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

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Chapter 38
The CAUSALTRT Procedure

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Overview: CAUSALTRT Procedure

The CAUSALTRT procedure estimates the average causal effect of a binary treatment, *T*, on a continuous or discrete outcome, *Y*. Although the causal effect that is defined and estimated in PROC CAUSALTRT is called a treatment effect, it is not confined to effects that result from controllable treatments (such as effects in an experiment). Depending on the application, the binary treatment variable *T* can represent an intervention (such as smoking cessation versus control), an exposure to a condition (such as attending a private versus public school), or an existing characteristic of subjects (such as high versus low socioeconomic status). The CAUSALTRT procedure can estimate two types of causal effects: the average treatment effect (ATE) and the average treatment effect for the treated (ATT). For more information about the causal effects that the CAUSALTRT procedure can estimate, see the section "Causal Effects: Definitions, Assumptions, and Identification" on page 2435.

The CAUSALTRT procedure implements causal inference methods that are designed primarily for use with data from nonrandomized trials or observational studies. In an observational study, you observe the treatment *T* and the outcome *Y* without assigning subjects randomly to the treatment conditions. Instead, subjects "select" themselves into the treatment conditions according to their pretreatment characteristics. If these pretreatment characteristics are also associated with the outcome *Y*, they induce a specious relationship between *T* and *Y* and hence cloud the causal interpretation of *T* on *Y*. Therefore, estimating the causal effect of *T* in observational studies usually requires adjustments that remove or counter the specious effects that are induced by the confounding variables.

To adjust for the effects of the confounding variables, you can model either the treatment assignment *T* or the outcome *Y*, or both. Modeling the treatment leads to inverse probability weighting methods, and modeling the outcome leads to regression adjustment methods. Combined modeling of the treatment and outcome leads to doubly robust methods that can provide unbiased estimates for the treatment effect even if one of the models is misspecified. For more information about which model specifications are required for different estimation methods and how default estimation methods are determined, see the section "Outline of Estimation Method Requirements" on page 2407. For an introduction to causal inference from nonrandomized data, see Imbens and Rubin (2015); Morgan and Winship (2015); Berzuini, Dawid, and Bernardinelli (2012).

Features of the CAUSALTRT Procedure

The CAUSALTRT procedure provides the following methods to estimate causal effects:

- inverse probability weighting methods
- regression adjustment
- doubly robust methods

You can estimate two types of causal effects:

- average treatment effect (ATE), also sometimes called the average causal effect (ACE)
- average treatment effect for the treated (ATT or ATET)

For more information about the causal effects that the CAUSALTRT procedure can estimate, see the section "Causal Effects: Definitions, Assumptions, and Identification" on page 2435.

PROC CAUSALTRT computes standard errors and confidence intervals for the causal effects by the following methods:

- asymptotic methods
- bootstrap methods (which you request by specifying the BOOTSTRAP statement)

For more information about how the CAUSALTRT procedure computes standard errors and confidence limits, see the section "Standard Errors and Confidence Intervals" on page 2445.

PROC CAUSALTRT provides the following types of graphical output:

- diagnostic plots for the propensity score model, including various plots of propensity scores or weights
- histograms for bootstrap estimates

Finally, you can save the propensity scores, inverse probability weights, and the predicted potential outcomes in a SAS data set.

Outline of Estimation Method Requirements

The CAUSALTRT procedure uses various estimation methods to adjust for the effects of confounding variables by fitting models for the treatment assignment T or the outcome Y, or both. For the estimation methods, you specify the outcome variable Y in the MODEL statement and the treatment assignment T in the PSMODEL statement.

Depending on the estimation method that you specify in the METHOD= option in the PROC CAUSALTRT statement, you must also provide specific additional modeling information in the MODEL and PSMODEL statements, as shown in Table 38.1.

Table 38.1 Estimation Method Requirements

METHOD=	Additional Specification
IPW, IPWR, or IPWS	A model for the treatment assignment in the PSMODEL statement.
REGADJ	A model for the outcome in the MODEL statement. If you do not specify an outcome model, PROC CAUSALTRT fits an intercept-only model separately for each treatment condition.
AIPW or IPWREG	Both an outcome model in the MODEL statement and a model for the treatment assignment in the PSMODEL statement.

The model for the treatment assignment is also called the propensity score model.

If you do not specify the METHOD= option in the PROC CAUSALTRT statement, the CAUSALTRT procedure determines a default estimation method based on which models are specified in the MODEL and

PSMODEL statements, according to following criteria:

- When only a treatment model is specified (in the PSMODEL statement), the default estimation method is IPWR. For example:

```
proc causaltrt;
   model y;
   psmodel trt = x1 x2;
run;
```

- When only an outcome model is specified (in the MODEL statement), the default estimation method is REGADJ. For example:

```
proc causaltrt;
   model y = x1 x2;
   psmodel trt;
run;
```

- When both the treatment and outcome models are specified, the default estimation method is AIPW. For example:

```
proc causaltrt;
   model y = x1 x2;
   psmodel trt = x1 x2;
run;
```

- When neither an outcome nor a treatment model is specified, the default estimation method is REGADJ with an intercept-only outcome model. For example:

```
proc causaltrt;
   model y;
   psmodel trt;
run;
```

If you specify the ATT option in the PROC CAUSALTRT statement, then you are estimating the average treatment effect for the treated (ATT) instead of the default average treatment effect (ATE). In this case, estimation methods are limited to either IPWR or regression adjustment. Therefore, if models for both the treatment assignment and outcome variable are specified without the METHOD=IPWR or METHOD=REGADJ option, PROC CAUSALTRT issues an error.

The CAUSALTRT procedure fits only the models necessary for the estimation method used. For example, if a model for the treatment assignment is specified but the REGADJ estimation method is requested, then PROC CAUSALTRT does not fit the treatment model and therefore does not produce output or displays that involve the propensity scores or weights.

For more information about the estimation methods that the CAUSALTRT procedure implements, see the sections "Estimating the Average Treatment Effect (ATE)" on page 2438 and "Estimating the Average Treatment Effect for the Treated (ATT)" on page 2443.

Getting Started: CAUSALTRT Procedure

This section illustrates some of the basic features of the CAUSALTRT procedure. This example uses data from a hypothetical nonrandomized trial.

Suppose that 486 patients in a trial are at risk for developing type 2 diabetes and are allowed to choose which of two preventive drugs they want to receive. For this study, the outcome of interest is whether a patient develops type 2 diabetes within five years. The nonrandom assignment of patients to treatment conditions does not control for confounding variables that might explain any observed difference between the treatment conditions. The hypothetical data set Drugs contains the following variables:

- Age: age at the start of the trial
- BMI: body mass index at the start of the trial
- Diabetes2: indicator for whether a patient developed type 2 diabetes, with values Yes and No
- Drug: indicator of treatment assignment, with values Drug_A and Drug_X
- Gender: gender

The first 10 observations in the Drugs data set are listed in Figure 38.1.

Figure 38.1 Drug Trial Data

Obs	Gender	Age	BMI	Drug	Diabetes2
1	Male	29	22.02	Drug_A	Yes
2	Female	30	23.83	Drug_X	Yes
3	Female	42	23.64	Drug_X	Yes
4	Male	47	23.67	Drug_A	No
5	Female	42	22.27	Drug_A	Yes
6	Male	45	26.90	Drug_A	Yes
7	Female	46	24.06	Drug_A	Yes
8	Female	45	23.41	Drug_A	Yes
9	Female	28	24.65	Drug_X	No
10	Male	36	20.13	Drug_X	Yes

The following statements invoke the CAUSALTRT procedure and request the estimation of the average treatment effect (ATE) by using the inverse probability weighting method with ratio adjustment (METHOD=IPWR):

```
proc causaltrt data=drugs method=ipwr ppsmodel;
   class Gender;
   psmodel Drug(ref='Drug_A') = Age Gender BMI;
   model Diabetes2(ref='No') / dist = bin;
run;
```

The results of this analysis are shown in the following figures. In Figure 38.2, PROC CAUSALTRT displays information about the estimation method used, the outcome variable, and the treatment variable.

Figure 38.2 Model Information

The CAUSALTRT Procedure

Model Information	
Data Set	WORK.DRUGS
Distribution	Binomial
Estimation Method	IPWR
Treatment Variable	Drug
Outcome Variable	Diabetes2

The METHOD= option in the PROC CAUSALTRT statement specifies the estimation method to be used. The outcome variable, Diabetes2, is specified in the MODEL statement, and the treatment variable, Drug, is specified in the PSMODEL statement.

The DIST=BIN option in the MODEL statement identifies the outcome as a binary variable, and the **`ref='No'`** option identifies No as the reference level. In the PSMODEL statement, the **`ref='Drug_A'`** option identifies Drug_A as the reference (control) condition when the treatment assignment is modeled and the ATE is estimated. The frequencies for the outcome and treatment variable categories are listed in the "Response Profile" (Figure 38.3) and "Treatment Profile" (Figure 38.4) tables, respectively.

Figure 38.3 Response Profile

Response Profile		
Ordered Value	**Diabetes2**	**Total Frequency**
1	Yes	287
2	No	199

Figure 38.4 Treatment Profile

Treatment Profile		
Ordered Value	**Drug**	**Total Frequency**
1	Drug_X	149
2	Drug_A	337

The IPWR estimation method uses inverse probability weighting to estimate the potential outcome means and ATE. The inverse probability weights are estimated by inverting the predicted probability of receiving treatment (that is, the Drug_X condition), which is estimated from a logistic regression model that is specified in the PSMODEL statement. The probability of receiving treatment is called the propensity score, and hence the regression model fit by the PSMODEL statement is also called the propensity score model. In this example, the predictors of the propensity score model are Age, Gender, and BMI. The PPSMODEL option in the PROC CAUSALTRT statement displays the parameter estimates for the propensity score model, as shown in Figure 38.5.

Figure 38.5 Propensity Score Model Estimates

The CAUSALTRT Procedure

Propensity Score Model Estimates

Parameter		Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		-0.6226	1.2738	-3.1193	1.8740	0.2389	0.6250
Age		-0.0888	0.0170	-0.1220	-0.0556	27.4228	<.0001
Gender	Female	-0.2103	0.2055	-0.6130	0.1924	1.0474	0.3061
Gender	Male	0	.	.	.	.	.
BMI		0.1434	0.0517	0.0422	0.2447	7.7115	0.0055

The estimates for the potential outcome means (POM) and ATE are displayed in the "Analysis of Causal Effect" table (Figure 38.6). The ATE estimate of –0.1787 indicates that Drug_X is more effective on average than Drug_A in preventing the development of type 2 diabetes. The ATE is significantly different from 0 at the 0.05 α-level, as indicated by the 95% confidence interval (–0.2771, –0.0803) or the p-value (0.0004).

Figure 38.6 IPWR Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	Drug_X	0.4681	0.0431	0.3835	0.5526	10.85	<.0001
POM	Drug_A	0.6468	0.0265	0.5948	0.6988	24.38	<.0001
ATE		-0.1787	0.0502	-0.2771	-0.08031	-3.56	0.0004

The ATE of Drug_X compared to Drug_A can also be estimated by using augmented inverse probability weights (AIPW). In addition to a propensity score model, the AIPW estimation method incorporates a model for the outcome variable, Diabetes2, into the estimation of the potential outcome means and ATE. The AIPW estimation method is doubly robust and provides unbiased estimates for the ATE even if one of the outcome or treatment models is misspecified.

The following statements invoke the CAUSALTRT procedure and use the AIPW estimation method to estimate the ATE:

```
proc causaltrt data=drugs method=aipw;
   class Gender;
   psmodel Drug(ref='Drug_A') = Age Gender BMI;
   model Diabetes2(ref='No') = Age Gender BMI / dist = bin;
run;
```

For this example, the same set of effects is specified in both the MODEL and PSMODEL statements, but in general this need not be the case. The use of the AIPW estimation method for this PROC CAUSALTRT step is reflected in the "Model Information" table (Figure 38.7).

Figure 38.7 Model Information

The CAUSALTRT Procedure

Model Information	
Data Set	WORK.DRUGS
Distribution	Binomial
Link Function	Logit
Estimation Method	AIPW
Treatment Variable	Drug
Outcome Variable	Diabetes2

As shown in Figure 38.8, the AIPW estimate for the ATE is –0.1709, which is similar to the IPWR estimate of –0.1787. Moreover, the AIPW standard error estimate for ATE is slightly smaller than that of the IPWR. The AIPW 95% confidence interval for ATE is also slightly narrower than that of the IPWR.

Figure 38.8 AIPW Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect							
Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	Drug_X	0.4782	0.0422	0.3954	0.5609	11.32	<.0001
POM	Drug_A	0.6491	0.0267	0.5968	0.7013	24.33	<.0001
ATE		-0.1709	0.0495	-0.2679	-0.07390	-3.45	0.0006

Syntax: CAUSALTRT Procedure

The following statements are available in the CAUSALTRT procedure. Items within < > are optional.

PROC CAUSALTRT < *options* > **;**
BOOTSTRAP < *options* > **;**
BY *variables* **;**
CLASS *variables* < **(***options***)** > . . . < *variable*< **(***options***)** > > < **/** *global-options* > **;**
FREQ *variable* **;**
MODEL *outcome* < **(***variable-options***)** >< **=** < *effects* > > < **/** *model-options* > **;**
OUTPUT < **OUT=***SAS-data-set* > < *keyword***=***name* . . . *keyword***=***name* > **;**
PSMODEL *treatment* < **(***variable-options***)** >< **=** *effects* < **/** *psmodel-options* > > **;**

The PROC CAUSALTRT, MODEL, and PSMODEL statements are required. The CLASS statement, if present, must precede the MODEL and PSMODEL statements. All statements can appear only once.

All the estimation methods implemented in PROC CAUSALTRT require the specification of both an outcome and a treatment variable. You specify the outcome variable in the MODEL statement and the treatment variable in the PSMODEL statement. In the MODEL and PSMODEL statements, you can use the same syntax to specify main effects and interaction terms for modeling the outcome and treatment assignment. This syntax is described in the section "Specification of Effects" on page 4083 in Chapter 52, "The GLM Procedure." For more information about which model specifications are required for different estimation

methods and how default estimation methods are determined, see the section "Outline of Estimation Method Requirements" on page 2407. The following sections describe the PROC CAUSALTRT statement and then describe the other statements in alphabetical order.

PROC CAUSALTRT Statement

PROC CAUSALTRT < *options* > **;**

The PROC CAUSALTRT statement invokes the CAUSALTRT procedure. Table 38.2 summarizes the *options* available in the PROC CAUSALTRT statement.

Table 38.2 PROC CAUSALTRT Statement Options

Option	Description
Input	
DATA=	Specifies the input data set
Response and Classification Variable Options	
DESCENDING	Sorts the outcome variable in reverse of the default order
NAMELEN=	Specifies the length of effect names
ORDER=	Specifies the sort order of the classification variables
RORDER=	Specifies the sort order of the outcome variable
Estimation and Analysis	
ATT	Estimates the average treatment effect for the treated
COVDIFFPS	Computes and displays standardized mean differences for the effects in the propensity score model
METHOD=	Specifies the estimation method
Displayed Output	
ALPHA=	Specifies the level for confidence limits
NOEFFECT	Suppresses all displayed output that involves the outcome variable
NOPRINT	Suppresses all displayed output
PALL	Displays all optional output
PLOTS	Produces ODS Graphics displays
POUTCOMEMOD	Displays outcome model parameter estimates
PPSMODEL	Displays propensity score model parameter estimates
Technical Details	
NLOPTIONS	Specifies optimization parameters for fitting the specified models
SINGULAR=	Specifies the singularity tolerance
THREADS=	Specifies the number of threads for the computation

You can specify the following *options*.

ALPHA=*number*

specifies a *number* to be used as the α level for $100(1-\alpha)\%$ confidence limits in the "Analysis of Causal Effect" table. The *number* must be between 0 and 1. This *number* is also used as the default level for propensity score and outcome model confidence limits. For the propensity score and outcome models, you can override this default level by specifying the ALPHA= options in the MODEL and PSMODEL statements, respectively. By default, ALPHA=0.05, which results in 95% confidence intervals.

ATT

ATET

estimates the average treatment effect for the treated. When this option is applied, it replaces the default estimation of the average treatment effect (ATE). For more information about the estimation methods implemented in the CAUSALTRT procedure and for comparisons between the average treatment effect and average treatment effect for the treated, see the sections "Estimating the Average Treatment Effect for the Treated (ATT)" on page 2443 and "Causal Effects: Definitions, Assumptions, and Identification" on page 2435. This option can be used only when METHOD=IPWR or REGADJ.

COVDIFFPS

computes weighted and unweighted standardized mean differences (between treatment and control conditions) and variance ratios (treatment to control) for the covariates (effects) in the propensity score model. This option is supported only for estimation methods that fit a propensity score model.

The results are displayed in the "Covariate Differences for Propensity Score Model" table. This table also includes columns for the weighted and unweighted mean and variance for propensity score model effects within each treatment condition; these columns are not displayed but are accessible if you save the table as an output data set by specifying the ODS OUTPUT statement. You can display these columns by modifying the corresponding template.

DATA=*SAS-data-set*

names the SAS data set that contains the data to be analyzed. If you omit this option, the procedure uses the most recently created SAS data set.

DESCENDING

DESCEND

DESC

sorts the levels of the outcome variable for a binary model in reverse of the specified order.

METHOD= AIPW | IPW | IPWR | IPWS | REGADJ | IPWREG

specifies the method to use to estimate the potential outcomes and treatment effect. You can specify one of the following values:

AIPW performs a doubly robust estimation by using augmented inverse probability weighting. You must specify a model for the outcome variable in the MODEL statement and a model for the treatment assignment in the PSMODEL statement.

IPW uses a basic inverse probability weighting method. You must specify a model for the treatment assignment in the PSMODEL statement.

IPWR uses an inverse probability weighting method with ratio adjustment. You must specify a model for the treatment assignment in the PSMODEL statement.

IPWS uses an inverse probability weighting method with ratio and scale adjustments. You must specify a model for the treatment assignment in the PSMODEL statement.

IPWREG performs a doubly robust estimation by using inverse probability weighted regression adjustment. You must specify a model for the outcome variable in the MODEL statement and a model for the treatment assignment in the PSMODEL statement.

REGADJ uses regression adjustment. You must specify a model for the outcome variable in the MODEL statement.

For all estimation methods, you specify the outcome variable in the MODEL statement and the treatment variable in the PSMODEL statement. For more information about the estimation methods that the CAUSALTRT procedure implements, see the sections "Estimating the Average Treatment Effect (ATE)" on page 2438 and "Estimating the Average Treatment Effect for the Treated (ATT)" on page 2443.

NAMELEN=*n*

specifies the maximum length of effect names in tables and output data sets to be *n* characters, where *n* is a value between 20 and 128. By default, NAMELEN=20.

NLOPTIONS(*nlo-options***)**

specifies options for the nonlinear optimization methods that are used for fitting the specified models. You can specify one or more of the following *nlo-options* separated by spaces:

ABSCONV=*r*

ABSTOL=*r*

specifies an absolute function convergence criterion by which minimization stops when $f(\boldsymbol{\psi}^{(k)}) \leq r$, where $\boldsymbol{\psi}$ is the vector of parameters in the optimization and $f(\cdot)$ is the objective function. The default value of *r* is the negative square root of the largest double-precision value.

ABSFCONV=*r*

ABSFTOL=*r*

specifies an absolute function difference convergence criterion. Termination requires a small change of the function value in successive iterations,

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

where $\boldsymbol{\psi}$ denotes the vector of parameters that participate in the optimization and $f(\cdot)$ is the objective function. By default, ABSFCONV=0.

ABSGCONV=*r*

ABSGTOL=*r*

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

$$\max_j |g_j(\boldsymbol{\psi}^{(k)})| \leq r$$

where $\boldsymbol{\psi}$ denotes the vector of parameters that participate in the optimization and $g_j(\cdot)$ is the gradient of the objective function with respect to the *j*th parameter. By default, ABSGCONV=1E–7.

FCONV=*r*

FTOL=*r*

specifies a relative function convergence criterion. Termination requires a small relative change of the function value in successive iterations,

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

where $\boldsymbol{\psi}$ denotes the vector of parameters that participate in the optimization and $f(\cdot)$ is the objective function. By default, FCONV=$10^{-\mathrm{FDIGITS}}$, where by default FDIGITS is $-\log_{10}\{\epsilon\}$, where ϵ is the machine precision.

GCONV=*r*

GTOL=*r*

specifies a relative gradient convergence criterion. For all values of the TECHNIQUE= suboption except CONGRA, termination requires the normalized predicted function reduction to be small,

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

where $\boldsymbol{\psi}$ denotes the vector of parameters that participate in the optimization, $f(\cdot)$ is the objective function, and $\mathbf{g}(\cdot)$ is the gradient. When TECHNIQUE=CONGRA (for which a reliable Hessian estimate $\mathbf{H}$ is not available), the following criterion is used:

$$\frac{\| \mathbf{g}(\boldsymbol{\psi}^{(k)}) \|_2^2 \quad \| \mathbf{g}(\boldsymbol{\psi}^{(k)}) \|_2}{\| \mathbf{g}(\boldsymbol{\psi}^{(k)}) - \mathbf{g}(\boldsymbol{\psi}^{(k-1)}) \|_2 \, |f(\boldsymbol{\psi}^{(k)})|} \leq r$$

By default, GCONV = 1E–8.

MAXFUNC=*n*

MAXFU=*n*

specifies the maximum number of function calls in the optimization process. The default values are as follows, depending on the value of the TECHNIQUE= suboption:

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

The optimization can terminate only after completing a full iteration. Therefore, the number of function calls that are actually performed can exceed *n*.

MAXITER=*n*

MAXIT=*n*

specifies the maximum number of iterations in the optimization process. The default values are as follows, depending on the value of the TECHNIQUE= suboption:

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

These default values also apply when *n* is specified as a missing value.

MAXTIME=*r*
specifies an upper limit of *r* seconds of CPU time for the optimization process. Because the time is checked only at the end of each iteration, the actual run time might be longer than *r*. By default, CPU time is not limited.

TECHNIQUE=CONGRA | DBLDOG | NEWRAP | NRRIDG | QUANEW | TRUREG
specifies the optimization technique to obtain maximum likelihood estimates. You can specify from the following values:

CONGRA	performs a conjugate-gradient optimization.
DBLDOG	performs a version of double-dogleg optimization.
NEWRAP	performs a Newton-Raphson optimization that combines a line-search algorithm with ridging.
NRRIDG	performs a Newton-Raphson optimization with ridging.
QUANEW	performs a dual quasi-Newton optimization.
TRUREG	performs a trust-region optimization.

By default, TECHNIQUE=NEWRAP.

For more information about these optimization methods, see the section "Choosing an Optimization Algorithm" on page 510 in Chapter 19, "Shared Concepts and Topics."

NOEFFECT
suppresses the display of all output that involves the outcome variable. This option is useful for investigating the balance of covariates between treatment conditions by exploring different propensity score models before displaying estimates for the causal effect. This option is effective only when METHOD=IPW, IPWR, or IPWS.

NOPRINT
suppresses all displayed output. 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*.

PALL

ALL

displays all optional output.

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

controls plots that are produced through ODS Graphics. For more information about controlling specific plots, see also the PLOTS options in the BOOTSTRAP and PSMODEL statements.

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

```
ods graphics on;

proc causaltrt plots=all method=ipwr;
   model y;
   psmodel trt = x1 x2;
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."

You can specify the following *plot-requests*:

ALL

produces all plots that are available for the specified estimation method.

BOOTHIST

produces histograms of the bootstrap estimates for the potential outcome means and treatment effect, which are displayed in a panel by default. This option is ignored if the BOOTSTRAP statement is not specified.

LOGITPSCORE

LPS

produces overlaid density plots for the logit of the propensity score within each treatment condition. These plots are not produced when METHOD=REGADJ.

NONE

suppresses all plots. If you specify this *plot-request*, then all plot requests that are specified in the BOOTSTRAP and PSMODEL statements are ignored.

OUTBYPSCORE

OUTBYPS

produces a scatter plot of the outcome variable by the propensity score for nonbinary outcomes. If the outcome is binary, box plots of the propensity scores within treatment conditions are produced for each outcome level. The whisker lengths for each box plot are determined by the maximum and minimum of the propensity scores. This plot is not produced when METHOD=REGADJ.

OUTBYWEIGHT

OUTBYWGT

produces a scatter plot of the outcome variable by weight for nonbinary outcomes. If the outcome is binary, box plots of the weights within treatment conditions are produced for each outcome level. The whisker lengths for each box plot are determined by the maximum and minimum of the weights. This plot is not produced when METHOD=REGADJ.

PSCLOUD

produces a point cloud of the propensity scores by jittering within the control and treatment conditions. This plot is not produced when METHOD=REGADJ.

PSCOVDEN

produces density plots for the covariates or continuous effects that are specified in the PSMODEL statement. Each plot displays the density of an effect for the treatment and control conditions. Two plots are produced for each effect: one plot displays unweighted densities, and the other plot displays densities that are weighted by inverse probability weights. By default, plots are produced for all continuous effects in the PSMODEL statement and are collected in panels. You can customize the density plots by using the PLOTS= option in the PSMODEL statement. This option is ignored when METHOD=REGADJ.

PSDIST

produces a box plot of the propensity score for each treatment condition. The whisker lengths for each box plot are determined by the maximum and minimum of the propensity scores. This plot is not produced when METHOD=REGADJ.

WEIGHTCLOUD

WCLOUD

produces a point cloud of the weights by jittering within the control and treatment conditions. This plot is not produced when METHOD=REGADJ.

WEIGHTDIST

WDIST

produces a box plot of the weights for each treatment condition. The whisker lengths for each box plot are determined by the maximum and minimum of the weights. This plot is not produced when METHOD=REGADJ.

You can specify the following *global-plot-options*:

UNPACK

UNPACKPANEL

suppresses paneling. By default, multiple plots can appear in the same output panel. You can use this option to display each plot separately.

POUTCOMEMOD

PREGADJ

displays parameter estimates for the outcome models for the control and treatment conditions.

PPSMODEL

PTREATMOD

displays parameter estimates for the propensity score model.

RORDER=DATA | FORMATTED | FREQ | INTERNAL

specifies the sort order for the levels of the outcome variable. In order for this option to apply, either the outcome variable must be specified in the CLASS statement or the DIST=BIN option must be specified in the MODEL statement. The following table shows how PROC CAUSALTRT interprets values of the RORDER= option.

Value of RORDER=	Levels Sorted By
DATA	Order of appearance in the input data set.
FORMATTED	External formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. The sort order is machine-dependent.
FREQ	Descending frequency count. Levels that have the most observations come first in the order.
INTERNAL	Unformatted value. The sort order is machine-dependent.

By default, RORDER=FORMATTED. The DESCENDING option in the PROC CAUSALTRT statement causes the response variable to be sorted in reverse of the order displayed in the previous table. For more information about sort order, see the chapter on the SORT procedure in the *Base SAS Procedures Guide*.

SINGULAR=*tolerance*

specifies the *tolerance* for testing the singularity of a matrix, where *tolerance* must be between 0 and 1. By default, *tolerance* is 1E7 times the machine epsilon.

THREADS=*n*

NTHREADS=*n*

specifies the number of threads for analytic computations and overrides the SAS system option THREADS | NOTHREADS. If you do not specify the THREADS= option or if you specify THREADS=0, the number of threads is determined from the number of CPUs in the host on which the analytic computations execute.

BOOTSTRAP Statement

BOOTSTRAP < *options* > **;**

A BOOTSTRAP statement requests bootstrap estimation of confidence intervals for the potential outcome means and treatment effect estimates. The bootstrap samples are taken from within the treatment conditions. To produce the plots that are controlled by the BOOTSTRAP statement, ODS Graphics must be enabled. PROC CAUSALTRT ignores the BOOTSTRAP statement if the initial estimation of the treatment effect results in an error or if the NOEFFECT option is specified in the PROC CAUSALTRT statement.

Table 38.3 summarizes the *options* available in the BOOTSTRAP statement.

Table 38.3 Summary of Options in BOOTSTRAP Statement

Option	Description
BOOTCI	Produces bootstrap confidence intervals of the estimates
BOOTDATA=	Specifies the bootstrap output data set
NBOOT=	Specifies the number of bootstrap sample data sets (replicates)
NOSKIP	Includes bootstrap samples that have inconsistent class levels
PLOTS=	Produces plots of the bootstrap estimates
SEED=	Specifies the seed that initializes the random number stream

You can specify the following *options*:

BOOTCI <(BC | NORMAL | PERC | ALL)>

computes bootstrap-based confidence intervals for the potential outcome means and the treatment effect estimates, and displays the values in the "Analysis of Causal Effect" table. This table includes a column that indicates the number of bootstrap samples used to compute the confidence intervals; this column is not displayed but is available if you save the table as an output data set by using the ODS OUTPUT statement. You can also display this column by modifying the corresponding template.

You can specify one or more of the following types of bootstrap confidence intervals separated by spaces:

BC produces bias-corrected confidence intervals. You must specify a value of 1,000 or more for the NBOOT= option, but the confidence intervals are not computed if fewer than 900 bootstrap replicates produce bootstrap estimates.

NORMAL produces confidence intervals that are based on the assumption that bootstrap estimates follow a normal distribution. You must specify a value of 50 or more for

the value NBOOT= option, but the corresponding standard errors and confidence intervals are not computed if fewer than 40 bootstrap replicates produce bootstrap estimates.

PERC produces percentile-based confidence intervals. You must specify a value of 1,000 or more for the NBOOT= option, but the confidence intervals are not computed if fewer than 900 bootstrap replicates produce bootstrap estimates.

ALL produces all three confidence intervals.

The ALPHA= option in the PROC CAUSALTRT statement sets the level of significance that is used to construct the bootstrap confidence intervals. For more information about how the bootstrap-based confidence intervals are computed, see the section "Bootstrap Methods" on page 2447. By default, BOOTCI=BC and PROC CAUSALTRT produces bias-corrected confidence intervals based on 1,000 bootstrap samples.

BOOTDATA=*SAS-data-set*

specifies the *SAS-data-set* that contains the estimates for the potential outcome means and treatment effect for each bootstrap sample that converges.

NBOOT=*n*

NSAMPLE=*n*

NSAMPLES=*n*

specifies the number of bootstrap sample data sets (replicates). A maximum of 10,000 bootstrap sample data sets can be requested. By default, NBOOT=1000.

NOSKIP

includes in the bootstrap estimation bootstrap samples that have inconsistent class levels in either the treatment or outcome model. By default, for any classification variable in a bootstrap sample data set that does not contain all levels that have been used in fitting either the treatment or outcome model for the original input data set, PROC CAUSALTRT treats the corresponding bootstrap sample estimates as nonconvergent and skips the estimation of the treatment effect. This option overrides the default and continues the estimation of the treatment effect for bootstrap samples that have inconsistent class levels.

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

produces ODS graphics of bootstrap estimates. By default, if you specify the PLOTS option, a panel is produced with the histograms of the bootstrap estimates for the potential outcome means and treatment effect. No graphics are produced if you specify the PLOTS=NONE option in the PROC CAUSALTRT statement.

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

```
ods graphics on;

proc causaltrt method=ipwr;
   model y;
   psmodel trt = x1 x2;
   bootstrap plot;
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."

You can specify the following *plot-requests*:

HIST<(EFFECT | POMCNT | POMTRT)>
HISTOGRAM<(EFFECT | POMCNT | POMTRT)>
produces histograms of the bootstrap estimates for the potential outcome means and treatment effect, which are displayed in a panel by default. You can request output of specific histograms by specifying one or more the following additional suboptions:

EFFECT produces a histogram of the bootstrap estimates for the treatment effect.

POMCNT produces a histogram of the bootstrap estimates for the potential outcome mean of the control condition.

POMTRT produces a histogram of the bootstrap estimates for the potential outcome mean of the treatment condition.

If you specify the ATT option in the PROC CAUSALTRT statement, then the histogram produced by the EFFECT suboption is the average treatment effect for the treated, and the histograms produced by the POMCNT and POMTRT suboptions are the potential outcome means conditioned on having received treatment. For more information about the differences between the average treatment effect and average treatment effect for the treated, see the section "Causal Effects: Definitions, Assumptions, and Identification" on page 2435.

NONE
suppresses all plots that are usually produced by the BOOTSTRAP statement. You can use this option to suppress output if the PLOTS=ALL option is specified in the PROC CAUSALTRT statement.

You can specify the following *global-plot-option*:

UNPACK
UNPACKPANEL
suppresses paneling. By default, multiple histograms of bootstrap estimates appear in the same output panel. You can use this option to display each histogram separately.

SEED=*n*
provides the seed that initializes the random number stream for generating the bootstrap sample data sets (replicates). If you do not specify this option or if you specify a value for *n* that is less than or equal to 0, the seed is generated from reading the time of day from the computer's clock. The largest possible value for the seed is $2^{31} - 1$.

You can use the SYSRANDOM and SYSRANEND macro variables after a PROC CAUSALTRT step to query the initial and final seed values. However, using the final seed value as the starting seed for a subsequent analysis does not continue the random number stream where the previous analysis ended. The SYSRANEND macro variable provides a mechanism to pass on seed values to ensure that the sequence of random numbers is the same every time you run an entire program. To reproduce the

random number stream that was used to generate bootstrap estimates, you must use the same SEED= value and the same number of threads for the analytic computations. When bootstrap resampling is performed, a column that indicates the number of threads used is added to the "Analysis of Causal Effect" table; this column is not displayed but is available if you use the ODS OUTPUT statement to save the table as an output data set. You can also display this column by modifying the corresponding template.

BY Statement

BY *variables* **;**

You can specify a BY statement in PROC CAUSALTRT 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 CAUSALTRT 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 *variable* < **(***options***)** > . . . < *variable* < **(***options***)** > > < / *global-options* > **;**

The CLASS statement names the classification variables to be used as explanatory variables in the analysis.

The CLASS statement must precede the MODEL and PSMODEL statements. Most options can be specified either as individual variable *options* or as *global-options*. You can specify *options* for each variable by enclosing the options in parentheses after the variable name. You can also specify *global-options* for the CLASS statement by placing them after a slash (/). *Global-options* are applied to all the variables specified in the CLASS statement. However, individual CLASS variable *options* override the *global-options*. Unless otherwise indicated, you can specify the following values for either an *option* or a *global-option*:

CPREFIX=*n*

uses at most the first *n* characters of a CLASS variable name in creating names for the corresponding design variables. The default is $32 - \min(32, \max(2, f))$, where f is the formatted length of the CLASS variable.

DESCENDING

DESC

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

LPREFIX=*n*

uses at most the first *n* characters of a CLASS variable label in creating labels for the corresponding design variables. The default is $256 - \min(256, \max(2, f))$, where f is the formatted length of the CLASS variable.

MISSING

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

ORDER=DATA | FORMATTED | FREQ | INTERNAL

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

The following table shows how PROC CAUSALTRT interprets values of the ORDER= option.

Value of ORDER=	Levels Sorted By
DATA	Order of appearance in the input data set.
FORMATTED	External formatted values, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) values. The sort order is machine-dependent.
FREQ	Descending frequency count. Levels that have more observations come earlier in the order.
INTERNAL	Unformatted value. The sort order is machine-dependent.

By default, ORDER=FORMATTED. For more information about sort order, see the chapter on the SORT procedure in the *Base SAS Procedures Guide* and the discussion of BY-group processing in *SAS Programmers Guide: Essentials*.

REF='*level***' | FIRST | LAST**

specifies a level of the classification variable to be put at the end of the list of levels. This level thus corresponds to the reference level in the usual interpretation of the linear estimates that have a singular parameterization.

You can specify the following values:

'*level*' specifies the *level* of the variable to use as the reference level. Specify the formatted value of the variable if a format is assigned. You cannot specify '*level*' as a *global-option*.

FIRST designates the first ordered level as reference.

LAST designates the last ordered level as reference.

By default, REF=LAST.

TRUNCATE< *=n* >
specifies the length (*n*) of variable values to use in determining the CLASS *variable* levels. The default is to use the full formatted length of the CLASS variable. If you specify this option without the length *n*, the first 16 characters of the formatted values are used. When formatted values are longer than 16 characters, you can use this option to revert to the levels as determined in releases before SAS 9. The TRUNCATE option is available only as a *global-option*.

FREQ Statement

FREQ *variable* **;**

The *variable* in the FREQ statement identifies a variable in the input data set that contains the frequency of occurrence of each observation. PROC CAUSALTRT treats each observation as if it appeared *n* times, where *n* is the value of the FREQ variable for the observation. If the frequency value is not an integer, it is truncated to an integer. If it is less than 1 or missing, the observation is not used.

MODEL Statement

MODEL *outcome* < *(variable-options)* >< **=** *effects* > < */ model-options* > **;**

For all the estimation methods that PROC CAUSALTRT implements, you must specify the *outcome* variable in the MODEL statement. For more information about the estimation methods implemented in PROC CAUSALTRT and the model specifications that are required, see the section "Outline of Estimation Method Requirements" on page 2407.

In addition to specifying the *outcome* variable, you can also specify the following:

effects
specify one or more explanatory variables or a combination of variables that are used to fit regression models for the *outcome* variable within each treatment condition. Explanatory variables that represent nominal (classification) data must be declared in the CLASS statement. For more information about specifying *effects*, see the section "Specification of Effects" on page 4083 in Chapter 52, "The GLM Procedure."

variable-options
specify one or more of the following options within parentheses for a binary *outcome* variable immediately after the variable:

DESCENDING

DESC

reverses the order of the outcome categories. If both the DESCENDING and ORDER= options are specified, PROC CAUSALTRT orders the outcome categories according to the ORDER= option and then reverses that order.

EVENT='*category***' | FIRST | LAST**

specifies the event category for the binary outcome model. PROC CAUSALTRT models the probability of the event category. You can specify one of the following:

'*category*'	specifies the value (formatted if a format is applied) of the event category in quotation marks.
FIRST	designates the first-ordered category as the event.
LAST	designates the last-ordered category as the event.

By default, EVENT=FIRST.

One of the most common sets of outcome levels is {0,1}, where 1 represents the event for which the probability is to be modeled. Consider the following example, where Y takes the values 1 and 0 for event and nonevent, respectively, and X is the explanatory variable. To specify the value 1 as the event category, use the following MODEL statement:

```
model Y(event='1') = X;
```

ORDER=DATA | FORMATTED | FREQ | INTERNAL

specifies the sort order for the levels of the outcome variable. The following table displays the available ORDER= options.

ORDER=	Levels Sorted By
DATA	Order of appearance in the input data set.
FORMATTED	External formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. The sort order is machine-dependent.
FREQ	Descending frequency count. Levels that have the most observations come first in the order.
INTERNAL	Unformatted value. The sort order is machine-dependent.

By default, ORDER=FORMATTED.

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

REFERENCE='*category***' | FIRST | LAST**

REF='*category***' | FIRST | LAST**

specifies the reference category for the binary outcome model. Specifying one outcome category as the reference is the same as specifying the other outcome category as the event category. You can specify one of the following:

'*category***'** specifies the value (formatted if a format is applied) of the reference category in quotation marks.

FIRST designates the first-ordered category as the reference.

LAST designates the last-ordered category as the reference.

By default, REF=LAST.

model-options

specify additional options for the outcome model after a slash (/). These *model-options* are summarized in Table 38.4 and described in detail after the table.

Table 38.4 *model-options* in the MODEL Statement

model-option	**Description**
ALPHA=	Specifies the level for confidence limits
DIST=	Specifies the probability distribution
LINK=	Specifies the link function
NOSCALE	Holds the scale parameter fixed
SCALE=	Specifies the value used for the scale

ALPHA=*number*

specifies a *number* to use as the α level for $100(1-\alpha)\%$ confidence limits that the MODEL statement computes. The value of *number* must be between 0 and 1. The default value of *number* is the set by the ALPHA= option in the PROC CAUSALTRT statement.

DIST=*keyword*

DISTRIBUTION=*keyword*

specifies the built-in probability distribution to use in the model. If you specify the DIST= option and you omit the LINK= option, a default link function is chosen as displayed in Table 38.5. If you specify neither the DIST= option nor the LINK= option, then the CAUSALTRT procedure defaults to the binomial distribution with logit link if the outcome variable is listed in the CLASS statement. If the outcome variable is not listed in the CLASS statement, then the CAUSALTRT procedure defaults to the normal distribution with the identity link function.

Table 38.5 Distributions and Default Link Functions

DIST=	Distribution	Default Link Function
BIN | **B**	Binary	Logit
GAMMA | **GAM** | **G**	Gamma	Reciprocal
IGAUSSIAN | **IG**	Inverse Gaussian	Reciprocal square
NORMAL | **NOR** | **N**	Normal	Identity
POISSON | **POI** | **P**	Poisson	Log

Responses for the inverse Gaussian and gamma distributions must be strictly positive. For the Poisson distribution, responses must be nonnegative, but they can take noninteger values. Observations whose response values are outside of the distribution's support are not used to estimate the causal effect, even if the estimation method does not fit an outcome model.

LINK=*keyword*
specifies the link function in the model. You can specify the *keywords* shown in Table 38.6.

Table 38.6 Built-In Link Functions of the CAUSALTRT Procedure

LINK=	Link Function	$g(\mu) = \eta =$
CLOGLOG | **CLL**	Complementary log-log	$\log(-\log(1-\mu))$
IDENTITY | **ID**	Identity	μ
INVERSE | **RECIPROCAL**	Reciprocal	$1/\mu$
LOG	Log	$\log(\mu)$
LOGIT	Logit	$\log(\mu/(1-\mu))$
POWERMINUS2	Power with exponent –2	$1/\mu^2$
PROBIT	Probit	$\Phi^{-1}(\mu)$

For the probit link, $\Phi^{-1}(\cdot)$ denotes the quantile function of the standard normal distribution. By default, the link function is chosen as shown in Table 38.5.

NOSCALE
holds the scale parameter fixed. If you omit the SCALE= option, the scale parameter is fixed at the value 1. If you do not specify the NOSCALE option, the scale parameter is estimated by maximum likelihood for the normal, inverse Gaussian, and gamma distributions.

SCALE=*number*
specifies the value used for the scale parameter when the NOSCALE option is specified. For the binomial and Poisson distributions, which have no free scale parameter, you can use this option to specify an overdispersed model. If the NOSCALE option is not specified, then *number* is used as an initial estimate of the scale parameter.

OUTPUT Statement

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

The OUTPUT statement creates a new SAS data set that contains all the variables in the input data set and optionally contains predicted values that are used to estimate the treatment effect. If the estimation of the causal effect requires that a regression model for the outcome variable be fit, then you can request that the predicted potential outcomes be included in the output data set. You can request that the predicted propensity scores and inverse probability weights be included if the estimation of the causal effect fits a model for the treatment assignment.

The output data set contains estimated potential outcomes and propensity scores for all observations in which the explanatory variables for the model are not missing, regardless of whether the outcome is missing.

This behavior enables you to predict potential outcomes and propensity scores of "new" observations without affecting the original model fit. These new observations must have nonmissing explanatory variable values and treatment assignment, but their outcome values are missing in the input data set. This way, these new observations cannot be used for model fitting but their predicted values are computed in the OUT= data set.

You can specify the following options:

OUT=*SAS-data-set*
: names the output data set. If you omit this option, an output data set is created and given a default name that uses the DATA*n* convention.

keyword=name
: specifies a statistic to be included in the output data set and assigns the specified *name* to the new variable that contains the statistic. Specify one or more of the following *keywords* and *names* (connect each *keyword* and *name* by an equal sign):

IPW=*name*
: requests the predicted inverse probability weight.

POCNT=*name*

PREDCNT=*name*
: requests the predicted potential outcome for the control condition.

POTRT=*name*

PREDTRT=*name*
: requests the predicted potential outcome for the treatment condition.

PSCORE=*name*

PS=*name*
: requests the predicted propensity score.

If you do not specify any *keyword=name* options, the output data set contains only the original variables.

PSMODEL Statement

PSMODEL *treatment* < *(variable-options)* >< **=** *effects* < */ psmodel-options* > > **;**

For all the estimation methods that PROC CAUSALTRT implements, you must specify a *treatment* variable in a PSMODEL statement. The regression model that is fit by the PSMODEL statement is called the propensity score model. The propensity score refers to the probability of receiving treatment conditional on the model *effects*. For more information about the estimation methods that PROC CAUSALTRT implements, see the section "Estimating the Average Treatment Effect (ATE)" on page 2438.

In addition to specifying the *treatment* variable, you can also specify the following:

effects
specify one or more explanatory variables or a combination of variables that are used to fit a regression model for the *treatment* variable. Explanatory variables that represent nominal (classification) data must be declared in the CLASS statement. For more information about specifying *effects*, see the section "Specification of Effects" on page 4083 in Chapter 52, "The GLM Procedure."

variable-options
specify one or more of the following options within parentheses for after the *treatment* variable:

DESCENDING
DESC
reverses the order of the treatment categories. If both the DESCENDING and ORDER= options are specified, PROC CAUSALTRT orders the treatment categories according to the ORDER= option and then reverses that order.

EVENT='*category***' | FIRST | LAST**
specifies the event category for the binary treatment model. PROC CAUSALTRT models the probability of the event category. You can specify one of the following:

'*category***'**	specifies the value (formatted if a format is applied) of the event category in quotation marks.
FIRST	designates the first-ordered category as the event.
LAST	designates the last-ordered category as the event.

By default, EVENT=FIRST.

One of the most common sets of treatment levels is {0,1}, where 1 represents the event for which the probability is to be modeled. Consider the following example, where T takes the values 1 and 0 for event and nonevent, respectively, and X is the explanatory variable. To specify the value 1 as the event category, use the following PSMODEL statement:

```
psmodel T(event='1') = X;
```

ORDER=DATA | FORMATTED | FREQ | INTERNAL
specifies the sort order for the levels of the treatment variable. The following table displays the available ORDER= options.

ORDER=	Levels Sorted By
DATA	Order of appearance in the input data set.
FORMATTED	External formatted value, except for numeric variables that have no explicit format, which are sorted by their unformatted (internal) value. The sort order is machine-dependent.
FREQ	Descending frequency count. Levels that have the most observations come first in the order.
INTERNAL	Unformatted value. The sort order is machine-dependent.

By default, ORDER=FORMATTED.

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

REFERENCE='*category***' | FIRST | LAST**
REF='*category***' | FIRST | LAST**
specifies the reference category for the binary treatment model. Specifying one treatment category as the reference is the same as specifying the other treatment category as the event category. You can specify one of the following:

'*category***'** specifies the value (formatted if a format is applied) of the reference category in quotation marks.

FIRST designates the first-ordered category as the reference.

LAST designates the last-ordered category as the reference.

By default, REF=LAST.

psmodel-options
specify additional options for the propensity score model after a slash (/). These *psmodel-options* are summarized in Table 38.7 and described in detail after the table. These options are applied only if the estimation method you request requires fitting a propensity score model.

Table 38.7 *psmodel-options* in the PSMODEL Statement

Option	Description
ALPHA=	Specifies the level for confidence limits
PLOTS=	Produces graphics for the propensity scores and weights
WGTFLAG=	Specifies a value to be used to flag large weights

ALPHA=*number*

specifies a *number* to use as the α level for $100(1-\alpha)\%$ confidence limits that the PSMODEL statement computes. The value of *number* must be between 0 and 1. The default value of *number* is the set by the ALPHA= option in the PROC CAUSALTRT statement.

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

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

produces ODS graphics by using the predicted propensity scores. No graphics are produced if you specify the PLOTS=NONE option in the PROC CAUSALTRT statement or if the estimation method used does not require fitting a propensity score model.

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

```
ods graphics on;

proc causaltrt method=ipwr;
   model y;
   psmodel trt = x1 x2 /plots=all;
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."

You can specify the following *plot-requests*:

ALL

produces all possible plots.

LOGITPSCORE

LPS

produces overlaid density plots for the logit of the propensity score within each treatment condition.

NONE

suppresses all plots that the PSMODEL statement could produce. This *plot-request* is used to suppress output if the PLOTS=ALL option is specified in the PROC CAUSALTRT statement.

OUTBYPSCORE

OUTBYPS

produces a scatter plot of the outcome variable by the propensity score for nonbinary outcomes. If the outcome is binary, box plots of the propensity scores within treatment conditions are produced for each outcome level. The whisker lengths for each box plot are determined by the maximum and minimum of the propensity scores.

OUTBYWEIGHT

OUTBYWGT

produces a scatter plot of the outcome variable by weight for nonbinary outcomes. If the outcome is binary, box plots of the weights within treatment conditions are produced for each outcome level. The whisker lengths for each box plot are determined by the maximum and minimum of the weights.

PSCLOUD

produces a point cloud of the propensity scores by jittering within the control and treatment conditions.

PSCOVDEN< *pscovden-options* **>**

produces density plots for the covariates or continuous effects that are specified in the PSMODEL statement. Each plot displays the density of effects for the treatment and control condition. Two plots are produced for each effect: one plot displays unweighted densities, and the other plot displays densities that are weighted by inverse probability weights. By default, plots are produced for all continuous effects that are specified in the PSMODEL statement, and the plots are collected in panels. You can specify the following *pscovden-options*:

EFFECTS(*effects***)**

specifies the effects for which density plots are produced. Plots are produced only for continuous effects that are specified in the PSMODEL statement. The *effects* consist of an explanatory variable or combination of variables. The syntax for specifying *effects* in this option is the same as the syntax for specifying *effects* in the MODEL and PSMODEL statements.

UNPACK

suppresses paneling. By default, multiple plots can appear in the same output panel. You can use this option to display each plot separately.

UNPACKEFFECTS

creates a separate panel for each effect. Each panel has a single row and two columns that contain the unweighted and weighted density plots. This option is ignored if you specify the UNPACK option in the PROC CAUSALTRT or PSMODEL statements.

PSDIST

produces a box plot of the propensity scores for each treatment condition. The whisker lengths for each box plot are determined by the maximum and minimum of the propensity scores.

WEIGHTCLOUD

WCLOUD

produces a point cloud of the weights by jittering within the control and treatment conditions.

WEIGHTDIST

WDIST

produces a box plot of the weights for each treatment condition. The whisker lengths for each box plot are determined by the maximum and minimum of the weights.

You can specify the following *global-plot-options*:

ONLY

suppresses plots that are not specified as a *plot-request*. This option applies only if the PLOTS= option is specified in the PROC CAUSALTRT statement.

UNPACK

UNPACKPANEL

suppresses paneling. By default, multiple plots can appear in the same output panel. You can specify UNPACK to display each plot separately.

WGTFLAG=*number*

specifies a *number* to use to flag large weights. The value of *number* must be greater than or equal to 1. If any observations have weights greater than *number*, a note is added to the SAS log. By default, WGTFLAG=50.

Details: CAUSALTRT Procedure

Causal Effects: Definitions, Assumptions, and Identification

The CAUSALTRT procedure estimates the causal effect of a binary treatment, T, on a continuous or discrete outcome, Y. This section defines causal effects and discusses the assumptions and conditions that enable researchers to establish causal interpretations.

Although the causal effects that PROC CAUSALTRT estimates are called treatment effects, the variable T might represent an intervention or exposure, depending on the problem nature. For example, consider that T is an intervention such as receiving subsidized access to a fitness center, and Y is measure of physical health. The researcher would like to assess the treatment or causal effect of the subsidized fitness program T on the physical health Y. But what exactly is the causal effect? This section uses Neyman-Rubin's potential outcomes framework (Rubin 1980, 1990) to define causal effects and to discuss their assumptions. Next, it explains the conditions that enable researchers to identify and establish causal effects.

The first important concept for defining a causal effect is potential outcomes. Potential outcomes describe an idealized source of data where you can observe a subject's response for all possible treatment assignments. For example, if you are estimating the causal effect of a binary variable for which $T = 0$ indicates assignment to the control and $T = 1$ assignment to treatment, then each subject has two potential outcomes $Y(0)$ and $Y(1)$. The subject-level (also called unit-level) treatment effect is defined as the difference in potential outcomes $Y(1) - Y(0)$.

To formally define the potential outcomes as unique and intrinsic values that are associated with a subject, Rubin (1980) states the stable unit treatment value assumption (SUTVA). See also Imbens and Rubin (2015). Two components of the SUTVA are the following:

- No interference. A subject's potential outcomes are not affected by the treatment assignments of the other subjects.
- No hidden variations of treatments. Subjects must receive the same form of treatment at each treatment level.

With a more refined statement, VanderWeele (2009) proposed a less restrictive version to the second component of SUTVA. Essentially, VanderWeele's version requires that the potential outcomes remain unchanged within certain degree of treatment variation for each treatment level. This version is also known as the treatment variation irrelevance assumption. See also Cole and Frangakis (2009).

Furthermore, Rubin (2005) points out an implicit but important assumption for constructing the potential outcome framework: the potential outcomes are not affected by the treatment assignment mechanism that the researchers use to learn about them. Whether in an observational study or a randomized experiment, potential outcomes remain unique to the subjects given the well-defined causal problem and SUTVA.

To summarize, the potential outcome framework with SUTVA ensures that the causal treatment effect is well defined. However, to actually attempt to estimate causal treatment effects from the data, the consistency assumption that relates an observed outcome to the potential outcome is needed:

$$Y = TY(1) + (1 - T)Y(0)$$

This equation states that the observed response Y is equal to the potential outcome with a treatment level that matches the actual assigned treatment level. In this setting, if j is an unobserved treatment condition, the unobserved potential outcome $Y(j)$ is defined using counterfactual conditionals as the outcome that would occur if, contrary to the observed assignment, the subject received treatment $T = j$. Because each subject can take part in only one treatment condition, at least half of the potential outcomes would not be observed in the data collection process. Therefore, the unit-level causal effect, as defined by $Y(1) - Y(0)$, is seldom the primary interest in research. Instead, average treatment effects in the population are the more common estimands.

The CAUSALTRT procedure estimates two types of treatment effects:

- The average treatment effect (ATE) for the entire population is given by

  $$\text{ATE} = \mu_1 - \mu_0 = E[Y(1)] - E[Y(0)]$$

  where $\mu_1 = E[Y(1)]$ and $\mu_0 = E[Y(0)]$ are potential outcome means (POMs) for the treatment and control conditions, respectively.
- The average treatment effect for the treated (ATT or ATET) is the average causal effect among only those individuals that receive treatment and is given by

  $$\text{ATT} = \mu_{1|T=1} - \mu_{0|T=1} = E[Y(1)|T = 1] - E[Y(0)|T = 1]$$

  where $\mu_{1|T=1} = E[Y(1)|T = 1]$ and $\mu_{0|T=1} = E[Y(0)|T = 1]$ are potential outcome means for the treatment and control conditions, respectively, conditional on receiving treatment.

It is important to notice that the preceding discussion of potential outcome framework, the associated assumptions, and the definitions of causal treatment effects apply to both experimental and observational

data (Rubin 1990). But for estimating causal treatment effects, statistical methodology for experimental and observational data would be differentiated.

The differentiation is caused by the following important condition (or assumption) for the identification of causal treatment effect: given the pretreatment covariates $\mathbf{X}$, the potential outcomes are independent of treatment assignment

This condition states that if all the covariates $\mathbf{X}$ have been included in the model appropriately (that is, there are no unmeasured covariates), the treatment effect of T on Y conditional on $\mathbf{X}$ would have a causal interpretation. Consequently, the causal treatment effects can be estimated as some functions of the observed conditional means.

Unfortunately, this condition cannot be 100% established in most applications; hence, this condition is usually referred to as an assumption in causal analysis literature. This assumption is called strong ignorability of treatment assignment or conditional exchangeability. This assumption sheds light on the different statistical methodology between randomized experiments and observational studies.

In experiments where randomization is used to assign subjects to treatment conditions, you can safely assume that the treatment assignment and potential outcomes are independent by design. Hence, for randomized experiments, traditional statistical methods such as t tests and ANOVA can be used without worrying about the confounding that can be caused by covariates $\mathbf{X}$.

However, in observational studies, subjects "select" the treatment conditions based on their pretreatment characteristics (covariates), $\mathbf{X}$, which could also be associated with the outcome variable. The treatment and outcome association would be confounded by the covariates. In this case, identification of causal effects requires that the strong ignorability or conditional exchangeability assumption be satisfied; that is, only when the estimation of the causal effects can successfully take into account all the confounding that is caused by the covariates $\mathbf{X}$.

The CAUSALTRT procedure implements several statistical techniques that enable you to estimate treatment effects when you specify confounding covariates $\mathbf{X}$. PROC CAUSALTRT uses the covariates $\mathbf{X}$ to fit generalized linear models for the treatment T, outcome Y, or both. Predicted values from these models are then incorporated into the estimation of the causal effects. In particular, you can estimate the ATE by the following methods:

- inverse probability weighting, where weights are predicted from the model for the treatment assignment T (also called the propensity score model)
- regression adjustment, where the model of the outcome Y is used to predict potential outcomes for each treatment assignment
- doubly robust estimation, which combines both inverse probability weighting and regression adjustment methods to estimate the causal effect; doubly robust estimation methods provide unbiased estimates even if one of the models is misspecified

Whenever your modeling involves a model for the treatment assignment T or propensity score (that is, when you use either the inverse probability weighting or doubly robust estimation), an additional assumption about positivity is needed: each subject should have a nonzero probability of receiving any treatment condition. This assumption is expressed as follows:

$$0 < \Pr(T = 1 \mid \mathbf{X} = \mathbf{x}) < 1$$

For more information about estimation of the ATE, see the section "Estimating the Average Treatment Effect (ATE)" on page 2438. For more information about the models that are required for the estimation methods that PROC CAUSALTRT implements and how default estimation methods are determined, see the section "Outline of Estimation Method Requirements" on page 2407. You can estimate the ATT by using either inverse probability weights or regression adjustment. For more information about estimation of the ATT, see the section "Estimating the Average Treatment Effect for the Treated (ATT)" on page 2443.

Estimating the Average Treatment Effect (ATE)

The CAUSALTRT procedure can estimate the average treatment effect (ATE) by using inverse probability weighting, regression adjustment, and doubly robust methods (doubly robust methods are combinations of the first two methods). The following sections describe each of these estimation methods.

Inverse Probability Weighting

The CAUSALTRT procedure estimates the potential outcome means and ATE by using the three inverse probability weighting methods that are described in Lunceford and Davidian (2004). All three methods compute weights using estimates for the conditional probability of receiving treatment,

$$e(\mathbf{x}) = \Pr(T = 1 \mid \mathbf{X} = \mathbf{x})$$

where $\mathbf{x}$ is a vector of the observed covariates. The conditional probability $e(\mathbf{x})$ is called the propensity score, and the model that is used to estimate $e(\mathbf{x})$ is called the propensity score model. The inverse probability weight for an observation is equal to

$$\frac{1}{\Pr(T = t \mid \mathbf{x})} = \frac{t}{e(\mathbf{x})} + \frac{1-t}{1-e(\mathbf{x})}$$

In addition to the stable unit treatment value assumption (SUTVA), two more assumptions on the propensity scores are required for the use of inverse probability weighting methods. The positivity assumption, that $0 < e(\mathbf{x}) < 1$, ensures that each observation has a nonzero probability of receiving each treatment condition. The assumption of no unmeasured confounders, also known as strong ignorability, requires that the potential outcomes $Y(0)$ and $Y(1)$ be independent of the treatment variable T conditional on the covariates $\mathbf{x}$. In practice, this assumption means that the set of covariates $\mathbf{x}$ should have included all the important confounders in the propensity score model. If these conditions are satisfied and the propensity score model is correctly specified, then it follows that

$$E\left[\frac{TY}{e(\mathbf{x})}\right] - E\left[\frac{(1-T)Y}{1-e(\mathbf{x})}\right] = E\left[\frac{Y(1)}{e(\mathbf{x})} E\left[T \mid \mathbf{x}\right]\right] - E\left[\frac{Y(0)}{1-e(\mathbf{x})} E\left[(1-T) \mid \mathbf{x}\right]\right] = E\left[Y(1)\right] - E\left[Y(0)\right]$$

The CAUSALTRT procedure uses the effects that are specified in the PSMODEL statement to fit a logistic regression to the propensity score model. The inverse probability weights are then computed by taking the inverse of the estimated propensity scores.

Suppose you have observations $(y_i, t_i, \mathbf{x}_i)$, for $i = 1, \ldots, n$. The parameter estimates for the propensity score model is given by $\hat{\boldsymbol{\beta}}_{\mathrm{ps}}$, and the predicted values for the propensity score are given by

$$\hat{e}_i = \hat{e}(\mathbf{x}_i) = \frac{\exp\left(\mathbf{x}_i' \hat{\boldsymbol{\beta}}_{\mathrm{ps}}\right)}{1 + \exp\left(\mathbf{x}_i' \hat{\boldsymbol{\beta}}_{\mathrm{ps}}\right)}$$

The three weighting methods that PROC CAUSALTRT implements obtain unbiased estimates of the potential outcome means by solving the equations

$$\mathbf{S}_{\text{ipw}}(\boldsymbol{\mu}) = \sum_{i=1}^{n} \mathbf{S}_{\text{ipw},i} = \mathbf{0}$$

for $\boldsymbol{\mu} = (\mu_0, \mu_1)$, where

$$\mathbf{S}_{\text{ipw},i} = \begin{bmatrix} \frac{(1-t_i)(y_i-\mu_0)}{1-\hat{e}_i} - \eta_0 \left(\frac{t_i-\hat{e}_i}{1-\hat{e}_i}\right) \\ \frac{t_i(y_i-\mu_1)}{\hat{e}_i} + \eta_1 \left(\frac{t_i-\hat{e}_i}{\hat{e}_i}\right) \end{bmatrix}$$

These estimation methods differ in the values of (η_0, η_1). The choices of (η_0, η_1) and the corresponding potential outcome mean estimates for each method are as follows:

- IPW:

$$(\eta_0, \eta_1) = (\mu_0, \mu_1)$$

$$\hat{\mu}_0^{\text{ipw}} = n^{-1} \sum_{i=1}^{n} \frac{(1-t_i)y_i}{1-\hat{e}_i}$$

$$\hat{\mu}_1^{\text{ipw}} = n^{-1} \sum_{i=1}^{n} \frac{t_i y_i}{\hat{e}_i}$$

- IPWR:

$$(\eta_0, \eta_1) = (0, 0)$$

$$\hat{\mu}_0^{\text{ipwr}} = \left[\sum_{i=1}^{n} \frac{(1-t_i)}{1-\hat{e}_i}\right]^{-1} \sum_{i=1}^{n} \frac{(1-t_i)y_i}{1-\hat{e}_i}$$

$$\hat{\mu}_1^{\text{ipwr}} = \left[\sum_{i=1}^{n} \frac{t_i}{\hat{e}_i}\right]^{-1} \sum_{i=1}^{n} \frac{t_i y_i}{\hat{e}_i}$$

- IPWS:

$$(\eta_0, \eta_1) = \left(-\frac{E\left[(1-T)(Y-\mu_0)/(1-e(\mathbf{x}))^2\right]}{E\left[(T-e(\mathbf{x}))^2/(1-e(\mathbf{x}))^2\right]}, -\frac{E\left[T(Y-\mu_1)/e(\mathbf{x})^2\right]}{E\left[(T-e(\mathbf{x}))^2/e(\mathbf{x})^2\right]}\right)$$

$$\hat{\mu}_0^{\text{ipws}} = -\left[\sum_{i=1}^{n} \frac{(1-t_i)}{1-\hat{e}_i}\left(1-\frac{C_0}{1-\hat{e}_i}\right)\right]^{-1} \sum_{i=1}^{n} \frac{(1-t_i)y_i}{1-\hat{e}_i}\left(1-\frac{C_0}{1-\hat{e}_i}\right)$$

$$\hat{\mu}_1^{\text{ipws}} = \left[\sum_{i=1}^{n} \frac{t_i}{\hat{e}_i}\left(1-\frac{C_1}{\hat{e}_i}\right)\right]^{-1} \sum_{i=1}^{n} \frac{t_i y_i}{\hat{e}_i}\left(1-\frac{C_1}{\hat{e}_i}\right)$$

where

$$C_0 = \left[-\sum_{j=1}^{n} \frac{t_j - \hat{e}_j}{1 - \hat{e}_j} \right] \left[\sum_{j=1}^{n} \left(\frac{t_j - \hat{e}_j}{1 - \hat{e}_j} \right)^2 \right]^{-1}$$

$$C_1 = \left[\sum_{j=1}^{n} \frac{t_j - \hat{e}_j}{\hat{e}_j} \right] \left[\sum_{j=1}^{n} \left(\frac{t_j - \hat{e}_j}{\hat{e}_j} \right)^2 \right]^{-1}$$

If the values of (η_0, η_1) that motivate the IPWS method were known constants, they would produce estimates for the potential outcome means that have the smallest asymptotic variance among the class of estimators that is defined by $\mathbf{S}_{\text{ipw}}(\boldsymbol{\mu})$. The IPWS method estimates $(\hat{\eta}_0, \hat{\eta}_1)$ by solving the estimating equations

$$\mathbf{S}(\boldsymbol{\eta}) = \sum_{i=1}^{n} \mathbf{S}_{\boldsymbol{\eta},i} = \mathbf{0}$$

for $\boldsymbol{\eta} = (\eta_0, \eta_1)$, where:

$$\mathbf{S}_{\boldsymbol{\eta},i} = \begin{bmatrix} \frac{(1-t_i)(y_i - \mu_0)}{(1-\hat{e}_i)^2} + \eta_0 \left(\frac{t_i - \hat{e}_i}{1-\hat{e}_i} \right)^2 \\ \frac{t_i (y_i - \mu_1)}{\hat{e}_i^2} + \eta_1 \left(\frac{t_i - \hat{e}_i}{\hat{e}_i} \right)^2 \end{bmatrix}$$

Although you do not need to specify an outcome model when you use the inverse probability weighting methods, you still need to specify the outcome variable in the MODEL statement. The IPW, IPWR, or IPWS estimation method can be requested using the METHOD= option in the PROC CAUSALTRT statement. For more information about which model specifications are required for different estimation methods and how default estimation methods are determined, see the section "Outline of Estimation Method Requirements" on page 2407.

The robust sandwich covariance estimate for $\hat{\boldsymbol{\mu}}$ is computed by stacking the equations $\mathbf{S}_{\text{ipw}}(\boldsymbol{\mu})$ and the score function for the logistic regression model that is used to obtain $\hat{\boldsymbol{\beta}}_{\text{ps}}$. By stacking the equations, PROC CAUSALTRT adjusts the covariance matrix for $\hat{\boldsymbol{\mu}}$ to account for the prediction of $\hat{\boldsymbol{\beta}}_{\text{ps}}$ and the propensity scores $\hat{e}_i$. For more information about using the robust sandwich covariance estimate to compute standard errors, see the section "Asymptotic Formulas" on page 2445.

The finite sample properties of $\hat{\boldsymbol{\mu}}$ and its covariance matrix can be affected by observations that have large weights. By default, a note is added to the SAS log if any observations have weights greater than 50. You can specify the value that is used to flag large weights in the WGTFLAG= option in the PSMODEL statement. You can also inspect the values of the predicted weights by requesting graphics in the PLOTS= option in the PROC CAUSALTRT or PSMODEL statements.

As described in Rosenbaum and Rubin (1983), the propensity score is also a balancing score. To assess the balance that is produced by a propensity score model, you can request the display of weighted and unweighted standardized mean differences and variance ratios for propensity score model effects in the COVDIFFPS option in the PROC CAUSALTRT statement. You can also request weighted and unweighted densities for propensity score model effects by specifying PSCOVDEN in the PLOTS= option in the PROC CAUSALTRT or PSMODEL statements. To inspect the balance of a propensity score model without showing the causal effects, specify the NOEFFECT option in the PROC CAUSALTRT statement.

Based on the balancing score property, you can use the propensity scores to create matched samples or strata for the data. For more information about applying the propensity score in matching and stratification see Chapter 100, "The PSMATCH Procedure."

Regression Adjustment

Regression adjustment estimates the ATE by using predicted values for the potential outcomes. The CAUSALTRT procedure predicts the potential outcomes from generalized linear models that are fit to the data by maximum likelihood estimation. For more information about generalized linear models, see the section "Generalized Linear Models Theory" on page 3544 in Chapter 50, "The GENMOD Procedure."

The effects that you specify in the MODEL statement are used to fit models for the outcome within each treatment condition. The predicted potential outcomes are then given by

$$\hat{y}_{i0} = g^{-1}(\mathbf{x}_i'\hat{\boldsymbol{\beta}}_c)$$

$$\hat{y}_{i1} = g^{-1}(\mathbf{x}_i'\hat{\boldsymbol{\beta}}_t)$$

where g is the link function being used and $\hat{\boldsymbol{\beta}}_{\mathrm{c}}$ and $\hat{\boldsymbol{\beta}}_{\mathrm{t}}$ are the parameter estimates for the control and treatment outcome models, respectively. The potential outcome mean μ_j is then estimated by averaging the predicted $\hat{y}_{ij}$ for all observations $i = 1, \ldots, n$, regardless of the observed treatment assignment. Therefore, the regression adjustment estimates for the potential outcome means solve the estimating equations

$$\mathbf{S}_{\mathrm{reg}}(\boldsymbol{\mu}) = \sum_{i=1}^{n} \mathbf{S}_{\mathrm{reg},i} = \mathbf{0}$$

where

$$\mathbf{S}_{\mathrm{reg},i} = \begin{bmatrix} \hat{y}_{i0} - \mu_0 \\ \hat{y}_{i1} - \mu_1 \end{bmatrix}$$

The regression adjustment estimates for the potential outcome means are equal to

$$\hat{\mu}_0^{\mathrm{reg}} = n^{-1} \sum_{i=1}^{n} \hat{y}_{i0}$$

$$\hat{\mu}_1^{\mathrm{reg}} = n^{-1} \sum_{i=1}^{n} \hat{y}_{i1}$$

If the outcome model is correctly specified and the assumption of no unmeasured confounders is satisfied, then regression adjustment produces unbiased estimates for the potential outcome means. The outcome model effects should also have similar distributions between treatment conditions to avoid extrapolation when the potential outcomes $\hat{y}_{ij}$ are predicted.

Although you do not need to specify a propensity score model in order to estimate the potential outcome means by the regression adjustment method, you still need to specify the treatment variable in the PSMODEL statement. You can specify METHOD=REGADJ in the PROC CAUSALTRT statement to request the regression adjustment method. For more information about which model specifications are required for different estimation methods and how default estimation methods are determined, see the section "Outline of Estimation Method Requirements" on page 2407.

The robust sandwich covariance estimate for $\hat{\boldsymbol{\mu}}^{\text{reg}}$ is estimated by stacking the equations $\mathbf{S}_{\text{reg}}(\boldsymbol{\mu})$ and the score function for the outcome models that are used to estimate $\hat{\boldsymbol{\beta}}_{\text{c}}$ and $\hat{\boldsymbol{\beta}}_{\text{t}}$. By stacking the equations, PROC CAUSALTRT adjusts the covariance matrix for $\hat{\boldsymbol{\mu}}^{\text{reg}}$ to account for the prediction of the potential outcomes $\hat{y}_{ij}$. For more information about using the robust sandwich covariance estimate to compute standard errors, see the section "Asymptotic Formulas" on page 2445.

Doubly Robust Estimation

Doubly robust estimation methods fit models for both the outcome and treatment variables. They combine inverse probability weighting and regression adjustment to estimate the potential outcome means. The methods are said to be doubly robust because they provide unbiased estimates for $\boldsymbol{\mu}$ even if one of the models is misspecified (Bang and Robins 2005). In this sense, you have two opportunities to obtain unbiased estimation of causal effects by specifying either a correct treatment or a correct outcome model. The CAUSALTRT procedure implements two doubly robust estimation methods: the augmented inverse probability weighting (AIPW) method described in Lunceford and Davidian (2004) and the inverse probability weighted regression adjustment (IPWREG) method described in Wooldridge (2010).

The AIPW estimation method estimates propensity scores $\hat{e}_i$ and the associated parameter estimates $\hat{\boldsymbol{\beta}}_{ps}$ by fitting a logistic regression model for treatment assignment, as described in section "Inverse Probability Weighting" on page 2438. It also estimates the potential outcomes $\hat{y}_{ij}$ by using the maximum likelihood fitting of the generalized linear models, as described in section "Regression Adjustment" on page 2441. Note that the treatment assignment and outcome models do not need to be fit using the same set of model effects.

The AIPW estimates for potential outcome means solve the estimating equations

$$\mathbf{S}_{\text{aipw}}(\boldsymbol{\mu}) = \sum_{i=1}^{n} \mathbf{S}_{\text{aipw},i}(\boldsymbol{\mu}) = \mathbf{0}$$

for (μ_0, μ_1), where

$$\mathbf{S}_{\text{aipw},i}(\boldsymbol{\mu}) = \begin{bmatrix} \frac{(1-t_i)y_i}{1-\hat{e}_i} + \hat{y}_{i0}\left(\frac{t_i-\hat{e}_i}{1-\hat{e}_i}\right) - \mu_0 \\ \frac{t_i y_i}{\hat{e}_i} - \hat{y}_{i1}\left(\frac{t_i-\hat{e}_i}{\hat{e}_i}\right) - \mu_1 \end{bmatrix} = \begin{bmatrix} \hat{y}_{i0} - \left(\frac{1-t_i}{1-\hat{e}_i}\right)(\hat{y}_{i0} - y_i) - \mu_0 \\ \hat{y}_{i1} - \left(\frac{t_i}{\hat{e}_i}\right)(\hat{y}_{i1} - y_i) - \mu_1 \end{bmatrix}$$

The AIPW estimates for the potential outcome means are given by

$$\hat{\mu}_0^{\text{aipw}} = n^{-1} \sum_{i=1}^{n} \frac{(1-t_i)y_i}{1-\hat{e}_i} + \hat{y}_{i0}\left(\frac{t_i-\hat{e}_i}{1-\hat{e}_i}\right)$$

$$\hat{\mu}_1^{\text{aipw}} = n^{-1} \sum_{i=1}^{n} \frac{t_i y_i}{\hat{e}_i} - \hat{y}_{i1}\left(\frac{t_i-\hat{e}_i}{\hat{e}_i}\right)$$

If one of the models is misspecified, $\hat{\boldsymbol{\mu}}^{\text{aipw}}$ remains an unbiased estimate of $\boldsymbol{\mu}$. However, the efficiency of $\hat{\boldsymbol{\mu}}^{\text{aipw}}$ and the estimation of its covariance matrix are affected.

The IPWREG estimation method uses the same logistic model for predicting $\hat{e}_i$, but it fits weighted models for the outcome variable separately for each treatment condition. To fit the outcome models, each observation is weighted by the inverse probability weights as follows:

$$\frac{1}{\Pr(T = t_i \mid \mathbf{x}_i)} = \frac{t_i}{e(\mathbf{x}_i)} + \frac{1-t_i}{1-e(\mathbf{x}_i)}$$

Let $\hat{\boldsymbol{\beta}}_{\mathrm{c}}^{w}$ and $\hat{\boldsymbol{\beta}}_{\mathrm{t}}^{w}$ denote the parameter estimates from the weighted regression outcome models for the control and treatment conditions, respectively. The predicted potential outcomes are then given by

$$\hat{y}_{i0}^{w} = g^{-1}(\mathbf{x}_i'\hat{\boldsymbol{\beta}}_{\mathrm{c}}^{w})$$

$$\hat{y}_{i1}^{w} = g^{-1}(\mathbf{x}_i'\hat{\boldsymbol{\beta}}_{\mathrm{t}}^{w})$$

where g is the link function being used. For the IPWREG method, PROC CAUSALTRT enforces the use of the canonical link for the distribution of the outcome variable. You cannot override the canonical link by the LINK= option. For information about the canonical link for each distribution, see Table 38.5.

The IPWREG estimates for the potential outcome means are given by

$$\hat{\mu}_0^{\mathrm{wreg}} = n^{-1}\sum_{i=1}^{n}\hat{y}_{i0}^{w}$$

$$\hat{\mu}_1^{\mathrm{wreg}} = n^{-1}\sum_{i=1}^{n}\hat{y}_{i1}^{w}$$

These estimates solve the following estimating equations:

$$\mathbf{S}_{\mathrm{reg}}^{w}(\boldsymbol{\mu}) = \sum_{i=1}^{n}\mathbf{S}_{\mathrm{reg},i}^{w} = \sum_{i=1}^{n}\begin{bmatrix} \hat{y}_{i0}^{w} - \mu_0 \\ \hat{y}_{i1}^{w} - \mu_1 \end{bmatrix} = \mathbf{0}$$

Estimating the Average Treatment Effect for the Treated (ATT)

In some research settings or program evaluation studies, instead of the average treatment effect (ATE), researchers or policy makers might be more interested in the causal treatment effects only for those who choose to participate in the treatment condition. Hence, the average treatment effect for the treated (ATT or ATET) becomes the focus.

The CAUSALTRT procedure enables you to estimate the ATT and the corresponding conditional potential outcome means by using either of the following methods:

- Inverse probability weighting with ratio adjustment (IPWR). To estimate the ATT, the inverse probability weights that are described in the section "Inverse Probability Weighting" on page 2438 are multiplied by the predicted propensity scores. The ATT weights are therefore given by

  $$\frac{e(\mathbf{x}_i)}{\Pr(T = t_i \mid \mathbf{x}_i)} = t_i + \frac{(1-t_i)e(\mathbf{x}_i)}{1-e(\mathbf{x}_i)}$$

  The estimating equations that are solved by the IPWR estimates for the conditional potential outcome means $\boldsymbol{\mu}_{T=1}$ are

  $$\mathbf{S}_{\mathrm{ipw}}(\boldsymbol{\mu}_{T=1}) = \sum_{i=1}^{n}\mathbf{S}_{\mathrm{ipw},i|T=1} = \mathbf{0}$$

  where

  $$\mathbf{S}_{\mathrm{ipw},i|T=1} = \begin{bmatrix} (1-t_i)(y_i - \mu_{0|T=1})\frac{\hat{e}_i}{1-\hat{e}_i} \\ t_i(y_i - \mu_{1|T=1}) \end{bmatrix}$$

The IPWR estimates for the conditional potential outcome means $\boldsymbol{\mu}_{T=1}$ are given by

$$\hat{\mu}^{\text{ipwr}}_{0|T=1} = \left[\sum_{i=1}^{n}(1-t_i)\frac{\hat{e}_i}{1-\hat{e}_i}\right]^{-1}\sum_{i=1}^{n}(1-t_i)y_i\frac{\hat{e}_i}{1-\hat{e}_i}$$

$$\hat{\mu}^{\text{ipwr}}_{1|T=1} = \left[\sum_{i=1}^{n}t_i\right]^{-1}\sum_{i=1}^{n}t_i y_i$$

If the propensity score model is correctly specified and the stable unit treatment value assumption (SUTVA), positivity, and no unmeasured confounders assumptions are satisfied, then the predicted conditional means are unbiased estimates for $\mu_{j|T=1}$.

- Regression adjustment (REGADJ). For this method, PROC CAUSALTRT obtains predicted potential outcomes $\hat{y}_{ij}$ from the outcome models that are fitted separately for each treatment condition. This approach is described in section "Regression Adjustment" on page 2441. To estimate $\boldsymbol{\mu}_{T=1}$, the predicted values are averaged only for individuals who received treatment. The REGADJ estimates for the conditional potential outcome means $\boldsymbol{\mu}_{T=1}$ are given by

$$\hat{\mu}^{\text{reg}}_{0|T=1} = \left[\sum_{i=1}^{n}t_i\right]^{-1}\sum_{i=1}^{n}t_i\hat{y}_{i0}$$

$$\hat{\mu}^{\text{reg}}_{1|T=1} = \left[\sum_{i=1}^{n}t_i\right]^{-1}\sum_{i=1}^{n}t_i\hat{y}_{i1}$$

The estimates therefore solve the estimating equations

$$\mathbf{S}_{\text{reg}}(\boldsymbol{\mu}_{T=1}) = \sum_{i=1}^{n}\mathbf{S}_{\text{reg},i|T=1} = \mathbf{0}$$

where

$$\mathbf{S}_{\text{reg},i|T=1} = \begin{bmatrix} t_i\left(\hat{y}_{i0}-\mu_{0|T=1}\right) \\ t_i\left(\hat{y}_{i1}-\mu_{1|T=1}\right) \end{bmatrix}$$

To request the estimation of the conditional potential outcome means and ATT, specify the ATT option in the PROC CAUSALTRT statement.

Comparing Weights for Estimating the ATE and ATT

This section describes and distinguishes the weights that are used in different estimation methods and analysis situations.

When the average treatment effect (ATE) is estimated, the inverse probability weight for an observation is equal to

$$\frac{1}{\Pr\left(T = t_i \mid \mathbf{x}_i\right)} = \frac{t_i}{e(\mathbf{x}_i)} + \frac{1 - t_i}{1 - e(\mathbf{x}_i)}$$

These are the weights that are used by the IPW, IPWR, IPWS, AIPW, and IPWREG methods to estimate the potential outcome means and ATE.

However, when you estimate the average treatment effect for the treated (ATT), the IPWR method uses the weights

$$\frac{\Pr\left(T = 1 \mid \mathbf{x}_i\right)}{\Pr\left(T = t_i \mid \mathbf{x}_i\right)} = t_i + \frac{(1 - t_i)e(\mathbf{x}_i)}{1 - e(\mathbf{x}_i)}$$

The differential uses of weights for ATE and ATT also apply to the following analyses or plots:

- weights that are flagged by the WGTFLAG= value
- the OUTBYWEIGHT, WDIST, and WCLOUD plots

Regardless of whether the ATT or ATE is estimated, the following analyses or plots always use the inverse probability weights (the first formula in this section):

- the weighted standardized mean differences and variance ratios for the covariates (effects) in the propensity score model, which are requested by the COVDIFFPS option
- the weighted density plots for the continuous covariates (effects) in the propensity score model, which are requested by the PLOTS=PSCOVDEN option

Standard Errors and Confidence Intervals

Asymptotic Formulas

PROC CAUSALTRT computes standard errors for the potential outcome means and treatment effect by using the robust sandwich covariance formula that is based on asymptotic theory. In general, let $\boldsymbol{\theta}_0$ denote the vector of parameters of interest. PROC CAUSALTRT considers all its estimation as an M-estimation problem that solves the following estimating equations:

$$\mathbf{S}(\boldsymbol{\theta}) = \sum_{i=1}^{n} \mathbf{S}_i = \mathbf{0}$$

When the function $S(\cdot)$ is evaluated at θ_0, it satisfies $E[S] = 0$. By the theory of M-estimation (Stefanski and Boos 2002), the robust sandwich covariance matrix, $\hat{V}(\hat{\boldsymbol{\theta}})$, for the estimates $\hat{\boldsymbol{\theta}}$ is given by

$$n^{-1}\mathbf{A}_n(\hat{\boldsymbol{\theta}})^{-1}\mathbf{B}_n(\hat{\boldsymbol{\theta}})\mathbf{A}_n(\hat{\boldsymbol{\theta}})^{-T}$$

where n is the sample size, $\mathbf{A}^{-T}$ denotes $\left(\mathbf{A}^T\right)^{-1}$, and

$$\mathbf{A}_n(\hat{\boldsymbol{\theta}}) = n^{-1}\sum_{i=1}^{n}\frac{-\partial S_i}{\partial \boldsymbol{\theta}^T}$$

$$\mathbf{B}_n(\hat{\boldsymbol{\theta}}) = n^{-1}\sum_{i=1}^{n} S_i S_i^T$$

PROC CAUSALTRT computes standard errors by taking the square roots of the diagonal elements of $\hat{V}(\hat{\boldsymbol{\theta}})$.

The form and dimension of $S(\boldsymbol{\theta})$, and hence those of the robust sandwich covariance matrix, depend on which estimation method is used. Whenever an outcome or treatment (propensity score) model is used in a particular estimation method, the estimating equations must also include the corresponding score vectors for that model.

Let $\boldsymbol{\beta}$ be a generic vector of parameters of a model, and let $\boldsymbol{\mu} = (\mu_0, \mu_1)$ be the vector of potential outcome means. Further, let $\mathbf{S}_{\text{ps}}$, $\mathbf{S}_{\text{out}}$, and $\mathbf{S}^{w}_{\text{out}}$ denote the score functions from the maximum likelihood estimation of the propensity score, outcome, and inverse probability weighted outcome models, respectively. Then the composition of $\boldsymbol{\theta}_0$ and $\mathbf{S}_i$ for each estimation method is as follows:

- AIPW

$$\boldsymbol{\theta}_0 = \left(\boldsymbol{\beta}_{\text{ps}}, \boldsymbol{\beta}_{\text{c}}, \boldsymbol{\beta}_{\text{t}}, \boldsymbol{\mu}\right)$$

$$\mathbf{S}_i = \left(\mathbf{S}_{\text{ps},i}, \mathbf{S}_{\text{out},i}, \mathbf{S}_{\text{ipw},i}\right)$$

- IPW and IPWR

$$\boldsymbol{\theta}_0 = \left(\boldsymbol{\beta}_{\text{ps}}, \boldsymbol{\mu}\right)$$

$$\mathbf{S}_i = \left(\mathbf{S}_{\text{ps},i}, \mathbf{S}_{\text{ipw},i}\right)$$

- IPWS

$$\boldsymbol{\theta}_0 = \left(\boldsymbol{\beta}_{\text{ps}}, \boldsymbol{\eta}, \boldsymbol{\mu}\right)$$

$$\mathbf{S}_i = \left(\mathbf{S}_{\text{ps},i}, \mathbf{S}_{\boldsymbol{\eta},i}, \mathbf{S}_{\text{ipw},i}\right)$$

- IPWREG

$$\boldsymbol{\theta}_0 = \left(\boldsymbol{\beta}_{\text{ps}}, \boldsymbol{\beta}^{w}_{\text{c}}, \boldsymbol{\beta}^{w}_{\text{t}}, \boldsymbol{\mu}\right)$$

$$\mathbf{S}_i = \left(\mathbf{S}_{\text{ps},i}, \mathbf{S}^{w}_{\text{out},i}, \mathbf{S}^{w}_{\text{reg},i}\right)$$

- REGADJ

$$\boldsymbol{\theta}_0 = (\boldsymbol{\beta}_{\mathrm{c}}, \boldsymbol{\beta}_{\mathrm{t}}, \boldsymbol{\mu})$$

$$\mathbf{S}_i = \left(\mathbf{S}_{\mathrm{out},i}, \mathbf{S}_{\mathrm{reg},i}\right)$$

The $(1-\alpha)100\%$ Wald confidence interval for the potential outcome mean μ_i is given by

$$\hat{\mu}_i \pm \mathrm{z}_{1-\alpha/2}\hat{\sigma}_i$$

where z_p is the $100p$th percentile of the standard normal distribution and $\hat{\sigma}_i$ is the standard error estimate for the potential outcome estimate $\hat{\mu}_i$. Because the ATE is the difference in potential outcome means, its standard error is computed by applying standard variance rules to the estimates from the covariance matrix for the potential outcomes. The corresponding Wald confidence interval for ATE is then constructed by the standard formula as shown in the previous expression. For the estimates of conditional potential outcome means, the standard errors and confidence limits are computed using the same approach but with $\mathbf{S}_{\mathrm{ipw},i}$ and $\mathbf{S}_{\mathrm{reg},i}$ replaced by $\mathbf{S}_{\mathrm{ipw},i|T=1}$ and $\mathbf{S}_{\mathrm{reg},i|T=1}$.

To provide better theoretical and computational properties, PROC CAUSALTRT uses modified expressions for components of A_n and B_n when the covariance matrix $\hat{V}(\hat{\boldsymbol{\theta}})$ is computed. For descriptions of the modifications, their motivation, and theoretical justification, see Pierce (1982); Robins, Rotnitzky, and Zhao (1995); Lunceford and Davidian (2004); Wooldridge (2010).

Bootstrap Methods

If you specify the BOOTSTRAP statement, PROC CAUSALTRT uses bootstrap resampling to compute standard errors and confidence intervals for the potential outcome means and treatment effect. The procedure samples as many bootstrap sample data sets (replicates) as you specify in the NBOOT= option and then estimates the potential outcome means and treatment effect for each replication. The bootstrap samples are taken from within the treatment conditions. Each bootstrap replicate contains the same numbers of usable observations in the control and treatment conditions as the number of usable observations that are included in the input data set.

Bootstrap confidence intervals are computed only for the potential outcome means and treatment effect. You can specify one or more the following types of bootstrap confidence intervals in the BOOTCI option in the BOOTSTRAP statement:

- The BOOTCI(NORMAL) option uses the normal approximation method to compute the bootstrap confidence interval. That is, the $(1-\alpha)100\%$ normal bootstrap confidence interval is given by

  $$\hat{\mu}_j \pm \sigma_{\mu_j^*} \times \mathrm{z}_{(1-\alpha/2)}$$

  where $\hat{\mu}_j$ is the estimate of μ_j from the original sample, $\sigma_{\mu_j^*}$ is the standard deviation of the bootstrap parameter estimates, and $\mathrm{z}_{(1-\alpha/2)}$ is the $100(1-\alpha/2)$th percentile of the standard normal distribution. PROC CAUSALTRT requires at least 50 bootstrap samples for normal bootstrap confidence intervals and does not compute them if 40 or fewer of the samples produce usable estimates.

- The BOOTCI(PERC) option requests the percentile method, which uses the $100(\alpha/2)$th and $100(1-\alpha/2)$th percentiles of the bootstrap parameter estimates as the confidence limits. These percentiles are

computed as follows. Let $\mu^*_{j,1}, \mu^*_{j,2}, \ldots, \mu^*_{j,B}$ represent the ordered values of the bootstrap estimates for the potential outcome mean μ_j. Let the kth weighted average percentile be q, set $p = \frac{k}{100}$, and let

$$np = l + g$$

where l is the integer part of np and g is the fractional part of np. Then the kth percentile, q, is computed as follows, which corresponds to the default percentile definition of the UNIVARIATE procedure:

$$q = \begin{cases} \frac{1}{2}\left(\mu^*_{j,l} + \mu^*_{j,l+1}\right) & \text{if } g = 0 \\ \mu^*_{j,l+1} & \text{if } g > 0 \end{cases}$$

- The BOOTCI(BC) option requests bias-corrected bootstrap confidence intervals, which use the cumulative distribution function (CDF), $G(\mu^*)$, of the bootstrap parameter estimates to determine the upper and lower endpoints of the confidence interval. The bias-corrected bootstrap confidence interval is given by

  $$G^{-1}\left(\Phi(2z_0 \pm z_{\alpha/2})\right)$$

  where Φ is the standard normal CDF, $z_{\alpha/2} = \Phi^{-1}(\alpha/2)$, and z_0 is a bias correction,

  $$z_0 = \Phi^{-1}\left(\frac{\mathrm{N}\left(\mu^*_j \le \hat{\mu}_j\right)}{\mathrm{B}}\right)$$

  where $\hat{\mu}_j$ is the original sample estimate of μ_j from the input data set; $\mathrm{N}(\mu^*_j \le \hat{\mu}_j)$ is the number of bootstrap estimates, μ^*_j, that are less than or equal to $\hat{\mu}_j$; and B is the number of bootstrap replicates for which an estimate for the treatment effect is obtained.

The bias-corrected bootstrap confidence intervals are the default intervals used if you do not override them by specifying the NORMAL or PERC suboptions in the BOOTCI option.

PROC CAUSALTRT requires at least 1,000 bootstrap samples for the percentile and bias-corrected bootstrap confidence intervals and does not compute them if fewer than 900 of the samples produce usable estimates. If the number of samples *n* specified in the NBOOT=*n* option is less than 1,000 and the percentile or bias-corrected bootstrap confidence intervals are requested, the value of *n* is ignored. Bootstrap confidence intervals and the bootstrap standard deviations are computed in the same manner for the estimates of the ATE and ATT.

Missing Values

When the CAUSALTRT procedure fits a model, it excludes observations that have missing values for the outcome variable, treatment variable, frequency variable, or predictor variables, which are specified in the MODEL and PSMODEL statements. It also excludes observations that have invalid response or frequency values. Invalid response values are determined by the probability distribution for the response as specified in the DIST= option in the MODEL statement. The exclusion of observations because of invalid responses applies to all estimation methods, even for methods that do not require an outcome model specification (such as IPW, IPWR, and IPWS). In particular, responses must be strictly positive for the inverse Gaussian and gamma distributions, and must be nonnegative for the Poisson distribution. In all cases, exclusion of observations almost certainly affects the estimation results.

ODS Table Names

PROC CAUSALTRT assigns a name to each table that it creates. You can use these names to refer to the table when you use the Output Delivery System (ODS) to select tables and create output data sets. These names are listed in Table 38.8. For more information about ODS, see Chapter 22, "Using the Output Delivery System."

Table 38.8 ODS Tables Produced by PROC CAUSALTRT

ODS Table Name	Description	Statement	Option
CausalEffects	Estimates for potential outcome means and treatment effect		Default
ClassLevels	Classification variable levels	CLASS	Default
ControlEstimates	Parameter estimates for the control condition outcome model	PROC CAUSALTRT	POUTCOMEMOD
ModelInfo	Model information		Default
NObs	Number of observations		Default
PSCovDiff	Standardized mean differences and variance ratios of propensity score model effects	PROC CAUSALTRT	COVDIFFPS
PSModelEstimates	Parameter estimates for the propensity score model	PROC CAUSALTRT	PPSMODEL
ResponseProfile	Frequency counts for a binary outcome variable	MODEL	DIST=BIN
TreatmentEstimates	Parameter estimates for the treatment condition outcome model	PROC CAUSALTRT	POUTCOMEMOD
TreatmentProfile	Frequency counts for the treatment variable		Default

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."

PROC CAUSALTRT assigns a name to each graph it creates using ODS. You can use these names to refer to the graphs when you use ODS. Table 38.9 lists the names.

To request these graphs, ODS Graphics must be enabled and you must specify the option indicated in Table 38.9.

Table 38.9 Graphs Produced by PROC CAUSALTRT

ODS Graph Name	Description	Statement	Option
BootHistPlot	Histogram of bootstrap sample estimates	BOOTSTRAP	PLOTS=HIST
LogitPSPlot	Kernel density plot for the logit of the propensity score	PSMODEL	PLOTS=LOGITPSCORE
OutcomeByPScore	Scatter plot of outcome by propensity score	PSMODEL	PLOTS=OUTBYPSCORE
OutcomeByWeight	Scatter plot of outcome by weight	PSMODEL	PLOTS=OUTBYWEIGHT
PSCloud	Point clouds of propensity scores	PSMODEL	PLOTS=PSCLOUD
PSCovDenPlot	Kernel density plots of PSMODEL effects	PSMODEL	PLOTS=PSCOVDEN
PSDistPlot	Box plot of propensity score	PSMODEL	PLOTS=PSDIST
WeightCloud	Point clouds of weights	PSMODEL	PLOTS=WEIGHTCLOUD
WeightDistPlot	Box plot of weights	PSMODEL	PLOTS=WEIGHTDIST

Examples: CAUSALTRT Procedure

The following examples illustrate some of the capabilities of the CAUSALTRT procedure. These examples are not intended to represent definitive analyses of the data sets that are presented here.

Example 38.1: Estimating the ATE Using Inverse Probability Weights

This example illustrates how the CAUSALTRT procedure uses inverse probability weights to estimate the average treatment effect (ATE). The question of interest is the effect that quitting smoking has on an individual's weight. The data for this example are a subset of data from the NHANES I Epidemiologic Follow-Up Study (NHEFS) in Hernán and Robins (2018). For the study, medical and behavioral information were collected during an initial physical examination, and again at follow-up interviews approximately one decade later.

The input data set SmokingWeight is shown in the following DATA step:

```
data SmokingWeight;
   input
   Sex Age Race Education Exercise BaseWeight Weight Change Activity
   YearsSmoke PerDay Quit;
   datalines;
   0 42 1 1 2 79.04 68.95 -10.09 0 29 30 0
   0 36 0 2 0 58.63 61.23 2.60 0 24 20 0
   1 56 1 2 2 56.81 66.22 9.41 0 26 20 0
   0 68 1 1 2 59.42 64.41 4.99 1 53 3 0
   0 40 0 2 1 87.09 92.08 4.99 1 19 20 0

   ... more lines ...

   0 45 0 1 0 63.05 64.41 1.36 0 29 40 0
   1 47 0 1 0 57.72 61.23 3.51 0 31 20 0
   1 51 0 3 0 62.71 . . 0 30 40 0
   0 68 0 1 1 52.39 57.15 4.76 1 46 15 0
   0 26 0 . 0 86.75 87.54 0.79 0 9 20 0
   0 29 0 2 1 90.83 106.59 15.76 1 14 30 1
;
```

The variables in the data are as follows:

- Activity: level of daily activity, with values 0, 1, and 2
- Age: age in 1971
- BaseWeight: weight in kilograms in 1971
- Change: difference in weight at the follow-up and baseline interviews (measured in kilograms)
- Education: level of education, with values 0, 1, 2, 3, and 4
- Exercise: amount of regular recreational exercise, with values 0, 1, and 2

- PerDay: number of cigarettes smoked per day in 1971
- Quit: 1 if an individual quit smoking between the initial and follow-up interviews; 0 otherwise
- Race: 0 for white; 1 otherwise
- Sex: 0 for male; 1 for female
- Weight: weight in kilograms at the follow-up interview
- YearsSmoke: number of years an individual has smoked

The following statements invoke PROC CAUSALTRT to estimate the average causal effect that quitting smoking has on weight gain:

```
ods graphics on;
proc causaltrt data=smokingweight covdiffps;
   class Sex Race Education Exercise Activity Quit /desc;
   psmodel Quit = Sex Age Education Exercise Activity YearsSmoke PerDay
          /plots=(PSDist pscovden(effects(Age YearsSmoke)) );
   model Change;
run;
```

The MODEL and PSMODEL statements are both required. A model for the treatment variable, Quit, is listed in the PSMODEL statement, and the outcome variable, Change, is specified in the MODEL statement. For estimation, the inverse probability weighting method with ratio adjustment (IPWR) is used by default because only a model for the treatment variable is specified. The estimation method, outcome variable, and treatment variable are all listed in the "Model Information" table in Output 38.1.1.

Output 38.1.1 Model Information

The CAUSALTRT Procedure

Model Information	
Data Set	WORK.SMOKINGWEIGHT
Distribution	Normal
Estimation Method	IPWR
Treatment Variable	Quit
Outcome Variable	Change

To examine whether the weights obtained from the propensity score model balance the covariates between the treatment and control conditions, you use the COVDIFFPS option in the PROC CAUSALTRT statement to request the computation of weighted and unweighted standardized mean differences (between treatment and control conditions) and variance ratios (treatment to control) for the covariates that are specified in the PSMODEL statement. These values are displayed in the "Covariate Differences for Propensity Score Model" table in Output 38.1.2. An improvement in the covariate balance after weighting would be indicated by the following two observations when you compare the unweighted and weighted columns in the table:

- smaller standardized mean differences in the weighted column
- variance ratios closer to one in the weighted column

Establishing covariate balance under the propensity score model is an important diagnostic step. Failing to achieve covariate balance would directly challenge the assumption of strong ignorability or conditional exchangeability, which is essential for estimating the causal effect. For more information about the assumptions and conditions required for the causal estimation methods, see the section "Causal Effects: Definitions, Assumptions, and Identification" on page 2435.

For the current example, Output 38.1.2 clearly shows that all standardized differences in the weighted column are smaller in magnitude than their counterparts in the unweighted column. All but one of the weighted standardized differences are smaller than 0.03 in magnitude. In addition, all but one of the variance ratios in the weighted column are closer to 1 than their counterparts in the unweighted column.

Notice that rows with blank values are for reference levels of the categorical covariates. The blank values indicate that they were not computed because they can be expressed in terms of the remaining levels.

Output 38.1.2 Standardized Mean Differences

The CAUSALTRT Procedure

Covariate Differences for Propensity Score Model

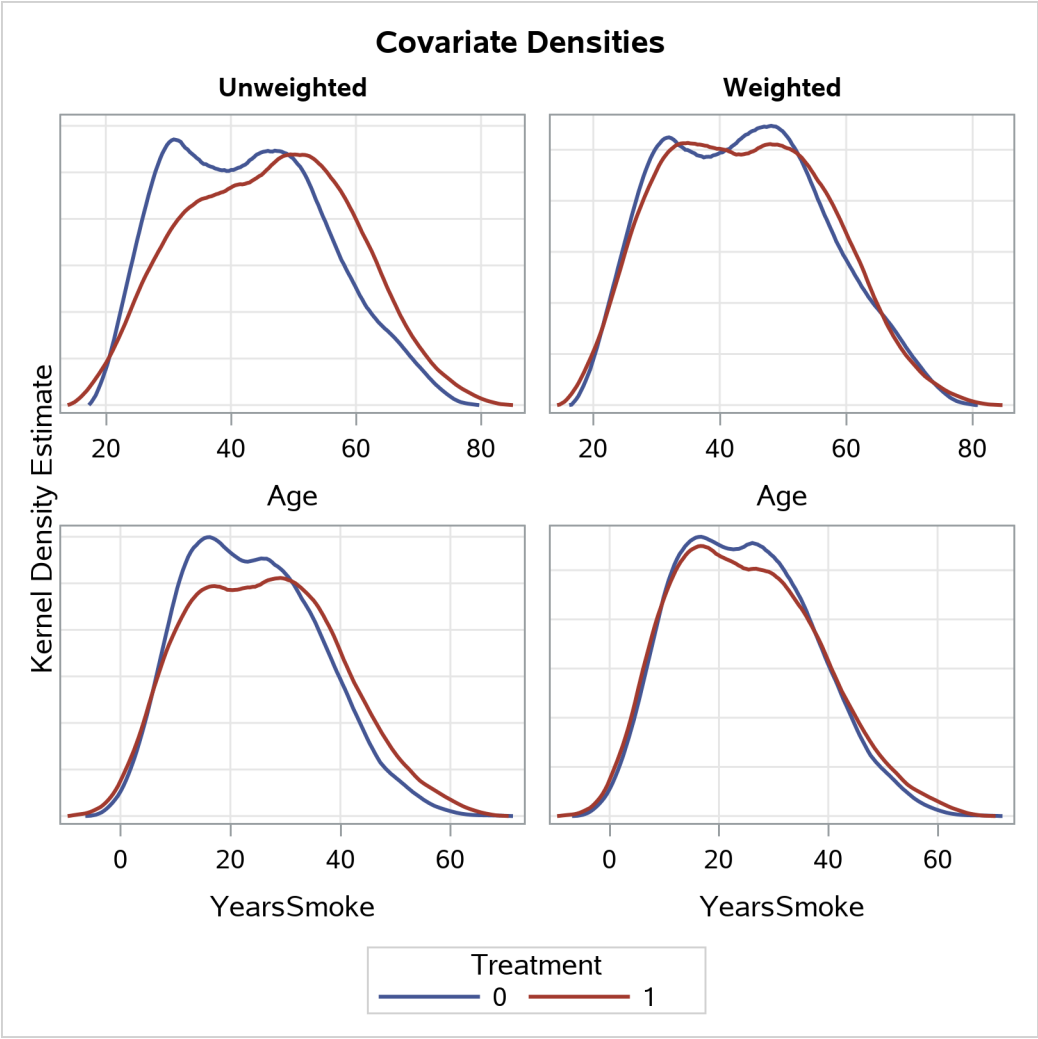
		Standardized Difference		Variance Ratio	
Parameter		**Unweighted**	**Weighted**	**Unweighted**	**Weighted**
Sex	**1**	-0.1603	-0.0200	0.9962	1.0006
Sex	**0**				
Age		0.2820	0.0318	1.0731	0.9847
Education	**5**	0.1660	0.0111	1.4610	1.0268
Education	**4**	-0.0270	0.0196	0.9167	1.0624
Education	**3**	-0.0472	-0.0015	0.9811	0.9994
Education	**2**	-0.1116	-0.0034	0.8498	0.9953
Education	**1**				
Exercise	**2**	0.0568	-0.0029	1.0252	0.9986
Exercise	**1**	0.0398	0.0166	1.0119	1.0049
Exercise	**0**				
Activity	**2**	0.0740	-0.0074	1.2182	0.9796
Activity	**1**	0.0268	0.0196	1.0043	1.0029
Activity	**0**				
YearsSmoke		0.1589	0.0253	1.1846	1.0894
PerDay		-0.2167	0.0027	1.1679	1.3323

Further diagnostics for assessing the covariate balance are requested by using the PLOTS= option in the PSMODEL statement.

The EFFECTS(Age YearsSmoke) suboption in the PSCOVDEN option requests that weighted and unweighted kernel density estimates be computed for the covariates Age and YearsSmoke. Output 38.1.3 displays the related paneled plots. The densities for both covariates show improved balance after weighting, as shown by the closely matched density curves in the weighted column. This observation echoes the preceding conclusion that the weights obtained from fitting the propensity score model lead to good covariate balance in Age and YearsSmoke. These density plots are available only for continuous covariates.

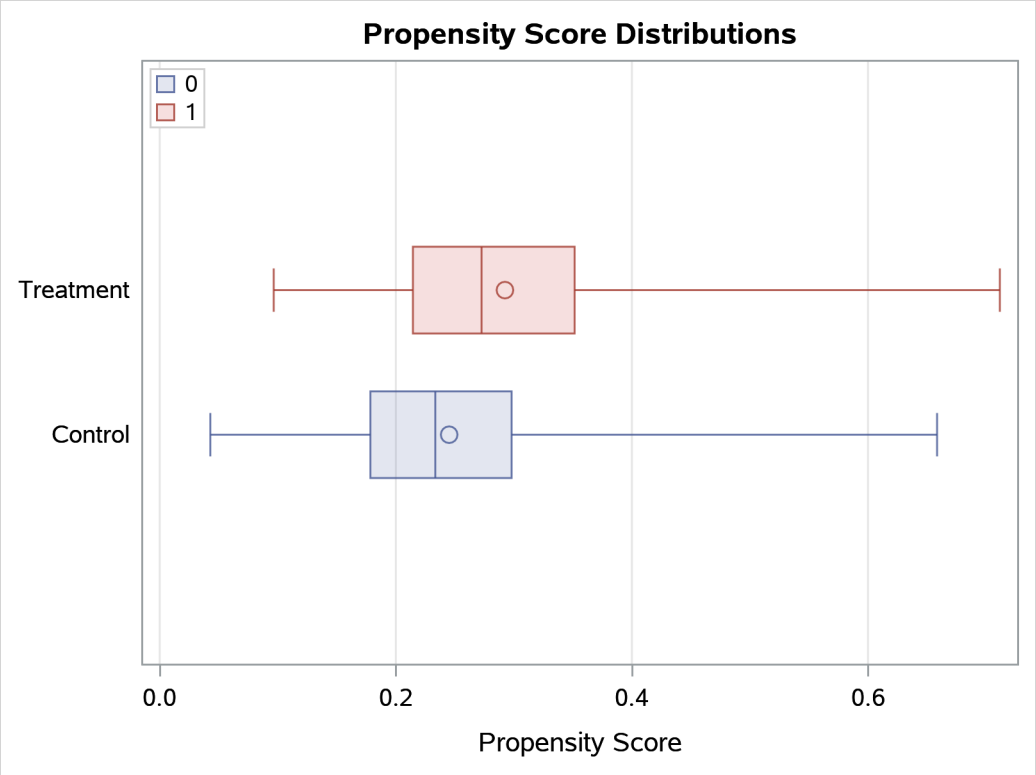
Output 38.1.4 shows the box plots that are requested by specifying PSDIST in the PLOTS= option. These box plots of propensity scores by treatment level indicate a similar distribution of propensity scores between treatment conditions.

Output 38.1.3 Density Estimates



The estimates for the potential outcome means and ATE are displayed in Output 38.1.5. The estimate for the ATE of 3.1876 indicates that, on average, quitting smoking leads to an increase of about three kilograms in an individual's weight.

Output 38.1.4 Propensity Score Distributions



Output 38.1.5 IPWR Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	1	4.9824	0.4528	4.0949	5.8699	11.00	<.0001
POM	0	1.7948	0.2163	1.3709	2.2187	8.30	<.0001
ATE		3.1876	0.4972	2.2132	4.1621	6.41	<.0001

As an alternative to estimating the ATE by using the IPWR estimation method, you can estimate it by using inverse probability weights with either the basic inverse probability weighting method (METHOD=IPW) or the inverse probability weighting method with ratio and scale adjustments (METHOD=IPWS). The following statements use the METHOD=IPWS option to estimate the ATE:

```
proc causaltrt data=smokingweight method=IPWS;
   class Sex Race Education Exercise Activity Quit /desc;
   psmodel Quit = Sex Age Education Exercise Activity YearsSmoke PerDay;
   model Change;
run;
```

Because the effects that are specified in the PSMODEL statement have not changed from the preceding analysis, the same model is fit for the treatment assignment in the current example. Therefore, the predicted weights and measures of covariate balance do not change. What has changed by using the IPWS instead of

the IPWR estimation method is how the weights are incorporated into the estimation of the potential outcome means and ATE. For this example, there is little difference between the IPWS estimate of 3.1896 for the ATE, shown in Output 38.1.6, and the IPWR estimate of 3.1876, shown in Output 38.1.5.

Output 38.1.6 IPWS Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	1	4.9850	0.4530	4.0972	5.8728	11.01	<.0001
POM	0	1.7954	0.2163	1.3715	2.2193	8.30	<.0001
ATE		3.1896	0.4973	2.2149	4.1643	6.41	<.0001

Example 38.2: Estimating the ATE Using Augmented Inverse Probability Weights

This example illustrates how the CAUSALTRT procedure uses augmented inverse probability weights (AIPW) to perform doubly robust estimation of the ATE. This example uses the SmokingWeight data set that is described in Example 38.1 and estimates the same causal effect: how quitting smoking might affect an individual's change in weight.

The AIPW method combines modeling the treatment assignment and modeling the outcome variable to estimate the potential outcome means and the ATE. The following statements invoke PROC CAUSALTRT to estimate the causal effect of quitting smoking on weight gain by using the AIPW method:

```
ods graphics on;
proc causaltrt data=smokingweight method=AIPW nthreads=4;
   class Sex Race Education Exercise Activity Quit /desc;
   psmodel Quit = Sex Age Education Exercise Activity YearsSmoke PerDay ;
   model Change = Sex Age Exercise Activity BaseWeight;
   bootstrap bootci(all) plot=hist seed=1234;
run;
```

The model for the treatment assignment is specified in the PSMODEL statement, and the outcome model is specified in the MODEL statement. The AIPW method is a doubly robust estimation method and provides unbiased estimates for the ATE even when one of the models is misspecified. The model for the treatment assignment is the same model that is used in Example 38.1. Therefore, the estimates for the weights and measures of covariate balance (Output 38.1.2 and Output 38.1.3) are the same for this example.

Although the AIPW estimates for the ATE and potential outcome means are doubly robust, the empirical estimates for their standard errors (the default estimates of standard errors) are not. You can request bootstrap-based estimation of the standard errors and confidence limits by using the BOOTSTRAP statement. The BOOTCI(ALL) option requests the estimation of all three bootstrap-based confidence intervals that PROC CAUSALTRT implements: the bias-corrected percentile method (default), percentile method, and normal approximation method. The bootstrap-based confidence intervals are added to the "Analysis of Causal Effect" table. The standard Wald confidence intervals and the three bootstrap-based confidence intervals all provide similar limits as shown in Output 38.2.1. The robust standard error estimate and the bootstrap standard error estimate are also very close. The AIPW estimate for the ATE of 3.3049 is larger than the IPWS estimate for

the ATE of 3.1896 (as shown in Output 38.1.6) and also larger than the IPWR estimate of 3.1876 (as shown in Output 38.1.5).

Output 38.2.1 AIPW Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

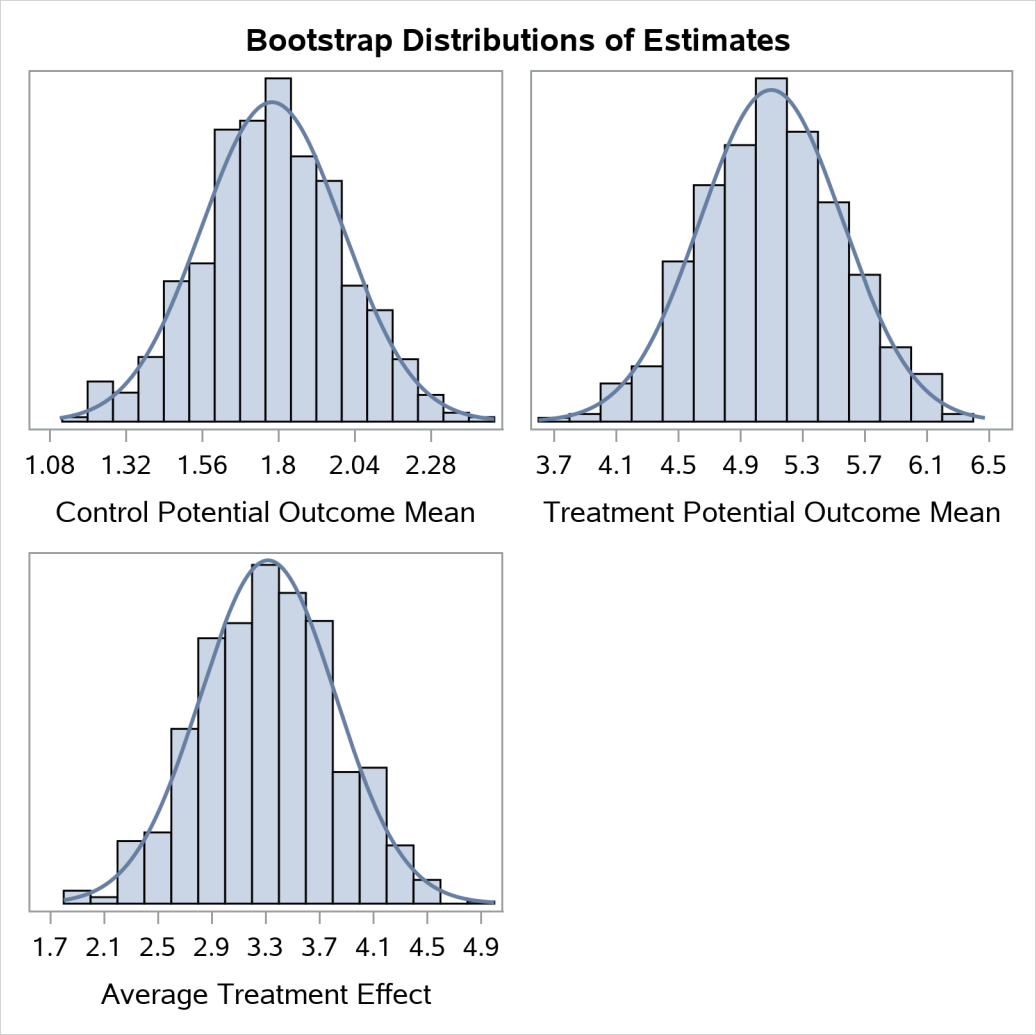
Parameter	Treatment Level	Estimate	Robust Std Err	Bootstrap Std Err	Wald 95% Confidence Limits		Bootstrap Wald 95% Confidence Limits		Bootstrap Percentile 95% Confidence Limits	
POM	1	5.0830	0.4495	0.4588	4.2019	5.9641	4.1839	5.9822	4.1907	6.0400
POM	0	1.7781	0.2156	0.2227	1.3556	2.2007	1.3416	2.2147	1.3175	2.2155
ATE		3.3049	0.4911	0.5016	2.3423	4.2675	2.3218	4.2879	2.3511	4.3029

Analysis of Causal Effect

Parameter	Bootstrap Bias Corrected 95% Confidence Limits		Z	Pr > |Z|
POM	4.1736	6.0079	11.31	<.0001
POM	1.3068	2.2127	8.25	<.0001
ATE	2.3502	4.2981	6.73	<.0001

To inspect the distribution of the bootstrap estimates, you request histograms of the estimates by specifying the PLOTS=HIST option in the BOOTSTRAP statement. In Output 38.2.2, the histograms are collected in a panel and show no extreme estimates. Normal densities are overlaid in the histograms. Output 38.2.2 shows that the distributions of the potential outcome means (POM) and ATE estimates are approximately normal. To reproduce the random number stream that was used to generate the bootstrap estimates, you must use the same SEED= value and the same number of threads for the analytic computations. When bootstrap resampling is performed, a column that indicates the number of threads used is added to the "Analysis of Causal Effect" table; this column is not displayed but is available if you use the ODS OUTPUT statement to save the table as an output data set. You can also display this column by modifying the corresponding template.

Output 38.2.2 Histograms of Bootstrap Estimates



Example 38.3: Estimating Treatment Effects Using Regression Adjustment

This example demonstrates how the CAUSALTRT procedure can use regression adjustment to estimate both the ATE (average treatment effect) and the ATT (average treatment effect for the treated). The question of interest in this example is the effect that attending a Catholic high school has on a student's performance in mathematics. The data for this example are a subset of data from the National Educational Longitudinal Study of 1988 in Murnane and Willett (2011). Demographic information was collected from the students and their families along with standardized test scores in 1988 and subsequent follow-up years. The outcome for this example is the student's score on the mathematics portion of the standardized tests in 1992.

The input data set School is shown in the following DATA step:

```
data School;
   input
   Income $ FatherEd $ MotherEd $ Math BaseMath  Catholic $;
   datalines;
```

```
   Middle HighSchool HighSchool 49.77 50.27 Yes
   Middle Unknown Unknown 59.84 51.52 Yes
   Middle NoHighSchool Postsecondary 50.38 47.56 Yes
   Middle Unknown Unknown 45.03 46.60 Yes
   High HighSchool HighSchool 54.26 60.22 Yes
   Low NoHighSchool HighSchool 55.37 58.63 Yes

   ... more lines ...

   High SomeSecondary HighSchool 43.28 43.27 Yes
   Middle HighSchool HighSchool 41.69 48.29 Yes
   High College College 56.60 60.15 Yes
   High College SomeSecondary 56.29 59.53 Yes
   High College Postsecondary 58.16 57.06 Yes
   High College SomeSecondary 63.57 63.51 Yes
;
```

The data set School consists of records for 5,671 high school students whose 1988 total family income was at most $75,000. The variables in the data are as follows:

- BaseMath: student's score on the mathematics portion of a standardized test in 1988
- Catholic: Yes if a student attended a Catholic high school; No otherwise
- FatherEd: highest level of education completed by the student's father, with six levels
- Income: classification based on total family income, with values of Low, Middle, and High
- Math: student's score on the mathematics portion of a standardized test in 1992
- MotherEd: highest level of education completed by the student's mother, with six levels

The following statements invoke the PROC CAUSALTRT procedure to estimate the ATE of attending a Catholic high school on math scores:

```
proc causaltrt data=school method=regadj poutcomemod;
   class Income FatherEd MotherEd;
   psmodel Catholic(ref='No');
   model Math = BaseMath Income FatherEd MotherEd;
run;
```

The METHOD=REGADJ option requests that regression adjustment be used to estimate the ATE. For this estimation method, models are fit for the outcome variable separately for each treatment condition. The treatment variable, Catholic, is listed in PSMODEL statement. The **ref='No'** option identifies Catholic='No' as the reference or control level. The outcome variable Math is specified in the MODEL statement along with the effects used to fit the outcome model.

The POUTCOMEMOD option in the PROC CAUSALTRT statement requests the display of the parameter estimates for the outcome model fit within each treatment condition. Two tables are produced: one for the control condition (Output 38.3.1) and one for the treatment condition (Output 38.3.2).

Output 38.3.1 Control Group Estimates

The CAUSALTRT Procedure

Outcome Model Estimates for Control Group

Parameter		Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		10.9061	0.4808	9.9638	11.8484	514.5891	<.0001
BaseMath		0.7774	0.0078	0.7622	0.7927	9950.9801	<.0001
Income	High	0.4244	0.1818	0.0681	0.7807	5.4516	0.0196
Income	Low	-0.7194	0.1944	-1.1004	-0.3385	13.7017	0.0002
Income	Middle	0	.	.	.	.	.
FatherEd	College	0.3857	0.3313	-0.2637	1.0351	1.3548	0.2444
FatherEd	HighScho	-0.3112	0.2903	-0.8803	0.2579	1.1488	0.2838
FatherEd	NoHighSc	-1.1478	0.3302	-1.7950	-0.5005	12.0806	0.0005
FatherEd	Postseco	0.5464	0.3827	-0.2037	1.2965	2.0381	0.1534
FatherEd	SomeSeco	0.1948	0.3066	-0.4061	0.7957	0.4036	0.5252
FatherEd	Unknown	0	.	.	.	.	.
MotherEd	College	0.6255	0.3747	-0.1089	1.3600	2.7863	0.0951
MotherEd	HighScho	-0.00768	0.3222	-0.6392	0.6238	0.0006	0.9810
MotherEd	NoHighSc	-0.5579	0.3610	-1.2654	0.1496	2.3890	0.1222
MotherEd	Postseco	0.1472	0.4370	-0.7093	1.0036	0.1134	0.7363
MotherEd	SomeSeco	0.4911	0.3346	-0.1647	1.1469	2.1540	0.1422
MotherEd	Unknown	0	.	.	.	.	.

Output 38.3.2 Treatment Group Estimates

The CAUSALTRT Procedure

Outcome Model Estimates for Treatment Group

Parameter		Estimate	Standard Error	Wald 95% Confidence Limits		Wald Chi-Square	Pr > ChiSq
Intercept		15.6156	1.7186	12.2471	18.9840	82.5561	<.0001
BaseMath		0.7274	0.0244	0.6795	0.7752	887.3010	<.0001
Income	High	-0.3734	0.5055	-1.3641	0.6173	0.5458	0.4600
Income	Low	-1.9732	0.6744	-3.2950	-0.6514	8.5605	0.0034
Income	Middle	0	.	.	.	.	.
FatherEd	College	2.3426	1.0035	0.3758	4.3095	5.4497	0.0196
FatherEd	HighScho	0.6428	1.0026	-1.3223	2.6080	0.4111	0.5214
FatherEd	NoHighSc	0.0547	1.0842	-2.0702	2.1796	0.0025	0.9598
FatherEd	Postseco	1.2191	1.0603	-0.8591	3.2973	1.3219	0.2503
FatherEd	SomeSeco	1.9739	0.9848	0.0436	3.9041	4.0171	0.0450
FatherEd	Unknown	0	.	.	.	.	.
MotherEd	College	-0.1707	1.0663	-2.2607	1.9193	0.0256	0.8728
MotherEd	HighScho	-1.3311	1.0506	-3.3903	0.7280	1.6053	0.2051
MotherEd	NoHighSc	-0.6978	1.3538	-3.3513	1.9557	0.2656	0.6063
MotherEd	Postseco	-0.8308	1.1261	-3.0379	1.3764	0.5442	0.4607
MotherEd	SomeSeco	-0.8607	1.0016	-2.8238	1.1025	0.7383	0.3902
MotherEd	Unknown	0	.	.	.	.	.

The potential outcome means and ATE are estimated by averaging predicted values for each student from each of the outcome models. The ATE estimate of 1.6920 in Output 38.3.3 indicates that attending a Catholic high school has a positive effect on math scores. This estimate for the treatment effect is much smaller than the estimate of 3.8949 that you would obtain by comparing the unadjusted average math scores for each treatment condition.

Output 38.3.3 Regression Adjustment Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	Yes	52.5790	0.2645	52.0605	53.0975	198.76	<.0001
POM	No	50.8871	0.1280	50.6363	51.1378	397.70	<.0001
ATE		1.6920	0.2536	1.1950	2.1889	6.67	<.0001

Conceptually, the ATE in this example is the average effect on the math scores for everyone in the population who would have attended a Catholic high school versus a non-Catholic high school. Causal effect analysis such as the current example enables you to estimate the ATE with causal interpretation, which is of general scientific interest.

However, for policy-making purposes, sometimes it is more interesting to examine the effectiveness of a program or treatment for those who did participate. The average treatment effect for the treated (ATT) is such a concept; it measures the treatment effect conditional on those who receive the treatment condition. PROC CAUSALTRT provides you two methods to estimate ATT: the inverse probability weighting method with ratio adjustment (METHOD=IPWR) or regression adjustment (METHOD=REGADJ).

The remainder of this section demonstrates the estimation of ATT for the Catholic high school data example. To estimate the average treatment effect for the treated, you specify the ATT option in the PROC CAUSALTRT statement. The following SAS statements estimate the ATT using the regression adjustment estimation method and the same outcome model as specified in the previous analysis for ATE:

```
proc causaltrt data=school method=regadj att;
   class Income FatherEd MotherEd;
   psmodel Catholic(ref='No');
   model Math = BaseMath Income FatherEd MotherEd;
run;
```

The "Analysis of Causal Effect" table now displays estimates for the ATT and the potential outcome means conditional on receiving the treatment condition. The estimate for the ATT is 1.5727, which is slightly smaller than the ATE estimate.

Output 38.3.4 Regression Adjustment ATT Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	Yes	54.5395	0.3475	53.8583	55.2207	156.93	<.0001
POM	No	52.9668	0.3034	52.3722	53.5614	174.59	<.0001
ATT		1.5727	0.2268	1.1281	2.0173	6.93	<.0001

From a policy-making point of view, the average effect that attending a Catholic high school would have on students who are in non-Catholic high school would also be of interest. Such a mirror concept of ATT is also known as ATU, average treatment effect for the untreated. Although the CAUSALTRT procedure does not provide a direct option for estimating ATU, you can still achieve that purpose by using the ATT option with the reverse treatment designation. In the following PROC CAUSALTRT statements, the **ref='Yes'** option in the PSMODEL statement redefines the treatment condition to be attending a non-Catholic high school.

```
proc causaltrt data=school method=regadj att;
   class Income FatherEd MotherEd;
   psmodel Catholic(ref='Yes');
   model Math = BaseMath Income FatherEd MotherEd;
run;
```

The ATT estimate of –1.7059 in Output 38.3.5 is the average causal effect that attending non-Catholic high schools has on the math scores of students in non-Catholic high schools. Reversing the sign of this estimate provides an estimate for the ATU: the average treatment effect that attending a Catholic school would have for those students in non-Catholic high schools. Hence, the ATU in the current example is 1.7059.

In some research studies, researchers would like to compare ATT and ATU to investigate the so-called effect heterogeneity issue. In the current example, the ATU is only slightly larger (by about 0.13 points) than the ATT. Considering the fact that all potential outcome means are about 50, it thus appears to be safe to say that effect heterogeneity, as indicated by the 0.13 point difference, is not an issue in the current example.

Output 38.3.5 AIPW Potential Outcome Means and ATE Estimates

The CAUSALTRT Procedure

Analysis of Causal Effect

Parameter	Treatment Level	Estimate	Robust Std Err	Wald 95% Confidence Limits		Z	Pr > |Z|
POM	No	50.6447	0.1338	50.3825	50.9068	378.60	<.0001
POM	Yes	52.3505	0.2717	51.8179	52.8831	192.66	<.0001
ATT		-1.7059	0.2608	-2.2171	-1.1947	-6.54	<.0001

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