROC QTRSELECT statement, 683
QTRSELECT procedure, CLASS statement, 684
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
QTRSELECT procedure, CODE statement, 685
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
QTRSELECT procedure, DISPLAY statement
CASESENSITIVE option, 18, 686
EXCLUDE option, 18, 686
EXCLUDEALL option, 18, 686
TRACE option, 18, 686
QTRSELECT procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 687
NOREPLACE option, 19, 687
REPEATED option, 19, 687
QTRSELECT procedure, EFFECT statement
BASIS option (spline), 26
DATABASE boundary option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
QTRSELECT procedure, MODEL statement, 689
CLB option, 689
INCLUDE option, 689
INFORMATIVE option, 690
NOINT option, 690
QUANTILES option, 690
START option, 690
STB option, 690
QTRSELECT procedure, MODEL statement,
QUANTILES option
NTAU option, 690
SORT option, 690
QTRSELECT procedure, OUTPUT statement, 691
COPYV AR= option, 691
keyword= option, 692
OUT= option, 691
QTRSELECT procedure, PARTITION statement
FRACTION option, 34, 693
ROLEVAR= option, 34, 694
QTRSELECT procedure, PROC QTRSELECT statement, 683
ABSCONV option, 42
ABSFCONV option, 42
ABSTOL option, 42
ABSFTOL option, 42
ABSXCONV option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
ALPHA= option, 684
COV=SPARSITY option, 684
DATA= option, 684
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NOCLPRINT option, 684
NORMALIZE= option, 45
TECHNIQUE= option, 46
XCONV option, 46
XTOL option, 46
QTRSELECT procedure, SELECTION statement, 694
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41
QUANTILES option
MODEL statement (QTRSELECT), 690
RANK option
PROC CORRELATION statement, 94
RBAIMP option
PROC TREESPLIT statement, 856
RCHART statement
RCHART procedure, 788
RDIF1 option
OUTPUT statement (FREQTAB), 143
RDIF2 option
OUTPUT statement (FREQTAB), 143
REDUCE statement
VARREDUCE procedure, 1008
REDUCEDERROR option
PRUNE statement (TREESPLIT), 868
REF= option
CLASS statement (ASSESS), 13
CLASS statement (BINNING), 13
CLASS statement (CARDINALITY), 13
CLASS statement (CORRELATION), 13
CLASS statement (GAMMOD), 13
CLASS statement (GENSELECT), 13
CLASS statement (KCLUS), 13
CLASS statement (LOGSELECT), 13
CLASS statement (NLMODE), 13
CLASS statement (PARTITION), 13
CLASS statement (PCA), 13
CLASS statement (PHSELECT), 13
CLASS statement (PLSMODE), 13
CLASS statement (QTRSELECT), 13
CLASS statement (REGENSELECT), 13
CLASS statement (TREESPLIT), 13
CLASS statement (VARIMPUTE), 13
CLASS statement (VARREDUCE), 13
REGSELECT procedure
MODEL statement, 743
OUTPUT statement, 745
PROC REGSELECT statement, 737
REGSELECT procedure, CLASS statement, 738
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13
REGSELECT procedure, CODE statement, 739
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINEWIDTH= option, 16
NOTRIM option, 16
OUT= option, 16
REGSELECT procedure, DISPLAY statement
CASESENSITIVE option, 18, 740
EXCLUDE option, 18, 740
EXCLUDEALL option, 18, 740
TRACE option, 18, 740
REGSELECT procedure, DISPLAYOUT statement
INCLUDEALL option, 19, 741
NOREPLACE option, 19, 741
REPEATED option, 19, 741
REGSELECT procedure, EFFECT statement
BASE option (spline), 26
DATABOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
REGSELECT procedure, MODEL statement, 743
  CLB option, 743
  INCLUDE option, 743
  INFORMATIVE option, 744
  NOINT option, 744
  SS3 option, 744
  START option, 744
  STB option, 744
  TOL option, 744
  VIF option, 744
REGSELECT procedure, OUTPUT statement, 745
  COPYV AR= option, 745
  keyword= option, 745
REGSELECT procedure, PARTITION statement
  FRACTION option, 34, 747
  ROLEVAR= option, 34, 747
REGSELECT procedure, PROC REGSELECT
  statement, 737
  ABSCONV option, 42
  ABSFCNV option, 42
  ABSFTOL option, 42
  ABSGCONV option, 42
  ABSGTOL option, 42
  ABSTOL option, 42
  ABSXCONV option, 42
  ABSXTOL option, 42
  ALPHA= option, 738
  DATA= option, 738
  FCONV option, 43
  FCONV2 option, 43
  FTOL option, 43
  FTOL2 option, 43
  GCONV option, 44
  GCONV2 option, 44
  GTOL option, 44
  GTOL2 option, 44
  MAXFUNCTION option, 45
  MAXITER= option, 45
  MAXTIME= option, 45
  MINITER= option, 45
NOCLPRINT option, 738
NORMALIZE option, 45
TECHNIQUE option, 46
XCONV option, 46
XTOL option, 46
REGSELECT procedure, SELECTION statement, 748
  ADAPTIVE option, 36
  CHOOSE= option, 36
  COMPETITIVE option, 36
  CRITERION= option, 36
  DETAILS= option, 38, 39
  FAST option, 37
  HIERARCHY= option, 39
  LSCEFFS option, 37
  MAXFUNCTION option, 37
  MAXSTEP= option, 37
  METHOD= option, 35
  MINEFFECTS= option, 37
  ORDERSELECT option, 39
  SELECT= option, 37
  SELECT= option, 41
  SLE= option, 37
  SLENTRY= option, 37
  SLS= option, 37
  STOP= option, 38
  STOP= option, 41
RELRISK option
  EXACT statement (FREQTAB), 129
  OUTPUT statement (FREQTAB), 143
  TABLES statement (FREQTAB), 181
REPEATED option
  DISPLAYOUT statement (ASSESS), 19
  DISPLAYOUT statement (BINNING), 19
  DISPLAYOUT statement (CARDINALITY), 19
  DISPLAYOUT statement (CORRELATION), 19, 96
  DISPLAYOUT statement (GAMMOD), 19, 312
  DISPLAYOUT statement (GENSELECT), 19, 370
  DISPLAYOUT statement (KCLUS), 19, 432
  DISPLAYOUT statement (LOGSELECT), 19
  DISPLAYOUT statement (NLMOD), 19, 472
  DISPLAYOUT statement (PARTITION), 19, 975
  DISPLAYOUT statement (PCA), 19, 565
  DISPLAYOUT statement (PHESELECT), 19, 602
  DISPLAYOUT statement (PLSMOD), 19, 649
  DISPLAYOUT statement (QTRSELECT), 19, 687
  DISPLAYOUT statement (REGSELECT), 19, 741
  DISPLAYOUT statement (TREESPLIT), 19
  DISPLAYOUT statement (VARIMPUTE), 19
DISPLAYOUT statement (VARREDUCE), 19, 1007
RESCHI= option
  OUTPUT statement (GENSELECT), 381
  OUTPUT statement (LOGSELECT), 481
RESDEV option
  OUTPUT statement (PHSELECT), 607
RESDEV= option
  OUTPUT statement (PHSELECT), 607
RESIDUAL= option
  OUTPUT statement (GENSELECT), 382
  OUTPUT statement (LOGSELECT), 481
RESLIK= option
  OUTPUT statement (GENSELECT), 382
  OUTPUT statement (LOGSELECT), 481
RESMART option
  OUTPUT statement (PHSELECT), 607
RESRAW= option
  OUTPUT statement (GENSELECT), 382
  OUTPUT statement (LOGSELECT), 481
RESSCH option
  OUTPUT statement (PHSELECT), 607
RESSCO option
  OUTPUT statement (PHSELECT), 608
RESTRICT statement
  NLMOD procedure, 535
RESWORK= option
  OUTPUT statement (GENSELECT), 382
  OUTPUT statement (LOGSELECT), 481
ROGDE= option
  MODEL statement (GAMMOD), 320
RISK1 option
  OUTPUT statement (FREQTAB), 143
RISK11 option
  OUTPUT statement (FREQTAB), 144
RISK12 option
  OUTPUT statement (FREQTAB), 144
RISK2 option
  OUTPUT statement (FREQTAB), 144
RISK21 option
  OUTPUT statement (FREQTAB), 144
RISK22 option
  OUTPUT statement (FREQTAB), 144
RISKDIFF option
  EXACT statement (FREQTAB), 130
  OUTPUT statement (FREQTAB), 143
  TABLES statement (FREQTAB), 184
RISKDIFF1 option
  OUTPUT statement (FREQTAB), 143
RISKDIFF2 option
  OUTPUT statement (FREQTAB), 143
ROCOUT= option
  PROC ASSESS statement, 912
ROLE option
  OUTPUT statement, 866
  OUTPUT statement (PHSELECT), 608
ROLE= option
  LD statement (PHSELECT), 607
  OUTPUT statement (GENSELECT), 382
  OUTPUT statement (LOGSELECT), 481
ROLEVAR= option
  PARTITION statement (ASSESS), 34
  PARTITION statement (BINNING), 34
  PARTITION statement (CARDINALITY), 34
  PARTITION statement (GENSELECT), 34, 383
  PARTITION statement (KCLUS), 34
  PARTITION statement (LOGSELECT), 34, 483
  PARTITION statement (NLMOD), 34
  PARTITION statement (PARTITION), 34
  PARTITION statement (PHSELECT), 34, 609
  PARTITION statement (PLSMOD), 34
  PARTITION statement (QTRSELECT), 34, 694
  PARTITION statement (REGSELECT), 34, 747
  PARTITION statement (TREESPLIT), 34, 866
  PARTITION statement (VARIIMPUTE), 34
  PARTITION statement (VARREDUCE), 34
  PLSMOD procedure, PARTITION statement, 655
RPREFIX= option
  PROC PCA statement, 562
RRC1 option
  OUTPUT statement (FREQTAB), 143
RRC2 option
  OUTPUT statement (FREQTAB), 143
RSS option
  GROW statement (TREESPLIT), 865
SAMPLESIZE= option
  AUTOTUNE statement, 860
SAMPPCT2= option
  PROC PARTITION statement, 973
SAMPPCT= option
  PROC PARTITION statement, 973
SAMPPCTEVT= option
  PROC PARTITION statement, 973
SCALE= option
  MODEL statement (GAMMOD), 320
SCHART statement
  SCHART procedure, 789
SCORE statement
  KCLUS procedure, 433
SCORES= option
  TABLES statement (FREQTAB), 189
SCOROUT option
  TABLES statement (FREQTAB), 189
SCORR option
  EXACT statement (FREQTAB), 131
  OUTPUT statement (FREQTAB), 144
TEST statement (FREQTAB), 192
SEARCHMETHOD= option
AUTOTUNE statement, 860
SEED= option
EXACT statement (FREQTAB), 134
PROC GAMMOD statement, 308
PROC KCLUS statement, 429
PROC PARTITION statement, 972
PROC PCA statement, METHOD=RANDOM option, 560
PROC PLSMOD statement, CVTEST option, 645
PROC TREESPLIT statement, 856
PROC VARIMPUTE statement, 989
SELECT= option
SELECTION statement (ASSESS), 37
SELECTION statement (BINNING), 37
SELECTION statement (CARDINALITY), 37
SELECTION statement (CORRELATION), 37
SELECTION statement (GAMMOD), 37
SELECTION statement (GENSELECT), 37
SELECTION statement (KCLUS), 37
SELECTION statement (LOGSELECT), 37
SELECTION statement (NLMOD), 37
SELECTION statement (PARTITION), 37
SELECTION statement (PCA), 37
SELECTION statement (PHSELECT), 41
SELECTION statement (PLSMOD), 41
SELECTION statement (QTRSELECT), 41
SELECTION statement (REGSELECT), 41
SELECTION statement (TREESPLIT), 41
SELECTION statement (VARIMPUTE), 41
SELECTION statement (VARREDUCE), 41
SEPARATE option
EFFECT statement, spline (ASSESS), 28
EFFECT statement, spline (BINNING), 28
EFFECT statement, spline (CARDINALITY), 28
EFFECT statement, spline (CORRELATION), 28
EFFECT statement, spline (GAMMOD), 28
EFFECT statement, spline (GENSELECT), 28
EFFECT statement, spline (KCLUS), 28
EFFECT statement, spline (LOGSELECT), 28
EFFECT statement, spline (NLMOD), 28
EFFECT statement, spline (PARTITION), 28
EFFECT statement, spline (PCA), 28
EFFECT statement, spline (PHSELECT), 28
EFFECT statement, spline (PLSMOD), 28
EFFECT statement, spline (QTRSELECT), 28
EFFECT statement, spline (REGSELECT), 28
EFFECT statement, spline (TREESPLIT), 28
EFFECT statement, spline (VARIMPUTE), 28
EFFECT statement, spline (VARREDUCE), 28
SHOWTIME option
CODE statement (PHSELECT), 16, 599
SIGMAS= option
chart statements (SPC), 795
SING= option
PROC PCA statement, 562
SINGCHOL= option
PROC GAMMOD statement, 308
SINGULAR= option
PROC GAMMOD statement, 309
PROC NLMOD statement, 527
PROC PCA statement, 562
SLE= option
SELECTION statement (ASSESS), 37
SELECTION statement (BINNING), 37
SELECTION statement (CARDINALITY), 37
SELECTION statement (CORRELATION), 37
SELECTION statement (GAMMOD), 37
SELECTION statement (GENSELECT), 37
<table>
<thead>
<tr>
<th>Selection Statement</th>
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**SLENTRY= Option**

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**SLS= Option**

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**SLSTAY= Option**

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**SMDCR Option**

(EXACT statement (FREQTAB), 131)

(OUTPUT statement (FREQTAB), 144)

(TEST statement (FREQTAB), 192)

**SMDCR Option**

(EXACT statement (FREQTAB), 131)

(OUTPUT statement (FREQTAB), 144)

(TEST statement (FREQTAB), 193)

**SMETH= Option**

(chart statements (SPC), 795)

**SMOOTH= Option**

(MODEL statement (GAMMOD), 317)

**SMOOTH OPTIONS Option**

(PROC GAMMOD statement, 309)

**SOLUTION Option**

(MODEL statement (PLSMOD), 651)

**SORT Option**

(QUANTILES option (QTRSELECT), 690)

**SPC Procedure**

(LIMITS= data table, 822)

(syntax, 781)

**SPC Procedure, BOXCHART Statement**

(783)

**SPC Procedure, CCHART Statement**

(784)

(LIMITN= option, 811)

(SIGMAS= option, 811)

**SPC Procedure, Chart Statements**

(793)

(ALLN option, 793)

(CONTROLSTAT= option, 793)

(EXCHART option, 793)

(LIMITN= option, 793)

(MEDCENTRAL= option, 794)

(NO3SIGMACHECK option, 794)

(NOPRINT option, 794)

(OUTLIMITS= option, 794)

(OUTTABLE= option, 794)

(PCTLDEF= option, 794)

(SIGMAS= option, 795)

(SMETH= option, 795)

(SUBGROUPN= option, 796)
TEST2RUN= option, 796
TEST3RUN= option, 796
TESTNSTD option, 796, 821
TESTOVERLAP option, 796
TESTS2= option, 798
TESTS= option, 797

SPC procedure, IRCHART statement, 785
LIMITN= option, 799
SIGMAS= option, 799

SPC procedure, MCHART statement, 785
LIMITN= option, 802
MEDCENTRAL= option, 802
SIGMAS= option, 802

SPC procedure, MRCHART statement, 786

SPC procedure, NPCHART statement, 787
LIMITN= option, 812
SIGMAS= option, 812

SPC procedure, PCHART statement, 788
LIMITN= option, 814
SIGMAS= option, 814

SPC procedure, PROC SPC statement, 782
DATA= option, 782, 822
NTHREADS= option, 782
PROCESSNAME= option, 783
SUBGROUPNAME= option, 783
SUBGROUPVALUE= option, 783

SPC procedure, RCHART statement, 788
LIMITN= option, 803
SIGMAS= option, 803

SPC procedure, SCHART statement, 789
LIMITN= option, 804
SIGMAS= option, 804

SPC procedure, UCHART statement, 790
LIMITN= option, 816
SIGMAS= option, 816

SPC procedure, XCHART statement, 790
LIMITN= option, 800
SIGMAS= option, 800

SPC procedure, XRCHART statement, 791

SPC procedure, XSCHART statement, 792

SPLIT option
CLASS statement (ASSESS), 13
CLASS statement (BINNING), 13
CLASS statement (CARDINALITY), 13
CLASS statement (CORRELATION), 13
CLASS statement (GAMMOD), 13
CLASS statement (GENSELECT), 13
CLASS statement (KCLUS), 13
CLASS statement (LOGSELECT), 13
CLASS statement (NLMOD), 13
CLASS statement (PARTITION), 13
CLASS statement (PCA), 13
CLASS statement (PHSELECT), 13
CLASS statement (PLSMOD), 13
CLASS statement (QTRSELECT), 13
CLASS statement (REGSELECT), 13
CLASS statement (TREESPLIT), 13
CLASS statement (VARIMPUTE), 13
CLASS statement (VARREDUCE), 13
EFFECT statement, spline (ASSESS), 29
EFFECT statement, spline (BINNING), 29
EFFECT statement, spline (CARDINALITY), 29
EFFECT statement, spline (CORRELATION), 29
EFFECT statement, spline (GAMMOD), 29
EFFECT statement, spline (GENSELECT), 29
EFFECT statement, spline (KCLUS), 29
EFFECT statement, spline (LOGSELECT), 29
EFFECT statement, spline (NLMOD), 29
EFFECT statement, spline (PARTITION), 29
EFFECT statement, spline (PCA), 29
EFFECT statement, spline (PHSELECT), 29
EFFECT statement, spline (PLSMOD), 29
EFFECT statement, spline (QTRSELECT), 29
EFFECT statement, spline (REGSELECT), 29
EFFECT statement, spline (TREESPLIT), 29
EFFECT statement, spline (VARIMPUTE), 29
EFFECT statement, spline (VARREDUCE), 29

SPLITONCE option
PROC TREESPLIT statement, 856

SS3 option
MODEL statement (REGSELECT), 744

SSCP option
PROC CORRELATION statement, 94

STANDARD option
PROC PCA statement, 563

STANDARDIZE option
EFFECT statement, polynomial (ASSESS), 24
EFFECT statement, polynomial (BINNING), 24
EFFECT statement, polynomial (CARDINALITY), 24
EFFECT statement, polynomial (CORRELATION), 24
EFFECT statement, polynomial (GAMMOD), 24
EFFECT statement, polynomial (GENSELECT), 24
EFFECT statement, polynomial (KCLUS), 24
EFFECT statement, polynomial (LOGSELECT), 24
EFFECT statement, polynomial (NLMOD), 24
EFFECT statement, polynomial (PARTITION), 24
EFFECT statement, polynomial (PCA), 24
EFFECT statement, polynomial (PHSELECT), 24
EFFECT statement, polynomial (PLSMOD), 24
EFFECT statement, polynomial (QTRSELECT), 24
EFFECT statement, polynomial (REGSELECT), 24
EFFECT statement, polynomial (TREESPLIT), 24
EFFECT statement, polynomial (VARIMPUTE), 24
EFFECT statement, polynomial (VARREDUCE), 24
STANDARDIZE= option
PROC KCLUS statement, 429
START option
MODEL statement (GENSELECT), 378
MODEL statement (LOGSELECT), 477
MODEL statement (QTRSELECT), 690
MODEL statement (REGSELECT), 744
START= option
MODEL statement (PHSELECT), 605
STAT= option
PROC PLSMOD statement, CVTEST option, 645
STB option
MODEL statement (QTRSELECT), 690
MODEL statement (REGSELECT), 744
PROC GENSELECT statement, 367
PROC LOGSELECT statement, 469
STD option
PROC PCA statement, 563
STDERR= option
PREDICT statement (NLMOD), 534
STDRES option (CROSSLIST)
TABLES statement (FREQTAB), 162
STDRESCHI= option
OUTPUT statement (GENSELECT), 382
OUTPUT statement (LOGSELECT), 482
STDRESDEV= option
OUTPUT statement (GENSELECT), 382
OUTPUT statement (LOGSELECT), 482
STDXBETA= option
OUTPUT statement (PHSELECT), 608
STDXBETA= option
OUTPUT statement (GENSELECT), 382
OUTPUT statement (LOGSELECT), 482
STOP= option
SELECTION statement (ASSESS), 38
SELECTION statement (BINNING), 38
SELECTION statement (CARDINALITY), 38
SELECTION statement (CORRELATION), 38
SELECTION statement (GAMMOD), 38
SELECTION statement (GENSELECT), 38
SELECTION statement (KCLUS), 38
SELECTION statement (LOGSELECT), 38
SELECTION statement (PARTITION), 38
SELECTION statement (PCA), 38
SELECTION statement (PHSELECT), 38
SELECTION statement (PLSMOD), 38
SELECTION statement (QTRSELECT), 38
SELECTION statement (REGSELECT), 38
SELECTION statement (TREESPLIT), 38
SELECTION statement (VARIMPUTE), 38
SELECTION statement (VARREDUCE), 38
STOPCRITERION= option
PROC KCLUS statement, 428, 430
STOPHORIZON= option
SELECTION statement (ASSESS), 41
SELECTION statement (BINNING), 41
SELECTION statement (CARDINALITY), 41
SELECTION statement (CORRELATION), 41
SELECTION statement (GAMMOD), 41
SELECTION statement (GENSELECT), 41
SELECTION statement (KCLUS), 41
SELECTION statement (LOGSELECT), 41
SELECTION statement (NLMOD), 41
SELECTION statement (PHSELECT), 41
SELECTION statement (PLSMOD), 41
SELECTION statement (QTRSELECT), 41
SELECTION statement (REGSELECT), 41
SELECTION statement (TREESPLIT), 41
SELECTION statement (VARIMPUTE), 41
SELECTION statement (VARREDUCE), 41
STRATA statement
PHSELECT procedure, 611
STUTC option
EXACT statement (FREQTAB), 131
OUTPUT statement (FREQTAB), 144
TEST statement (FREQTAB), 193
SUBGROUPN= option
chart statements (SPC), 796
SUBGROUPNAME= option
PROC SPC statement, 783
SUBGROUPVALUE= option
PROC SPC statement, 783
SUPERIORITY option (BINOMIAL)
TABLES statement (FREQTAB), 155
SUPERIORITY option (RELRISK)
TABLES statement (FREQTAB), 184
SUPERIORITY option (RISKDIFF)
TABLES statement (FREQTAB), 189
SURVIVAL option
OUTPUT statement (PHSELECT), 608
SVMACHINE procedure, OUTPUT statement
COPYVARS= option, 991
SYMMETRY option
EXACT statement (FREQTAB), 132
syntax
GENSELECT procedure, 364
GAMMOD procedure, 306
NLMOD procedure, 525

TABLES statement
  FREQTAB procedure, 145

TARGET statement
  ASSSESS procedure, 914
  BINNING procedure, 937
  TREESPLIT procedure, 892

TARGETEVENT= option
  AUTOTUNE statement, 860

TAUB option
  OUTPUT statement (FREQTAB), 140
  TEST statement (FREQTAB), 192

TAUC option
  OUTPUT statement (FREQTAB), 144
  TEST statement (FREQTAB), 193

TECHNIQUE= option
  PROC ASSESS statement, 46
  PROC BINNING statement, 46
  PROC CARDINALITY statement, 46
  PROC CORRELATION statement, 46
  PROC GAMMOD statement, 46
  PROC GENSELECT statement, 46
  PROC KCLUS statement, 46
  PROC LOGSELECT statement, 46
  PROC NLMOD statement, 46
  PROC PARTITION statement, 46
  PROC PCA statement, 46
  PROC PHSELECT statement, 46
  PROC PLSMOD statement, 46
  PROC QTRSELECT statement, 46
  PROC REGSELECT statement, 46
  PROC TREESPLIT statement, 46
  PROC VARIMPUTE statement, 46
  PROC VARREDUCE statement, 46, 1005

TEST statement
  FREQTAB procedure, 190
  TEST2RUN= option
    chart statements (SPC), 796
    SHEWHART procedure, 821
  TEST3RUN= option
    chart statements (SPC), 796
    SHEWHART procedure, 821
  TEST= option (COMMONRISKDIFF)
    TABLES statement (FREQTAB), 161
  TEST=MH option (COMMONRISKDIFF)
    TABLES statement (FREQTAB), 161
  TEST=MR option (COMMONRISKDIFF)
    TABLES statement (FREQTAB), 161
  TEST=SCORE option (COMMONRISKDIFF)
    TABLES statement (FREQTAB), 161
  TESTF= option
    TABLES statement (FREQTAB), 200
    TESTF= option (CHISQ)

TESTNSTD option
  chart statements (SPC), 796
  SPC procedure, 821

TESTOVERLAP option
  chart statements (SPC), 796

TESTP= option
  TABLES statement (FREQTAB), 200
  TESTP= option (CHISQ)
    TABLES statement (FREQTAB), 157

TESTS2= option
  chart statements (SPC), 798

TESTS= option
  chart statements (SPC), 797

TIME= option
  CODE statement (PHSELECT), 599

TIMEPOINT= option
  CODE statement (PHSELECT), 16, 599

TOL option
  MODEL statement (REGSELECT), 744

TOTPCT option
  TABLES statement (FREQTAB), 189

TRACE option
  DISPLAY statement (ASSESS), 18
  DISPLAY statement (BINNING), 18
  DISPLAY statement (CARDINALITY), 18
  DISPLAY statement (CORRELATION), 18, 96
  DISPLAY statement (GAMMOD), 18, 311
  DISPLAY statement (GENSELECT), 18, 369
  DISPLAY statement (KCLUS), 18, 432
  DISPLAY statement (LOGSELECT), 18, 471
  DISPLAY statement (NLMOD), 18, 529
  DISPLAY statement (PARTITION), 18, 974
  DISPLAY statement (PCA), 18, 565
  DISPLAY statement (PHSELECT), 18, 601
  DISPLAY statement (PLSMOD), 18, 649
  DISPLAY statement (QTRSELECT), 18, 686
  DISPLAY statement (REGSELECT), 18, 740
  DISPLAY statement (TREESPLIT), 18
  DISPLAY statement (VARIMPUTE), 18
  DISPLAY statement (VARREDUCE), 18, 1007

TREESPLIT procedure
  AUTOTUNE statement, 856
  INPUT statement, 892
  MODEL statement, 865
  PROC TREESPLIT statement, 849
  TARGET statement, 892

TREESPLIT procedure, AUTOTUNE statement, 856
  TUNINGPARAMETERS= option, 860

TREESPLIT procedure, CLASS statement, 862
  DESCENDING option, 11, 1005
  MISSING option, 11, 1005
  ORDER= option, 11
  PARAM= option, 12
REF= option, 13
SPLIT option, 13
TREESPLIT procedure, CODE statement, 863
COMMENT option, 15
FILE= option, 15
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16
TREESPLIT procedure, DISPLAY statement
CASESENSITIVE option, 18
EXCLUDE option, 18
EXCLUDEALL option, 18
TRACE option, 18
TREESPLIT procedure, DISPLAYOUT statement
INCLUDEALL option, 19
NOREPLACE option, 19
REPEATED option, 19
TREESPLIT procedure, EFFECT statement
BASIS option (spline), 26
DATABASEBOUNDARY option (spline), 26
DEGREE option (polynomial), 24
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24
TREESPLIT procedure, GROW statement, 863
ALPHA= option, 864
BONFERRONI option, 864
CHAID option, 863
CHISQUARE option, 864
ENTROPY option, 864
FTEST option, 864
GINI option, 864
IGR option, 864
RSS option, 865
TREESPLIT procedure, INPUT statement, 892
TREESPLIT procedure, MODEL statement, 865
TREESPLIT procedure, OUTPUT statement, 865
COPYV ARS= option, 866
OUT= option, 865
ROLE option, 866
TREESPLIT procedure, PARTITION statement
FRAGMENT option, 34, 866
ROLEVAR= option, 34, 866
TREESPLIT procedure, PROC TREESPLIT statement, 849
ABSCONV option, 42
ABSFCONV option, 42
ABSFTOL option, 42
ABSGCONV option, 42
ABSGTOL option, 42
ABSTOL option, 42
ABSXCONV option, 42
ABSXTOL option, 42
ASSIGNMISSING= option, 850
BINMETHOD = option, 851
CVCC option, 852
DATA= option, 852
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MAXBRANCH= option, 852
MAXDEPTH= option, 852
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
MINLEAFSIZE= option, 852
MINUSEINSEARCH= option, 852
NOREPRINT option, 853
NORMALIZE= option, 45
NSURROGATES= option, 853
NUMBIN= option, 853
OUTMODEL option, 853
OUTMODELVAR option, 853
PLOTS= option, 853
PRINTTARGET option, 855
PRUNINGTABLE option, 855
RBAIMP option, 856
SEED= option, 856
SPLITONCE option, 856
TECHNIQUE= option, 46
VII= option, 856
XCONV option, 46
XTOL option, 46
TREESPLIT procedure, PRUNE statement, 867
ALPHA= option, 867
C45 option, 867
CONFIDENCE= option, 867
COSTCOMPLEXITY option, 867
KFOLD= option, 867
LEAVES= option, 867, 868
OFF option, 868
REDUCEDERROR option, 868

TREESPLIT procedure, SELECTION statement
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

TREESPLIT procedure, syntax, 849
TREESPLIT procedure, TARGET statement, 892

TREND option
EXACT statement (FREQTAB), 132
OUTPUT statement (FREQTAB), 145
TABLES statement (FREQTAB), 190

TSYMM option
OUTPUT statement (FREQTAB), 145

TUNINGPARAMETERS= option
AUTOTUNE statement, 860

TVALUE= option
PREDICT statement (NLMOD), 534

TYPE3 option
MODEL statement (GENSELECT), 378
MODEL statement (LOGSELECT), 477
MODEL statement (PHSELECT), 605

U option
OUTPUT statement (FREQTAB), 145

UCHART statement
UCHART procedure, 790

UCL= option
OUTPUT statement (GENSELECT), 383
OUTPUT statement (LOGSELECT), 482

UCLM= option
OUTPUT statement (GENSELECT), 383
OUTPUT statement (LOGSELECT), 482

UCR option
OUTPUT statement (FREQTAB), 145

unpack option
PROC GAMMOD statement, 308

UPPER= option
OUTPUT statement (GENSELECT), 383
OUTPUT statement (LOGSELECT), 482
PREDICT statement (NLMOD), 534

UPPERXBETA= option
OUTPUT statement (GENSELECT), 383
OUTPUT statement (LOGSELECT), 482

URC option
OUTPUT statement (FREQTAB), 145

USEPARAMETERS= option
AUTOTUNE statement, 862

VAR statement
ASSESS procedure, 914
CARDINALITY procedure, 957
CORRELATION procedure, 97
PCA procedure, 568
VAR= option (BINOMIAL)
TABLES statement (FREQTAB), 155
VAR= option (RISKDIFF)
TABLES statement (FREQTAB), 189

VARDEF= option
PROC CORRELATION statement, 94
PROC PCA statement, 563
VAREXP= option
REDUCE statement, 1009

VARIANCEEXPLAINED= option
REDUCE statement, 1009

VARIMPUTE procedure, CLASS statement
DESCENDING option, 11, 1005
MISSING option, 11, 1005
ORDER= option, 11
PARAM= option, 12
REF= option, 13
SPLIT option, 13

VARIMPUTE procedure, CODE statement, 989
COMMENT option, 15
FILE= option, 15, 989
FORMATWIDTH= option, 15
INDENTSIZE= option, 15
LABELID= option, 16
LINESIZE= option, 16
NOTRIM option, 16
OUT= option, 16

VARIMPUTE procedure, DISPLAY statement
CASESENSITIVE option, 18
EXCLUDE option, 18
EXCLUDEALL option, 18
TRACE option, 18

VARIMPUTE procedure, DISPLAYOUT statement
INCLUDEALL option, 19
NOREPLACE option, 19
VARIMPUTE procedure, EFFECT statement
- BASIS option (spline), 26
- DATABOUNDARY option (spline), 26
- DEGREE option (polynomial), 24
- DEGREE option (spline), 27
- DETAILS option (multimember), 23
- DETAILS option (polynomial), 24
- DETAILS option (spline), 27
- KNOTMAX= option (spline), 27
- KNOTMETHOD option (spline), 27
- KNOTMIN= option (spline), 28
- MDEGREE option (polynomial), 24
- NATURALCUBIC option (spline), 28
- NOEFFECT option (multimember), 23
- NOSEPARATE option (polynomial), 24
- SEPARATE option (spline), 28
- SPLIT option (spline), 29
- STANDARDIZE option (polynomial), 24

VARIMPUTE procedure, INPUT statement, 989
- OUT= option, 990

VARIMPUTE procedure, OUTPUT statement, 990
- OUT= option, 990

VARIMPUTE procedure, PARTITION statement
- FRACTION option, 34
- ROLEVAR= option, 34

VARIMPUTE procedure, PROC VARIMPUTE statement, 988
- ABSCONV option, 42
- ABSFCNV option, 42
- ABSFTOL option, 42
- ABSGCONV option, 42
- ABSGTOL option, 42
- ABSTOL option, 42
- ABSXCONV option, 42
- ABSTOL option, 42
- DATA= option, 988
- FCONV option, 43
- FCONV2 option, 43
- FTOL option, 43
- FTOL2 option, 43
- GCONV option, 44
- GCONV2 option, 44
- GTOL option, 44
- GTOL2 option, 44
- MAXFUNC= option, 45
- MAXITER= option, 45
- MAXTIME= option, 45
- MINTER= option, 45
- NORMALIZE= option, 45
- NTHREADS= option, 988
- SEED= option, 989
- TECHNIQUE= option, 46
- XCONV option, 46
- XTOL option, 46

VARIMPUTE procedure, SELECTION statement
- ADAPTIVE option, 36
- CHOOSE= option, 36
- COMPETITIVE option, 36
- CRITERION= option, 36
- DETAILS= option, 38, 39
- FAST option, 37
- HIERARCHY= option, 39
- LSCOEFFS option, 37
- MAXEFFECTS= option, 37
- MAXSTEPS= option, 37
- METHOD= option, 35
- MINEFFECTS= option, 37
- ORDERSELECT option, 39
- SELECT= option, 37
- SELECTION= option, 41
- SLE= option, 37
- SLENTRY= option, 37
- SLS= option, 37
- SLSTAY= option, 37
- STOP= option, 38
- STOPHORIZON= option, 41

VARIMPUTE procedure, syntax, 988
- VARINC= option
  - REDUCE statement, 1009

VARREDUCE procedure, CLASS statement, 1005
- DESCENDING option, 11, 1005
- MISSING option, 11, 1005
- ORDER= option, 11
- PARAM= option, 12
- REF= option, 13
- SPLIT option, 13

VARREDUCE procedure, CODE statement
- COMMENT option, 15
- FILE= option, 15
- FORMATWIDTH= option, 15
- INDENTSIZE= option, 15
- LABELID= option, 16
- LINESIZE= option, 16
- NOTRIM option, 16
- OUT= option, 16

VARREDUCE procedure, DISPLAY statement
- CASESENSITIVE option, 18, 1006
- EXCLUDE option, 18, 1006
- EXCLUDEALL option, 18, 1006
- TRACE option, 18, 1007

VARREDUCE procedure, DISPLAYOUT statement
- INCLUDEALL option, 19, 1007
- NOREPLACE option, 19, 1007
- REPEATED option, 19, 1007

VARREDUCE procedure, EFFECT statement
- BASIS option (spline), 26
- DATABOUNDARY option (spline), 26
- DEGREE option (polynomial), 26
DEGREE option (spline), 27
DETAILS option (multimember), 23
DETAILS option (polynomial), 24
DETAILS option (spline), 27
KNOTMAX= option (spline), 27
KNOTMETHOD option (spline), 27
KNOTMIN= option (spline), 28
MDEGREE option (polynomial), 24
NATURALCUBIC option (spline), 28
NOEFFECT option (multimember), 23
NOSEPARATE option (polynomial), 24
SEPARATE option (spline), 28
SPLIT option (spline), 29
STANDARDIZE option (polynomial), 24

VARREDUCE procedure, PARTITION statement
FRACTION option, 34
ROLEVAR= option, 34

VARREDUCE procedure, PROC VARREDUCE statement
FCONV option, 43
FCONV2 option, 43
FTOL option, 43
FTOL2 option, 43
GCONV option, 44
GCONV2 option, 44
GTOL option, 44
GTOL2 option, 44
MATRIX= option, 1004
MAXFUNC= option, 45
MAXITER= option, 45
MAXTIME= option, 45
MINITER= option, 45
NOPRINT option, 1004
NORMALIZE= option, 45
OUTCP= option, 1004
TECHNIQUE= option, 46, 1005
XCONV option, 46
XTOL option, 46

VARREDUCE procedure, REDUCE statement, 1008
AIC option, 1009
AICC option, 1009
BIC option, 1009
MAXEFFECTS= option, 1009
MAXITER= option, 1009
MINVARIANCEINCREMENT= option, 1009
VAREXP= option, 1009
VARIANCEEXPLAINED= option, 1009
VARINC= option, 1009

VARREDUCE procedure, SELECTION statement
ADAPTIVE option, 36
CHOOSE= option, 36
COMPETITIVE option, 36
CRITERION= option, 36
DETAILS= option, 38, 39
FAST option, 37
HIERARCHY= option, 39
LSCOEFFS option, 37
MAXEFFECTS= option, 37
MAXSTEPS= option, 37
METHOD= option, 35
MINEFFECTS= option, 37
ORDERSELECT option, 39
SELECT= option, 37
SELECTION= option, 41
SLE= option, 37
SLENTRY= option, 37
SLS= option, 37
SLSTAY= option, 37
STOP= option, 38
STOPHORIZON= option, 41

VARREDUCE procedure, syntax, 1003
VARSS option
PROC PLSMOD statement, 647
VIF option
MODEL statement (REGSELECT), 744
VII= option
PROC TREESPLIT statement, 856

WARN= option (CHISQ)
TABLES statement (FREQTAB), 157

WEIGHT statement
CORRELATION procedure, 97
FREQTAB procedure, 193
GAMMOD procedure, 322
GENSELECT procedure, 385
LOGSELECT procedure, 485
PCA procedure, 568
PHSELECT procedure, 611
QTRSELECT procedure, 695
REGSELECT procedure, 749
TREESPLIT procedure, 868
WITH statement
CORRELATION procedure, 97
WOE(WOEADJUST=) option
PROC BINNING statement, 935
WTKAPPA option
EXACT statement (FREQTAB), 132
OUTPUT statement (FREQTAB), 145
TEST statement (FREQTAB), 193
WTRESSCH option
   OUTPUT statement (PHSELECT), 608

XBETA option
   OUTPUT statement (PHSELECT), 608

XBETA= option
   OUTPUT statement (GENSELECT), 383
   OUTPUT statement (LOGSELECT), 482

XCHART statement
   XCHART procedure, 790

XCONV option
   PROC ASSESS statement, 46
   PROC BINNING statement, 46
   PROC CARDINALITY statement, 46
   PROC CORRELATION statement, 46
   PROC GAMMOD statement, 46
   PROC GENSELECT statement, 46
   PROC KCLUS statement, 46
   PROC LOGSELECT statement, 46
   PROC NLMODE statement, 46
   PROC PARTITION statement, 46
   PROC PCA statement, 46
   PROC PHSELECT statement, 46
   PROC PLSMOD statement, 46
   PROC QTRSELECT statement, 46
   PROC REGSELECT statement, 46
   PROC TREESPLIT statement, 46
   PROC VARIMPUTE statement, 46
   PROC VARREDUCE statement, 46

XRCHART statement
   XRCHART procedure, 791

XSCHART statement
   XSCHART procedure, 792

XTOL option
   PROC ASSESS statement, 46
   PROC BINNING statement, 46
   PROC CARDINALITY statement, 46
   PROC CORRELATION statement, 46
   PROC GAMMOD statement, 46
   PROC GENSELECT statement, 46
   PROC KCLUS statement, 46
   PROC LOGSELECT statement, 46
   PROC NLMODE statement, 46
   PROC PARTITION statement, 46
   PROC PCA statement, 46
   PROC PHSELECT statement, 46
   PROC PLSMOD statement, 46
   PROC QTRSELECT statement, 46
   PROC REGSELECT statement, 46
   PROC TREESPLIT statement, 46
   PROC VARIMPUTE statement, 46
   PROC VARREDUCE statement, 46

ZELEN option
   EXACT statement (FREQTAB), 127
   OUTPUT statement (FREQTAB), 139

ZEROS option
   WEIGHT statement (FREQTAB), 194
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