

SAS/STAT[®] 15.1

User's Guide

The TTEST Procedure

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Chapter 125

The TTEST Procedure

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Overview: TTEST Procedure

The TTEST procedure performs t tests and computes confidence limits for one sample, paired observations, two independent samples, and the AB/BA crossover design. Two-sided, TOST (two one-sided test) equivalence, and upper and lower one-sided hypotheses are supported for means, mean differences, and mean ratios for either normal or lognormal data. PROC TTEST also computes bootstrap standard error, bias estimates, and confidence limits.

Table 125.1 summarizes the designs, analysis criteria, hypotheses, and distributional assumptions supported in the TTEST procedure, along with the syntax that you use to specify them.

Table 125.1 Features Supported in the TTEST Procedure

Feature	Syntax
Design	
One-sample	VAR statement
Paired	PAIRED statement
Two-independent-sample	CLASS statement, VAR statement
AB/BA crossover	VAR / Crossover=
Analysis Criterion	
Mean difference	PROC TTEST TEST=DIFF
Mean ratio	PROC TTEST TEST=RATIO
Hypothesis	
Two-sided	PROC TTEST SIDES=2
Equivalence	PROC TTEST TOST (< lower , > upper)
Lower one-sided	PROC TTEST SIDES=L
Upper one-sided	PROC TTEST SIDES=U
Distribution	
Normal	PROC TTEST DIST=NORMAL
Lognormal	PROC TTEST DIST=LOGNORMAL
Empirical, resampled with replacement	BOOTSTRAP statement

FREQ and WEIGHT statements are available. Data can be input in the form of observations or, in certain cases, summary statistics. Output includes summary statistics; confidence limits for means, standard deviations, and coefficients of variation; hypothesis tests; bootstrap analyses; and a variety of graphical displays for both the input data set and bootstrap samples, including histograms, densities, box plots, confidence intervals, Q-Q plots, profiles, agreement plots, and correlation plots.

PROC TTEST uses ODS Graphics to create graphs as part of its output. For general information about ODS Graphics, see Chapter 21, “Statistical Graphics Using ODS.” For specific information about the statistical graphics available with the TTEST procedure, see the **PLOTS** option in the **PROC TTEST** statement and the section “ODS Graphics” on page 10519.

Getting Started: TTEST Procedure

One-Sample t Test

A one-sample t test can be used to compare a sample mean to a given value. This example, taken from Huntsberger and Billingsley (1989, p. 290), tests whether the mean length of a certain type of court case is more than 80 days by using 20 randomly chosen cases. The data are read by the following DATA step:

```
data time;
  input time @@;
  datalines;
  43 90 84 87 116 95 86 99 93 92
  121 71 66 98 79 102 60 112 105 98
  ;
```

The only variable in the data set, *time*, is assumed to be normally distributed. The trailing at signs (@@) indicate that there is more than one observation on a line. The following statements invoke PROC TTEST for a one-sample t test:

```
ods graphics on;

proc ttest h0=80 plots(showh0) sides=u alpha=0.1;
  var time;
run;

ods graphics off;
```

The **VAR** statement indicates that the *time* variable is being studied, while the **H0=** option specifies that the mean of the *time* variable should be compared to the null value 80 rather than the default of 0. The **PLOTS(SHOWH0)** option requests that this null value be displayed on all relevant graphs. The **SIDES=U** option reflects the focus of the research question, namely whether the mean court case length is *greater than* 80 days, rather than *different than* 80 days (in which case you would use the default **SIDES=2** option). The **ALPHA=0.1** option requests 90% confidence intervals rather than the default 95% confidence intervals. The output is displayed in Figure 125.1.

Figure 125.1 One-Sample t Test Results
The TTEST Procedure
Variable: *time*

N	Mean	Std Dev	Std Err	Minimum	Maximum
20	89.8500	19.1456	4.2811	43.0000	121.0

Figure 125.1 continued

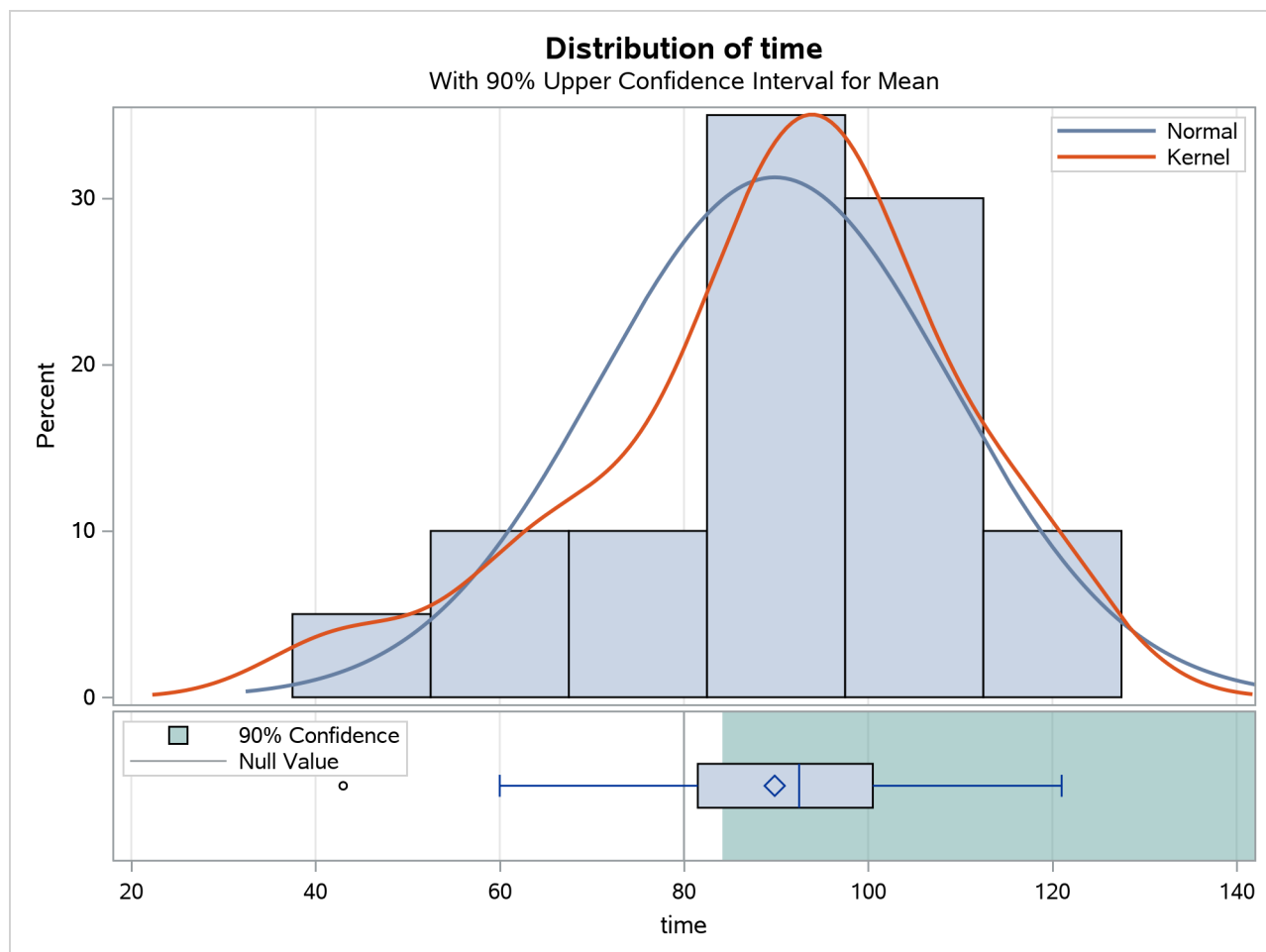
	90%			90%	
Mean	CL Mean	Std Dev		CL Std Dev	
89.8500	84.1659	Infty	19.1456	15.2002	26.2374

DF	t Value	Pr > t
19	2.30	0.0164

Summary statistics appear at the top of the output. The sample size (N), mean, standard deviation, and standard error are displayed with the minimum and maximum values of the time variable. The 90% confidence limits for the mean and standard deviation are shown next. Due to the `SIDES=U` option, the interval for the mean is an upper one-sided interval with a finite lower bound (84.1659 days). The limits for the standard deviation are the equal-tailed variety, per the default `CI=EQUAL` option in the `PROC TTEST` statement. At the bottom of the output are the degrees of freedom, t statistic value, and p -value for the t test. At the 10% α level, this test indicates that the mean length of the court cases is significantly greater than from 80 days ($t = 2.30$, $p = 0.0164$).

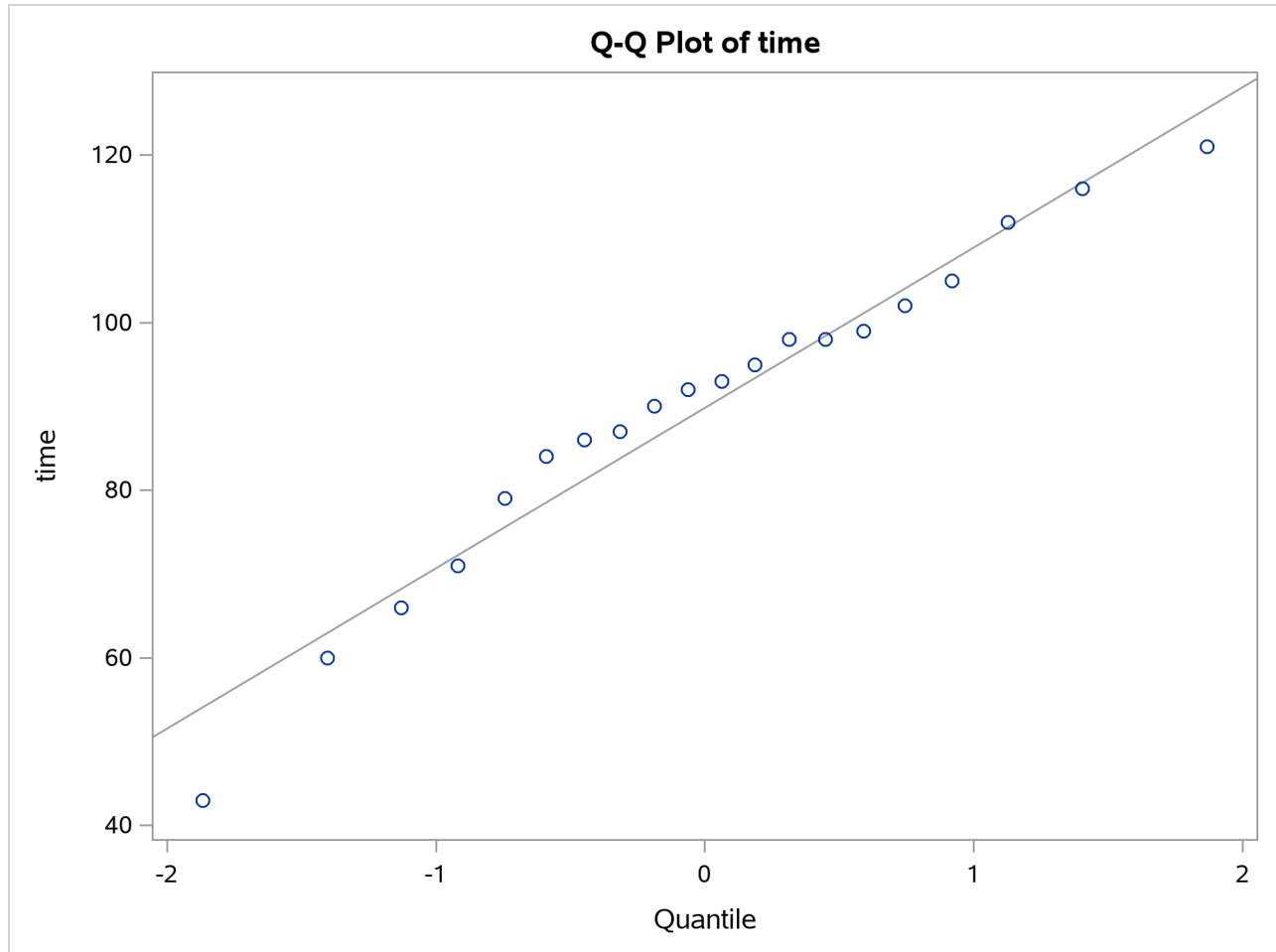
The summary panel in Figure 125.2 shows a histogram with overlaid normal and kernel densities, a box plot, the 90% confidence interval for the mean, and the null value of 80 days.

Figure 125.2 Summary Panel



The confidence interval excludes the null value, consistent with the rejection of the null hypothesis at $\alpha = 0.1$. The Q-Q plot in Figure 125.3 assesses the normality assumption.

Figure 125.3 Q-Q Plot



The curvilinear shape of the Q-Q plot suggests a possible slight deviation from normality. You could use the UNIVARIATE procedure with the NORMAL option to numerically check the normality assumptions.

Comparing Group Means

If you want to compare values obtained from two different groups, and if the groups are independent of each other and the data are normally or lognormally distributed in each group, then a group t test can be used. Examples of such group comparisons include the following:

- test scores for two third-grade classes, where one of the classes receives tutoring
- fuel efficiency readings of two automobile nameplates, where each nameplate uses the same fuel
- sunburn scores for two sunblock lotions, each applied to a different group of people
- political attitude scores of males and females

In the following example, the golf scores for males and females in a physical education class are compared. The sample sizes from each population are equal, but this is not required for further analysis. The scores are thought to be approximately normally distributed within gender. The data are read by the following statements:

```
data scores;
  input Gender $ Score @@;
  datalines;
f 75 f 76 f 80 f 77 f 80 f 77 f 73
m 82 m 80 m 85 m 85 m 78 m 87 m 82
;
```

The dollar sign (\$) following Gender in the INPUT statement indicates that Gender is a character variable. The trailing at signs (@@) enable the procedure to read more than one observation per line.

You can use a group *t* test to determine whether the mean golf score for the men in the class differs significantly from the mean score for the women. If you also suspect that the distributions of the golf scores of males and females have unequal variances, then you might want to specify the **COCHRAN** option in order to use the Cochran approximation (in addition to the Satterthwaite approximation, which is included by default). The following statements invoke PROC TTEST for the case of unequal variances, along with both types of confidence limits for the pooled standard deviation.

```
ods graphics on;

proc ttest cochrn ci=equal umpu;
  class Gender;
  var Score;
run;

ods graphics off;
```

The **CLASS** statement contains the variable that distinguishes the groups being compared, and the **VAR** statement specifies the response variable to be used in calculations. The **COCHRAN** option produces *p*-values for the unequal variance situation by using the Cochran and Cox (1950) approximation. Equal-tailed and uniformly most powerful unbiased (UMPU) confidence intervals for σ are requested by the **CI=** option. Output from these statements is displayed in Figure 125.4 through Figure 125.7.

Figure 125.4 Simple Statistics

The TTEST Procedure

Variable: Score

Gender	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
f		7	76.8571	2.5448	0.9619	73.0000	80.0000
m		7	82.7143	3.1472	1.1895	78.0000	87.0000
Diff (1-2) Pooled			-5.8571	2.8619	1.5298		
Diff (1-2) Satterthwaite			-5.8571		1.5298		

Simple statistics for the two populations being compared, as well as for the difference of the means between the populations, are displayed in Figure 125.4. The Gender column indicates the population that corresponds to the statistics in that row, and the Method column indicates the method for estimating the standard deviation, either pooled (assuming equal variances for males and females) or Satterthwaite (assuming unequal

variances). The sample size (N), mean, standard deviation, standard error, and minimum and maximum values are displayed.

Confidence limits for means and standard deviations are shown in [Figure 125.5](#).

Figure 125.5 Confidence Limits

Gender	Method	Mean	95% CL Mean	Std Dev	95% CL Std Dev		95% UMPU CL Std Dev	
					CL	Std Dev	CL	Std Dev
f		76.8571	74.5036 79.2107	2.5448	1.6399	5.6039	1.5634	5.2219
m		82.7143	79.8036 85.6249	3.1472	2.0280	6.9303	1.9335	6.4579
Diff (1-2) Pooled		-5.8571	-9.1902 -2.5241	2.8619	2.0522	4.7242	2.0019	4.5727
Diff (1-2) Satterthwaite		-5.8571	-9.2064 -2.5078					

For the mean difference, both pooled and Satterthwaite 95% intervals are shown. Equal-tailed and UMPU confidence limits are shown for the standard deviation under the assumption of equal variances.

The test statistics, associated degrees of freedom, and p -values are displayed in [Figure 125.6](#).

Figure 125.6 t Tests

Method	Variances	DF	t Value	Pr > t
Pooled	Equal	12	-3.83	0.0024
Satterthwaite	Unequal	11.496	-3.83	0.0026
Cochran	Unequal	6	-3.83	0.0087

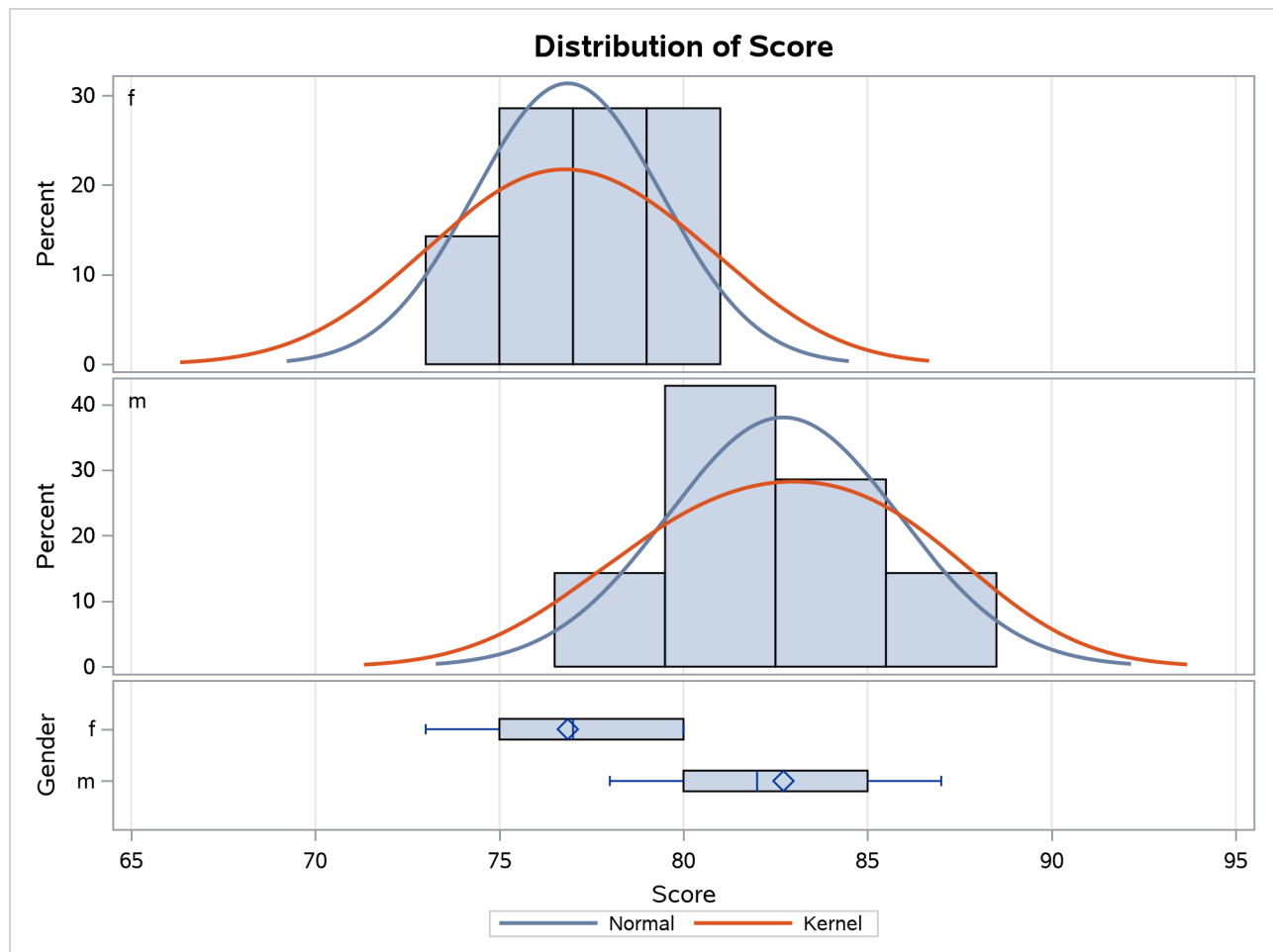
The Method column denotes which t test is being used for that row, and the Variances column indicates what assumption about variances is being made. The pooled test assumes that the two populations have equal variances and uses degrees of freedom $n_1 + n_2 - 2$, where n_1 and n_2 are the sample sizes for the two populations. The remaining two tests do not assume that the populations have equal variances. The Satterthwaite test uses the Satterthwaite approximation for degrees of freedom, while the Cochran test uses the Cochran and Cox approximation for the p -value. All three tests result in highly significant p -values, supporting the conclusion of a significant difference between males' and females' golf scores.

The “Equality of Variances” test in [Figure 125.7](#) reveals insufficient evidence of unequal variances (the Folded F statistic $F' = 1.53$, with $p = 0.6189$).

Figure 125.7 Tests of Equality of Variances

Equality of Variances				
Method	Num DF	Den DF	F Value	Pr > F
Folded F	6	6	1.53	0.6189

The summary panel in [Figure 125.8](#) shows comparative histograms, normal and kernel densities, and box plots, comparing the distribution of golf scores between genders.

Figure 125.8 Summary Panel

The Q-Q plots in Figure 125.9 assess the normality assumption for each gender.

Figure 125.9 Q-Q Plot



The plots for both males and females show no obvious deviations from normality. You can check the assumption of normality more rigorously by using PROC UNIVARIATE with the NORMAL option; if the assumption of normality is not reasonable, you should analyze the data with the nonparametric Wilcoxon rank sum test by using PROC NPAR1WAY.

Syntax: TTEST Procedure

The following statements are available in the TTEST procedure:

```
PROC TTEST < options > ;
  BOOTSTRAP < / options > ;
  CLASS variable ;
  PAIRED variables ;
  BY variables ;
  VAR variables < / options > ;
  FREQ variable ;
  WEIGHT variable ;
```

No statement can be used more than once. There is no restriction on the order of the statements after the PROC TTEST statement. The following sections describe the PROC TTEST statement and then describe the other statements in alphabetical order.

PROC TTEST Statement

PROC TTEST < options > ;

The **PROC TTEST** statement invokes the TTEST procedure. Table 125.2 summarizes the *options* available in the **PROC TTEST** statement. The *options* are then described fully in alphabetical order.

Table 125.2 PROC TTEST Statement Options

Option	Description
Basic Options	
DATA=	Specifies input data set
ORDER=	Determines sort order of CLASS variable or CROSSOVER= treatment variables
Analysis Options	
ALPHA=	Specifies 1 – confidence level
DIST=	Specifies distributional assumption (normal or lognormal)
H0=	Specifies null value
SIDES=	Specifies number of sides and direction
TEST=	Specifies test criterion (difference or ratio)
TOST	Requests equivalence test and specifies bounds
Displayed Output	
CI=	Requests confidence interval for standard deviation or coefficient of variation
COCHRAN	Requests Cochran <i>t</i> test
PLOTS	Produces ODS statistical graphics
Output Ordering	
BYVAR	Groups results by variables that are specified in the PAIRED or VAR statement
NOBYVAR	Groups results by tables

You can specify the following *options*:

ALPHA=*p*

specifies that confidence intervals (except test-based mean confidence intervals when you specify the **TOST** option) are to be $100(1 - p)\%$ confidence intervals, where $0 < p < 1$. When you specify the **TOST** option, the test-based mean confidence intervals are $100(1 - 2p)\%$ confidence intervals. For the **PLOTS=BOOTSTRAP(CORRELATION)** option, the **ALPHA=** option specifies that the elliptical prediction region is to be a $100(1 - p)\%$ prediction region. If *p* is 0 or less, or 1 or more, an error message is printed. By default, **ALPHA=0.05**.

BYVAR

groups the results by the variables that are specified in the **PAIRED** or **VAR** statement. The **BYVAR** option is enabled by default. Note that this represents a change from previous releases for how the results are grouped with respect to variables and tables. Prior to SAS 9.2, multiple variables were included in each table, similar to the new **NOBYVAR** option.

CI=EQUAL | UMPU | NONE**CL=EQUAL | UMPU | NONE**

specifies whether a confidence interval is displayed for σ and, if so, what kind. You can specify one or more of the following values:

EQUAL	specifies an equal-tailed confidence interval.
UMPU	specifies an interval based on the uniformly most powerful unbiased test of $H_0: \sigma = \sigma_0$.
NONE	requests that no confidence interval be displayed for σ .

The values **EQUAL** and **UMPU** together request that both types of confidence intervals be displayed. If the value **NONE** is specified with one or both of the values **EQUAL** and **UMPU**, **NONE** takes precedence. For more information, see the section “[Two-Independent-Sample Design](#)” on page 10498. By default, **CI=EQUAL**.

COCHRAN

requests the Cochran and Cox (1950) approximation of the probability level for the unequal variances situation. For more information, see the section “[Two-Independent-Sample Design](#)” on page 10498.

DATA=SAS-data-set

names the SAS data set for the procedure to use. By default, PROC TTEST uses the most recently created SAS data set. The input data set can contain summary statistics of the observations instead of the observations themselves. The number, mean, and standard deviation of the observations are required for each **BY** group (one sample and paired differences) or for each class within each **BY** group (two samples). For more information about the **DATA=** option, see the section “[Input Data Set of Statistics](#)” on page 10492.

DIST=LOGNORMAL | NORMAL

specifies the underlying distribution assumed for the data. You can specify the following values:

LOGNORMAL	specifies that the underlying distribution is lognormal.
NORMAL	specifies that the underlying distribution is normal.

By default, **DIST=NORMAL**, unless **TEST=RATIO** is specified, in which case the default is **DIST=LOGNORMAL**.

H0=m

requests tests against a null value of m , unless the **TOST** option is used, in which case m is merely used to derive the lower and upper equivalence bounds. For the crossover design, the value m applies for both treatment and period tests. By default, $H_0=0$ when **TEST=DIFF** (or **DIST=NORMAL** for a one-sample design) and $H_0=1$ when **TEST=RATIO** (or **DIST=LOGNORMAL** for a one-sample design).

NOBYVAR

includes all variables that are specified in the **PAIRED** or **VAR** statement together in each output table. If the **NOBYVAR** option is not specified, then the **BYVAR** option is enabled, grouping the results by the **PAIRED** and **VAR** variables.

ORDER=DATA | FORMATTED | FREQ | INTERNAL | MIXED

specifies the order in which to sort the levels of the classification variables (which are specified in the **CLASS** statement) and treatment variables (which are specified in the **CROSSOVER=** option in the **VAR** statement).

This option applies to the levels for all classification or treatment variables, except when you use the **ORDER=FORMATTED** option with numeric classification or treatment variables that have no explicit format. With this option, the levels of such variables are ordered by their internal value.

You can specify 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 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 greatest number of observations come first in the order. In the event of a tie, ORDER=MIXED is used.
INTERNAL MIXED	Unformatted value. The sort order is machine-dependent. Same as ORDER=FORMATTED if the unformatted variable is character-valued; same as ORDER=INTERNAL otherwise (the unformatted variable is numeric-valued).

For **FORMATTED** and **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*.

By default, **ORDER=MIXED**, which corresponds to the ordering in releases previous to SAS 9.2.

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

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

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

```
plots=none
plots=(histogram boxplot interval qq profiles agreement)
plots(unpack)=summary
plots(showh0)=interval(type=pergroup)
plots=(summary(unpack) interval(type=period))
```

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

```
ods graphics on;

proc ttest plots=all;
    var oxygen;
run;

ods graphics off;
```

For more information about enabling and disabling ODS Graphics, see the section “[Enabling and Disabling ODS Graphics](#)” on page 623 in Chapter 21, “[Statistical Graphics Using ODS](#).”

If ODS Graphics is enabled but you do not specify the **PLOTS** option, then PROC TTEST produces a default set of plots. (**NOTE:** The graphical results are unavailable if your input data set contains summary statistics rather than observation values.)

For a one-sample design, the default plots are the following:

- summary plot (histogram with overlaid normal and kernel densities, box plot, and confidence interval band) for the input data set
- Q-Q plot for the input data set
- summary plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- Q-Q plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- correlation plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement

For a two-independent-sample design, the default plots are the following:

- summary plot (comparative histograms with overlaid densities and box plots) for the input data set
- Q-Q plot for the input data set
- summary plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- Q-Q plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- correlation plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement

For a paired design, the default plots are the following:

- summary plot (histogram, densities, box plot, and confidence interval) of the difference or ratio for the input data set
- Q-Q plot of the difference or ratio for the input data set
- profiles plot for the input data set
- agreement plot for the input data set
- summary plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- Q-Q plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement
- correlation plot of bootstrap statistics, if you specify the **BOOTSTRAP** statement

For a crossover design, the default plots are the following:

- comparative histograms with overlaid densities by treatment and period for the input data set
- comparative box plots by treatment and period for the input data set
- Q-Q plots by treatment and period for the input data set
- profiles over treatment plot for the input data set
- agreement of treatments plot for the input data set

For more detailed descriptions of plots, see the section “[Interpreting Graphs](#)” on page 10522.

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

ONLY

suppresses the default plots. Only plots that you specifically request are displayed.

SHOWH0

SHOWNULL

shows the null value (as specified by the **H0=** option in the **PROC TTEST** statement) in all relevant plots. For one-sample and paired designs, the null value can appear when you also specify the **SUMMARY**, **BOOTSTRAP(SUMMARY)**, **BOOTSTRAP(BOX)**, **BOOTSTRAP(INTERVAL)**, **BOX**, or **INTERVAL plot-request**. For two-independent-sample designs and crossover designs, the null value can appear when you specify the **BOOTSTRAP(INTERVAL)** or **INTERVAL plot-request**. For crossover designs, the null value can appear only when you specify the **INTERVAL plot-request**.

UNPACKPANEL

UNPACK

suppresses paneling. By default, multiple plots can appear in some output panels. Specify this option to get each plot in a separate panel. You can specify **PLOTS(UNPACKPANEL)** to unpack the default plots.

You can specify the following *plot-requests*:

ALL

produces all appropriate plots. You can specify other *plot-requests* with **ALL**; for example, to request all plots and specify that intervals should be for the period difference in a crossover design, specify **PLOTS=(ALL INTERVAL(TYPE=PERIOD))**.

AGREEMENT < TYPE=type >

AGREEMENTPLOT < TYPE=type >

produces an agreement plot for the input data set. This plot is produced by default for paired and crossover designs, the only designs for which this option is valid.

For paired designs, the second response in each pair is plotted against the first response. For more information, see the section “[Agreement Plots for Paired Designs](#)” on page 10522.

For crossover designs, you can specify the following options:

TYPE=PERIOD

plots the response in the second period against the response in the first period. For more information, see the section “[Period Agreement Plots for Crossover Designs](#)” on page 10522.

TYPE=TREATMENT

plots the response associated with the second treatment against the response associated with the first treatment. For more information, see the section “[Treatment Agreement Plots for Crossover Designs](#)” on page 10523.

By default, TYPE=TREATMENT for crossover designs.

BOOTSTRAP <(bootstrap-plot-requests)>**BOOT** <(bootstrap-plot-requests)>

controls the bootstrap-related plots that are produced through ODS Graphics.

You can specify the following *bootstrap-plot-requests*:

BOX**BOXPLOT**

produces box plots of bootstrap mean and standard deviation.

A bootstrap confidence interval is shown as a band in the background if the specified value of the **BOOTCI=** option in the **BOOTSTRAP** statement is capable of producing confidence intervals for the bootstrap statistic.

For more information, see the section “[Box Plots](#)” on page 10523.

CORRELATION**CORR**

produces a scatter plot of bootstrap standard deviation versus mean statistics with an overlaid elliptical prediction region.

This correlation plot is produced by default for one-sample, two-sample, and paired designs if you specify the **BOOTSTRAP** statement.

For more information, see the section “[Bootstrap Correlation Plots](#)” on page 10524.

HISTOGRAM**HIST****HISTDENS**

produces histograms along with overlaid normal and kernel densities for bootstrap mean and standard deviation.

For more information, see the section “[Histograms](#)” on page 10523.

INTERVAL**INTERVALPLOT**

produces plots of bootstrap confidence intervals for the mean and standard deviation.

For more information, see the section “[Confidence Intervals](#)” on page 10523.

QQ**QQPLOT**

produces normal quantile-quantile (Q-Q) plots of the bootstrap mean and standard deviation. These plots are produced by default for one-sample, two-sample, and paired designs if you specify the **BOOTSTRAP** statement.

For more information, see the section “[Q-Q Plots](#)” on page 10524.

SUMMARY < UNPACK >**SUMMARYPLOT < UNPACK >**

produces bootstrap histogram and box plots together in a single panel, where the plots share common X axes. These plots are produced by default for one-sample, paired, and two-independent-sample designs if you specify the **BOOTSTRAP** statement. For more information, see the documentation for **BOX** and **HISTOGRAM** *bootstrap-plot-requests*. You can specify the following option:

UNPACK

plots bootstrap histograms along with overlaid densities in one panel and bootstrap box plots (along with confidence interval bands, if applicable) in another panel. Note that specifying **PLOTS(ONLY)=BOOTSTRAP(SUMMARY(UNPACK))** is exactly the same as specifying **PLOTS(ONLY)=BOOTSTRAP(BOX HISTOGRAM)**.

By default, if you specify the **BOOTSTRAP** statement, then the **SUMMARY**, **QQ**, and **CORRELATION** *bootstrap-plot-requests* are included unless you exclude them by specifying the **ONLY** *global-plot-option*.

The **BOOTSTRAP** *plot-request* is ignored if you omit the **BOOTSTRAP** statement.

BOX**BOXPLOT**

produces a box plot or comparative box plots for the input data set. A box plot is produced by default for crossover designs. For other designs, a box plot appears by default if you specify the **SUMMARY** or **ALL** *plot-request*.

For one-sample and paired designs, a confidence interval for the mean is shown as a band in the background, along with the equivalence bounds if the **TOST** option is used in the **PROC TTEST** statement.

For a two-independent-sample design, comparative box plots (one for each class) are shown. For a crossover design, comparative box plots for all four combinations of the two treatments and two periods are shown.

For more information, see the section “**Box Plots**” on page 10523.

HISTOGRAM**HIST****HISTDENS**

produces a histogram or comparative histograms along with overlaid normal and kernel densities for the input data set. A histogram is produced by default for crossover designs. For other designs, it appears by default if you specify the **SUMMARY** or **ALL** *plot-request*.

For one-sample and paired designs, the histogram and densities are based on the test criterion (which is the mean difference or ratio for a paired design). For a two-independent-sample design, comparative histograms (one for each class) are shown. For a crossover design, histograms for all four combinations of the two treatments and two periods are shown.

For more information, see the section “**Histograms**” on page 10523.

INTERVAL < TYPE=*type* >**INTERVALPLOT** < TYPE=*type* >

produces plots of confidence interval for means of the input data set.

For a two-independent-sample design, you can specify one of the following options:

TYPE=PERGROUP

shows two separate two-sided confidence intervals, one for each class. You cannot use this option along with the [SHOWHO](#) *global-plot-option*.

TYPE=TEST

shows pooled and Satterthwaite confidence intervals.

By default, TYPE=TEST for two-independent-sample designs.

For a crossover design, you can specify the following options:

TYPE=PERGROUP

shows four separate two-sided intervals, one for each treatment-by-period combination. You cannot use this option along with the [SHOWHO](#) *global-plot-option*.

TYPE=PERIOD

shows pooled and Satterthwaite confidence intervals for the period difference or ratio. This option is invalid if you specify the [IGNOREPERIOD](#) option in the [VAR](#) statement.

TYPE=TREATMENT

shows pooled and Satterthwaite confidence intervals for the treatment difference or ratio.

By default, TYPE=TREATMENT for crossover designs.

For more information, see the section “[Confidence Intervals](#)” on page 10523.

NONE

suppresses all plots.

PROFILES < TYPE=*type* >**PROFILESPLOT** < TYPE=*type* >

produces a profiles plot for the input data set. This plot is produced by default for paired and crossover designs, the only designs for which this option is valid.

For paired designs, a line is drawn for each observation from left to right connecting the first response to the second response. For more information, see the section “[Profiles for Paired Designs](#)” on page 10524.

For crossover designs, you can specify one of the following options:

TYPE=PERIOD

shows response profiles over period, connecting the first period on the left to the second period on the right for each subject. For more information, see the section “[Profiles over Period for Crossover Designs](#)” on page 10524.

TYPE=TREATMENT

shows response profiles over treatment values, connecting the first treatment on the left to the second treatment on the right for each observation. For more information, see the section “[Profiles over Treatment for Crossover Designs](#)” on page 10524.

By default, TYPE=TREATMENT for crossover designs.

QQ**QQPLOT**

produces a normal quantile-quantile (Q-Q) plot for the input data set. This plot is produced by default for all designs.

For two-sample designs, separate plots are shown for each class in a single panel. For crossover design, separate plots are shown for each treatment-by-period combination in a single panel.

For more information, see the section “[Q-Q Plots](#)” on page 10524.

SUMMARY < UNPACK >**SUMMARYPLOT < UNPACK >**

produces histogram and box plots for the input data set together in a single panel, where the plots share common X axes. These plots are produced by default for one-sample, paired, and two-independent-sample designs, the only designs for which this option is valid. For more information, see the documentation for the [BOX](#) and [HISTOGRAM plot-requests](#). You can specify the following option:

UNPACK

plots histograms along with overlaid densities in one panel and box plots (along with confidence interval bands, for one-sample and paired designs) in another panel. Note that specifying [PLOTS\(ONLY\)=SUMMARY\(UNPACK\)](#) is exactly the same as specifying [PLOTS\(ONLY\)=\(BOX HISTOGRAM\)](#).

SIDES=2 | L | U

SIDED=2 | L | U

SIDE=2 | L | U

specifies the number of sides (or tails) and direction of the statistical tests and test-based confidence intervals. The values are interpreted as follows:

- | | |
|----------|--|
| 2 | specifies two-sided tests and confidence intervals. |
| L | specifies lower one-sided tests (in which the alternative hypothesis indicates a parameter value less than the null value) and lower one-sided confidence intervals between minus infinity and the upper confidence limit. |
| U | specifies upper one-sided tests (in which the alternative hypothesis indicates a parameter value greater than the null value) and upper one-sided confidence intervals between the lower confidence limit and infinity. |

By default, SIDES=2.

TEST=DIFF | RATIO

specifies the test criterion. This option is ignored for one-sample designs. You can specify the following values:

DIFF tests the difference of means.

RATIO tests the ratio of means.

By default, TEST=DIFF, unless you specify **DIST=LOGNORMAL**, in which case the default is TEST=RATIO.

TOST (< lower , > upper)

performs Schuirmann's TOST equivalence test. The *upper* equivalence bound must be specified. If **TEST=DIFF**, then the default value for the *lower* equivalence bound is $2m - upper$, where m is the value of the **H0=** option. If **TEST=RATIO**, then the default value for *lower* is $m / upper$.

BOOTSTRAP Statement

BOOTSTRAP < / options > ;

The BOOTSTRAP statement requests bootstrap standard error, bias estimates, and confidence intervals.

These bootstrap statistics are currently available only for one-sample, paired, and two-sample designs and only for analyses that assume normal data—although the bootstrap methods themselves do not necessarily assume normality.

Bootstrap results are unavailable if you specify the **TEST=RATIO**, **DIST=LOGNORMAL**, or **TOST** option in the **PROC TTEST** statement; if you specify the **CROSSOVER=** option in the **VAR** statement; or if you specify the **WEIGHT** statement. They are also unavailable if your input data set contains summary statistics rather than raw observed values.

The sample statistics for which bootstrap standard error, bias estimates, and confidence intervals are provided are as follows:

- For a one-sample design: mean and standard deviation of the observations
- For a paired design: mean and standard deviation of the paired difference—that is, the difference between the first and second members of an observation pair
- For a two-sample design: mean, pooled standard deviation, and unpooled standard deviation of the class difference—that is, the difference between an observation from the first class and an observation from the second class

For more information about how these statistics are computed, see the section “Statistics That Are Resampled” on page 10509.

You can specify the **BOOTSTRAP plot-request** option in the **PROC TTEST** statement to request plots that are based on bootstrap samples.

Summary of Options

Table 125.4 summarizes the *options* available in the BOOTSTRAP statement.

Table 125.4 Summary of Options in BOOTSTRAP Statement

Option	Description
BOOTCI=	Produces bootstrap confidence intervals for the mean and variability parameter estimates
BOOTDATA=	Specifies the bootstrap output data set
NSAMPLES=	Specifies the number of bootstrap sample data sets (replicates)
SEED=	Provides the seed that initializes the random number stream

Dictionary of Options

BOOTCI < = < BC | BOOTT | EXPANDEDPERC | NORMAL | PERCENTILE | TBOOTSE >>

produces bootstrap-based confidence intervals. You can request the following types of bootstrap confidence interval:

BC	produces bias-corrected percentile intervals.
BOOTT	produces bootstrap <i>t</i> intervals, which use a traditional standard error estimate and quantiles of the bootstrap distribution of the <i>t</i> statistic.
EXPANDEDPERC	produces percentile-based confidence intervals that include a narrowness bias adjustment.
NORMAL	produces normal-based confidence intervals that use the bootstrap standard error estimate.
PERCENTILE	produces percentile-based confidence intervals.
TBOOTSE	produces <i>t</i> -based confidence intervals that use the bootstrap standard error estimate.

The default option is BOOTCI=BC.

Table 125.5 shows which analysis parameters are supported for each type of bootstrap confidence interval. A bullet enclosed in parentheses indicates that the confidence limits are the same as for the other method for the same parameter.

Table 125.5 Parameters That Are Supported for Each Type of Bootstrap Confidence Interval in the BOOTSTRAP Statement

Design	Parameter	Method	BOOTCI Type					
			BC	BOOTT	EXPERC	NORMAL	PERC	TBOOTSE
One-sample	Mean		•	•	•	•	•	•
	Std Dev		•				•	
Paired	Mean (1–2)		•	•	•	•	•	•
	Std Dev (1–2)		•				•	
Two-sample	Mean (1–2)	Pooled	•	•	•	•	•	•

Table 125.5 *continued*

Design	Parameter	Method	BOOTCI Type					
			BC	BOOTT	EXPERC	NORMAL	PERC	TBOOTSE
	Mean (1–2)	Satterthwaite	(•)	•	•	(•)	(•)	•
	Std Dev (1–2)	Pooled	•				•	
	Std Dev (1–2)	Satterthwaite	•				•	

All six types include confidence intervals for the mean parameter estimate on which the usual hypothesis test is based, for example, the mean for a one-sample design or the mean difference for a paired or two-sample design. For BOOTCI=BC and BOOTCI=PERCENTILE, confidence intervals based on the variability parameter estimate are also produced; these are based on the variability parameter estimate that is used to compute the standard error of the usual hypothesis test for the mean parameter, for example, the standard deviation for a one-sample design or the standard deviation of the difference for a paired or two-sample design.

The **ALPHA=** and **SIDES=** options in the **PROC TTEST** statement set the direction and level of significance that is used in constructing the bootstrap confidence intervals.

For more information about the bootstrap confidence intervals supported by PROC TTEST, see the section “[Bootstrap Confidence Intervals](#)” on page 10511.

BOOTDATA=SAS-data-set

specifies the SAS data set that contains the bootstrap sample data when you use a **BOOTSTRAP** statement. This data set has the number of observations that you specify in the **NSAMPLES=** option and contains the mean and standard deviation estimates that are calculated for each bootstrap sample.

NSAMPLES=*n*

specifies the number of bootstrap sample data sets (replicates). The value must be greater than 1. By default, NSAMPLES=10000.

SEED=*n*

provides the seed that initializes the random number stream for generating the bootstrap sample data sets (replicates). If you do not specify the **SEED=** value, or if you specify a value less than or equal to 0, the seed is generated from reading the time of day from the computer's clock.

BY Statement

BY variables ;

You can specify a BY statement in PROC TTEST 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 TTEST 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* ;

A **CLASS** statement giving the name of the classification (or grouping) variable must accompany the **PROC TTEST** statement in the two-independent-sample case. It should be omitted for the one-sample, paired, and AB/BA crossover designs. If it is used without the **VAR** statement, all numeric variables in the input data set (except those that appear in the **CLASS**, **BY**, **FREQ**, or **WEIGHT** statement) are included in the analysis.

The classification variable must have two, and only two, levels. PROC TTEST divides the observations into the two groups for the *t* test by using the levels of this variable. You can use either a numeric or a character variable in the **CLASS** statement.

Classification levels are determined from the formatted values of the **CLASS** variable. Thus, you can use formats to define group levels. For more information, see the discussions of the **FORMAT** procedure, the **FORMAT** statement, formats, and informats in *SAS Formats and Informats: Reference*.

FREQ Statement

FREQ *variable* ;

The *variable* in the **FREQ** statement identifies a variable that contains the frequency of occurrence of each observation. PROC TTEST treats each observation as if it appears *n* times, where *n* is the value of the **FREQ** variable for the observation. If the value is not an integer, only the integer portion is used. If the frequency value is less than 1 or is missing, the observation is not used in the analysis. When the **FREQ** statement is not specified, each observation is assigned a frequency of 1. The **FREQ** statement cannot be used if the **DATA=** data set contains statistics instead of the original observations.

PAIRED Statement

PAIRED *pair-lists* ;

The *pair-lists* in the **PAIRED** statement identifies the variables to be compared in paired comparisons. You can use one or more *pair-lists*. Variables or lists of variables are separated by an asterisk (*) or a colon (:). The asterisk requests that each variable on the left be compared with each variable on the right. The colon requests that the first variable on the left be compared with the first on the right, the second on the left with

the second on the right, and so on. The number of variables on the left must equal the number on the right when the colon is used. The differences are calculated by taking the variable on the left minus the variable on the right for both the asterisk and colon. A pair that is formed by a variable with itself is ignored. Use the **PAIRED** statement only for paired comparisons. The **CLASS** and **VAR** statements cannot be used with the **PAIRED** statement.

Examples of the use of the asterisk and the colon are shown in Table 125.6.

Table 125.6 PAIRED Statement in the TTEST Procedure

These PAIRED Statements	Yield These Comparisons
PAIRED A*B;	A-B
PAIRED A*B C*D;	A-B and C-D
PAIRED (A B) * (C D) ;	A-C, A-D, B-C, and B-D
PAIRED (A B) * (C B) ;	A-C, A-B, and B-C
PAIRED (A1-A2) * (B1-B2) ;	A1-B1, A1-B2, A2-B1, and A2-B2
PAIRED (A1-A2) : (B1-B2) ;	A1-B1 and A2-B2

VAR Statement

VAR *variables* *</ options>* ;

The **VAR** statement names the variables to be used in the analyses. One-sample comparisons are conducted when the **VAR** statement is used without the **CROSSOVER=** option or **CLASS** statement. Two-independent-sample comparisons are conducted when the **VAR** statement is used with a **CLASS** statement.

An AB/BA crossover analysis is conducted when the **CROSSOVER=** option is used in the **VAR** statement. In this case, you must specify an even number of variables. Each set of two variables represents the responses in the first and second periods of the AB/BA crossover design. For example, if you use the **CROSSOVER=** option and specify **VAR x1 x2 x3 x4**, then you will get two analyses. One analysis will have x1 as the period 1 response and x2 as the period 2 response. The other analysis will have x3 as the period 1 response and x4 as the period 2 response.

The **VAR** statement cannot be used with the **PAIRED** statement. If the **VAR** statement is omitted, all numeric variables in the input data set (except a numeric variable that appears in the **BY**, **CLASS**, **FREQ**, or **WEIGHT** statement) are included in the analysis.

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

CROSSOVER= (*variable1 variable2*)

specifies the variables that represent the treatment applied in each of the two periods in an AB/BA crossover design. The treatment variables must have two, and only two, levels. For any particular observation, the levels for the two variables must be different, due to the restrictions of the AB/BA crossover design. You can use either numeric or character variables.

Treatment levels are determined from the formatted values of the variables. Thus, you can use formats to define the treatment levels. For more information, see the discussions of the **FORMAT** procedure, the **FORMAT** statement, formats, and informats in *SAS Formats and Informats: Reference*.

IGNOREPERIOD

ignores the period effect—that is, the period effect is assumed to be equal to 0 (if **TEST=DIFF**) or 1 (if **TEST=RATIO**). This assumption increases the degrees of freedom for the test of the treatment difference by 1 and is usually more powerful, but it risks incorrect results if there is actually a period effect.

WEIGHT Statement

WEIGHT *variable* ;

The **WEIGHT** statement weights each observation in the input data set by the value of the *variable*. The values of the *variable* can be nonintegral, and they are not truncated. Observations that have negative, zero, or missing values for the *variable* are not used in the analyses. Each observation is assigned a weight of 1 when the **WEIGHT** statement is not used. The **WEIGHT** statement cannot be used with an input data set of summary statistics.

Details: TTEST Procedure

Input Data Set of Statistics

PROC TTEST accepts data containing either observation values or summary statistics. Observation values are supported for all analyses, whereas summary statistics are supported only for a subset of analyses. If the analysis involves the paired design, the AB/BA crossover design, or the lognormal distributional assumption (**DIST=LOGNORMAL**), then observation values must be used. The graphical results are unavailable if your input data set contains summary statistics rather than raw observed values.

PROC TTEST assumes that the **DATA=** data set contains statistics if it contains a character variable with name **_TYPE_** or **_STAT_**. The TTEST procedure expects this character variable to contain the names of statistics. If both **_TYPE_** and **_STAT_** variables exist and are of type character, PROC TTEST expects **_TYPE_** to contain the names of statistics including 'N', 'MEAN', and 'STD' for each **BY** group (or for each class within each **BY** group for two-sample *t* tests). If no 'N', 'MEAN', or 'STD' statistics exist, an error message is printed.

FREQ, **WEIGHT**, and **PAIRED** statements cannot be used with input data sets of statistics. **BY**, **CLASS**, and **VAR** statements are the same regardless of data set type. For paired comparisons, see the **_DIF_** values for the **_TYPE_=T** observations in output produced by the **OUTSTATS=** option in the PROC COMPARE statement (see the *Base SAS Procedures Guide*).

Missing Values

An observation is omitted from the calculations if it has a missing value for either the **CLASS** variable, a **CROSSOVER=** variable, a **PAIRED** variable, the variable to be tested (in a one-sample or two-independent-sample design), or either of the two response variables (in a crossover design). If more than one variable or pair of variables is listed in the **VAR** statement, a missing value in one variable or pair does not eliminate the observation from the analysis of other nonmissing variables or variable pairs.

Computational Methods

This section describes the computational formulas for the estimates, confidence limits, and tests for each analysis in the TTEST procedure. The first subsection defines some common notation. The second subsection discusses the distinction between arithmetic and geometric means. The third subsection explains the concept of the coefficient of variation. The next four subsections address the four supported designs (one-sample, paired, two-independent-sample, and AB/BA crossover). The content in each of those subsections is divided into separate discussions according to different values of the **DIST=** and **TEST=** options in the **PROC TTEST** statement. The next-to-last subsection describes TOST equivalence analyses. The last subsection discusses bootstrap methods.

Common Notation

Table 125.7 displays notation for some of the commonly used symbols.

Table 125.7 Common Notation

Symbol	Description
μ	Population value of (arithmetic) mean
μ_0	Null value of test (value of H0= option in PROC TTEST statement)
σ^2	Population variance
σ	Population value of standard deviation
γ	Population value of geometric mean
CV	Population value of coefficient of variation (ratio of population standard deviation and population arithmetic mean)
α	Value of ALPHA= option in PROC TTEST statement
$t_{p,v}$	p th percentile of t distribution with v degrees of freedom (df)
F_{p,v_1,v_2}	p th percentile of F distribution with v_1 numerator df and v_2 denominator df
$\chi^2_{p,v}$	p th percentile of chi-square distribution with v df

Arithmetic and Geometric Means

The *arithmetic mean* (more commonly called simply the *mean*) of the distribution of a random variable X is its expected value, $E(X)$. The arithmetic mean is the natural parameter of interest for a normal distribution because the distribution of the difference of normal random variables has a known normal distribution, and the arithmetic mean of a normal difference is equal to the difference of the individual arithmetic means. (No such convenient property holds for geometric means with normal data, with either differences or ratios.)

The usual estimate of an arithmetic mean is the sum of the values divided by the number of values:

$$\text{arithmetic mean} = \frac{1}{n} \sum_{i=1}^n y_i$$

The *geometric mean* of the distribution of a random variable X is $\exp(E(\log(X)))$, the exponentiation of the mean of the natural logarithm. The geometric mean is the natural parameter of interest for a lognormal distribution because the distribution of a ratio of lognormal random variables has a known lognormal distribution, and the geometric mean of a lognormal ratio is equal to the ratio of the individual geometric means. (No such convenient property holds for arithmetic means with lognormal data, with either differences or ratios.)

The usual estimate of a geometric mean is the product of the values raised to the power $1/n$, where n is the number of values:

$$\text{geometric mean} = \left(\prod_{i=1}^n y_i \right)^{\frac{1}{n}}$$

Coefficient of Variation

The *coefficient of variation* (abbreviated “CV”) of the distribution of a random variable X is the ratio of the standard deviation to the (arithmetic) mean, or $\sqrt{\text{Var}(X)}/E(X)$. Conceptually, it is a measure of the variability of X expressed in units corresponding to the mean of X .

For lognormal data, the CV is the natural measure of variability (rather than the standard deviation) because the CV is invariant to multiplication of a lognormal variable by a constant. For a two-independent-sample design, the assumption of equal CVs on a lognormal scale is analogous to the assumption of equal variances on the normal scale. When the CVs of two independent samples of lognormal data are assumed equal, the pooled estimate of variability is used.

One-Sample Design

Define the following notation:

n^* = number of observations in data set

y_i = value of i th observation, $i \in \{1, \dots, n^*\}$

f_i = frequency of i th observation, $i \in \{1, \dots, n^*\}$

w_i = weight of i th observation, $i \in \{1, \dots, n^*\}$

$$n = \text{sample size} = \sum_i^{n^*} f_i$$

Normal Data (DIST=NORMAL)

The mean estimate \bar{y} , standard deviation estimate s , and standard error SE are computed as follows:

$$\bar{y} = \frac{\sum_i^{n^*} f_i w_i y_i}{\sum_i^{n^*} f_i w_i}$$

$$s = \left(\frac{\sum_i^{n^*} f_i w_i (y_i - \bar{y})^2}{n - 1} \right)^{\frac{1}{2}}$$

$$SE = \frac{s}{\left(\sum_i^{n^*} f_i w_i \right)^{\frac{1}{2}}}$$

The $100(1 - \alpha)\%$ confidence interval for the mean μ is

$$\left(\bar{y} - t_{1-\frac{\alpha}{2}, n-1} SE, \bar{y} + t_{1-\frac{\alpha}{2}, n-1} SE \right), \text{ SIDES}=2$$

$$\left(-\infty, \bar{y} + t_{1-\alpha, n-1} SE \right), \text{ SIDES}=L$$

$$\left(\bar{y} - t_{1-\alpha, n-1} SE, \infty \right), \text{ SIDES}=U$$

The t value for the test is computed as

$$t = \frac{\bar{y} - \mu_0}{SE}$$

The p -value of the test is computed as

$$p\text{-value} = \begin{cases} P(t^2 > F_{1-\alpha, 1, n-1}) & , \text{ two-sided} \\ P(t < t_{\alpha, n-1}) & , \text{ lower one-sided} \\ P(t > t_{1-\alpha, n-1}) & , \text{ upper one-sided} \end{cases}$$

The equal-tailed confidence interval for the standard deviation (**CI=EQUAL**) is based on the acceptance region of the test of $H_0: \sigma = \sigma_0$ that places an equal amount of area ($\frac{\alpha}{2}$) in each tail of the chi-square distribution:

$$\left\{ \chi_{\frac{\alpha}{2}, n-1}^2 \leq \frac{(n-1)s^2}{\sigma_0^2} \leq \chi_{\frac{1-\alpha}{2}, n-1}^2 \right\}$$

The acceptance region can be algebraically manipulated to give the following $100(1 - \alpha)\%$ confidence interval for σ^2 :

$$\left(\frac{(n-1)s^2}{\chi_{1-\frac{\alpha}{2}, n-1}^2}, \frac{(n-1)s^2}{\chi_{\frac{\alpha}{2}, n-1}^2} \right)$$

Taking the square root of each side yields the $100(1 - \alpha)\%$ **CI=EQUAL** confidence interval for σ :

$$\left(\left(\frac{(n-1)s^2}{\chi_{1-\frac{\alpha}{2}, n-1}^2} \right)^{\frac{1}{2}}, \left(\frac{(n-1)s^2}{\chi_{\frac{\alpha}{2}, n-1}^2} \right)^{\frac{1}{2}} \right)$$

The other confidence interval for the standard deviation (**CI=UMPU**) is derived from the uniformly most powerful unbiased test of $H_0: \sigma = \sigma_0$ (Lehmann 1986). This test has acceptance region

$$\left\{ c_1 \leq \frac{(n-1)s^2}{\sigma_0^2} \leq c_2 \right\}$$

where the critical values c_1 and c_2 satisfy

$$\int_{c_1}^{c_2} f_{n-1}(y) dy = 1 - \alpha$$

and

$$\int_{c_1}^{c_2} y f_{n-1}(y) dy = (n-1)(1 - \alpha)$$

where $f_v(y)$ is the PDF of the chi-square distribution with v degrees of freedom. This acceptance region can be algebraically manipulated to arrive at

$$P \left\{ \frac{(n-1)s^2}{c_2} \leq \sigma^2 \leq \frac{(n-1)s^2}{c_1} \right\} = 1 - \alpha$$

where c_1 and c_2 solve the preceding two integrals. To find the area in each tail of the chi-square distribution to which these two critical values correspond, solve $c_1 = \chi_{1-\alpha_2, n-1}^2$ and $c_2 = \chi_{\alpha_1, n-1}^2$ for α_1 and α_2 ; the resulting α_1 and α_2 sum to α . Hence, a $100(1 - \alpha)\%$ confidence interval for σ^2 is given by

$$\left(\frac{(n-1)s^2}{\chi_{1-\alpha_2, n-1}^2}, \frac{(n-1)s^2}{\chi_{\alpha_1, n-1}^2} \right)$$

Taking the square root of each side yields the $100(1 - \alpha)\%$ **CI=UMPU** confidence interval for σ :

$$\left(\left(\frac{(n-1)s^2}{\chi_{1-\alpha_2, n-1}^2} \right)^{\frac{1}{2}}, \left(\frac{(n-1)s^2}{\chi_{\alpha_1, n-1}^2} \right)^{\frac{1}{2}} \right)$$

Lognormal Data (DIST=LOGNORMAL)

The **DIST=LOGNORMAL** analysis is handled by log-transforming the data and null value, performing a **DIST=NORMAL** analysis, and then transforming the results back to the original scale. This simple technique is based on the properties of the lognormal distribution as discussed in Johnson, Kotz, and Balakrishnan (1994, Chapter 14).

Taking the natural logarithms of the observation values and the null value, define

$$z_i = \log(y_i) \quad , \quad i \in \{1, \dots, n^*\}$$

$$\gamma_0 = \log(\mu_0)$$

First, a **DIST=NORMAL** analysis is performed on $\{z_i\}$ with the null value γ_0 , producing the mean estimate \bar{z} , the standard deviation estimate s_z , a t value, and a p -value. The geometric mean estimate $\hat{\gamma}$ and the CV estimate \widehat{CV} of the original lognormal data are computed as follows:

$$\hat{\gamma} = \exp(\bar{z})$$

$$\widehat{CV} = (\exp(s_z^2) - 1)^{\frac{1}{2}}$$

The t value and p -value remain the same. The confidence limits for the geometric mean and CV on the original lognormal scale are computed from the confidence limits for the arithmetic mean and standard deviation in the **DIST=NORMAL** analysis on the log-transformed data, in the same way that $\hat{\gamma}$ is derived from \bar{z} and \widehat{CV} is derived from s_z .

Paired Design

Define the following notation:

n^* = number of observations in data set

y_{1i} = value of i th observation for first PAIRED variable, $i \in \{1, \dots, n^*\}$

y_{2i} = value of i th observation for second PAIRED variable, $i \in \{1, \dots, n^*\}$

f_i = frequency of i th observation, $i \in \{1, \dots, n^*\}$

w_i = weight of i th observation, $i \in \{1, \dots, n^*\}$

$$n = \text{sample size} = \sum_i^{n^*} f_i$$

Normal Difference (DIST=NORMAL TEST=DIFF)

The analysis is the same as the analysis for the one-sample design in the section “Normal Data (DIST=NORMAL)” on page 10495 based on the differences

$$d_i = y_{1i} - y_{2i} \quad , \quad i \in \{1, \dots, n^*\}$$

Lognormal Ratio (DIST=LOGNORMAL TEST=RATIO)

The analysis is the same as the analysis for the one-sample design in the section “Lognormal Data (DIST=LOGNORMAL)” on page 10496 based on the ratios

$$r_i = y_{1i}/y_{2i} \quad , \quad i \in \{1, \dots, n^*\}$$

Normal Ratio (DIST=NORMAL TEST=RATIO)

The hypothesis $H_0: \mu_1/\mu_2 = \mu_0$, where μ_1 and μ_2 are the means of the first and second PAIRED variables, respectively, can be rewritten as $H_0: \mu_1 - \mu_0\mu_2 = 0$. The t value and p -value are computed in the same way as in the one-sample design in the section “Normal Data (DIST=NORMAL)” on page 10495 based on the transformed values

$$z_i = y_{1i} - \mu_0 y_{2i} \quad , \quad i \in \{1, \dots, n^*\}$$

Estimates and confidence limits are not computed for this situation.

Two-Independent-Sample Design

Define the following notation:

$$\begin{aligned}
 n_1^* &= \text{number of observations at first class level} \\
 n_2^* &= \text{number of observations at second class level} \\
 y_{1i} &= \text{value of } i\text{th observation at first class level, } i \in \{1, \dots, n_1^*\} \\
 y_{2i} &= \text{value of } i\text{th observation at second class level, } i \in \{1, \dots, n_2^*\} \\
 f_{1i} &= \text{frequency of } i\text{th observation at first class level, } i \in \{1, \dots, n_1^*\} \\
 f_{2i} &= \text{frequency of } i\text{th observation at second class level, } i \in \{1, \dots, n_2^*\} \\
 w_{1i} &= \text{weight of } i\text{th observation at first class level, } i \in \{1, \dots, n_1^*\} \\
 w_{2i} &= \text{weight of } i\text{th observation at second class level, } i \in \{1, \dots, n_2^*\} \\
 n_1 &= \text{sample size for first class level} = \sum_i^{n_1^*} f_{1i} \\
 n_2 &= \text{sample size for second class level} = \sum_i^{n_2^*} f_{2i}
 \end{aligned}$$

Normal Difference (DIST=NORMAL TEST=DIFF)

Observations at the first class level are assumed to be distributed as $N(\mu_1, \sigma_1^2)$, and observations at the second class level are assumed to be distributed as $N(\mu_2, \sigma_2^2)$, where μ_1 , μ_2 , σ_1 , and σ_2 are unknown.

The within-class-level mean estimates (\bar{y}_1 and \bar{y}_2), standard deviation estimates (s_1 and s_2), standard errors (SE_1 and SE_2), and confidence limits for means and standard deviations are computed in the same way as for the one-sample design in the section “Normal Data (DIST=NORMAL)” on page 10495.

The mean difference $\mu_1 - \mu_2 = \mu_d$ is estimated by

$$\bar{y}_d = \bar{y}_1 - \bar{y}_2$$

Under the assumption of equal variances ($\sigma_1^2 = \sigma_2^2$), the pooled estimate of the common standard deviation is

$$s_p = \left(\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2} \right)^{\frac{1}{2}}$$

The pooled standard error (the estimated standard deviation of \bar{y}_d assuming equal variances) is

$$SE_p = s_p \left(\frac{1}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{1}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^{\frac{1}{2}}$$

The pooled $100(1 - \alpha)\%$ confidence interval for the mean difference μ_d is

$$\begin{aligned}
 &(\bar{y}_d - t_{1-\frac{\alpha}{2}, n_1+n_2-2} SE_p, \bar{y}_d + t_{1-\frac{\alpha}{2}, n_1+n_2-2} SE_p), \text{ SIDES=2} \\
 &(-\infty, \bar{y}_d + t_{1-\alpha, n_1+n_2-2} SE_p), \text{ SIDES=L} \\
 &(\bar{y}_d - t_{1-\alpha, n_1+n_2-2} SE_p, \infty), \text{ SIDES=U}
 \end{aligned}$$

The t value for the pooled test is computed as

$$t_p = \frac{\bar{y}_d - \mu_0}{SE_p}$$

The p -value of the test is computed as

$$p\text{-value} = \begin{cases} P(t_p^2 > F_{1-\alpha, 1, n_1+n_2-2}) & , \quad \text{two-sided} \\ P(t_p < t_{\alpha, n_1+n_2-2}) & , \quad \text{lower one-sided} \\ P(t_p > t_{1-\alpha, n_1+n_2-2}) & , \quad \text{upper one-sided} \end{cases}$$

Under the assumption of unequal variances (the Behrens-Fisher problem), the unpooled standard error is computed as

$$SE_u = \left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^{\frac{1}{2}}$$

Satterthwaite's (1946) approximation for the degrees of freedom, extended to accommodate weights, is computed as

$$df_u = \frac{SE_u^4}{\frac{s_1^4}{(n_1-1)\left(\sum_{i=1}^{n_1^*} f_{1i} w_{1i}\right)^2} + \frac{s_2^4}{(n_2-1)\left(\sum_{i=1}^{n_2^*} f_{2i} w_{2i}\right)^2}}$$

The unpooled Satterthwaite $100(1-\alpha)\%$ confidence interval for the mean difference μ_d is

$$\begin{aligned} & \left(\bar{y}_d - t_{1-\frac{\alpha}{2}, df_u} SE_u, \bar{y}_d + t_{1-\frac{\alpha}{2}, df_u} SE_u \right), \text{ SIDES}=2 \\ & \left(-\infty, \bar{y}_d + t_{1-\alpha, df_u} SE_u \right), \text{ SIDES}=L \\ & \left(\bar{y}_d - t_{1-\alpha, df_u} SE_u, \infty \right), \text{ SIDES}=U \end{aligned}$$

The t value for the unpooled Satterthwaite test is computed as

$$t_u = \frac{\bar{y}_d - \mu_0}{SE_u}$$

The p -value of the unpooled Satterthwaite test is computed as

$$p\text{-value} = \begin{cases} P(t_u^2 > F_{1-\alpha, 1, df_u}) & , \quad \text{two-sided} \\ P(t_u < t_{\alpha, df_u}) & , \quad \text{lower one-sided} \\ P(t_u > t_{1-\alpha, df_u}) & , \quad \text{upper one-sided} \end{cases}$$

When the **COCHRAN** option is specified in the **PROC TTEST** statement, the Cochran and Cox (1950) approximation of the p -value of the t_u statistic is the value of p such that

$$t_u = \frac{\left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} \right) t_1 + \left(\frac{s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right) t_2}{\left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} \right) + \left(\frac{s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)}$$

where t_1 and t_2 are the critical values of the t distribution corresponding to a significance level of p and sample sizes of n_1 and n_2 , respectively. The number of degrees of freedom is undefined when $n_1 \neq n_2$. In general, the Cochran and Cox test tends to be conservative (Lee and Gurland 1975).

The $100(1 - \alpha)\%$ **CI=EQUAL** and **CI=UMPU** confidence intervals for the common population standard deviation σ assuming equal variances are computed as discussed in the section “**Normal Data (DIST=NORMAL)**” on page 10495 for the one-sample design, except replacing s^2 by s_p^2 and $(n - 1)$ by $(n_1 + n_2 - 1)$.

The folded form of the F statistic, F' , tests the hypothesis that the variances are equal (Steel and Torrie 1980), where

$$F' = \frac{\max(s_1^2, s_2^2)}{\min(s_1^2, s_2^2)}$$

A test of F' is a two-tailed F test because you do not specify which variance you expect to be larger. The p -value (Steel and Torrie 1980) is equal-tailed and is computed as

$$\begin{aligned} p\text{-value} &= 2P(F' > F_{1-\alpha, df_a, df_b}) \\ &= \begin{cases} P(s_1^2/s_2^2 > F_{1-\alpha, df_1, df_2}) + P(s_2^2/s_1^2 \leq F_{1-\alpha, df_2, df_1}) & , \quad s_1^2/s_2^2 \geq 1 \\ P(s_1^2/s_2^2 \leq F_{1-\alpha, df_1, df_2}) + P(s_2^2/s_1^2 > F_{1-\alpha, df_2, df_1}) & , \quad s_1^2/s_2^2 < 1 \end{cases} \end{aligned}$$

where df_1 , df_2 , df_a , and df_b are the degrees of freedom that correspond to s_1^2 , s_2^2 , $\max(s_1^2, s_2^2)$, and $\min(s_1^2, s_2^2)$, respectively.

Note that the p -value is similar to the probability p^* of a greater F' value under the null hypothesis that $\sigma_1^2 = \sigma_2^2$,

$$p^* = \begin{cases} P(s_1^2/s_2^2 > F_{1-\alpha, df_1, df_2}) + P(s_2^2/s_1^2 \leq F_{1-\alpha, df_1, df_2}) & , \quad s_1^2/s_2^2 \geq 1 \\ P(s_1^2/s_2^2 \leq F_{1-\alpha, df_1, df_2}) + P(s_2^2/s_1^2 > F_{1-\alpha, df_1, df_2}) & , \quad s_1^2/s_2^2 < 1 \end{cases}$$

The F' test is not very robust to violations of the assumption that the data are normally distributed, and thus it is not recommended without confidence in the normality assumption.

Lognormal Ratio (DIST=LOGNORMAL TEST=RATIO)

The **DIST=LOGNORMAL** analysis is handled by log-transforming the data and null value, performing a **DIST=NORMAL** analysis, and then transforming the results back to the original scale. See the section “**Normal Data (DIST=NORMAL)**” on page 10495 for the one-sample design for details on how the **DIST=NORMAL** computations for means and standard deviations are transformed into the **DIST=LOGNORMAL** results for geometric means and CVs. As mentioned in the section “**Coefficient of Variation**” on page 10494, the assumption of equal CVs on the lognormal scale is analogous to the assumption of equal variances on the normal scale.

Normal Ratio (DIST=NORMAL TEST=RATIO)

The distributional assumptions, equality of variances test, and within-class-level mean estimates (\bar{y}_1 and \bar{y}_2), standard deviation estimates (s_1 and s_2), standard errors (SE_1 and SE_2), and confidence limits for means and standard deviations are the same as in the section “**Normal Difference (DIST=NORMAL TEST=DIFF)**” on page 10498 for the two-independent-sample design.

The mean ratio $\mu_1/\mu_2 = \mu_r$ is estimated by

$$\hat{\mu}_r = \bar{y}_1/\bar{y}_2$$

No estimates or confidence intervals for the ratio of standard deviations are computed.

Under the assumption of equal variances ($\sigma_1^2 = \sigma_2^2$), the pooled confidence interval for the mean ratio is the Fieller (1954) confidence interval, extended to accommodate weights. Let

$$\begin{aligned} a_p &= \frac{s_p^2 t_{1-\frac{\alpha}{2}, n_1+n_2-2}^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} - \bar{y}_2^2 \\ b_p &= \bar{y}_1 \bar{y}_2 \\ c_p &= \frac{s_p^2 t_{1-\frac{\alpha}{2}, n_1+n_2-2}^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} - \bar{y}_1^2 \end{aligned}$$

where s_p is the pooled standard deviation defined in the section “**Normal Difference (DIST=NORMAL TEST=DIFF)**” on page 10498 for the two-independent-sample design. If $a_p \geq 0$ (which occurs when \bar{y}_2 is too close to zero), then the pooled two-sided $100(1 - \alpha)\%$ Fieller confidence interval for μ_r does not exist. If $a < 0$, then the interval is

$$\left(-\frac{b_p}{a_p} + \frac{(b_p^2 - a_p c_p)^{\frac{1}{2}}}{a_p}, -\frac{b_p}{a_p} - \frac{(b_p^2 - a_p c_p)^{\frac{1}{2}}}{a_p} \right)$$

For the one-sided intervals, let

$$\begin{aligned} a_p^* &= \frac{s_p^2 t_{1-\alpha, n_1+n_2-2}^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} - \bar{y}_2^2 \\ c_p^* &= \frac{s_p^2 t_{1-\alpha, n_1+n_2-2}^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} - \bar{y}_1^2 \end{aligned}$$

which differ from a_p and c_p only in the use of α in place of $\alpha/2$. If $a_p^* \geq 0$, then the pooled one-sided $100(1 - \alpha)\%$ Fieller confidence intervals for μ_r do not exist. If $a_p^* < 0$, then the intervals are

$$\begin{aligned} &\left(-\infty, -\frac{b_p}{a_p^*} - \frac{(b_p^2 - a_p^* c_p^*)^{\frac{1}{2}}}{a_p^*} \right), \text{ SIDES=L} \\ &\left(-\frac{b_p}{a_p^*} + \frac{(b_p^2 - a_p^* c_p^*)^{\frac{1}{2}}}{a_p^*}, \infty \right), \text{ SIDES=U} \end{aligned}$$

The pooled t test assuming equal variances is the Sasabuchi (1988a, b) test. The hypothesis $H_0: \mu_r = \mu_0$ is rewritten as $H_0: \mu_1 - \mu_0 \mu_2 = 0$, and the pooled t test in the section “**Normal Difference (DIST=NORMAL TEST=DIFF)**” on page 10498 for the two-independent-sample design is conducted on the original y_{1i} values ($i \in \{1, \dots, n_1^*\}$) and transformed values of y_{2i}

$$y_{2i}^* = \mu_0 y_{2i}, \quad i \in \{1, \dots, n_2^*\}$$

with a null difference of 0. The t value for the Sasabuchi pooled test is computed as

$$t_p = \frac{\bar{y}_1 - \mu_0 \bar{y}_2}{s_p \left(\frac{1}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{\mu_0^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^{\frac{1}{2}}}$$

The p -value of the test is computed as

$$p\text{-value} = \begin{cases} P(t_p^2 > F_{1-\alpha, 1, n_1+n_2-2}) & , \quad \text{two-sided} \\ P(t_p < t_{\alpha, n_1+n_2-2}) & , \quad \text{lower one-sided} \\ P(t_p > t_{1-\alpha, n_1+n_2-2}) & , \quad \text{upper one-sided} \end{cases}$$

Under the assumption of unequal variances, the unpooled Satterthwaite-based confidence interval for the mean ratio μ_r is computed according to the method in Dilba, Schaarschmidt, and Hothorn (2007, the section “Two-sample Problem” on page 20), extended to accommodate weights. The degrees of freedom for the confidence interval are based on the same approximation as in Tamhane and Logan (2004) for the unpooled t test but with the null mean ratio μ_0 replaced by the maximum likelihood estimate $\hat{\mu}_r = \bar{y}_1/\bar{y}_2$:

$$df_u = \frac{\left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{\hat{\mu}_r^2 s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^2}{\frac{s_1^4}{(n_1-1) \left(\sum_{i=1}^{n_1^*} f_{1i} w_{1i} \right)^2} + \frac{\hat{\mu}_r^4 s_2^4}{(n_2-1) \left(\sum_{i=1}^{n_2^*} f_{2i} w_{2i} \right)^2}}$$

Let

$$\begin{aligned} a_u &= \frac{s_2^2 t_{1-\frac{\alpha}{2}, df_u}^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} - \bar{y}_2^2 \\ b_u &= \bar{y}_1 \bar{y}_2 \\ c_u &= \frac{s_1^2 t_{1-\frac{\alpha}{2}, df_u}^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} - \bar{y}_1^2 \end{aligned}$$

where s_1 and s_2 are the within-class-level standard deviations defined in the section “[Normal Difference \(DIST=NORMAL TEST=DIFF\)](#)” on page 10498 for the two-independent-sample design. If $a_u \geq 0$ (which occurs when \bar{y}_2 is too close to zero), then the unpooled Satterthwaite-based two-sided $100(1-\alpha)\%$ confidence interval for μ_r does not exist. If $a_u < 0$, then the interval is

$$\left(-\frac{b_u}{a_u} + \frac{(b_u^2 - a_u c_u)^{\frac{1}{2}}}{a_u}, -\frac{b_u}{a_u} - \frac{(b_u^2 - a_u c_u)^{\frac{1}{2}}}{a_u} \right)$$

The t test assuming unequal variances is the test derived in Tamhane and Logan (2004). The hypothesis $H_0: \mu_r = \mu_0$ is rewritten as $H_0: \mu_1 - \mu_0 \mu_2 = 0$, and the Satterthwaite t test in the section “[Normal Difference \(DIST=NORMAL TEST=DIFF\)](#)” on page 10498 for the two-independent-sample design is conducted on the original y_{1i} values ($i \in \{1, \dots, n_1^*\}$) and transformed values of y_{2i}

$$y_{2i}^* = \mu_0 y_{2i} \quad , \quad i \in \{1, \dots, n_2^*\}$$

with a null difference of 0. The degrees of freedom are computed as

$$df_u = \frac{\left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{\mu_0^2 s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^2}{\frac{s_1^4}{(n_1-1) \left(\sum_{i=1}^{n_1^*} f_{1i} w_{1i} \right)^2} + \frac{\mu_0^4 s_2^4}{(n_2-1) \left(\sum_{i=1}^{n_2^*} f_{2i} w_{2i} \right)^2}}$$

The t value for the Satterthwaite-based unpooled test is computed as

$$t_u = \frac{\bar{y}_1 - \mu_0 \bar{y}_2}{\left(\frac{s_1^2}{\sum_{i=1}^{n_1^*} f_{1i} w_{1i}} + \frac{\mu_0^2 s_2^2}{\sum_{i=1}^{n_2^*} f_{2i} w_{2i}} \right)^{\frac{1}{2}}}$$

The p -value of the test is computed as

$$p\text{-value} = \begin{cases} P\left(t_u^2 > F_{1-\alpha, 1, \text{df}_u^*}\right) & , \quad \text{two-sided} \\ P\left(t_u < t_{\alpha, \text{df}_u^*}\right) & , \quad \text{lower one-sided} \\ P\left(t_u > t_{1-\alpha, \text{df}_u^*}\right) & , \quad \text{upper one-sided} \end{cases}$$

AB/BA Crossover Design

Let “A” and “B” denote the two treatment values. Define the following notation:

n_1^* = number of observations with treatment sequence AB

n_2^* = number of observations with treatment sequence BA

y_{11i} = response value of i th observation in sequence AB during period 1, $i \in \{1, \dots, n_1^*\}$

y_{12i} = response value of i th observation in sequence AB during period 2, $i \in \{1, \dots, n_1^*\}$

y_{21i} = response value of i th observation in sequence BA during period 1, $i \in \{1, \dots, n_2^*\}$

y_{22i} = response value of i th observation in sequence BA during period 2, $i \in \{1, \dots, n_2^*\}$

So $\{y_{11i}, \dots, y_{11n_1^*}\}$ and $\{y_{22i}, \dots, y_{22n_2^*}\}$ are all observed at treatment level A, and $\{y_{12i}, \dots, y_{12n_1^*}\}$ and $\{y_{21i}, \dots, y_{21n_2^*}\}$ are all observed at treatment level B.

Define the *period difference* for an observation as the difference between period 1 and period 2 response values:

$$\text{pd}_{kji} = y_{k1i} - y_{k2i}$$

for $k \in \{1, 2\}$ and $i \in \{1, \dots, n_k^*\}$. Similarly, the *period ratio* is the ratio between period 1 and period 2 response values:

$$\text{pr}_{kji} = y_{k1i} / y_{k2i}$$

The *crossover difference* for an observation is the difference between treatment A and treatment B response values:

$$\text{cd}_{kji} = \begin{cases} y_{k1i} - y_{k2i} & , \quad k = 1 \\ y_{k2i} - y_{k1i} & , \quad k = 2 \end{cases}$$

Similarly, the *crossover ratio* is the ratio between treatment A and treatment B response values:

$$\text{cr}_{kji} = \begin{cases} y_{k1i} / y_{k2i} & , \quad k = 1 \\ y_{k2i} / y_{k1i} & , \quad k = 2 \end{cases}$$

In the absence of the **IGNOREPERIOD** option in the **PROC TTEST** statement, the data are split into two groups according to treatment sequence and analyzed as a two-independent-sample design. If **DIST=NORMAL**, then the analysis of the treatment effect is based on the half period differences $\{pd_{kji}/2\}$, and the analysis for the period effect is based on the half crossover differences $\{cd_{kji}/2\}$. The computations for the normal difference analysis are the same as in the section “**Normal Difference (DIST=NORMAL TEST=DIFF)**” on page 10498 for the two-independent-sample design. The normal ratio analysis without the **IGNOREPERIOD** option is not supported for the AB/BA crossover design. If **DIST=LOGNORMAL**, then the analysis of the treatment effect is based on the square root of the period ratios $\{\sqrt{pr_{kji}}\}$, and the analysis for the period effect is based on the square root of the crossover ratios $\{\sqrt{cr_{kji}}\}$. The computations are the same as in the section “**Lognormal Ratio (DIST=LOGNORMAL TEST=RATIO)**” on page 10500 for the two-independent-sample design.

If the **IGNOREPERIOD** option is specified, then the treatment effect is analyzed as a paired analysis on the (treatment A, treatment B) response value pairs, regardless of treatment sequence. So the set of pairs is taken to be the concatenation of $\{(y_{111}, y_{121}), \dots, (y_{11n_1^*}, y_{12n_1^*})\}$ and $\{(y_{221}, y_{211}), \dots, (y_{22n_2^*}, y_{21n_2^*})\}$. The computations are the same as in the section “**Paired Design**” on page 10497.

See Senn (2002, Chapter 3) for a more detailed discussion of the AB/BA crossover design.

TOST Equivalence Test

The hypotheses for an equivalence test are

$$H_0: \mu < \theta_L \quad \text{or} \quad \mu > \theta_U$$

$$H_1: \theta_L \leq \mu \leq \theta_U$$

where θ_L and θ_U are the lower and upper bounds specified in the **TOST** option in the **PROC TTEST** statement, and μ is the analysis criterion (mean, mean ratio, or mean difference, depending on the analysis). Following the two one-sided tests (TOST) procedure of Schuirmann (1987), the equivalence test is conducted by performing two separate tests:

$$H_{a0}: \mu < \theta_L$$

$$H_{a1}: \mu \geq \theta_L$$

and

$$H_{b0}: \mu > \theta_U$$

$$H_{b1}: \mu \leq \theta_U$$

The overall p -value is the larger of the two p -values of those tests.

Rejection of H_0 in favor of H_1 at significance level α occurs if and only if the $100(1 - 2\alpha)\%$ confidence interval for μ is contained completely within (θ_L, θ_U) . So, the $100(1 - 2\alpha)\%$ confidence interval for μ is displayed in addition to the usual $100(1 - \alpha)\%$ interval.

For further discussion of equivalence testing for the designs supported in the TTEST procedure, see Phillips (1990); Diletti, Hauschke, and Steinijans (1991); Hauschke et al. (1999).

Bootstrap Methods

Overview of the Bootstrap

The bootstrap is based on the *plug-in principle* and is an extension of the practice of replacing unknown parameters with estimates (for example, substituting a sample mean for a population mean). The extension goes all the way to the entire population F from which the data being analyzed are a sample.

The most popular variety of bootstrap is the *nonparametric bootstrap*, which relies on random sampling with replacement from the data to estimate the distribution of a sample estimate (or the joint distribution of multiple sample estimates).

The bootstrap methods in PROC TTEST are all based on the nonparametric bootstrap. The other two main varieties are the *parametric bootstrap* (sampling from a model that has estimated parameters) and *smoothed bootstrap* (sampling from a continuous distribution estimate).

The heuristic for the nonparametric bootstrap is as follows:

1. Draw n observations with replacement from the original n data points to create a “bootstrap sample.”
2. Calculate a statistic of interest, θ , from the bootstrap sample and denote its computed value as $\hat{\theta}$.
3. Repeat for a total of r samples.

The statistics of primary interest in PROC TTEST are the sample mean and sample standard deviation.

Purpose of the Bootstrap

The main purpose of bootstrapping is to assess the accuracy and precision of one or more sample estimates in terms of bias, standard error, and confidence intervals.

In typical situations, the bootstrap is *not* useful for estimating a population parameter or the CDF or quantiles of sample estimates. This is because the bootstrap distribution is centered around the observed statistic, not the population parameter. For example, the bootstrap cannot improve on a sample mean estimate.

Bootstrapping can also be a useful tool for inference in various situations, such as the following:

- Parametric assumptions are violated. For example, χ^2 intervals for a variance and F -based intervals for the ratio of variances are not robust to deviations from normality, and their coverage does not improve even with increasing sample size.
- It is too difficult to derive formulas.
- The data are stored in a way that makes calculating formulas impractical.

Useful Applications and Notable Shortcomings

Popular and useful applications of bootstrapping include the following:

- Better standard error estimates
- Bias estimates
- Percentile intervals, optionally with corrections for median bias or narrowness bias (or both)
- t -based intervals, which are traditional t -based confidence intervals either with the bootstrap standard error in place of the traditional standard error or with bootstrap quantiles of the t statistic in place of t distribution quantiles

The two most notable shortcomings of the bootstrap are as follows:

- It tends to perform poorly for small samples.
- Bootstrap bias-corrected *estimates* are usually worse than estimates that are based on the original sample. Even though they tend to be more accurate, they also tend to have much higher variance.

Educational Value

Hesterberg (2015) points out several educational benefits of the bootstrap:

- Because the bootstrap works the same way with a wide variety of statistics, students can focus on ideas rather than formulas. They can also focus on statistics that are appropriate rather than “well-behaved.”
- Plots of the bootstrap distribution can help make the abstract concrete for concepts such as sampling distributions, standard errors, bias, the central limit theorem, and confidence intervals.
- The action of drawing bootstrap samples reinforces the role that random sampling plays in statistics.
- The relationship between the bootstrap distribution and the original sample is fundamentally the same as the relationship between the original sample and the population. Patterns that are observed in bootstrap samples (for example, excessive narrowness) usually imply similar patterns in random sampling from the population (for example, the same narrowness that is corrected for with the $n/(n-1)$ factor in the traditional sample standard deviation estimate).

Politis (2016) explains how bootstrapping can help ease students into understanding the notion of resampling from an empirical distribution, instilling confidence in mean and variance estimates without relying on the (often unjustifiable) assumption of normality. He suggests a three-stage approach for guiding students through this transition:

1. Introduce Monte Carlo simulation as an alternative to distribution theory.
2. Demonstrate the parametric bootstrap as an alternative to critical value tables.
3. Abandon the parametric paradigm altogether by generating quantiles and percentile intervals from the resampling distribution. Show when the bootstrap works better or worse than the parametric approach.

Weights and Frequencies

The TTEST procedure does not support the use of the WEIGHT statement with the bootstrap because there is no consensus on weighted bootstrap methods.

The FREQ statement is supported with the bootstrap.

Review of Common Notation and Formulas

Most notation and formulas involved in the descriptions of bootstrap methods in subsequent sections have already been discussed in previous sections, but they are presented here for easier reference. Estimates that involve the empirical distribution derived from the data are newly presented in this section and are denoted as “ZE,” sometimes with a subscript to distinguish among alternative assumptions.

Table 125.8 summarizes the basic notation for each design that is supported in bootstrap methods in PROC TTEST.

Table 125.8 Common Notation

Symbol	Description
One-Sample Design	
n	Number of observations
μ	Population mean
σ^2	Population variance
α	Value of ALPHA= option in PROC TTEST statement, such that the confidence level for all bootstrap confidence intervals is $100(1 - \alpha)\%$
y_i	Value of i th observation, $i \in \{1, \dots, n\}$
Two-Sample Design	
n_1	Number of observations at the first class level
n_2	Number of observations at the second class level
y_{1i}	Value of i th observation at the first class level, $i \in \{1, \dots, n_1\}$
y_{2i}	Value of i th observation at the second class level, $i \in \{1, \dots, n_2\}$
General	
z_p	100 p percentile of standard normal distribution
$t_{p,v}$	100 p percentile of t distribution with v degrees of freedom

The standard error of $\hat{\theta}$ is the standard deviation of its sampling distribution. The degrees of freedom discussed in this section reflect the values that would be used for t tests for the corresponding designs in PROC TTEST.

One-sample estimates for mean (\bar{y}), standard deviation (s), standard error of mean (SE), and degrees of freedom (df) are as follows:

$$\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$$

$$s = \left(\frac{1}{n-1} \sum_{i=1}^n (y_i - \bar{y})^2 \right)^{\frac{1}{2}}$$

$$\text{SE} = s / \sqrt{n}$$

$$\text{df} = n - 1$$

Two-sample estimates for within-group means (\bar{y}_1 and \bar{y}_2), mean difference (\bar{y}_d), and within-group standard deviations (s_1 and s_2) are as follows:

$$\begin{aligned}\bar{y}_1 &= \frac{1}{n_1} \sum_{i=1}^{n_1} y_{1i} \\ \bar{y}_2 &= \frac{1}{n_2} \sum_{i=1}^{n_2} y_{2i} \\ \bar{y}_d &= \bar{y}_1 - \bar{y}_2 \\ s_1 &= \left(\frac{1}{n_1 - 1} \sum_{i=1}^{n_1} (y_{1i} - \bar{y}_1)^2 \right)^{\frac{1}{2}} \\ s_2 &= \left(\frac{1}{n_2 - 1} \sum_{i=1}^{n_2} (y_{2i} - \bar{y}_2)^2 \right)^{\frac{1}{2}}\end{aligned}$$

Two-sample pooled estimates for standard deviation that is assumed to be common within groups (s_p), standard error of mean difference (SE_p), and degrees of freedom (df_p) are as follows:

$$\begin{aligned}s_p &= \left(\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2} \right)^{\frac{1}{2}} \\ SE_p &= s_p \left(\frac{1}{n_1} + \frac{1}{n_2} \right)^{\frac{1}{2}} \\ df_p &= n_1 + n_2 - 2\end{aligned}$$

Note that s^2 , s_1^2 , s_2^2 , and s_p^2 are all unbiased estimators of their respective variances.

The two-sample unpooled standard error estimate of the mean difference (SE_u) and degrees of freedom estimate for unpooled (Satterthwaite) t statistic (df_u) are as follows:

$$\begin{aligned}SE_u &= \left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2} \right)^{\frac{1}{2}} \\ df_u &= \frac{SE_u^4}{\frac{s_1^4}{(n_1 - 1)n_1^2} + \frac{s_2^4}{(n_2 - 1)n_2^2}}\end{aligned}$$

The one-sample variance of the empirical distribution ($\hat{\sigma}^2$) and the standard error of the empirical distribution of the mean (ZE) are as follows:

$$\begin{aligned}\hat{\sigma}^2 &= \left(\frac{n - 1}{n} \right) s^2 \\ ZE &= \hat{\sigma} / \sqrt{n}\end{aligned}$$

The two-sample pooled variance of the empirical distribution ($\hat{\sigma}_p^2$) and the pooled standard error estimate of the empirical distribution of mean difference (ZE_p) are as follows:

$$\hat{\sigma}_p^2 = \frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2}$$

$$ZE_p = \hat{\sigma}_p \left(\frac{1}{n_1} + \frac{1}{n_2} \right)^{\frac{1}{2}}$$

The two-sample unpooled standard error of the empirical distribution of mean difference is defined as

$$ZE_u = \left(\frac{(n_1 - 1)s_1^2}{n_1^2} + \frac{(n_2 - 1)s_2^2}{n_2^2} \right)^{\frac{1}{2}}$$

Resampling

For the nonparametric bootstrap for a one-sample design, a *bootstrap sample* is a random draw of n observations with replacement from the original data set, where $\hat{\theta}$ is the statistic that is calculated from a sample of n iid observations (for example, \bar{y} or s), r is the number of independent bootstrap samples, and $\hat{\theta}_i^*$ is the value of $\hat{\theta}$ for the i th bootstrap sample from the original data, where $i \in \{1, \dots, r\}$.

The bootstrap for a paired design is identical to the bootstrap for a one-sample design if y_i is defined as the difference between the first and second members of the i th pair.

In a bootstrap for a two-sample design, random draws of size n_1 and n_2 are taken with replacement from the first and second groups, respectively, and combined to produce a single bootstrap sample.

Statistics That Are Resampled

The sample estimates $\hat{\theta}$ for statistics θ that are supported in bootstrap analyses are computed as follows.

For a one-sample design, the mean μ is estimated by

$$\bar{y} = \frac{1}{n} \sum_{i=1}^n y_i$$

and the standard deviation σ is estimated by

$$s = \left(\frac{1}{n-1} \sum_{i=1}^n (y_i - \bar{y})^2 \right)^{\frac{1}{2}}$$

For a paired design, the mean of the paired difference $d_i = y_{1i} - y_{2i}$ is estimated by

$$\bar{d} = \frac{1}{n} \sum_{i=1}^n d_i$$

and the standard deviation of the paired difference is estimated by

$$s_d = \left(\frac{1}{n-1} \sum_{i=1}^n (d_i - \bar{d})^2 \right)^{\frac{1}{2}}$$

For a two-sample design, the mean μ_d of the class difference $d_{ij} = y_{1i} - y_{2j}$ is estimated by

$$\bar{y}_d = \bar{y}_1 - \bar{y}_2 = \frac{1}{n_1} \sum_{i=1}^{n_1} y_{1i} - \frac{1}{n_2} \sum_{j=1}^{n_2} y_{2j}$$

Under the assumption of equal variances ($\sigma_1^2 = \sigma_2^2$), the pooled estimate of the standard deviation of the class difference is

$$s_{pd} = \sqrt{2}s_p = \sqrt{2} \left(\frac{(n_1 - 1)s_1^2 + (n_2 - 1)s_2^2}{n_1 + n_2 - 2} \right)^{\frac{1}{2}}$$

Under the assumption of unequal variances, the Satterthwaite estimate of the standard deviation of the class difference is

$$s_{ud} = \sqrt{s_1^2 + s_2^2}$$

Bootstrap Standard Error, Bias Estimate, and Quantiles

The *bootstrap standard error* is the sample standard deviation of the bootstrap distribution:

$$s_b = \left(\frac{1}{r-1} \sum_{i=1}^r (\hat{\theta}_i^* - \bar{\hat{\theta}}^*)^2 \right)^{\frac{1}{2}}$$

The *bootstrap bias estimate* is

$$\hat{\text{bias}}_b = \left(\frac{1}{r} \sum_{i=1}^r \hat{\theta}_i^* \right) - \hat{\theta}$$

Several confidence intervals in the next section are based on quantiles of bootstrap samples. Following the convention in Efron and Tibshirani (1993, section 12.5), the quantile for an ambiguous case is chosen as the nearest sample value in the direction toward the center of the bootstrap distribution. This choice ensures that confidence intervals that are constructed from the quantiles satisfy the desired coverage. In particular, the p th quantile (100 p percentile) q_p of the bootstrap distribution of $\hat{\theta}_i^*$ (or some function of $\hat{\theta}_i^*$) is computed as follows:

- If rp is an integer, then q_p is the rp th largest value.
- Otherwise, if $p \leq 0.5$ and $L = \text{floor}((r+1)p) \geq 1$, then q_p is the L th largest value.
- Otherwise, if $p > 0.5$ and $U = \text{ceil}((r+1)p) \leq r$, then q_p is the U th largest value.
- Otherwise (either $p \leq 0.5$ and $L = \text{floor}((r+1)p) < 1$, or $p > 0.5$ and $U = \text{ceil}((r+1)p) > r$), then q_p is undefined and the bootstrap sample must be larger to yield a valid quantile-based confidence interval.

Bootstrap Confidence Intervals

The bootstrap confidence intervals that PROC TTEST implements are based primarily on recommendations from Hesterberg (2015). The recommendations are based on a combination of educational value and good performance in practice.

See Table 125.5 for a summary of which parameters are supported for each type of confidence interval.

For the following sections, let \hat{S} denote the estimate of the standard error based on unbiased variance estimates—that is, SE for a one-sample or paired design, SE_p for a pooled analysis for a two-sample design, or SE_u for an unpooled analysis for a two-sample design. Similarly, let \hat{Z} denote the estimate of the standard error based on the variances of the empirical distribution—that is, ZE , ZE_p , or ZE_u . Finally, let \hat{df} denote the degrees of freedom that would be used for t tests for the corresponding designs—that is, df , df_p , or df_u .

Normal Interval with Bootstrap Standard Error

Perhaps the most crude confidence interval based on the bootstrap is the *normal interval with bootstrap standard error*, which is simply the normal-based confidence interval with the usual standard error replaced by the bootstrap standard error:

$$\begin{cases} \left(\hat{\theta} - z_{1-\alpha/2} s_b, \hat{\theta} + z_{1-\alpha/2} s_b \right) & , \quad \text{two-sided} \\ \left(-\infty, \hat{\theta} + z_{1-\alpha} s_b \right) & , \quad \text{lower one-sided} \\ \left(\hat{\theta} - z_{1-\alpha} s_b, \infty \right) & , \quad \text{upper one-sided} \end{cases}$$

In PROC TTEST, the normal interval with bootstrap standard error is computed only for the mean or mean difference. Standard confidence intervals for standard deviations are based on the chi-square distribution rather than on the normal distribution and thus do not have a bootstrap analog of this type.

Bootstrap Percentile Interval

The *bootstrap percentile interval* is recommended by Hesterberg (2015) as one of two “quick and dirty” intervals to begin with when introducing students to the bootstrap. Depending on the sidedness, it is the middle, lower, or upper $100(1 - \alpha)\%$ of the bootstrap distribution:

$$\begin{cases} \left(q_{\frac{\alpha}{2}}, q_{1-\frac{\alpha}{2}} \right) & , \quad \text{two-sided} \\ \left(-\infty, q_{1-\alpha} \right) & , \quad \text{lower one-sided} \\ \left(q_{\alpha}, \infty \right) & , \quad \text{upper one-sided} \end{cases}$$

where q are quantiles of $\hat{\theta}^*$.

This interval is usually the most intuitive one for students. It is robust to skewness in the data, but it performs poorly for small sample sizes. It tends to be too narrow, and it is only “first-order accurate.” For a one-sample design, first-order accuracy means that the one-sided coverage probability differs from the nominal value by $O(n^{-\frac{1}{2}})$.

t Interval with Bootstrap Standard Error

The other “quick and dirty interval” is the *t interval with bootstrap standard error*, which is the traditional t -based confidence interval with the usual standard error replaced by the bootstrap standard error:

$$\begin{cases} \left(\hat{\theta} - t_{1-\alpha/2, \hat{df}} s_b, \hat{\theta} + t_{1-\alpha/2, \hat{df}} s_b \right) & , \quad \text{two-sided} \\ \left(-\infty, \hat{\theta} + t_{1-\alpha, \hat{df}} s_b \right) & , \quad \text{lower one-sided} \\ \left(\hat{\theta} - t_{1-\alpha, \hat{df}} s_b, \infty \right) & , \quad \text{upper one-sided} \end{cases}$$

This interval is also the same as the normal interval with bootstrap standard error where normal quantiles are replaced by t quantiles.

In PROC TTEST, the t interval with bootstrap standard error is computed only for the mean or mean difference. Standard confidence intervals for standard deviations are based on the chi-square distribution rather than on the t distribution and thus do not have a bootstrap analog of this type.

The t interval with bootstrap standard error can help students learn formula methods. It performs relatively well for small n but is not robust to skewness in the data.

Students can compare percentile and t intervals: if they are similar, then they are both probably acceptable.

Bootstrap Expanded Percentile Interval

Whereas the usual bootstrap percentile interval has coverage properties similar to the normal interval with bootstrap standard error (robustness to skewness notwithstanding), the *expanded bootstrap percentile interval* alleviates the narrowness bias by “upgrading” the coverage properties to be more like the t interval with bootstrap standard error. The expanded bootstrap percentile is produced by replacing the α in the bootstrap percentile interval with the value α' that solves the equation $h_z(\alpha') = h_t(\alpha)$, where $h_z(p)$ is the half-width of the normal-based $100(1 - p)\%$ confidence interval that uses the variance of the empirical distribution and $h_t(p)$ is the half-width of the t -based $100(1 - p)\%$ confidence interval that uses the unbiased variance estimate. The *half-width* of a two-sided interval is the length of the interval divided by two, and the half-width of a one-sided interval is the absolute difference between the point estimate and the finite limit.

The general solution of $h_z(\alpha') = h_t(\alpha)$ is

$$\alpha' = d\Phi\left(\frac{\hat{S}}{\hat{Z}}t_{\alpha/d, \hat{df}}\right)$$

where d is the number of sides.

The solutions for different designs are as follows:

$$\alpha' = \begin{cases} d\Phi\left(\sqrt{\frac{n}{n-1}}t_{\alpha/d, n-1}\right) & , \quad \text{one-sample or paired analysis} \\ d\Phi\left(\sqrt{\frac{n_1+n_2}{n_1+n_2-2}}t_{\alpha/d, n_1+n_2-2}\right) & , \quad \text{two-sample pooled analysis} \\ d\Phi\left(\frac{SE_u}{Z_{E_u}}t_{\alpha/d, df_u}\right) & , \quad \text{two-sample unpooled analysis} \end{cases}$$

The resulting expanded percentile interval for each case is

$$\begin{cases} \left(q_{\frac{\alpha'}{2}}, q_{1-\frac{\alpha'}{2}}\right) & , \quad \text{two-sided} \\ (-\infty, q_{1-\alpha'}) & , \quad \text{lower one-sided} \\ (q_{\alpha'}, \infty) & , \quad \text{upper one-sided} \end{cases}$$

where q are quantiles of $\hat{\theta}^*$.

In PROC TTEST, the bootstrap expanded percentile interval is computed only for the mean or mean difference. Standard confidence intervals for standard deviations are based on the chi-square distribution rather than on the normal or t distributions and thus do not have a bootstrap analog of this type.

The expanded interval is better than the bootstrap percentile interval and the t interval with bootstrap standard error but not as good as the bootstrap t interval, which is described in the following section.

Bootstrap t Interval

The *bootstrap t interval* eschews the assumption of the t statistic having a t distribution and instead uses quantiles of its bootstrap distribution, along with traditional standard error estimates,

$$\begin{cases} \left(\hat{\theta} - q_{1-\frac{\alpha}{2}} \hat{S}, \hat{\theta} - q_{\frac{\alpha}{2}} \hat{S} \right) & , \quad \text{two-sided} \\ \left(-\infty, \hat{\theta} - q_{\alpha} \hat{S} \right) & , \quad \text{lower one-sided} \\ \left(\hat{\theta} - q_{1-\alpha} \hat{S}, \infty \right) & , \quad \text{upper one-sided} \end{cases}$$

where q are quantiles of $(\hat{\theta}^* - \hat{\theta}) / \hat{S}^*$ and \hat{S} is the (non-bootstrap) standard error estimate of $\hat{\theta}$ based on unbiased variance estimates.

In PROC TTEST, the bootstrap t interval is computed only for the mean or mean difference. There is no reasonable general formula for the standard error of the sample standard deviation.

The bootstrap t interval allows for asymmetry and is “second-order accurate,” satisfying the following properties for a one-sample design:

- $O(n^{-1})$ difference in one-sided coverage probability from nominal value
- robust to bias
- robust to skewness
- transformation-invariant—that is, intervals for some function of θ can be obtained by applying the same transformation to the endpoints

Bootstrap Bias-Corrected Percentile Interval

The *bootstrap bias-corrected percentile interval (BC)* is

$$\begin{cases} (q_{\alpha_1}, q_{\alpha_2}) & , \quad \text{two-sided} \\ (-\infty, q_{\alpha_3}) & , \quad \text{lower one-sided} \\ (q_{\alpha_4}, \infty) & , \quad \text{upper one-sided} \end{cases}$$

where

$$\begin{aligned} \alpha_1 &= \Phi(2z_0 + z_{\alpha/2}) \\ \alpha_2 &= \Phi(2z_0 + z_{1-\alpha/2}) \\ \alpha_3 &= \Phi(2z_0 + z_{1-\alpha}) \\ \alpha_4 &= \Phi(2z_0 + z_{\alpha}) \\ z_0 &= \Phi^{-1}(\#\{\hat{\theta}_i^* < \hat{\theta}\}/r) \end{aligned}$$

and q are quantiles of $\hat{\theta}^*$.

The BC interval is the default bootstrap confidence interval in PROC TTEST (and also in the NLIN and CAUSALTRT procedures). It corrects for median bias, which occurs when the median of the sampling distribution differs from θ . The two-sided version is given in Efron and Tibshirani (1993, equation 14.10), and the one-sided version is given in Carpenter and Bithell (2000, equation 9).

Displayed Output

For an AB/BA crossover design, the CrossoverVarInfo table shows the variables that are specified for the response and treatment values in each period of the design.

The summary statistics in the Statistics table and confidence limits in the ConfLimits table are displayed for certain variables and/or transformations or subgroups of the variables in the analysis, depending on the design. For a one-sample design, results are displayed for all variables. For a paired design, results are displayed for the paired difference if you specify the **TEST=DIFF** option in the **PROC TTEST** statement, or for the paired ratio if you specify **TEST=RATIO**.

For a two-independent-sample design, most of the results are displayed for each of the two classes, for the difference (if **TEST=DIFF**) or ratio of means between classes (if **TEST=RATIO**), and for the assumed-common within-class standard deviation (if **DIST=NORMAL**) or coefficient of variation (if **TEST=RATIO**). Results are *not* displayed for the standard *deviation* of the class difference or ratio or for the coefficient of variation of the class ratio. However, the standard *errors* that are displayed if you specify **TEST=DIFF** are the standard deviation estimates of the means of each of the two classes and the pooled and unpooled (Satterthwaite) standard deviation estimates of the mean class difference. These standard errors are the same ones that are used in hypothesis tests and confidence limits for means and mean differences.

For an AB/BA crossover design, statistics and confidence limits are displayed for each of the four cells in the design (all four combinations of the two periods and two treatments). If the **IGNOREPERIOD** option is specified in the **VAR** statement, then results are also displayed for the overall treatment difference or ratio, the same as they are for the paired design. If the **IGNOREPERIOD** option is absent, then results are also displayed for the treatment difference or ratio within each sequence and overall, and also for the period difference or ratio, the same as they are for the two-sample design.

The Statistics table displays the following summary statistics:

- the names of the variables, displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- the name of the classification variable (if the two-independent-sample design is used) or treatment and period (if the AB/BA crossover design is used)
- the Method for estimating standard deviation and standard error for a two-independent-sample design, either pooled (for the equal-variance assumption) or Satterthwaite (for the unequal-variance assumption)
- N, the number of nonmissing values
- the (arithmetic) Mean, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Geometric Mean, displayed if the **DIST=LOGNORMAL** option is specified in the **PROC TTEST** statement
- Std Dev, the standard deviation, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Coefficient of Variation, displayed if the **DIST=LOGNORMAL** option is specified in the **PROC TTEST** statement

- Std Err, the standard error of the mean, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Minimum value
- the Maximum value

The **ConfLimits** table displays the following:

- the names of the variables, displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- the name of the classification variable (if the two-independent-sample design is used) or treatment and period (if the AB/BA crossover design is used)
- the method for estimating standard deviation and standard error for a two-independent-sample design, either pooled (for the equal-variance assumption) or Satterthwaite (for the unequal-variance assumption)
- the (arithmetic) Mean, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Geometric Mean, displayed if the **DIST=LOGNORMAL** option is specified in the **PROC TTEST** statement
- 100(1 – α)% CL Mean, the lower and upper confidence limits for the mean. Separate pooled and Satterthwaite confidence limits are shown for the difference or ratio transformations in two-independent-sample designs and AB/BA crossover designs without the **IGNOREPERIOD** option.
- Std Dev, the standard deviation, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Coefficient of Variation, displayed if the **DIST=LOGNORMAL** option is specified in the **PROC TTEST** statement
- 100(1 – α)% CL Std Dev, the equal-tailed confidence limits for the standard deviation, displayed if the **DIST=NORMAL** and **CI=EQUAL** options are specified in the **PROC TTEST** statement
- 100(1 – α)% UMPU CL Std Dev, the UMPU confidence limits for the standard deviation, displayed if the **DIST=NORMAL** and **CI=UMPU** options are specified in the **PROC TTEST** statement
- 100(1 – α)% CL CV, the equal-tailed confidence limits for the coefficient of variation, displayed if the **DIST=LOGNORMAL** and **CI=EQUAL** options are specified in the **PROC TTEST** statement
- 100(1 – α)% UMPU CL CV, the UMPU confidence limits for the coefficient of variation, displayed if the **DIST=LOGNORMAL** and **CI=UMPU** options are specified in the **PROC TTEST** statement

The confidence limits in the **EquivLimits** table and test results in the **TTests** and **EquivTests** tables are displayed only for the test criteria—that is, the variables or transformations being tested. For a one-sample design, results are displayed for all variables in the analysis. For a paired design, results are displayed for the difference if you specify the **TEST=DIFF** option in the **PROC TTEST** statement, or for the ratio if you specify **TEST=RATIO**. For a two-independent-sample design, the results for the difference (if **TEST=DIFF**) or ratio (if **TEST=RATIO**) are displayed. For an AB/BA crossover design, results are displayed for the

treatment difference (if **TEST=DIFF**) or ratio (if **TEST=RATIO**). If the **IGNOREPERIOD** option is absent, then results are also displayed for the period difference (if **TEST=DIFF**) or ratio (if **TEST=RATIO**).

The **EquivLimits** table, produced only if the **TOST** option is specified in the **PROC TTEST** statement, displays the following:

- the name of the variable(s), displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- the (arithmetic) Mean, displayed if the **DIST=NORMAL** option is specified in the **PROC TTEST** statement
- the Geometric Mean, displayed if the **DIST=LOGNORMAL** option is specified in the **PROC TTEST** statement
- Lower Bound, the lower equivalence bound for the mean specified in the **TOST** option in the **PROC TTEST** statement
- $100(1 - 2\alpha)\%$ CL Mean, the lower and upper confidence limits for the mean relevant to the equivalence test. Separate pooled and Satterthwaite confidence limits are shown for two-independent-sample designs and AB/BA crossover designs without the **IGNOREPERIOD** option.
- Upper Bound, the upper equivalence bound for the mean specified in the **TOST** option in the **PROC TTEST** statement
- Assessment, the result of the equivalence test at the significance level specified by the **ALPHA=** option in the **PROC TTEST** statement, either “Equivalent” or “Not equivalent”

The **TTests** table is produced only if the **TOST** option is *not* specified in the **PROC TTEST** statement. Separate results for pooled and Satterthwaite tests (and also the Cochran and Cox test, if the **COCHRAN** option is specified in the **PROC TTEST** statement) are displayed for two-independent-sample designs and AB/BA crossover designs without the **IGNOREPERIOD** option. The table includes the following results:

- the name of the variable(s), displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- *t* Value, the *t* statistic for comparing the mean to the null value as specified by the **H0=** option in the **PROC TTEST** statement
- DF, the degrees of freedom
- the *p*-value, the probability of obtaining a *t* statistic at least as extreme as the observed *t* value under the null hypothesis

The **EquivTests** table is produced only if the **TOST** option is specified in the **PROC TTEST** statement. Separate results for pooled and Satterthwaite tests are displayed for two-independent-sample designs and AB/BA crossover designs without the **IGNOREPERIOD** option. Each test consists of two separate one-sided tests. The overall *p*-value is the larger *p*-value from these two tests. The table includes the following results:

- the name of the variable(s), displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- Null, the lower equivalence bound for the Upper test or the upper equivalence bound for the Lower test, as specified by the **TOST** option in the **PROC TTEST** statement
- t Value, the t statistic for comparing the mean to the Null value
- DF, the degrees of freedom
- the p -value, the probability of obtaining a t statistic at least as extreme as the observed t value under the null hypothesis

The Equality table gives the results of the test of equality of variances. It is displayed for two-independent-sample designs and AB/BA crossover designs without the **IGNOREPERIOD** option. The table includes the following results:

- the name of the variable(s), displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- Num DF and Den DF, the numerator and denominator degrees of freedom
- F Value, the F' (folded) statistic
- Pr > F, the probability of a greater F' value. This is the two-tailed p -value.

The Bootstrap table displays bootstrap standard error, bias estimates, and confidence limits. These results are displayed for certain variables in the analysis, their transformations, or their subgroups (or any combination of these), depending on the design and the analysis options. Results are currently displayed only for one-sample, paired, and two-sample designs and for analyses that assume normal data and involve means and standard deviations of either variables or differences between variables or class levels. Bootstrap standard error and bias estimates are always displayed for these designs and analyses, and [Table 125.5](#) shows which analysis parameters are supported for each type of bootstrap confidence interval.

Bootstrap results are unavailable if you specify any of the **TEST=RATIO**, **DIST=LOGNORMAL**, or **TOST** options in the **PROC TTEST** statement; if you specify the **CROSSOVER=** option in the **VAR** statement; or if you specify the **WEIGHT** statement. They are also unavailable if your input data set contains summary statistics rather than raw observed values.

For a one-sample design, results are displayed for all variables. For a paired design, results are displayed for the paired difference.

For a two-sample design, results are displayed for the class difference—that is, the difference between an observation from the first class and an observation from the second class. Note in particular that whereas the limits displayed for standard deviation in the ConfLimits table are for the assumed-common within-class standard deviation, the limits displayed for standard deviation in the Bootstrap table are for the standard deviation of the *difference*. The estimated standard deviation of the difference is equal to $\sqrt{2}s_p$ under the equal-variance assumption and is equal to $\sqrt{s_1^2 + s_2^2}$ under the unequal-variance assumption.

The Bootstrap table includes the following results:

- the names of the variables, displayed if the **NOBYVAR** option is used in the **PROC TTEST** statement
- the name of the classification variable (if the two-independent-sample design is used)
- the method for estimating standard deviation for a two-independent-sample design, either pooled (for the equal-variance assumption) or Satterthwaite (for the unequal-variance assumption); this choice of method determines both the form of the standard deviation difference estimate on which the bootstrap standard error and bias estimates are based and also the formulas for some of the confidence limits for both mean and standard deviation parameters
- the parameter, either mean or standard deviation
- the bootstrap estimate of the standard error of the statistic
- the bootstrap estimate of the bias
- $100(1 - \alpha)\%$ CL, the lower and upper bootstrap confidence limits for the relevant transformation of each parameter, based on the choice of BOOTCI method

ODS Table Names

PROC TTEST assigns a name to each table it creates. You can use these names to reference the table when using the Output Delivery System (ODS) to select tables and create output data sets. These names are listed in Table 125.9. For more information about ODS, see Chapter 20, “Using the Output Delivery System.”

Table 125.9 ODS Tables Produced by PROC TTEST

ODS Table Name	Description	Syntax
ConfLimits	$100(1 - \alpha)\%$ confidence limits for means, standard deviations, and/or coefficients of variation	By default
Equality	Tests for equality of variance	CLASS statement or VAR / CROSSOVER=
EquivLimits	$100(1 - 2\alpha)\%$ confidence limits for means	PROC TTEST TOST
EquivTests	Equivalence t tests	PROC TTEST TOST
Statistics	Univariate summary statistics	By default
TTtests	t tests	By default
Bootstrap	Bootstrap standard error and bias estimates and $100(1 - \alpha)\%$ bootstrap confidence limits	BOOTSTRAP statement

ODS Graphics

Statistical procedures use ODS Graphics to create graphs as part of their output. ODS Graphics is described in detail in Chapter 21, “[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 623 in Chapter 21, “[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 622 in Chapter 21, “[Statistical Graphics Using ODS](#).”

ODS Graph Names

You can refer to every graph that is produced through ODS Graphics by its name. The names of the graphs that PROC TTEST generates are listed in [Table 125.10](#) and [Table 125.11](#). [Table 125.10](#), which is alphabetized by graph name, shows required statements and options. [Table 125.11](#) is organized by required *bootstrap-plot-request*.

Table 125.10 Graphs Produced by PROC TTEST

ODS Graph Name	Plot Description	Statement / Option
AgreementOfPeriods	Plot of period 2 against period 1 response values for an AB/BA crossover design	VAR / CROSSEVER= PLOTS=AGREEMENT(TYPE=PERIOD)
AgreementOfTreatments	Plot of second treatment against first treatment response values for an AB/BA crossover design	VAR / CROSSEVER= PLOTS=AGREEMENT
AgreementPlot	Plot of second response against first response for a paired design	PAIRED statement PLOTS=AGREEMENT
BoxPlot	Box plots, also with confidence band for one-sample or paired design	PLOTS=BOX PLOTS=SUMMARY(UNPACK)
Histogram	Histograms with overlaid kernel densities, and also normal densities if DIST=NORMAL	PLOTS=HISTOGRAM PLOTS=SUMMARY(UNPACK)
Interval	Confidence intervals for means	PLOTS=INTERVAL
ProfilesOverPrd	Plot of response profiles over periods 1 and 2 for an AB/BA crossover design	VAR / CROSSEVER= PLOTS=PROFILES(TYPE=PERIOD)
ProfilesOverTrt	Plot of response profiles over first and second treatments for an AB/BA crossover design	VAR / CROSSEVER= PLOTS=PROFILES
ProfilesPlot	Plot of response profiles over first and second response values for a paired design	PAIRED statement PLOTS=PROFILES

Table 125.10 *continued*

ODS Graph Name	Plot Description	Statement / Option
QQPlot	Normal quantile-quantile plots	PLOTS=QQ
SummaryPanel	Histograms with overlaid kernel densities (and also normal densities if DIST=NORMAL) and box plots (and also with confidence band for one-sample or paired design)	PLOTS=SUMMARY
(various)	Bootstrap plots (see Table 125.11)	BOOTSTRAP statement PLOTS=BOOTSTRAP (<i>bootstrap-plot-request</i>)

Table 125.11 Bootstrap Graphs Produced by PROC TTEST

ODS Graph Name	Plot Description	Statistic	Design	<i>bootstrap-plot-request</i>
BootstrapMeanBoxPlot	Box plots and confidence bands	Mean	One-sample Paired Certain two-sample cases	BOX SUMMARY(UNPACK)
BootMeanPooledBoxPlot	Box plots and pooled confidence bands	Mean	Certain two-sample cases	BOX SUMMARY(UNPACK)
BootMeanSattBoxPlot	Box plots and Satterthwaite confidence bands	Mean	Certain two-sample cases	BOX SUMMARY(UNPACK)
BootstrapStdDevBoxPlot	Box plots and confidence bands	Standard deviation	One-sample Paired	BOX SUMMARY(UNPACK)
BootPooledStdDevBoxPlot	Box plots and confidence bands	Pooled standard deviation	Two-sample	BOX SUMMARY(UNPACK)
BootSattStdDevBoxPlot	Box plots and confidence bands	Satterthwaite standard deviation	Two-sample	BOX SUMMARY(UNPACK)
BootCorrMeanStdDevPlot	Scatter plots with overlaid elliptical prediction regions	Mean and standard deviation	One-sample Paired	CORRELATION
BootCorrMeanPoolStdDevPlot	Scatter plots with overlaid elliptical prediction regions	Mean and pooled standard deviation	Two-sample	CORRELATION
BootCorrMeanSattStdDevPlot	Scatter plots with overlaid elliptical prediction regions	Mean and Satterthwaite standard deviation	Two-sample	CORRELATION

Table 125.11 *continued*

ODS Graph Name	Plot Description	Statistic	Design	<i>bootstrap-plot-request</i>
BootstrapMeanHistogram	Histograms with overlaid normal and kernel densities	Mean	One-sample Paired Two-sample	HISTOGRAM SUMMARY(UNPACK)
BootstrapStdDevHistogram	Histograms with overlaid normal and kernel densities	Standard deviation	One-sample Paired	HISTOGRAM SUMMARY(UNPACK)
BootPooledStdDevHistogram	Histograms with overlaid normal and kernel densities	Pooled standard deviation	Two-sample	HISTOGRAM SUMMARY(UNPACK)
BootSattStdDevHistogram	Histograms with overlaid normal and kernel densities	Satterthwaite standard deviation	Two-sample	HISTOGRAM SUMMARY(UNPACK)
BootstrapMeanIntervalPlot	Bootstrap confidence intervals	Mean	One-sample Paired Two-sample	INTERVAL
BootstrapStdDevIntervalPlot	Bootstrap confidence intervals	Standard deviation Pooled and Satterthwaite standard deviations	One-sample Paired Two-sample	INTERVAL
BootstrapMeanQQPlot	Normal quantile-quantile plots	Mean	One-sample Paired Two-sample	QQ
BootstrapStdDevQQPlot	Normal quantile-quantile plots	Standard deviation	One-sample Paired	QQ
BootPooledStdDevQQPlot	Normal quantile-quantile plots	Pooled standard deviation	Two-sample	QQ
BootSattStdDevQQPlot	Normal quantile-quantile plots	Satterthwaite standard deviation	Two-sample	QQ
BootstrapMeanSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and confidence bands	Mean	One-sample Paired Certain two-sample cases	SUMMARY
BootMeanPooledSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and pooled confidence bands	Mean	Certain two-sample cases	SUMMARY

Table 125.11 *continued*

ODS Graph Name	Plot Description	Statistic	Design	<i>bootstrap-plot-request</i>
BootMeanSattSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and Satterthwaite confidence bands	Mean	Certain two-sample cases	SUMMARY
BootstrapStdDevSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and confidence bands	Standard deviation	One-sample Paired	SUMMARY
BootPoolStdDevSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and confidence bands	Pooled standard deviation	Two-sample	SUMMARY
BootSattStdDevSummaryPanel	Histograms with overlaid normal and kernel densities, box plots, and confidence bands	Satterthwaite standard deviation	Two-sample	SUMMARY

Interpreting Graphs

Agreement Plots for Paired Designs

For paired designs, the second response of each pair is plotted against the first response, with the mean shown as a large bold symbol. If the **WEIGHT** statement is used, then the mean is the weighted mean. A diagonal line with a slope of 1 and a y-intercept of 0 is overlaid. The location of the points with respect to the diagonal line reveals the strength and direction of the difference or ratio. The tighter the clustering along the same direction as the line, the stronger the positive correlation of the two measurements for each subject. Clustering along a direction perpendicular to the line indicates negative correlation.

Period Agreement Plots for Crossover Designs

The response in the second period is plotted against the response in the first period, with plot symbols distinguishing the two treatment sequences and the two sequence means shown larger in bold. If the **WEIGHT** statement is used, then the means are weighted means. A diagonal line with a slope of 1 and a y-intercept of 0 is overlaid.

In the absence of a strong period effect, the points from each sequence will appear as mirror images about the diagonal line, farther apart with stronger treatment effects. Deviations from symmetry about the diagonal line indicate a period effect. The spread of points within each treatment sequence is an indicator of between-subject variability. The tighter the clustering along the same direction as the line (within each treatment sequence), the stronger the positive correlation of the two measurements for each subject. Clustering along a direction perpendicular to the line indicates negative correlation.

The period agreement plot is usually less informative than the treatment agreement plot. The exception is when the period effect is stronger than the treatment effect.

Treatment Agreement Plots for Crossover Designs

The response associated with the second treatment is plotted against the response associated with the first treatment, with plot symbols distinguishing the two treatment sequences and the two sequence means shown larger in bold. If the **WEIGHT** statement is used, then the means are weighted means. A diagonal line with a slope of 1 and a y-intercept of 0 is overlaid.

The location of the points with respect to the diagonal line reveals the strength and direction of the treatment effect. Substantial location differences between the two sequences indicates a strong period effect. The spread of points within each treatment sequence is an indicator of between-subject variability. The tighter the clustering along the same direction as the line (within each treatment sequence), the stronger the positive correlation of the two measurements for each subject. Clustering along a direction perpendicular to the line indicates negative correlation.

Box Plots

The box is drawn from the 25th percentile (lower quartile) to the 75th percentile (upper quartile). The vertical line inside the box shows the location of the median. If **DIST=NORMAL**, then a diamond symbol shows the location of the mean. The whiskers extend to the minimum and maximum observations, and circles beyond the whiskers identify outliers.

For one-sample and paired designs, a confidence interval for the mean is shown as a band in the background. If the analysis is an equivalence analysis (with the **TOST** option in the **PROC TTEST** statement), then the interval is a $100(1 - 2\alpha)\%$ confidence interval shown along with the equivalence bounds. The inclusion of this interval completely within the bounds is indicative of a significant p -value. If the analysis is not an equivalence analysis, then the confidence level is $100(1 - \alpha)\%$. If the **SHOWH0** global plot option is used, then the null value for the test is shown. If the **WEIGHT** statement is used, then weights are incorporated in the confidence intervals.

Histograms

The **WEIGHT** statement is ignored in the computation of the normal and kernel densities.

Confidence Intervals

If the analysis is an equivalence analysis (with the **TOST** option in the **PROC TTEST** statement), then unless the **TYPE=PERGROUP** option is used, the interval is a $100(1 - 2\alpha)\%$ mean confidence interval shown along with the equivalence bounds. The inclusion of this interval completely within the bounds is indicative of a significant p -value.

If the analysis is not an equivalence analysis, or if the **TYPE=PERGROUP** option is used, then the confidence level is $100(1 - \alpha)\%$. If the **SHOWH0** *global-plot-option* is used, then the null value for the test is shown.

If the **SIDES=L** or **SIDES=U** option is used in the **PROC TTEST** statement, then the unbounded side of the one-sided interval is represented with an arrowhead. Note that the actual location of the arrowhead is irrelevant.

If the **WEIGHT** statement is used, then weights are incorporated in the confidence intervals.

Profiles for Paired Designs

For paired designs, a line is drawn for each observation from left to right connecting the first response to the second response. The mean first response and mean second response are connected with a bold line. If the **WEIGHT** statement is used, then the means are weighted means. The more extreme the slope, the stronger the effect. A wide spread of profiles indicates high between-subject variability. Consistent positive slopes indicate strong positive correlation. Widely varying slopes indicate lack of correlation, while consistent negative slopes indicate strong negative correlation.

Profiles over Period for Crossover Designs

For each observation, the response for the first period is connected to the response for second period, regardless of the treatment applied in each period. The means for each treatment sequence are shown in bold. If the **WEIGHT** statement is used, then the means are weighted means.

In the absence of a strong period effect, the profiles for each sequence will appear as mirror images about an imaginary horizontal line in the center. Deviations from symmetry about this imaginary horizontal line indicate a period effect. A wide spread of profiles within sequence indicates high between-subject variability.

The **TYPE=PERIOD** plot is usually less informative than the **TYPE=TREATMENT** plot. The exception is when the period effect is stronger than the treatment effect.

Profiles over Treatment for Crossover Designs

For each observation, the response for the first treatment is connected to the response for the second treatment, regardless of the periods in which they occur. The means for each treatment sequence are shown in bold. If the **WEIGHT** statement is used, then the means are weighted means.

In general, the more extreme the slope, the stronger the treatment effect. Slope differences between the two treatment sequences measure the period effect. A wide spread of profiles within sequence indicates high between-subject variability.

Q-Q Plots

Q-Q plots are useful for diagnosing violations of the normality and homoscedasticity assumptions. If the data in a Q-Q plot come from a normal distribution, the points will cluster tightly around the reference line. You can use the **UNIVARIATE** procedure with the **NORMAL** option to numerically check the normality assumption.

Bootstrap Correlation Plots

The bootstrap correlation plot is useful for visualizing the correlation between the bootstrap mean and standard deviation across bootstrap samples. The elliptical prediction region is the $100(1 - p)\%$ prediction region that assumes a bivariate normal distribution, where p is the value of the **ALPHA=** option in the **PROC TTEST** statement. The more elongated the shape of the ellipse, the higher the correlation.

Examples: TTEST Procedure

Example 125.1: Using Summary Statistics to Compare Group Means

This example, taken from Huntsberger and Billingsley (1989), compares two grazing methods using 32 steers. Half of the steers are allowed to graze continuously while the other half are subjected to controlled grazing time. The researchers want to know if these two grazing methods affect weight gain differently. The data are read by the following DATA step:

```
data graze;
  length GrazeType $ 10;
  input GrazeType $ WtGain @@;
  datalines;
controlled 45    controlled 62
controlled 96    controlled 128
controlled 120   controlled 99
controlled 28    controlled 50
controlled 109   controlled 115
controlled 39    controlled 96
controlled 87    controlled 100
controlled 76    controlled 80
continuous 94    continuous 12
continuous 26    continuous 89
continuous 88    continuous 96
continuous 85    continuous 130
continuous 75    continuous 54
continuous 112   continuous 69
continuous 104   continuous 95
continuous 53    continuous 21
;
```

The variable `GrazeType` denotes the grazing method: “controlled” is controlled grazing and “continuous” is continuous grazing. The dollar sign (\$) following `GrazeType` makes it a character variable, and the trailing at signs (@@) tell the procedure that there is more than one observation per line.

If you have summary data—that is, just means and standard deviations, as computed by PROC MEANS—then you can still use PROC TTEST to perform a simple *t* test analysis. This example demonstrates this mode of input for PROC TTEST. Note, however, that graphics are unavailable when summary statistics are used as input.

The MEANS procedure is invoked to create a data set of summary statistics with the following statements:

```
proc sort;
  by GrazeType;
run;

proc means data=graze noprint;
  var WtGain;
  by GrazeType;
  output out=newgraze;
run;
```

The NOPRINT option eliminates all printed output from the MEANS procedure. The **VAR** statement tells PROC MEANS to compute summary statistics for the WtGain variable, and the **BY** statement requests a separate set of summary statistics for each level of GrazeType. The OUTPUT OUT= statement tells PROC MEANS to put the summary statistics into a data set called newgraze so that it can be used in subsequent procedures. This new data set is displayed in [Output 125.1.1](#) by using PROC PRINT as follows:

```
proc print data=newgraze;
run;
```

The **_STAT_** variable contains the names of the statistics, and the GrazeType variable indicates which group the statistic is from.

Output 125.1.1 Output Data Set of Summary Statistics

Obs	GrazeType	_TYPE_	_FREQ_	_STAT_	WtGain
1	continuous	0	16	N	16.000
2	continuous	0	16	MIN	12.000
3	continuous	0	16	MAX	130.000
4	continuous	0	16	MEAN	75.188
5	continuous	0	16	STD	33.812
6	controlled	0	16	N	16.000
7	controlled	0	16	MIN	28.000
8	controlled	0	16	MAX	128.000
9	controlled	0	16	MEAN	83.125
10	controlled	0	16	STD	30.535

The following statements invoke PROC TTEST with the newgraze data set, as denoted by the **DATA=** option:

```
proc ttest data=newgraze;
  class GrazeType;
  var WtGain;
run;
```

The **CLASS** statement contains the variable that distinguishes between the groups being compared, in this case GrazeType. The summary statistics and confidence intervals are displayed first, as shown in [Output 125.1.2](#).

Output 125.1.2 Summary Statistics and Confidence Limits

The TTEST Procedure

Variable: WtGain

GrazeType	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
continuous		16	75.1875	33.8117	8.4529	12.0000	130.0
controlled		16	83.1250	30.5350	7.6337	28.0000	128.0
Diff (1-2)	Pooled		-7.9375	32.2150	11.3897		
Diff (1-2)	Satterthwaite		-7.9375		11.3897		

Output 125.1.2 *continued*

GrazeType	Method	95%					
		Mean	95% CL Mean		Std Dev	CL Std Dev	
continuous		75.1875	57.1705	93.2045	33.8117	24.9768	52.3300
controlled		83.1250	66.8541	99.3959	30.5350	22.5563	47.2587
Diff (1-2)	Pooled	-7.9375	-31.1984	15.3234	32.2150	25.7434	43.0609
Diff (1-2)	Satterthwaite	-7.9375	-31.2085	15.3335			

In [Output 125.1.2](#), The GrazeType column specifies the group for which the statistics are computed. For each class, the sample size, mean, standard deviation and standard error, and maximum and minimum values are displayed. The confidence bounds for the mean are also displayed.

[Output 125.1.3](#) shows the results of tests for equal group means and equal variances.

Output 125.1.3 *t Tests*

Method	Variances	DF	t Value	Pr > t
Pooled	Equal	30	-0.70	0.4912
Satterthwaite	Unequal	29.694	-0.70	0.4913

Equality of Variances				
Method	Num DF	Den DF	F Value	Pr > F
Folded F	15	15	1.23	0.6981

A group test statistic for the equality of means is reported for both equal and unequal variances. Both tests indicate a lack of evidence for a significant difference between grazing methods ($t = -0.70$ and $p = 0.4912$ for the pooled test, $t = -0.70$ and $p = 0.4913$ for the Satterthwaite test). The equality of variances test does not indicate a significant difference in the two variances ($F' = 1.23$, $p = 0.6981$). Note that this test assumes that the observations in both data sets are normally distributed; this assumption can be checked in PROC UNIVARIATE by using the NORMAL option with the raw data.

Although the ability to use summary statistics as input is useful if you lack access to the original data, some of the output that would otherwise be produced in an analysis on the original data is unavailable. There are also limitations on the designs and distributional assumptions that can be used with summary statistics as input. For more information, see the section “[Input Data Set of Statistics](#)” on page 10492.

Example 125.2: One-Sample Comparison with the FREQ Statement

This example examines children’s reading skills. The data consist of Degree of Reading Power (DRP) test scores from 44 third-grade children and are taken from Moore (1995, p. 337). Their scores are given in the following DATA step:

```
data read;
  input score count @@;
  datalines;
40 2   47 2   52 2   26 1   19 2
25 2   35 4   39 1   26 1   48 1
14 2   22 1   42 1   34 2   33 2
18 1   15 1   29 1   41 2   44 1
51 1   43 1   27 2   46 2   28 1
49 1   31 1   28 1   54 1   45 1
;
```

The following statements invoke the TTEST procedure to test if the mean test score is equal to 30.

```
ods graphics on;

proc ttest data=read h0=30;
    var score;
    freq count;
run;

ods graphics off;
```

The count variable contains the frequency of occurrence of each test score; this is specified in the **FREQ** statement. The output, shown in [Output 125.2.1](#), contains the results.

Output 125.2.1 TTEST Results

The TTEST Procedure

Variable: score

Frequency: count

N	Mean	Std Dev	Std Err	Minimum	Maximum
44	34.8636	11.2303	1.6930	14.0000	54.0000

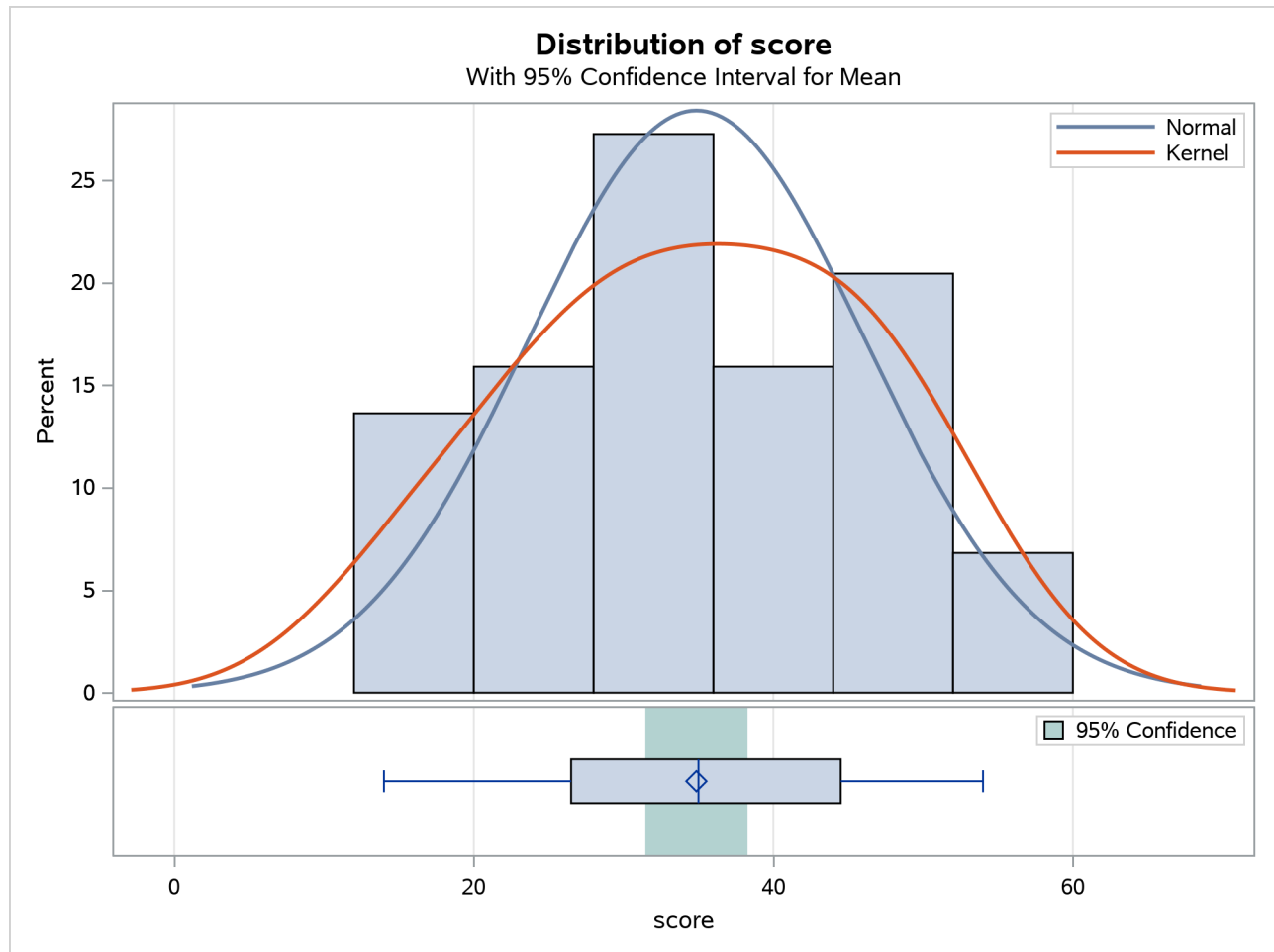
				95%	
Mean	95% CL Mean	Std Dev	CL	Std Dev	
34.8636	31.4493 38.2780	11.2303	9.2788	14.2291	

DF	t Value	Pr > t
43	2.87	0.0063

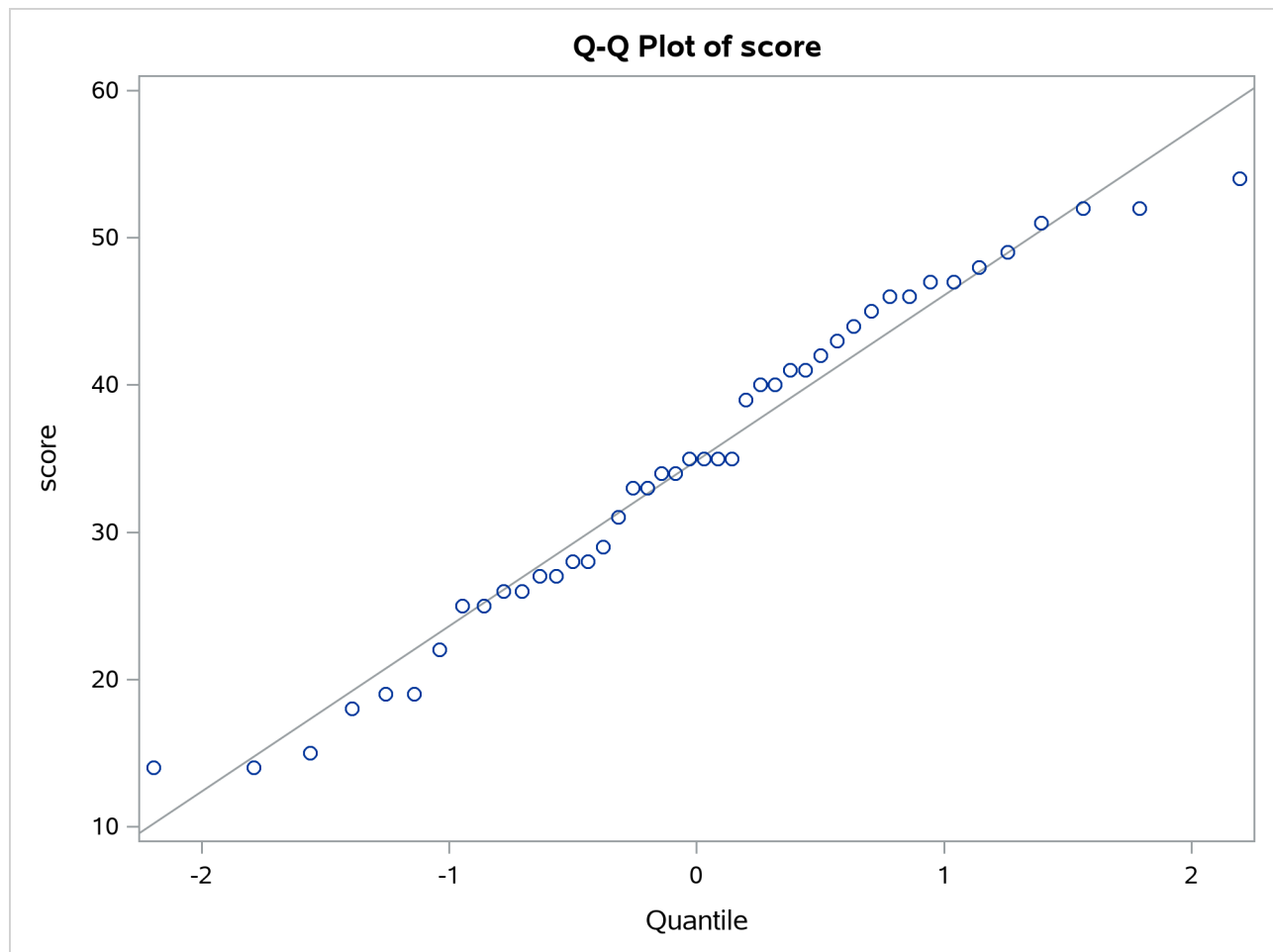
The SAS log states that 30 observations and two variables have been read. However, the sample size given in the TTEST output is N=44. This is due to specifying the count variable in the **FREQ** statement. The test is significant ($t = 2.87$, $p = 0.0063$) at the 5% level, so you can conclude that the mean test score is different from 30.

The summary panel in [Output 125.2.2](#) shows a histogram with overlaid normal and kernel densities, a box plot, and the 95% confidence interval for the mean.

Output 125.2.2 Summary Panel



The Q-Q plot in [Output 125.2.3](#) assesses the normality assumption.

Output 125.2.3 Q-Q Plot

The tight clustering of the points around the diagonal line is consistent with the normality assumption. You could use the UNIVARIATE procedure with the NORMAL option to numerically check the normality assumption.

Example 125.3: Paired Comparisons

When it is not feasible to assume that two groups of data are independent, and a natural pairing of the data exists, it is advantageous to use an analysis that takes the correlation into account. Using this correlation results in higher power to detect existing differences between the means. The differences between paired observations are assumed to be normally distributed. Some examples of this natural pairing are as follows:

- pre- and post-test scores for a student receiving tutoring
- fuel efficiency readings of two fuel types observed on the same automobile
- sunburn scores for two sunblock lotions, one applied to the individual's right arm, one to the left arm
- political attitude scores of husbands and wives

In this example, taken from the *SUGI Supplemental Library User's Guide, Version 5 Edition*, a stimulus is being examined to determine its effect on systolic blood pressure. Twelve men participate in the study. Each man's systolic blood pressure is measured both before and after the stimulus is applied. The following statements input the data:

```
data pressure;
  input SBPbefore SBPafter @@;
  datalines;
120 128   124 131   130 131   118 127
140 132   128 125   140 141   135 137
126 118   130 132   126 129   127 135
;
```

The variables SBPbefore and SBPafter denote the systolic blood pressure before and after the stimulus, respectively.

The statements to perform the test follow:

```
ods graphics on;

proc ttest;
  paired SBPbefore*SBPafter;
run;

ods graphics off;
```

The **PAIRED** statement is used to test whether the mean change in systolic blood pressure is significantly different from zero. The tabular output is displayed in [Output 125.3.1](#).

Output 125.3.1 TTEST Results

The TTEST Procedure

Difference: SBPbefore - SBPafter

N	Mean	Std Dev	Std Err	Minimum	Maximum
12	-1.8333	5.8284	1.6825	-9.0000	8.0000

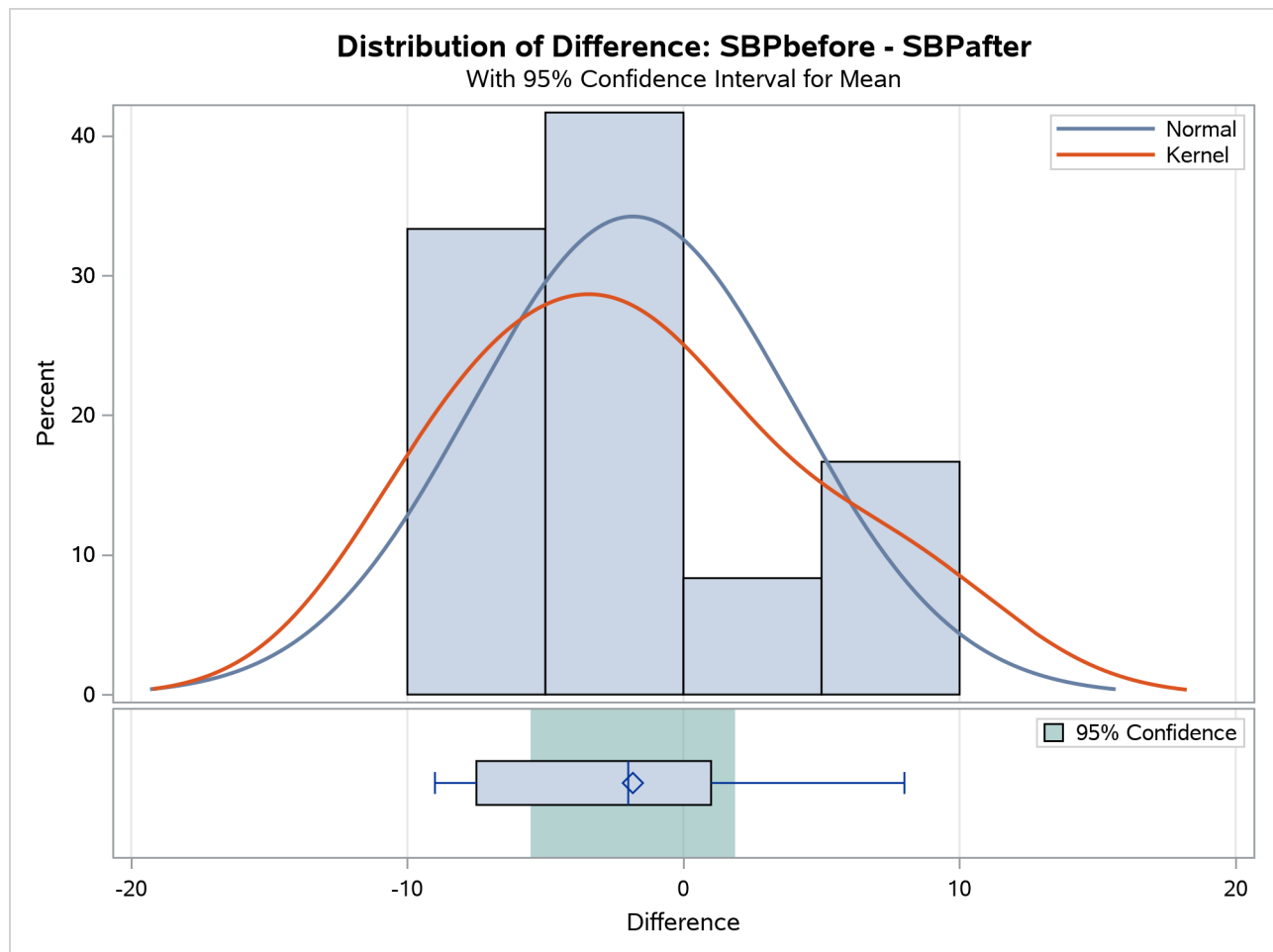
95%					
Mean	95% CL Mean	Std Dev	CL Std Dev		
-1.8333	-5.5365	1.8698	5.8284	4.1288	9.8958

DF	t Value	Pr > t
11	-1.09	0.2992

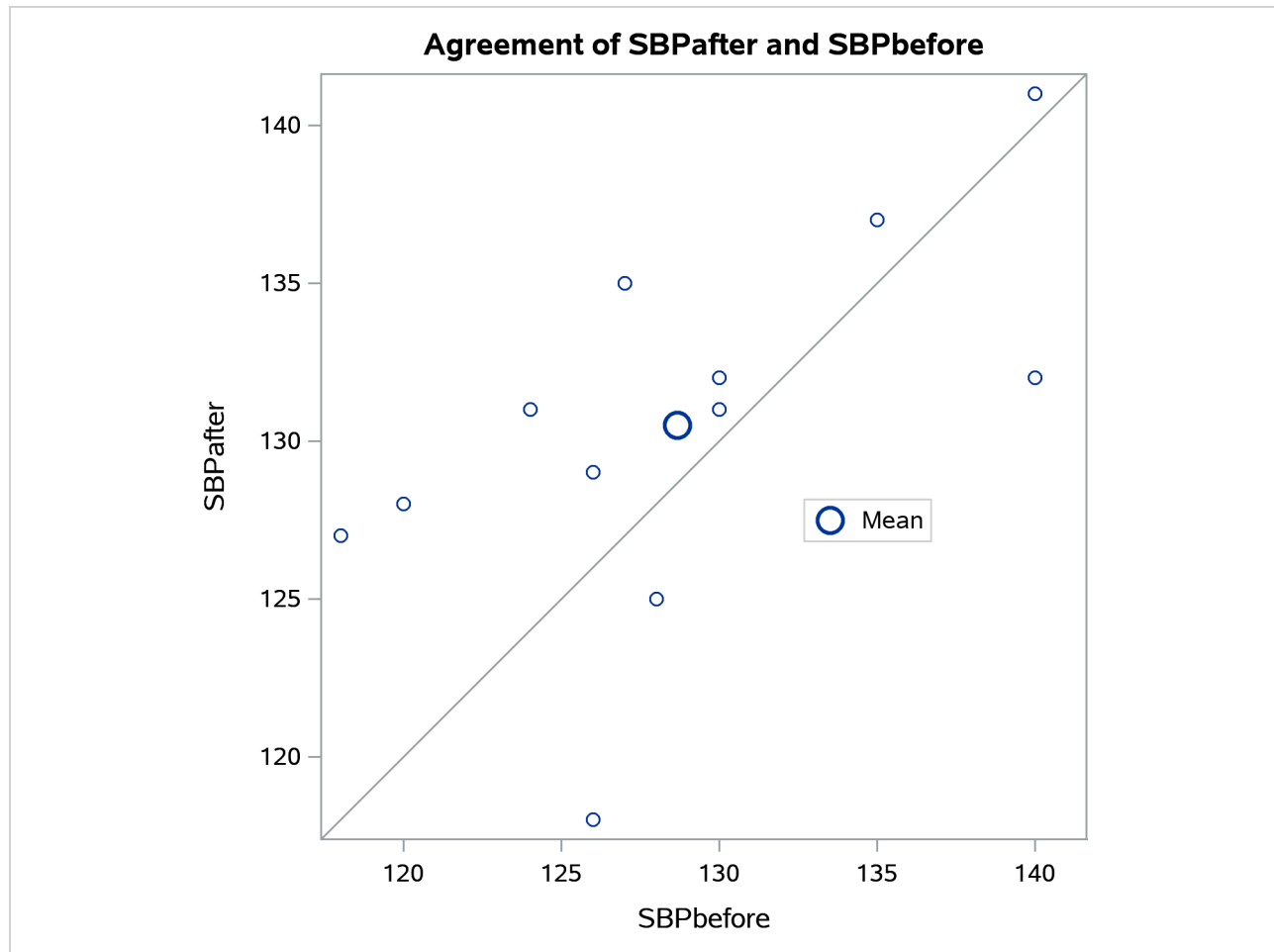
The variables SBPbefore and SBPafter are the paired variables with a sample size of 12. The summary statistics of the difference are displayed (mean, standard deviation, and standard error) along with their confidence limits. The minimum and maximum differences are also displayed. The t test is not significant ($t = -1.09$, $p = 0.2992$), indicating that the stimuli did not significantly affect systolic blood pressure.

The summary panel in [Output 125.3.2](#) shows a histogram, normal and kernel densities, box plot, and $100(1 - \alpha)\% = 95\%$ confidence interval of the SBPbefore – SBPafter difference.

Output 125.3.2 Summary Panel

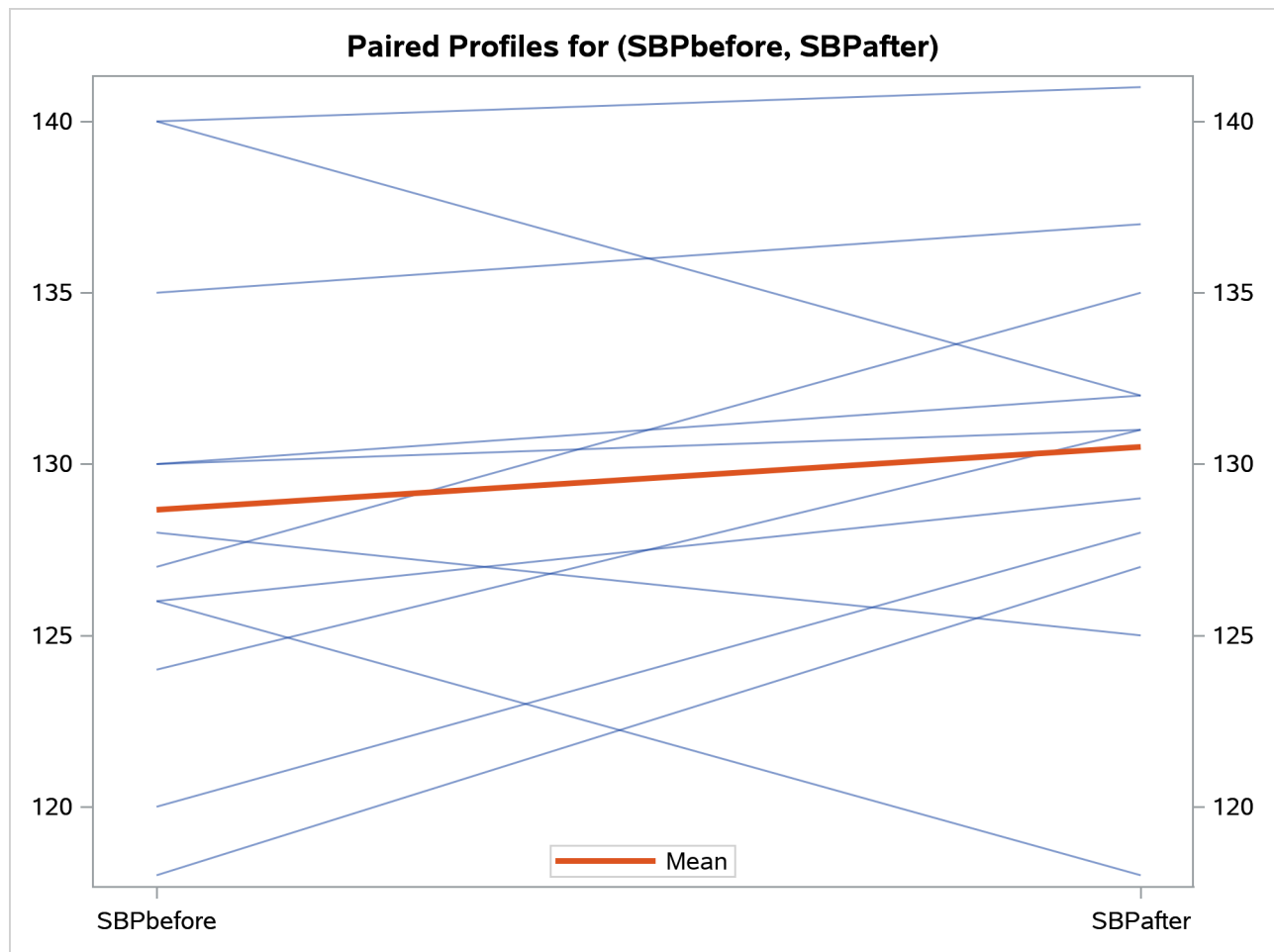


The agreement plot in [Output 125.3.3](#) reveals that only three men have higher blood pressure before the stimulus than after.

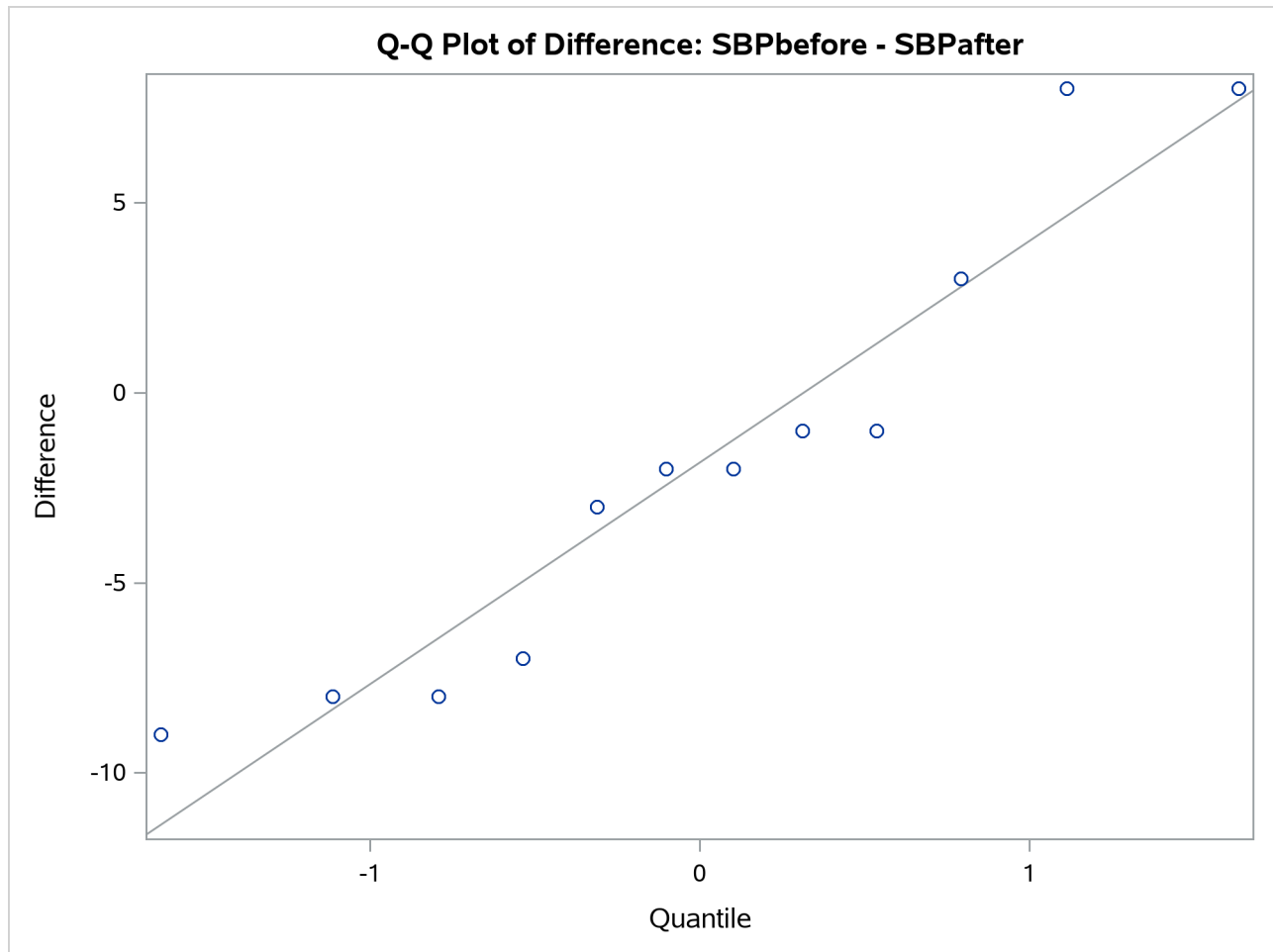
Output 125.3.3 Agreement of Treatments

But the differences for these men are relatively large, keeping the mean difference only slightly negative.

The profiles plot in [Output 125.3.4](#) is a different view of the same information contained in [Output 125.3.3](#), plotting the blood pressure from before to after the stimulus.

Output 125.3.4 Profiles over Treatments

The Q-Q plot in [Output 125.3.5](#) assesses the normality assumption.

Output 125.3.5 Q-Q Plot

The Q-Q plot shows no obvious deviations from normality. You can check the assumption of normality more rigorously by using PROC UNIVARIATE with the NORMAL option.

Example 125.4: AB/BA Crossover Design

Senn (2002, Chapter 3) discusses a study comparing the effectiveness of two bronchodilators, formoterol (“for”) and salbutamol (“sal”), in the treatment of childhood asthma. A total of 13 children are recruited for an AB/BA crossover design. A random sample of 7 of the children are assigned to the treatment sequence for/sal, receiving a dose of formoterol upon an initial visit (“period 1”) and then a dose of salbutamol upon a later visit (“period 2”). The other 6 children are assigned to the sequence sal/for, receiving the treatments in the reverse order but otherwise in a similar manner. Periods 1 and 2 are sufficiently spaced so that no carryover effects are suspected. After a child inhales a dose of a bronchodilator, peak expiratory flow (PEF) is measured. Higher PEF indicates greater effectiveness. The data are assumed to be approximately normally distributed.

The data set is generated with the following statements:

```
data asthma;
  input Drug1 $ Drug2 $ PEF1 PEF2 @@;
  datalines;
for sal 310 270   for sal 310 260   for sal 370 300
for sal 410 390   for sal 250 210   for sal 380 350
for sal 330 365
sal for 370 385   sal for 310 400   sal for 380 410
sal for 290 320   sal for 260 340   sal for 90  220
;
```

You can display the data by using the following statements, which produce [Output 125.4.1](#):

```
proc print data=asthma;
run;
```

Output 125.4.1 Asthma Study Data

Obs	Drug1	Drug2	PEF1	PEF2
1	for	sal	310	270
2	for	sal	310	260
3	for	sal	370	300
4	for	sal	410	390
5	for	sal	250	210
6	for	sal	380	350
7	for	sal	330	365
8	sal	for	370	385
9	sal	for	310	400
10	sal	for	380	410
11	sal	for	290	320
12	sal	for	260	340
13	sal	for	90	220

The variables PEF1 and PEF2 represent the responses for the first and second periods, respectively. The variables Drug1 and Drug2 represent the treatment in each period.

You can analyze this crossover design by using the **CROSSOVER=** option after a slash (/) in the **VAR** statement:

```
ods graphics on;

proc ttest data=asthma plots=interval;
  var PEF1 PEF2 / crossover= (Drug1 Drug2);
run;

ods graphics off;
```

With the default **PROC TTEST** options **TEST=DIFF** and **DIST=NORMAL** and the lack of the **IGNOREPERIOD** option in the **VAR** statement, both the treatment difference and the period difference are assessed. The **PROC TTEST** default options **H0=0**, **SIDES=2**, and **ALPHA=0.05** specify a two-sided analysis with 95% confidence limits comparing treatment and period differences to a default difference of zero. The default **CI=EQUAL** option in the **PROC TTEST** statement requests equal-tailed confidence intervals for

standard deviations. The **PLOTS=INTERVAL** option produces **TYPE=TREATMENT** confidence intervals, in addition to the default plots **AGREEMENT(TYPE=TREATMENT)**, **BOX**, **HISTOGRAM**, **PROFILES(TYPE=TREATMENT)**, and **QQ**.

Output 125.4.2 summarizes the response and treatment variables for each period.

Output 125.4.2 Crossover Variable Information

The TTEST Procedure

Response Variables: PEF1, PEF2

Crossover Variable Information		
Period	Response	Treatment
1	PEF1	Drug1
2	PEF2	Drug2

Output 125.4.3 displays basic summary statistics (sample size, mean, standard deviation, standard error, minimum, and maximum) for each of the four cells in the design, the treatment difference within each treatment sequence, the overall treatment difference, and the overall period difference.

Output 125.4.3 Statistics

Sequence	Treatment	Period	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
1	for	1		7	337.1	53.7631	20.3206	250.0	410.0
2	for	2		6	345.8	70.8814	28.9372	220.0	410.0
2	sal	1		6	283.3	105.4	43.0245	90.0000	380.0
1	sal	2		7	306.4	64.7247	24.4636	210.0	390.0
1	Diff (1-2)			7	30.7143	32.9682	12.4608	-35.0000	70.0000
2	Diff (1-2)			6	62.5000	44.6934	18.2460	15.0000	130.0
Both	Diff (1-2)		Pooled		46.6071	19.3702	10.7766		
Both	Diff (1-2)		Satterthwaite		46.6071		11.0475		
Both		Diff (1-2)	Pooled		-15.8929	19.3702	10.7766		
Both		Diff (1-2)	Satterthwaite		-15.8929		11.0475		

The treatment difference “Diff (1–2)” corresponds to the “for” treatment minus the “sal” treatment, because “for” appears before “sal” in the output, according to the **ORDER=MIXED** default **PROC TTEST** option. Its mean estimate is 46.6071, favoring formoterol over salbutamol.

The standard deviation (Std Dev) reported for a “difference” is actually the pooled standard deviation across both treatment sequence (for/sal and sal/for), assuming equal variances. The standard error (Std Err) is the standard deviation of the mean estimate.

The top half of the table in Output 125.4.4 shows 95% two-sided confidence limits for the means for the same criteria addressed in the table in Output 125.4.3.

Output 125.4.4 Confidence Limits

Sequence	Treatment	Period	Method	Mean	95% CL Mean	Std Dev	95% CL Std Dev	
1	for	1		337.1	287.4	386.9	53.7631	34.6446
2	for	2		345.8	271.4	420.2	70.8814	44.2447
2	sal	1		283.3	172.7	393.9	105.4	65.7841
1	sal	2		306.4	246.6	366.3	64.7247	41.7082
1	Diff (1-2)			30.7143	0.2238	61.2048	32.9682	21.2445
2	Diff (1-2)			62.5000	15.5972	109.4	44.6934	27.8980
Both	Diff (1-2)			Pooled	46.6071	22.8881	70.3262	19.3702
Both	Diff (1-2)			Satterthwaite	46.6071	21.6585	71.5558	32.8882
Both	Diff (1-2)			Pooled	-15.8929	-39.6119	7.8262	19.3702
Both	Diff (1-2)			Satterthwaite	-15.8929	-40.8415	9.0558	32.8882

For the mean differences, both pooled (assuming equal variances for both treatment sequences) and Satterthwaite (assuming unequal variances) intervals are shown. For example, the pooled confidence limits for the overall treatment mean difference (for – sal) assuming equal variances are 22.8881 and 70.3262.

The bottom half of [Output 125.4.4](#) shows 95% equal-tailed confidence limits for the standard deviations within each cell and for the treatment difference within each sequence. It also shows confidence limits for the pooled common standard deviation assuming equal variances. Note that the pooled standard deviation of 19.3702 and associated confidence limits 13.7217 and 32.8882 apply to both difference tests (treatment and period), since each of those tests involves the same pooled standard deviation.

[Output 125.4.5](#) shows the results of *t* tests of treatment and period differences.

Output 125.4.5 *t* Tests

Treatment	Period	Method	Variances	DF	t Value	Pr > t
Diff (1-2)		Pooled	Equal	11	4.32	0.0012
Diff (1-2)		Satterthwaite	Unequal	9.1017	4.22	0.0022
	Diff (1-2)	Pooled	Equal	11	-1.47	0.1683
	Diff (1-2)	Satterthwaite	Unequal	9.1017	-1.44	0.1838

Both pooled and Satterthwaite versions of the test of treatment difference are highly significant ($p = 0.0012$ and $p = 0.0022$), and both versions of the test of period difference are insignificant ($p = 0.1683$ and $p = 0.1838$).

The folded *F* test of equal variances in each treatment sequence is shown in [Output 125.4.6](#).

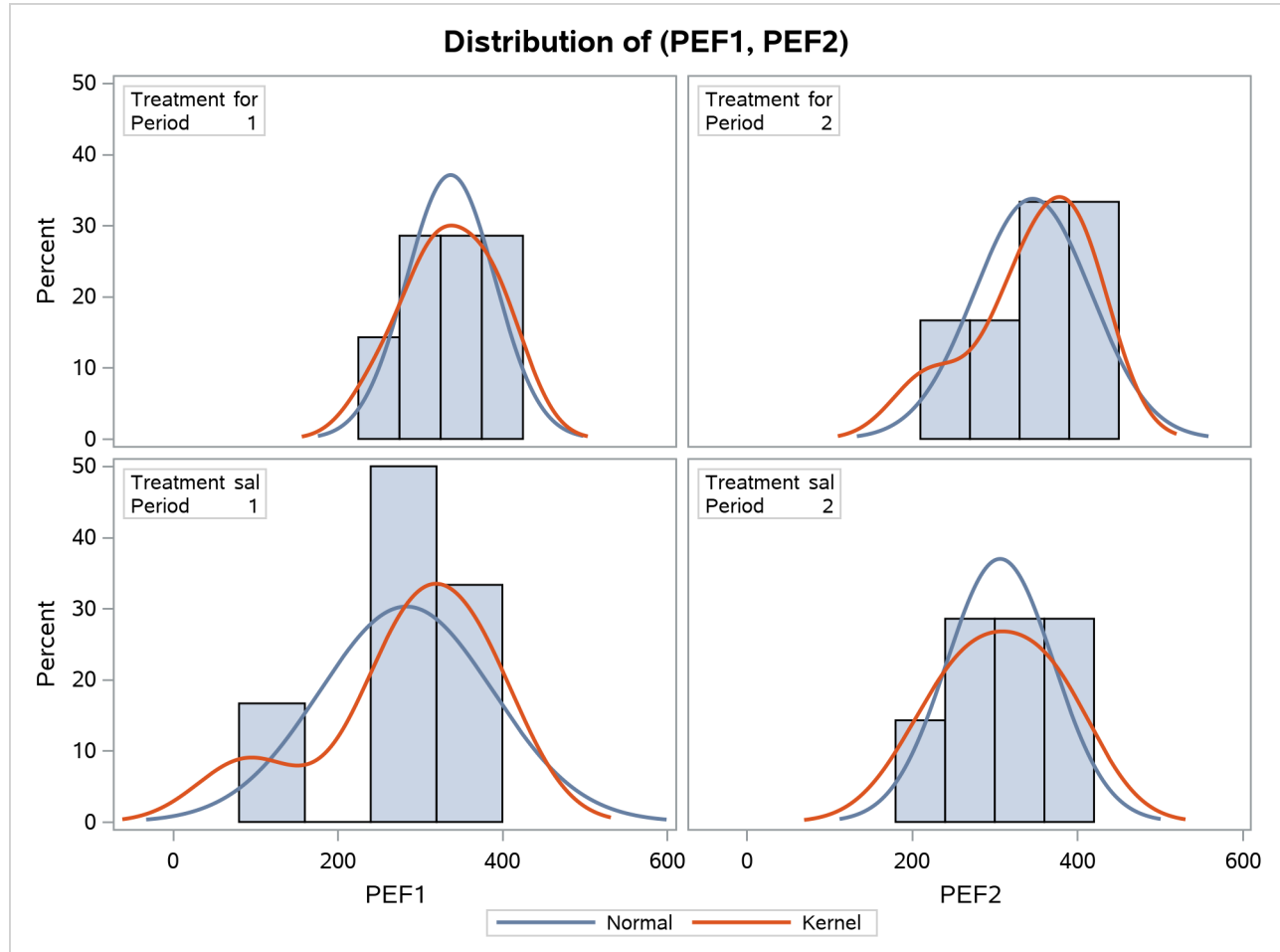
Output 125.4.6 Equality of Variances Test

Equality of Variances				
Method	Num DF	Den DF	F Value	Pr > F
Folded F	5	6	1.84	0.4797

The insignificant result ($p = 0.48$) implies a lack of evidence for unequal variances. However, it does not demonstrate equal variances, and it is not very robust to deviations from normality.

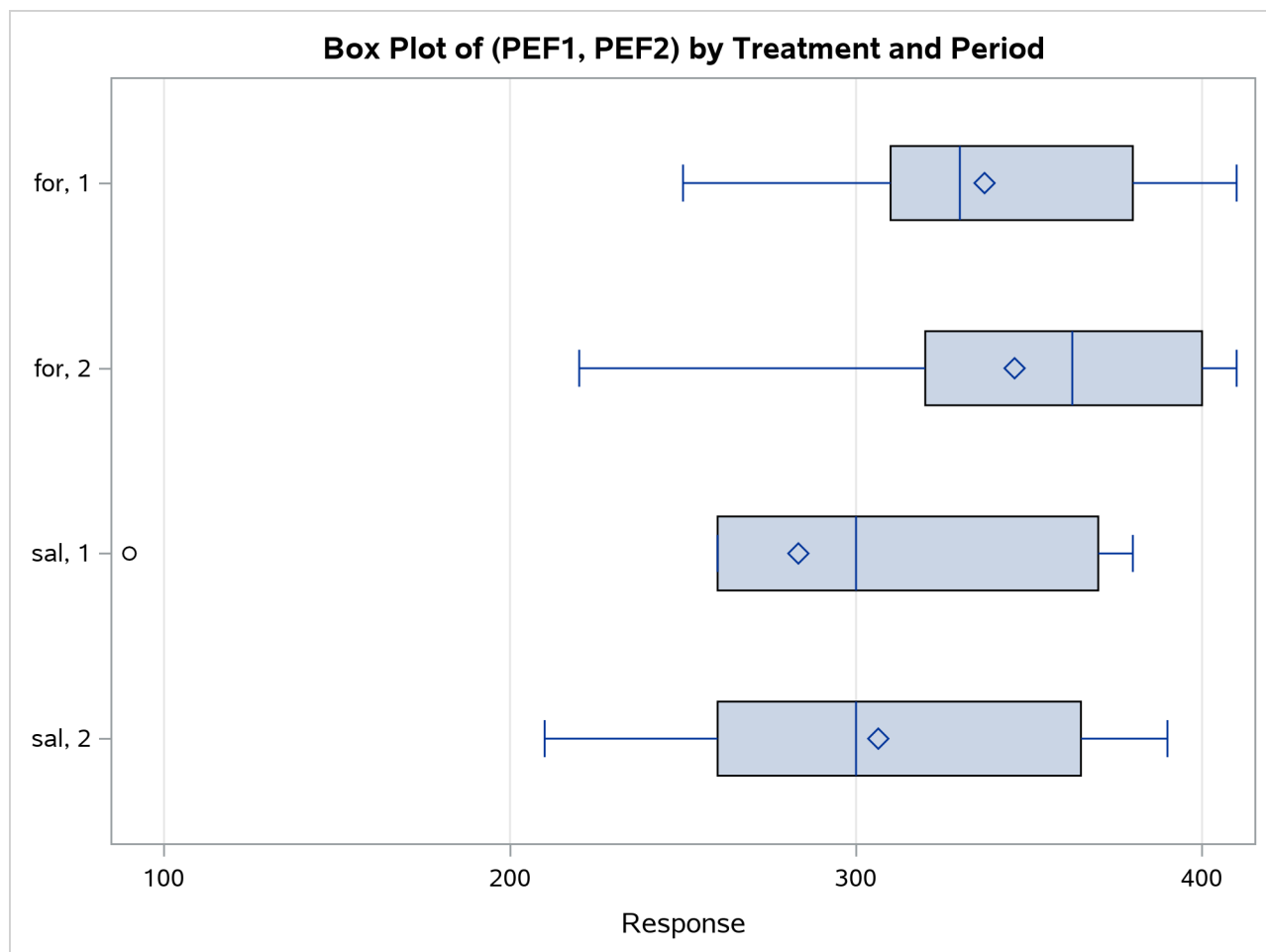
Output 125.4.7 shows the distribution of the response variables PEF1 and PEF2 within each of the four cells (combinations of two treatments and two periods) of the AB/BA crossover design, in terms of histograms and normal and kernel density estimates.

Output 125.4.7 Comparative Histograms



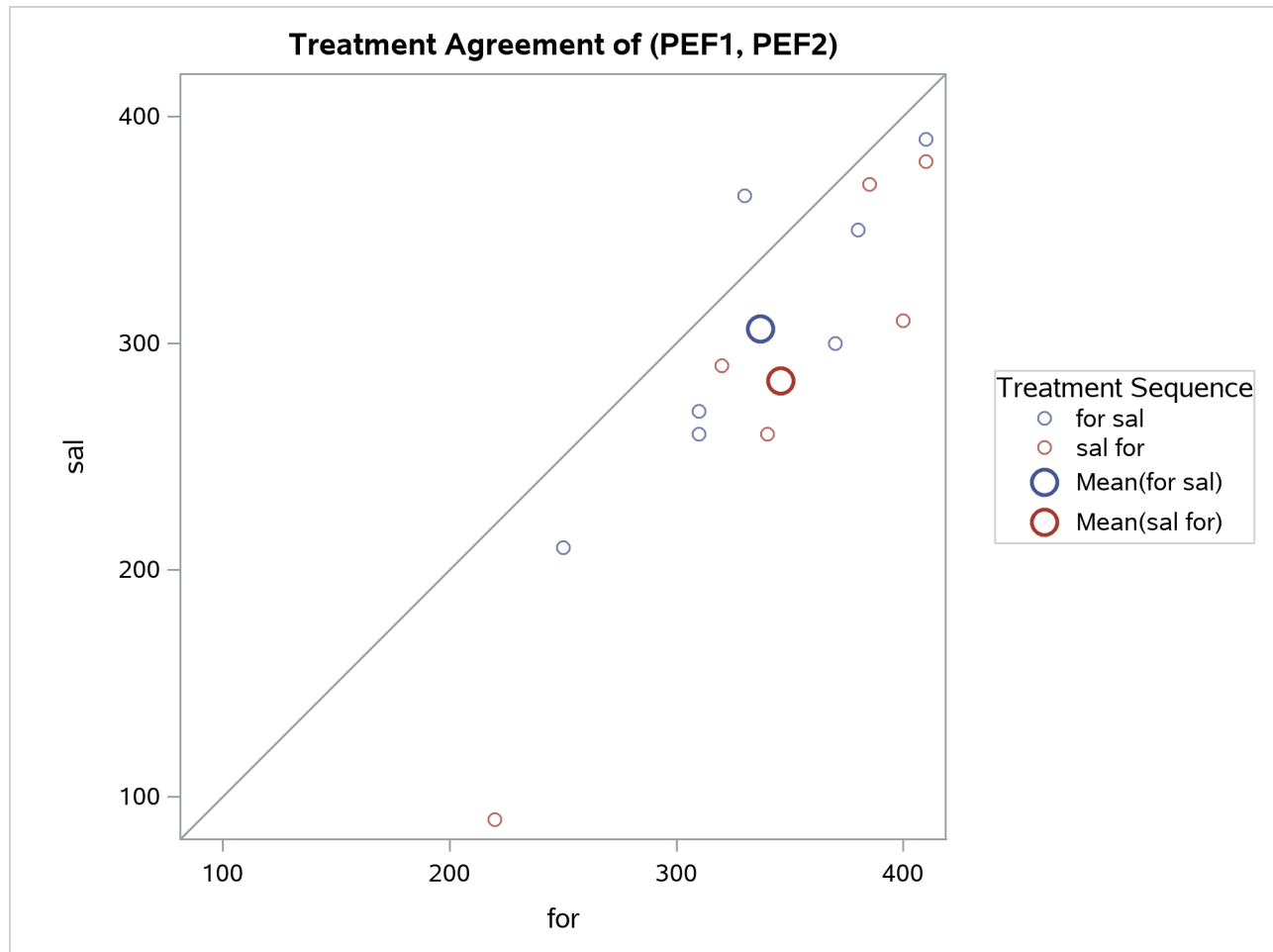
The distributions for the first treatment sequence (for/sal) appear to be somewhat symmetric, and the distributions for the sal/for sequence appear to be skewed to the left.

Output 125.4.8 shows a similar distributional summary but in terms of box plots.

Output 125.4.8 Comparative Box Plots

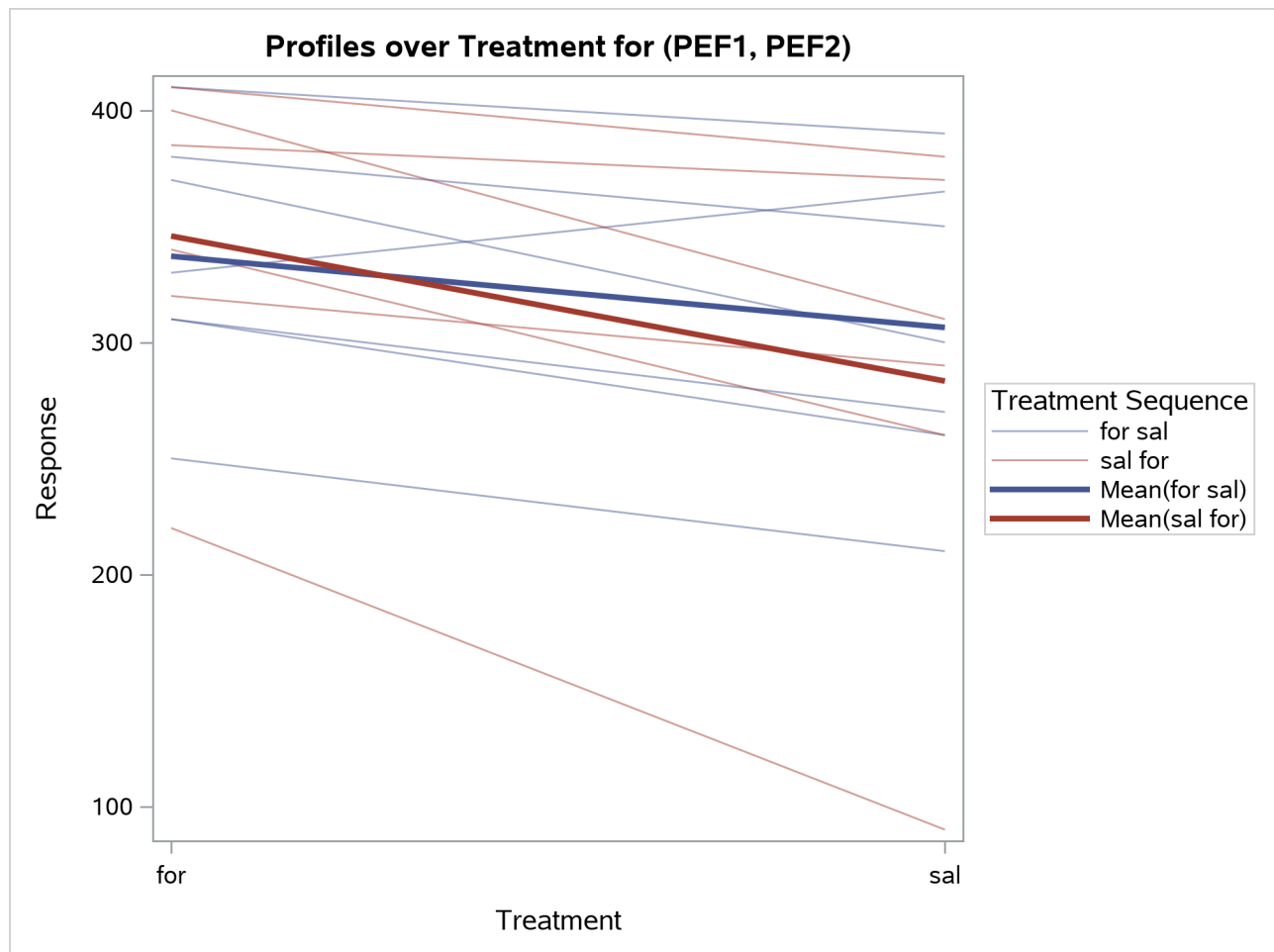
The relative locations of means and medians in each box plot corroborate the fact that the distributions for the sal/for sequence are skewed to the left. The distributions for the for/sal sequence appear to be skewed slightly to the right. The box plot for the salbutamol treatment in the first period shows an outlier (the circle on the far left side of the plot).

The treatment agreement plot in [Output 125.4.9](#) reveals that only a single observation has a higher peak expiratory flow for salbutamol.

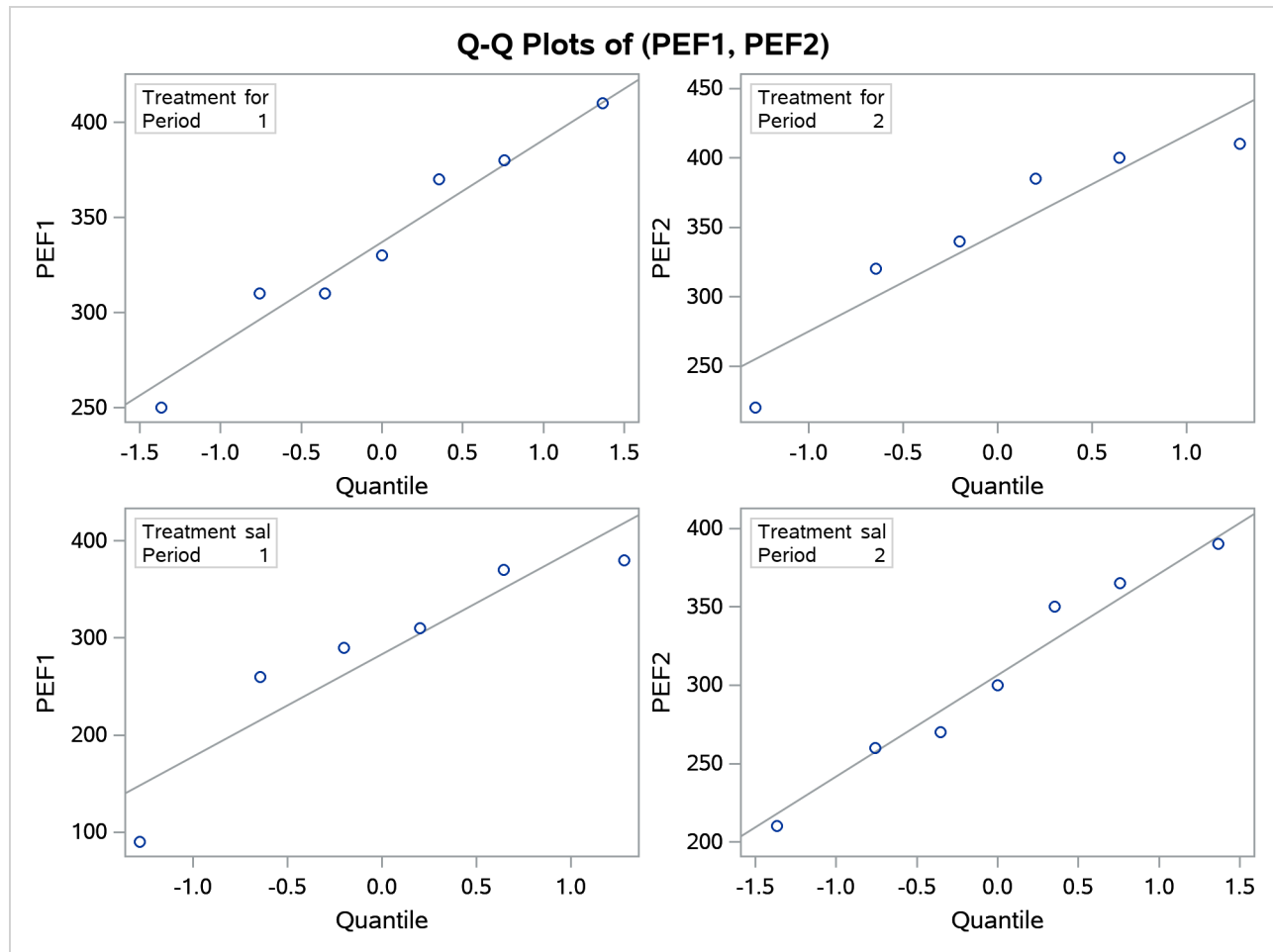
Output 125.4.9 Agreement of Treatments Plot

The mean for the sal/for treatment sequence is farther from the diagonal equivalence line, revealing that the treatment difference is more pronounced for the 6 observations in the sal/for sequence than for the 7 observations in the for/sal sequence. This fact is also seen numerically in [Output 125.4.3](#) and [Output 125.4.4](#), which show within-sequence treatment differences of 30.7 for for/sal and 62.5 for sal/for.

The profiles over treatment plot in [Output 125.4.10](#) is a different view of the same information contained in [Output 125.4.9](#), plotting the profiles from formoterol to salbutamol treatments. The lone observation for which the peak expiratory flow is higher for salbutamol appears as the only line with negative slope.

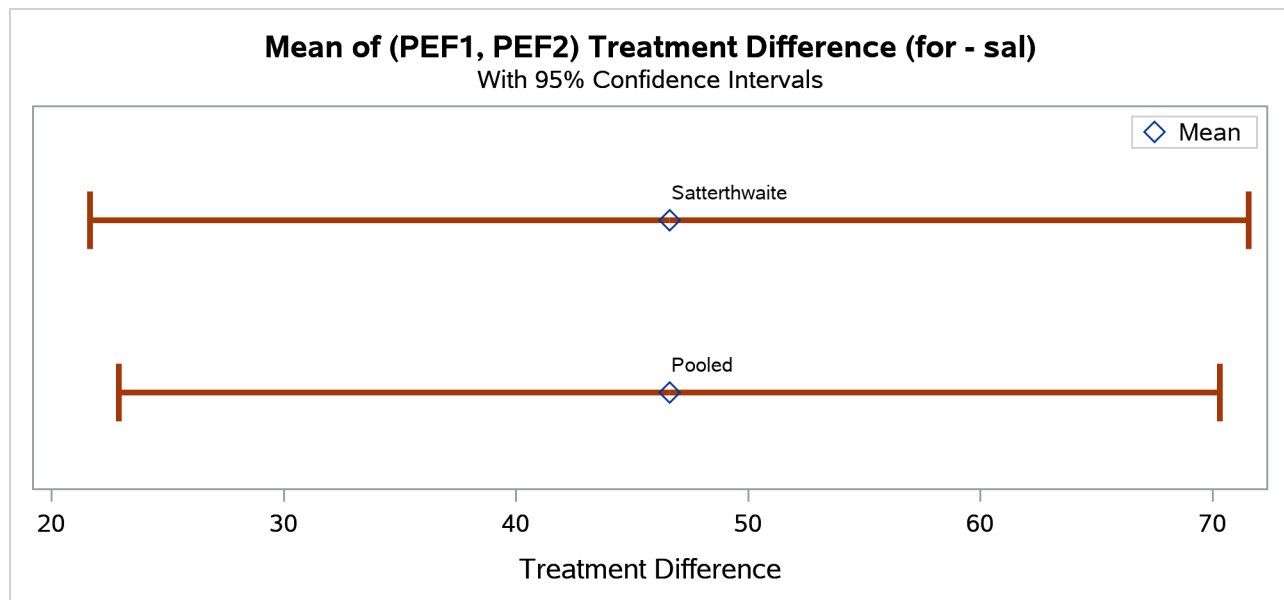
Output 125.4.10 Profiles over Treatment

The Q-Q plots in [Output 125.4.11](#) assess normality assumption within each of the four cells of the design.

Output 125.4.11 Q-Q Plots

The two Q-Q plots for the sal/for sequence (lower left and upper right) suggest some possible normality violations in the tails, but the sample size is too small to make any strong conclusions. You could use the UNIVARIATE procedure with the NORMAL option to numerically check the normality assumptions.

Finally, [Output 125.4.12](#) shows both pooled and Satterthwaite two-sided 95% confidence intervals for the treatment difference.

Output 125.4.12 Confidence Intervals for Treatment Difference

The pooled interval is slightly smaller than the Satterthwaite interval. (This is not always the case.)

Example 125.5: Equivalence Testing with Lognormal Data

Wellek (2003, p. 212) discusses an average bioequivalence study comparing the AUC (area under serum-concentration curve) measurements for two different drugs, denoted “Test” and “Reference,” over a period of 20 hours. This example looks at a portion of Wellek’s data, conducting an equivalence analysis with a paired design that uses AUC values on the original scale (assumed to be lognormally distributed). Each subject in the study received the Test drug upon one visit and then the Reference drug upon a later visit, sufficiently spaced so that no carryover effects would occur.

The goal is to test whether the geometric mean AUC ratio between Test and Reference is between 0.8 and 1.25, corresponding to the traditional FDA (80%, 125%) equivalence criterion. See the section “[Arithmetic and Geometric Means](#)” on page 10494 for a discussion of the use of geometric means for lognormal data.

The following SAS statements generate the data set:

```
data auc;
  input TestAUC RefAUC @@;
  datalines;
103.4 90.11 59.92 77.71 68.17 77.71 94.54 97.51
69.48 58.21 72.17 101.3 74.37 79.84 84.44 96.06
96.74 89.30 94.26 97.22 48.52 61.62 95.68 85.80
;
```

You can display the data by using the following statements, which produce [Output 125.5.1](#):

```
proc print data=auc;
run;
```

Output 125.5.1 AUC Data for Test and Reference Drugs

Obs	TestAUC	RefAUC
1	103.40	90.11
2	59.92	77.71
3	68.17	77.71
4	94.54	97.51
5	69.48	58.21
6	72.17	101.30
7	74.37	79.84
8	84.44	96.06
9	96.74	89.30
10	94.26	97.22
11	48.52	61.62
12	95.68	85.80

The TestAUC and RefAUC variables represent the AUC measurements for each subject under the Test and Reference drugs, respectively. Use the following SAS statements to perform the equivalence analysis:

```
ods graphics on;

proc ttest data=auc dist=lognormal tost(0.8, 1.25);
  paired TestAUC*RefAUC;
run;

ods graphics off;
```

The **DIST=LOGNORMAL** option specifies the lognormal distributional assumption and requests an analysis in terms of geometric mean and coefficient of variation. The **TOST** option specifies the equivalence bounds 0.8 and 1.25.

[Output 125.5.2](#) shows basic summary statistics for the ratio of TestAUC to RefAUC.

Output 125.5.2 Summary Statistics

The TTEST Procedure

Ratio: TestAUC / RefAUC

N	Geometric Mean	Coefficient of Variation	Minimum	Maximum
12	0.9412	0.1676	0.7124	1.1936

The geometric mean ratio of 0.9412 is the sample mean of the log-transformed data exponentiated to bring it back to the original scale. So the plasma concentration over the 20-hour period is slightly lower for the Test drug than for the Reference drug. The CV of 0.1676 is the ratio of the standard deviation to the (arithmetic) mean.

Output 125.5.3 shows the $100(1 - \alpha)\% = 95\%$ confidence limits for the geometric mean ratio (0.8467 and 1.0462) and CV (0.1183 and 0.2884).

Output 125.5.3 Confidence Limits

Geometric			Coefficient		
Mean	95% CL	Mean	of Variation	95% CL	CV
0.9412	0.8467	1.0462	0.1676	0.1183	0.2884

Output 125.5.4 shows the $100(1 - 2\alpha)\% = 90\%$ confidence limits for the geometric mean ratio, 0.8634 and 1.0260.

Output 125.5.4 Equivalence Limits

Geometric	Lower			Upper	
Mean	Bound	90% CL	Mean	Bound	Assessment
0.9412	0.8	<	0.8634	1.0260	< 1.25 Equivalent

The assessment of “Equivalent” reflects the fact that these limits are contained within the equivalence bounds 0.8 and 1.25. This result occurs if and only if the p -value of the test is less than the α value specified in the ALPHA= option in the PROC TTEST statement, and it is the reason that $100(1 - 2\alpha)\%$ confidence limits are shown in addition to the usual $100(1 - \alpha)\%$ limits.

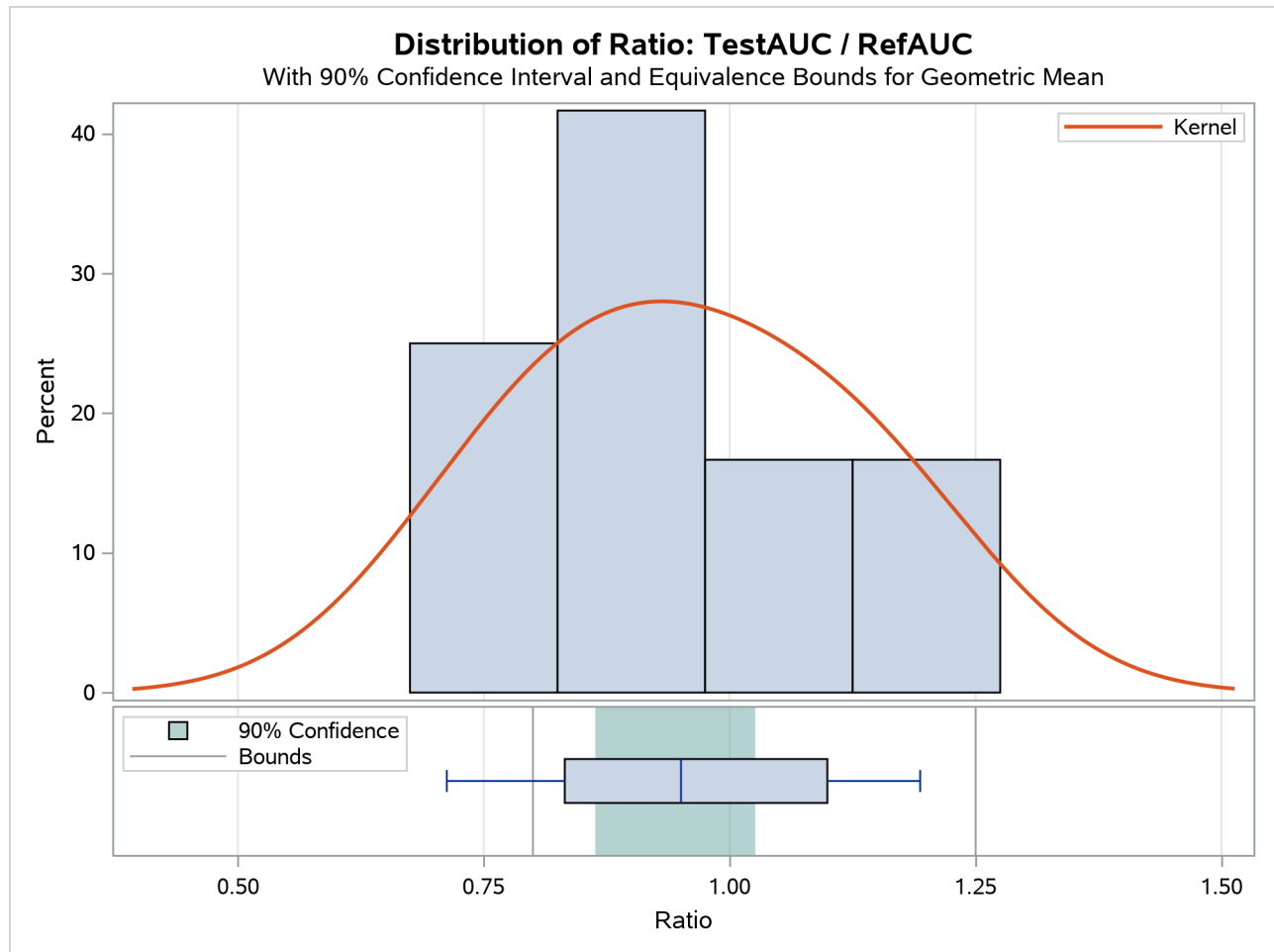
Output 125.5.5 shows the p -values for the two one-sided tests against the upper and lower equivalence bounds.

Output 125.5.5 TOST Equivalence Test

Test	Null	DF	t Value	P-Value
Upper	0.8	11	3.38	0.0031
Lower	1.25	11	-5.90	<.0001
Overall				0.0031

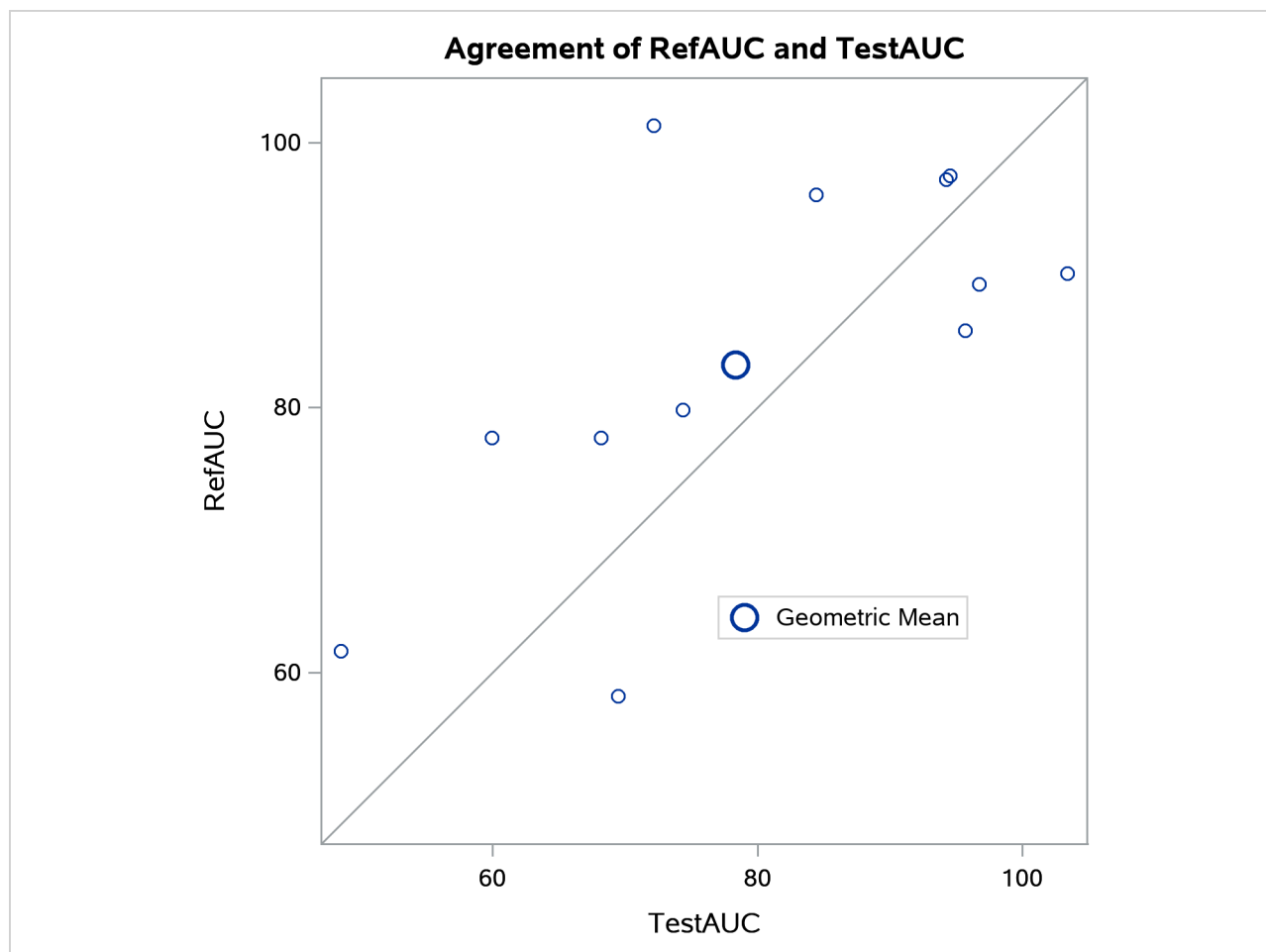
The overall p -value of 0.0031, the larger of the two one-sided p -values, indicates significant evidence of equivalence between the Test and Reference drugs.

The summary panel in Output 125.5.6 shows a histogram, kernel density, box plot, and $100(1 - 2\alpha)\% = 90\%$ confidence interval of the Test-to-Reference ratio of AUC, along with the equivalence bounds.

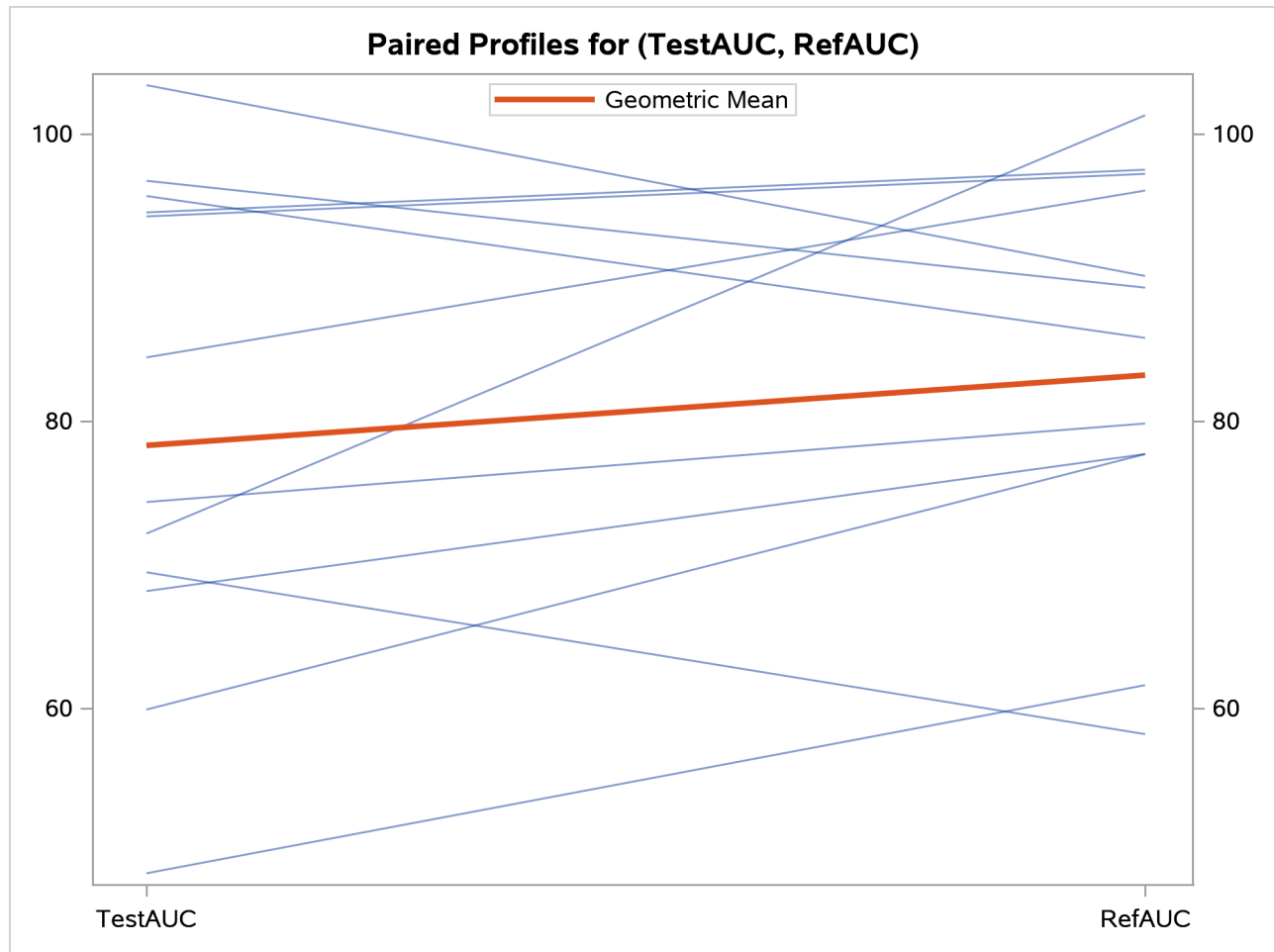
Output 125.5.6 Summary Panel

The confidence interval is closer to the lower equivalence bound than the upper bound and contained entirely within the bounds.

The agreement plot in [Output 125.5.7](#) reveals that the only four subjects with higher AUC for the Test drug are at the far lower or far upper end of the AUC distribution. This might merit further investigation.

Output 125.5.7 Agreement Plot

The profiles plot in [Output 125.5.8](#) is a different view of the same information contained in [Output 125.5.7](#), plotting the AUC from Test to Reference drug.

Output 125.5.8 Profiles Plot

Example 125.6: Bootstrap with Two-Sample Design

As discussed in the section “[Bootstrap Methods](#)” on page 10505, the bootstrap is a useful technique for producing improved estimates of standard error and bias and improved confidence intervals that adjust for narrowness bias and median bias. The following example illustrates the use of the bootstrap for the same golf score data as are analyzed in the Getting Started example in the section “[Comparing Group Means](#)” on page 10473.

The golf scores for males and females in a physical education class are contained in the scores data set, which is created by the following SAS statements:

```
data scores;
  input Gender $ Score @@;
  datalines;
f 75 f 76 f 80 f 77 f 80 f 77 f 73
m 82 m 80 m 85 m 85 m 78 m 87 m 82
;
```

The addition of the **BOOTSTRAP** statement to the SAS statements specified in the section “[Comparing Group Means](#)” on page 10473 requests bootstrap results for the comparison of female and male golf scores, as follows:

```
ods graphics on;

proc ttest ci=equal umpu plots=bootstrap(interval);
  class Gender;
  var Score;
  bootstrap / seed=837;
run;
```

The **SEED=** option in the **BOOTSTRAP** statement is specified to enable reproducibility of the results. Because the **NSAMPLES=** option is not included, PROC TTEST uses 10,000 bootstrap samples by default. Because the **BOOTCI=** option is not specified, PROC TTEST uses bootstrap bias-corrected percentile intervals by default.

The **PLOTS=BOOTSTRAP(INTERVAL)** option produces bootstrap interval plots in addition to the default summary panel, Q-Q, and correlation plots.

[Output 125.6.1](#) shows simple statistics for the female and male golf scores being compared, as well as for the difference of the female and male means. The Gender column indicates the population that corresponds to the statistics in that row, and the Method column indicates the method for estimating the standard deviation, either pooled (assuming equal variances for females and males) or Satterthwaite (assuming unequal variances).

Output 125.6.1 Simple Statistics

The TTEST Procedure

Variable: Score

Gender	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
f		7	76.8571	2.5448	0.9619	73.0000	80.0000
m		7	82.7143	3.1472	1.1895	78.0000	87.0000
Diff (1-2)	Pooled		-5.8571	2.8619	1.5298		
Diff (1-2)	Satterthwaite		-5.8571		1.5298		

Let y_f and y_m denote the random variables for female and male scores, respectively. The mean of -5.8571 in [Output 125.6.1](#) is computed as $\bar{y}_f - \bar{y}_m$, the estimated mean of the difference $y_f - y_m$. The standard deviation of 2.8619 is the pooled estimate of the standard deviation of either y_f or y_m , which are assumed in the pooled method to have equal variances. The standard error of 1.5298 is the estimated standard deviation of $\bar{y}_f - \bar{y}_m$. This standard error is identical for both pooled and Satterthwaite methods because the group sample sizes are equal ($n_f = n_m$).

[Output 125.6.2](#) displays both pooled and Satterthwaite 95% intervals for the mean of the difference $y_f - y_m$. It also shows equal-tailed and uniformly most powerful unbiased confidence limits for the assumed-common standard deviation of y_f and y_m under the assumption of equal variances.

Output 125.6.2 Confidence Limits

Gender	Method	Mean	95% CL	Mean	Std Dev	95% UMPU CL Std Dev			
						CL	Std Dev	CL	Std Dev
f		76.8571	74.5036	79.2107	2.5448	1.6399	5.6039	1.5634	5.2219
m		82.7143	79.8036	85.6249	3.1472	2.0280	6.9303	1.9335	6.4579
Diff (1-2)	Pooled	-5.8571	-9.1902	-2.5241	2.8619	2.0522	4.7242	2.0019	4.5727
Diff (1-2)	Satterthwaite	-5.8571	-9.2064	-2.5078					

Output 125.6.3 shows the bootstrap results for the golf score data.

Output 125.6.3 Bootstrap Analysis with Bias-Corrected Percentile Intervals

Bootstrap Statistics and Confidence Limits						
Gender	Method	Parameter	Std			
			Error	Bias	95% CL	
Diff (1-2)		Mean	1.4184	0.00440	-8.8571	-3.2857
Diff (1-2)	Pooled	Std Dev	0.5776	-0.3472	3.2071	5.2372
Diff (1-2)	Satterthwaite	Std Dev	0.5776	-0.3472	3.2071	5.2372

Each of the 10,000 bootstrap samples in the bootstrap analysis consists of a collection of $n_f = 7$ random draws with replacement from the female scores and $n_m = 7$ random draws with replacement from the male scores. For each of these samples, three statistics are computed:

- the sample mean estimate of the difference $y_f - y_m$
- the pooled standard deviation estimate of $y_f - y_m$, assuming equal variances
- the Satterthwaite standard deviation estimate of $y_f - y_m$, assuming unequal variances

It is these three statistics that correspond to the three rows in [Output 125.6.3](#), identified by the Method and Parameter columns.

The bootstrap estimate of the standard error of the mean difference, 1.4184, is slightly lower than the estimate of 1.5298 from the original sample. The bootstrap estimate of the bias of $\bar{y}_1 - \bar{y}_2$ is 0.0044, very small compared to either estimate of the standard error.

There is only one row for the mean difference parameter in [Output 125.6.3](#) because the bias-corrected percentile interval is invariant to the choice between pooled and Satterthwaite methods for estimating the standard deviation. The 95% bootstrap bias-corrected confidence interval for the mean difference is substantially narrower than either of the t -based confidence intervals shown in [Output 125.6.2](#). This is not too surprising because the bootstrap bias-corrected interval corrects only for *median* bias—that is, a difference between the parameter θ and the median of its distribution—and not for *narrowness* bias. Narrowness bias in this context is the tendency of uncorrected bootstrap percentile intervals to be too narrow, especially for small sample sizes such as in this case ($n_f = n_m = 7$).

The second and third rows in [Output 125.6.3](#) show bootstrap results for the pooled and Satterthwaite estimates, respectively, of the standard deviation of $y_f - y_m$. These estimates are identical to each other—both in the original sample and in the bootstrap results—because the group sample sizes are equal. The bootstrap standard error estimate, 0.5776, has no straightforward basis for comparison among the estimates that are computed

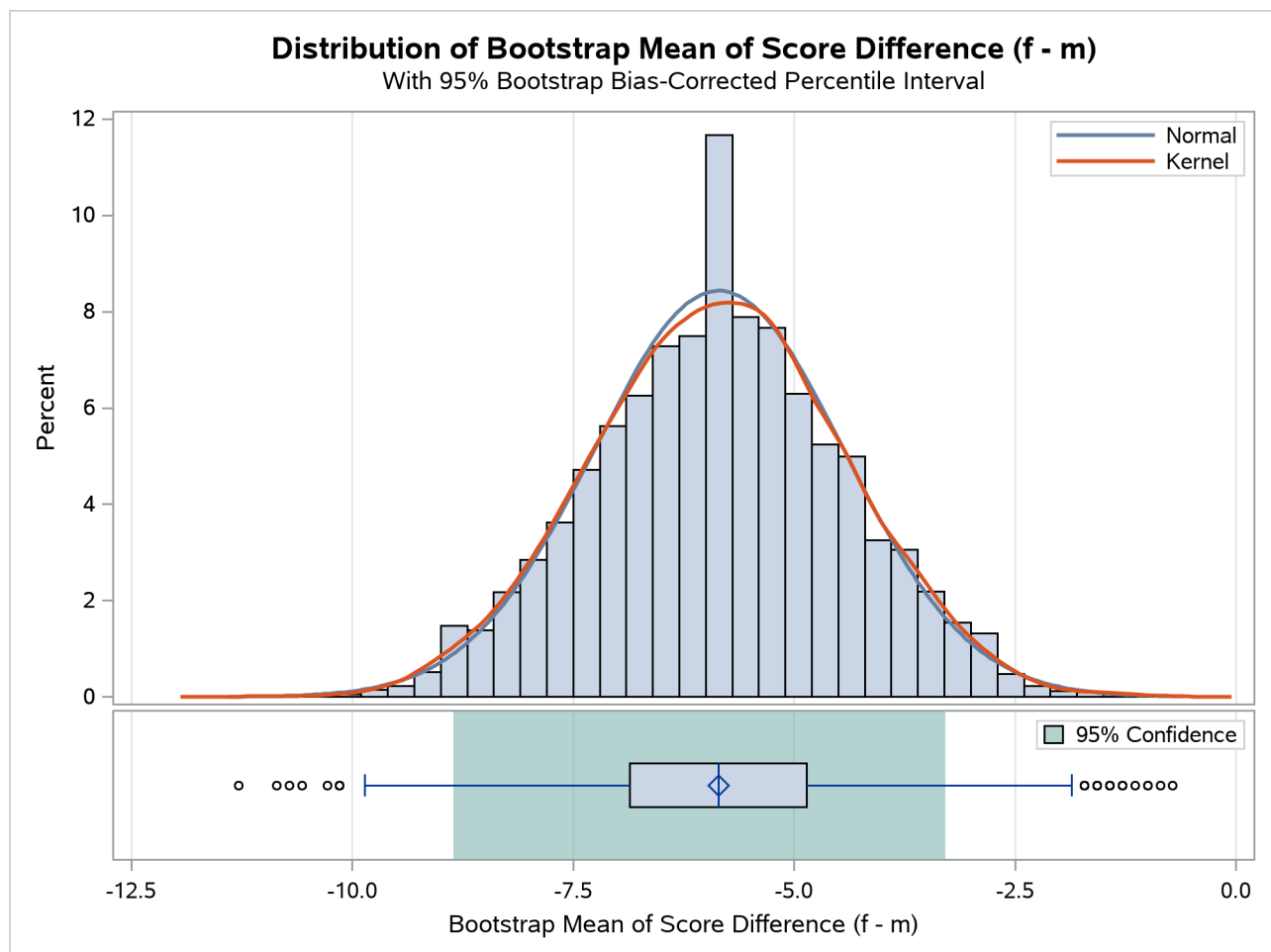
directly from the original sample in [Output 125.6.1](#) and [Output 125.6.2](#) because there is no reasonable closed-form estimate for the standard deviation of a standard deviation estimate. This demonstrates one of the advantages of the bootstrap—that it can produce standard error estimates for any statistical estimator.

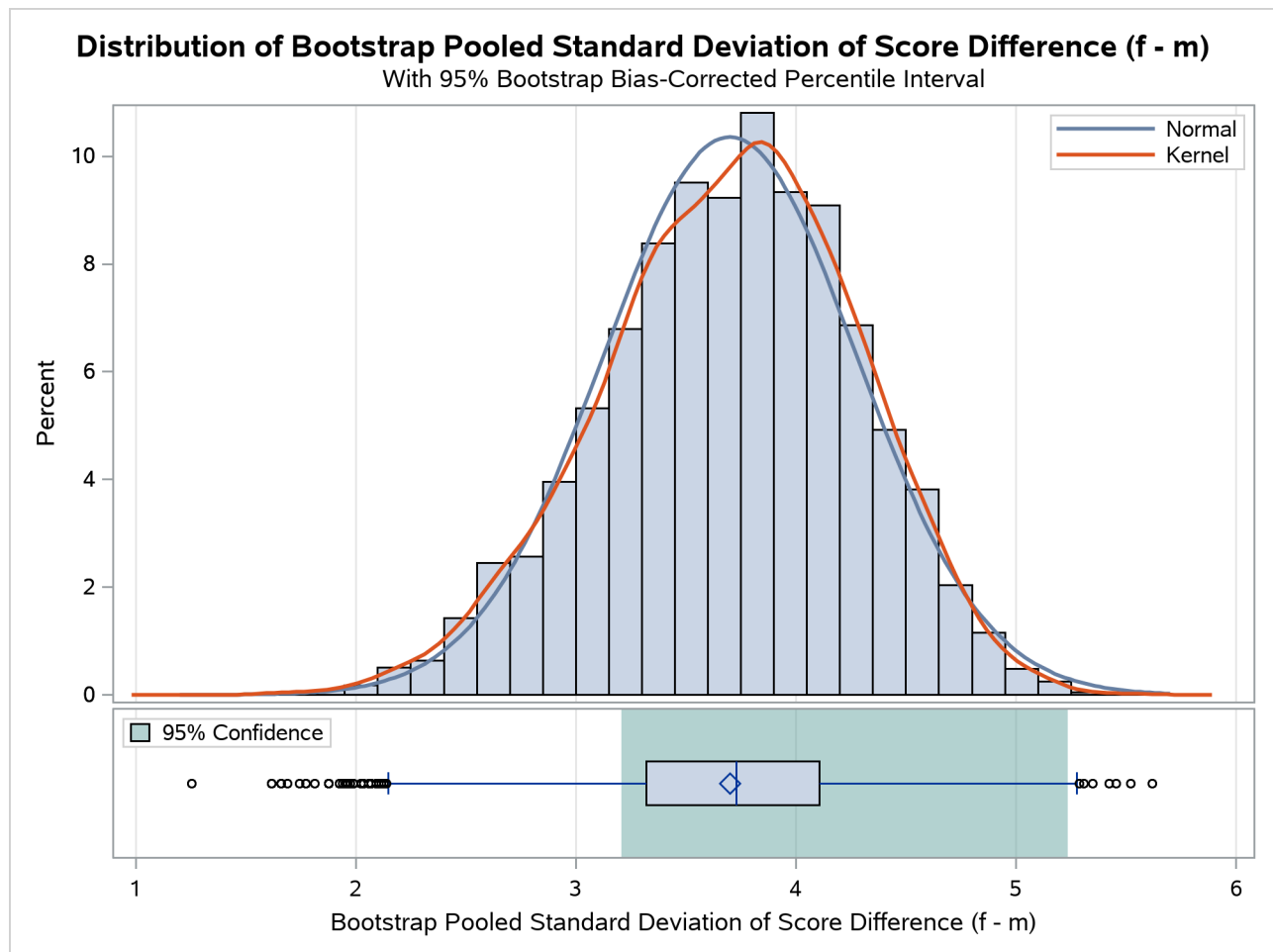
The estimated bias of the standard deviation of the difference is relatively large compared to the standard error and implies that the standard deviation of $y_f - y_m$ is being underestimated in the original sample.

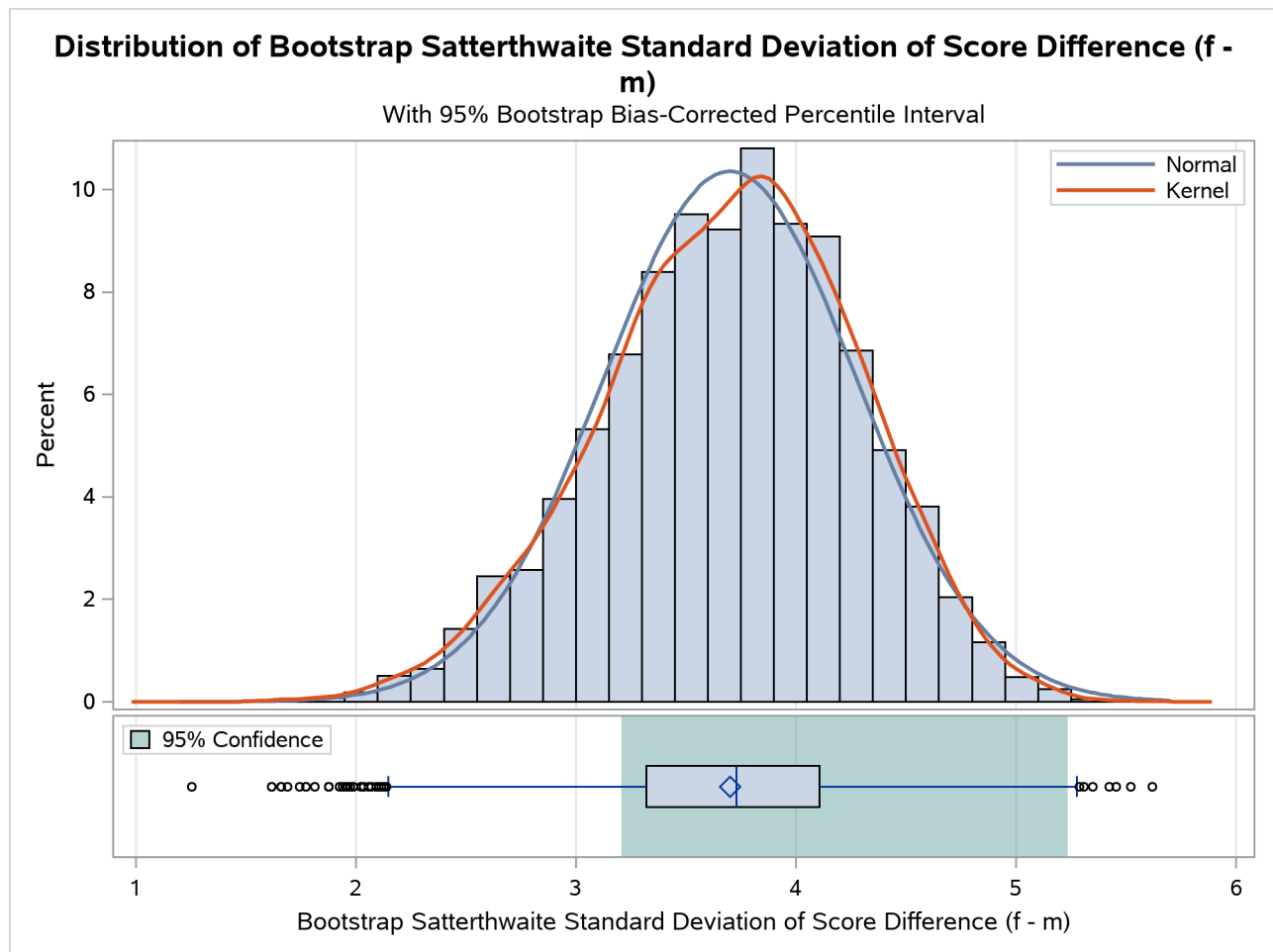
The bootstrap bias-corrected percentile interval for the standard deviation of $y_f - y_m$, (3.2071, 5.2372), cannot be directly compared with the estimate and confidence limits of the pooled standard deviation that are computed from the original sample in [Output 125.6.2](#). However, you can transform the statistics for the pooled standard deviation into statistics for the standard deviation of $y_f - y_m$ simply by multiplying them by $\sqrt{2}$, because the pooled estimate of $\text{Var}(y_f - y_m)$ is $2s_p^2$. The resulting point estimate from the original sample is $2.8619 \times \sqrt{2} = 4.0473$. The transformed equal-tail and UMPU confidence intervals are, respectively, (2.9022, 6.6810) and (2.8311, 6.4668).

The bootstrap summary panels in [Output 125.6.4](#) through [Output 125.6.6](#) show histograms, normal and kernel densities, box plots, and $100(1 - \alpha)\% = 95\%$ bootstrap bias-corrected percentile intervals for the mean, pooled standard deviation, and Satterthwaite standard deviation of the difference between female and male scores.

Output 125.6.4 Summary Panel of Bootstrap Mean

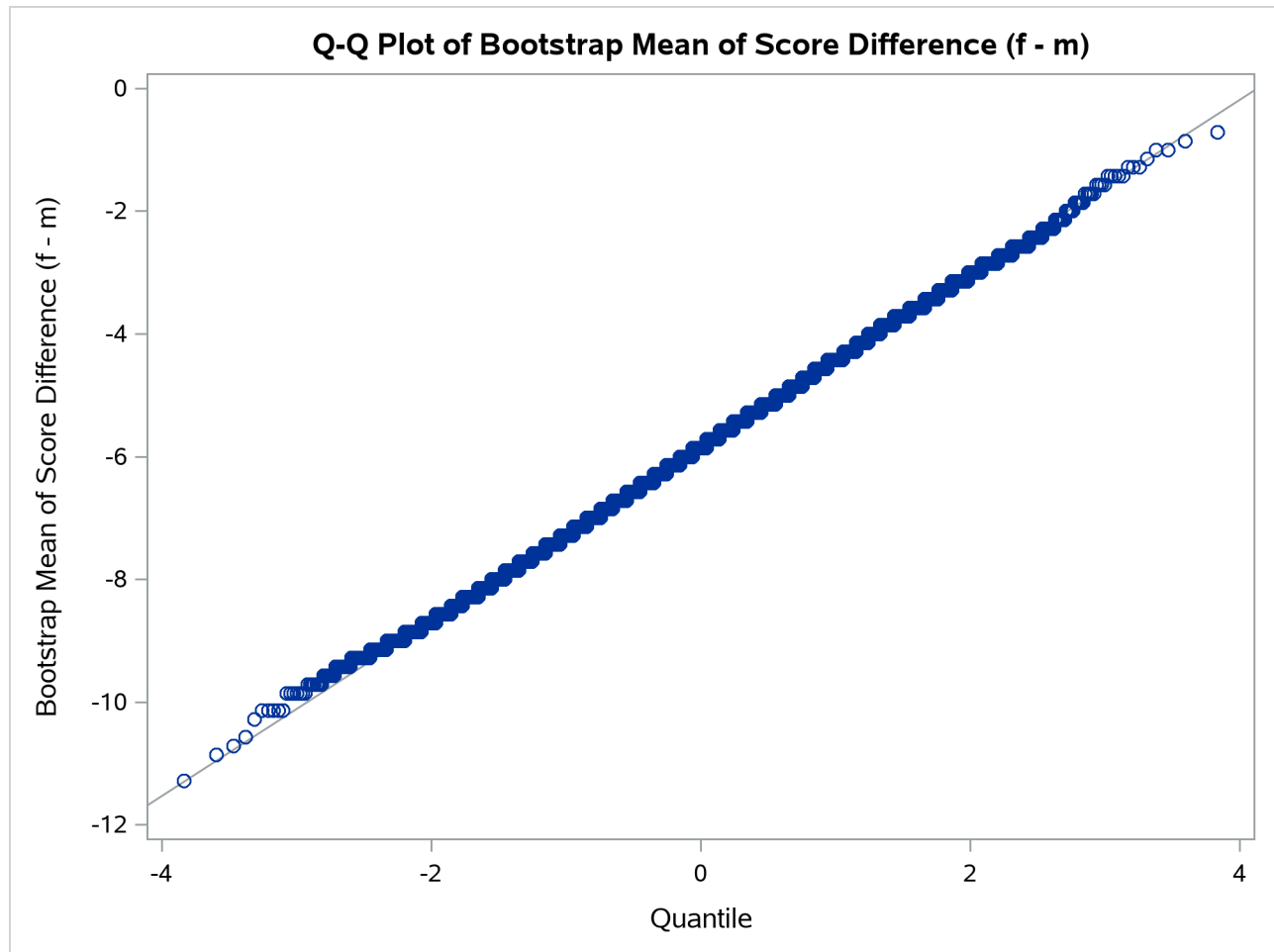


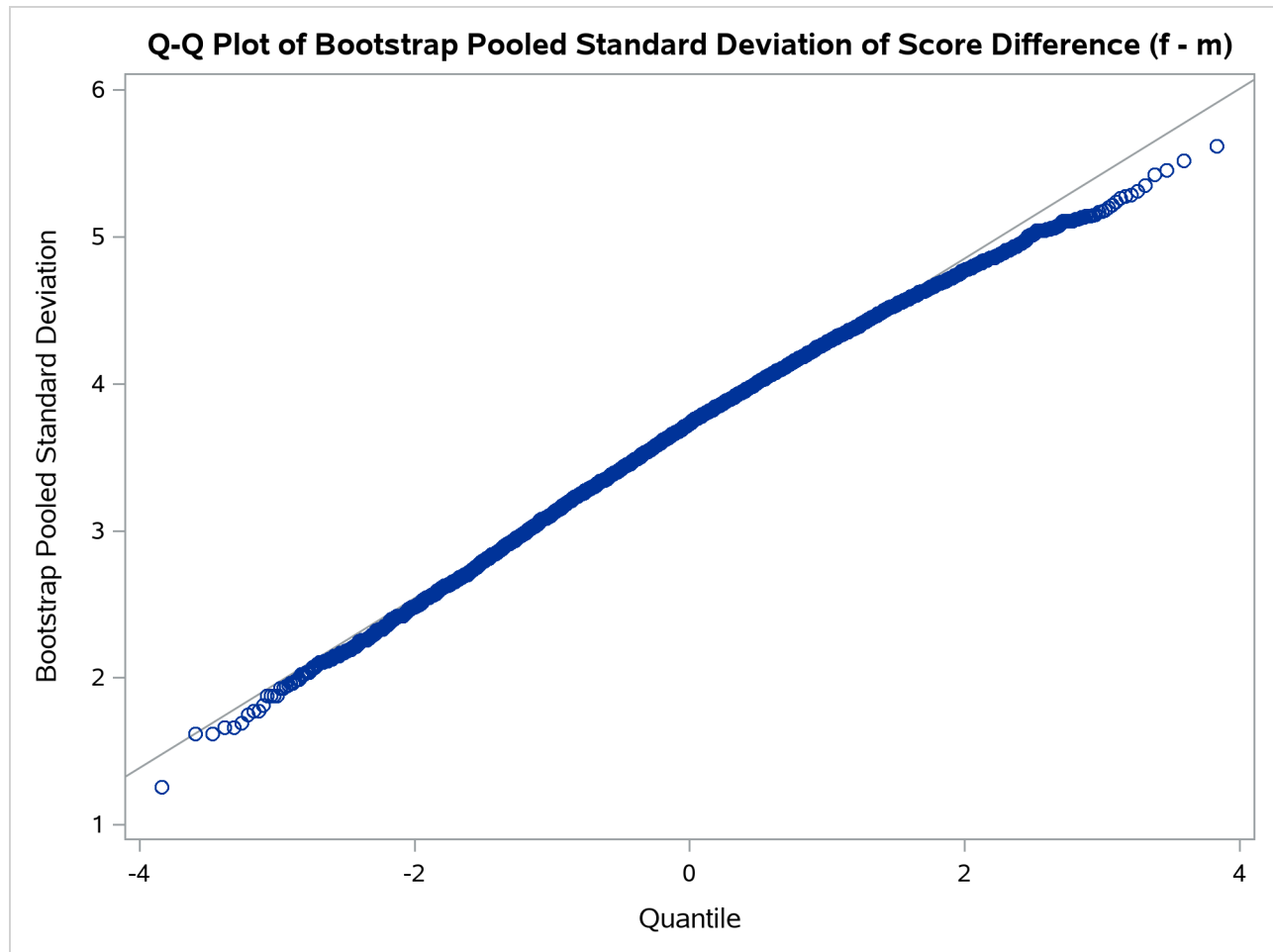
Output 125.6.5 Summary Panel of Bootstrap Pooled Standard Deviation

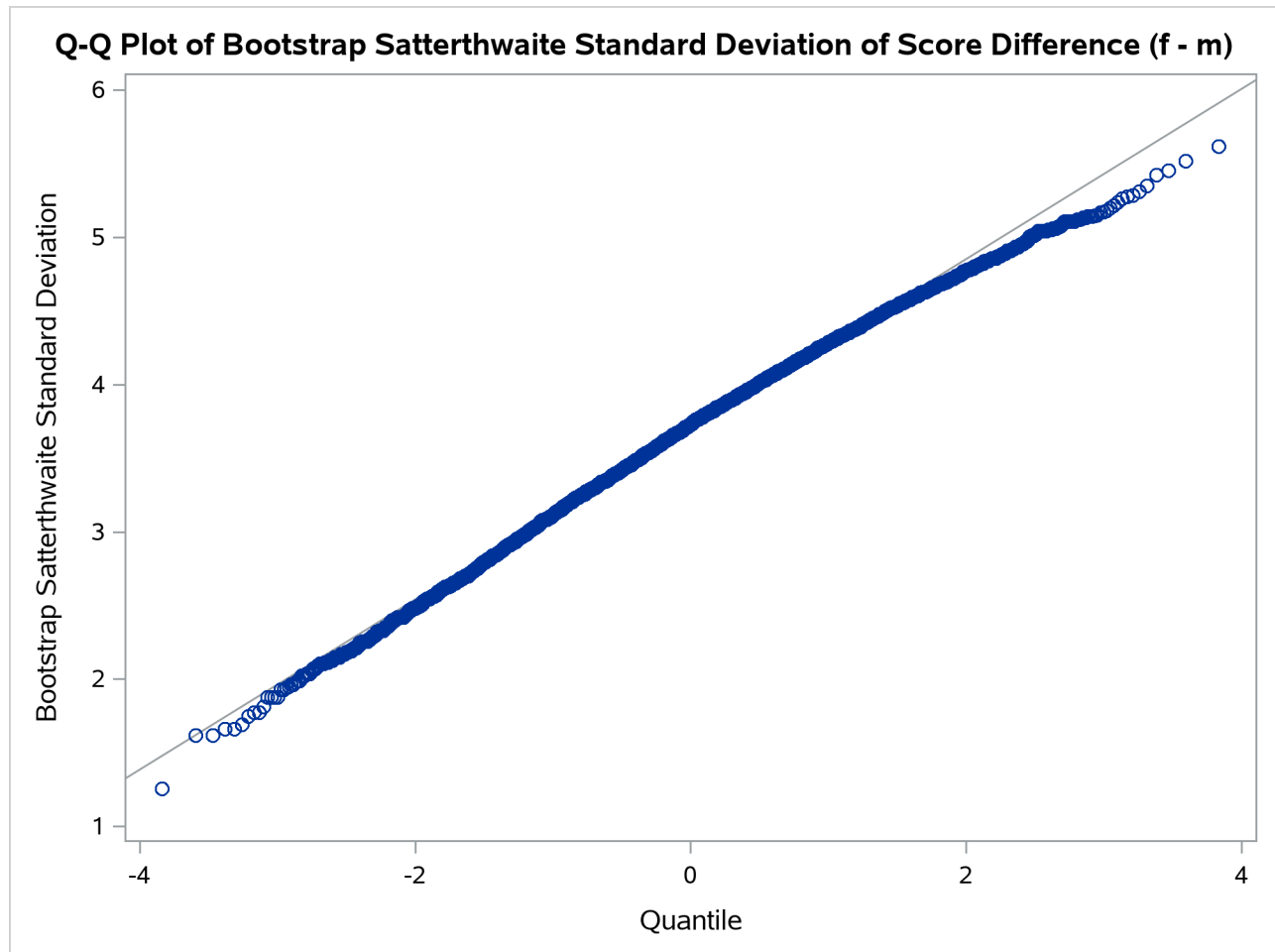
Output 125.6.6 Summary Panel of Bootstrap Satterthwaite Standard Deviation

The bootstrap Q-Q plots in [Output 125.6.7](#) through [Output 125.6.9](#) assess the normality of the distributions of the bootstrap mean, pooled standard deviation, and Satterthwaite standard deviation of the difference between female and male scores. The deviations from normality in the upper tail of the standard deviations are not surprising, because they have approximate chi-square distributions for normal data.

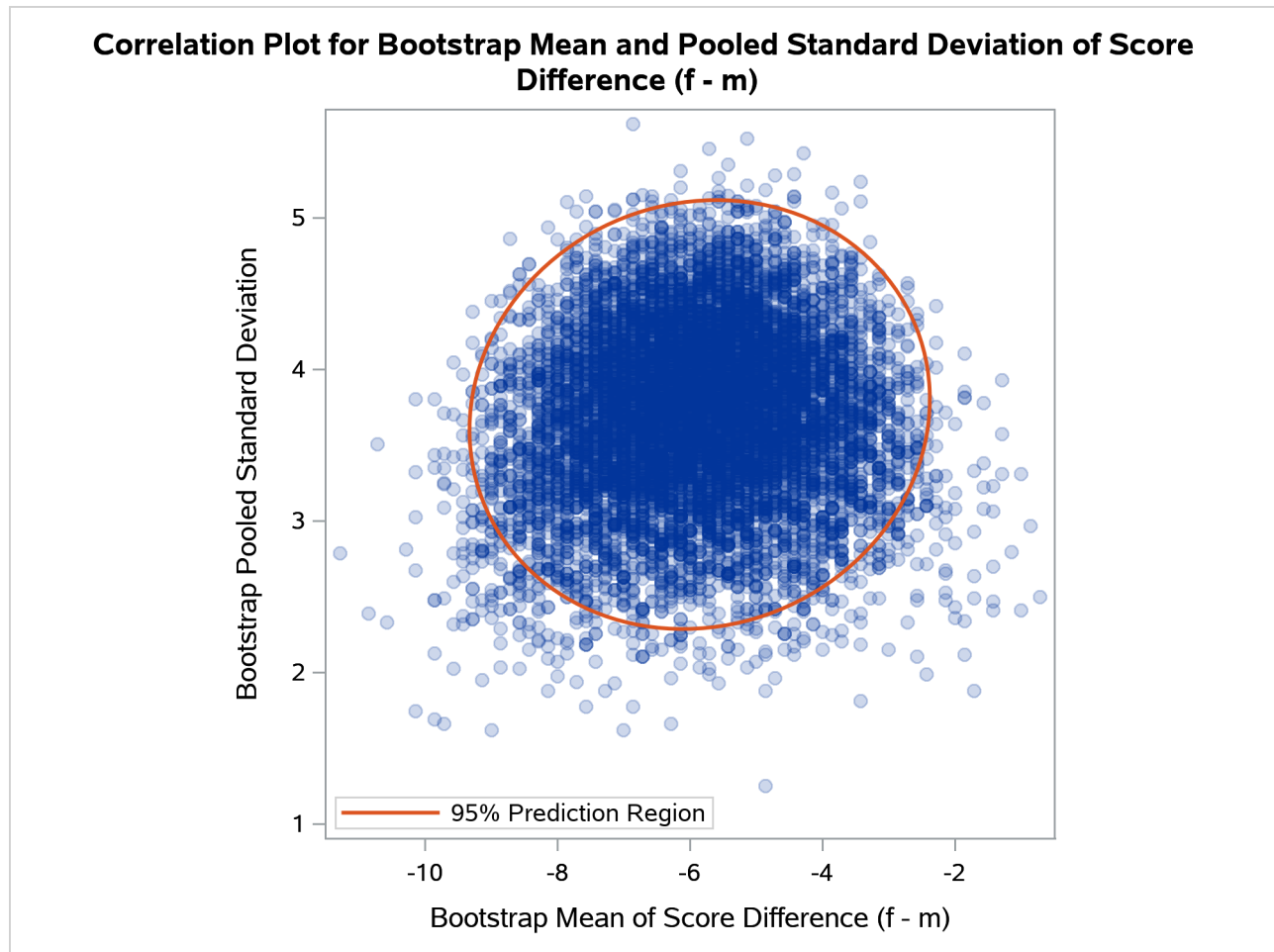
Output 125.6.7 Q-Q Plot of Bootstrap Mean

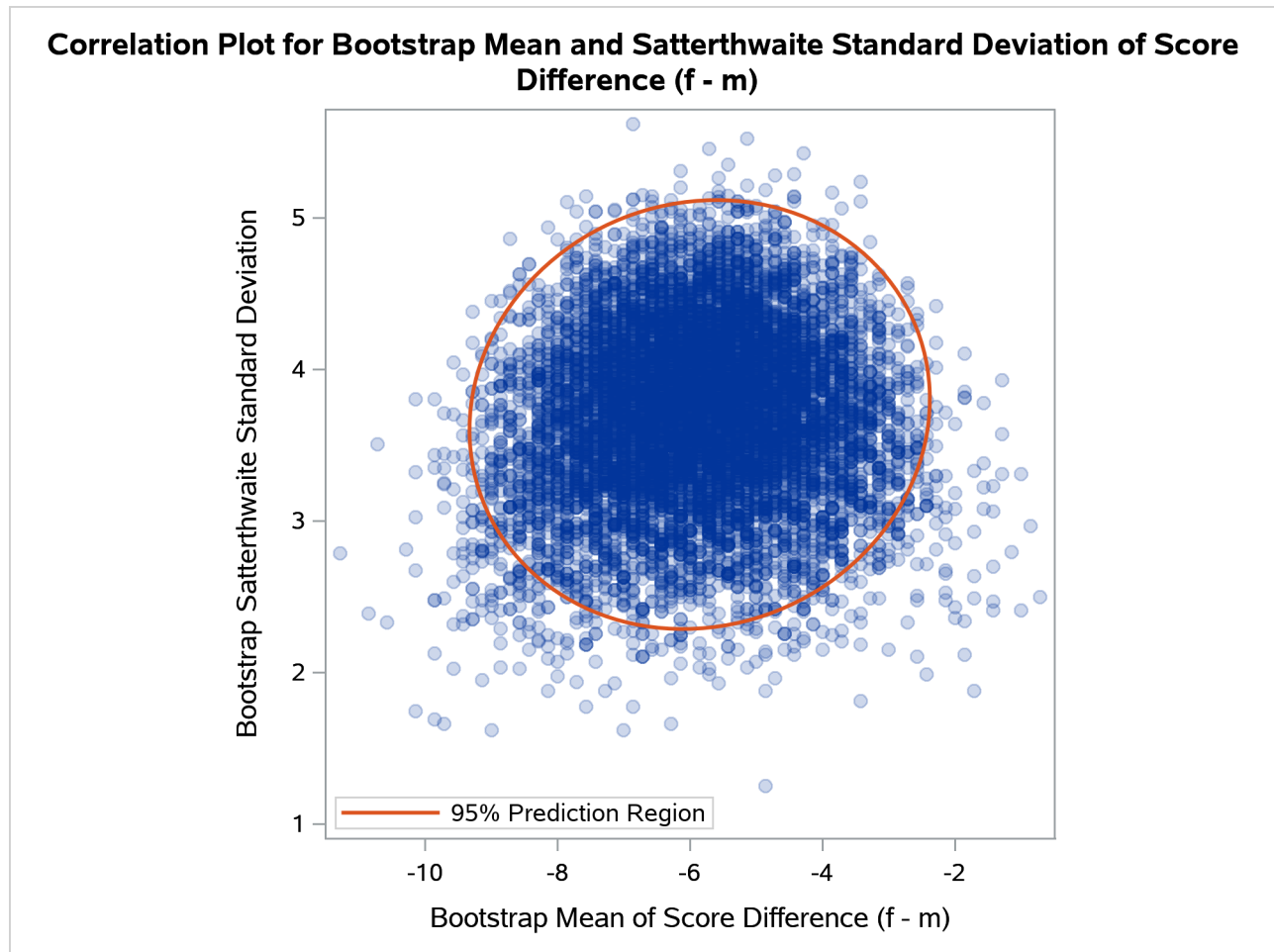


Output 125.6.8 Q-Q Plot of Bootstrap Pooled Standard Deviation

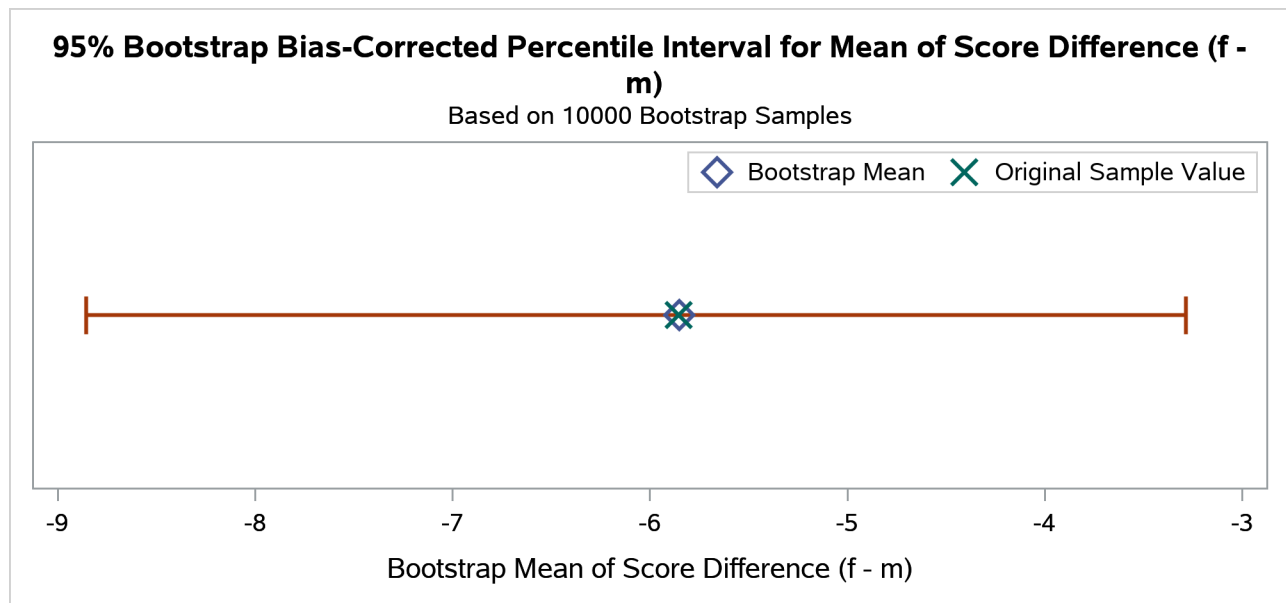
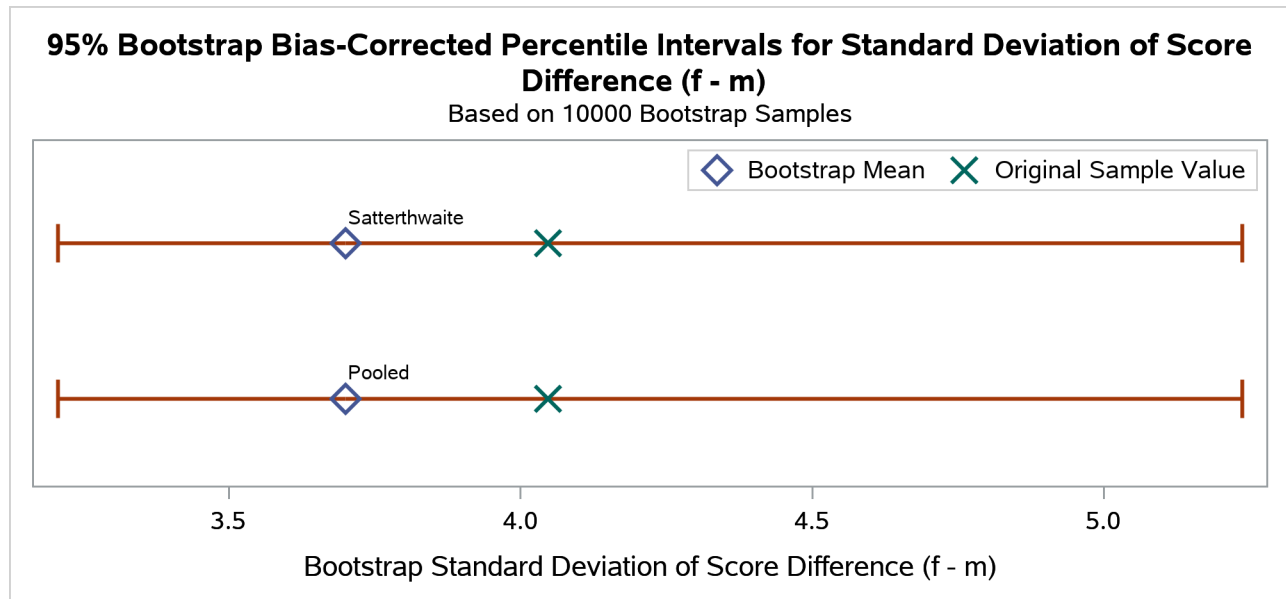
Output 125.6.9 Q-Q Plot of Bootstrap Satterthwaite Standard Deviation

The bootstrap correlation plots in [Output 125.6.10](#) and [Output 125.6.11](#) show the relationship between the bootstrap mean and the bootstrap pooled and Satterthwaite standard deviations of the difference between female and male scores. The approximately circular (as opposed to elongated elliptical) shapes of the prediction regions suggest unusually low correlations between the mean and standard deviation.

Output 125.6.10 Correlation Plot of Bootstrap Mean and Pooled Standard Deviation

Output 125.6.11 Correlation Plot of Bootstrap Mean and Satterthwaite Standard Deviation

The bootstrap interval plots in [Output 125.6.12](#) and [Output 125.6.13](#) show $100(1 - \alpha)\% = 95\%$ bootstrap bias-corrected percentile intervals of the mean, pooled standard deviation, and Satterthwaite standard deviation of the difference between female and male scores. The distance and direction between the sample and bootstrap means that are marked on the interval for each statistic reflect the size and sign of the bootstrap-estimated bias of the sample mean of the statistic.

Output 125.6.12 Bootstrap Bias-Corrected Percentile Interval Plot of Mean**Output 125.6.13** Bootstrap Bias-Corrected Percentile Interval Plot of Pooled and Satterthwaite Standard Deviations

For the purpose of illustration, it is informative to compare the bootstrap bias-corrected percentile intervals to both unadjusted and expanded percentile intervals. The following SAS statements request unadjusted bootstrap percentile intervals:

```
proc ttest plots(only)=bootstrap(interval);
  class Gender;
  var Score;
  bootstrap / seed=810 bootci=percentile;
run;
```

Output 125.6.14 through Output 125.6.16 show very similar confidence limits for the mean difference but substantially lower limits for the standard deviation of the difference, compared to the bootstrap bias-corrected confidence limits in Output 125.6.3, Output 125.6.12, and Output 125.6.13. This is consistent with both the magnitudes and directions of the bootstrap bias estimates. The minor differences in the bootstrap standard error and bias estimates between Output 125.6.3 and Output 125.6.14 are due only to random variation in the bootstrap resampling.

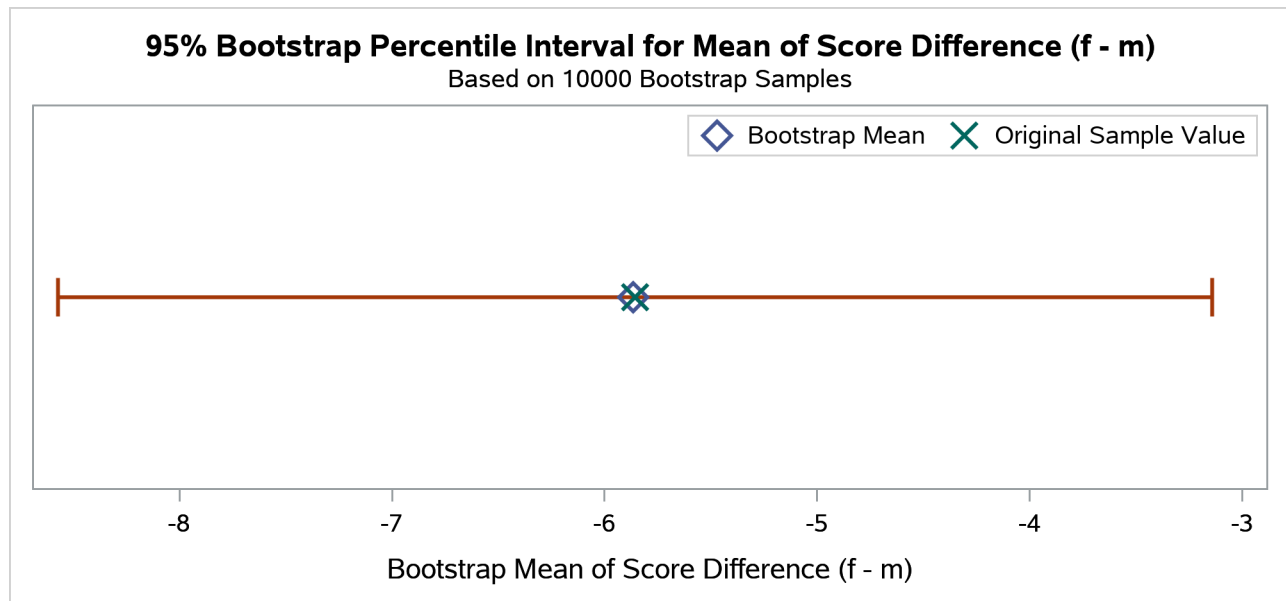
Output 125.6.14 Bootstrap Analysis with Percentile Intervals

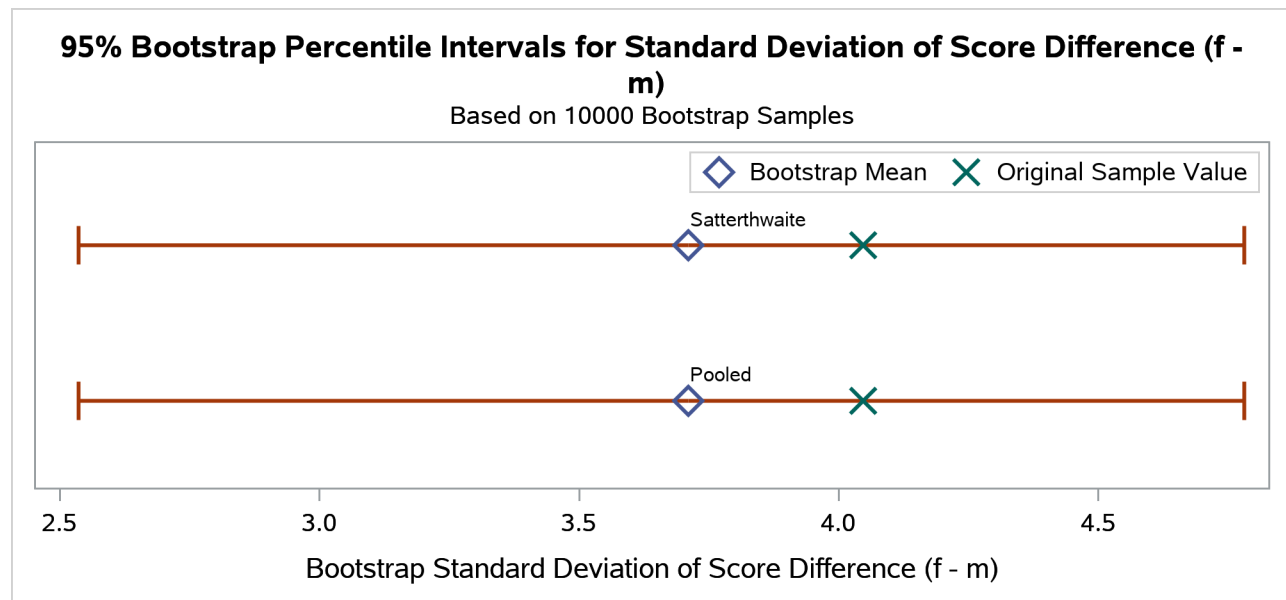
The TTEST Procedure

Variable: Score

Bootstrap Statistics and Confidence Limits					
Gender	Method	Parameter	Std Error	Bias	95% CL
Diff (1-2)		Mean	1.4046	-0.00934	-8.5714 -3.1429
Diff (1-2)	Pooled	Std Dev	0.5757	-0.3373	2.5355 4.7809
Diff (1-2)	Satterthwaite	Std Dev	0.5757	-0.3373	2.5355 4.7809

Output 125.6.15 Bootstrap Percentile Interval Plot of Mean



Output 125.6.16 Bootstrap Percentile Interval Plot of Pooled and Satterthwaite Standard Deviations

The following SAS statements request bootstrap expanded percentile intervals:

```
proc ttest plots(only)=bootstrap(interval);
  class Gender;
  var Score;
  bootstrap / seed=249 bootci=expandedperc;
run;

ods graphics off;
```

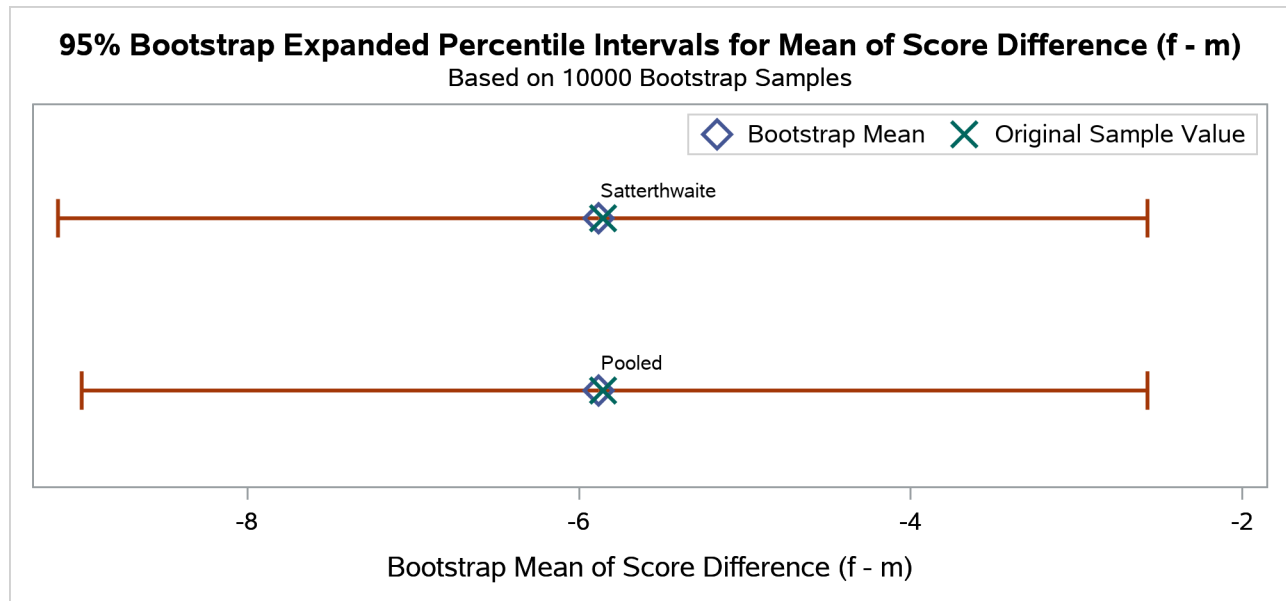
Output 125.6.17 and Output 125.6.18 show a substantially wider confidence interval for the mean difference when compared to Output 125.6.14 through Output 125.6.16. This makes sense because the expanded percentile interval, unlike the bias-corrected confidence interval, corrects for narrowness bias, which is especially problematic for small sample sizes.

Output 125.6.17 Bootstrap Analysis with Expanded Percentile Intervals

The TTEST Procedure

Variable: Score

Bootstrap Statistics and Confidence Limits						
Gender	Method	Parameter	Std Error	Bias	95% CL	
Diff (1-2)	Pooled	Mean	1.4024	-0.0265	-9.0000	-2.5714
Diff (1-2)	Satterthwaite	Mean	1.4024	-0.0265	-9.1429	-2.5714
Diff (1-2)	Pooled	Std Dev	0.5817	-0.3515		
Diff (1-2)	Satterthwaite	Std Dev	0.5817	-0.3515		

Output 125.6.18 Bootstrap Expanded Percentile Interval Plot of Mean

There are distinct pooled and Satterthwaite versions of the expanded percentile intervals for the mean in [Output 125.6.17](#) and [Output 125.6.18](#), because the two methods compute degrees of freedom differently and the degrees of freedom are involved in the “expanded” adjustment.

Expanded percentile intervals are not computed for the standard deviation parameters because the method that is specified in the `BOOTCI=EXPANDEDPERC` option is based on the assumption of approximate normality of the bootstrapped statistic $\hat{\theta}$. However, both the pooled and Satterthwaite standard deviation estimates have approximate chi-square distributions under normality. Because they are not sample mean estimates, they are not subject to the central limit theorem.

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