THE POWER TO KNOW.

SAS/STAT 15.2®
User's Guide
The LIFEREG Procedure

SAS® Documentation
November 06, 2020

This document is an individual chapter from *SAS/STAT® 15.2 User's Guide*.

The correct bibliographic citation for this manual is as follows: SAS Institute Inc. 2020. *SAS/STAT® 15.2 User's Guide*. Cary, NC: SAS Institute Inc.

SAS/STAT® 15.2 User's Guide

SAS Institute Inc., SAS Campus Drive, Cary, NC 27513-2414

November 2020

Chapter 75
The LIFEREG Procedure

Contents

Overview: LIFEREG Procedure

The LIFEREG procedure fits parametric models to failure time data that can be uncensored, right censored, left censored, or interval censored. The models for the response variable consist of a linear effect composed of the covariates and a random disturbance term. The distribution of the random disturbance can be taken from a class of distributions that includes the extreme value, normal, logistic, and, by using a log transformation, the exponential, Weibull, lognormal, log-logistic, and three-parameter gamma distributions.

The model assumed for the response $\mathbf{y}$ is

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \sigma\boldsymbol{\epsilon}$$

where $\mathbf{y}$ is a vector of response values, often the log of the failure times, $\mathbf{X}$ is a matrix of covariates or independent variables (usually including an intercept term), $\boldsymbol{\beta}$ is a vector of unknown regression parameters, σ is an unknown scale parameter, and $\boldsymbol{\epsilon}$ is a vector of errors assumed to come from a known distribution (such as the standard normal distribution). If an offset variable O is specified, the form of the model is $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{O} + \sigma\boldsymbol{\epsilon}$, where $\mathbf{O}$ is a vector of values of the offset variable O. The distribution might also depend on additional shape parameters. These models are equivalent to accelerated failure time models when the log of the response is the quantity being modeled. The effect of the covariates in an accelerated failure time model is to change the scale, and not the location, of a baseline distribution of failure times.

The LIFEREG procedure estimates the parameters by maximum likelihood with a Newton-Raphson algorithm. PROC LIFEREG estimates the standard errors of the parameter estimates from the inverse of the observed information matrix.

The accelerated failure time model assumes that the effect of independent variables on an event time distribution is multiplicative on the event time. Usually, the scale function is $\exp(\mathbf{x}_c'\boldsymbol{\beta}_c)$, where $\mathbf{x}_c$ is the vector of covariate values (not including the intercept term) and $\boldsymbol{\beta}_c$ is a vector of unknown parameters. Thus, if T_0 is an event time sampled from the baseline distribution corresponding to values of zero for the covariates, then the accelerated failure time model specifies that, if the vector of covariates is $\mathbf{x}_c$, the event time is $T = \exp(\mathbf{x}_c'\boldsymbol{\beta}_c)T_0$. If $y = \log(T)$ and $y_0 = \log(T_0)$, then

$$y = \mathbf{x}_c'\boldsymbol{\beta}_c + y_0$$

This is a linear model with y_0 as the error term.

In terms of survival or exceedance probabilities, this model is

$$\Pr(T > t \mid \mathbf{x}_c) = \Pr(T_0 > \exp(-\mathbf{x}_c'\boldsymbol{\beta}_c)t)$$

The probability on the left-hand side of the equal sign is evaluated given the value $\mathbf{x}_c$ for the covariates, and the right-hand side is computed using the baseline probability distribution but at a scaled value of the argument. The right-hand side of the equation represents the value of the baseline survival function evaluated at $\exp(-\mathbf{x}_c'\boldsymbol{\beta}_c)t$.

Models usually have an intercept parameter and a scale parameter. In terms of the original untransformed event times, the effects of the intercept term and the scale term are to scale the event time and to raise the event time to a power, respectively. That is, if

$$\log(T_0) = \mu + \sigma \log(T_\epsilon)$$

then

$$T_0 = \exp(\mu) T_\epsilon^\sigma$$

Although it is possible to fit these models to the original response variable by using the NOLOG option, it is more common to model the log of the response variable. Because of this log transformation, zero values for the observed failure times are not allowed unless the NOLOG option is specified. Similarly, small values for the observed failure times lead to large negative values for the transformed response. The NOLOG option should be used only if you want to fit a distribution appropriate for the untransformed response, such as the extreme value instead of the Weibull. If you specify the normal or logistic distributions, the responses are not log transformed; that is, the NOLOG option is implicitly assumed.

Parameter estimates for the normal distribution are sensitive to large negative values, and care must be taken that the fitted model is not unduly influenced by them. Large negative values for the normal distribution can occur when fitting the lognormal distribution by log transforming the response, and some response values are near zero. Likewise, values that are extremely large after the log transformation have a strong influence in fitting the Weibull distribution (that is, the extreme value distribution for log responses). You should examine the residuals and check the effects of removing observations with large residuals or extreme values of covariates on the model parameters. The logistic distribution gives robust parameter estimates in the sense that the estimates have a bounded influence function.

The standard errors of the parameter estimates are computed from large sample normal approximations by using the observed information matrix. In small samples, these approximations might be poor. See Lawless (2003) for additional discussion and references. You can sometimes construct better confidence intervals by transforming the parameters. For example, large sample theory is often more accurate for $\log(\sigma)$ than σ. Therefore, it might be more accurate to construct confidence intervals for $\log(\sigma)$ and transform these into confidence intervals for σ. The parameter estimates and their estimated covariance matrix are available in an output SAS data set and can be used to construct additional tests or confidence intervals for the parameters. Alternatively, tests of parameters can be based on log-likelihood ratios. See Cox and Oakes (1984) for a discussion of the merits of some possible test methods including score, Wald, and likelihood ratio tests. Likelihood ratio tests are generally more reliable for small samples than tests based on the information matrix.

The log-likelihood function is computed using the log of the failure time as a response. This log likelihood differs from the log likelihood obtained using the failure time as the response by an additive term of $\sum \log(t_i)$,

where the sum is over the uncensored failure times. This term does not depend on the unknown parameters and does not affect parameter or standard error estimates. However, many published values of log likelihoods use the failure time as the basic response variable and, hence, differ by the additive term from the value computed by the LIFEREG procedure.

The classic Tobit model also fits into this class of models but with data usually censored on the left. The data considered by Tobin (1958) in his original paper came from a survey of consumers where the response variable is the ratio of expenditures on durable goods to the total disposable income. The two explanatory variables are the age of the head of household and the ratio of liquid assets to total disposable income. Because many observations in this data set have a value of zero for the response variable, the model fit by Tobin is

$$\mathbf{y} = \max(\mathbf{x}'\boldsymbol{\beta} + \epsilon, 0)$$

which is a regression model with left censoring, where $\mathbf{x}' = (1, \mathbf{x}_c')$.

Bayesian analysis of parametric survival models can be requested by using the BAYES statement in the LIFEREG procedure. In Bayesian analysis, the model parameters are treated as random variables, and inference about parameters is based on the posterior distribution of the parameters, given the data. The posterior distribution is obtained using Bayes' theorem as the likelihood function of the data weighted with a prior distribution. The prior distribution enables you to incorporate knowledge or experience of the likely range of values of the parameters of interest into the analysis. If you have no prior knowledge of the parameter values, you can use a noninformative prior distribution, and the results of the Bayesian analysis will be very similar to a classical analysis based on maximum likelihood. A closed form of the posterior distribution is often not feasible, and a Markov chain Monte Carlo method by Gibbs sampling is used to simulate samples from the posterior distribution. See Chapter 7, "Introduction to Bayesian Analysis Procedures," for an introduction to the basic concepts of Bayesian statistics. Also see the section "Bayesian Analysis: Advantages and Disadvantages" on page 132 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for a discussion of the advantages and disadvantages of Bayesian analysis. See Ibrahim, Chen, and Sinha (2001) and Gilks, Richardson, and Spiegelhalter (1996) for more information about Bayesian analysis, including guidance in choosing prior distributions.

For Bayesian analysis, PROC LIFEREG generates a Gibbs chain for the posterior distribution of the model parameters. Summary statistics (mean, standard deviation, quartiles, HPD and credible intervals, correlation matrix) and convergence diagnostics (autocorrelations; Gelman-Rubin, Geweke, Raftery-Lewis, and Heidelberger and Welch tests; and the effective sample size) are computed for each parameter, as well as the correlation matrix of the posterior sample. Trace plots, posterior density plots, and autocorrelation function plots that are created using ODS Graphics are also provided for each parameter.

The LIFEREG procedure uses ODS Graphics to create graphs as part of its output. For general information about ODS Graphics, see Chapter 23, "Statistical Graphics Using ODS."

Getting Started: LIFEREG Procedure

The following examples demonstrate how you can use the LIFEREG procedure to fit a parametric model to failure time data.

Suppose you have a response variable y that represents failure time; a binary variable, censor, with censor=0 indicating censored values; and two linearly independent variables, x1 and x2. The following statements perform a typical accelerated failure time model analysis. Higher-order effects such as interactions and nested effects are allowed in the independent variables list, but they are not shown in this example.

```
proc lifereg;
   model y*censor(0) = x1 x2;
run;
```

PROC LIFEREG can fit models to interval-censored data. The syntax for specifying interval-censored data is as follows:

```
proc lifereg;
   model (begin, end) = x1 x2;
run;
```

You can also model binomial data by using the *events/trials* syntax for the response, as illustrated in the following statements:

```
proc lifereg;
   model r/n=x1 x2;
run;
```

The variable n represents the number of trials, and the variable r represents the number of events.

Modeling Right-Censored Failure Time Data

The following example demonstrates how you can use the LIFEREG procedure to fit a model to right-censored failure time data.

Suppose you conduct a study of two headache pain relievers. You divide patients into two groups, with each group receiving a different type of pain reliever. You record the time taken (in minutes) for each patient to report headache relief. Because some of the patients never report relief for the entire study, some of the observations are censored.

The following DATA step creates the SAS data set headache:

```
data Headache;
   input Minutes Group Censor @@;
   datalines;
11  1  0   12  1  0   19  1  0   19  1  0
19  1  0   19  1  0   21  1  0   20  1  0
21  1  0   21  1  0   20  1  0   21  1  0
20  1  0   21  1  0   25  1  0   27  1  0
30  1  0   21  1  1   24  1  1   14  2  0
16  2  0   16  2  0   21  2  0   21  2  0
```

```
23  2  0   23  2  0   23  2  0   23  2  0
25  2  1   23  2  0   24  2  0   24  2  0
26  2  1   32  2  1   30  2  1   30  2  0
32  2  1   20  2  1
;
```

The data set Headache contains the variable Minutes, which represents the reported time to headache relief; the variable Group, the group to which the patient is assigned; and the variable Censor, a binary variable indicating whether the observation is censored. Valid values of the variable Censor are 0 (no) and 1 (yes). Figure 75.1 shows the first five records of the data set Headache.

Figure 75.1 Headache Data

Obs	Minutes	Group	Censor
1	11	1	0
2	12	1	0
3	19	1	0
4	19	1	0
5	19	1	0

The following statements invoke the LIFEREG procedure:

```
proc lifereg data=Headache;
   class Group;
   model Minutes*Censor(1)=Group;
   output out=New cdf=Prob;
run;
```

The CLASS statement specifies the variable Group as the classification variable. The MODEL statement syntax indicates that the response variable Minutes is right censored when the variable Censor takes the value 1. The MODEL statement specifies the variable Group as the single explanatory variable. Because the MODEL statement does not specify the DISTRIBUTION= option, the LIFEREG procedure fits the default type 1 extreme-value distribution by using $\log$(Minutes) as the response. This is equivalent to fitting the Weibull distribution.

The OUTPUT statement creates the output data set New. In addition to containing the variables in the original data set Headache, the SAS data set New also contains the variable Prob. This new variable is created by the CDF= option to contain the estimates of the cumulative distribution function evaluated at the observed response.

The results of this analysis are displayed in the following figures.

Figure 75.2 Model Fitting Information from the LIFEREG Procedure

The LIFEREG Procedure

Model Information	
Data Set	WORK.HEADACHE
Dependent Variable	Log(Minutes)
Censoring Variable	Censor
Censoring Value(s)	1
Number of Observations	38
Noncensored Values	30
Right Censored Values	8
Left Censored Values	0
Interval Censored Values	0
Number of Parameters	3
Name of Distribution	Weibull
Log Likelihood	-9.37930239

Class Level Information		
Name	**Levels**	**Values**
Group	2	1 2

Figure 75.2 displays the class level information and model fitting information. There are 30 uncensored observations and 8 right-censored observations. The log likelihood for the Weibull distribution is –9.3793. The log-likelihood value can be used to compare the goodness of fit for nested models with different covariates, but with the same distribution.

Figure 75.3 Model Fit Statistics from the LIFEREG Procedure

Fit Statistics	
-2 Log Likelihood	18.759
AIC (smaller is better)	24.759
AICC (smaller is better)	25.464
BIC (smaller is better)	29.671

Fit Statistics (Unlogged Response)	
-2 Log Likelihood	199.747
Weibull AIC (smaller is better)	205.747
Weibull AICC (smaller is better)	206.453
Weibull BIC (smaller is better)	210.660

Figure 75.3 displays fit statistics for the model. The "Fit Statistics" table displays statistics based on the maximum extreme-value log likelihood fit by using log(Minutes) as the response. These statistics are useful in comparing the fit of a different model when the fit criteria from the model that you compare is also based on the log likelihood using log(Minutes) as the response. The "Fit Statistics (Unlogged Response)" table is based on the maximum Weibull log likelihood using Minutes as the response. The AIC, BIC, and AICC statistics in this table can be used to compare models with different covariates, in addition to models with different distributions, as long as the fit statistics for the models that you compare use Minutes as the response.

Figure 75.4 Model Parameter Estimates from the LIFEREG Procedure

Analysis of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept		1	3.3091	0.0589	3.1938	3.4245	3161.70	<.0001
Group	1	1	-0.1933	0.0786	-0.3473	-0.0393	6.05	0.0139
Group	2	0	0.0000	.	.	.	.	.
Scale		1	0.2122	0.0304	0.1603	0.2809		
Weibull Shape		1	4.7128	0.6742	3.5604	6.2381		

The table of parameter estimates is displayed in Figure 75.4. Both the intercept and the slope parameter for the variable group are significantly different from 0 at the 0.05 level. Because the variable group has only one degree of freedom, parameter estimates are given for only one level of the variable group (group=1). However, the estimate for the intercept parameter provides a baseline for group=2.

The resulting model is as follows:

$$\log(\text{minutes}) = \begin{cases} 3.30911843 - 0.1933025 & \text{for group} = 1 \\ 3.30911843 & \text{for group} = 2 \end{cases}$$

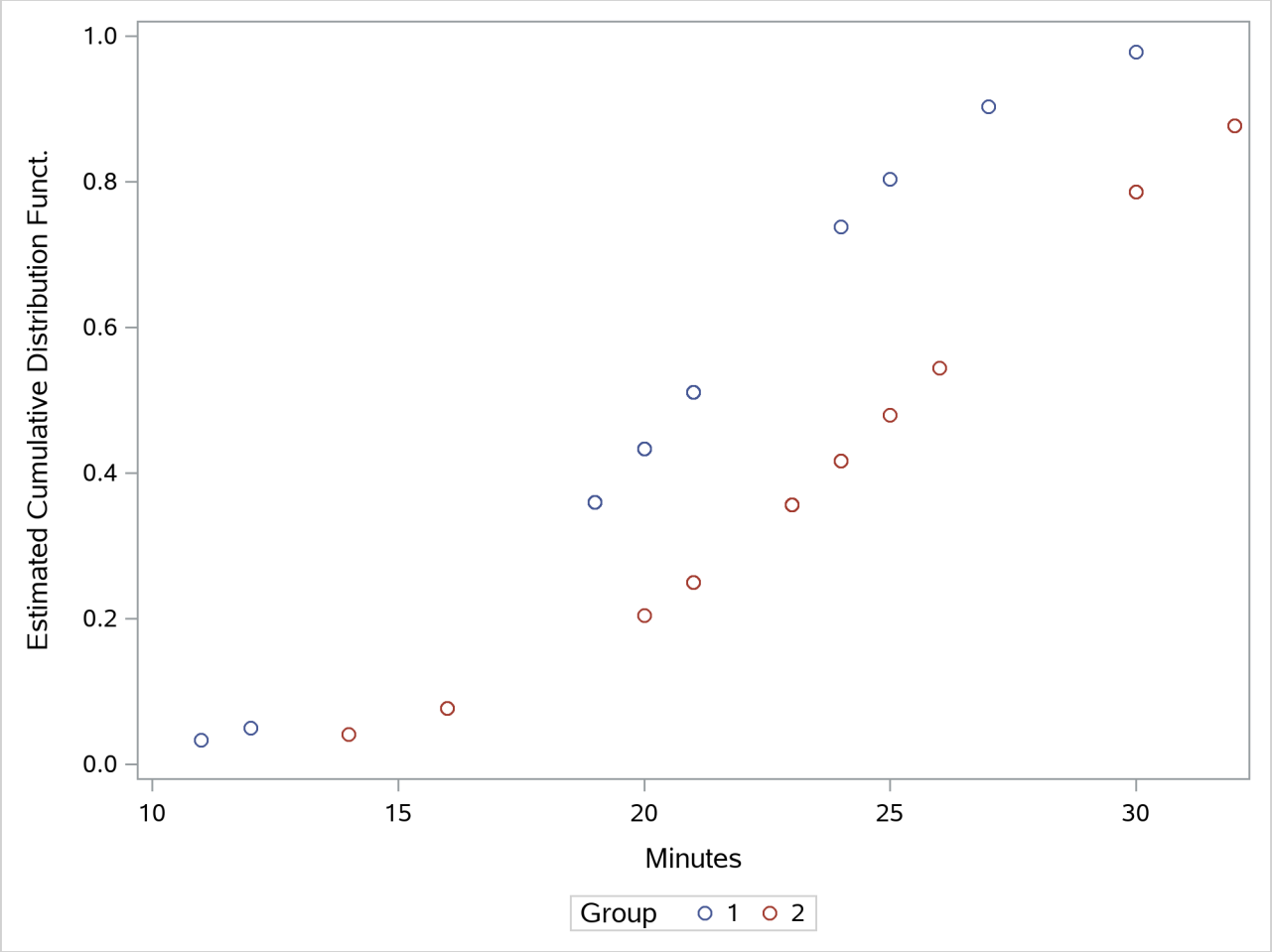
Note that the Weibull shape parameter for this model is the reciprocal of the extreme-value scale parameter estimate shown in Figure 75.4 ($1/0.21219 = 4.7128$).

The following statements produce a graph of the cumulative distribution values versus the variable Minutes.

```
proc sgplot data=New;
   scatter x=Minutes y=Prob / group=Group;
   discretelegend;
run;
```

Figure 75.5 displays the estimated cumulative distribution function values contained in the output data set New for each group.

Figure 75.5 Plot of the Estimated Cumulative Distribution Function



Bayesian Analysis of Right-Censored Data

Nelson (1982) describes a study of the lifetimes of locomotive engine fans. This example shows how to use PROC LIFEREG to carry out a Bayesian analysis of the engine fan data. In this example, a lognormal distribution is used to model the engine lifetimes, but other survival time distributions, such as the Weibull, can also be used.

The following SAS statements create the SAS data set Fan. This data set contains a censoring indicator variable and right-censored survival times for the 70 locomotive engine fans in the study.

```
data Fan;
   input Lifetime Censor@@;
   datalines;
 450 0    460 1   1150 0   1150 0   1560 1
1600 0   1660 1   1850 1   1850 1   1850 1
1850 1   1850 1   2030 1   2030 1   2030 1
2070 0   2070 0   2080 0   2200 1   3000 1
3000 1   3000 1   3000 1   3100 0   3200 1
```

```
3450 0   3750 1   3750 1   4150 1   4150 1
4150 1   4150 1   4300 1   4300 1   4300 1
4300 1   4600 0   4850 1   4850 1   4850 1
4850 1   5000 1   5000 1   5000 1   6100 1
6100 0   6100 1   6100 1   6300 1   6450 1
6450 1   6700 1   7450 1   7800 1   7800 1
8100 1   8100 1   8200 1   8500 1   8500 1
8500 1   8750 1   8750 0   8750 1   9400 1
9900 1  10100 1  10100 1  10100 1  11500 1
;
```

Some of the fans had not failed at the time the data were collected, and the unfailed units have right-censored lifetimes. The variable Lifetime represents either a failure time or a censoring time. The variable Censor is equal to 0 if the value of Lifetime is a failure time, and it is equal to 1 if the value is a censoring time.

The following SAS statements specify a Bayesian analysis that uses a lognormal model for the engine lifetimes. There are no covariates, so the model is an intercept-only model. The OUTPOST= option saves the samples from the posterior distribution in the SAS data set Post for further processing.

```
ods graphics on;
proc lifereg data=Fan;
   model Lifetime*Censor( 1 )= / dist=lognormal;
   bayes seed=1  outpost=Post;
run;
```

The SEED= option is specified to maintain reproducibility; no other options are specified in the BAYES statement. By default, a uniform prior distribution is assumed for the intercept coefficient. The uniform prior is a flat prior on the real line with a distribution that reflects ignorance of the location of the parameter, placing equal probability on all possible values the regression coefficient can take. Using the uniform prior in the following example, you would expect the Bayesian estimates to resemble the classical results of maximizing the likelihood. If you can elicit an informative prior on the regression coefficients, you should use the COEFFPRIOR= option to specify it. A default noninformative gamma prior is used for the lognormal scale parameter σ.

You should make sure that the posterior distribution samples have achieved convergence before using them for Bayesian inference. If you do not specify additional options, PROC LIFEREG produces by default three convergence diagnostics: autocorrelations of the posterior sample, effective sample size, and the Geweke statistic. See the section "Assessing Markov Chain Convergence" on page 140 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for information about assessing the convergence of the chain of posterior samples. Trace plots, posterior density plots, and autocorrelation function plots that are created using ODS Graphics are also provided for each parameter. See the section "Visual Analysis via Trace Plots" on page 141 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for help in interpreting these plots.

The "Analysis of Maximum Likelihood Parameter Estimates" table in Figure 75.6 summarizes maximum likelihood estimates of the lognormal intercept and scale parameters.

Figure 75.6 Maximum Likelihood Estimates from the LIFEREG Procedure

The LIFEREG Procedure

Bayesian Analysis

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits	
Intercept	1	10.1432	0.5211	9.1219	11.1646
Scale	1	1.6796	0.3893	1.0664	2.6453

Since no prior distribution for the intercept was specified, the default uniform improper distribution shown in the "Uniform Prior for Regression Coefficients" table in Figure 75.7 is used.

Noninformative prior distributions are appropriate if you have no prior knowledge of the likely range of values of the parameters, and if you want to make probability statements about the parameters or functions of the parameters. Refer, for example, to Ibrahim, Chen, and Sinha (2001) for more information about choosing prior distributions.

The default noninformative gamma prior distribution for the lognormal scale parameter is shown in the "Independent Prior Distributions for Model Parameters" table in Figure 75.7.

Figure 75.7 Noninformative Prior Distributions

The LIFEREG Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients

Parameter	Prior
Intercept	Constant

Independent Prior Distributions for Model Parameters

Parameter	Prior Distribution	Hyperparameters			
Scale	Gamma	Shape	0.001	Inverse Scale	0.001

By default, posterior mode estimates of the model parameters are used as the starting value for the simulation. These are listed in the "Initial Values of the Chain" table in Figure 75.8.

Figure 75.8 Markov Chain Initial Values

Initial Values of the Chain

Chain	Seed	Intercept	Scale
1	1	10.0501	1.59544

Summary statistics for the posterior sample are displayed in the "Fit Statistics," "Descriptive Statistics for the Posterior Sample," "Interval Statistics for the Posterior Sample," and "Posterior Correlation Matrix" tables

in Figure 75.9. Since noninformative prior distributions were used, these results are consistent with the maximum likelihood estimates shown in Figure 75.6.

Figure 75.9 Posterior Sample Summary Statistics

Fit Statistics	
DIC (smaller is better)	87.244
pD (effective number of parameters)	1.822

The LIFEREG Procedure

Bayesian Analysis

Posterior Summaries

Parameter	N	Mean	Standard Deviation	Percentiles 25%	50%	75%
Intercept	10000	10.4198	0.6171	9.9671	10.3261	10.7959
Scale	10000	1.9197	0.4808	1.5676	1.8476	2.1931

Posterior Intervals

Parameter	Alpha	Equal-Tail Interval		HPD Interval	
Intercept	0.050	9.4478	11.8994	9.3224	11.6752
Scale	0.050	1.1908	3.0570	1.1104	2.8833

Posterior Correlation Matrix

Parameter	Intercept	Scale
Intercept	1.0000	0.8296
Scale	0.8296	1.0000

By default, PROC LIFEREG computes three convergence diagnostics: the lag1, lag5, lag10, and lag50 autocorrelations; the Geweke diagnostic; and the effective sample size. These are displayed in Figure 75.10. There is no indication that the Markov chain has not converged. See the section "Assessing Markov Chain Convergence" on page 140 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for more information about convergence diagnostics and their interpretation.

Figure 75.10 Posterior Sample Summary Statistics

The LIFEREG Procedure

Bayesian Analysis

Posterior Autocorrelations

Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.6973	0.1764	0.0188	-0.0016
Scale	0.6955	0.1711	0.0171	-0.0003

Figure 75.10 *continued*

Geweke Diagnostics		
Parameter	**z**	**Pr > |z|**
Intercept	-0.9716	0.3313
Scale	-0.9363	0.3491

Effective Sample Sizes			
		Autocorrelation	
Parameter	**ESS**	**Time**	**Efficiency**
Intercept	1773.7	5.6380	0.1774
Scale	1805.7	5.5381	0.1806

Summary statistics of the posterior distribution samples are produced by default. However, these statistics might not be sufficient for carrying out your Bayesian inference. The samples from the posterior distribution saved in the SAS data set Post created with the OUTPOST= option can be used for further analysis.

Trace, autocorrelation, and density plots for the three model parameters shown in Figure 75.11 and Figure 75.12 are useful in diagnosing whether the Markov chain of posterior samples has converged. These plots show no evidence that the chain has not converged. See the section "Visual Analysis via Trace Plots" on page 141 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for more information about interpreting these types of diagnostic plots.

Figure 75.11 Diagnostic Plots

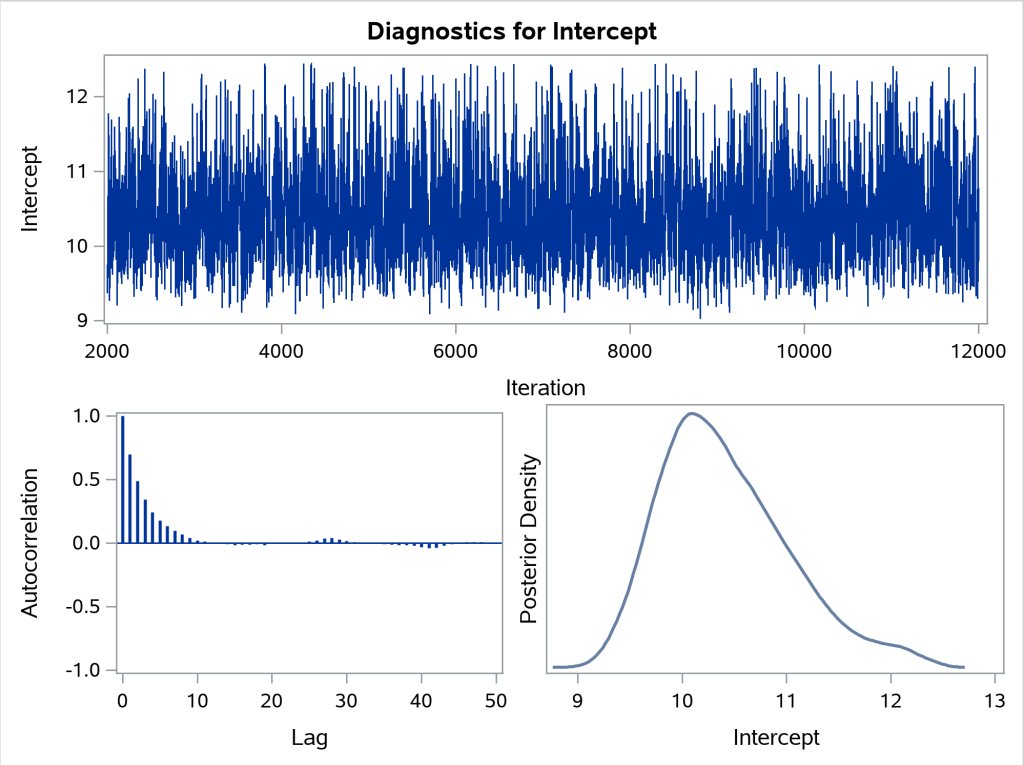
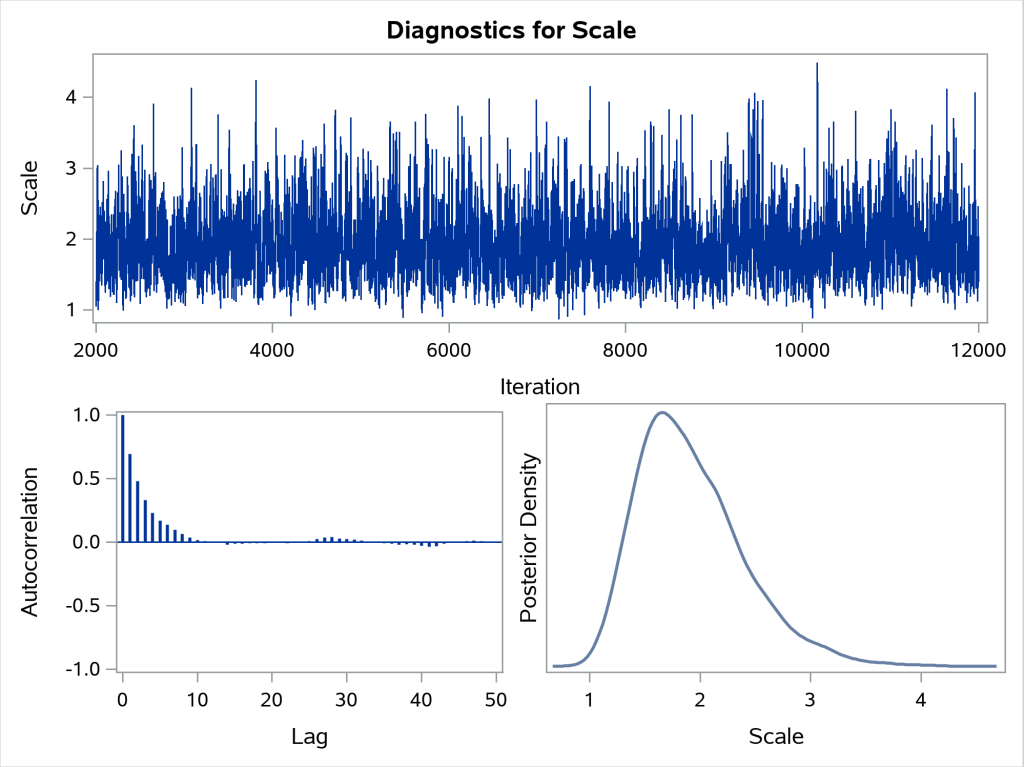


Figure 75.12 Diagnostic Plots



The fraction failing in the first 8000 hours of operation might be a quantity of interest. This kind of information could be useful, for example, in determining whether to improve the reliability of the engine components due to warranty considerations. The following SAS statements compute the mean and percentiles of the distribution of the fraction failing in the first 8000 hours from the posterior sample data set Post:

```
data Prob;
   set Post;
   Frac = ProbNorm(( log(8000) - Intercept ) / Scale );
   label Frac= 'Fraction Failing in 8000 Hours';
run;

proc means data = Prob(keep=Frac) n mean p10 p25 p50 p75 p90;
run;
```

The mean fraction of failures in the first 8000 hours, shown in Figure 75.13, is about 0.24, which could be used in further analysis of warranty costs. The 10th percentile is about 0.16 and the 90th percentile is about 0.32, which gives an assessment of the probable range of the fraction failing in the first 8000 hours.

Figure 75.13 Fraction Failing in 8000 Hours

The MEANS Procedure

Analysis Variable : Frac Fraction Failing in 8000 Hours						
N	Mean	10th Pctl	25th Pctl	50th Pctl	75th Pctl	90th Pctl
10000	0.2381259	0.1628591	0.1953658	0.2336532	0.2765736	0.3190248

Syntax: LIFEREG Procedure

The following statements are available in the LIFEREG procedure:

PROC LIFEREG < *options* > **;**
BAYES < *options* > **;**
BY *variables* **;**
CLASS *variables* **;**
ESTIMATE < '*label*' > *estimate-specification* < **(***divisor***=***n***)** >
< **,** . . . < '*label*' > *estimate-specification* < **(***divisor***=***n***)** > > < / *options* > **;**
INSET < *keyword-list* > < / *options* > **;**
LSMEANS < *model-effects* > < / *options* > **;**
LSMESTIMATE *model-effect* < '*label*' > *values* < **(***divisor***=***n***)** >
< **,** . . . < '*label*' > *values* < **(***divisor***=***n***)** > > < / *options* > **;**
MODEL *response* **=** < *effects* > < / *options* > **;**
OUTPUT < **OUT=***SAS-data-set* > < *keyword***=***name* . . . *keyword***=***name* > < *options* > **;**
PROBPLOT < / *options* > **;**
SLICE *model-effect* < / *options* > **;**
STORE < **OUT=** >*item-store-name* < / **LABEL=**'*label*' > **;**
TEST < *model-effects* > < / *options* > **;**
WEIGHT *variable* **;**

The MODEL statement is required; it specifies both the variables that are used in the regression part of the model and the distribution that is used for the error (random) component of the model. Each invocation of the LIFEREG procedure can use only one MODEL statement. If multiple MODEL statements are present, only the last is used. You can specify main effects and interaction terms in the MODEL statement, as in the GLM procedure. You can specify initial values in the MODEL statement or in an INEST= data set. If no initial values are specified, the starting estimates are obtained by ordinary least squares. The CLASS statement determines which explanatory variables are treated as categorical. The WEIGHT statement identifies a *variable* with values that are used to weight the observations. Observations with zero or negative weights are not used to fit the model, although predicted values can be computed for them. The OUTPUT statement creates an output data set that contains predicted values and residuals.

The ESTIMATE, LSMEANS, LSMESTIMATE, SLICE, STORE, and TEST statements are common to many procedures. Summary descriptions of functionality and syntax for these statements are also given after the PROC LIFEREG statement in alphabetical order, and full documentation about them is available in Chapter 19, "Shared Concepts and Topics."

PROC LIFEREG Statement

PROC LIFEREG < *options* > **;**

The PROC LIFEREG statement invokes the LIFEREG procedure. Table 75.1 summarizes the *options* available in the PROC LIFEREG statement.

Table 75.1 PROC LIFEREG Statement Options

Option	Description
COVOUT	Writes the estimated covariance matrix to the OUTEST= data set
DATA=	Specifies the input SAS data set
INEST=	Specifies an input SAS data set that contains initial estimates
NAMELEN=	Specifies the length of effect names
NOPRINT	Suppresses the display of the output
ORDER=	Specifies the sort order for the levels of the classification variables
OUTEST=	Specifies an output SAS data set
PLOTS=	Controls graphics created by ODS Graphics
XDATA=	Specifies a SAS input data containing values for the independent variables

You can specify the following *options* in the PROC LIFEREG statement.

COVOUT
writes the estimated covariance matrix to the OUTEST= data set if convergence is attained.

DATA=*SAS-data-set*
specifies the input SAS data set used by PROC LIFEREG. By default, the most recently created SAS data set is used.

INEST=*SAS-data-set*
specifies an input SAS data set that contains initial estimates for all the parameters in the model. See the section "INEST= Data Set" on page 5557 for a detailed description of the contents of the INEST= data set.

NAMELEN=*n*
specifies the length of effect names in tables and output data sets to be *n* characters, where *n* is a value between 20 and 200. The default length is 20 characters.

NOPRINT
suppresses the display of the output. Note that this option temporarily disables the Output Delivery System (ODS). For more information, see Chapter 22, "Using the Output Delivery System."

ORDER=DATA | FORMATTED | FREQ | INTERNAL
specifies the sort order for the levels of the classification variables (which are specified in the CLASS statement).

This option applies to the levels for all classification variables, except when you use the (default) ORDER=FORMATTED option with numeric classification variables that have no explicit format. In that case, the levels of such variables are ordered by their internal value.

The ORDER= option can take the following values:

Value of ORDER=	Levels Sorted By
DATA	Order of appearance in the input data set
FORMATTED	External formatted value, except for numeric variables with no explicit format, which are sorted by their unformatted (internal) value
FREQ	Descending frequency count; levels with the most observations come first in the order
INTERNAL	Unformatted value

By default, ORDER=FORMATTED. For ORDER=FORMATTED and ORDER=INTERNAL, the sort order is machine-dependent.

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

OUTEST=*SAS-data-set*
specifies an output SAS data set containing the parameter estimates, the maximized log likelihood, and, if the COVOUT option is specified, the estimated covariance matrix. See the section "OUTEST= Data Set" on page 5557 for a detailed description of the contents of the OUTEST= data set.

PLOTS=NONE | PROBPLOT
specifies options that control graphics created by ODS Graphics.

ODS Graphics must be enabled before plots can be requested. For example:

```
ods graphics on;

proc lifereg plots=probplot;
   model y = x;
run;

ods graphics off;
```

For more information about enabling and disabling ODS Graphics, see the section "Enabling and Disabling ODS Graphics" on page 651 in Chapter 23, "Statistical Graphics Using ODS."

The following *plot-requests* are available.

NONE suppresses any plots created by ODS Graphics specified in other LIFEREG statements, such as the BAYES or PROBPLOT statement.

PROBPLOT creates a default probability plot based on information in the MODEL statement. If a PROBPLOT statement is also specified, the probability plot specified in that statement is created, and this option is ignored.

XDATA=*SAS-data-set*

specifies an input SAS data set that contains values for all the independent variables in the MODEL statement and variables in the CLASS statement for probability plotting. If there are covariates specified in a MODEL statement and a probability plot is requested with a PROBPLOT statement, you specify fixed values for the effects in the MODEL statement with the XDATA= data set. See the section "XDATA= Data Set" on page 5558 for a detailed description of the contents of the XDATA= data set.

BAYES Statement

BAYES < *options* > **;**

The BAYES statement requests a Bayesian analysis of the regression model by using Gibbs sampling. The Bayesian posterior samples (also known as the chain) for the regression parameters are not tabulated. The Bayesian posterior samples (also known as the chain) for the model parameters can be output to a SAS data set.

Table 75.2 summarizes the *options* available in the BAYES statement.

Table 75.2 BAYES Statement Options

Option	Description
Monte Carlo Options	
INITIAL=	Specifies initial values of the chain
INITIALMLE	Specifies that maximum likelihood estimates be used as initial values of the chain
METROPOLIS=	Specifies the use of a Metropolis step
NBI=	Specifies the number of burn-in iterations
NMC=	Specifies the number of iterations after burn-in
SEED=	Specifies the random number generator seed
THINNING=	Controls the thinning of the Markov chain
Model and Prior Options	
COEFFPRIOR=	Specifies the prior of the regression coefficients
EXPONENTIALSCALEPRIOR=	Specifies the prior of the exponential scale parameter
GAMMASHAPEPRIOR=	Specifies the prior of the three-parameter gamma shape parameter
SCALEPRIOR=	Specifies the prior of the scale parameter
WEIBULLSCALEPRIOR=	Specifies the prior of the Weibull scale parameter
WEIBULLSHAPEPRIOR=	Specifies the prior of the Weibull shape parameter
Summary Statistics and Convergence Diagnostics	
DIAGNOSTICS=	Displays convergence diagnostics
PLOTS=	Displays diagnostic plots
STATISTICS=	Displays summary statistics of the posterior samples
Posterior Samples	
OUTPOST=	Names a SAS data set for the posterior samples

The following list describes these *options* and their suboptions.

COEFFPRIOR=UNIFORM | NORMAL <(*normal-options*)>

CPRIOR=UNIFORM | NORMAL <(*option*)>

COEFF=UNIFORM | NORMAL <(*option*)>

specifies the prior distribution for the regression coefficients. The default is COEFFPRIOR=UNIFORM. The available prior distributions are as follows:

NORMAL<(*normal-option*)>

specifies a normal distribution. The *normal-options* include the following:

CONDITIONAL

specifies that the normal prior, conditional on the current Markov chain value of the location-scale model precision parameter $\tau = \frac{1}{\sigma^2}$, is $N(\boldsymbol{\mu}, \tau^{-1}\boldsymbol{\Sigma})$, where $\boldsymbol{\mu}$ and $\boldsymbol{\Sigma}$ are the mean and covariance of the normal prior specified by other normal options.

INPUT= *SAS-data-set*

specifies a SAS data set that contains the mean and covariance information of the normal prior. The data set must have a _TYPE_ variable to represent the type of each observation and a variable for each regression coefficient. If the data set also contains a _NAME_ variable, the values of this variable are used to identify the covariances for the _TYPE_='COV' observations; otherwise, the _TYPE_='COV' observations are assumed to be in the same order as the explanatory variables in the MODEL statement. PROC LIFEREG reads the mean vector from the observation with _TYPE_='MEAN' and reads the covariance matrix from observations with _TYPE_='COV'. For an independent normal prior, the variances can be specified with _TYPE_='VAR'; alternatively, the precisions (inverse of the variances) can be specified with _TYPE_='PRECISION'.

RELVAR<=c>

specifies the normal prior $N(\mathbf{0}, c\mathbf{J})$, where $\mathbf{J}$ is a diagonal matrix with diagonal elements equal to the variances of the corresponding ML estimator. By default, $c = 10^6$.

VAR<=c>

specifies the normal prior $N(\mathbf{0}, c\mathbf{I})$, where $\mathbf{I}$ is the identity matrix.

If you do not specify an option, the normal prior $N(\mathbf{0}, 10^6\mathbf{I})$, where $\mathbf{I}$ is the identity matrix, is used. See the section "Normal Prior" on page 5561 for more details.

UNIFORM

specifies a flat prior—that is, the prior that is proportional to a constant ($p(\beta_1, \ldots, \beta_k) \propto 1$ for all $-\infty < \beta_i < \infty$).

DIAGNOSTICS=ALL | NONE | (*keyword-list*)

DIAG=ALL | NONE | (*keyword-list*)

controls the number of diagnostics produced. You can request all the following diagnostics by specifying DIAGNOSTICS=ALL. If you do not want any of these diagnostics, specify DIAGNOSTICS=NONE. If you want some but not all of the diagnostics, or if you want to change certain settings of these diagnostics, specify a subset of the following *keywords*. The default is DIAGNOSTICS=(AUTOCORR ESS GEWEKE).

AUTOCORR <(LAGS= *numeric-list*) >
computes the autocorrelations of lags given by LAGS= list for each parameter. Elements in the list are truncated to integers and repeated values are removed. If the LAGS= option is not specified, autocorrelations of lags 1, 5, 10, and 50 are computed for each variable. See the section "Autocorrelations" on page 152 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

ESS
computes Carlin's estimate of the effective sample size, the correlation time, and the efficiency of the chain for each parameter. See the section "Effective Sample Size" on page 153 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

GELMAN <(*gelman-options***) >**
computes the Gelman and Rubin convergence diagnostics. You can specify one or more of the following *gelman-options*:

NCHAIN=*number*

N=*number*
specifies the number of parallel chains used to compute the diagnostic, and must be 2 or larger. The default is NCHAIN=3. If an INITIAL= data set is used, NCHAIN defaults to the number of rows in the INITIAL= data set. If any number other than this is specified with the NCHAIN= option, the NCHAIN= value is ignored.

ALPHA=*value*
specifies the significance level for the upper bound. The default is ALPHA=0.05, resulting in a 97.5% bound.

See the section "Gelman and Rubin Diagnostics" on page 145 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

GEWEKE <(*geweke-options***) >**
computes the Geweke spectral density diagnostics, which are essentially a two-sample t test between the first f_1 portion and the last f_2 portion of the chain. The default is $f_1 = 0.1$ and $f_2 = 0.5$, but you can choose other fractions by using the following *geweke-options*:

FRAC1=*value*
specifies the fraction f_1 for the first window.

FRAC2=*value*
specifies the fraction f_2 for the second window.

See the section "Geweke Diagnostics" on page 147 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

HEIDELBERGER <(*heidel-options***) >**
computes the Heidelberger and Welch diagnostic for each variable, which consists of a stationarity test of the null hypothesis that the sample values form a stationary process. If the stationarity test is not rejected, a halfwidth test is then carried out. Optionally, you can specify one or more of the following *heidel-options*:

SALPHA=*value*
specifies the α level ($0 < \alpha < 1$) for the stationarity test.

HALPHA=*value*
specifies the α level ($0 < \alpha < 1$) for the halfwidth test.

EPS=*value*
specifies a positive number ϵ such that if the halfwidth is less than ϵ times the sample mean of the retained iterates, the halfwidth test is passed.

See the section "Heidelberger and Welch Diagnostics" on page 148 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

MCSE

MCERROR
computes the Monte Carlo standard error for each parameter. The Monte Caro standard error, which measures the simulation accuracy, is the standard error of the posterior mean estimate and is calculated as the posterior standard deviation divided by the square root of the effective sample size. See the section "Standard Error of the Mean Estimate" on page 154 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

RAFTERY<(*raftery-options***)>**
computes the Raftery and Lewis diagnostics that evaluate the accuracy of the estimated quantile ($\hat{\theta}_Q$ for a given $Q \in (0,1)$) of a chain. $\hat{\theta}_Q$ can achieve any degree of accuracy when the chain is allowed to run for a long time. A stopping criterion is when the estimated probability $\hat{P}_Q = \Pr(\theta \leq \hat{\theta}_Q)$ reaches within $\pm R$ of the value Q with probability S; that is, $\Pr(Q - R \leq \hat{P}_Q \leq Q + R) = S$. The following *raftery-options* enable you to specify Q, R, S, and a precision level ϵ for the test:

QUANTILE | Q=*value*
specifies the order (a value between 0 and 1) of the quantile of interest. The default is 0.025.

ACCURACY | R=*value*
specifies a small positive number as the margin of error for measuring the accuracy of estimation of the quantile. The default is 0.005.

PROBABILITY | S=*value*
specifies the probability of attaining the accuracy of the estimation of the quantile. The default is 0.95.

EPSILON | EPS=*value*
specifies the tolerance level (a small positive number) for the stationary test. The default is 0.001.

See the section "Raftery and Lewis Diagnostics" on page 150 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

EXPSCALEPRIOR=GAMMA< (*options*) > | IMPROPER

ESCALEPRIOR=GAMMA< (*options*) > | IMPROPER

ESCPRIOR=GAMMA< (*options*) > | IMPROPER

specifies that Gibbs sampling be performed on the exponential distribution scale parameter and the prior distribution for the scale parameter. This prior distribution applies only when the exponential distribution and no covariates are specified.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by EXPSCALEPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 5560 for more details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* >

specifies independent $G(c\hat{\alpha}, c)$ distribution, where $\hat{\alpha}$ is the MLE of the exponential scale parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\alpha}$ and the variance is $\frac{\hat{\alpha}}{c^2}$. By default, *c*=10^{-4}.

SHAPE=*a*

ISCALE=*b*

when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*

when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*

when specified alone, results in a $G(c, c)$ prior.

An improper prior with density $f(t)$ proportional to t^{-1} is specified with EXPSCALEPRIOR=IMPROPER.

GAMMASHAPEPRIOR=NORMAL< (*options*) >

GAMASHAPEPRIOR=NORMAL< (*options*) >

SHAPE1PRIOR=NORMAL< (*options*) >

specifies the prior distribution for the gamma distribution shape parameter. If you do not specify any options in a gamma model, the $N(0, 10^6)$ prior for the shape is used. You can specify MEAN= and VAR= or RELVAR= options, either alone or together, to specify the mean and variance of the normal prior for the gamma shape parameter.

MEAN=*a*

specifies a normal prior $N(a, 10^6)$. By default, *a*=0.

RELVAR< =*b* >

specifies the normal prior $N(0, bJ)$, where J is the variance of the MLE of the shape parameter. By default, *b*=10^6.

VAR=*c*

specifies the normal prior $N(0, c)$. By default, *c*=10^6.

INITIAL=*SAS-data-set*
specifies the SAS data set that contains the initial values of the Markov chains. The INITIAL= data set must contain all the variables of the model. You can specify multiple rows as the initial values of the parallel chains for the Gelman-Rubin statistics, but posterior summaries, diagnostics, and plots are computed only for the first chain. If the data set also contains the variable _SEED_, the value of the _SEED_ variable is used as the seed of the random number generator for the corresponding chain.

INITIALMLE
specifies that maximum likelihood estimates of the model parameters be used as initial values of the Markov chain. If this option is not specified, estimates of the mode of the posterior distribution obtained by optimization are used as initial values.

METROPOLIS=YES | NO
specifies the use of a Metropolis step to generate Gibbs samples for posterior distributions that are not log concave. The default value is METROPOLIS=YES.

NBI=*number*
specifies the number of burn-in iterations before the chains are saved. The default is 2000.

NMC=*number*
specifies the number of iterations after the burn-in. The default is 10000.

OUTPOST=*SAS-data-set*

OUT=*SAS-data-set*
names the SAS data set that contains the posterior samples. See the section "OUTPOST= Output Data Set" on page 5562 for more information. Alternatively, you can create the output data set by specifying an ODS OUTPUT statement as follows:

ODS OUTPUT POSTERIORSAMPLE=*SAS-data-set*

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

PLOTS<(*global-plot-options***)>=(***plot-request* < *. . . plot-request* >**)**
controls the display of diagnostic plots. Three types of plots can be requested: trace plots, autocorrelation function plots, and kernel density plots. By default, the plots are displayed in panels unless the global plot option UNPACK is specified. Also, when specifying more than one type of plots, the plots are displayed by parameters unless the global plot option GROUPBY is specified. When you specify only one plot request, you can omit the parentheses around the plot request. For example:

```
plots=none
plots(unpack)=trace
plots=(trace autocorr)
```

ODS Graphics must be enabled before plots can be requested. For example:

```
ods graphics on;
proc lifereg;
   model y=x;
   bayes plots=trace;
run;
ods graphics off;
```

For more information about enabling and disabling ODS Graphics, see the section "Enabling and Disabling ODS Graphics" on page 651 in Chapter 23, "Statistical Graphics Using ODS."

The *global-plot-options* are as follows:

FRINGE
creates a fringe plot on the X axis of the density plot.

GROUPBY=PARAMETER | TYPE
specifies how the plots are grouped when there is more than one type of plot.

GROUPBY=TYPE
specifies that the plots be grouped by type.

GROUPBY=PARAMETER
specifies that the plots be grouped by parameter.

GROUPBY=PARAMETER is the default.

LAGS=*n*
specifies that autocorrelations be plotted up to lag *n*. If this option is not specified, autocorrelations are plotted up to lag 50.

SMOOTH
displays a fitted penalized B-spline curve for each trace plot.

UNPACKPANEL
UNPACK
specifies that all paneled plots be unpacked, meaning that each plot in a panel is displayed separately.

The *plot-requests* include the following:

ALL
specifies all types of plots. PLOTS=ALL is equivalent to specifying PLOTS=(TRACE AUTOCORR DENSITY).

AUTOCORR
displays the autocorrelation function plots for the parameters.

DENSITY
displays the kernel density plots for the parameters.

NONE
suppresses all diagnostic plots.

TRACE
displays the trace plots for the parameters. See the section "Visual Analysis via Trace Plots" on page 141 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details.

SCALEPRIOR=GAMMA< (*options*) >
specifies that Gibbs sampling be performed on the location-scale model scale parameter and the prior distribution for the scale parameter.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by SCALEPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 5560 for details. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* >
specifies independent $G(c\hat{\sigma}, c)$ distribution, where $\hat{\sigma}$ is the MLE of the scale parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\sigma}$ and the variance is $\frac{\hat{\sigma}}{c}$. By default, *c*=10^{-4}.

SHAPE=*a*

ISCALE=*b*
when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*
when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*
when specified alone, results in a $G(c, c)$ prior.

SEED=*number*
specifies an integer seed in the range 1 to $2^{31} - 1$ for the random number generator in the simulation. Specifying a seed enables you to reproduce identical Markov chains for the same specification. If the SEED= option is not specified, or if you specify a nonpositive seed, a random seed is derived from the time of day.

STATISTICS < (*global-options*) > = ALL | NONE | *keyword* | (*keyword-list*)

STATS < (*global-statoptions*) > = ALL | NONE | *keyword* | (*keyword-list*)
controls the number of posterior statistics produced. Specifying STATISTICS=ALL is equivalent to specifying STATISTICS= (SUMMARY INTERVAL COV CORR). If you do not want any posterior statistics, you specify STATISTICS=NONE. The default is STATISTICS=(SUMMARY INTERVAL). See the section "Summary Statistics" on page 153 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for details. The *global-options* include the following:

ALPHA=*numeric-list*
controls the probabilities of the credible intervals. The ALPHA= values must be between 0 and 1. Each ALPHA= value produces a pair of 100(1–ALPHA)% equal-tail and HPD intervals for each parameters. The default is ALPHA=0.05, which yields the 95% credible intervals for each parameter.

PERCENT=*numeric-list*
requests the percentile points of the posterior samples. The PERCENT= values must be between 0 and 100. The default is PERCENT=25, 50, 75, which yields the 25th, 50th, and 75th percentile points, respectively, for each parameter.

The list of *keywords* includes the following:

CORR
produces the posterior correlation matrix.

COV
produces the posterior covariance matrix.

SUMMARY
produces the means, standard deviations, and percentile points for the posterior samples. The default is to produce the 25th, 50th, and 75th percentile points, but you can use the global PERCENT= option to request specific percentile points.

INTERVAL
produces equal-tail credible intervals and HPD intervals. The default is to produce the 95% equal-tail credible intervals and 95% HPD intervals, but you can use the global ALPHA= option to request intervals of any probabilities.

NONE
suppresses printing all summary statistics.

THINNING=*number*

THIN=*number*
controls the thinning of the Markov chain. Only one in every k samples is used when THINNING=k, and if NBI=n_0 and NMC=n, the number of samples kept is

$$\left[\frac{n_0+n}{k}\right]-\left[\frac{n_0}{k}\right]$$

where $[a]$ represents the integer part of the number a. The default is THINNING=1.

WEIBULLSCALEPRIOR=GAMMA<(*options***)>**

WSCALEPRIOR=GAMMA<(*options***)>**

WSCPRIOR=GAMMA<(*options***)>**
specifies that Gibbs sampling be performed on the Weibull model scale parameter and the prior distribution for the scale parameter. This option applies only when a Weibull distribution and no covariates are specified. When this option is specified, PROC LIFEREG performs Gibbs sampling on the Weibull scale parameter, which is defined as $\exp(\mu)$, where μ is the intercept term.

A gamma prior $G(a,b)$ is specified by WEIBULLSCALEPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The gamma probability density is given by $g(t)=\frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 5560 for details about the gamma prior. The default is $G(10^{-4},10^{-4})$.

RELSHAPE<=*c***>**
specifies independent $G(c\hat{\alpha},c)$ distribution, where $\hat{\alpha}$ is the MLE of the Weibull scale parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\alpha}$ and the variance is $\frac{\hat{\alpha}}{c}$. By default, c=10^{-4}.

SHAPE=*a*

ISCALE=*b*

when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*

when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*

when specified alone, results in a $G(c, c)$ prior.

WEIBULLSHAPEPRIOR=GAMMA< (*options***) >**

WSHAPEPRIOR=GAMMA< (*options***) >**

WSHPRIOR=GAMMA< (*options***) >**

specifies that Gibbs sampling be performed on the Weibull model shape parameter and the prior distribution for the shape parameter. When this option is specified, PROC LIFEREG performs Gibbs sampling on the Weibull shape parameter, which is defined as σ^{-1}, where σ is the location-scale model scale parameter.

A gamma prior $G(a, b)$ with density $f(t) = \frac{b(bt)^{a-1}\mathrm{e}^{-bt}}{\Gamma(a)}$ is specified by WEIBULL-SHAPEPRIOR=GAMMA, which can be followed by one of the following *gamma-options* enclosed in parentheses. The hyperparameters a and b are the shape and inverse-scale parameters of the gamma distribution, respectively. See the section "Gamma Prior" on page 5560 for details about the gamma prior. The default is $G(10^{-4}, 10^{-4})$.

RELSHAPE< =*c* **>**

specifies independent $G(c\hat{\beta}, c)$ distribution, where $\hat{\beta}$ is the MLE of the Weibull shape parameter. With this choice of hyperparameters, the mean of the prior distribution is $\hat{\beta}$ and the variance is $\frac{\hat{\beta}}{c}$. By default, *c*=10^{-4}.

SHAPE< =*a* **>**

ISCALE=*b*

when both specified, results in a $G(a, b)$ prior.

SHAPE=*c*

when specified alone, results in a $G(c, c)$ prior.

ISCALE=*c*

when specified alone, results in a $G(c, c)$ prior.

BY Statement

BY *variables* **;**

You can specify a BY statement in PROC LIFEREG to obtain separate analyses of observations in groups that are defined by the BY variables. When a BY statement appears, the procedure expects the input data set to be sorted in order of the BY variables. If you specify more than one BY statement, only the last one specified is used.

If your input data set is not sorted in ascending order, use one of the following alternatives:

- Sort the data by using the SORT procedure with a similar BY statement.
- Specify the NOTSORTED or DESCENDING option in the BY statement in the LIFEREG procedure. The NOTSORTED option does not mean that the data are unsorted but rather that the data are arranged in groups (according to values of the BY variables) and that these groups are not necessarily in alphabetical or increasing numeric order.
- Create an index on the BY variables by using the DATASETS procedure (in Base SAS software).

For more information about BY-group processing, see the discussion in *SAS Language Reference: Concepts*. For more information about the DATASETS procedure, see the discussion in the *Base SAS Procedures Guide*.

CLASS Statement

CLASS *variables* < / **TRUNCATE** > **;**

The CLASS statement names the classification variables to be used in the model. Typical classification variables are Treatment, Sex, Race, Group, and Replication. If you use the CLASS statement, it must appear before the MODEL statement.

Classification variables can be either character or numeric. By default, class levels are determined from the entire set of formatted values of the CLASS variables.

NOTE: Prior to SAS 9, class levels were determined by using no more than the first 16 characters of the formatted values. To revert to this previous behavior, you can use the TRUNCATE option in the CLASS statement.

In any case, you can use formats to group values into levels. See the discussion of the FORMAT procedure in the *Base SAS Procedures Guide* and the discussions of the FORMAT statement and SAS formats in *SAS Formats and Informats: Reference*. You can adjust the order of CLASS variable levels with the ORDER= option in the PROC LIFEREG statement.

You can specify the following *option* in the CLASS statement after a slash (/):

TRUNCATE
specifies that class levels should be determined by using only up to the first 16 characters of the formatted values of CLASS variables. When formatted values are longer than 16 characters, you can use this option to revert to the levels as determined in releases prior to SAS 9.

ESTIMATE Statement

ESTIMATE < '*label*' > *estimate-specification* < **(***divisor***=***n***)** >
< **,** . . . < '*label*' > *estimate-specification* < **(***divisor***=***n***)** > >
< **/** *options* > **;**

The ESTIMATE statement provides a mechanism for obtaining custom hypothesis tests. Estimates are formed as linear estimable functions of the form $\mathbf{L}\boldsymbol{\beta}$. You can perform hypothesis tests for the estimable functions, construct confidence limits, and obtain specific nonlinear transformations.

Table 75.3 summarizes the *options* available in the ESTIMATE statement.

Table 75.3 ESTIMATE Statement Options

Option	Description
Construction and Computation of Estimable Functions	
DIVISOR=	Specifies a list of values to divide the coefficients
NOFILL	Suppresses the automatic fill-in of coefficients for higher-order effects
SINGULAR=	Tunes the estimability checking difference
Degrees of Freedom and *p*-Values	
ADJUST=	Determines the method of multiple comparison adjustment of estimates
ALPHA=α	Determines the confidence level $(1-\alpha)$
LOWER	Performs one-sided, lower-tailed inference
STEPDOWN	Adjusts multiplicity-corrected p-values further in a step-down fashion
TESTVALUE=	Specifies values under the null hypothesis for tests
UPPER	Performs one-sided, upper-tailed inference
Statistical Output	
CL	Constructs confidence limits
CORR	Displays the correlation matrix of estimates
COV	Displays the covariance matrix of estimates
E	Prints the $\mathbf{L}$ matrix
JOINT	Produces a joint F or chi-square test for the estimable functions
PLOTS=	Produces ODS statistical graphics if the analysis is sampling-based
SEED=	Specifies the seed for computations that depend on random numbers

Table 75.3 *continued*

Option	Description
Generalized Linear Modeling	
CATEGORY=	Specifies how to construct estimable functions for multinomial data
EXP	Exponentiates and displays estimates
ILINK	Computes and displays estimates and standard errors on the inverse linked scale

For more information about the syntax of the ESTIMATE statement, see the section "ESTIMATE Statement" on page 448 in Chapter 19, "Shared Concepts and Topics."

INSET Statement

INSET < *keyword-list* > < / *options* > **;**

The box or table of summary information produced on plots made with the PROBPLOT statement is called an *inset*. You can use the INSET statement to customize the information that is displayed in the inset box as well as to customize the appearance of the inset box. To supply the information that is displayed in the inset box, you specify *keywords* corresponding to the information that you want shown. For example, the following statements produce a probability plot with the number of observations, the number of right-censored observations, the name of the distribution, and the estimated Weibull shape parameter in the inset:

```
proc lifereg data=epidemic;
   model life = dose / dist = Weibull;
   probplot;
   inset nobs right dist shape;
run;
```

By default, inset entries are identified with appropriate labels. However, you can provide a customized label by specifying the *keyword* for that entry followed by the equal sign (=) and the label in quotes. For example, the following INSET statement produces an inset containing the number of observations and the name of the distribution, labeled "Sample Size" and "Distribution" in the inset:

```
inset nobs='Sample Size' dist='Distribution';
```

If you specify a *keyword* that does not apply to the plot you are creating, then the *keyword* is ignored.

If you specify more than one INSET statement, only the first one is used.

Table 75.4 lists *keywords* available in the INSET statement to display summary statistics, distribution parameters, and distribution fitting information.

Table 75.4 INSET Statement Keywords

Keyword	Description
CONFIDENCE	Confidence coefficient for all confidence intervals
DIST	Name of the distribution
INTERVAL	Number of interval-censored observations
LEFT	Number of left-censored observations
NOBS	Number of observations
NMISS	Number of observations with missing values
RIGHT	Number of right-censored observations
SCALE	Value of the scale parameter
SHAPE	Value of the shape parameter
UNCENSORED	Number of uncensored observations

LSMEANS Statement

LSMEANS < *model-effects* > < / *options* > **;**

The LSMEANS statement computes and compares least squares means (LS-means) of fixed effects. LS-means are *predicted population margins*—that is, they estimate the marginal means over a balanced population. In a sense, LS-means are to unbalanced designs as class and subclass arithmetic means are to balanced designs.

Table 75.5 summarizes the *options* available in the LSMEANS statement.

Table 75.5 LSMEANS Statement Options

Option	Description
Construction and Computation of LS-Means	
AT	Modifies the covariate value in computing LS-means
BYLEVEL	Computes separate margins
DIFF	Computes differences of LS-means
OM=	Specifies the weighting scheme for LS-means computation as determined by the input data set
SINGULAR=	Tunes estimability checking
Degrees of Freedom and *p*-Values	
ADJUST=	Determines the method of multiple-comparison adjustment of LS-means differences
ALPHA=α	Determines the confidence level ($1 - \alpha$)
STEPDOWN	Adjusts multiple-comparison *p*-values further in a step-down fashion

Table 75.5 *continued*

Option	Description
Statistical Output	
CL	Constructs confidence limits for means and mean differences
CORR	Displays the correlation matrix of LS-means
COV	Displays the covariance matrix of LS-means
E	Prints the **L** matrix
LINES	Uses connecting lines to indicate nonsignificantly different subsets of LS-means
LINESTABLE	Displays the results of the LINES option as a table
MEANS	Prints the LS-means
PLOTS=	Produces graphs of means and mean comparisons
SEED=	Specifies the seed for computations that depend on random numbers
Generalized Linear Modeling	
EXP	Exponentiates and displays estimates of LS-means or LS-means differences
ILINK	Computes and displays estimates and standard errors of LS-means (but not differences) on the inverse linked scale
ODDSRATIO	Reports (simple) differences of least squares means in terms of odds ratios if permitted by the link function

For more information about the syntax of the LSMEANS statement, see the section "LSMEANS Statement" on page 465 in Chapter 19, "Shared Concepts and Topics."

LSMESTIMATE Statement

LSMESTIMATE *model-effect* < '*label*' > *values* < *divisor*=*n* >
< **,** . . . < '*label*' > *values* < *divisor*=*n* > >
< / *options* > **;**

The LSMESTIMATE statement provides a mechanism for obtaining custom hypothesis tests among least squares means.

Table 75.6 summarizes the *options* available in the LSMESTIMATE statement.

Table 75.6 LSMESTIMATE Statement Options

Option	Description
Construction and Computation of LS-Means	
AT	Modifies covariate values in computing LS-means
BYLEVEL	Computes separate margins
DIVISOR=	Specifies a list of values to divide the coefficients
OM=	Specifies the weighting scheme for LS-means computation as determined by a data set
SINGULAR=	Tunes estimability checking
Degrees of Freedom and *p*-Values	
ADJUST=	Determines the method of multiple-comparison adjustment of LS-means differences
ALPHA=α	Determines the confidence level ($1 - \alpha$)
LOWER	Performs one-sided, lower-tailed inference
STEPDOWN	Adjusts multiple-comparison *p*-values further in a step-down fashion
TESTVALUE=	Specifies values under the null hypothesis for tests
UPPER	Performs one-sided, upper-tailed inference
Statistical Output	
CL	Constructs confidence limits for means and mean differences
CORR	Displays the correlation matrix of LS-means
COV	Displays the covariance matrix of LS-means
E	Prints the $\mathbf{L}$ matrix
ELSM	Prints the $\mathbf{K}$ matrix
JOINT	Produces a joint *F* or chi-square test for the LS-means and LS-means differences
PLOTS=	Produces graphs of means and mean comparisons
SEED=	Specifies the seed for computations that depend on random numbers
Generalized Linear Modeling	
CATEGORY=	Specifies how to construct estimable functions for multinomial data
EXP	Exponentiates and displays LS-means estimates
ILINK	Computes and displays estimates and standard errors of LS-means (but not differences) on the inverse linked scale

For more information about the syntax of the LSMESTIMATE statement, see the section "LSMESTIMATE Statement" on page 486 in Chapter 19, "Shared Concepts and Topics."

MODEL Statement

< *label* **:>** **MODEL** *response* **<** ∗*censor* **(** *list* **)>** **=** *effects* **<** / *options* **>** **;**

< *label* **:>** **MODEL** **(** *lower* **,** *upper* **)=** *effects* **<** / *options* **>** **;**

< *label* **:>** **MODEL** *events/trials* **=** *effects* **<** / *options* **>** **;**

Only a single MODEL statement can be used with one invocation of the LIFEREG procedure. If multiple MODEL statements are present, only the last is used. The optional *label* is used to label the model estimates in the output SAS data set and OUTEST= data set.

The first MODEL syntax is appropriate for right censoring. The variable *response* is possibly right censored. If the *response* variable can be right censored, then a second variable, denoted *censor*, must appear after the *response* variable with a list of parenthesized values, separated by commas or blanks, to indicate censoring. That is, if the *censor* variable takes on a value given in the list, the *response* is a right-censored value; otherwise, it is an observed value.

The second MODEL syntax specifies two variables, *lower* and *upper*, that contain values of the endpoints of the censoring interval. If the two values are the same (and not missing), it is assumed that there is no censoring and the actual response value is observed. If the lower value is missing, then the upper value is used as a left-censored value. If the upper value is missing, then the lower value is taken as a right-censored value. If both values are present and the lower value is less than the upper value, it is assumed that the values specify a censoring interval. If the lower value is greater than the upper value or both values are missing, then the observation is not used in the analysis, although predicted values can still be obtained if none of the covariates are missing.

The following table summarizes the ways of specifying censoring.

lower	*upper*	**Comparison**	**Interpretation**
Not missing	Not missing	Equal	No censoring
Not missing	Not missing	Lower < upper	Censoring interval
Missing	Not missing		Upper used as left-censoring value
Not missing	Missing		Lower used as right-censoring value
Not missing	Not missing	Lower > upper	Observation not used
Missing	Missing		Observation not used

The third MODEL syntax specifies two variables that contain count data for a binary response. The value of the first variable, *events*, is the number of successes. The value of the second variable, *trials*, is the number of tries. The values of both *events* and (*trials-events*) must be nonnegative, and *trials* must be positive for the response to be valid. The values of the two variables do not need to be integers and are not modified to be integers.

The *effects* following the equal sign are the covariates in the model. Higher-order effects, such as interactions and nested terms, are allowed in the list, similar to the GLM procedure. Variable names and combinations of variable names representing higher-order terms are allowed to appear in this list. Classification, or CLASS,

variables can be used as effects, and indicator variables are generated for the class levels. If you do not specify any covariates following the equal sign, an intercept-only model is fit.

Examples of three valid MODEL statements follow:

```
a: model time*flag(1,3)=temp;

b: model (start, finish)=;

c: model r/n=dose;
```

MODEL statement a indicates that the response is contained in a variable named time and that, if the variable flag takes on the values 1 or 3, the observation is right censored. The explanatory variable is temp, which could be a CLASS variable. MODEL statement b indicates that the response is known to be in the interval between the values of the variables start and finish and that there are no covariates except for a default intercept term. MODEL statement c indicates a binary response, with the variable r containing the number of responses and the variable n containing the number of trials.

Table 75.7 summarizes the *options* available in the MODEL statement.

Table 75.7 MODEL Statement Options

Option	Description
Model Specification	
ALPHA=	Sets the significance level
DISTRIBUTION=	Specifies the distribution type for failure time
NOLOG	Requests no log transformation of response
INTERCEPT=	Specifies initial estimate for intercept term
NOINT	Holds the intercept term fixed
INITIAL=	Specifies initial estimates for regression parameters
OFFSET=	Specifies an offset variable
SCALE=	Initializes the scale parameter
NOSCALE	Holds the scale parameter fixed
SHAPE1=	Initializes the first shape parameter
NOSHAPE1	Holds the first shape parameter fixed
Model Fitting	
CONVERGE=	Sets the convergence criterion
CONVG=	Sets the relative Hessian convergence criterion
MAXITER=	Sets the maximum number of iterations
SINGULAR=	Sets the tolerance for testing singularity
Output	
CORRB	Displays the estimated correlation matrix
COVB	Displays the estimated covariance matrix
ITPRINT	Displays the iteration history, final gradient, and second derivative matrix

The following *options* can appear in the MODEL statement.

ALPHA=*value*
sets the significance level for the confidence intervals for regression parameters and estimated survival probabilities. The value must be between 0 and 1. By default, ALPHA=0.05.

CONVERGE=*value*
sets the convergence criterion. Convergence is declared when the maximum change in the parameter estimates between Newton-Raphson steps is less than the value specified. The change is a relative change if the parameter is greater than 0.01 in absolute value; otherwise, it is an absolute change. By default, CONVERGE=1E–8.

CONVG=*value*
sets the relative Hessian convergence criterion; *value* must be between 0 and 1. After convergence is determined with the change in parameter criterion specified with the CONVERGE= option, the quantity $tc = \frac{\mathbf{g}'\mathbf{H}^{-1}\mathbf{g}}{|f|}$ is computed and compared to *value*, where $\mathbf{g}$ is the gradient vector, $\mathbf{H}$ is the Hessian matrix for the model parameters, and f is the log-likelihood function. If *tc* is greater than *value*, a warning that the relative Hessian convergence criterion has been exceeded is displayed. This criterion detects the occasional case where the change in parameter convergence criterion is satisfied, but a maximum in the log-likelihood function has not been attained. By default, CONVG=1E–4.

CORRB
produces the estimated correlation matrix of the parameter estimates.

COVB
produces the estimated covariance matrix of the parameter estimates.

DISTRIBUTION=*distribution-type*

DIST=*distribution-type*

D=*distribution-type*
specifies the distribution type assumed for the failure time. By default, PROC LIFEREG fits a type 1 extreme-value distribution to the log of the response. This is equivalent to fitting the Weibull distribution, since the scale parameter for the extreme-value distribution is related to a Weibull shape parameter and the intercept is related to the Weibull scale parameter in this case. When the NOLOG option is specified, PROC LIFEREG models the untransformed response with a type 1 extreme-value distribution as the default. See the section "Supported Distributions" on page 5545 for descriptions of the distributions. The following are valid values for *distribution-type*:

EXPONENTIAL	the exponential distribution, which is treated as a restricted Weibull distribution
GAMMA	a generalized gamma distribution (Lawless 2003, p. 240). The standard two-parameter gamma distribution is not available in PROC LIFEREG.
LLOGISTIC	a log-logistic distribution
LNORMAL	a lognormal distribution
LOGISTIC	a logistic distribution (equivalent to LLOGISTIC when the NOLOG option is specified)
NORMAL	a normal distribution (equivalent to LNORMAL when the NOLOG option is specified)
WEIBULL	a Weibull distribution. If NOLOG is specified, it fits a type 1 extreme-value distribution to the raw, untransformed data.

By default, PROC LIFEREG transforms the response with the natural logarithm before fitting the specified model when you specify the GAMMA, LLOGISTIC, LNORMAL, or WEIBULL option. You can suppress the log transformation with the NOLOG option. The following table summarizes the resulting distributions when the preceding distribution options are used in combination with the NOLOG option.

DISTRIBUTION=	NOLOG Specified?	Resulting Distribution
EXPONENTIAL	No	Exponential
EXPONENTIAL	Yes	One-parameter extreme value
GAMMA	No	Generalized log-gamma using the log of the response. (This is the same as fitting the generalized gamma using the untransformed response.)
GAMMA	Yes	Generalized log-gamma with untransformed responses
LOGISTIC	No	Logistic
LOGISTIC	Yes	Logistic (NOLOG has no effect)
LLOGISTIC	No	Log-logistic
LLOGISTIC	Yes	Logistic
LNORMAL	No	Lognormal
LNORMAL	Yes	Normal
NORMAL	No	Normal
NORMAL	Yes	Normal (NOLOG has no effect)
WEIBULL	No	Weibull
WEIBULL	Yes	Extreme value

INITIAL=*values*

sets initial values for the regression parameters. This option can be helpful in the case of convergence difficulty. Specified values are used to initialize the regression coefficients for the covariates specified in the MODEL statement. The intercept parameter is initialized with the INTERCEPT= option and is not included here. The values are assigned to the variables in the MODEL statement in the same order in which they are listed in the MODEL statement. Note that a CLASS variable requires $k - 1$ values when the CLASS variable takes on k different levels. The order of the CLASS levels is determined by the ORDER= option. If there is no intercept term, the first CLASS variable requires k initial values. If a BY statement is used, all CLASS variables must take on the same number of levels in each BY group or no meaningful initial values can be specified. The INITIAL= option can be specified as follows.

Type of List	Specification
List separated by blanks	`initial=3 4 5`
List separated by commas	`initial=3,4,5`
x to y	`initial=3 to 5`
x to y by z	`initial=3 to 5 by 1`
Combination of methods	`initial=1,3 to 5,9`

By default, PROC LIFEREG computes initial estimates with ordinary least squares. See the section "Computational Method" on page 5543 for details.

NOTE: The INITIAL= option is overwritten by the INEST= option. See the section "INEST= Data Set" on page 5557 for details.

INTERCEPT=*value*
initializes the intercept term to *value*. By default, the intercept is initialized by an ordinary least squares estimate.

ITPRINT
displays the iteration history for computing maximum likelihood estimates, the final evaluation of the gradient, and the final evaluation of the negative of the second derivative matrix—that is, the negative of the Hessian. If you perform a Bayesian analysis by specifying the BAYES statement, the iteration history for computing the mode of the posterior distribution is also displayed.

MAXITER=*n*
sets the maximum allowable number of iterations during the model estimation. By default, MAXITER=50.

NOINT
holds the intercept term fixed. Because of the usual log transformation of the response, the intercept parameter is usually a scale parameter for the untransformed response, or a location parameter for a transformed response.

NOLOG
requests that no log transformation of the response variable be performed. By default, PROC LIFEREG models the log of the response variable for the GAMMA, LLOGISTIC, LOGNORMAL, and WEIBULL distribution options. NOLOG is implicitly assumed for the NORMAL and LOGISTIC distribution options.

NOSCALE
holds the scale parameter fixed. Note that if the log transformation has been applied to the response, the effect of the scale parameter is a power transformation of the original response. If no SCALE= value is specified, the scale parameter is fixed at the value 1.

NOSHAPE1
holds the first shape parameter, SHAPE1, fixed. If no SHAPE1= value is specified, SHAPE1 is fixed at a value that depends on the DISTRIBUTION type.

OFFSET=*variable*
specifies a variable in the input data set to be used as an offset variable. This variable cannot be a CLASS variable, and it cannot be the response variable or one of the explanatory variables.

SCALE=*value*
initializes the scale parameter to *value*. If the Weibull distribution is specified, this scale parameter is the scale parameter of the type 1 extreme-value distribution, not the Weibull scale parameter. Note that, with a log transformation, the exponential model is the same as a Weibull model with the scale parameter fixed at the value 1.

SHAPE1=*value*
initializes the first shape parameter to *value*. If the specified distribution does not depend on this parameter, then this option has no effect. The only distribution that depends on this shape parameter is the generalized gamma distribution. See the section "Supported Distributions" on page 5545 for descriptions of the parameterizations of the distributions.

SINGULAR=*value*
sets the tolerance for testing singularity of the information matrix and the crossproducts matrix for the initial least squares estimates. Roughly, the test requires that a pivot be at least this value times the original diagonal value. By default, SINGULAR=1E–12.

OUTPUT Statement

OUTPUT < **OUT=***SAS-data-set* > < *keyword*=*name* > . . . < *keyword*=*name* > **;**

The OUTPUT statement creates a new SAS data set containing statistics calculated after fitting the model. At least one specification of the form *keyword=name* is required.

All variables in the original data set are included in the new data set, along with the variables created as options for the OUTPUT statement. These new variables contain fitted values and estimated quantiles. If you want to create a SAS data set in a permanent library, you must specify a two-level name. For more information about permanent libraries and SAS data sets, see *SAS Programmers Guide: Essentials*. Each OUTPUT statement applies to the preceding MODEL statement. See Example 75.1 for illustrations of the OUTPUT statement.

The following specifications can appear in the OUTPUT statement:

OUT=*SAS-data-set*
specifies the new data set. By default, the procedure uses the DATA*n* convention to name the new data set.

keyword=name
specifies the statistics to include in the output data set and gives names to the new variables. Specify a *keyword* for each desired statistic (see the following list of *keywords*), an equal sign, and the variable to contain the statistic.

The *keywords* allowed and the statistics they represent are as follows:

CENSORED=*variable*
specifies a *variable* to signal whether an observation is censored, and the type of censoring. The variable takes on values according to Table 75.8.

Table 75.8 Censoring Variable Values

Type of Response	CENSORED Variable Value
Uncensored	0
Right-censored	1
Left-censored	2
Interval-censored	3

CDF=*variable*

specifies a *variable* to contain the estimates of the cumulative distribution function evaluated at the observed response. If the data are interval censored, then the cumulative distribution function is evaluated at the response lower interval endpoint. See the section "Predicted Values" on page 5548 for more information.

CONTROL=*variable*

specifies a *variable* in the input data set to control the estimation of quantiles. See Example 75.1 for an illustration. If the specified variable has the value 1, estimates for all the values listed in the QUANTILE= list are computed for that observation in the input data set; otherwise, no estimates are computed. If no CONTROL= variable is specified, all quantiles are estimated for all observations. If the response variable in the MODEL statement is binomial, then this option has no effect.

CRESIDUAL | CRES=*variable*

specifies a *variable* to contain the Cox-Snell residuals

$$-\log(S(u_i))$$

where S is the standard survival function and

$$u_i = \frac{y_i - \mathbf{x}_i'\mathbf{b}}{\sigma}$$

If the data are interval censored, residuals are computed for y_i values corresponding to lower interval endpoints. If the response variable in the corresponding model statement is binomial, then the residuals are not computed, and this variable contains missing values.

SRESIDUAL | SRES=*variable*

specifies a *variable* to contain the standardized residuals

$$\frac{y_i - \mathbf{x}_i'\mathbf{b}}{\sigma}$$

If the data are interval censored, residuals are computed for y_i values corresponding to lower interval endpoints. If the response variable in the corresponding model statement is binomial, then the residuals are not computed, and this variable contains missing values.

PREDICTED | P=*variable*

specifies a *variable* to contain the quantile estimates. If the response variable in the corresponding model statement is binomial, then this variable contains the estimated probabilities, $1 - F(-\mathbf{x}'\mathbf{b})$.

QUANTILES | QUANTILE | Q=*value-list*

gives a list of *values* for which quantiles are calculated. The values must be between 0 and 1, noninclusive. For each value, a corresponding quantile is estimated. This option is not used if the response variable in the corresponding MODEL statement is binomial.

By default, QUANTILES=0.5. When the response is not binomial, a numeric variable, _PROB_, is added to the OUTPUT data set whenever the QUANTILES= option is specified. The variable _PROB_ gives the probability value for the quantile estimates. These are the values taken from the QUANTILES= list and are given as values between 0 and 1, not as values between 0 and 100. The list of QUANTILES values can be specified as in Table 75.9.

Table 75.9 Types of Value Lists

Type of List	Specification
List separated by blanks	`.2 .4 .6 .8`
List separated by commas	`.2,.4,.6,.8`
x to y	`.2 to .8`
x to y by z	`.2 to .8 by .1`
Combination of methods	`.1,.2 to .8 by .2`

STD_ERR | STD=*variable*

specifies a *variable* to contain the estimates of the standard errors of the estimated quantiles or $\mathbf{x}'\mathbf{b}$. If the response used in the MODEL statement is a binomial response, then these are the standard errors of $\mathbf{x}'\mathbf{b}$. Otherwise, they are the standard errors of the quantile estimates. These estimates can be used to compute confidence intervals for the quantiles. However, if the model is fit to the log of the event time, better confidence intervals can usually be computed by transforming the confidence intervals for the log response. See Example 75.1 for such a transformation.

XBETA=*variable*

specifies a *variable* to contain the computed value of $\mathbf{x}'\mathbf{b}$, where $\mathbf{x}$ is the covariate vector and $\mathbf{b}$ is the vector of parameter estimates.

PROBPLOT Statement

PROBPLOT | PPLOT < */options* > **;**

You can use the PROBPLOT statement to create a probability plot from lifetime data. The data can be uncensored, right censored, or arbitrarily censored. You can specify any number of PROBPLOT statements after a MODEL statement. The syntax used for the response in the MODEL statement determines the type of censoring assumed in creating the probability plot. The model fit with the MODEL statement is plotted along with the data. If there are covariates in the model, they are set to constant values specified in the XDATA= data set when creating the probability plot. If no XDATA= data set is specified, continuous variables are set to their overall mean values and categorical variables specified in the CLASS statement are set to their highest levels.

Table 75.10 summarizes the *options* available in the PROBPLOT statement.

Table 75.10 PROBPLOT Statement Options

Option	Description
HCL	Computes and draws confidence limits for the predicted probabilities
HLOWER=	Specifies *value* as the lower lifetime axis tick mark
HUPPER=	Specifies *value* as the upper lifetime axis tick mark
HREF	Draws reference lines perpendicular to the horizontal axis
HREFLABELS=	Specifies labels for the lines requested by the HREF= option
ITPRINTEM	Displays the iteration history for the Turnbull algorithm

Table 75.10 *continued*

Option	Description
MAXITEM=	Specifies the maximum number of iterations for the Turnbull algorithm
NOCENPLOT	Suppresses the plotting of censored data points
NOCONF	Suppresses the default confidence bands
NODATA	Suppresses plotting of the estimated empirical probability plot
NOFIT	Suppresses the fitted probability (percentile) line and confidence bands
NOFRAME	Suppresses the frame around plotting areas
NOGRID	Suppresses grid lines
NOPOLISH	Suppresses setting small interval probabilities to zero in the Turnbull algorithm
NPINTERVALS=	Displays one of the two kinds of confidence limits
PCTLIST=	Specifies the list of percentages for which to compute percentile estimates
PLOWER=	Specifies the lower limit on the probability axis scale
PPOS=	Specifies the plotting position type
PPOUT	Displays a table of the cumulative probabilities
PRINTPROBS	Displays intervals and associated probabilities for the Turnbull algorithm
PROBLIST=	Specifies the list of initial values for the Turnbull algorithm
PUPPER=	Specifies the upper limit on the probability axis scale
ROTATE	Requests probability plots with probability scale on the horizontal axis
SQUARE	Makes the layout of the probability plots square
TOLLIKE=	Specifies the criterion for convergence in the Turnbull algorithm
TOLPROB=	Specifies the criterion for setting the interval probability to zero in the Turnbull algorithm
VREF	Draws reference lines perpendicular to the vertical axis
VREFLABELS=	Specifies labels for the lines requested by the VREF= option

You can specify the following *options* to control the content, layout, and appearance of a probability plot.

The following *options* are available if ODS Graphics is enabled.

HCL
computes and draws confidence limits for the predicted probabilities in the horizontal direction.

HLOWER=*value*
specifies the lower limit on the lifetime axis scale. The HLOWER= option specifies *value* as the lower lifetime axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

HUPPER=*value*
specifies *value* as the upper lifetime axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

HREF < (INTERSECT) > =*value-list*
requests reference lines perpendicular to the horizontal axis be drawn at horizontal axis values in the *value-list*. If (INTERSECT) is specified, a second reference line perpendicular to the vertical axis is drawn that intersects the fit line at the same point as the horizontal axis reference line. If a horizontal axis reference line label is specified with the HREFLABELS= option, the intersecting vertical axis

reference line is labeled with the vertical axis value. See also the CHREF=, HREFLABELS=, and LHREF= options.

HREFLABELS=*'label1'* **...** *'labeln'*

HREFLABEL=*'label1'* **...** *'labeln'*

HREFLAB=*'label1'* **...** *'labeln'*

specifies labels for the lines requested by the HREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

ITPRINTEM

displays the iteration history for the Turnbull algorithm.

MAXITEM=*n1 <,n2>*

specifies the maximum number of iterations for the Turnbull algorithm. Iteration history will be displayed in increments of *n2* if requested with the ITPRINTEM option. See the section "Arbitrarily Censored Data" on page 5554 for details.

NOCENPLOT

suppresses the plotting of censored data points.

NOCONF

suppresses the default confidence bands on the probability plot.

NODATA

suppresses plotting of the estimated empirical probability plot.

NOFIT

suppresses the fitted probability (percentile) line and confidence bands.

NOFRAME

suppresses the frame around plotting areas.

NOGRID

suppresses grid lines.

NOPOLISH

suppresses setting small interval probabilities to zero in the Turnbull algorithm.

NPINTERVALS=*interval-type*

specifies one of the two kinds of confidence limits for the estimated cumulative probabilities, pointwise (NPINTERVALS=POINT) or simultaneous (NPINTERVALS=SIMUL), requested by the PPOUT option to be displayed in the tabular output.

PCTLIST=*value-list*

specifies the list of percentages for which to compute percentile estimates; *value-list* must be a list of values separated by blanks or commas. Each value in the list must be between 0 and 100.

PLOWER=*value*
specifies the lower limit on the probability axis scale. The PLOWER= option specifies *value* as the lower probability axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

PPOS=*plotting-position-type*
specifies the plotting position type. See the section "Probability Plotting" on page 5552 for details.

PPOS=	Method
EXPRANK	Expected ranks
MEDRANK	Median ranks
MEDRANK1	Median ranks (exact formula)
KM	Kaplan-Meier
MKM	Modified Kaplan-Meier (default)

PPOUT
specifies that a table of the cumulative probabilities plotted on the probability plot be displayed. Kaplan-Meier estimates of the cumulative probabilities are also displayed, along with standard errors and confidence limits. The confidence limits can be pointwise or simultaneous, as specified by the NPINTERVALS= option.

PRINTPROBS
displays intervals and associated probabilities for the Turnbull algorithm.

PROBLIST=*value-list*
specifies the list of initial values for the Turnbull algorithm.

PUPPER=*value*
specifies the upper limit on the probability axis scale. The PUPPER= option specifies *value* as the upper probability axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

ROTATE
requests probability plots with probability scale on the horizontal axis.

SQUARE
makes the layout of the probability plots square.

TOLLIKE=*value*
specifies the criterion for convergence in the Turnbull algorithm.

TOLPROB=*value*
specifies the criterion for setting the interval probability to zero in the Turnbull algorithm.

VREF<(INTERSECT)>=*value-list*
requests reference lines perpendicular to the vertical axis be drawn at vertical axis values in the *value-list*. If (INTERSECT) is specified, a second reference line perpendicular to the horizontal axis is drawn that intersects the fit line at the same point as the vertical axis reference line. If a vertical axis reference line label is specified with the VREFLABELS= option, the intersecting horizontal axis reference line is labeled with the horizontal axis value. See also the CVREF=, LVREF=, and VREFLABELS= options.

VREFLABELS=*'label1' . . . 'labeln'*

VREFLABEL=*'label1' . . . 'labeln'*

VREFLAB=*'label1' . . . 'labeln'*

specifies labels for the lines requested by the VREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

SLICE Statement

SLICE *model-effect* < / *options* > **;**

The SLICE statement provides a general mechanism for performing a partitioned analysis of the LS-means for an interaction. This analysis is also known as an analysis of simple effects.

This statement uses the same *options* as the LSMEANS statement, which are summarized in Table 19.23 in Chapter 19, "Shared Concepts and Topics." For more information about the syntax of the SLICE statement, see the section "SLICE Statement" on page 515 in Chapter 19, "Shared Concepts and Topics."

STORE Statement

STORE < **OUT=** >*item-store-name* < / **LABEL=**'*label*' > **;**

The STORE statement saves the context and results of the statistical analysis. The resulting item store has a binary file format that cannot be modified. The contents of the item store can be processed using the PLM procedure. For more information about the syntax of the STORE statement, see the section "STORE Statement" on page 519 in Chapter 19, "Shared Concepts and Topics."

TEST Statement

TEST < *model-effects* > < / *options* > **;**

The TEST statement enables you to perform chi-square tests for model effects that test Type I, Type II, or Type III hypotheses. By default, the Type III tests are performed. For more information, see Chapter 19, "Shared Concepts and Topics."

WEIGHT Statement

WEIGHT *variable* **;**

If you want to use weights for each observation in the input data set, place the weights in a variable in the data set and specify the name in a WEIGHT statement. The values of the WEIGHT variable can be nonintegral and are not truncated. Observations with nonpositive or missing values for the weight variable do not contribute to the fit of the model. The WEIGHT variable multiplies the contribution to the log likelihood for each observation.

Details: LIFEREG Procedure

Missing Values

Any observation with missing values for the dependent variable is not used in the model estimation unless it is one and only one of the values in an interval specification. Also, if one of the explanatory variables or the censoring variable is missing, the observation is not used. For any observation to be used in the estimation of a model, only the variables needed in that model have to be nonmissing. Predicted values are computed for all observations with no missing explanatory variable values. If the censoring variable is missing, the CENSORED= variable in the OUT= SAS data set is also missing.

Model Specification

Main effects as well as interaction terms are allowed in the model specification, similar to the GLM procedure. For numeric variables, a main effect is a linear term equal to the value of the variable unless the variable appears in the CLASS statement. For variables listed in the CLASS statement, PROC LIFEREG creates indicator variables (variables taking the values zero or one) for every level of the variable except the last level. If there is no intercept term, the first CLASS variable has indicator variables created for all levels including the last level. The levels are ordered according to the ORDER= option. Estimates of a main effect depend upon other effects in the model and, therefore, are adjusted for the presence of other effects in the model.

Computational Method

By default, the LIFEREG procedure computes initial values for the parameters by using ordinary least squares (OLS) and ignoring censoring. This might not be the best set of starting values for a given set of data. For example, if there are extreme values in your data, the OLS fit might be excessively influenced by the extreme observations, causing an overflow or convergence problems. See Example 75.3 for one way to deal with convergence problems.

You can specify the INITIAL= option in the MODEL statement to override these starting values. You can also specify the INTERCEPT=, SCALE=, and SHAPE= options to set initial values of the intercept, scale, and shape parameters. For models with multilevel interaction effects, it is a little difficult to use the INITIAL= option to provide starting values for all parameters. In this case, you can use the INEST= data set. See the section "INEST= Data Set" on page 5557 for details. The INEST= data set overrides all previous specifications for starting values of parameters.

The rank of the design matrix $\mathbf{X}$ is estimated before the model is fit. Columns of $\mathbf{X}$ that are judged linearly dependent on other columns have the corresponding parameters set to zero. The test for linear dependence is controlled by the SINGULAR= option in the MODEL statement. Variables are included in the model in the order in which they are listed in the MODEL statement with the continuous variables included in the model before any classification variables.

The log-likelihood function is maximized by means of a ridge-stabilized Newton-Raphson algorithm. The maximized value of the log likelihood can take positive or negative values, depending on the specified model and the values of the maximum likelihood estimates of the model parameters.

If convergence of the maximum likelihood estimates is attained, a Type III chi-square test statistic is computed for each effect, testing whether there is any contribution from any of the levels of the effect. This statistic is computed as a quadratic form in the appropriate parameter estimates by using the corresponding submatrix of the asymptotic covariance matrix estimate. See Chapter 52, "The GLM Procedure," and Chapter 15, "The Four Types of Estimable Functions," for more information about Type III estimable functions. The asymptotic covariance matrix is computed as the inverse of the observed information matrix. Note that if the NOINT option is specified and CLASS variables are used, the first CLASS variable contains a contribution from an intercept term. The results are displayed in an ODS table named "Type3Analysis." Chi-square tests for individual parameters are Wald tests based on the observed information matrix and the parameter estimates. If an effect has a single degree of freedom in the parameter estimates table, the chi-square test for this parameter is equivalent to the Type III test for this effect.

Before SAS 8.2, a multiple-degree-of-freedom statistic was computed for each effect to test for contribution from any level of the effect. In general, the Type III test statistic in a main-effect-only model (no interaction terms) will be equal to the previously computed effect statistic, unless there are collinearities among the effects. If there are collinearities, the Type III statistic will adjust for them, and the value of the Type III statistic and the number of degrees of freedom might not be equal to those of the previous effect statistic.

Suppose there are n observations from the model $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \sigma\boldsymbol{\epsilon}$ (or $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{O} + \sigma\boldsymbol{\epsilon}$ if there is an offset variable), where $\mathbf{X}$ is an $n \times k$ matrix of covariate values (including the intercept), $\mathbf{y}$ is a vector of responses, $\mathbf{O}$ is a vector of offset variable values, and $\boldsymbol{\epsilon}$ is a vector of errors with survival function S, cumulative distribution function F, and probability density function f. That is, $S(t) = \Pr(\epsilon_i > t)$, $F(t) = \Pr(\epsilon_i \leq t)$, and $f(t) = dF(t)/dt$, where ϵ_i is a component of the error vector. Then, if all the responses are observed,

the log likelihood, L, can be written as

$$L = \sum \log\left(\frac{f(u_i)}{\sigma}\right)$$

where $u_i = \frac{1}{\sigma}(y_i - \mathbf{x}_i'\boldsymbol{\beta})$.

If some of the responses are left, right, or interval censored, the log likelihood can be written as

$$L = \sum \log\left(\frac{f(u_i)}{\sigma}\right) + \sum \log\left(S(u_i)\right) + \sum \log\left(F(u_i)\right) + \sum \log\left(F(u_i) - F(v_i)\right)$$

with the first sum over uncensored observations, the second sum over right-censored observations, the third sum over left-censored observations, the last sum over interval-censored observations, and

$$v_i = \frac{1}{\sigma}(z_i - \mathbf{x}_i'\boldsymbol{\beta})$$

where z_i is the lower end of a censoring interval.

If the response is specified in the binomial format, *events*/*trials*, then the log-likelihood function is

$$L = \sum r_i \log(P_i) + (n_i - r_i)\log(1 - P_i)$$

where r_i is the number of events and n_i is the number of trials for the ith observation. In this case, $P_i = 1 - F(-\mathbf{x}_i'\boldsymbol{\beta})$. For the symmetric distributions, logistic and normal, this is the same as $F(\mathbf{x}_i'\boldsymbol{\beta})$. Additional information about censored and limited dependent variable models can be found in Kalbfleisch and Prentice (1980) and Maddala (1983).

The estimated covariance matrix of the parameter estimates is computed as the negative inverse of $\mathbf{I}$, which is the information matrix of second derivatives of L with respect to the parameters evaluated at the final parameter estimates. If $\mathbf{I}$ is not positive definite, a positive-definite submatrix of $\mathbf{I}$ is inverted, and the remaining rows and columns of the inverse are set to zero. If some of the parameters, such as the scale and intercept, are restricted, the corresponding elements of the estimated covariance matrix are set to zero. The standard error estimates for the parameter estimates are taken as the square roots of the corresponding diagonal elements.

For restrictions placed on the intercept, scale, and shape parameters, one-degree-of-freedom Lagrange multiplier test statistics are computed. These statistics are computed as

$$\chi^2 = \frac{g^2}{V}$$

where g is the derivative of the log likelihood with respect to the restricted parameter at the restricted maximum and

$$V = \mathbf{I}_{11} - \mathbf{I}_{12}\mathbf{I}_{22}^{-1}\mathbf{I}_{21}$$

where the 1 subscripts refer to the restricted parameter and the 2 subscripts refer to the unrestricted parameters. The information matrix is evaluated at the restricted maximum. These statistics are asymptotically distributed as chi-squares with one degree of freedom under the null hypothesis that the restrictions are valid, provided that some regularity conditions are satisfied. See Rao (1973, p. 418) for a more complete discussion. It is possible for these statistics to be missing if the observed information matrix is not positive definite. Higher-degree-of-freedom tests for multiple restrictions are not currently computed.

A Lagrange multiplier test statistic is computed to test this constraint. Notice that this test statistic is comparable to the Wald test statistic for testing that the scale is one. The Wald statistic is the result of squaring the difference of the estimate of the scale parameter from one and dividing this by the square of its estimated standard error.

Supported Distributions

For most distributions, the baseline survival function (S) and the probability density function(f) are listed for the additive random disturbance (y_0 or $\log(T_0)$) with location parameter μ and scale parameter σ. See the section "Overview: LIFEREG Procedure" on page 5498 for more information. These distributions apply when the log of the response is modeled (this is the default analysis). The corresponding survival function (G) and its density function (g) are given for the untransformed baseline distribution (T_0).

For the normal and logistic distributions, the response is not log transformed by PROC LIFEREG, and the survival functions and probability density functions listed apply to the untransformed response.

For example, for the WEIBULL distribution, $S(w)$ and $f(w)$ are the survival function and the probability density function for the extreme-value distribution (distribution of the log of the response), while $G(t)$ and $g(t)$ are the survival function and the probability density function of a Weibull distribution (using the untransformed response).

The chosen baseline functions define the meaning of the intercept, scale, and shape parameters. Only the gamma distribution has a free shape parameter in the following parameterizations. Notice that some of the distributions do not have mean zero and that σ is not, in general, the standard deviation of the baseline distribution.

For the Weibull distribution, the accelerated failure time model is also a proportional-hazards model. However, the parameterization for the covariates differs by a multiple of the scale parameter from the parameterization commonly used for the proportional hazards model.

The distributions supported in the LIFEREG procedure follow. If there are no covariates in the model, μ = Intercept in the output; otherwise, $\mu = \mathbf{x}'\boldsymbol{\beta}$. σ = Scale in the output.

Exponential

$$
\begin{aligned}
S(w) &= \exp(-\exp(w-\mu)) \\
f(w) &= \exp(w-\mu)\exp(-\exp(w-\mu)) \\
G(t) &= \exp(-\alpha t) \\
g(t) &= \alpha \exp(-\alpha t)
\end{aligned}
$$

where $\exp(-\mu) = \alpha$.

Generalized Gamma

$S(w) = S'(u)$, $f(w) = \sigma^{-1} f'(u)$, $G(t) = G'(v)$, $g(t) = \frac{v}{t\sigma} g'(v)$, $u = \frac{w-\mu}{\sigma}$, $v = \exp(\frac{\log(t)-\mu}{\sigma})$, and

$$
\begin{aligned}
S'(u) &= \begin{cases} 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2}\exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ \frac{\Gamma(\delta^{-2}, \delta^{-2}\exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases} \\
f'(u) &= \frac{|\delta|}{\Gamma\left(\delta^{-2}\right)} \left(\delta^{-2}\exp(\delta u)\right)^{\delta^{-2}} \exp\left(-\exp(\delta u)\delta^{-2}\right) \\
G'(v) &= \begin{cases} 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2} v^{\delta})}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ \frac{\Gamma(\delta^{-2}, \delta^{-2} v^{\delta})}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases} \\
g'(v) &= \frac{|\delta|}{v\Gamma\left(\delta^{-2}\right)} \left(\delta^{-2} v^{\delta}\right)^{\delta^{-2}} \exp\left(-v^{\delta}\delta^{-2}\right)
\end{aligned}
$$

where $\Gamma(a)$ denotes the complete gamma function, $\Gamma(a, z)$ denotes the incomplete gamma function, and δ is a free shape parameter. The δ parameter is called Shape by PROC LIFEREG. See Lawless (2003, p. 240), and Klein and Moeschberger (1997, p. 386) for a description of the generalized gamma distribution.

Logistic

$$
\begin{aligned}
S(w) &= \left(1 + \exp\left(\frac{w-\mu}{\sigma}\right)\right)^{-1} \\
f(w) &= \frac{\exp\left(\frac{w-\mu}{\sigma}\right)}{\sigma\left(1 + \exp\left(\frac{w-\mu}{\sigma}\right)\right)^2}
\end{aligned}
$$

Log-Logistic

$$
\begin{aligned}
S(w) &= \left(1 + \exp\left(\frac{w-\mu}{\sigma}\right)\right)^{-1} \\
f(w) &= \frac{\exp\left(\frac{w-\mu}{\sigma}\right)}{\sigma\left(1 + \exp\left(\frac{w-\mu}{\sigma}\right)\right)^2} \\
G(t) &= \frac{1}{1 + \alpha t^{\gamma}} \\
g(t) &= \frac{\alpha\gamma t^{\gamma-1}}{(1 + \alpha t^{\gamma})^2}
\end{aligned}
$$

where $\gamma = 1/\sigma$ and $\alpha = \exp(-\mu/\sigma)$.

Lognormal

$$
\begin{aligned}
S(w) &= 1 - \Phi\left(\frac{w-\mu}{\sigma}\right) \\
f(w) &= \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2}\left(\frac{w-\mu}{\sigma}\right)^2\right) \\
G(t) &= 1 - \Phi\left(\frac{\log(t)-\mu}{\sigma}\right) \\
g(t) &= \frac{1}{\sqrt{2\pi}\sigma t} \exp\left(-\frac{1}{2}\left(\frac{\log(t)-\mu}{\sigma}\right)^2\right)
\end{aligned}
$$

where Φ is the cumulative distribution function for the normal distribution.

Normal

$$
\begin{aligned}
S(w) &= 1 - \Phi\left(\frac{w-\mu}{\sigma}\right) \\
f(w) &= \frac{1}{\sqrt{2\pi}\sigma} \exp\left(-\frac{1}{2}\left(\frac{w-\mu}{\sigma}\right)^2\right)
\end{aligned}
$$

where Φ is the cumulative distribution function for the normal distribution.

Weibull

$$
\begin{aligned}
S(w) &= \exp\left(-\exp\left(\frac{w-\mu}{\sigma}\right)\right) \\
f(w) &= \frac{1}{\sigma} \exp\left(\frac{w-\mu}{\sigma}\right) \exp\left(-\exp\left(\frac{w-\mu}{\sigma}\right)\right) \\
G(t) &= \exp\left(-\alpha t^{\gamma}\right) \\
g(t) &= \gamma\alpha t^{\gamma-1} \exp\left(-\alpha t^{\gamma}\right)
\end{aligned}
$$

where $\sigma = 1/\gamma$ and $\alpha = \exp(-\mu/\sigma)$.

If your parameterization is different from the ones shown here, you can still use the procedure to fit your model. For example, a common parameterization for the Weibull distribution is

$$g(t;\lambda,\beta) = \left(\frac{\beta}{\lambda}\right)\left(\frac{t}{\lambda}\right)^{\beta-1}\exp\left(-\left(\frac{t}{\lambda}\right)^{\beta}\right)$$

$$G(t;\lambda,\beta) = \exp\left(-\left(\frac{t}{\lambda}\right)^{\beta}\right)$$

so that $\lambda = \exp(\mu)$ and $\beta = 1/\sigma$.

Again note that the expected value of the baseline log response is, in general, not zero and that the distributions are not symmetric in all cases. Thus, for a given set of covariates, $\mathbf{x}$, the expected value of the log response is not always $\mathbf{x}'\boldsymbol{\beta}$.

Some relations among the distributions are as follows:

- The gamma with Shape=1 is a Weibull distribution.
- The gamma with Shape=0 is a lognormal distribution.
- The Weibull with Scale=1 is an exponential distribution.

Predicted Values

For a given set of covariates, $\mathbf{x}$ (including the intercept term), the pth quantile of the log response, y_p, is given by

$$y_p = \mathbf{x}'\boldsymbol{\beta} + \sigma u_p$$

if no offset variable has been specified, or

$$y_p = \mathbf{x}'\boldsymbol{\beta} + \mathrm{o} + \sigma u_p$$

for a given value o of an offset variable, where u_p is the pth quantile of the baseline distribution. The estimated quantile is computed by replacing the unknown parameters with their estimates, including any shape parameters on which the baseline distribution might depend. The estimated quantile of the original response is obtained by taking the exponential of the estimated log quantile unless the NOLOG option is specified in the preceding MODEL statement.

The following table shows how u_p is computed from the baseline distribution $F(u)$:

Table 75.11 Baseline Probability Functions and u_p

Distribution	$F(u)$		u_p
Exponential	$1 - \exp(-\exp(u))$		$\log(-\log(1-p))$
Generalized gamma	$\begin{cases} \frac{\Gamma(\delta^{-2}, \delta^{-2}\exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta > 0 \\ 1 - \frac{\Gamma(\delta^{-2}, \delta^{-2}\exp(\delta u))}{\Gamma(\delta^{-2})} & \text{if } \delta < 0 \end{cases}$		$F^{-1}(p)$
Logistic	$1 - (1 + \exp(u))^{-1}$		$\log(p/(1-p))$
Log-logistic	$1 - (1 + \exp(u))^{-1}$		$\log(p/(1-p))$
Lognormal	$\Phi(u)$		$\Phi^{-1}(p)$
Normal	$\Phi(u)$		$\Phi^{-1}(p)$
Weibull	$1 - \exp(-\exp(u))$		$\log(-\log(1-p))$

For the generalized gamma distribution, u_p is computed numerically.

The standard errors of the quantile estimates are computed using the estimated covariance matrix of the parameter estimates and a Taylor series expansion of the quantile estimate. The standard error is computed as

$$\text{STD} = \sqrt{\mathbf{z}'\mathbf{V}\mathbf{z}}$$

where $\mathbf{V}$ is the estimated covariance matrix of the parameter vector $(\boldsymbol{\beta}', \sigma, \delta)'$, and $\mathbf{z}$ is the vector

$$\mathbf{z} = \begin{bmatrix} \mathbf{x} \\ \hat{u}_p \\ \hat{\sigma}\frac{\partial u_p}{\partial \delta} \end{bmatrix}$$

where δ is the vector of the shape parameters. Unless the NOLOG option is specified, this standard error estimate is converted into a standard error estimate for $\exp(y_p)$ as $\exp(\hat{y}_p)$STD. It might be more desirable to compute confidence limits for the log response and convert them back to the original response variable than to use the standard error estimates for $\exp(y_p)$ directly. See Example 75.1 for a 90% confidence interval of the response constructed by exponentiating a confidence interval for the log response.

The variable CDF is computed as

$$\text{CDF}_i = F(u_i)$$

where the residual is defined by

$$u_i = \left(\frac{y_i - \mathbf{x}_i'\mathbf{b}}{\hat{\sigma}}\right)$$

and F is the baseline cumulative distribution function. If the data are interval-censored, then the cumulative distribution function, $\text{CDF}_i = F(u_i)$, is evaluated at the lower interval endpoint.

Confidence Intervals

Confidence intervals are computed for all model parameters and are reported in the "Analysis of Parameter Estimates" table. The confidence coefficient can be specified with the ALPHA=α MODEL statement option, resulting in a $(1-\alpha)\times 100\%$ two-sided confidence coefficient. The default confidence coefficient is 95%, corresponding to $\alpha = 0.05$.

Regression Parameters

A two-sided $(1-\alpha)\times 100\%$ confidence interval $[\beta_{iL},\ \ \beta_{iU}]$ for the regression parameter β_i is based on the asymptotic normality of the maximum likelihood estimator $\hat{\beta}_i$ and is computed by

$$\beta_{iL} = \hat{\beta}_i - z_{1-\alpha/2}(\mathrm{SE}_{\hat{\beta}_i})$$
$$\beta_{iU} = \hat{\beta}_i + z_{1-\alpha/2}(\mathrm{SE}_{\hat{\beta}_i})$$

where $\mathrm{SE}_{\hat{\beta}_i}$ is the estimated standard error of $\hat{\beta}_i$, and z_p is the $p\times 100$ percentile of the standard normal distribution.

Scale Parameter

A two-sided $(1-\alpha)\times 100\%$ confidence interval $[\sigma_L,\ \ \sigma_U]$ for the scale parameter σ in the location-scale model is based on the asymptotic normality of the logarithm of the maximum likelihood estimator $\log(\hat{\sigma})$, and is computed by

$$\sigma_L = \hat{\sigma}/\exp[z_{1-\alpha/2}(\mathrm{SE}_{\hat{\sigma}})/\hat{\sigma}]$$
$$\sigma_U = \hat{\sigma}\exp[z_{1-\alpha/2}(\mathrm{SE}_{\hat{\sigma}})/\hat{\sigma}]$$

See Meeker and Escobar (1998) for more information.

Weibull Scale and Shape Parameters

The Weibull distribution scale parameter η and shape parameter β are obtained by transforming the extreme-value location parameter μ and scale parameter σ:

$$\eta = \exp(\mu)$$
$$\beta = 1/\sigma$$

Consequently, two-sided $(1-\alpha)\times 100\%$ confidence intervals for the Weibull scale and shape parameters are computed as

$$[\eta_L,\ \ \eta_U] = [\exp(\mu_L),\ \ \exp(\mu_U)]$$
$$[\beta_L,\ \ \beta_U] = [1/\sigma_U,\ \ 1/\sigma_L]$$

Gamma Shape Parameter

A two-sided $(1-\alpha)\times 100\%$ confidence interval for the three-parameter gamma shape parameter δ is computed by

$$[\delta_L,\ \ \delta_U] = [\hat{\delta} - z_{1-\alpha/2}(\mathrm{SE}_{\hat{\delta}}),\ \ \hat{\delta} + z_{1-\alpha/2}(\mathrm{SE}_{\hat{\delta}})]$$

Fit Statistics

Suppose that the model contains p parameters and that n observations are used in model fitting. The fit criteria displayed by the LIFEREG procedure are calculated as follows:

- –2 log likelihood:

  $$-2\log(\mathrm{L})$$

  where L is the maximized likelihood for the model.

- Akaike's information criterion:

  $$\mathrm{AIC} = -2\log(\mathrm{L}) + 2p$$

- corrected Akaike's information criterion:

  $$\mathrm{AICC} = \mathrm{AIC} + \frac{2p(p+1)}{n-p-1}$$

- Bayesian information criterion:

  $$\mathrm{BIC} = -2\log(\mathrm{L}) + p\log(n)$$

If you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, then maximum likelihood estimates of model parameters are computed by maximizing the log likelihood of the distribution of the logarithm of the response. This is equivalent to computing maximum likelihood parameter estimates based on the response on the original, rather than log, scale. If you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, then fit statistics based on the maximized log likelihood $\log(\mathrm{L})$ of the log of the response are reported in the "Fit Statistics" table. Fit criteria computed in this way cannot be meaningfully compared with fit criteria that are based on the log likelihood of the unlogged response. If you specify the normal or logistic distribution, or if you specify the NOLOG option in the MODEL statement, then the fit criteria reported in the "Fit Statistics" table are based on the response on the original, rather than log, scale.

In addition to the "Fit Statistics" table described previously, if you specify the Weibull, exponential, lognormal, log-logistic, or gamma distribution, fit criteria that are based on the distribution of the response on the original scale, rather than the log of the response, are reported in the "Fit Statistics (Unlogged Response)" table.

When comparing models, you should compare fit criteria based on the log likelihood that is computed by using the response on the same scale, either always based on the log of the response or always based on the response on the original scale.

See Akaike (1981, 1979) for details of AIC and BIC. See Simonoff (2003) for a discussion of using AIC, AICC, and BIC in statistical modeling.

Probability Plotting

Probability plots are useful tools for the display and analysis of lifetime data. Probability plots use an inverse distribution scale so that a cumulative distribution function (CDF) plots as a straight line. A nonparametric estimate of the CDF of the lifetime data will plot approximately as a straight line, thus providing a visual assessment of goodness of fit.

You can use the PROBPLOT statement in PROC LIFEREG to create probability plots of data that are complete, right censored, interval censored, or a combination of censoring types (arbitrarily censored). A line representing the maximum likelihood fit from the MODEL statement and pointwise parametric confidence bands for the cumulative probabilities are also included in the plot.

A random variable Y belongs to a *location-scale* family of distributions if its CDF F is of the form

$$\Pr\{Y \leq y\} = F(y) = G\left(\frac{y-\mu}{\sigma}\right)$$

where μ is the location parameter and σ is the scale parameter. Here, G is a CDF that cannot depend on any unknown parameters, and G is the CDF of Y if $\mu = 0$ and $\sigma = 1$. For example, if Y is a normal random variable with mean μ and standard deviation σ,

$$G(u) = \Phi(u) = \int_{-\infty}^{u} \frac{1}{\sqrt{2\pi}} \exp\left(-\frac{u^2}{2}\right) du$$

and

$$F(y) = \Phi\left(\frac{y-\mu}{\sigma}\right)$$

The normal, extreme-value, and logistic distributions are location-scale models. The three-parameter gamma distribution is a location-scale model if the shape parameter δ is fixed. If T has a lognormal, Weibull, or log-logistic distribution, then $\log(T)$ has a distribution that is a location-scale model. These distributions are said to be of type log-location-scale. Probability plots are constructed for lognormal, Weibull, and log-logistic distributions by using $\log(T)$ instead of T in the plots.

Let $y_{(1)} \leq y_{(2)} \leq \ldots \leq y_{(n)}$ be ordered observations of a random sample with distribution function $F(y)$. A probability plot is a plot of the points $y_{(i)}$ against $m_i = G^{-1}(a_i)$, where $a_i = \hat{F}(y_i)$ is an estimate of the CDF $F(y_{(i)}) = G\left(\frac{y_{(i)}-\mu}{\sigma}\right)$. The nonparametric CDF estimates a_i are sometimes called *plotting positions*. The axis on which the points m_i are plotted is usually labeled with a probability scale (the scale of a_i).

If F is one of the location-scale distributions, then y is the lifetime; otherwise, the log of the lifetime is used to transform the distribution to a location-scale model.

If the data actually have the stated distribution, then $\hat{F} \approx F$,

$$m_i = G^{-1}(\hat{F}(y_i)) \approx G^{-1}\left(G\left(\frac{y_{(i)}-\mu}{\sigma}\right)\right) = \frac{y_{(i)}-\mu}{\sigma}$$

and points $(y_{(i)}, m_i)$ should fall approximately in a straight line.

There are several ways to compute the nonparametric CDF estimates used in probability plots from lifetime data. These are discussed in the next two sections.

Complete and Right-Censored Data

The censoring times must be taken into account when you compute plotting positions for right-censored data. The modified Kaplan-Meier method described in the following section is the default method for computing nonparametric CDF estimates for display on probability plots. See Abernethy (1996), Meeker and Escobar (1998), and Nelson (1982) for discussions of the methods described in the following sections.

Expected Ranks, Kaplan-Meier, and Modified Kaplan-Meier Methods

Let $y_{(1)} \leq y_{(2)} \leq \ldots \leq y_{(n)}$ be ordered observations of a random sample including failure times and censor times. Order the data in increasing order. Label all the data with reverse ranks r_i, with $r_1 = n, \ldots, r_n = 1$. For the lifetime (not censoring time) corresponding to reverse rank r_i, compute the survival function estimate

$$S_i = \left[\frac{r_i}{r_i + 1}\right] S_{i-1}$$

with $S_0 = 1$. The expected rank plotting position is computed as $a_i = 1 - S_i$. The option PPOS=EXPRANK specifies the expected rank plotting position.

For the Kaplan-Meier method,

$$S_i = \left[\frac{r_i - 1}{r_i}\right] S_{i-1}$$

The Kaplan-Meier plotting position is then computed as $a'_i = 1 - S_i$. The option PPOS=KM specifies the Kaplan-Meier plotting position.

For the modified Kaplan-Meier method, use

$$S'_i = \frac{S_i + S_{i-1}}{2}$$

where S_i is computed from the Kaplan-Meier formula with $S_0 = 1$. The plotting position is then computed as $a''_i = 1 - S'_i$. The option PPOS=MKM specifies the modified Kaplan-Meier plotting position. If the PPOS option is not specified, the modified Kaplan-Meier plotting position is used as the default method.

For complete samples, $a_i = i/(n+1)$ for the expected rank method, $a'_i = i/n$ for the Kaplan-Meier method, and $a''_i = (i - 0.5)/n$ for the modified Kaplan-Meier method. If the largest observation is a failure for the Kaplan-Meier estimator, then $F_n = 1$ and the point is not plotted.

Median Ranks

Let $y_{(1)} \leq y_{(2)} \leq \ldots \leq y_{(n)}$ be ordered observations of a random sample including failure times and censor times. A failure order number j_i is assigned to the ith failure: $j_i = j_{i-1} + \Delta$, where $j_0 = 0$. The increment Δ is initially 1 and is modified when a censoring time is encountered in the ordered sample. The new increment is computed as

$$\Delta = \frac{(n+1) - \text{ previous failure order number}}{1 + \text{ number of items beyond previous censored item}}$$

The plotting position is computed for the ith failure time as

$$a_i = \frac{j_i - 0.3}{n + 0.4}$$

For complete samples, the failure order number j_i is equal to i, the order of the failure in the sample. In this case, the preceding equation for a_i is an approximation of the median plotting position computed as the median of the ith-order statistic from the uniform distribution on (0, 1). In the censored case, j_i is not necessarily an integer, but the preceding equation still provides an approximation to the median plotting position. The PPOS=MEDRANK option specifies the median rank plotting position.

Arbitrarily Censored Data

The LIFEREG procedure can create probability plots for data that consist of combinations of exact, left-censored, right-censored, and interval-censored lifetimes—that is, arbitrarily censored data. The LIFEREG procedure uses an iterative algorithm developed by Turnbull (1976) to compute a nonparametric maximum likelihood estimate of the cumulative distribution function for the data. Since the technique is maximum likelihood, standard errors of the cumulative probability estimates are computed from the inverse of the associated Fisher information matrix. This algorithm is an example of the expectation-maximization (EM) algorithm. The default initial estimate assigns equal probabilities to each interval. You can specify different initial values with the PROBLIST= option. Convergence is determined if the change in the log likelihood between two successive iterations is less than delta, where the default value of delta is 10^{-8}. You can specify a different value for delta with the TOLLIKE= option. Iterations will be terminated if the algorithm does not converge after a fixed number of iterations. The default maximum number of iterations is 1000. Some data might require more iterations for convergence. You can specify the maximum allowed number of iterations with the MAXITEM= option in the PROBPLOT statement. The iteration history of the log likelihood is displayed if you specify the ITPRINTEM option. The iteration history of the estimated interval probabilities are also displayed if you specify both options ITPRINTEM and PRINTPROBS.

If an interval probability is smaller than a tolerance (10^{-6} by default) after convergence, the probability is set to zero, the interval probabilities are renormalized so that they add to one, and iterations are restarted. Usually the algorithm converges in just a few more iterations. You can change the default value of the tolerance with the TOLPROB= option. You can specify the NOPOLISH option to avoid setting small probabilities to zero and restarting the algorithm.

If you specify the ITPRINTEM option, a table summarizing the Turnbull estimate of the interval probabilities is displayed. The columns labeled "Reduced Gradient" and "Lagrange Multiplier" are used in checking final convergence of the maximum likelihood estimate. The Lagrange multipliers must all be greater than or equal to zero, or the solution is not maximum likelihood. See Gentleman and Geyer (1994) for more details of the convergence checking. Also see Meeker and Escobar (1998, Chapter 3) for more information.

See Example 75.6 for an illustration.

Nonparametric Confidence Intervals

You can use the PPOUT option in the PROBPLOT statement to create a table containing the nonparametric CDF estimates computed by the selected method, Kaplan-Meier CDF estimates, standard errors of the Kaplan-Meier estimator, and nonparametric confidence limits for the CDF. The confidence limits are either pointwise or simultaneous, depending on the value of the NPINTERVALS= option in the PROBPLOT statement. The method used in the LIFEREG procedure for computation of approximate pointwise and simultaneous confidence intervals for cumulative failure probabilities relies on the Kaplan-Meier estimator of the cumulative distribution function of failure time and approximate standard deviation of the Kaplan-Meier estimator. For the case of arbitrarily censored data, the Turnbull algorithm, discussed previously, provides an extension of the Kaplan-Meier estimator. Both the Kaplan-Meier and the Turnbull estimators provide an estimate of the standard error of the CDF estimator, $\mathrm{se}_{\hat{F}}$, that is used in computing confidence intervals.

Pointwise Confidence Intervals

Approximate $(1-\alpha)100\%$ pointwise confidence intervals are computed as in Meeker and Escobar (1998, Section 3.6) as

$$[F_L,\ \ F_U] = \left[\frac{\hat{F}}{\hat{F}+(1-\hat{F})w},\ \ \frac{\hat{F}}{\hat{F}+(1-\hat{F})/w}\right]$$

where

$$w = \exp\left[\frac{z_{1-\alpha/2}\mathrm{se}_{\hat{F}}}{(\hat{F}(1-\hat{F}))}\right]$$

where z_p is the pth quantile of the standard normal distribution.

Simultaneous Confidence Intervals

Approximate $(1-\alpha)100\%$ simultaneous confidence bands valid over the lifetime interval (t_a, t_b) are computed as the "Equal Precision" case of Nair (1984) and Meeker and Escobar (1998, Section 3.8) as

$$[F_L,\ \ F_U] = \left[\frac{\hat{F}}{\hat{F}+(1-\hat{F})w},\ \ \frac{\hat{F}}{\hat{F}+(1-\hat{F})/w}\right]$$

where

$$w = \exp\left[\frac{e_{a,b,1-\alpha/2}\mathrm{se}_{\hat{F}}}{(\hat{F}(1-\hat{F}))}\right]$$

where the factor $x = e_{a,b,1-\alpha/2}$ is the solution of

$$x\exp(-x^2/2)\log\left[\frac{(1-a)b}{(1-b)a}\right]/\sqrt{8\pi} = \alpha/2$$

The time interval (t_a, t_b) over which the bands are valid depends in a complicated way on the constants a and b defined in Nair (1984), $0 < a < b < 1$. The constants a and b are chosen by default so that the confidence bands are valid between the lowest and highest times corresponding to failures in the case of multiply censored data, or to the lowest and highest intervals for which probabilities are computed for arbitrarily censored data. You can optionally specify a and b directly with the NPINTERVALS=SIMULTANEOUS(a, b) option in the PROBPLOT statement.

Parametric Confidence Intervals

Pointwise parametric confidence bands are displayed in a probability plot, unless you specify the NOCONF option in the PROBPLOT statement. Two kinds of confidence intervals are available for display in a probability plot: confidence limits for the estimated cumulative distribution function (CDF) and confidence limits for estimated distribution percentiles.

Confidence Limits for the Estimated CDF

If the distribution is of type log-location-scale, let $y = \log(t)$ where t is the value of time at which the confidence limits are to be computed. If the distribution is of type location-scale, let y be the value at which you want to evaluate confidence limits for the estimated CDF $\hat{F}(y)$. Let

$$\hat{u} = \frac{\mathbf{y} - \mathbf{x}'\hat{\boldsymbol{\beta}}}{\hat{\sigma}}$$

where the column vector $\mathbf{x}$ of covariate values is determined by the rules summarized in the section "XDATA= Data Set" on page 5558. If an offset variable is specified, the mean of the offset variable values is included in $\mathbf{x}'\boldsymbol{\beta}$.

The CDF estimate is given by

$$\hat{F}(y) = G(\hat{u})$$

where G is the baseline distribution. The approximate standard error of $\hat{F}(y)$ is computed as in Meeker and Escobar (1998, Section 8.4.3) as

$$\mathrm{SE}_{\hat{F}} = \frac{g(\hat{u})}{\hat{\sigma}}\left[\mathrm{Var}(\mathbf{x}'\hat{\boldsymbol{\beta}}) + 2\hat{u}\mathrm{Cov}(\mathbf{x}'\hat{\boldsymbol{\beta}}, \hat{\sigma}) + \hat{u}^2\mathrm{Var}(\hat{\sigma})\right]^{\frac{1}{2}}$$

where g is the probability density function corresponding to G. Two-sided $(1-\alpha)\times 100\%$ confidence limits are given by

$$[F_L,\ \ F_U] = \left[\frac{\hat{F}}{\hat{F} + (1-\hat{F})\times w},\ \ \frac{\hat{F}}{\hat{F} + (1-\hat{F})/w}\right]$$

where

$$w = \exp\left[\frac{z_{1-\alpha/2}\mathrm{SE}_{\hat{F}}}{\hat{F}(1-\hat{F})}\right]$$

and z_p is the $p \times 100$ percentile of the standard normal distribution. The quantities $\mathrm{Var}(\mathbf{x}'\hat{\boldsymbol{\beta}})$, $\mathrm{Cov}(\mathbf{x}'\hat{\boldsymbol{\beta}}, \hat{\sigma})$, and $\mathrm{Var}(\hat{\sigma})$ are computed based on the covariance matrix of the estimated parameter vector $(\hat{\boldsymbol{\beta}}, \hat{\sigma})$.

Confidence Limits for Percentiles

If the HCL option is specified in the PROBPLOT statement, confidence limits based on estimated distribution percentiles instead of the default CDF limits are displayed in the probability plot.

For location-scale distributions, the estimated $p \times 100$ percentile of the distribution F is given by

$$y_p = \mathbf{x}'\hat{\boldsymbol{\beta}} + G^{-1}(p)\hat{\sigma}$$

where G is the baseline distribution and the column vector $\mathbf{x}$ of covariate values is determined by the rules summarized in the section "XDATA= Data Set" on page 5558. The standard error of y_p is estimated by

$\mathrm{SE}_y = z'\Sigma z$ where $\mathbf{z} = (\mathbf{x}', G^{-1}(p))'$ and Σ is the covariance matrix of the parameter estimates $(\hat{\boldsymbol{\beta}}', \hat{\sigma})'$. Two-sided $(1-\alpha)\times 100\%$ confidence limits for y_p are given by

$$[y_L,\ \ y_U] = [y_p - z_{1-\alpha/2}\mathrm{SE}_y,\ \ y_p + z_{1-\alpha/2}\mathrm{SE}_y]$$

For distributions of type log-location-scale, the confidence limits are computed as

$$[t_L = \exp(y_L),\ \ t_U = \exp(y_U)]$$

For example, if T has the Weibull distribution, G is the standardized extreme value distribution, $[y_L,\ \ y_U]$ are confidence limits for the $p\times 100$ percentile of the extreme value distribution for $\log(T)$, and $[t_L = \exp(y_L),\ \ t_U = \exp(y_U)]$ are confidence limits for the $p\times 100$ percentile of the Weibull distribution for T.

INEST= Data Set

If specified, the INEST= data set specifies initial estimates for all the parameters in the model. The INEST= data set must contain the intercept variable (named Intercept) and all independent variables in the MODEL statement.

If BY processing is used, the INEST= data set should also include the BY variables, and there must be at least one observation for each BY group. If there is more than one observation in one BY group, the first observation read is used for that BY group.

If the INEST= data set also contains the _TYPE_ variable, only observations with _TYPE_ value 'PARMS' are used as starting values. Combining the INEST= data set and the MAXITER= option in the MODEL statement, partial scoring can be done, such as predicting on a validation data set by using the model built from a training data set.

You can specify starting values for the iterative algorithm in the INEST= data set. This data set overwrites the INITIAL= option in the MODEL statement, which is a little difficult to use for models including multilevel interaction effects. The INEST= data set has the same structure as the OUTEST= data set but is not required to have all the variables or observations that appear in the OUTEST= data set. One simple use of the INEST= option is passing the previous OUTEST= data set directly to the next model as an INEST= data set, assuming that the two models have the same parameterization. See Example 75.3 for an illustration.

OUTEST= Data Set

The OUTEST= data set contains parameter estimates and the log likelihood for the model. You can specify a label in the MODEL statement to distinguish between the estimates for different models fit with the LIFEREG procedure. If the COVOUT option is specified, the OUTEST= data set also contains the estimated covariance matrix of the parameter estimates. Note that, if the LIFEREG procedure does not converge, the parameter estimates are set to missing in the OUTEST data set.

The OUTEST= data set contains all variables specified in the MODEL statement and the BY statement. One observation consists of parameter values for the model with the dependent variable having the value –1. If the COVOUT option is specified, there are additional observations containing the rows of the estimated covariance matrix. For these observations, the dependent variable contains the parameter estimate for the corresponding row variable. The following variables are also added to the data set:

MODEL	a character variable containing the label of the MODEL statement, if present. Otherwise, the variable's value is blank.
NAME	a character variable containing the name of the dependent variable for the parameter estimates observations or the name of the row for the covariance matrix estimates
TYPE	a character variable containing the type of the observation, either PARMS for parameter estimates or COV for covariance estimates
DIST	a character variable containing the name of the distribution modeled
LNLIKE	a numeric variable containing the last computed value of the log likelihood
INTERCEPT	a numeric variable containing the intercept parameter estimates and covariances
SCALE	a numeric variable containing the scale parameter estimates and covariances
SHAPE1	a numeric variable containing the first shape parameter estimates and covariances if the specified distribution has additional shape parameters

Any BY variables specified are also added to the OUTEST= data set.

XDATA= Data Set

The XDATA= data set is used for plotting the predicted probability when there are covariates specified in a MODEL statement and a probability plot is specified with a PROBPLOT statement. See Example 75.4 for an illustration.

The XDATA= data set is an input SAS data set that contains values for all the independent variables in the MODEL statement and variables in the CLASS statement. The XDATA= data set has the same structure as the DATA= data set but is not required to have all the variables or observations that appear in the DATA= data set.

The XDATA= data set must contain all the independent variables in the MODEL statement and variables in the CLASS statement. Even though variables in the CLASS statement might not be used, valid values are required for these variables in the XDATA= data set. Missing values are not allowed. Missing values are not allowed in the XDATA= data set for any of the independent variables, either. Missing values are allowed for the dependent variables and other variables if they are included in the XDATA= data set.

If BY processing is used, the XDATA= data set should also include the BY variables, and there must be at least one valid observation for each BY group. If there is more than one valid observation in a BY group, the last one read is used for that BY group.

If there is no XDATA= data set in the PROC LIFEREG statement, by default, the LIFEREG procedure will use the overall mean for effects containing a continuous variable (or variables) and the highest level of a single classification variable as reference level. The rules are summarized as follows:

- If the effect contains a continuous variable (or variables), the overall mean of this effect (not the variables) is used.
- If the effect is a single classification variable, the highest level of the variable is used.

Computational Resources

Let p be the number of parameters estimated in the model. The minimum working space (in bytes) needed is

$$16p^2 + 100p$$

However, if sufficient space is available, the input data set is also kept in memory; otherwise, the input data set is reread for each evaluation of the likelihood function and its derivatives, with the resulting execution time of the procedure substantially increased.

Let n be the number of observations used in the model estimation. Each evaluation of the likelihood function and its first and second derivatives requires $O(np^2)$ multiplications and additions, n individual function evaluations for the log density or log distribution function, and n evaluations of the first and second derivatives of the function. The calculation of each updating step from the gradient and Hessian requires $O(p^3)$ multiplications and additions. The $O(v)$ notation means that, for large values of the argument, v, $O(v)$ is approximately a constant times v.

Bayesian Analysis

Gibbs Sampling

This section provides details about Bayesian analysis by Gibbs sampling in the location-scale models for survival data available in PROC LIFEREG. See the section "Gibbs Sampler" on page 135 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for a general discussion of Gibbs sampling. PROC LIFEREG fits parametric location-scale survival models. That is, the probability density of the response Y can expressed in the general form

$$f(y) = g\left(\frac{y-\mu}{\sigma}\right)$$

where $Y = \log(T)$ for lifetimes T. The function g determines the specific distribution. The location parameter μ_i is modeled through regression parameters as $\mu_i = \mathbf{x}_i'\boldsymbol{\beta}$. The LIFEREG procedure can provide Bayesian estimates of the regression parameters and σ. The OUTPUT and PROBPLOT statements, if specified, are ignored. The PLOTS=PROBPLOT option in the PROC LIFEREG statement and the CORRB and COVB options in the MODEL statement are also ignored.

For the Weibull distribution, you can specify that Gibbs sampling be performed on the Weibull shape parameter $\beta = \sigma^{-1}$ instead of the scale parameter σ by specifying a prior distribution for the shape parameter with the WEIBULLSHAPEPRIOR= option. In addition, if there are no covariates in the model, you can specify Gibbs sampling on the Weibull scale parameter $\alpha = \exp(\mu)$, where μ is the intercept term, with the WEIBULLSCALEPRIOR= option.

In the case of the exponential distribution with no covariates, you can specify Gibbs sampling on the exponential scale parameter $\alpha = \exp(\mu)$, where μ is the intercept term, with the EXPSCALEPRIOR= option.

Let $\boldsymbol{\theta} = (\theta_1, \ldots, \theta_k)\prime$ be the parameter vector. For location-scale models, the θ_i's are the regression coefficients β_i's and the scale parameter σ. In the case of the three-parameter gamma distribution, there is an

additional gamma shape parameter τ. Let $L(D|\boldsymbol{\theta})$ be the likelihood function, where D is the observed data. Let $\pi(\boldsymbol{\theta})$ be the prior distribution. The full conditional distribution of $[\theta_i|\theta_j, i \neq j]$ is proportional to the joint distribution; that is,

$$\pi(\theta_i|\theta_j, i \neq j, D) \propto L(D|\boldsymbol{\theta})p(\boldsymbol{\theta})$$

For instance, the one-dimensional conditional distribution of θ_1 given $\theta_j = \theta_j^*, 2 \leq j \leq k$, is computed as

$$\pi(\theta_1|\theta_j = \theta_j^*, 2 \leq j \leq k, D) = L(D|(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \ldots, \theta_k^*)')p(\boldsymbol{\theta} = (\theta_1, \theta_2^*, \ldots, \theta_k^*)')$$

Suppose you have a set of arbitrary starting values $\{\theta_1^{(0)}, \ldots, \theta_k^{(0)}\}$. Using the ARMS (adaptive rejection Metropolis sampling) algorithm of Gilks and Wild (1992) and Gilks, Best, and Tan (1995), you can do the following:

draw $\theta_1^{(1)}$ from $[\theta_1|\theta_2^{(0)}, \ldots, \theta_k^{(0)}]$

draw $\theta_2^{(1)}$ from $[\theta_2|\theta_1^{(1)}, \theta_3^{(0)}, \ldots, \theta_k^{(0)}]$

...

draw $\theta_k^{(1)}$ from $[\theta_k|\theta_1^{(1)}, \ldots, \theta_{k-1}^{(1)}]$

This completes one iteration of the Gibbs sampler. After one iteration, you have $\{\theta_1^{(1)}, \ldots, \theta_k^{(1)}\}$. After n iterations, you have $\{\theta_1^{(n)}, \ldots, \theta_k^{(n)}\}$. PROC LIFEREG implements the ARMS algorithm based on a program provided by Gilks (2003) to draw a sample from a full conditional distribution. See the section "Assessing Markov Chain Convergence" on page 140 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for information about assessing the convergence of the chain of posterior samples.

You can output these posterior samples into a SAS data set. The following *option* in the BAYES statement outputs the posterior samples into the SAS data set Post: OUTPOST=Post. The data set also includes the variables LogPost and LogLike, which represent the log of the posterior distribution and the log of the likelihood, respectively.

Priors for Model Parameters

The model parameters are the regression coefficients and the dispersion parameter (or the precision or scale), if the model has one. The priors for the dispersion parameter and the priors for the regression coefficients are assumed to be independent, while you can have a joint multivariate normal prior for the regression coefficients.

Scale and Shape Parameters

Gamma Prior The gamma distribution $G(a, b)$ has a PDF

$$f_{a,b}(u) = \frac{b(bu)^{a-1}\mathrm{e}^{-bu}}{\Gamma(a)}, \qquad u > 0$$

where a is the shape parameter and b is the inverse-scale parameter. The mean is $\frac{a}{b}$ and the variance is $\frac{a}{b^2}$.

Improper Prior The joint prior density is given by

$$p(u) \propto u^{-1}, \qquad u > 0$$

Regression Coefficients

Let $\boldsymbol{\beta}$ be the regression coefficients.

Normal Prior Assume $\boldsymbol{\beta}$ has a multivariate normal prior with mean vector $\boldsymbol{\beta}_0$ and covariance matrix $\boldsymbol{\Sigma}_0$. The joint prior density is given by

$$p(\boldsymbol{\beta}) \propto \mathrm{e}^{-\frac{1}{2}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)'\boldsymbol{\Sigma}_0^{-1}(\boldsymbol{\beta}-\boldsymbol{\beta}_0)}$$

Uniform Prior The joint prior density is given by

$$p(\boldsymbol{\beta}) \propto 1$$

Posterior Distribution

Denote the observed data by D.

The posterior distribution is

$$\pi(\boldsymbol{\theta}|D) \propto L_P(D|\boldsymbol{\theta})p(\boldsymbol{\theta})$$

where $L_P(D|\boldsymbol{\theta})$ is the likelihood function with regression coefficients and any additional parameters, such as scale or shape, $\boldsymbol{\theta}$ as parameters; and $p(\boldsymbol{\theta})$ is the joint prior distribution of the parameters.

Deviance Information Criterion

Let $\boldsymbol{\theta}_i$ be the model parameters at iteration i of the Gibbs sampler, and let $\mathrm{LL}(\boldsymbol{\theta}_i)$ be the corresponding model log likelihood. PROC LIFEREG computes the following fit statistics defined by Spiegelhalter et al. (2002):

- effective number of parameters:

$$p_D = \overline{\mathrm{LL}(\boldsymbol{\theta})} - \mathrm{LL}(\bar{\boldsymbol{\theta}})$$

- deviance information criterion (DIC):

$$\mathrm{DIC} = \overline{\mathrm{LL}(\boldsymbol{\theta})} + p_D$$

where

$$\overline{\mathrm{LL}(\boldsymbol{\theta})} = \frac{1}{n}\sum_{i=1}^{n}\mathrm{LL}(\boldsymbol{\theta}_i)$$

$$\bar{\boldsymbol{\theta}} = \frac{1}{n}\sum_{i=1}^{n}\boldsymbol{\theta}_i$$

and n is the number of Gibbs samples.

Starting Values of the Markov Chains

When the BAYES statement is specified, PROC LIFEREG generates one Markov chain containing the approximate posterior samples of the model parameters. Additional chains are produced when the Gelman-Rubin diagnostics are requested. Starting values (or initial values) can be specified in the INITIAL= data set in the BAYES statement. If INITIAL= option is not specified, PROC LIFEREG picks its own initial values for the chains.

Denote $[x]$ as the integral value of x. Denote $\hat{s}(X)$ as the estimated standard error of the estimator X.

Regression Coefficients and Gamma Shape Parameter

For the first chain that the summary statistics and regression diagnostics are based on, the default initial values are estimates of the mode of the posterior distribution. If the INITIALMLE option is specified, the initial values are the maximum likelihood estimates; that is,

$$\beta_i^{(0)} = \hat{\beta}_i$$

Initial values for the rth chain ($r \geq 2$) are given by

$$\beta_i^{(0)} = \hat{\beta}_i \pm \left(2 + \left[\frac{r}{2}\right]\right)\hat{s}(\hat{\beta}_i)$$

with the plus sign for odd r and minus sign for even r.

Scale, Exponential Scale, Weibull Scale, or Weibull Shape Parameter λ

Let λ be the parameter sampled.

For the first chain that the summary statistics and diagnostics are based on, the initial values are estimates of the mode of the posterior distribution; or the maximum likelihood estimates if the INITIALMLE option is specified; that is,

$$\lambda^{(0)} = \hat{\lambda}$$

The initial values of the rth chain ($r \geq 2$) are given by

$$\lambda^{(0)} = \hat{\lambda}\mathrm{e}^{\pm\left([\frac{r}{2}]+2\right)\hat{s}(\hat{\lambda})}$$

with the plus sign for odd r and minus sign for even r.

OUTPOST= Output Data Set

The OUTPOST= data set contains the generated posterior samples. There are 2+n variables, where n is the number of model parameters. The variable Iteration represents the iteration number and the variable LogPost contains the log posterior likelihood values. The other n variables represent the draws of the Markov chain for the model parameters.

Displayed Output for Classical Analysis

For each model, PROC LIFEREG displays the following.

Model Information

The "Model Information" table displays the two-level name of the input data set, the distribution name, and the name and label of the dependent variable; the name and label of the censor indicator variable, for right-censored data; if you specify the WEIGHT statement, the name and label of the weight variable; and the maximum value of the log likelihood.

Number of Observations

The "Number of Observations" table displays the number of observations read from the input data set, and the number of observations used in the analysis.

Class Level Information

The "Class Level Information" table displays the levels of classification variables if you specify a CLASS statement.

Fit Statistics

The "Fit Statistics" table displays the negative of twice the log likelihood, Akaike's information criterion (AIC), the corrected Akaike's information criterion (AICC), and the Bayesian information criterion (BIC). If the specified distribution is Weibull, lognormal, log-logistic, or gamma, the fit criteria are based on the log likelihood for the log of the response, rather than for the response on the original scale.

Fit Statistics (Unlogged Response)

If the specified distribution is Weibull, lognormal, log-logistic, or gamma, the "Fit Statistics (Unlogged Response)" table displays fit criteria that are based on the log likelihood for the response on the original, rather than log, scale. The negative of twice the log likelihood, Akaike's information criterion (AIC), the corrected Akaike's information criterion (AICC), and the Bayesian information criterion (BIC) are displayed.

Type III Analysis of Effects

The "Type III Analysis of Effects" table displays, for each effect in the model, the effect name, the degrees of freedom associated with the type III contrast for the effect, the chi-square statistic for the contrast, and the *p*-value for the statistic.

Analysis of Maximum Likelihood Parameter Estimates

The "Analysis of Maximum Likelihood Parameter Estimates" table displays the parameter name, the degrees of freedom for each parameter, the maximum likelihood estimate of each parameter, the estimated standard error of the parameter estimator, confidence limits for each parameter, a chi-square statistic for testing whether the parameter is zero, and the associated *p*-value for the statistic.

Lagrange Multiplier Statistics

If there are constrained parameters in the model, such as the scale or intercept, then the "Lagrange Multiplier Statistics" table displays a Lagrange multiplier test for the constraint.

Displayed Output for Bayesian Analysis

If a Bayesian analysis is requested with a BAYES statement, the displayed output includes the following.

Model Information

The "Model Information" table displays the two-level name of the input data set, the number of burn-in iterations, the number of iterations after the burn-in, the number of thinning iterations, the distribution name, and the name and label of the dependent variable; the name and label of the censor indicator variable, for right-censored data; if you specify the WEIGHT statement, the name and label of the weight variable; and the maximum value of the log likelihood.

Class Level Information

The "Class Level Information" table displays the levels of classification variables if you specify a CLASS statement.

Maximum Likelihood Estimates

The "Analysis of Maximum Likelihood Parameter Estimates" table displays the maximum likelihood estimate of each parameter, the estimated standard error of the parameter estimator, and confidence limits for each parameter.

Coefficient Prior

The "Coefficient Prior" table displays the prior distribution of the regression coefficients.

Independent Prior Distributions for Model Parameters

The "Independent Prior Distributions for Model Parameters" table displays the prior distributions of additional model parameters (scale, exponential scale, Weibull scale, Weibull shape, gamma shape).

Initial Values and Seeds

The "Initial Values and Seeds" table displays the initial values and random number generator seeds for the Gibbs chains.

Fit Statistics

The "Fit Statistics" table displays the deviance information criterion (DIC) and the effective number of parameters.

Posterior Summaries

The "Posterior Summaries" table contains the size of the sample, the mean, the standard deviation, and the quartiles for each model parameter.

Posterior Intervals

The "Posterior Intervals" table contains the HPD intervals and the credible intervals for each model parameter.

Correlation Matrix of the Posterior Samples

The "Correlation Matrix of the Posterior Samples" table is produced if you include the CORR suboption in the SUMMARY= option in the BAYES statement. This table displays the sample correlation of the posterior samples.

Covariance Matrix of the Posterior Samples

The "Covariance Matrix of the Posterior Samples" table is produced if you include the COV suboption in the SUMMARY= option in the BAYES statement. This table displays the sample covariance of the posterior samples.

Autocorrelations of the Posterior Samples

The "Autocorrelations of the Posterior Samples" table displays the lag1, lag5, lag10, and lag50 autocorrelations for each parameter.

Gelman and Rubin Diagnostics

The "Gelman and Rubin Diagnostics" table is produced if you include the GELMAN suboption in the DIAGNOSTIC= option in the BAYES statement. This table displays the estimate of the potential scale reduction factor and its 97.5% upper confidence limit for each parameter.

Geweke Diagnostics

The "Geweke Diagnostics" table displays the Geweke statistic and its p-value for each parameter.

Raftery and Lewis Diagnostics

The "Raftery Diagnostics" tables is produced if you include the RAFTERY suboption in the DIAGNOSTIC= option in the BAYES statement. This table displays the Raftery and Lewis diagnostics for each variable.

Heidelberger and Welch Diagnostics

The "Heidelberger and Welch Diagnostics" table is displayed if you include the HEIDELBERGER suboption in the DIAGNOSTIC= option in the BAYES statement. This table shows the results of a stationary test and a halfwidth test for each parameter.

Effective Sample Size

The "Effective Sample Size" table displays, for each parameter, the effective sample size, the correlation time, and the efficiency.

Monte Carlo Standard Errors

The "Monte Carlo Standard Errors" table displays, for each parameter, the Monte Carlo standard error, the posterior sample standard deviation, and the ratio of the two.

Plot Options Superseded by ODS Graphics

You can select one of the following two types of graphics in PROC LIFEREG: ODS and traditional. ODS Graphics is the preferred method of creating graphs, superseding traditional graphs.

When ODS Graphics is enabled, you can use the PLOTS= option in the PROC LIFEREG statement to create plots by using ODS Graphics. For more information about ODS Graphics options, see the PLOTS= option. If ODS Graphics is not enabled, then traditional graphics are produced.

You can specify the following option in the PROC LIFEREG statement:

GOUT=*graphics-catalog*
specifies a graphics catalog in which to save traditional graphical output.

The following *options* control the appearance of the box in the INSET statement when you use traditional graphics. These *options* are not available if ODS Graphics is enabled. Table 75.12 summarizes the *options* available in the INSET statement.

Table 75.12 INSET Statement Options

Option	Description
CFILL=	Specifies the color for the filling box
CFILLH=	Specifies the color for the filling box header
CFRAME=	Specifies the color for the frame
CHEADER=	Specifies the color for text in the header
CTEXT=	Specifies the color for the text
FONT=	Specifies the software font for the text
HEADER=	Specifies the text for the header or box title
HEIGHT=	Specifies the height of the text
NOFRAME	Omits the frame around the box
POS=	Determines the position of the inset
REFPOINT=	Specifies the reference point for an inset

All *options* are specified after the slash (/) in the INSET statement.

CFILL=*color*
specifies the color for the filling box.

CFILLH=*color*
specifies the color for the filling box header.

CFRAME=*color*
specifies the color for the frame.

CHEADER=*color*
specifies the color for text in the header.

CTEXT=*color*
specifies the color for the text.

FONT=*font*
specifies the software font for the text.

HEADER=*'quoted string'*
specifies the text for the header or box title.

HEIGHT=*value*
specifies the height of the text.

NOFRAME
omits the frame around the box.

POS=*value* **< DATA | PERCENT >**
determines the position of the inset. The *value* can be a compass point (N, NE, E, SE, S, SW, W, NW) or a pair of coordinates (x, y) enclosed in parentheses. The coordinates can be specified in screen percentage units or axis data units. The default is screen percentage units.

REFPOINT=*name*
specifies the reference point for an inset that is positioned by a pair of coordinates with the POS= option. You use the REFPOINT= option in conjunction with the POS= coordinates. The REFPOINT= option specifies which corner of the inset frame you have specified with coordinates (x, y), and it can take the value of BR (bottom right), BL (bottom left), TR (top right), or TL (top left). The default is REFPOINT=BL. If the inset position is specified as a compass point, then the REFPOINT= option is ignored.

Table 75.13 summarizes the *options* available in the PROBPLOT statement for traditional graphics.

Table 75.13 PROBPLOT Statement Options

Option	Description
Traditional Graphics	
ANNOTATE=	Specifies an Annotate data set
CAXIS=	Specifies the color for the axes and tick marks
CCENSOR=	Specifies the color for filling the censor plot area

Table 75.13 *continued*

Option	Description
CENBIN	Plots censored data as frequency counts
CENCOLOR=	Specifies the color for the censor symbol
CENSYMBOL=	Specifies symbols for censored values
CFIT=	Specifies the color for the fitted probability line and confidence curves
CFRAME=	Specifies the color for the area enclosed by the axes and frame
CGRID=	Specifies the color for grid lines
CHREF=	Specifies the color for lines requested by the HREF= option
CTEXT=	Specifies the color for tick mark values and axis labels
CVREF=	Specifies the color for lines requested by the VREF= option
DESCRIPTION=	Specifies a description that appears in the PROC GREPLAY master menu
FONT=	Specifies a software font for reference line and axis labels
HCL	Computes and draws confidence limits
HEIGHT=	Specifies the height of text used outside framed areas
HLOWER=	Specifies the lower limit on the lifetime axis scale
HOFFSET=	Specifies the offset for the horizontal axis
HREF	Draws reference lines perpendicular to the horizontal axis
HREFLABELS=	Specifies labels for the lines requested by the HREF= option
HREFLABPOS=	Specifies the vertical position of labels for HREF= lines
HUPPER=	Specifies *value* as the upper lifetime axis tick mark
INBORDER	Requests a border around probability plots
INTERTILE=	Specifies the distance between tiles
ITPRINTEM	Displays the iteration history for the Turnbull algorithm
JITTER=	Specifies the amount to jitter overlaid plot symbols, in units of symbol width
LFIT=	Specifies a line style for fitted curves and confidence limits
LGRID=	Specifies a line style for all grid lines
LHREF=	Specifies the line type for lines requested by the HREF= option
LVREF=	Specifies the line type for lines requested by the VREF= option
MAXITEM=	Specifies the maximum number of iterations for the Turnbull algorithm
NAME=	Specifies a name for the plot
NOCENPLOT	Suppresses the plotting of censored data points
NOCONF	Suppresses the default confidence bands
NODATA	Suppresses plotting of the estimated empirical probability plot
NOFIT	Suppresses the fitted probability (percentile) line and confidence bands
NOFRAME	Suppresses the frame around plotting areas
NOGRID	Suppresses grid lines
NOHLABEL	Suppresses horizontal label
NOHTICK	Suppresses horizontal tick marks
NOPOLISH	Suppresses setting small interval probabilities to zero
NOVLABEL	Suppresses vertical labels
NOVTICK	Suppresses vertical tick marks
NPINTERVALS=	Displays one of the two kinds of confidence limit
PCTLIST=	Specifies the list of percentages for which to compute percentile estimates
PLOWER=	Specifies the lower limit on the probability axis scale
PPOS=	Specifies the plotting position type

Table 75.13 *continued*

Option	Description
PPOUT	Displays a table of the cumulative probabilities
PRINTPROBS	Displays intervals and associated probabilities for the Turnbull algorithm
PROBLIST=	Specifies the list of initial values for the Turnbull algorithm
PUPPER=	Specifies the upper limit on the probability axis scale
ROTATE	Requests probability plots with probability scale on the horizontal axis
SQUARE	Makes the layout of the probability plots square
TOLLIKE=	Specifies the criterion for convergence in the Turnbull algorithm
TOLPROB=	Specifies the criterion for setting the interval probability to zero in the Turnbull algorithm
VAXISLABEL=	Specifies a label for the vertical axis
VREF	Draws reference lines perpendicular to the vertical axis
VREFLABELS=	Specifies labels for the lines requested by the VREF= option
VREFLABPOS=	Specifies the horizontal position of labels for VREF= lines
WAXIS=	Specifies line thickness for axes and frame
WFIT=	Specifies line thickness for fitted curves
WGRID=	Specifies line thickness for grids
WREFL=	Specifies line thickness for reference lines

The following *options* are available in the PROBPLOT statement if you use traditional graphics—that is, if ODS Graphics is not enabled.

ANNOTATE=*SAS-data-set*

ANNO=*SAS-data-set*

specifies an Annotate data set, as described in *SAS/GRAPH: Reference*, that enables you to add features to the probability plot. The data set you specify with the ANNOTATE= option in the PROBPLOT statement provides the Annotate data set for all plots created by the statement.

CAXIS=*color*

CAXES=*color*

specifies the color for the axes and tick marks. This option overrides any COLOR= specifications in an AXIS statement. The default is the first color in the device color list.

CCENSOR=*color*

specifies the color for filling the censor plot area. The default is the first color in the device color list.

CENBIN

plots censored data as frequency counts (rounding for noninteger frequency) rather than as individual points.

CENCOLOR=*color*

specifies the color for the censor symbol. The default is the first color in the device color list.

CENSYMBOL=*symbol* | **(***symbol list***)**
specifies symbols for censored values. The *symbol* is one of the symbol names (plus, star, square, diamond, triangle, hash, paw, point, dot, and circle) or a letter (A–Z). If you do not specify the CENSYMBOL= option, the symbol used for censored values is the same as for failures.

CFIT=*color*
specifies the color for the fitted probability line and confidence curves. The default is the first color in the device color list.

CFRAME=*color*

CFR=*color*
specifies the color for the area enclosed by the axes and frame. This area is not shaded by default.

CGRID=*color*
specifies the color for grid lines. The default is the first color in the device color list.

CHREF=*color*

CH=*color*
specifies the color for lines requested by the HREF= option. The default is the first color in the device color list.

CTEXT=*color*
specifies the color for tick mark values and axis labels. The default is the color specified for the CTEXT= option in the most recent GOPTIONS statement.

CVREF=*color*

CV=*color*
specifies the color for lines requested by the VREF= option. The default is the first color in the device color list.

DESCRIPTION='*string***'**

DES='*string***'**
specifies a description, up to 40 characters, that appears in the PROC GREPLAY master menu. The default is the variable name.

FONT=*font*
specifies a software font for reference line and axis labels. You can also specify fonts for axis labels in an AXIS statement. The FONT= font takes precedence over the FTEXT= font specified in the most recent GOPTIONS statement. Hardware characters are used by default.

HCL
computes and draws confidence limits for the predicted probabilities based on distribution percentiles instead of the default CDF limits. See the section "Confidence Limits for Percentiles" on page 5556 for details of the computation.

HEIGHT=*value*
specifies the height of text outside framed areas. The default value is 3.846 (in percentage).

HLOWER=*value*
specifies the lower limit on the lifetime axis scale. The HLOWER= option specifies *value* as the lower lifetime axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

HOFFSET=*value*
specifies the offset for the horizontal axis. The default value is 1.

HUPPER=*value*
specifies *value* as the upper lifetime axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

HREF < (INTERSECT) > =*value-list*
requests that reference lines perpendicular to the horizontal axis be drawn at horizontal axis values in the *value-list*. If (INTERSECT) is specified, a second reference line perpendicular to the vertical axis is drawn that intersects the fit line at the same point as the horizontal axis reference line. If a horizontal axis reference line label is specified with the HREFLABELS= option, the intersecting vertical axis reference line is labeled with the vertical axis value. See also the CHREF=, HREFLABELS=, and LHREF= options.

HREFLABELS=*'label1'* **...** *'labeln'*
HREFLABEL=*'label1'* **...** *'labeln'*
HREFLAB=*'label1'* **...** *'labeln'*
specifies labels for the lines requested by the HREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

HREFLABPOS=*n*
specifies the vertical position of labels for HREF= lines. The following table shows the valid values for *n* and the corresponding label placements.

n	**Label Placement**
1	Top
2	Staggered from top
3	Bottom
4	Staggered from bottom
5	Alternating from top
6	Alternating from bottom

INBORDER
requests a border around probability plots.

INTERTILE=*value*
specifies the distance between tiles.

ITPRINTEM
displays the iteration history for the Turnbull algorithm.

JITTER=*value*
specifies the amount to jitter overlaid plot symbols, in units of symbol width.

LFIT=*linetype*
specifies a line style for fitted curves and confidence limits. By default, fitted curves are drawn by connecting solid lines (*linetype = 1*), and confidence limits are drawn by connecting dashed lines (*linetype = 3*).

LGRID=*linetype*
specifies a line style for all grid lines; *linetype* is between 1 and 46. The default is 35.

LHREF=*linetype*
LH=*linetype*
specifies the line type for lines requested by the HREF= option. The default is 2, which produces a dashed line.

LVREF=*linetype*
LV=*linetype*
specifies the line type for lines requested by the VREF= option. The default is 2, which produces a dashed line.

MAXITEM=*n1 <,n2>*
specifies the maximum number of iterations for the Turnbull algorithm. Iteration history will be displayed in increments of *n2* if requested with the ITPRINTEM option. See the section "Arbitrarily Censored Data" on page 5554 for details.

NAME=*'string'*
specifies a name for the plot, up to eight characters, that appears in the PROC GREPLAY master menu. The default is 'LIFEREG'.

NOCENPLOT
suppresses the plotting of censored data points.

NOCONF
suppresses the default confidence bands on the probability plot.

NODATA
suppresses plotting of the estimated empirical probability plot.

NOFIT
suppresses the fitted probability (percentile) line and confidence bands.

NOFRAME
suppresses the frame around plotting areas.

NOGRID
suppresses grid lines.

NOHLABEL
suppresses horizontal labels.

NOHTICK
suppresses horizontal tick marks.

NOPOLISH
suppresses setting small interval probabilities to zero in the Turnbull algorithm.

NOVLABEL
suppresses vertical labels.

NOVTICK
suppresses vertical tick marks.

NPINTERVALS=*interval-type*
specifies one of the two kinds of confidence limits for the estimated cumulative probabilities, pointwise (NPINTERVALS=POINT) or simultaneous (NPINTERVALS=SIMUL), requested by the PPOUT option to be displayed in the tabular output.

PCTLIST=*value-list*
specifies the list of percentages for which to compute percentile estimates; *value-list* must be a list of values separated by blanks or commas. Each value in the list must be between 0 and 100.

PLOWER=*value*
specifies the lower limit on the probability axis scale. The PLOWER= option specifies *value* as the lower probability axis tick mark. The tick mark interval and the upper axis limit are determined automatically.

PPOS=*character-list*
specifies the plotting position type. See the section "Probability Plotting" on page 5552 for details.

PPOS=	Method
EXPRANK	Expected ranks
MEDRANK	Median ranks
MEDRANK1	Median ranks (exact formula)
KM	Kaplan-Meier
MKM	Modified Kaplan-Meier (default)

PPOUT
specifies that a table of the cumulative probabilities plotted on the probability plot be displayed. Kaplan-Meier estimates of the cumulative probabilities are also displayed, along with standard errors and confidence limits. The confidence limits can be pointwise or simultaneous, as specified by the NPINTERVALS= option.

PRINTPROBS
displays intervals and associated probabilities for the Turnbull algorithm.

PROBLIST=*value-list*
specifies the list of initial values for the Turnbull algorithm.

PUPPER=*value*
specifies the upper limit on the probability axis scale. The PUPPER= option specifies *value* as the upper probability axis tick mark. The tick mark interval and the lower axis limit are determined automatically.

ROTATE
requests probability plots with probability scale on the horizontal axis.

SQUARE
makes the layout of the probability plots square.

TOLLIKE=*value*
specifies the criterion for convergence in the Turnbull algorithm.

TOLPROB=*value*
specifies the criterion for setting the interval probability to zero in the Turnbull algorithm.

VAXISLABEL='*string*'
specifies a label for the vertical axis.

VREF< (INTERSECT) >=*value-list*
requests that reference lines perpendicular to the vertical axis be drawn at vertical axis values in the *value-list*. If (INTERSECT) is specified, a second reference line perpendicular to the horizontal axis is drawn that intersects the fit line at the same point as the vertical axis reference line. If a vertical axis reference line label is specified with the VREFLABELS= option, the intersecting horizontal axis reference line is labeled with the horizontal axis value. See also the CVREF=, LVREF=, and VREFLABELS= options.

VREFLABELS=*'label1' . . . 'labeln'*
VREFLABEL=*'label1' . . . 'labeln'*
VREFLAB=*'label1' . . . 'labeln'*
specifies labels for the lines requested by the VREF= option. The number of labels must equal the number of lines. Enclose each label in quotes. Labels can be up to 16 characters.

VREFLABPOS=*n*
specifies the horizontal position of labels for VREF= lines. The valid values for *n* and the corresponding label placements are shown in the following table.

n	**Label Placement**
1	Left
2	Right

WAXIS=*n*
specifies line thickness for axes and frame. The default value is 1.

WFIT=*n*
specifies line thickness for fitted curves. The default value is 1.

WGRID=*n*
specifies line thickness for grids. The default value is 1.

WREFL=*n*
specifies line thickness for reference lines. The default value is 1.

ODS Table Names

PROC LIFEREG assigns a name to each table it creates. You can use these names to reference the table when using the Output Delivery System (ODS) to select tables and create output data sets. These names are listed separately in Table 75.14 for a maximum likelihood analysis and in Table 75.15 for a Bayesian analysis. For more information about ODS, see Chapter 22, "Using the Output Delivery System."

Table 75.14 ODS Tables Produced in PROC LIFEREG for a Classical Analysis

ODS Table Name	Description	Statement	Option
ClassLevels	Classification variable levels	CLASS	Default*
ConvergenceStatus	Convergence status	MODEL	Default
CorrB	Parameter estimate correlation matrix	MODEL	CORRB
CovB	Parameter estimate covariance matrix	MODEL	COVB
IterEM	Iteration history for Turnbull algorithm	PROBPLOT	ITPRINTEM
FitStatistics	Fit statistics	MODEL	Default
FitStatisticsUL	Fit statistics for unlogged response	MODEL	DISTRIBUTION=WEIBULL, LOGNORMAL, LLOGISTIC, or GAMMA
IterHistory	Iteration history	MODEL	ITPRINT
LagrangeStatistics	Lagrange statistics	MODEL	NOINT | NOSCALE
LastGrad	Last evaluation of the gradient	MODEL	ITPRINT
LastHess	Last evaluation of the Hessian	MODEL	ITPRINT
ModelInfo	Model information	MODEL	Default
NObs	Number of observations	MODEL	Default
ParameterEstimates	Parameter estimates	MODEL	Default
ParmInfo	Parameter indices	MODEL	Default
ProbabilityEstimates	Nonparametric CDF estimates	PROBPLOT	PPOUT
TConvergenceStatus	Convergence status for Turnbull algorithm	PROBPLOT	Default
Turnbull	Probability estimates from Turnbull algorithm	PROBPLOT	ITPRINTEM
Type3Analysis	Type 3 tests	MODEL	Default*

* Depending on the data.

Table 75.15 ODS Tables Produced in PROC LIFEREG for a Bayesian Analysis

ODS Table Name	Description	Statement	Option
AutoCorr	Autocorrelations of the posterior samples	BAYES	Default
ClassLevels	Classification variable levels	CLASS	Default*
CoeffPrior	Prior distribution of the regression coefficients	BAYES	Default
ConvergenceStatus	Convergence status of maximum likelihood estimation	MODEL	Default
Corr	Correlation matrix of the posterior samples	BAYES	SUMMARY=CORR
ESS	Effective sample size	BAYES	Default
FitStatistics	Fit statistics	BAYES	Default
Gelman	Gelman and Rubin convergence diagnostics	BAYES	DIAG=GELMAN
Geweke	Geweke convergence diagnostics	BAYES	Default
Heidelberger	Heidelberger and Welch convergence diagnostics	BAYES	DIAG=HEIDELBERGER
InitialValues	Initial values of the Markov chains	BAYES	Default
MCError	Monte Carlo standard errors	BAYES	DIAG=MCSE
ModelInfo	Model information	MODEL	Default
NObs	Number of observations	MODEL	Default
ParameterEstimates	Maximum likelihood estimates of model parameters	MODEL	Default
ParmPrior	Prior distribution for scale and shape	BAYES	Default
PostIntervals	HPD and equal-tail intervals of the posterior samples	BAYES	Default
PosteriorSample	Posterior samples (for output data set only)	BAYES	
PostSummaries	Summary statistics of the posterior samples	BAYES	Default
Raftery	Raftery and Lewis convergence diagnostics	BAYES	DIAG=RAFTERY

* Depending on the data.

ODS Graphics

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in Chapter 23, "Statistical Graphics Using ODS."

Before you create graphs, ODS Graphics must be enabled (for example, by specifying the ODS GRAPHICS ON statement). For more information about enabling and disabling ODS Graphics, see the section "Enabling and Disabling ODS Graphics" on page 651 in Chapter 23, "Statistical Graphics Using ODS."

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" on page 650 in Chapter 23, "Statistical Graphics Using ODS."

Some graphs are produced by default; other graphs are produced by using statements and options.

ODS Graph Names

PROC LIFEREG assigns a name to each graph it creates using ODS. You can use these names to reference the graphs when using ODS. The names of the graphs that PROC LIFEREG generates are listed in Table 75.16, along with the required statements and options.

Table 75.16 Graphs Produced by PROC LIFEREG

ODS Graph Name	Description	Statement	Option
ADPanel	Autocorrelation function and density panel	BAYES	PLOTS=(AUTOCORR DENSITY)
AutocorrPanel	Autocorrelation function panel	BAYES	PLOTS= AUTOCORR
AutocorrPlot	Autocorrelation function plot	BAYES	PLOTS(UNPACK)=AUTOCORR
ProbPlot	Probability plot	PROBPLOT	Default
TAPanel	Trace and autocorrelation function panel	BAYES	PLOTS=(TRACE AUTOCORR)
TADPanel	Trace, autocorrelation, and density function panel	BAYES	Default
TDPanel	Trace and density panel	BAYES	PLOTS=(TRACE DENSITY)
TracePanel	Trace panel	BAYES	PLOTS=TRACE
TracePlot	Trace plot	BAYES	PLOTS(UNPACK)=TRACE

Examples: LIFEREG Procedure

Example 75.1: Motorette Failure

This example fits a Weibull model and a lognormal model to the example given in Kalbfleisch and Prentice (1980, p. 5). An output data set called models is specified to contain the parameter estimates. By default, the natural log of the variable time is used by the procedure as the response. After this log transformation, the Weibull model is fit using the extreme-value baseline distribution, and the lognormal is fit using the normal baseline distribution.

Since the extreme-value and normal distributions do not contain any shape parameters, the variable SHAPE1 is missing in the models data set. An additional output data set, out, is created that contains the predicted quantiles and their standard errors for values of the covariate corresponding to temp=130 and temp=150. This is done with the control variable, which is set to 1 for only two observations.

Using the standard error estimates obtained from the output data set, approximate 90% confidence limits for the predicted quantities are then created in a subsequent DATA step for the log response. The logs of the predicted values are obtained because the values of the P= variable in the OUT= data set are in the same units as the original response variable, time. The standard errors of the quantiles of log(time) are approximated (using a Taylor series approximation) by the standard deviation of time divided by the mean value of time. These confidence limits are then converted back to the original scale by the exponential function.

The following statements produce Output 75.1.1:

```
title 'Motorette Failures With Operating Temperature as a Covariate';
data motors;
   input time censor temp @@;
   if _N_=1 then
      do;
         temp=130;
         time=.;
         control=1;
         z=1000/(273.2+temp);
         output;
         temp=150;
         time=.;
         control=1;
         z=1000/(273.2+temp);
         output;
      end;
   if temp>150;
   control=0;
   z=1000/(273.2+temp);
   output;
   datalines;
8064 0 150 8064 0 150 8064 0 150 8064 0 150 8064 0 150
8064 0 150 8064 0 150 8064 0 150 8064 0 150 8064 0 150
1764 1 170 2772 1 170 3444 1 170 3542 1 170 3780 1 170
4860 1 170 5196 1 170 5448 0 170 5448 0 170 5448 0 170
 408 1 190  408 1 190 1344 1 190 1344 1 190 1440 1 190
```

```
1680 0 190 1680 0 190 1680 0 190 1680 0 190 1680 0 190
 408 1 220  408 1 220  504 1 220  504 1 220  504 1 220
 528 0 220  528 0 220  528 0 220  528 0 220  528 0 220
;

proc print data=motors;
run;
```

Output 75.1.1 Motorette Failure Data

Motorette Failures With Operating Temperature as a Covariate

Obs	time	censor	temp	control	z
1	.	0	130	1	2.48016
2	.	0	150	1	2.36295
3	1764	1	170	0	2.25632
4	2772	1	170	0	2.25632
5	3444	1	170	0	2.25632
6	3542	1	170	0	2.25632
7	3780	1	170	0	2.25632
8	4860	1	170	0	2.25632
9	5196	1	170	0	2.25632
10	5448	0	170	0	2.25632
11	5448	0	170	0	2.25632
12	5448	0	170	0	2.25632
13	408	1	190	0	2.15889
14	408	1	190	0	2.15889
15	1344	1	190	0	2.15889
16	1344	1	190	0	2.15889
17	1440	1	190	0	2.15889
18	1680	0	190	0	2.15889
19	1680	0	190	0	2.15889
20	1680	0	190	0	2.15889
21	1680	0	190	0	2.15889
22	1680	0	190	0	2.15889
23	408	1	220	0	2.02758
24	408	1	220	0	2.02758
25	504	1	220	0	2.02758
26	504	1	220	0	2.02758
27	504	1	220	0	2.02758
28	528	0	220	0	2.02758
29	528	0	220	0	2.02758
30	528	0	220	0	2.02758
31	528	0	220	0	2.02758
32	528	0	220	0	2.02758

The following statements produce Output 75.1.2 and Output 75.1.3:

```
proc lifereg data=motors outest=modela covout;
   a: model time*censor(0)=z;
      output out=outa quantiles=.1 .5 .9 std=std p=predtime
         control=control;
run;

proc lifereg data=motors outest=modelb covout;
   b: model time*censor(0)=z / dist=lnormal;
      output out=outb quantiles=.1 .5 .9 std=std p=predtime
         control=control;
run;
```

Output 75.1.2 Motorette Failure: Model A

Motorette Failures With Operating Temperature as a Covariate

The LIFEREG Procedure

Model Information	
Data Set	WORK.MOTORS
Dependent Variable	Log(time)
Censoring Variable	censor
Censoring Value(s)	0
Number of Observations	30
Noncensored Values	17
Right Censored Values	13
Left Censored Values	0
Interval Censored Values	0
Number of Parameters	3
Name of Distribution	Weibull
Log Likelihood	-22.95148315

Type III Analysis of Effects

Effect	DF	Wald Chi-Square	Pr > ChiSq
z	1	99.5239	<.0001

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-11.8912	1.9655	-15.7435	-8.0389	36.60	<.0001
z	1	9.0383	0.9060	7.2626	10.8141	99.52	<.0001
Scale	1	0.3613	0.0795	0.2347	0.5561		
Weibull Shape	1	2.7679	0.6091	1.7982	4.2605		

Output 75.1.3 Motorette Failure: Model B

Motorette Failures With Operating Temperature as a Covariate

The LIFEREG Procedure

Model Information	
Data Set	WORK.MOTORS
Dependent Variable	Log(time)
Censoring Variable	censor
Censoring Value(s)	0
Number of Observations	30
Noncensored Values	17
Right Censored Values	13
Left Censored Values	0
Interval Censored Values	0
Number of Parameters	3
Name of Distribution	Lognormal
Log Likelihood	-24.47381031

Type III Analysis of Effects

Effect	DF	Wald Chi-Square	Pr > ChiSq
z	1	42.0001	<.0001

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-10.4706	2.7719	-15.9034	-5.0377	14.27	0.0002
z	1	8.3221	1.2841	5.8052	10.8389	42.00	<.0001
Scale	1	0.6040	0.1107	0.4217	0.8652		

The following statements produce Output 75.1.4:

```
data models;
   set modela modelb;
run;

proc print data=models;
   id _model_;
   title 'Fitted Models';
run;
```

Output 75.1.4 Motorette Failure: Fitted Models

Fitted Models

MODEL	_NAME_	_TYPE_	_DIST_	_STATUS_	_LNLIKE_	time	Intercept	z	_SCALE_
a	time	PARMS	Weibull	0 Converged	-22.9515	-1.0000	-11.8912	9.03834	0.36128
a	Intercept	COV	Weibull	0 Converged	-22.9515	-11.8912	3.8632	-1.77878	0.03448
a	z	COV	Weibull	0 Converged	-22.9515	9.0383	-1.7788	0.82082	-0.01488
a	Scale	COV	Weibull	0 Converged	-22.9515	0.3613	0.0345	-0.01488	0.00632
b	time	PARMS	Lognormal	0 Converged	-24.4738	-1.0000	-10.4706	8.32208	0.60403
b	Intercept	COV	Lognormal	0 Converged	-24.4738	-10.4706	7.6835	-3.55566	0.03267
b	z	COV	Lognormal	0 Converged	-24.4738	8.3221	-3.5557	1.64897	-0.01285
b	Scale	COV	Lognormal	0 Converged	-24.4738	0.6040	0.0327	-0.01285	0.01226

The following statements produce Output 75.1.5:

```
data out;
   set outa outb;
run;

data out1;
   set out;
   ltime=log(predtime);
   stde=std/predtime;
   upper=exp(ltime+1.64*stde);
   lower=exp(ltime-1.64*stde);
run;

title 'Quantile Estimates and Confidence Limits';
proc print data=out1;
   id temp;
run;
title;
```

Output 75.1.5 Motorette Failure: Quantile Estimates and Confidence Limits

Quantile Estimates and Confidence Limits

temp	time	censor	control	z	_PROB_	predtime	std	ltime	stde	upper	lower
130	.	0	1	2.48016	0.1	16519.27	5999.85	9.7123	0.36320	29969.51	9105.47
130	.	0	1	2.48016	0.5	32626.65	9874.33	10.3929	0.30265	53595.71	19861.63
130	.	0	1	2.48016	0.9	50343.22	15044.35	10.8266	0.29884	82183.49	30838.80
150	.	0	1	2.36295	0.1	5726.74	1569.34	8.6529	0.27404	8976.12	3653.64
150	.	0	1	2.36295	0.5	11310.68	2299.92	9.3335	0.20334	15787.62	8103.28
150	.	0	1	2.36295	0.9	17452.49	3629.28	9.7672	0.20795	24545.37	12409.24
130	.	0	1	2.48016	0.1	12033.19	5482.34	9.3954	0.45560	25402.68	5700.09
130	.	0	1	2.48016	0.5	26095.68	11359.45	10.1695	0.43530	53285.36	12779.95
130	.	0	1	2.48016	0.9	56592.19	26036.90	10.9436	0.46008	120349.65	26611.42
150	.	0	1	2.36295	0.1	4536.88	1443.07	8.4200	0.31808	7643.71	2692.83
150	.	0	1	2.36295	0.5	9838.86	2901.15	9.1941	0.29487	15957.38	6066.36
150	.	0	1	2.36295	0.9	21336.97	7172.34	9.9682	0.33615	37029.72	12294.62

Example 75.2: Computing Predicted Values for a Tobit Model

The LIFEREG procedure can be used to perform a Tobit analysis. The Tobit model, described by Tobin (1958), is a regression model for left-censored data assuming a normally distributed error term. The model parameters are estimated by maximum likelihood. PROC LIFEREG provides estimates of the parameters of the distribution of the *uncensored* data. See Greene (1993) and Maddala (1983) for a more complete discussion of censored normal data and related distributions. This example shows how you can use PROC LIFEREG and the DATA step to compute two of the three types of predicted values discussed there.

Consider a continuous random variable Y and a constant C. If you were to sample from the distribution of Y but discard values less than (greater than) C, the distribution of the remaining observations would be *truncated* on the left (right). If you were to sample from the distribution of Y and report values less than (greater than) C as C, the distribution of the sample would be left (right) *censored*.

The probability density function of the truncated random variable Y' is given by

$$f_{\mathrm{Y}'}(y) = \frac{f_{\mathrm{Y}}(y)}{\Pr(\mathrm{Y} > \mathrm{C})} \quad \text{for} \quad y > \mathrm{C}$$

where $f_{\mathrm{Y}}(y)$ is the probability density function of Y. PROC LIFEREG cannot compute the proper likelihood function to estimate parameters or predicted values for a truncated distribution. Suppose the model being fit is specified as follows:

$$\mathrm{Y}_i^* = \mathbf{x}_i'\boldsymbol{\beta} + \epsilon_i$$

where ϵ_i is a normal error term with zero mean and standard deviation σ.

Define the censored random variable Y_i as

$$\begin{aligned} \mathrm{Y}_i &= 0 \text{ if } \mathrm{Y}_i^* \le 0 \\ \mathrm{Y}_i &= \mathrm{Y}_i^* \text{ if } \mathrm{Y}_i^* > 0 \end{aligned}$$

This is the Tobit model for left-censored normal data. Y_i^* is sometimes called the *latent variable*. PROC LIFEREG estimates parameters of the distribution of Y_i^* by maximum likelihood.

You can use the LIFEREG procedure to compute predicted values based on the mean functions of the latent and observed variables. The mean of the latent variable Y_i^* is $\mathbf{x}_i'\boldsymbol{\beta}$, and you can compute values of the mean for different settings of $\mathbf{x}_i$ by specifying XBETA=*variable-name* in an OUTPUT statement. Estimates of $\mathbf{x}_i'\boldsymbol{\beta}$ for each observation will be written to the OUT= data set. Predicted values of the observed variable Y_i can be computed based on the mean

$$E(\mathrm{Y}_i) = \Phi\left(\frac{\mathbf{x}_i'\boldsymbol{\beta}}{\sigma}\right)(\mathbf{x}_i'\boldsymbol{\beta} + \sigma\lambda_i)$$

where

$$\lambda_i = \frac{\phi(\mathbf{x}_i'\boldsymbol{\beta}/\sigma)}{\Phi(\mathbf{x}_i'\boldsymbol{\beta}/\sigma)}$$

ϕ and Φ represent the normal probability density and cumulative distribution functions.

Although the distribution of ϵ_i in the Tobit model is often assumed normal, you can use other distributions for the Tobit model in the LIFEREG procedure by specifying a distribution with the DISTRIBUTION= option in the MODEL statement. One distribution that should be mentioned is the logistic distribution. For this distribution, the MLE has bounded influence function with respect to the response variable, but not the design variables. If you believe your data have outliers in the response direction, you might try this distribution for some robust estimation of the Tobit model.

With the logistic distribution, the predicted values of the observed variable Y_i can be computed based on the mean of Y_i^*,

$$E(\mathrm{Y}_i) = \sigma \ln(1 + \exp(\mathbf{x}_i'\boldsymbol{\beta}/\sigma))$$

The following table shows a subset of the Mroz (1987) data set. In these data, Hours is the number of hours the wife worked outside the household in a given year, Yrs_Ed is the years of education, and Yrs_Exp is the years of work experience. A Tobit model will be fit to the hours worked with years of education and experience as covariates.

Hours	Yrs_Ed	Yrs_Exp
0	8	9
0	8	12
0	9	10
0	10	15
0	11	4
0	11	6
1000	12	1
1960	12	29
0	13	3
2100	13	36
3686	14	11
1920	14	38
0	15	14
1728	16	3
1568	16	19
1316	17	7
0	17	15

If the wife was not employed (worked 0 hours), her hours worked will be left censored at zero. In order to accommodate left censoring in PROC LIFEREG, you need two variables to indicate censoring status of observations. You can think of these variables as lower and upper endpoints of interval censoring. If there is no censoring, set both variables to the observed value of Hours. To indicate left censoring, set the lower endpoint to missing and the upper endpoint to the censored value, zero in this case.

The following statements create a SAS data set with the variables Hours, Yrs_Ed, and Yrs_Exp from the preceding data. A new variable, Lower, is created such that Lower=. if Hours=0 and Lower=Hours if Hours>0.

```
data subset;
   input Hours Yrs_Ed Yrs_Exp @@;
   if Hours eq 0
      then Lower=.;
      else Lower=Hours;
   datalines;
0 8 9 0 8 12 0 9 10 0 10 15 0 11 4 0 11 6
1000 12 1 1960 12 29 0 13 3 2100 13 36
3686 14 11 1920 14 38 0 15 14 1728 16 3
1568 16 19 1316 17 7 0 17 15
;
```

The following statements fit a normal regression model to the left-censored Hours data with Yrs_Ed and Yrs_Exp as covariates. You need the estimated standard deviation of the normal distribution to compute the predicted values of the censored distribution from the preceding formulas. The data set OUTEST contains the standard deviation estimate in a variable named _SCALE_. You also need estimates of $\mathbf{x}_i'\boldsymbol{\beta}$. These are contained in the data set OUT as the variable Xbeta.

```
proc lifereg data=subset outest=OUTEST(keep=_scale_);
   model (lower, hours) = yrs_ed yrs_exp / d=normal;
   output out=OUT xbeta=Xbeta;
run;
```

Output 75.2.1 shows the results of the model fit. These tables show parameter estimates for the uncensored, or latent variable, distribution.

Output 75.2.1 Parameter Estimates from PROC LIFEREG

The LIFEREG Procedure

Model Information	
Data Set	WORK.SUBSET
Dependent Variable	Lower
Dependent Variable	Hours
Number of Observations	17
Noncensored Values	8
Right Censored Values	0
Left Censored Values	9
Interval Censored Values	0
Number of Parameters	4
Name of Distribution	Normal
Log Likelihood	-74.9369977

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-5598.64	2850.248	-11185.0	-12.2553	3.86	0.0495
Yrs_Ed	1	373.1477	191.8872	-2.9442	749.2397	3.78	0.0518
Yrs_Exp	1	63.3371	38.3632	-11.8533	138.5276	2.73	0.0987
Scale	1	1582.870	442.6732	914.9433	2738.397		

The following statements combine the two data sets created by PROC LIFEREG to compute predicted values

for the censored distribution. The OUTEST= data set contains the estimate of the standard deviation from the uncensored distribution, and the OUT= data set contains estimates of $\mathbf{x}_i'\boldsymbol{\beta}$.

```
data predict;
   drop lambda _scale_ _prob_;
   set out;
   if _n_ eq 1 then set outest;
   lambda = pdf('NORMAL',Xbeta/_scale_)
            / cdf('NORMAL',Xbeta/_scale_);
   Predict = cdf('NORMAL', Xbeta/_scale_)
             * (Xbeta + _scale_*lambda);
   label Xbeta='MEAN OF UNCENSORED VARIABLE'
         Predict = 'MEAN OF CENSORED VARIABLE';
run;
```

Output 75.2.2 shows the original variables, the predicted means of the uncensored distribution, and the predicted means of the censored distribution.

Output 75.2.2 Predicted Means from PROC LIFEREG

Hours	Lower	Yrs_Ed	Yrs_Exp	MEAN OF UNCENSORED VARIABLE	MEAN OF CENSORED VARIABLE
0	.	8	9	-2043.42	73.46
0	.	8	12	-1853.41	94.23
0	.	9	10	-1606.94	128.10
0	.	10	15	-917.10	276.04
0	.	11	4	-1240.67	195.76
0	.	11	6	-1113.99	224.72
1000	1000	12	1	-1057.53	238.63
1960	1960	12	29	715.91	1052.94
0	.	13	3	-557.71	391.42
2100	2100	13	36	1532.42	1672.50
3686	3686	14	11	322.14	805.58
1920	1920	14	38	2032.24	2106.81
0	.	15	14	885.30	1170.39
1728	1728	16	3	561.74	951.69
1568	1568	16	19	1575.13	1708.24
1316	1316	17	7	1188.23	1395.61
0	.	17	15	1694.93	1809.97

Example 75.3: Overcoming Convergence Problems by Specifying Initial Values

This example illustrates the use of parameter initial value specification to help overcome convergence difficulties.

The following statements create a SAS data set.

```
data raw;
   input censor x c1 @@;
   datalines;
0 16   0.00  0 17  0.00  0 18  0.00  0 17   0.04  0 18   0.04  0 18   0.04
0 23   0.40  0 22  0.40  0 22  0.40  0 33   4.00  0 34   4.00  0 35   4.00
1 54  40.00  1 54 40.00  1 54 40.00  1 54 400.00  1 54 400.00  1 54 400.00
;
```

Output 75.3.1 shows the contents of the data set raw.

Output 75.3.1 Contents of the Data Set

Obs	censor	x	c1
1	0	16	0.00
2	0	17	0.00
3	0	18	0.00
4	0	17	0.04
5	0	18	0.04
6	0	18	0.04
7	0	23	0.40
8	0	22	0.40
9	0	22	0.40
10	0	33	4.00
11	0	34	4.00
12	0	35	4.00
13	1	54	40.00
14	1	54	40.00
15	1	54	40.00
16	1	54	400.00
17	1	54	400.00
18	1	54	400.00

The following SAS statements request that a Weibull regression model be fit to the data:

```
title 'OLS (Default) Initial Values';
proc lifereg data=raw;
   model x*censor(1) = c1 / distribution = Weibull itprint;
run;
```

Convergence was not attained in 50 iterations for this model, as the following messages to the log indicate:

```
WARNING: Convergence was not attained in 50 iterations. You might want to
         increase the maximum number of iterations (MAXITER= option) or change
```

```
          the convergence criteria (CONVERGE = value) in the MODEL statement.
WARNING: The procedure is continuing in spite of the above warning. Results
          shown are based on the last maximum likelihood iteration. Validity
          of the model fit is questionable.
```

The first line (iter=0) of the iteration history table, shown in Output 75.3.2, shows the default initial ordinary least squares (OLS) estimates of the parameters.

Output 75.3.2 Initial Least Squares

OLS (Default) Initial Values

The LIFEREG Procedure

Iteration History for Parameter Estimates

Iter	Ridge	Loglikelihood	Intercept	c1	Scale
0	0	-22.891088	3.2324769714	0.0020664542	0.3995754195
1	0	-16.427074	3.5337141598	0.0028713635	0.3283544365
2	0	-13.216768	3.4480787541	0.0052801225	0.3816964358
3	0	-5.0786635	3.1966395335	0.0191439929	0.2325418958
4	0	-2.0018885	3.1848047525	0.0275425402	0.1963590539
5	0	-0.1814984	3.1478989655	0.0374731819	0.2103607621
6	0	2.90712131	3.0858183316	0.0659946149	0.1818245261
7	0.063	2.9991781	3.1014479187	0.0661096622	0.1648677081
8	0.063	3.01557837	3.0995493638	0.0662333056	0.1670552505
9	0.063	3.0301815	3.0992317977	0.0663580659	0.1669529486
10	0.063	3.0448013	3.0989901232	0.0664827053	0.1667371524
11	0.063	3.05941254	3.0987507448	0.0666071514	0.1665197313
12	0.063	3.07401474	3.0985118143	0.0667314052	0.1663026517
13	0.063	3.08860788	3.0982732928	0.066855467	0.1660859472
14	0.063	3.10319193	3.0980351787	0.0669793371	0.1658696184
15	0.063	3.11776689	3.0977974713	0.0671030156	0.1656536651
16	0.063	3.13233272	3.0975601698	0.0672265029	0.1654380873
17	0.063	3.1468894	3.0973232737	0.0673497993	0.165222885
18	0.063	3.16143692	3.0970867821	0.0674729049	0.1650080579
19	0.063	3.17597526	3.0968506943	0.06759582	0.1647936061
20	0.063	3.19050439	3.0966150098	0.0677185449	0.1645795293
21	0.063	3.2050243	3.0963797277	0.0678410799	0.1643658275
22	0.063	3.21953496	3.0961448474	0.0679634252	0.1641525006
23	0.063	3.23403635	3.0959103682	0.068085581	0.1639395483
24	0.063	3.24852845	3.0956762896	0.0682075476	0.1637269705
25	0.063	3.26301123	3.0954426107	0.0683293253	0.1635147672
26	0.063	3.27748468	3.095209331	0.0684509143	0.163302938
27	0.063	3.29194878	3.0949764498	0.0685723149	0.1630914829
28	0.063	3.3064035	3.0947439665	0.0686935273	0.1628804017
29	0.063	3.32084881	3.0945118805	0.0688145517	0.1626696942
30	0.063	3.3352847	3.0942801911	0.0689353885	0.1624593601
31	0.063	3.34971114	3.0940488977	0.0690560378	0.1622493994
32	0.063	3.36412812	3.0938179997	0.0691765	0.1620398118
33	0.063	3.3785356	3.0935874965	0.0692967752	0.1618305971
34	0.063	3.39293356	3.0933573875	0.0694168637	0.161621755
35	0.063	3.40732199	3.093127672	0.0695367658	0.1614132855
36	0.063	3.42170085	3.0928983495	0.0696564816	0.1612051882
37	0.063	3.43607013	3.0926694194	0.0697760116	0.1609974629
38	0.063	3.45042979	3.0924408811	0.0698953558	0.1607901095
39	0.063	3.46477983	3.092212734	0.0700145146	0.1605831276
40	0.063	3.4791202	3.0919849776	0.0701334882	0.160376517
41	0.063	3.4934509	3.0917576112	0.0702522768	0.1601702775
42	0.063	3.50777188	3.0915306343	0.0703708808	0.1599644088
43	0.063	3.52208314	3.0913040464	0.0704893002	0.1597589108

Output 75.3.2 *continued*

OLS (Default) Initial Values

The LIFEREG Procedure

Iteration History for Parameter Estimates

Iter	Ridge	Loglikelihood	Intercept	c1	Scale
44	0.063	3.53638465	3.0910778468	0.0706075354	0.159553783
45	0.063	3.55067637	3.0908520349	0.0707255867	0.1593490254
46	0.063	3.5649583	3.0906266104	0.0708434542	0.1591446376
47	0.063	3.57923039	3.0904015725	0.0709611382	0.1589406193
48	0.063	3.59349263	3.0901769207	0.0710786389	0.1587369703
49	0.063	3.607745	3.0899526546	0.0711959567	0.1585336903
50	0.063	3.62198746	3.0897287734	0.0713130916	0.1583307791

The log-logistic distribution is more robust to large values of the response than the Weibull distribution, so one approach to improving the convergence performance is to fit a log-logistic distribution, and if this converges, use the resulting parameter estimates as initial values in a subsequent fit of a model with the Weibull distribution.

The following statements fit a log-logistic distribution to the data:

```
proc lifereg data=raw;
   model x*censor(1) = c1 / distribution = llogistic;
run;
```

The algorithm converges, and the maximum likelihood estimates for the log-logistic distribution are shown in Output 75.3.3

Output 75.3.3 Estimates from the Log-Logistic Distribution

OLS (Default) Initial Values

The LIFEREG Procedure

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	2.8983	0.0318	2.8360	2.9606	8309.43	<.0001
c1	1	0.1592	0.0133	0.1332	0.1852	143.85	<.0001
Scale	1	0.0498	0.0122	0.0308	0.0804		

The following statements refit the Weibull model by using the maximum likelihood estimates from the log-logistic fit as initial values:

```
proc lifereg data=raw outest=outest;
   model x*censor(1) = c1 / itprint distribution = weibull
                            intercept=2.898 initial=0.16 scale=0.05;
   output out=out xbeta=xbeta;
run;
```

Examination of the resulting output in Output 75.3.4 shows that the convergence problem has been solved by specifying different initial values.

Output 75.3.4 Final Estimates from the Weibull Distribution

OLS (Default) Initial Values

The LIFEREG Procedure

Model Information	
Data Set	WORK.RAW
Dependent Variable	Log(x)
Censoring Variable	censor
Censoring Value(s)	1
Number of Observations	18
Noncensored Values	12
Right Censored Values	6
Left Censored Values	0
Interval Censored Values	0
Number of Parameters	3
Name of Distribution	Weibull
Log Likelihood	11.232023272

Algorithm converged.

Analysis of Maximum Likelihood Parameter Estimates

Parameter	DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	2.9699	0.0326	2.9059	3.0338	8278.86	<.0001
c1	1	0.1435	0.0165	0.1111	0.1758	75.43	<.0001
Scale	1	0.0844	0.0189	0.0544	0.1308		
Weibull Shape	1	11.8526	2.6514	7.6455	18.3749		

As an example of an alternative way of specifying initial values, the following invocation of PROC LIFEREG, using the INEST= data set to provide starting values for the three parameters, is equivalent to the previous invocation:

```
data in;
   input  intercept c1 _scale_;
   datalines;
2.898 0.16 0.05
;

proc lifereg data=raw inest=in outest=outest;
   model x*censor(1) = c1 / itprint distribution = weibull;
   output out=out xbeta=xbeta;
run;
```

Example 75.4: Analysis of Arbitrarily Censored Data with Interaction Effects

The artificial data in this example are from a study of the natural recovery time of mice after injection of a certain toxin. Twenty mice were grouped by sex (sex: 1 = Male, 2 = Female) with equal sizes. Their ages (in days) were recorded at the injection. Their recovery times (in minutes) were also recorded. Toxin density in blood was used to decide whether a mouse recovered. Mice were checked at two times for recovery. If a mouse had recovered at the first time, the observation is left censored, and no further measurement is made. The variable time1 is set to missing and time2 is set to the measurement time to indicate left censoring. If a mouse had not recovered at the first time, it was checked later at a second time. If it had recovered by the second measurement time, the observation is interval censored, and the variable time1 is set to the first measurement time and time2 is set to the second measurement time. If there was no recovery at the second measurement, the observation is right censored, and time1 is set to the second measurement time and time2 is set to missing to indicate right censoring.

The following statements create a SAS data set containing the data from the experiment:

```
title 'Natural Recovery Time';
data mice;
   input sex age time1 time2;
   datalines;
1  57  631   631
1  45  .     170
1  54  227   227
1  43  143   143
1  64  916   .
1  67  691   705
1  44  100   100
1  59  730   .
1  47  365   365
1  74  1916  1916
2  79  1326  .
2  75  837   837
2  84  1200  1235
2  54  .     365
2  74  1255  1255
2  71  1823  .
2  65  537   637
2  33  583   683
2  77  955   .
2  46  577   577
;
```

The following SAS statements create the SAS data sets xrow1 and xrow2:

```
data xrow1;
   input sex age time1 time2;
   datalines;
1  50  .  .
;

data xrow2;
   input sex age time1 time2;
```

```
   datalines;
2  60.6  .  .
;
```

The following SAS statements fit a Weibull model with age, sex, and an age-by-sex interaction term as covariates, and create a plot of predicted probabilities against recovery time for the fixed values of age and sex specified in the SAS data set xrow1:

```
ods graphics on;
proc lifereg data=mice xdata=xrow1;
   class sex;
   model (time1, time2) = age sex age*sex / dist=Weibull;

   probplot  / nodata
       plower=.5
       vref(intersect) = 75
       vreflab = '75 Percent';
   inset;
run;
```

Standard output is shown in Output 75.4.1. Tables containing general model information, Type III tests for the main effects and interaction terms, and parameter estimates are created.

Output 75.4.1 Parameter Estimates for the Interaction Model

Natural Recovery Time

The LIFEREG Procedure

Model Information	
Data Set	WORK.MICE
Dependent Variable	Log(time1)
Dependent Variable	Log(time2)
Number of Observations	20
Noncensored Values	9
Right Censored Values	5
Left Censored Values	2
Interval Censored Values	4
Number of Parameters	5
Name of Distribution	Weibull
Log Likelihood	-25.91033295

Type III Analysis of Effects

Effect	DF	Wald Chi-Square	Pr > ChiSq
age	1	33.8496	<.0001
sex	1	14.0245	0.0002
age*sex	1	10.7196	0.0011

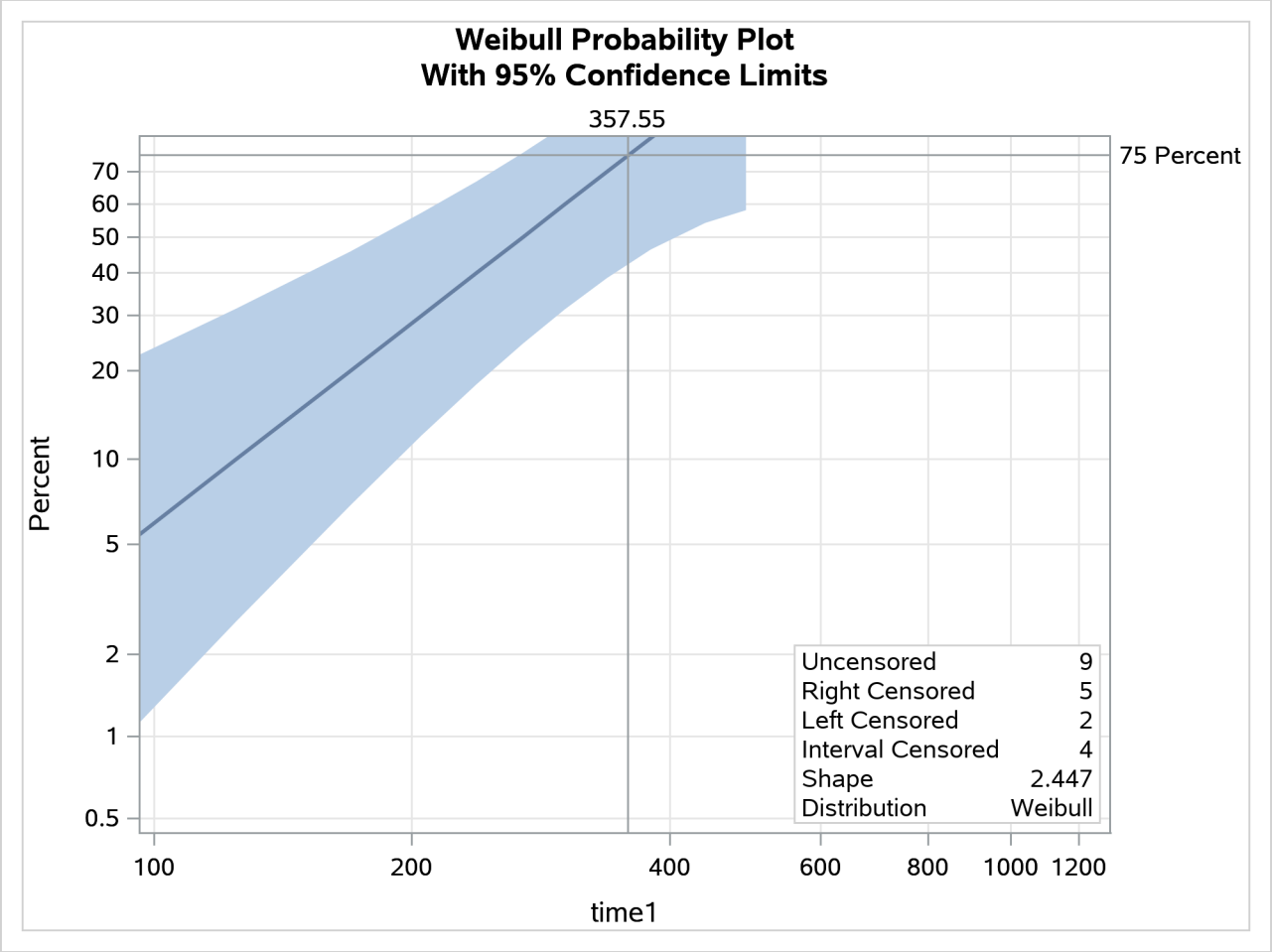
Output 75.4.1 *continued*

Analysis of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept		1	5.4110	0.5549	4.3234	6.4986	95.08	<.0001
age		1	0.0250	0.0086	0.0081	0.0419	8.42	0.0037
sex	1	1	-3.9808	1.0630	-6.0643	-1.8974	14.02	0.0002
sex	2	0	0.0000	.	.	.	.	.
age*sex	1	1	0.0613	0.0187	0.0246	0.0980	10.72	0.0011
age*sex	2	0	0.0000	.	.	.	.	.
Scale		1	0.4087	0.0900	0.2654	0.6294		
Weibull Shape		1	2.4468	0.5391	1.5887	3.7682		

The following two plots display the predicted probability against the recovery time for two different populations. Output 75.4.2 is created with the PROBPLOT statement with the option XDATA= xrow1, which specifies the population with sex = 1, age = 50. Output 75.4.3 is created with the PROBPLOT statement with the option XDATA= xrow2, which specifies the population with sex = 2, age = 60.6. These are the default values that the LIFEREG procedure would use for the probability plot if the XDATA= option had not been specified. Reference lines are used to display specified predicted probability points and their relative locations in the plot.

Output 75.4.2 Probability Plot for Recovery Time with sex = 1, age = 50

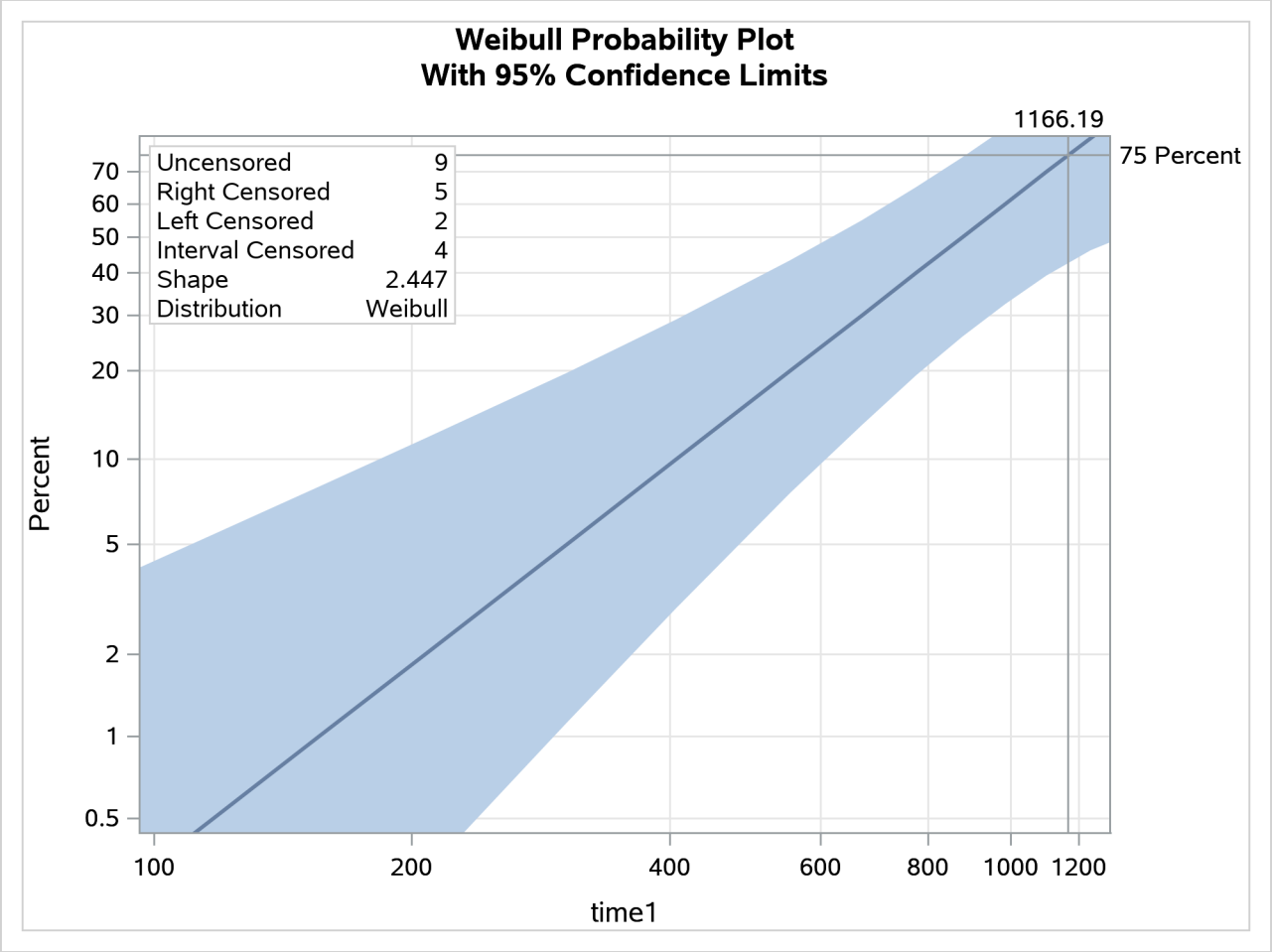


The following SAS statements fit a Weibull model with age, sex, and an age-by-sex interaction term as covariates, and create the plot of predicted probabilities against recovery time shown in Output 75.4.3, for the fixed values of age and sex specified in the SAS data set xrow2:

```
proc lifereg data=mice xdata=xrow2;
   class sex;
   model (time1, time2) = age sex age*sex / dist=Weibull;

   probplot  / nodata
       plower=.5
       vref(intersect) = 75
       vreflab = '75 Percent';
   inset;
run;
title;
```

Output 75.4.3 Probability Plot for Recovery Time with sex = 2, age = 60.6



Example 75.5: Probability Plotting—Right Censoring

The following statements create a SAS data set containing observed and right-censored lifetimes of 70 diesel engine fans (Nelson 1982):

```
data Fan;
   input Lifetime Censor@@;
   Lifetime = Lifetime / 1000;
   datalines;
 450 0    460 1   1150 0   1150 0   1560 1
1600 0   1660 1   1850 1   1850 1   1850 1
1850 1   1850 1   2030 1   2030 1   2030 1
2070 0   2070 0   2080 0   2200 1   3000 1
3000 1   3000 1   3000 1   3100 0   3200 1
3450 0   3750 1   3750 1   4150 1   4150 1
4150 1   4150 1   4300 1   4300 1   4300 1
4300 1   4600 0   4850 1   4850 1   4850 1
4850 1   5000 1   5000 1   5000 1   6100 1
6100 0   6100 1   6100 1   6300 1   6450 1
```

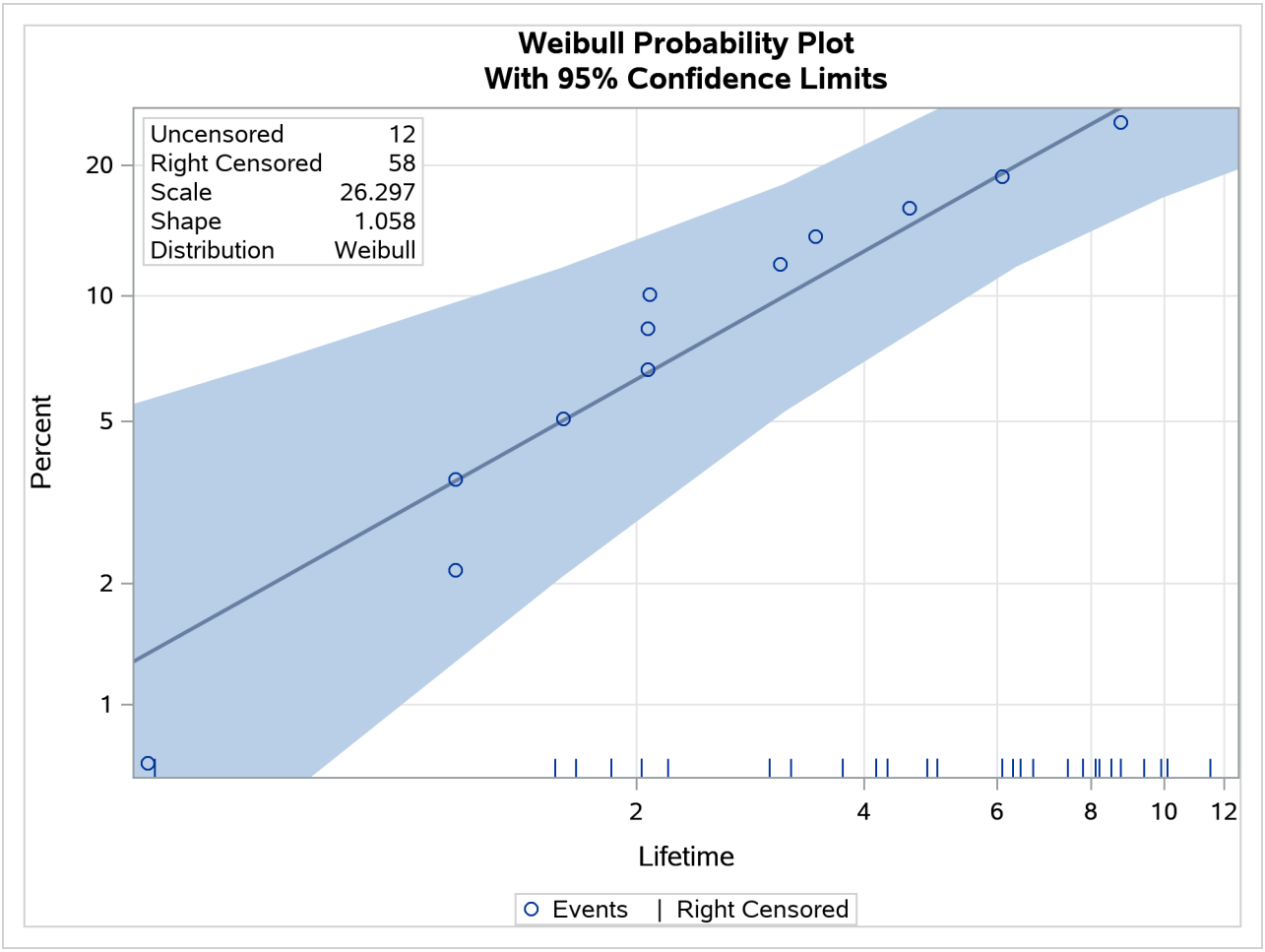
```
6450 1   6700 1   7450 1   7800 1   7800 1
8100 1   8100 1   8200 1   8500 1   8500 1
8500 1   8750 1   8750 0   8750 1   9400 1
9900 1  10100 1  10100 1  10100 1  11500 1
;
```

Some of the fans had not failed at the time the data were collected, and the unfailed units have right-censored lifetimes. The variable LIFETIME represents either a failure time or a censoring time, in thousands of hours. The variable CENSOR is equal to 0 if the value of LIFETIME is a failure time, and it is equal to 1 if the value is a censoring time. The following statements use the LIFEREG procedure to produce the probability plot with an inset for the engine lifetimes:

```
ods graphics on;
proc lifereg data=Fan;
   model Lifetime*Censor( 1 ) = / d = Weibull;
   probplot
   ppout
   npintervals=simul;
   inset;
run;
```

The resulting graphical output is shown in Output 75.5.1. The estimated CDF, a line representing the maximum likelihood fit, and pointwise parametric confidence bands are plotted in the body of Output 75.5.1. The values of right-censored observations are plotted along the bottom of the graph. The "Cumulative Probability Estimates" table is also created in Output 75.5.2.

Output 75.5.1 Probability Plot for the Fan Data



Output 75.5.2 CDF Estimates

Cumulative Probability Estimates					
		Simultaneous 95% Confidence Limits			
Lifetime	Cumulative Probability	Lower	Upper	Kaplan-Meier Estimate	Kaplan-Meier Standard Error
0.45	0.0071	0.0007	0.2114	0.0143	0.0142
1.15	0.0215	0.0033	0.2114	0.0288	0.0201
1.15	0.0360	0.0073	0.2168	0.0433	0.0244
1.6	0.0506	0.0125	0.2304	0.0580	0.0282
2.07	0.0666	0.0190	0.2539	0.0751	0.0324
2.07	0.0837	0.0264	0.2760	0.0923	0.0361
2.08	0.1008	0.0344	0.2972	0.1094	0.0392
3.1	0.1189	0.0436	0.3223	0.1283	0.0427
3.45	0.1380	0.0535	0.3471	0.1477	0.0460
4.6	0.1602	0.0653	0.3844	0.1728	0.0510
6.1	0.1887	0.0791	0.4349	0.2046	0.0581
8.75	0.2488	0.0884	0.6391	0.2930	0.0980

Example 75.6: Probability Plotting—Arbitrary Censoring

Table 75.17 contains microprocessor failure data (Nelson 1990). Units were inspected at predetermined time intervals. The data consist of inspection interval endpoints (in hours) and the number of units failing in each interval. A missing (.) lower endpoint indicates left censoring, and a missing upper endpoint indicates right censoring. These can be thought of as semi-infinite intervals with a lower (upper) endpoint of negative (positive) infinity for left (right) censoring.

Table 75.17 Interval-Censored Data

Lower Endpoint	Upper Endpoint	Number Failed
.	6	6
6	12	2
24	48	2
24	.	1
48	168	1
48	.	839
168	500	1
168	.	150
500	1000	2
500	.	149
1000	2000	1
1000	.	147
2000	.	122

The following SAS statements create the SAS data set Micro:

```
data Micro;
   input t1 t2 f;
   datalines;
. 6 6
6 12 2
12 24 0
24 48 2
24 .  1
48 168 1
48 .   839
168 500 1
168 .   150
500 1000 2
500 .    149
1000 2000 1
1000 . 147
2000 . 122
;
```

The following SAS statements compute the nonparametric Turnbull estimate of the cumulative distribution function and create a lognormal probability plot:

```
ods graphics on;
proc lifereg data=Micro;
   model ( t1 t2 ) = / d=lognormal intercept=25 scale=5;
   weight f;
   probplot
   pupper = 10
   itprintem
   printprobs
   maxitem = (1000,25)
   ppout;
   inset;
run;
```

The two initial values INTERCEPT=25 and SCALE=5 in the MODEL statement are used to aid convergence in the model-fitting algorithm.

The following tables are created by the PROBPLOT statement in addition to the standard tabular output from the MODEL statement. Output 75.6.1 shows the iteration history for the Turnbull estimate of the CDF for the microprocessor data. With both options ITPRINTEM and PRINTPROBS specified in the PROBPLOT statement, this table contains the log likelihoods and interval probabilities for every 25th iteration and the last iteration. It would contain only the log likelihoods if the option PRINTPROBS were not specified.

Output 75.6.1 Iteration History for the Turnbull Estimate

The LIFEREG Procedure

Iteration History for the Turnbull Estimate of the CDF									
Iteration	**Loglikelihood**	**(., 6)**	**(6, 12)**	**(24, 48)**	**(48, 168)**	**(168, 500)**	**(500, 1000)**	**(1000, 2000)**	**(2000, .)**
0	-1133.4051	0.125	0.125	0.125	0.125	0.125	0.125	0.125	0.125
25	-104.16622	0.00421644	0.00140548	0.00140648	0.00173338	0.00237846	0.00846094	0.04565407	0.93474475
50	-101.15151	0.00421644	0.00140548	0.00140648	0.00173293	0.00234891	0.00727679	0.01174486	0.96986811
75	-101.06641	0.00421644	0.00140548	0.00140648	0.00173293	0.00234891	0.00727127	0.00835638	0.9732621
100	-101.06534	0.00421644	0.00140548	0.00140648	0.00173293	0.00234891	0.00727125	0.00801814	0.97360037
125	-101.06533	0.00421644	0.00140548	0.00140648	0.00173293	0.00234891	0.00727125	0.00798438	0.97363413
130	-101.06533	0.00421644	0.00140548	0.00140648	0.00173293	0.00234891	0.00727125	0.007983	0.97363551

The table in Output 75.6.2 summarizes the Turnbull estimates of the interval probabilities, the reduced gradients, and Lagrange multipliers as described in the section "Arbitrarily Censored Data" on page 5554.

Output 75.6.2 Summary for the Turnbull Algorithm

Lower Lifetime	Upper Lifetime	Probability	Reduced Gradient	Lagrange Multiplier
.	6	0.0042	0	0
6	12	0.0014	0	0
24	48	0.0014	0	0
48	168	0.0017	0	0
168	500	0.0023	0	0
500	1000	0.0073	-7.219342E-9	0
1000	2000	0.0080	-0.037063236	0
2000	.	0.9736	0.0003038877	0

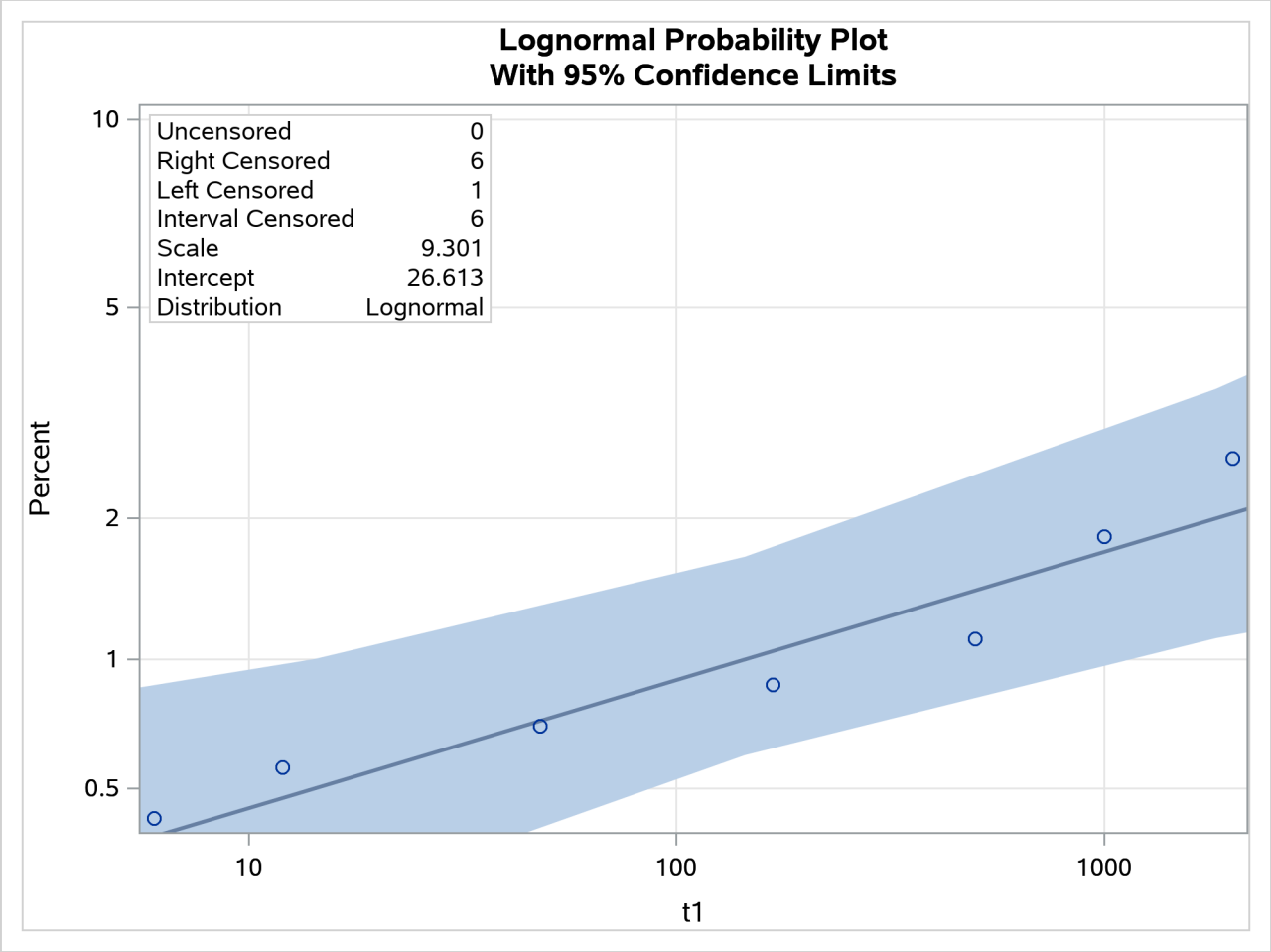
Output 75.6.3 shows the final estimate of the CDF, along with standard errors and nonparametric confidence limits. Two kinds of nonparametric confidence limits, pointwise or simultaneous, are available. The default is the pointwise nonparametric confidence limits. You can specify the simultaneous nonparametric confidence limits by using the NPINTERVALS=SIMUL option.

Output 75.6.3 Final CDF Estimates for Turnbull Algorithm

Cumulative Probability Estimates					
			Pointwise 95% Confidence Limits		
Lower Lifetime	**Upper Lifetime**	**Cumulative Probability**	**Lower**	**Upper**	**Standard Error**
6	6	0.0042	0.0019	0.0094	0.0017
12	24	0.0056	0.0028	0.0112	0.0020
48	48	0.0070	0.0038	0.0130	0.0022
168	168	0.0088	0.0047	0.0164	0.0028
500	500	0.0111	0.0058	0.0211	0.0037
1000	1000	0.0184	0.0094	0.0357	0.0063
2000	2000	0.0264	0.0124	0.0553	0.0101

Output 75.6.4 shows the CDF estimates, maximum likelihood fit, and pointwise parametric confidence limits plotted on a lognormal probability plot.

Output 75.6.4 Lognormal Probability Plot for the Microprocessor Data



Example 75.7: Bayesian Analysis of Clinical Trial Data

Consider the data on melanoma patients from a clinical trial described in Ibrahim, Chen, and Sinha (2001). A partial listing of the data is shown in Output 75.7.1.

The survival time is modeled by a Weibull regression model with three covariates. An analysis of the right-censored survival data is performed with PROC LIFEREG to obtain Bayesian estimates of the regression coefficients by using the following SAS statements:

```
ods graphics on;
proc lifereg data=e1684;
   class Sex;
   model Survtime*Survcens(1)=Age Sex Perform / dist=Weibull;
   bayes WeibullShapePrior=gamma seed=9999;
run;
```

Output 75.7.1 Clinical Trial Data

Obs	survtime	survcens	age	sex	perform
1	1.57808	2	35.9945	1	0
2	1.48219	2	41.9014	1	0
3	7.33425	1	70.2164	2	0
4	0.65479	2	58.1753	2	1
5	2.23288	2	33.7096	1	0
6	9.38356	1	47.9726	1	0
7	3.27671	2	31.8219	2	0
8	0.00000	1	72.3644	2	0
9	0.80274	2	40.7151	2	0
10	9.64384	1	32.9479	1	0
11	1.66575	2	35.9205	1	0
12	0.94247	2	40.5068	2	0
13	1.68767	2	57.0384	1	0
14	5.94247	2	63.1452	1	0
15	2.34247	2	62.0630	1	0
16	0.89863	2	56.5342	1	1
17	9.03288	1	22.9945	2	0
18	9.63014	1	18.4712	1	0
19	0.52603	2	41.2521	1	0
20	1.82192	2	29.5178	1	0

Maximum likelihood estimates of the model parameters shown in Output 75.7.2 are displayed by default.

Output 75.7.2 Maximum Likelihood Parameter Estimates

The LIFEREG Procedure

Bayesian Analysis

Analysis of Maximum Likelihood Parameter Estimates

Parameter		DF	Estimate	Standard Error	95% Confidence Limits	
Intercept		1	2.4402	0.3716	1.7119	3.1685
age		1	-0.0115	0.0070	-0.0253	0.0023
sex	1	1	-0.1170	0.1978	-0.5046	0.2707
sex	2	0	0.0000	.	.	.
perform		1	0.2905	0.3222	-0.3411	0.9220
Scale		1	1.2537	0.0824	1.1021	1.4260
Weibull Shape		1	0.7977	0.0524	0.7012	0.9073

Since no prior distributions for the regression coefficients were specified, the default uniform improper distributions shown in the "Uniform Prior for Regression Coefficients" table in Output 75.7.3 are used. The specified gamma prior for the Weibull shape parameter is also shown in Output 75.7.3.

Output 75.7.3 Model Parameter Priors

The LIFEREG Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients	
Parameter	**Prior**
Intercept	Constant
age	Constant
sex1	Constant
perform	Constant

Independent Prior Distributions for Model Parameters					
Parameter	**Prior Distribution**	**Hyperparameters**			
Weibull Shape	Gamma	Shape	0.001	Inverse Scale	0.001

Fit statistics, descriptive statistics, interval statistics, and the sample parameter correlation matrix for the posterior sample are displayed in the tables in Output 75.7.4. Since noninformative prior distributions for the regression coefficients were used, the mean and standard deviations of the posterior distributions for the model parameters are close to the maximum likelihood estimates and standard errors.

Output 75.7.4 Posterior Sample Statistics

Fit Statistics	
DIC (smaller is better)	875.512
pD (effective number of parameters)	5.115

The LIFEREG Procedure

Bayesian Analysis

Posterior Summaries						
				Percentiles		
Parameter	**N**	**Mean**	**Standard Deviation**	**25%**	**50%**	**75%**
Intercept	10000	2.4754	0.3868	2.2101	2.4711	2.7309
age	10000	-0.0117	0.00731	-0.0165	-0.0117	-0.00664
sex1	10000	-0.1247	0.2068	-0.2650	-0.1240	0.0167
perform	10000	0.3212	0.3436	0.0826	0.3091	0.5365
WeibShape	10000	0.7829	0.0521	0.7473	0.7815	0.8180

Posterior Intervals					
		Equal-Tail Interval		HPD Interval	
Parameter	**Alpha**				
Intercept	0.050	1.7382	3.2573	1.6951	3.2070
age	0.050	-0.0261	0.00250	-0.0256	0.00281
sex1	0.050	-0.5299	0.2715	-0.5224	0.2744
perform	0.050	-0.3071	1.0463	-0.3358	1.0044
WeibShape	0.050	0.6841	0.8893	0.6811	0.8857

Output 75.7.4 *continued*

Posterior Correlation Matrix

Parameter	Intercept	age	sex1	perform	WeibShape
Intercept	1.0000	-.8976	-.3075	-.0663	-.1313
age	-.8976	1.0000	-.0422	-.0460	0.0663
sex1	-.3075	-.0422	1.0000	0.0898	0.0412
perform	-.0663	-.0460	0.0898	1.0000	-.0418
WeibShape	-.1313	0.0663	0.0412	-.0418	1.0000

The default diagnostic statistics are displayed in Output 75.7.5. See the section "Assessing Markov Chain Convergence" on page 140 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for more details on Bayesian convergence diagnostics.

Output 75.7.5 Convergence Diagnostics

The LIFEREG Procedure

Bayesian Analysis

Posterior Autocorrelations

Parameter	Lag 1	Lag 5	Lag 10	Lag 50
Intercept	0.0794	-0.0050	0.0004	-0.0182
age	0.0069	-0.0085	-0.0038	-0.0104
sex1	0.6385	0.0666	-0.0001	-0.0154
perform	0.6676	0.0896	0.0215	0.0094
WeibShape	0.0844	0.0123	-0.0013	0.0025

Geweke Diagnostics

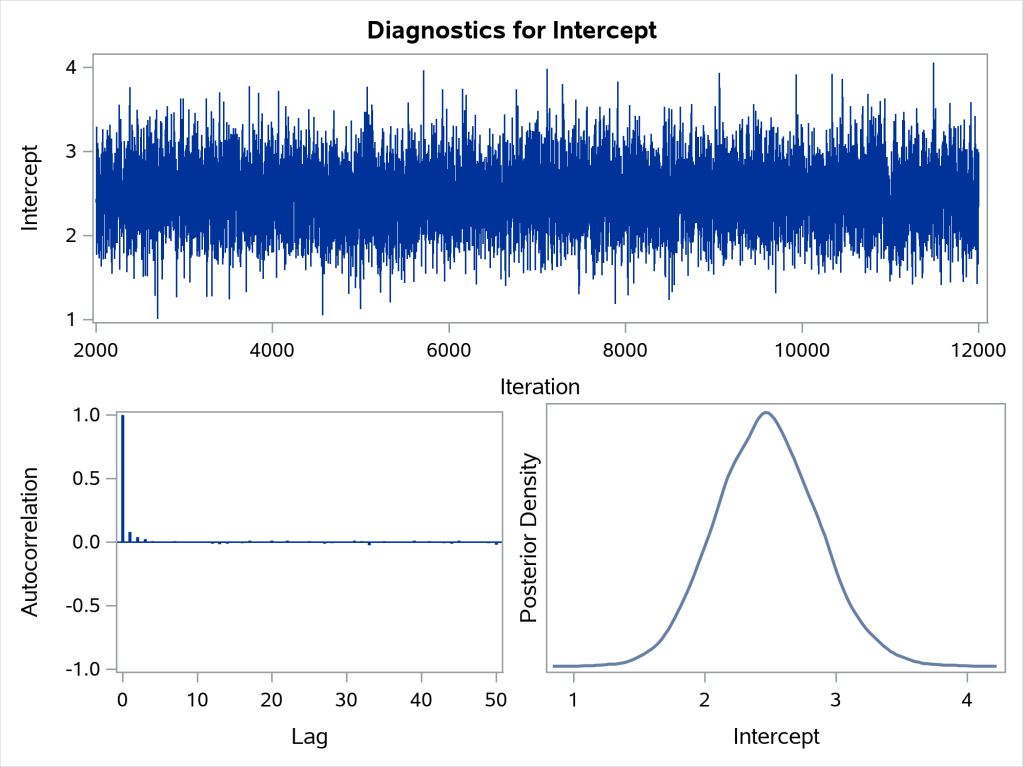
Parameter	z	Pr > |z|
Intercept	0.4727	0.6364
age	-0.9149	0.3603
sex1	0.4041	0.6862
perform	1.1278	0.2594
WeibShape	-0.3212	0.7481

Effective Sample Sizes

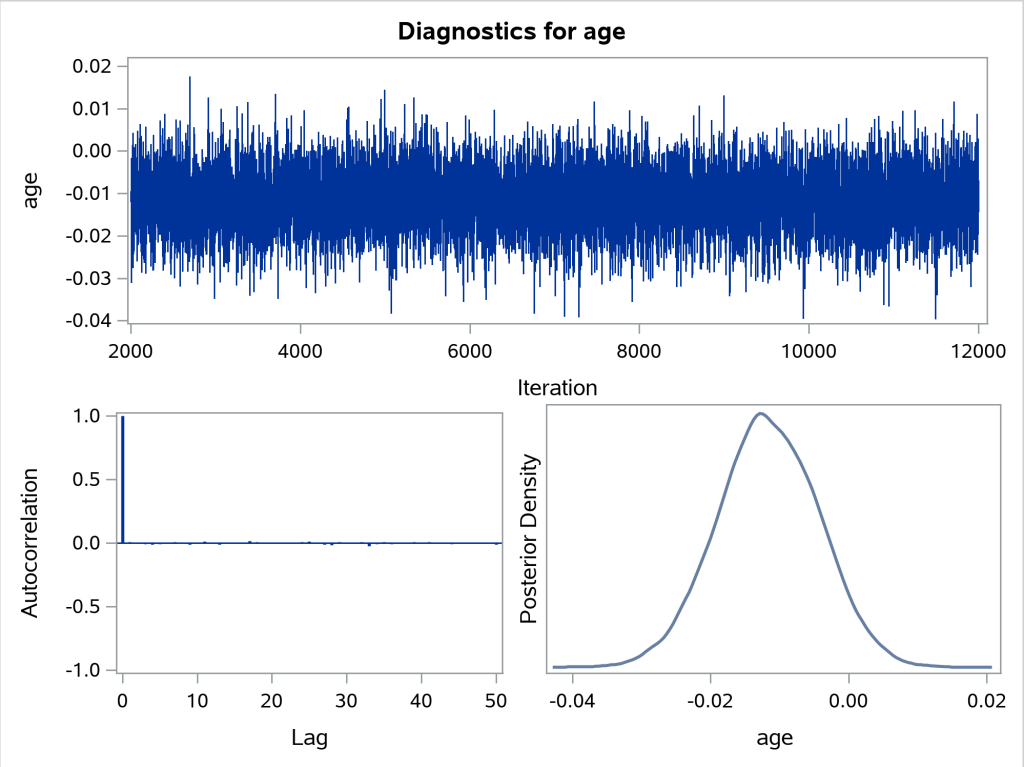
Parameter	ESS	Autocorrelation Time	Efficiency
Intercept	7732.1	1.2933	0.7732
age	10000.0	1.0000	1.0000
sex1	2503.2	3.9948	0.2503
perform	2263.9	4.4172	0.2264
WeibShape	8226.0	1.2157	0.8226

Trace, autocorrelation, and density plots for the seven model parameters are shown in Output 75.7.6 through Output 75.7.10. These plots show no indication that the Markov chains have not converged. See the sections "Assessing Markov Chain Convergence" on page 140 and "Visual Analysis via Trace Plots" on page 141 in Chapter 7, "Introduction to Bayesian Analysis Procedures," for more information about assessing the convergence of the chain of posterior samples.

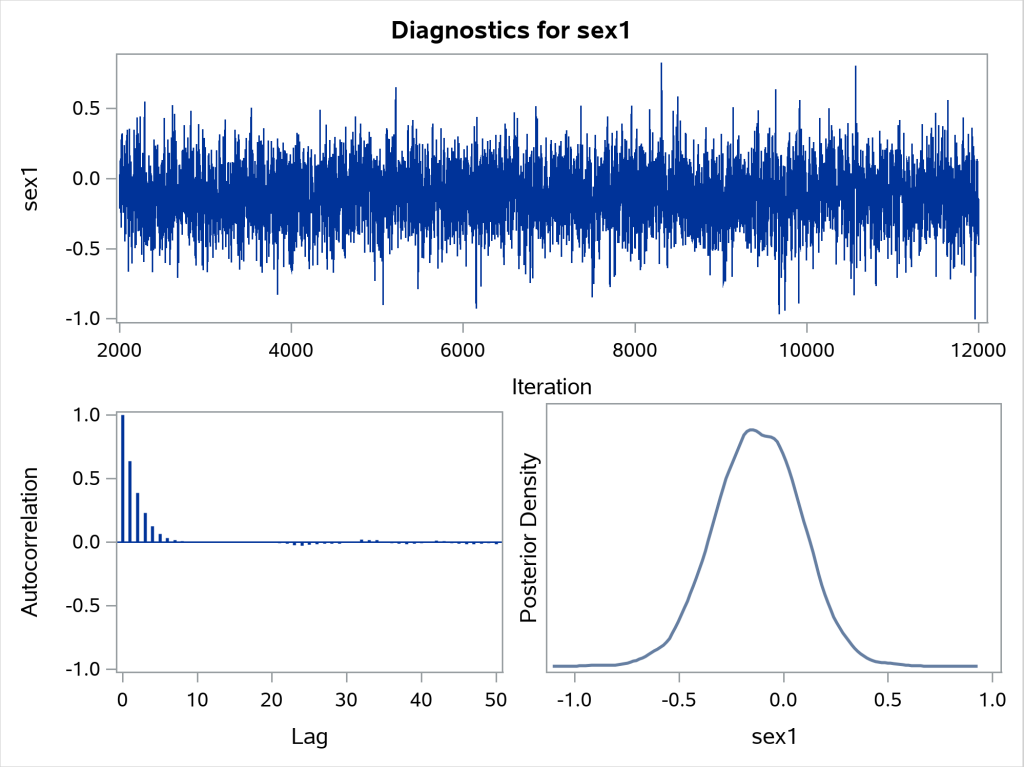
Output 75.7.6 Diagnostic Plots



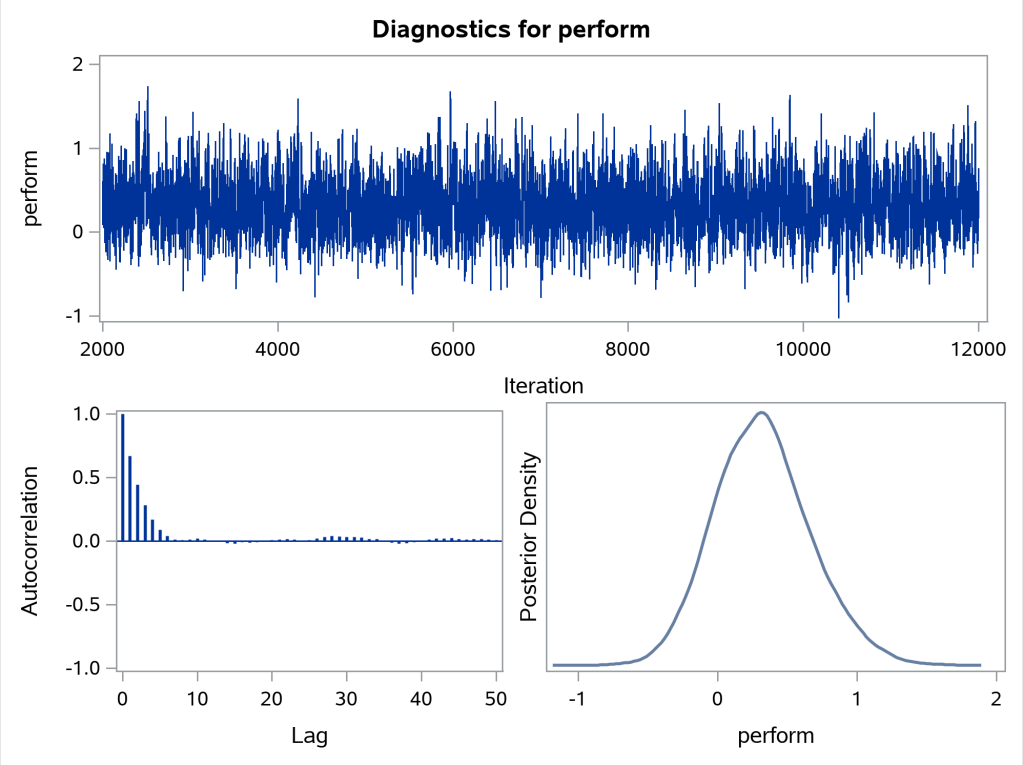
Output 75.7.7 Diagnostic Plots



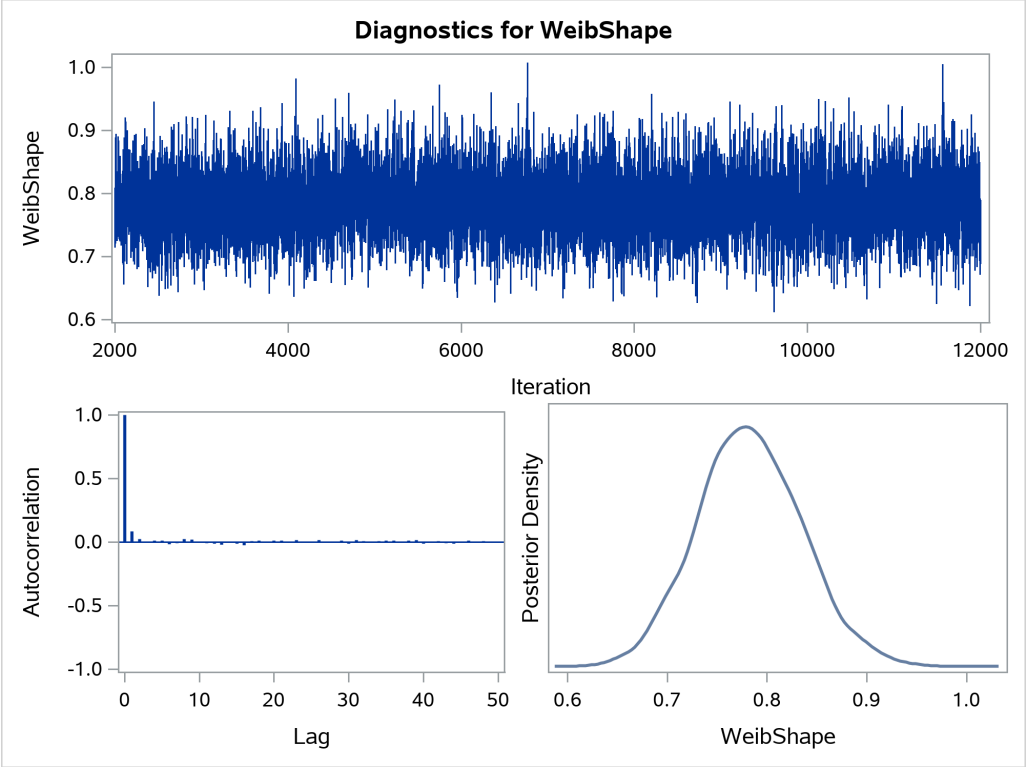
Output 75.7.8 Diagnostic Plots



Output 75.7.9 Diagnostic Plots



Output 75.7.10 Diagnostic Plots



Example 75.8: Model Postfitting Analysis

PROC LIFEREG enables you to make model-based inferences. This example uses the larynx cancer data (Klein and Moeschberger 1997) to illustrate usage of the LSMEANS and LSMESTIMATE statements for model postfitting analysis.

The survival time is modeled by a proportional odds model with two covariates: patient age and cancer stage (1, 2, 3, 4). The following statements use PROC LIFEREG to fit this model:

```
ods graphics on;

proc sort data=Larynx;
   by DESCENDING Stage;
run;

proc lifereg data=Larynx order=data;
   class Stage;
   model Time*Death(0) = Age Stage / dist = llogistic;
   lsmeans Stage / diff adjust=Sidak;
run;
```

The LSMEANS statement compares pairwise differences in survival times among the four different cancer stages, while adjusting for age. The ADJUST=SIDAK option uses the Sidak method to control the overall Type I error rate of these comparisons. Results are displayed in Output 75.8.1.

Output 75.8.1 LS-Means Differences between Disease Stages

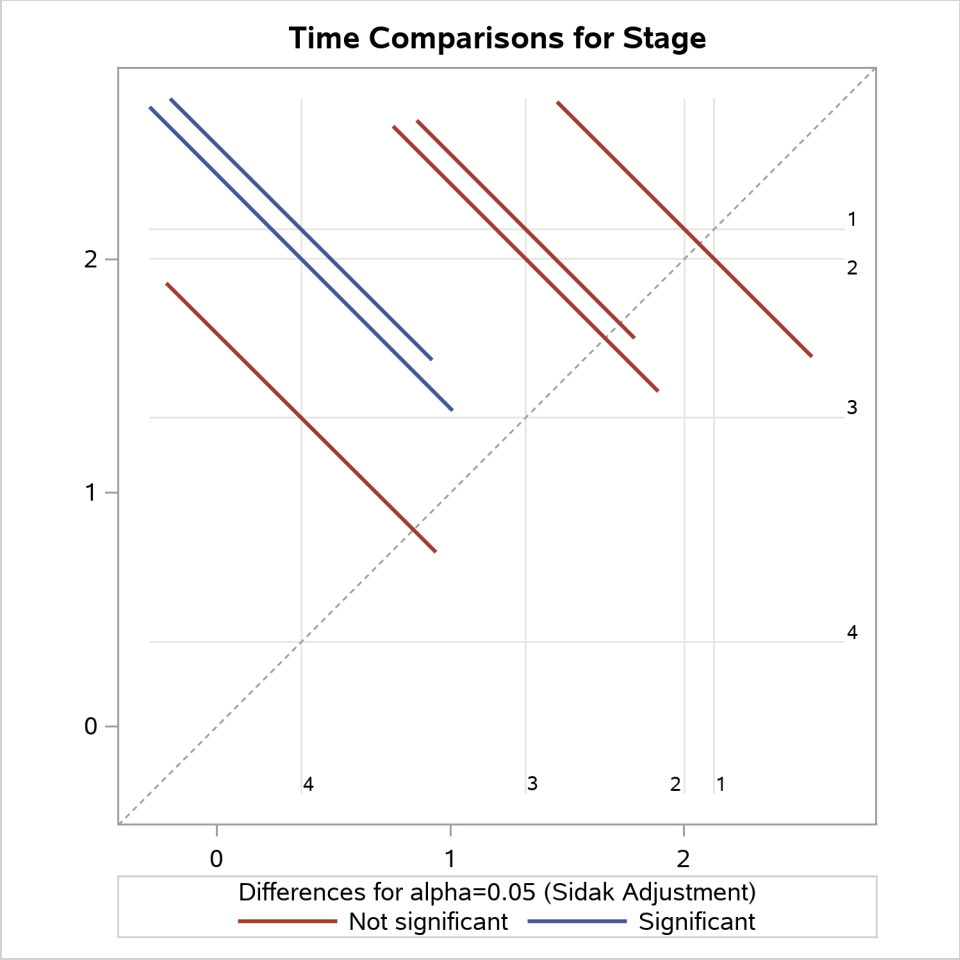
The LIFEREG Procedure

Differences of Stage Least Squares Means
Adjustment for Multiple Comparisons: Sidak

Stage	_Stage	Estimate	Standard Error	z Value	Pr > |z|	Adj P
4	3	-0.9604	0.4379	-2.19	0.0283	0.1581
4	2	-1.6404	0.4931	-3.33	0.0009	0.0053
4	1	-1.7661	0.4257	-4.15	<.0001	0.0002
3	2	-0.6800	0.4316	-1.58	0.1151	0.5199
3	1	-0.8057	0.3539	-2.28	0.0228	0.1292
2	1	-0.1257	0.4152	-0.30	0.7621	0.9998

All the LS-means differences and their significance are displayed by the mean-mean scatter plot in Output 75.8.2.

Output 75.8.2 Plot of Pairwise LS-Means Differences



Suppose you want to jointly test whether the effects of stages 2, 3, and 4 are different from stage 1. The following LSMESTIMATE statement contrasts the LS-means of stages 2, 3, and 4 against the LS-means of

stage 1:

```
proc lifereg data=Larynx order=data;
   class Stage year;
   model Time*Death(0) = Age Stage / dist = llogistic;
   lsmestimate Stage 'Stage 4 vs 1' 1 0 0 -1,
                     'Stage 3 vs 1' 0 1 0 -1,
                     'Stage 2 vs 1' 0 0 1 -1 / cl adjust=Sidak;
run;
```

The CL option produces 95% confidence limits, including both unadjusted ones and those adjusted for multiple comparisons according to the ADJUST= option. Results are displayed in Output 75.8.3.

Output 75.8.3 Custom LS-Means Tests and Relative Odds

The LIFEREG Procedure

Least Squares Means Estimates
Adjustment for Multiplicity: Sidak

Effect	Label	Estimate	Standard Error	z Value	Pr > |z|	Adj P	Alpha	Lower	Upper	Adj Lower	Adj Upper
Stage	Stage 4 vs 1	-1.7661	0.4257	-4.15	<.0001	0.0001	0.05	-2.6004	-0.9319	-2.7825	-0.7498
Stage	Stage 3 vs 1	-0.8057	0.3539	-2.28	0.0228	0.0668	0.05	-1.4993	-0.1122	-1.6507	0.03921
Stage	Stage 2 vs 1	-0.1257	0.4152	-0.30	0.7621	0.9865	0.05	-0.9395	0.6881	-1.1171	0.8657

You can also perform the preceding analysis for a Bayesian model. The following statements generate posterior samples from a Bayesian model and request an LS-means analysis to compare the stage effects:

```
proc lifereg data=Larynx order=data;
   class Stage;
   model Time*Death(0) = Age Stage / dist = llogistic;
   bayes seed=100 nmc=500 nbi=500 diagnostic=none outpost=OOO;
   lsmeans Stage / diff exp;
   lsmestimate Stage 'Stage 4 vs 1' 1 0 0 -1,
                     'Stage 3 vs 1' 0 1 0 -1,
                     'Stage 2 vs 1' 0 0 1 -1
                        / cl plots=boxplot(orient=horizontal);
run;
```

Because no prior distributions for the regression coefficients were specified, the default uniform improper distributions shown in the "Uniform Prior for Regression Coefficients" table in Output 75.8.4 are used. The specified gamma prior for the scale parameter is also shown in Output 75.8.4.

Output 75.8.4 Model Parameter Priors

The LIFEREG Procedure

Bayesian Analysis

Uniform Prior for Regression Coefficients

Parameter	Prior
Intercept	Constant
Age	Constant
Stage4	Constant
Stage3	Constant
Stage2	Constant

Independent Prior Distributions for Model Parameters

Parameter	Prior Distribution	Hyperparameters
Scale	Gamma	Shape 0.001 Inverse Scale 0.001

Under the Bayesian framework, the LS-means differences are treated as random variables for which posterior samples are readily available according to the linear relationship of LS-means and the regression coefficients. Output 75.8.5 lists the sample mean, standard deviation, and percentiles for each LS-means difference.

Output 75.8.5 LS-Means Differences between Disease Stages

Sample Differences of Stage Least Squares Means

					Percentiles					Percentiles for Exponentiated		
Stage	_Stage	N	Estimate	Standard Deviation	25th	50th	75th	Exponentiated	Standard Error of Exponentiated	25th	50th	75th
4	3	500	-0.9307	0.4752	-1.2743	-0.9446	-0.6086	0.4426	0.232690	0.2796	0.3888	0.5441
4	2	500	-1.6591	0.5327	-2.0161	-1.6573	-1.2861	0.2181	0.115808	0.1332	0.1907	0.2763
4	1	500	-1.8001	0.4321	-2.0951	-1.7943	-1.5491	0.1815	0.082975	0.1231	0.1663	0.2124
3	2	500	-0.7284	0.4828	-1.0488	-0.7219	-0.3975	0.5410	0.268735	0.3504	0.4858	0.6720
3	1	500	-0.8694	0.3727	-1.1199	-0.8541	-0.6149	0.4488	0.168055	0.3263	0.4257	0.5407
2	1	500	-0.1410	0.4413	-0.4126	-0.1417	0.1363	0.9585	0.462376	0.6619	0.8679	1.1461

The LSMESTIMATE statement produces summary statistics of the posterior samples for the specified LS-means contrasts. Results are presented in Output 75.8.6; they are very similar to the results based on maximum likelihood in Output 75.8.3.

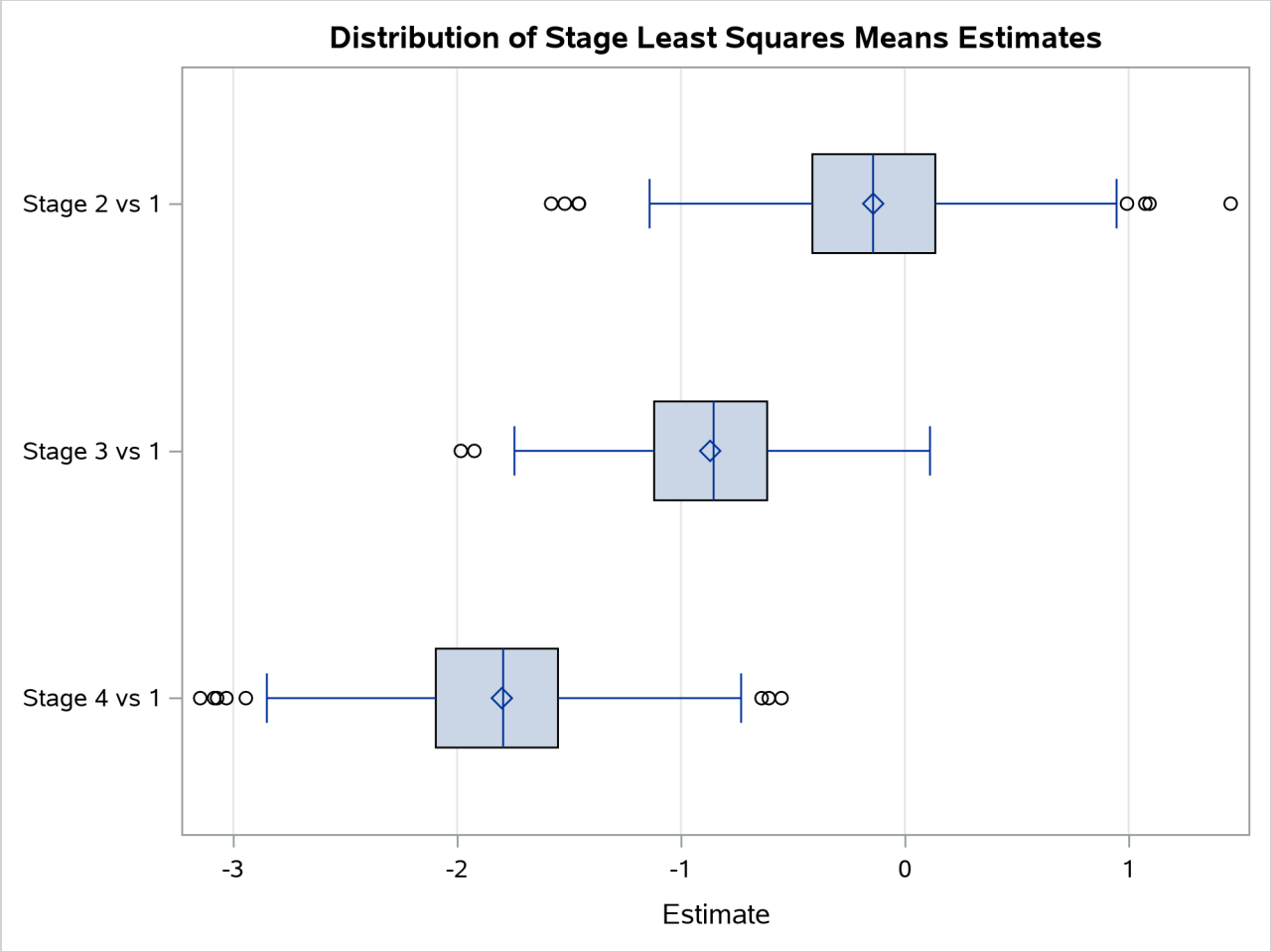
Output 75.8.6 Summary Statistics of Custom LS-Means Differences

Sample Least Squares Means Estimates

					Percentiles					
Effect	Label	N	Estimate	Standard Deviation	25th	50th	75th	Alpha	Lower HPD	Upper HPD
Stage	**Stage 4 vs 1**	500	-1.8001	0.4321	-2.0951	-1.7943	-1.5491	0.05	-2.6279	-0.8897
Stage	**Stage 3 vs 1**	500	-0.8694	0.3727	-1.1199	-0.8541	-0.6149	0.05	-1.6033	-0.2031
Stage	**Stage 2 vs 1**	500	-0.1410	0.4413	-0.4126	-0.1417	0.1363	0.05	-1.1401	0.6252

The PLOTS= option uses ODS Graphics to display the Bayesian samples. A box plot is presented in Output 75.8.7.

Output 75.8.7 Box Plot of Sampled LS-Means Differences



References

Abernethy, R. B. (1996). *The New Weibull Handbook*. 2nd ed. North Palm Beach, FL: Robert B. Abernethy.

Akaike, H. (1979). "A Bayesian Extension of the Minimum AIC Procedure of Autoregressive Model Fitting." *Biometrika* 66:237–242.

Akaike, H. (1981). "Likelihood of a Model and Information Criteria." *Journal of Econometrics* 16:3–14.

Cox, D. R., and Oakes, D. (1984). *Analysis of Survival Data*. London: Chapman & Hall.

Gentleman, R., and Geyer, C. J. (1994). "Maximum Likelihood for Interval Censored Data: Consistency and Computation." *Biometrika* 81:618–623.

Gilks, W. R. (2003). "Adaptive Metropolis Rejection Sampling (ARMS)." Software from MRC Biostatistics Unit, Cambridge, UK. http://www.maths.leeds.ac.uk/~wally.gilks/adaptive.rejection/web_page/Welcome.html.

Gilks, W. R., Best, N. G., and Tan, K. K. C. (1995). "Adaptive Rejection Metropolis Sampling within Gibbs Sampling." *Journal of the Royal Statistical Society, Series C* 44:455–472.

Gilks, W. R., Richardson, S., and Spiegelhalter, D. J. (1996). *Markov Chain Monte Carlo in Practice*. London: Chapman & Hall.

Gilks, W. R., and Wild, P. (1992). "Adaptive Rejection Sampling for Gibbs Sampling." *Journal of the Royal Statistical Society, Series C* 41:337–348.

Greene, W. H. (1993). *Econometric Analysis*. 2nd ed. New York: Macmillan.

Ibrahim, J. G., Chen, M.-H., and Sinha, D. (2001). *Bayesian Survival Analysis*. New York: Springer-Verlag.

Kalbfleisch, J. D., and Prentice, R. L. (1980). *The Statistical Analysis of Failure Time Data*. New York: John Wiley & Sons.

Klein, J. P., and Moeschberger, M. L. (1997). *Survival Analysis: Techniques for Censored and Truncated Data*. New York: Springer-Verlag.

Lawless, J. F. (2003). *Statistical Model and Methods for Lifetime Data*. 2nd ed. New York: John Wiley & Sons.

Maddala, G. S. (1983). *Limited-Dependent and Qualitative Variables in Econometrics*. New York: Cambridge University Press.

Meeker, W. Q., and Escobar, L. A. (1998). *Statistical Methods for Reliability Data*. New York: John Wiley & Sons.

Mroz, T. A. (1987). "The Sensitivity of an Empirical Model of Married Women's Work to Economic and Statistical Assumptions." *Econometrica* 55:765–799.

Nair, V. N. (1984). "Confidence Bands for Survival Functions with Censored Data: A Comparative Study." *Technometrics* 26:265–275.

Nelson, W. (1982). *Applied Life Data Analysis*. New York: John Wiley & Sons.

Nelson, W. (1990). *Accelerated Testing: Statistical Models, Test Plans, and Data Analyses*. New York: John Wiley & Sons.

Rao, C. R. (1973). *Linear Statistical Inference and Its Applications*. 2nd ed. New York: John Wiley & Sons.

Simonoff, J. S. (2003). *Analyzing Categorical Data*. New York: Springer-Verlag.

Spiegelhalter, D. J., Best, N. G., Carlin, B. P., and Van der Linde, A. (2002). "Bayesian Measures of Model Complexity and Fit." *Journal of the Royal Statistical Society, Series B* 64:583–616. With discussion.

Tobin, J. (1958). "Estimation of Relationships for Limited Dependent Variables." *Econometrica* 26:24–36.

Turnbull, B. W. (1976). "The Empirical Distribution Function with Arbitrarily Grouped, Censored, and Truncated Data." *Journal of the Royal Statistical Society, Series B* 38:290–295.

Subject Index

Syntax Index