



THE  
POWER  
TO KNOW.

# **SAS/STAT® 9.22 User's Guide**

## **The ACECLUS Procedure**

### **(Book Excerpt)**



This document is an individual chapter from *SAS/STAT® 9.22 User's Guide*.

The correct bibliographic citation for the complete manual is as follows: SAS Institute Inc. 2010. *SAS/STAT® 9.22 User's Guide*. Cary, NC: SAS Institute Inc.

Copyright © 2010, SAS Institute Inc., Cary, NC, USA

All rights reserved. Produced in the United States of America.

**For a Web download or e-book:** Your use of this publication shall be governed by the terms established by the vendor at the time you acquire this publication.

**U.S. Government Restricted Rights Notice:** Use, duplication, or disclosure of this software and related documentation by the U.S. government is subject to the Agreement with SAS Institute and the restrictions set forth in FAR 52.227-19, Commercial Computer Software-Restricted Rights (June 1987).

SAS Institute Inc., SAS Campus Drive, Cary, North Carolina 27513.

1st electronic book, May 2010

SAS® Publishing provides a complete selection of books and electronic products to help customers use SAS software to its fullest potential. For more information about our e-books, e-learning products, CDs, and hard-copy books, visit the SAS Publishing Web site at [support.sas.com/publishing](http://support.sas.com/publishing) or call 1-800-727-3228.

SAS® and all other SAS Institute Inc. product or service names are registered trademarks or trademarks of SAS Institute Inc. in the USA and other countries. ® indicates USA registration.

Other brand and product names are registered trademarks or trademarks of their respective companies.

## Chapter 22

# The ACECLUS Procedure

### Contents

|                                                                             |            |
|-----------------------------------------------------------------------------|------------|
| Overview: ACECLUS Procedure . . . . .                                       | <b>779</b> |
| Background . . . . .                                                        | 780        |
| Getting Started: ACECLUS Procedure . . . . .                                | <b>786</b> |
| Syntax: ACECLUS Procedure . . . . .                                         | <b>793</b> |
| PROC ACECLUS Statement . . . . .                                            | 794        |
| BY Statement . . . . .                                                      | 798        |
| FREQ Statement . . . . .                                                    | 799        |
| VAR Statement . . . . .                                                     | 799        |
| WEIGHT Statement . . . . .                                                  | 799        |
| Details: ACECLUS Procedure . . . . .                                        | <b>799</b> |
| Missing Values . . . . .                                                    | 799        |
| Output Data Sets . . . . .                                                  | 800        |
| Computational Resources . . . . .                                           | 801        |
| Displayed Output . . . . .                                                  | 802        |
| ODS Table Names . . . . .                                                   | 803        |
| Example: ACECLUS Procedure . . . . .                                        | <b>803</b> |
| Example 22.1: Transformation and Cluster Analysis of Fisher Iris Data . . . | 803        |
| References . . . . .                                                        | <b>810</b> |

---

## Overview: ACECLUS Procedure

The ACECLUS (approximate covariance estimation for clustering) procedure obtains approximate estimates of the pooled within-cluster covariance matrix when the clusters are assumed to be multivariate normal with equal covariance matrices. Neither cluster membership nor the number of clusters needs to be known. PROC ACECLUS is useful for preprocessing data to be subsequently clustered by the CLUSTER or FASTCLUS procedure.

Many clustering methods perform well with spherical clusters but poorly with elongated elliptical clusters (Everitt 1980, pp. 77–97). If the elliptical clusters have roughly the same orientation and eccentricity, you can apply a linear transformation to the data to yield a spherical within-cluster covariance matrix—that is, a covariance matrix proportional to the identity. Equivalently, the distance between observations can be measured in the metric of the inverse of the pooled within-cluster covariance matrix. The remedy is difficult to apply, however, because you need to know what

the clusters are in order to compute the sample within-cluster covariance matrix. One approach is to estimate iteratively both cluster membership and within-cluster covariance (Wolfe 1970; Hartigan 1975). Another approach is provided by Art, Gnanadesikan, and Kettenring (1982). They have devised an ingenious method for estimating the within-cluster covariance matrix without knowledge of the clusters. The method can be applied before any of the usual clustering techniques, including hierarchical clustering methods.

First, Art, Gnanadesikan, and Kettenring (1982) obtain a decomposition of the total-sample sum-of-squares-and-crossproducts (SSCP) matrix into within-cluster and between-cluster SSCP matrices computed from pairwise differences between observations, rather than differences between observations and means. Then, they show how the within-cluster SSCP matrix based on pairwise differences can be approximated without knowing the number or the membership of the clusters. The approximate within-cluster SSCP matrix can be used to compute distances for cluster analysis, or it can be used in a canonical analysis similar to canonical discriminant analysis. For more information, see Chapter 27, “[The CANDISC Procedure](#).”

Art, Gnanadesikan, and Kettenring demonstrate by Monte Carlo calculations that their method can produce better clusters than the Euclidean metric even when the approximation to the within-cluster SSCP matrix is poor or the within-cluster covariances are moderately heterogeneous. The algorithm used by the ACECLUS procedure differs slightly from the algorithm used by Art, Gnanadesikan, and Kettenring. In the following sections, the PROC ACECLUS algorithm is described first; then, differences between PROC ACECLUS and the method used by Art, Gnanadesikan, and Kettenring are summarized.

---

## Background

It is well known from the literature on nonparametric statistics that variances and, hence, covariances can be computed from pairwise differences instead of deviations from means. (For example, Puri and Sen (1971, pp. 51–52) show that the variance is a  $U$  statistic of degree 2.) Let  $\mathbf{X} = (x_{ij})$  be the data matrix with  $n$  observations (rows) and  $v$  variables (columns), and let  $\bar{x}_j$  be the mean of the  $j$ th variable. The sample covariance matrix  $\mathbf{S} = (s_{jk})$  is usually defined as

$$s_{jk} = \frac{1}{n-1} \sum_{i=1}^n (x_{ij} - \bar{x}_j)(x_{ik} - \bar{x}_k)$$

The matrix  $\mathbf{S}$  can also be computed as

$$s_{jk} = \frac{1}{n(n-1)} \sum_{i=2}^n \sum_{h=1}^{i-1} (x_{ij} - x_{hj})(x_{ik} - x_{hk})$$

Let  $\mathbf{W} = (w_{jk})$  be the pooled within-cluster covariance matrix,  $q$  be the number of clusters,  $n_c$  be the number of observations in the  $c$ th cluster, and

$$d''_{ic} = \begin{cases} 1 & \text{if observation } i \text{ is in cluster } c \\ 0 & \text{otherwise} \end{cases}$$



The matrix  $\mathbf{W}$  is normally defined as

$$w_{jk} = \frac{1}{n-q} \sum_{c=1}^q \sum_{i=1}^n d''_{ic} (x_{ij} - \bar{x}_{cj})(x_{ik} - \bar{x}_{ck})$$

where  $\bar{x}_{cj}$  is the mean of the  $j$ th variable in cluster  $c$ . Let

$$d'_{ih} = \begin{cases} \frac{1}{n_c} & \text{if observations } i \text{ and } h \text{ are in cluster } c \\ 0 & \text{otherwise} \end{cases}$$

The matrix  $\mathbf{W}$  can also be computed as

$$w_{jk} = \frac{1}{n-q} \sum_{i=2}^n \sum_{h=1}^{i-1} d'_{ih} (x_{ij} - x_{hj})(x_{ik} - x_{hk})$$

If the clusters are not known,  $d'_{ih}$  cannot be determined. However, an approximation to  $\mathbf{W}$  can be obtained by using instead

$$d_{ih} = \begin{cases} 1 & \text{if } \sum_{j=1}^v \sum_{k=1}^v m_{jk} (x_{ij} - x_{hj})(x_{ik} - x_{hk}) \leq u^2 \\ 0 & \text{otherwise} \end{cases}$$

where  $u$  is an appropriately chosen value and  $\mathbf{M} = (m_{jk})$  is an appropriate metric. Let  $\mathbf{A} = (a_{jk})$  be defined as

$$a_{jk} = \frac{\sum_{i=2}^n \sum_{h=1}^{i-1} d_{ih} (x_{ij} - x_{hj})(x_{ik} - x_{hk})}{2 \sum_{i=2}^n \sum_{h=1}^{i-1} d_{ih}}$$

If all of the following conditions hold,  $\mathbf{A}$  equals  $\mathbf{W}$ :

- All within-cluster distances in the metric  $\mathbf{M}$  are less than or equal to  $u$ .
- All between-cluster distances in the metric  $\mathbf{M}$  are greater than  $u$ .
- All clusters have the same number of members  $n_c$ .

If the clusters are of unequal size,  $\mathbf{A}$  gives more weight to large clusters than  $\mathbf{W}$  does, but this discrepancy should be of little importance if the population within-cluster covariance matrices are equal. There might be large differences between  $\mathbf{A}$  and  $\mathbf{W}$  if the cutoff  $u$  does not discriminate between pairs in the same cluster and pairs in different clusters. Lack of discrimination might occur for one of the following reasons:

- The clusters are not well separated.
- The metric  $\mathbf{M}$  or the cutoff  $u$  is not chosen appropriately.

In the former case, little can be done to remedy the problem. The remaining question concerns how to choose  $\mathbf{M}$  and  $u$ . Consider  $\mathbf{M}$  first. The best choice for  $\mathbf{M}$  is  $\mathbf{W}^{-1}$ , but  $\mathbf{W}$  is not known. The solution is to use an iterative algorithm:

1. Obtain an initial estimate of  $\mathbf{A}$ , such as the identity or the total-sample covariance matrix. See the **INITIAL=** option in the PROC ACECLUS statement for more information.
2. Let  $\mathbf{M}$  equal  $\mathbf{A}^{-1}$ .
3. Recompute  $\mathbf{A}$  by using the preceding formula.
4. Repeat steps 2 and 3 until the estimate stabilizes.

Convergence is assessed by comparing values of  $\mathbf{A}$  on successive iterations. Let  $\mathbf{A}_i$  be the value of  $\mathbf{A}$  on the  $i$ th iteration and  $\mathbf{A}_0$  be the initial estimate of  $\mathbf{A}$ . Let  $\mathbf{Z}$  be a user-specified  $v \times v$  matrix. See the **METRIC=** option in the PROC ACECLUS statement for more information. The convergence measure is

$$e_i = \frac{1}{v} \| \mathbf{Z}'(\mathbf{A}_i - \mathbf{A}_{i-1})\mathbf{Z} \|$$

where  $\| \cdots \|$  indicates the Euclidean norm—that is, the square root of the sum of the squares of the elements of the matrix. In PROC ACECLUS,  $\mathbf{Z}$  can be the identity or an inverse factor of  $\mathbf{S}$  or  $\text{diag}(\mathbf{S})$ . Iteration stops when  $e_i$  falls below a user-specified value. See the **CONVERGE=** option or the **MAXITER=** option in the PROC ACECLUS statement for more information.

The remaining question of how to choose  $u$  has no simple answer. In practice, you must try several different values. PROC ACECLUS provides four different ways of specifying  $u$ :

- You can specify a constant value for  $u$ . This method is useful if the initial estimate of  $\mathbf{A}$  is quite good. See the **ABSOLUTE** option and the **THRESHOLD=** option in the PROC ACECLUS statement for more information.
- You can specify a threshold value  $t > 0$  that is multiplied by the root mean square distance between observations in the current metric on each iteration to give  $u$ . Thus, the value of  $u$  changes from iteration to iteration. This method is appropriate if the initial estimate of  $\mathbf{A}$  is poor. See the **THRESHOLD=** option in the PROC ACECLUS statement for more information.
- You can specify a value  $p$ ,  $0 < p < 1$ , to be transformed into a distance  $u$  such that approximately a proportion  $p$  of the pairwise Mahalanobis distances between observations in a random sample from a multivariate normal distribution will be less than  $u$  in repeated sampling. The transformation can be computed only if the number of observations exceeds the number of variables, preferably by at least 10 percent. This method also requires a good initial estimate of  $\mathbf{A}$ . See the **PROPORTION=** option and the **ABSOLUTE** option in the PROC ACECLUS statement for more information.
- You can specify a value  $p$ ,  $0 < p < 1$ , to be transformed into a value  $t$  that is then multiplied by  $1/\sqrt{2v}$  times the root mean square distance between observations in the current metric on each iteration to yield  $u$ . The value of  $u$  changes from iteration to iteration. This method can be used with a poor initial estimate of  $\mathbf{A}$ . See the **PROPORTION=** option in the PROC ACECLUS statement for more information.

In most cases, the analysis should begin with the last method, using values of  $p$  between 0.5 and 0.01 and using the full covariance matrix as the initial estimate of  $\mathbf{A}$ .

Proportions  $p$  are transformed to distances  $t$  by using the formula

$$t^2 = 2v \left\{ \left[ F_{v, n-v}^{-1}(p) \right]^{\frac{n-v}{n-1}} \right\}$$

where  $F_{v, n-v}^{-1}$  is the quantile (inverse cumulative distribution) function of an  $F$  random variable with  $v$  and  $n - v$  degrees of freedom. The squared Mahalanobis distance between a single pair of observations sampled from a multivariate normal distribution is distributed as  $2v$  times an  $F$  random variable with  $v$  and  $n - v$  degrees of freedom. The distances between two pairs of observations are correlated if the pairs have an observation in common. The quantile function is raised to the power given in the preceding formula to compensate approximately for the correlations among distances between pairs of observations that share a member. Monte Carlo studies indicate that the approximation is acceptable if the number of observations exceeds the number of variables by at least 10 percent.

If  $\mathbf{A}$  becomes singular, step 2 in the iterative algorithm cannot be performed because  $\mathbf{A}$  cannot be inverted. In this case, let  $\mathbf{Z}$  be the matrix as defined in discussing the convergence measure, and let  $\mathbf{Z}'\mathbf{A}\mathbf{Z} = \mathbf{R}'\mathbf{\Lambda}\mathbf{R}$ , where  $\mathbf{R}'\mathbf{R} = \mathbf{R}\mathbf{R}' = \mathbf{I}$  and  $\mathbf{\Lambda} = (\lambda_{jk})$  is diagonal. Let  $\mathbf{\Lambda}^* = (\lambda_{jk}^*)$  be a diagonal matrix, where  $\lambda_{jj}^* = \max(\lambda_{jj}, g \text{ trace}(\mathbf{\Lambda}))$ , and  $0 < g < 1$  is a user-specified singularity criterion (see the **SINGULAR=** option in the PROC ACECLUS statement for more information). Then  $\mathbf{M}$  is computed as  $\mathbf{Z}\mathbf{R}'(\mathbf{\Lambda}^*)^{-1}\mathbf{R}\mathbf{Z}'$ .

The ACECLUS procedure differs from the method used by Art, Gnanadesikan, and Kettenring (1982) in several respects:

- The Art, Gnanadesikan, and Kettenring method uses the identity matrix as the initial estimate, whereas the ACECLUS procedure enables you to specify any symmetric matrix as the initial estimate and defaults to the total-sample covariance matrix. The default initial estimate in PROC ACECLUS is chosen to yield invariance under nonsingular linear transformations of the data but might sometimes obscure clusters that become apparent if the identity matrix is used.
- The Art, Gnanadesikan, and Kettenring method carries out all computations with SSCP matrices, whereas the ACECLUS procedure uses estimated covariance matrices because covariances are easier to interpret than crossproducts.
- The Art, Gnanadesikan, and Kettenring method uses the  $m$  pairs with the smallest distances to form the new estimate at each iteration, where  $m$  is specified by the user, whereas the ACECLUS procedure uses all pairs closer than a given cutoff value. Kettenring (1984) says that the  $m$ -closest-pairs method seems to give the user more direct control. PROC ACECLUS uses a distance cutoff because it yields a slight decrease in computer time and because in some cases, such as widely separated spherical clusters, the results are less sensitive to the choice of distance cutoff than to the choice of  $m$ . Much research remains to be done on this issue.
- The Art, Gnanadesikan, and Kettenring method uses a different convergence measure. Let  $\mathbf{A}_i$  be computed on each iteration by using the  $m$ -closest-pairs method, and let  $\mathbf{B}_i = \mathbf{A}_{i-1}^{-1}\mathbf{A}_i - \mathbf{I}$ , where  $\mathbf{I}$  is the identity matrix. The convergence measure is equivalent to  $\text{trace}(\mathbf{B}_i^2)$ .

Analyses of the Fisher (1936) iris data, consisting of measurements of petal and sepal length and width for 50 specimens from each of three iris species, are summarized in Table 22.1. The number of misclassified observations out of 150 is given for four clustering methods:

- $k$ -means as implemented in PROC FASTCLUS with MAXC=3, MAXITER=99, and CONV=0
- Ward's minimum variance method as implemented in PROC CLUSTER
- average linkage on Euclidean distances as implemented in PROC CLUSTER
- the centroid method as implemented in PROC CLUSTER

Each hierarchical analysis is followed by the TREE procedure with NCL=3 to determine cluster assignments at the three-cluster level. Clusters with 20 or fewer observations are discarded by using the DOCK=20 option. The observations in a discarded cluster are considered unclassified.

Each method is applied to the following data:

- the raw data
- the data standardized to unit variance by the STANDARD procedure
- two standardized principal components accounting for 95 percent of the standardized variance and having an identity total-sample covariance matrix, computed by the PRINCOMP procedure with the STD option
- four standardized principal components having an identity total-sample covariance matrix, computed by PROC PRINCOMP with the STD option
- the data transformed by PROC ACECLUS, using seven different settings of the PROPORTION= (P=) option
- four canonical variables having an identity pooled within-species covariance matrix, computed using the CANDISC procedure

Theoretically, the best results should be obtained by using the canonical variables from PROC CANDISC. PROC ACECLUS yields results comparable to those from PROC CANDISC for values of the PROPORTION= option ranging from 0.005 to 0.02. At PROPORTION=0.04, average linkage and the centroid method show some deterioration, but  $k$ -means and Ward's method continue to produce excellent classifications. At larger values of the PROPORTION= option, all methods perform poorly, although no worse than with four standardized principal components.

**Table 22.1** Number of Misclassified and Unclassified Observations Using Fisher's (1936) Iris Data

| Data                                   | Clustering Method |        |                 |          |
|----------------------------------------|-------------------|--------|-----------------|----------|
|                                        | <i>k</i> -means   | Ward's | Average Linkage | Centroid |
| raw data                               | 16*               | 16*    | 25 + 12**       | 14*      |
| standardized data                      | 25                | 26     | 33+4            | 33+4     |
| two standardized principal components  | 29                | 31     | 30+9            | 27+32    |
| four standardized principal components | 39                | 27     | 32+7            | 45+11    |
| transformed by ACECLUS P=0.32          | 39                | 10+9   | 7+25            |          |
| transformed by ACECLUS P=0.16          | 39                | 18+9   | 7+19            | 7+26     |
| transformed by ACECLUS P=0.08          | 19                | 9      | 3+13            | 5+16     |
| transformed by ACECLUS P=0.04          | 4                 | 5      | 1+19            | 3+12     |
| transformed by ACECLUS P=0.02          | 4                 | 3      | 3               | 3        |
| transformed by ACECLUS P=0.01          | 4                 | 4      | 3               | 4        |
| transformed by ACECLUS P=0.005         | 4                 | 4      | 4               | 4        |
| canonical variables                    | 3                 | 5      | 4               | 4+1      |

\* A single number represents misclassified observations with no unclassified observations.

\*\* Where two numbers are separated by a plus sign, the first is the number of misclassified observations; the second is the number of unclassified observations.

This example demonstrates the following:

- PROC ACECLUS can produce results as good as those from the optimal transformation.
- PROC ACECLUS can be useful even when the within-cluster covariance matrices are moderately heterogeneous.
- The choice of the distance cutoff as specified by the PROPORTION= or the THRESHOLD= option is important, and several values should be tried.
- Commonly used transformations such as standardization and principal components can produce poor classifications.

Although experience with the Art, Gnanadesikan, and Kettenring and PROC ACECLUS methods is limited, the results so far suggest that these methods help considerably more often than they hinder the subsequent cluster analysis, especially with normal-mixture techniques such as *k*-means and Ward's minimum variance method.

## Getting Started: ACECLUS Procedure

The following example demonstrates how you can use the ACECLUS procedure to obtain approximate estimates of the pooled within-cluster covariance matrix and to compute canonical variables for subsequent analysis. You use PROC ACECLUS to preprocess data before you cluster it by using the FASTCLUS or CLUSTER procedure.

Suppose you want to determine whether national figures for birth rates, death rates, and infant death rates can be used to determine certain types or categories of countries. You want to perform a cluster analysis to determine whether the observations can be formed into groups suggested by the data. Previous studies indicate that the clusters computed from this type of data can be elongated and elliptical. Thus, you need to perform a linear transformation on the raw data before the cluster analysis.

The following data<sup>1</sup> from Rouncefield (1995) are the birth rates, death rates, and infant death rates for 97 countries. The following statements create the SAS data set Poverty:

```
data poverty;
    input Birth Death InfantDeath Country &$20. @@;
    datalines;
24.7 5.7 30.8 Albania 12.5 11.9 14.4 Bulgaria
13.4 11.7 11.3 Czechoslovakia 12 12.4 7.6 Former E. Germany
11.6 13.4 14.8 Hungary 14.3 10.2 16 Poland
13.6 10.7 26.9 Romania 14 9 20.2 Yugoslavia
17.7 10 23 USSR 15.2 9.5 13.1 Byelorussia
13.4 11.6 13 Ukrainian SSR 20.7 8.4 25.7 Argentina
46.6 18 111 Bolivia 28.6 7.9 63 Brazil
23.4 5.8 17.1 Chile 27.4 6.1 40 Columbia
32.9 7.4 63 Ecuador 28.3 7.3 56 Guyana
34.8 6.6 42 Paraguay 32.9 8.3 109.9 Peru
18 9.6 21.9 Uruguay 27.5 4.4 23.3 Venezuela
29 23.2 43 Mexico 12 10.6 7.9 Belgium
13.2 10.1 5.8 Finland 12.4 11.9 7.5 Denmark
13.6 9.4 7.4 France 11.4 11.2 7.4 Germany
10.1 9.2 11 Greece 15.1 9.1 7.5 Ireland
9.7 9.1 8.8 Italy 13.2 8.6 7.1 Netherlands
14.3 10.7 7.8 Norway 11.9 9.5 13.1 Portugal
10.7 8.2 8.1 Spain 14.5 11.1 5.6 Sweden
12.5 9.5 7.1 Switzerland 13.6 11.5 8.4 U.K.
14.9 7.4 8 Austria 9.9 6.7 4.5 Japan
14.5 7.3 7.2 Canada 16.7 8.1 9.1 U.S.A.
40.4 18.7 181.6 Afghanistan 28.4 3.8 16 Bahrain
42.5 11.5 108.1 Iran 42.6 7.8 69 Iraq
22.3 6.3 9.7 Israel 38.9 6.4 44 Jordan
26.8 2.2 15.6 Kuwait 31.7 8.7 48 Lebanon
45.6 7.8 40 Oman 42.1 7.6 71 Saudi Arabia
29.2 8.4 76 Turkey 22.8 3.8 26 United Arab Emirates
```

<sup>1</sup> These data have been compiled from the United Nations *Demographic Yearbook* 1990 (United Nations publications, Sales No. E/F.91.XII.1, copyright 1991, United Nations, New York) and are reproduced with the permission of the United Nations.

|      |      |       |              |      |      |      |             |
|------|------|-------|--------------|------|------|------|-------------|
| 42.2 | 15.5 | 119   | Bangladesh   | 41.4 | 16.6 | 130  | Cambodia    |
| 21.2 | 6.7  | 32    | China        | 11.7 | 4.9  | 6.1  | Hong Kong   |
| 30.5 | 10.2 | 91    | India        | 28.6 | 9.4  | 75   | Indonesia   |
| 23.5 | 18.1 | 25    | Korea        | 31.6 | 5.6  | 24   | Malaysia    |
| 36.1 | 8.8  | 68    | Mongolia     | 39.6 | 14.8 | 128  | Nepal       |
| 30.3 | 8.1  | 107.7 | Pakistan     | 33.2 | 7.7  | 45   | Philippines |
| 17.8 | 5.2  | 7.5   | Singapore    | 21.3 | 6.2  | 19.4 | Sri Lanka   |
| 22.3 | 7.7  | 28    | Thailand     | 31.8 | 9.5  | 64   | Vietnam     |
| 35.5 | 8.3  | 74    | Algeria      | 47.2 | 20.2 | 137  | Angola      |
| 48.5 | 11.6 | 67    | Botswana     | 46.1 | 14.6 | 73   | Congo       |
| 38.8 | 9.5  | 49.4  | Egypt        | 48.6 | 20.7 | 137  | Ethiopia    |
| 39.4 | 16.8 | 103   | Gabon        | 47.4 | 21.4 | 143  | Gambia      |
| 44.4 | 13.1 | 90    | Ghana        | 47   | 11.3 | 72   | Kenya       |
| 44   | 9.4  | 82    | Libya        | 48.3 | 25   | 130  | Malawi      |
| 35.5 | 9.8  | 82    | Morocco      | 45   | 18.5 | 141  | Mozambique  |
| 44   | 12.1 | 135   | Namibia      | 48.5 | 15.6 | 105  | Nigeria     |
| 48.2 | 23.4 | 154   | Sierra Leone | 50.1 | 20.2 | 132  | Somalia     |
| 32.1 | 9.9  | 72    | South Africa | 44.6 | 15.8 | 108  | Sudan       |
| 46.8 | 12.5 | 118   | Swaziland    | 31.1 | 7.3  | 52   | Tunisia     |
| 52.2 | 15.6 | 103   | Uganda       | 50.5 | 14   | 106  | Tanzania    |
| 45.6 | 14.2 | 83    | Zaire        | 51.1 | 13.7 | 80   | Zambia      |
| 41.7 | 10.3 | 66    | Zimbabwe     |      |      |      |             |

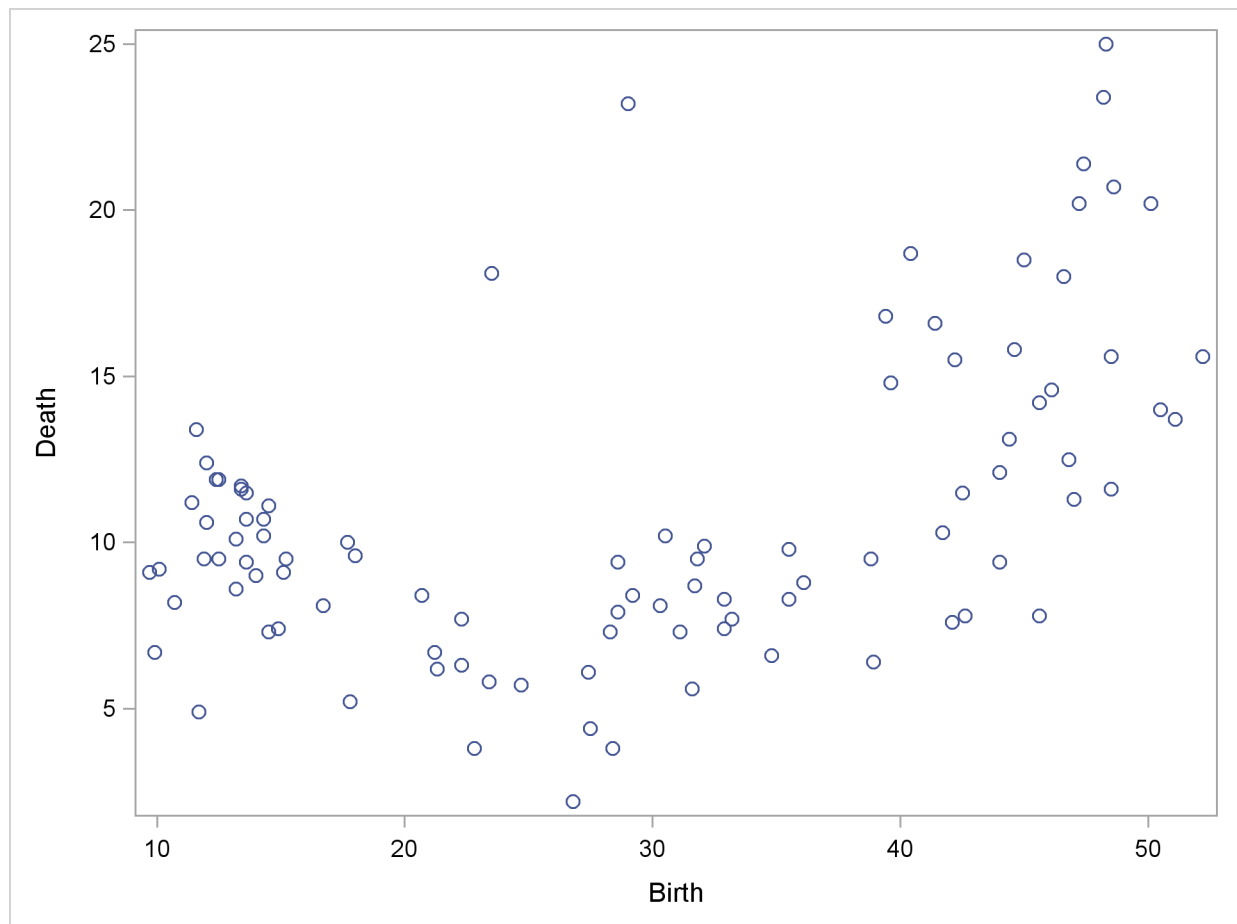
;

The data set `Poverty` contains the character variable `Country` and the numeric variables `Birth`, `Death`, and `InfantDeath`, which represent the birth rate per thousand, death rate per thousand, and infant death rate per thousand, respectively. The `$20.` format in the `INPUT` statement specifies that the variable `Country` is a character variable with a length of 20. The preceding `&` enables the reading of blanks in the middle of the country names. The double trailing at sign (`@@`) in the `INPUT` statement specifies that observations are input from each line until all values have been read.

It is often useful when beginning a cluster analysis to look at the data graphically. The following statements use the `SGPLOT` procedure to make a scatter plot of the variables `Birth` and `Death`.

```
proc sgplot data=poverty;
    scatter y=Death x=Birth;
run;
```

The plot, displayed in [Figure 22.1](#), indicates the difficulty of dividing the points into clusters. Plots of the other variable pairs (not shown) display similar characteristics. The clusters that comprise these data might be poorly separated and elongated. Data with poorly separated or elongated clusters must be transformed.

**Figure 22.1** Scatter Plot of Original Poverty Data: Birth Rate versus Death Rate

If you know the within-cluster covariances, you can transform the data to make the clusters spherical. However, since you do not know what the clusters are, you cannot calculate exactly the within-cluster covariance matrix. The ACECLUS procedure estimates the within-cluster covariance matrix to transform the data, even when you have no knowledge of cluster membership or the number of clusters.

The following statements perform the ACECLUS procedure transformation by using the SAS data set `Poverty`:

```
proc aceclus data=poverty out=ace proportion=.03;
  var Birth Death InfantDeath;
run;
```

The `OUT=` option creates an output data set called `Ace` to contain the canonical variable scores. The `PROPORTION=` option specifies that approximately 3 percent of the pairs are included in the estimation of the within-cluster covariance matrix. The `VAR` statement specifies that the variables `Birth`, `Death`, and `InfantDeath` are used in computing the canonical variables.



The results of this analysis are displayed in [Figure 22.2](#) through [Figure 22.5](#).

[Figure 22.2](#) displays the number of observations, the number of variables, and the settings for the PROPORTION and CONVERGE options. The PROPORTION option is set at 0.03, as specified in the previous statements. The CONVERGE parameter is set at its default value of 0.001. [Figure 22.2](#) next displays the means, standard deviations, and sample covariance matrix of the analytical variables.

**Figure 22.2** Means, Standard Deviations, and Covariance Matrix from the ACECLUS Procedure

| The ACECLUS Procedure                                  |            |                    |             |
|--------------------------------------------------------|------------|--------------------|-------------|
| Approximate Covariance Estimation for Cluster Analysis |            |                    |             |
| Observations                                           | 97         | Proportion         | 0.0300      |
| Variables                                              | 3          | Converge           | 0.00100     |
| Means and Standard Deviations                          |            |                    |             |
| Variable                                               | Mean       | Standard Deviation |             |
| Birth                                                  | 29.2299    | 13.5467            |             |
| Death                                                  | 10.8361    | 4.6475             |             |
| InfantDeath                                            | 54.9010    | 45.9926            |             |
| COV: Total Sample Covariances                          |            |                    |             |
|                                                        | Birth      | Death              | InfantDeath |
| Birth                                                  | 183.512951 | 30.610056          | 534.794969  |
| Death                                                  | 30.610056  | 21.599205          | 139.925900  |
| InfantDeath                                            | 534.794969 | 139.925900         | 2115.317811 |

The type of matrix used for the initial within-cluster covariance estimate is displayed in [Figure 22.3](#). In this example, that initial estimate is the full covariance matrix. The threshold value that corresponds to the PROPORTION=0.03 setting is given as 0.292815.

**Figure 22.3** Table of Iteration History from the ACECLUS Procedure

| Initial Within-Cluster Covariance Estimate = Full Covariance Matrix |          |
|---------------------------------------------------------------------|----------|
| Threshold =                                                         | 0.292815 |

**Figure 22.3** *continued*

| Iteration History    |                 |                    |                           |                        |
|----------------------|-----------------|--------------------|---------------------------|------------------------|
| Iteration            | RMS<br>Distance | Distance<br>Cutoff | Pairs<br>Within<br>Cutoff | Convergence<br>Measure |
| 1                    | 2.449           | 0.717              | 385.0                     | 0.552025               |
| 2                    | 12.534          | 3.670              | 446.0                     | 0.008406               |
| 3                    | 12.851          | 3.763              | 521.0                     | 0.009655               |
| 4                    | 12.882          | 3.772              | 591.0                     | 0.011193               |
| 5                    | 12.716          | 3.723              | 628.0                     | 0.008784               |
| 6                    | 12.821          | 3.754              | 658.0                     | 0.005553               |
| 7                    | 12.774          | 3.740              | 680.0                     | 0.003010               |
| 8                    | 12.631          | 3.699              | 683.0                     | 0.000676               |
| Algorithm converged. |                 |                    |                           |                        |

Figure 22.3 displays the iteration history. For each iteration, PROC ACECLUS displays the following measures:

- root mean square distance between all pairs of observations
- distance cutoff for including pairs of observations in the estimate of within-cluster covariances (equal to  $\text{RMS} \times \text{Threshold}$ )
- number of pairs within the cutoff
- convergence measure

Figure 22.4 displays the approximate within-cluster covariance matrix and the table of eigenvalues from the canonical analysis. The first column of the eigenvalues table contains numbers for the eigenvectors. The next column of the table lists the eigenvalues of  $\text{Inv}(\text{ACE}) * (\text{COV} - \text{ACE})$ .

**Figure 22.4** Approximate Within-Cluster Covariance Estimates

| ACE: Approximate Covariance Estimate Within Clusters |             |             |             |            |
|------------------------------------------------------|-------------|-------------|-------------|------------|
|                                                      | Birth       | Death       | InfantDeath |            |
| Birth                                                | 5.94644949  | -0.63235725 | 6.28151537  |            |
| Death                                                | -0.63235725 | 2.33464129  | 1.59005857  |            |
| InfantDeath                                          | 6.28151537  | 1.59005857  | 35.10327233 |            |
| Eigenvalues of Inv(ACE) * (COV-ACE)                  |             |             |             |            |
|                                                      | Eigenvalue  | Difference  | Proportion  | Cumulative |
| 1                                                    | 63.5500     | 54.7313     | 0.8277      | 0.8277     |
| 2                                                    | 8.8187      | 4.4038      | 0.1149      | 0.9425     |
| 3                                                    | 4.4149      |             | 0.0575      | 1.0000     |

The next three columns of the eigenvalue table (Figure 22.4) display measures of the relative size and importance of the eigenvalues. The first column lists the difference between each eigenvalue and its successor. The last two columns display the individual and cumulative proportions that each eigenvalue contributes to the total sum of eigenvalues.

The raw and standardized canonical coefficients are displayed in Figure 22.5. The coefficients are standardized by multiplying the raw coefficients with the standard deviation of the associated variable. The ACECLUS procedure uses these standardized canonical coefficients to create the transformed canonical variables, which are the linear transformations of the original input variables, Birth, Death, and InfantDeath.

**Figure 22.5** Raw and Standardized Canonical Coefficients from the ACECLUS Procedure

| Eigenvectors (Raw Canonical Coefficients) |          |          |          |
|-------------------------------------------|----------|----------|----------|
|                                           | Can1     | Can2     | Can3     |
| Birth                                     | 0.125610 | 0.457037 | 0.003875 |
| Death                                     | 0.108402 | 0.163792 | 0.663538 |
| InfantDeath                               | 0.134704 | -.133620 | -.046266 |
| Standardized Canonical Coefficients       |          |          |          |
|                                           | Can1     | Can2     | Can3     |
| Birth                                     | 1.70160  | 6.19134  | 0.05249  |
| Death                                     | 0.50380  | 0.76122  | 3.08379  |
| InfantDeath                               | 6.19540  | -6.14553 | -2.12790 |

The following statements invoke the CLUSTER procedure, using the SAS data set Ace created in the previous ACECLUS procedure:

```
proc cluster data=ace outtree=tree noprint method=ward;
  var can1 can2 can3 ;
  copy Birth--Country;
run;
```

The OUTTREE= option creates the output SAS data set Tree that is used in subsequent statements to draw a tree diagram. The NOPRINT option suppresses the display of the output. The METHOD= option specifies Ward's minimum-variance clustering method.

The VAR statement specifies that the canonical variables computed in the ACECLUS procedure are used in the cluster analysis. The COPY statement specifies that all the variables from the SAS data set Poverty (Birth—Country) are added to the output data set Tree.

The following statements use the TREE procedure to create an output SAS data set called New. The NCLUSTERS= option specifies the number of clusters desired in the SAS data set New. The NOPRINT option suppresses the display of the output.

```
proc tree data=tree out=new nclusters=3 noprint;
  copy Birth Death InfantDeath can1 can2 ;
  id Country;
run;
```

The COPY statement copies the canonical variables Can1 and Can2 (computed in the preceding ACECLUS procedure) and the original analytical variables Birth, Death, and InfantDeath into the output SAS data set New.

The following statements invoke the SGPLOT procedure, using the SAS data set created by PROC TREE:

```
proc sgplot data=new;
  scatter y=Death x=Birth / group=cluster;
  keylegend / title="Cluster Membership";
run;

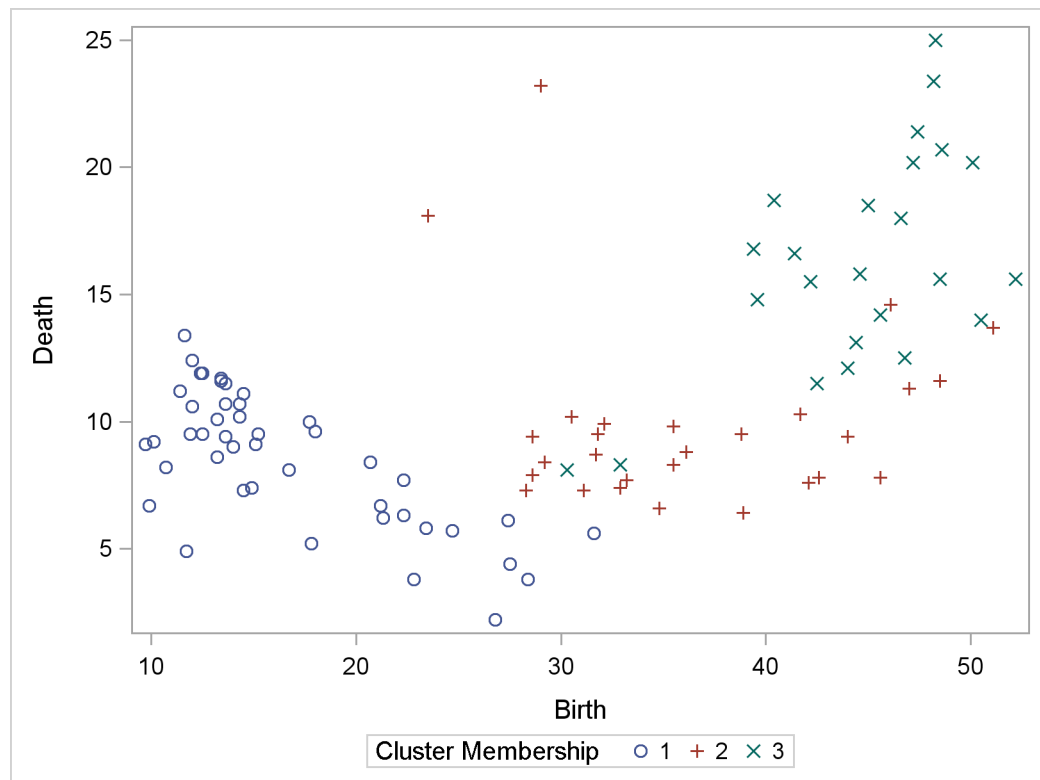
proc sgplot data=new;
  scatter y=can2 x=can1 / group=cluster;
  keylegend / title="Cluster Membership";
run;
```

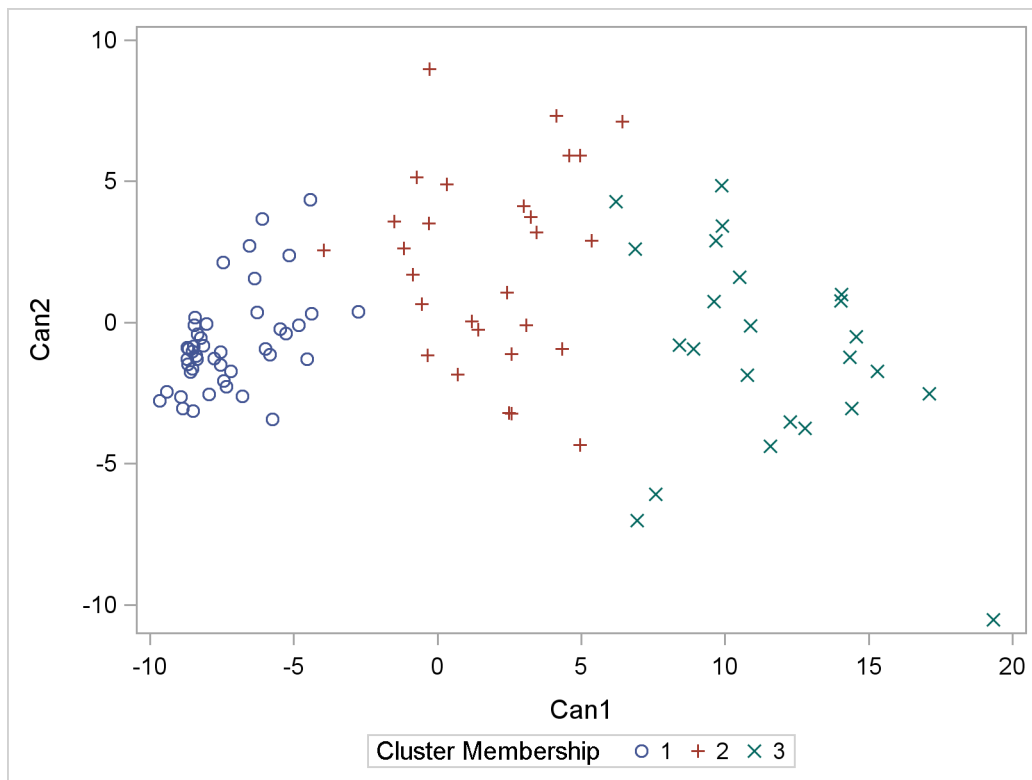
The first PROC SGPLOT statement requests a scatter plot of the two variables Birth and Death, using the variable CLUSTER as the identification variable.

The second PROC SGPLOT statement requests a plot of the two canonical variables, using the value of the variable CLUSTER as the identification variable.

Figure 22.6 and Figure 22.7 display the separation of the clusters when three clusters are calculated.

**Figure 22.6** Scatter Plot of Poverty Data, Identified by Cluster



**Figure 22.7** Scatter Plot of Canonical Variables


---

## Syntax: ACECLUS Procedure

The following statements are available in the ACECLUS procedure:

**PROC ACECLUS** **PROPORTION**=*p* / **THRESHOLD**=*t* <options> ;

**BY** *variables* ;

**FREQ** *variable* ;

**VAR** *variables* ;

**WEIGHT** *variable* ;

Usually you need only the VAR statement in addition to the required PROC ACECLUS statement. The optional BY, FREQ, VAR, and WEIGHT statements are described in alphabetical order after the PROC ACECLUS statement.

## PROC ACECLUS Statement

**PROC ACECLUS** **PROPORTION**=*p* / **THRESHOLD**=*t* < *options* > ;

The PROC ACECLUS statement starts the ACECLUS procedure. The options available with the PROC ACECLUS statement are summarized in Table 22.2 and discussed in the following sections. Note that, if you specify the METHOD=COUNT option, you must specify either the PROPORTION= or the MPAIRS= option. Otherwise, you must specify either the PROPORTION= or THRESHOLD= option.

**Table 22.2** Summary of PROC ACECLUS Statement Options

| Options                                   | Description                                                                                                   |
|-------------------------------------------|---------------------------------------------------------------------------------------------------------------|
| <b>Specify clustering options</b>         |                                                                                                               |
| METHOD=                                   | specifies the clustering method                                                                               |
| MPAIRS=                                   | specifies number of pairs for estimating within-cluster covariance (when you specify the option METHOD=COUNT) |
| PROPORTION=                               | specifies proportion of pairs for estimating within-cluster covariance                                        |
| THRESHOLD=                                | specifies the threshold for including pairs in the estimation of the within-cluster covariance                |
| <b>Specify input and output data sets</b> |                                                                                                               |
| DATA=                                     | specifies input data set name                                                                                 |
| OUT=                                      | specifies output data set name                                                                                |
| OUTSTAT=                                  | specifies output data set name containing various statistics                                                  |
| <b>Specify iteration options</b>          |                                                                                                               |
| ABSOLUTE                                  | uses absolute instead of relative threshold                                                                   |
| CONVERGE=                                 | specifies convergence criterion                                                                               |
| INITIAL=                                  | specifies initial estimate of within-cluster covariance matrix                                                |
| MAXITER=                                  | specifies maximum number of iterations                                                                        |
| METRIC=                                   | specifies metric in which computations are performed                                                          |
| SINGULAR=                                 | specifies singularity criterion                                                                               |
| <b>Specify canonical analysis options</b> |                                                                                                               |
| N=                                        | specifies number of canonical variables                                                                       |
| PREFIX=                                   | specifies prefix for naming canonical variables                                                               |
| <b>Control displayed output</b>           |                                                                                                               |
| NOPRINT                                   | suppresses the display of the output                                                                          |
| PP                                        | produces PP-plot of distances between pairs from last iteration                                               |
| QQ                                        | produces QQ-plot of power transformation of distances between pairs from last iteration                       |
| SHORT                                     | omits all output except for iteration history and eigenvalue table                                            |

The following list provides details about the options. The list is in alphabetical order.

### **ABSOLUTE**

causes the THRESHOLD= value or the threshold computed from the PROPORTION= option to be treated absolutely rather than relative to the root mean square distance between observations. Use the ABSOLUTE option only when you are confident that the initial estimate of the within-cluster covariance matrix is close to the final estimate, such as when the INITIAL= option specifies a data set created by a previous execution of PROC ACECLUS by using the OUTSTAT= option.

### **CONVERGE=c**

specifies the convergence criterion. By default, CONVERGE= 0.001. Iteration stops when the convergence measure falls below the value specified by the CONVERGE= option or when the iteration limit as specified by the MAXITER= option is exceeded, whichever happens first.

### **DATA=SAS-data-set**

specifies the SAS data set to be analyzed. By default, PROC ACECLUS uses the most recently created SAS data set.

### **INITIAL=name**

specifies the matrix for the initial estimate of the within-cluster covariance matrix. Valid values for *name* are as follows:

|                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| DIAGONAL   D       | uses the diagonal matrix of sample variances as the initial estimate of the within-cluster covariance matrix.                                                                                                                                                                                                                                                                                                                                     |
| FULL   F           | uses the total-sample covariance matrix as the initial estimate of the within-cluster covariance matrix.                                                                                                                                                                                                                                                                                                                                          |
| IDENTITY   I       | uses the identity matrix as the initial estimate of the within-cluster covariance matrix.                                                                                                                                                                                                                                                                                                                                                         |
| INPUT=SAS-data-set | specifies a SAS data set from which to obtain the initial estimate of the within-cluster covariance matrix. The data set can be TYPE=CORR, COV, UCORR, UCOV, SSCP, or ACE, or it can be an ordinary SAS data set. See Appendix A, “ <a href="#">Special SAS Data Sets</a> ,” for descriptions of CORR, COV, UCORR, UCOV, and SSCP data sets. See the section “ <a href="#">Output Data Sets</a> ” on page 800 for a description of ACE data sets. |

If you do not specify the INITIAL= option, the default is the matrix specified by the METRIC= option. If neither the INITIAL= nor the METRIC= option is specified, INITIAL=FULL is used if there are enough observations to obtain a nonsingular total-sample covariance matrix; otherwise, INITIAL=DIAGONAL is used.

### **MAXITER=n**

specifies the maximum number of iterations. By default, MAXITER=10.

### **METHOD=COUNT | C | THRESHOLD | T**

specifies the clustering method. The METHOD=THRESHOLD option requests a method (also

the default) that uses all pairs closer than a given cutoff value to form the estimate at each iteration. The METHOD=COUNT option requests a method that uses a number of pairs,  $m$ , with the smallest distances to form the estimate at each iteration.

**METRIC=***name*

specifies the metric in which the computations are performed, implies the default value for the INITIAL= option, and specifies the matrix **Z** used in the formula for the convergence measure  $e_i$  and for checking singularity of the **A** matrix. Valid values for *name* are as follows:

|              |                                                                                                                                                                                                           |
|--------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| DIAGONAL   D | uses the diagonal matrix of sample variances $\text{diag}(\mathbf{S})$ and sets $\mathbf{Z} = \text{diag}(\mathbf{S})^{-\frac{1}{2}}$ , where the superscript $-\frac{1}{2}$ indicates an inverse factor. |
| FULL   F     | uses the total-sample covariance matrix <b>S</b> and sets $\mathbf{Z} = \mathbf{S}^{-\frac{1}{2}}$ .                                                                                                      |
| IDENTITY   I | uses the identity matrix <b>I</b> and sets $\mathbf{Z} = \mathbf{I}$ .                                                                                                                                    |

If you do not specify the METRIC= option, METRIC=FULL is used if there are enough observations to obtain a nonsingular total-sample covariance matrix; otherwise, METRIC=DIAGONAL is used.

The option METRIC= is rather technical. It affects the computations in a variety of ways, but for well-conditioned data the effects are subtle. For most data sets, the METRIC= option is not needed.

**MPAIRS=***m*

specifies the number of pairs to be included in the estimation of the within-cluster covariance matrix when METHOD=COUNT is requested. The values of  $m$  must be greater than 0 but less than or equal to  $(\text{totfq} \times (\text{totfq} - 1)) / 2$ , where *totfq* is the sum of nonmissing frequencies specified in the FREQ statement. If there is no FREQ statement, *totfq* equals the number of total nonmissing observations.

**N=***n*

specifies the number of canonical variables to be computed. The default is the number of variables analyzed. N=0 suppresses the canonical analysis.

**NOPRINT**

suppresses the display of all output. Note that this option temporarily disables the Output Delivery System (ODS). For more information, see Chapter 20, [“Using the Output Delivery System.”](#)

**OUT=***SAS-data-set*

creates an output SAS data set that contains all the original data as well as the canonical variables having an estimated within-cluster covariance matrix equal to the identity matrix. If you want to create a permanent SAS data set, you must specify a two-level name. See *SAS Language Reference: Concepts* for more information about permanent SAS data sets.

**OUTSTAT=***SAS-data-set*

specifies a TYPE=ACE output SAS data set that contains means, standard deviations, number of observations, covariances, estimated within-cluster covariances, eigenvalues, and canonical coefficients. If you want to create a permanent SAS data set, you must specify a two-level



name. See *SAS Language Reference: Concepts* for more information about permanent SAS data sets.

**PROPORTION**=*p*

**PERCENT**=*p*

**P**=*p*

specifies the percentage of pairs to be included in the estimation of the within-cluster covariance matrix. The value of *p* must be greater than 0. If *p* is greater than or equal to 1, it is interpreted as a percentage and divided by 100; PROPORTION=0.02 and PROPORTION=2 are equivalent. When you specify METHOD=THRESHOLD, a threshold value is computed from the PROPORTION= option under the assumption that the observations are sampled from a multivariate normal distribution.

When you specify METHOD=COUNT, the number of pairs, *m*, is computed from PROPORTION=*p* as

$$m = \text{floor} \left( \frac{p}{2} \times \text{totfq} \times (\text{totfq} - 1) \right)$$

where *totfq* is the number of total nonmissing observations.

**PP**

produces a PP probability plot of distances between pairs of observations computed in the last iteration.

**PREFIX**=*name*

specifies a prefix for naming the canonical variables. By default the names are Can1, Can2, ..., CAN*N*. If you specify PREFIX=ABC, the variables are named ABC1, ABC2, ABC3, and so on. The number of characters in the prefix plus the number of digits required to designate the variables should not exceed the name length defined by the VALIDVARNAME= system option. For more information about the VALIDVARNAME= system option, see *SAS Language Reference: Dictionary*.

**QQ**

produces a QQ probability plot of a power transformation of the distances between pairs of observations computed in the last iteration. **CAUTION:** The QQ plot can require an enormous amount of computer time.

**SHORT**

omits all items from the standard output except for the iteration history and the eigenvalue table.

**SINGULAR**=*g*

**SING**=*g*

specifies a singularity criterion  $0 < g < 1$  for the total-sample covariance matrix **S** and the approximate within-cluster covariance estimate **A**. The default is SINGULAR=1E-4.

**THRESHOLD**=*t*

**T**=*t*

specifies the threshold for including pairs of observations in the estimation of the within-cluster

covariance matrix. A pair of observations is included if the Euclidean distance between them is less than or equal to  $t$  times the root mean square distance computed over all pairs of observations.

---

## BY Statement

**BY** *variables* ;

You can specify a BY statement with PROC ACECLUS to obtain separate analyses on 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 for the ACECLUS 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).

If you specify the INITIAL=INPUT= option and the INITIAL=INPUT= data set does not contain any of the BY variables, the entire INITIAL=INPUT= data set provides the initial value for the matrix **A** for each BY group in the DATA= data set.

If the INITIAL=INPUT= data set contains some but not all of the BY variables, or if some BY variables do not have the same type or length in the INITIAL=INPUT= data set as in the DATA= data set, then PROC ACECLUS displays an error message and stops.

If all the BY variables appear in the INITIAL=INPUT= data set with the same type and length as in the DATA= data set, then each BY group in the INITIAL=INPUT= data set provides the initial value for **A** for the corresponding BY group in the DATA= data set. All BY groups in the DATA= data set must also appear in the INITIAL= INPUT= data set. The BY groups in the INITIAL=INPUT= data set must be in the same order as in the DATA= data set. If you specify NOTSORTED in the BY statement, identical BY groups must occur in the same order in both data sets. If you do not specify NOTSORTED, some BY groups can appear in the INITIAL= INPUT= data set, but not in the DATA= data set; such BY groups are not used in the analysis.

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*.

---

## FREQ Statement

**FREQ** *variable* ;

If a variable in your data set represents the frequency of occurrence for the observation, include the name of that variable in the FREQ statement. The procedure then treats the data set as if each observation appears  $n$  times, where  $n$  is the value of the FREQ variable for the observation. If a value of the FREQ variable is not integral, it is truncated to the largest integer not exceeding the given value. Observations with FREQ values less than one are not included in the analysis. The total number of observations is considered equal to the sum of the FREQ variable.

---

## VAR Statement

**VAR** *variables* ;

The VAR statement specifies the numeric variables to be analyzed. If the VAR statement is omitted, all numeric variables not specified in other statements are analyzed.

---

## WEIGHT Statement

**WEIGHT** *variable* ;

If you want to specify relative weights for each observation in the input data set, place the weights in a variable in the data set and specify that variable name in a WEIGHT statement. This is often done when the variance associated with each observation is different and the values of the weight variable are proportional to the reciprocals of the variances. The values of the WEIGHT variable can be nonintegral and are not truncated. An observation is used in the analysis only if the value of the WEIGHT variable is greater than zero.

The WEIGHT and FREQ statements have a similar effect, except in calculating the divisor of the **A** matrix.

---

## Details: ACECLUS Procedure

---

### Missing Values

Observations with missing values are omitted from the analysis and are given missing values for canonical variable scores in the OUT= data set.

## Output Data Sets

### OUT= Data Set

The OUT= data set contains all the variables in the original data set plus new variables containing the canonical variable scores. The N= option determines the number of new variables. The OUT= data set is not created if N=0. The names of the new variables are formed by concatenating the value given by the PREFIX= option (or the prefix CAN if the PREFIX= option is not specified) and the numbers 1, 2, 3, and so on. The OUT= data set can be used as input to PROC CLUSTER or PROC FASTCLUS. The cluster analysis should be performed on the canonical variables, not on the original variables.

### OUTSTAT= Data Set

The OUTSTAT= data set is a TYPE=ACE data set containing the following variables:

- the BY variables, if any
- the two new character variables, \_TYPE\_ and \_NAME\_
- the variables analyzed—that is, those in the VAR statement, or, if there is no VAR statement, all numeric variables not listed in any other statement

Each observation in the new data set contains some type of statistic as indicated by the \_TYPE\_ variable. The values of the \_TYPE\_ variable are as follows:

|          |                                                                                                                                                                                                                                   |
|----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| MEAN     | mean of each variable                                                                                                                                                                                                             |
| STD      | standard deviation of each variable                                                                                                                                                                                               |
| N        | number of observations on which the analysis is based. This value is the same for each variable.                                                                                                                                  |
| SUMWGT   | sum of the weights if a WEIGHT statement is used. This value is the same for each variable.                                                                                                                                       |
| COV      | covariances between each variable and the variable named by the _NAME_ variable. The number of observations with _TYPE_=COV is equal to the number of variables being analyzed.                                                   |
| ACE      | estimated within-cluster covariances between each variable and the variable named by the _NAME_ variable. The number of observations with _TYPE_=ACE is equal to the number of variables being analyzed.                          |
| EIGENVAL | eigenvalues of $INV(ACE) * (COV - ACE)$ . If the N= option requests fewer than the maximum number of canonical variables, only the specified number of eigenvalues are produced, with missing values filling out the observation. |

|          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
|----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RAWScore | raw canonical coefficients.<br><br>To obtain the canonical variable scores, these coefficients should be multiplied by the raw data centered by means obtained from the observation with <code>_TYPE_='MEAN'</code> .                                                                                                                                                                                                                                                                                                                                                                |
| SCORE    | standardized canonical coefficients. The <code>_NAME_</code> variable contains the name of the corresponding canonical variable as constructed from the <code>PREFIX=</code> option. The number of observations with <code>_TYPE_=SCORE</code> equals the number of canonical variables computed.<br><br>To obtain the canonical variable scores, these coefficients should be multiplied by the standardized data, using means obtained from the observation with <code>_TYPE_='MEAN'</code> and standard deviations obtained from the observation with <code>_TYPE_='STD'</code> . |

The OUTSTAT= data set can be used in the following conditions:

- to initialize another execution of PROC ACECLUS
- to compute canonical variable scores with the SCORE procedure
- as input to the FACTOR procedure, specifying `METHOD=SCORE`, to rotate the canonical variables

---

## Computational Resources

Let

- $n$  = number of observations
- $v$  = number of variables
- $i$  = number of iterations

## Memory

The memory in bytes required by PROC ACECLUS is approximately

$$8(2n(v + 1) + 21v + 5v^2)$$

bytes. If you request the PP or QQ option, an additional  $4n(n - 1)$  bytes are needed.

## Time

The time required by PROC ACECLUS is roughly proportional to

$$2nv^2 + 10v^3 + i \left( \frac{n^2v}{2} + nv^2 + 5v^3 \right)$$

---

## Displayed Output

Unless the SHORT option is specified, the ACECLUS procedure displays the following items:

- Means and Standard Deviations of the input variables
- the **S** matrix, labeled COV: Total Sample Covariances
- the name or value of the matrix used for the Initial Within-Cluster Covariance Estimate
- the Threshold value if the PROPORTION= option is specified

For each iteration, PROC ACECLUS displays the following items:

- the Iteration number
- RMS Distance, the root mean square distance between all pairs of observations
- the Distance Cutoff ( $u$ ) for including pairs of observations in the estimate of the within-cluster covariances, which equals the RMS distance times the threshold
- the number of Pairs Within Cutoff
- the Convergence Measure ( $e_i$ ) as specified by the METRIC= option

If the SHORT option is not specified, PROC ACECLUS also displays the **A** matrix, labeled ACE: Approximate Covariance Estimate Within Clusters.

The ACECLUS procedure displays a table of eigenvalues from the canonical analysis containing the following items:

- Eigenvalues of  $\text{Inv}(\text{ACE}) * (\text{COV} - \text{ACE})$
- the Difference between successive eigenvalues
- the Proportion of variance explained by each eigenvalue
- the Cumulative proportion of variance explained

If the SHORT option is not specified, PROC ACECLUS displays the following items:

- the Eigenvectors or raw canonical coefficients
- the standardized eigenvectors or standard canonical coefficients

## ODS Table Names

PROC ACECLUS 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 the following table. For more information about ODS, see Chapter 20, “Using the Output Delivery System.”

**Table 22.3** ODS Tables Produced by PROC ACECLUS

| ODS Table Name    | Description                                                            | Statement | Option        |
|-------------------|------------------------------------------------------------------------|-----------|---------------|
| ConvergenceStatus | Convergence status                                                     | PROC      | default       |
| DataOptionInfo    | Data and option information                                            | PROC      | default       |
| Eigenvalues       | Eigenvalues of<br>$\text{Inv}(\text{ACE}) * (\text{COV} - \text{ACE})$ | PROC      | default       |
| Eigenvectors      | Eigenvectors (raw canonical coefficients)                              | PROC      | default       |
| InitWithin        | Initial within-cluster covariance estimate                             | PROC      | INITIAL=INPUT |
| IterHistory       | Iteration history                                                      | PROC      | default       |
| SimpleStatistics  | Simple statistics                                                      | PROC      | default       |
| StdCanCoef        | Standardized canonical coefficients                                    | PROC      | default       |
| Threshold         | Threshold value                                                        | PROC      | PROPORTION=   |
| TotSampleCov      | Total sample covariances                                               | PROC      | default       |
| Within            | Approximate covariance estimate within clusters                        | PROC      | default       |

## Example: ACECLUS Procedure

### Example 22.1: Transformation and Cluster Analysis of Fisher Iris Data

The iris data published by Fisher (1936) have been widely used for examples in discriminant analysis and cluster analysis. The sepal length, sepal width, petal length, and petal width are measured in millimeters on 50 iris specimens from each of three species, *Iris setosa*, *I. versicolor*, and *I. virginica*. Mezzich and Solomon (1980) discuss a variety of cluster analyses of the iris data.

In this example PROC ACECLUS is used to transform the data, and the clustering is performed by PROC FASTCLUS. Compare this with the example in Chapter 34, “The FASTCLUS Procedure.” The results from the FREQ procedure display fewer misclassifications when PROC ACECLUS is used.

The following statements produce [Output 22.1.1](#) through [Output 22.1.5](#):

```
proc format;
  value specname
    1='Setosa      '
    2='Versicolor'
    3='Virginica  ';
run;

data iris;
  title 'Fisher (1936) Iris Data';
  input SepalLength SepalWidth PetalLength PetalWidth Species @@;
  format Species specname.;
  label SepalLength='Sepal Length in mm.'
        SepalWidth  ='Sepal Width in mm.'
        PetalLength ='Petal Length in mm.'
        PetalWidth  ='Petal Width in mm.';
  datalines;
50 33 14 02 1 64 28 56 22 3 65 28 46 15 2 67 31 56 24 3
63 28 51 15 3 46 34 14 03 1 69 31 51 23 3 62 22 45 15 2
59 32 48 18 2 46 36 10 02 1 61 30 46 14 2 60 27 51 16 2

... more lines ...

63 33 60 25 3 53 37 15 02 1
;

proc aceclus data=iris out=ace p=.02 outstat=score;
  var SepalLength SepalWidth PetalLength PetalWidth ;
run;

proc sgplot data=ace;
  scatter y=can2 x=can1 / group=Species;
  keylegend / title="Species";
  format Species specname. ;
run;

proc fastclus data=ace maxc=3 maxiter=10 conv=0 out=clus;
  var can;;
run;

proc freq;
  tables cluster*Species;
run;
```

**Output 22.1.1** Using PROC ACECLUS to Transform Fisher's Iris Data

| Fisher (1936) Iris Data                                |     |            |         |
|--------------------------------------------------------|-----|------------|---------|
| The ACECLUS Procedure                                  |     |            |         |
| Approximate Covariance Estimation for Cluster Analysis |     |            |         |
| Observations                                           | 150 | Proportion | 0.0200  |
| Variables                                              | 4   | Converge   | 0.00100 |



Output 22.1.1 continued

| Means and Standard Deviations |         |                    |                     |
|-------------------------------|---------|--------------------|---------------------|
| Variable                      | Mean    | Standard Deviation | Label               |
| SepalLength                   | 58.4333 | 8.2807             | Sepal Length in mm. |
| SepalWidth                    | 30.5733 | 4.3587             | Sepal Width in mm.  |
| PetalLength                   | 37.5800 | 17.6530            | Petal Length in mm. |
| PetalWidth                    | 11.9933 | 7.6224             | Petal Width in mm.  |

| COV: Total Sample Covariances |             |             |             |             |
|-------------------------------|-------------|-------------|-------------|-------------|
|                               | SepalLength | SepalWidth  | PetalLength | PetalWidth  |
| SepalLength                   | 68.5693512  | -4.2434004  | 127.4315436 | 51.6270694  |
| SepalWidth                    | -4.2434004  | 18.9979418  | -32.9656376 | -12.1639374 |
| PetalLength                   | 127.4315436 | -32.9656376 | 311.6277852 | 129.5609396 |
| PetalWidth                    | 51.6270694  | -12.1639374 | 129.5609396 | 58.1006264  |

Initial Within-Cluster Covariance Estimate = Full Covariance Matrix

Threshold = 0.334211

Iteration History

| Iteration | RMS Distance | Distance Cutoff | Pairs Within Cutoff | Convergence Measure |
|-----------|--------------|-----------------|---------------------|---------------------|
| 1         | 2.828        | 0.945           | 408.0               | 0.465775            |
| 2         | 11.905       | 3.979           | 559.0               | 0.013487            |
| 3         | 13.152       | 4.396           | 940.0               | 0.029499            |
| 4         | 13.439       | 4.491           | 1506.0              | 0.046846            |
| 5         | 13.271       | 4.435           | 2036.0              | 0.046859            |
| 6         | 12.591       | 4.208           | 2285.0              | 0.025027            |
| 7         | 12.199       | 4.077           | 2366.0              | 0.009559            |
| 8         | 12.121       | 4.051           | 2402.0              | 0.003895            |
| 9         | 12.064       | 4.032           | 2417.0              | 0.002051            |
| 10        | 12.047       | 4.026           | 2429.0              | 0.000971            |

Algorithm converged.

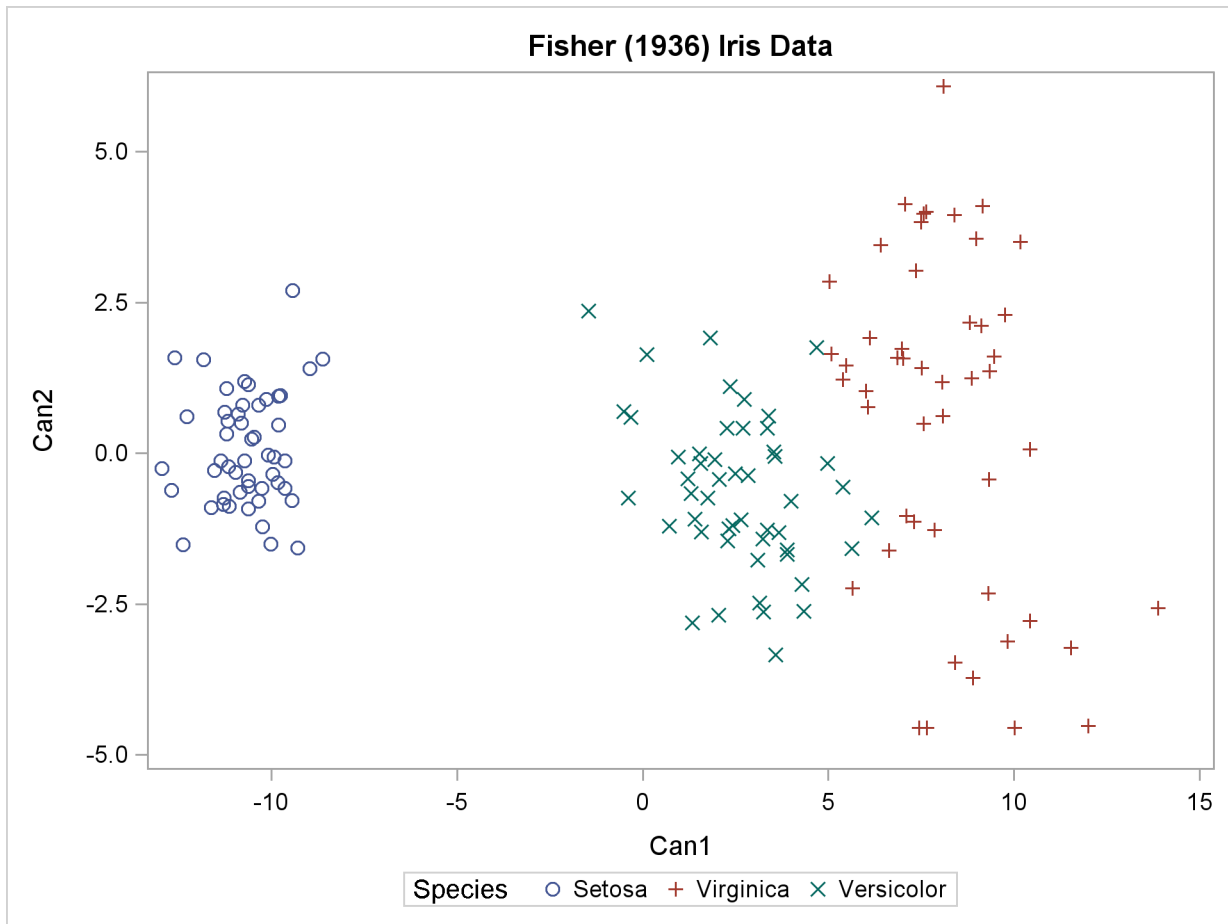
Output 22.1.2 Eigenvalues, Raw Canonical Coefficients, and Standardized Canonical Coefficients

| ACE: Approximate Covariance Estimate Within Clusters |             |            |             |            |
|------------------------------------------------------|-------------|------------|-------------|------------|
|                                                      | SepalLength | SepalWidth | PetalLength | PetalWidth |
| SepalLength                                          | 11.73342939 | 5.47550432 | 4.95389049  | 2.02902429 |
| SepalWidth                                           | 5.47550432  | 6.91992590 | 2.42177851  | 1.74125154 |
| PetalLength                                          | 4.95389049  | 2.42177851 | 6.53746398  | 2.35302594 |
| PetalWidth                                           | 2.02902429  | 1.74125154 | 2.35302594  | 2.05166735 |

Output 22.1.2 *continued*

| Eigenvalues of Inv (ACE) * (COV-ACE)      |                     |            |            |            |          |
|-------------------------------------------|---------------------|------------|------------|------------|----------|
|                                           | Eigenvalue          | Difference | Proportion | Cumulative |          |
| 1                                         | 63.7716             | 61.1593    | 0.9367     | 0.9367     |          |
| 2                                         | 2.6123              | 1.5561     | 0.0384     | 0.9751     |          |
| 3                                         | 1.0562              | 0.4167     | 0.0155     | 0.9906     |          |
| 4                                         | 0.6395              |            | 0.00939    | 1.0000     |          |
| Eigenvectors (Raw Canonical Coefficients) |                     |            |            |            |          |
|                                           |                     | Can1       | Can2       | Can3       | Can4     |
| SepalLength                               | Sepal Length in mm. | -.012009   | -.098074   | -.059852   | 0.402352 |
| SepalWidth                                | Sepal Width in mm.  | -.211068   | -.000072   | 0.402391   | -.225993 |
| PetalLength                               | Petal Length in mm. | 0.324705   | -.328583   | 0.110383   | -.321069 |
| PetalWidth                                | Petal Width in mm.  | 0.266239   | 0.870434   | -.085215   | 0.320286 |
| Standardized Canonical Coefficients       |                     |            |            |            |          |
|                                           |                     | Can1       | Can2       | Can3       | Can4     |
| SepalLength                               | Sepal Length in mm. | -0.09944   | -0.81211   | -0.49562   | 3.33174  |
| SepalWidth                                | Sepal Width in mm.  | -0.91998   | -0.00031   | 1.75389    | -0.98503 |
| PetalLength                               | Petal Length in mm. | 5.73200    | -5.80047   | 1.94859    | -5.66782 |
| PetalWidth                                | Petal Width in mm.  | 2.02937    | 6.63478    | -0.64954   | 2.44134  |

**Output 22.1.3** Plot of Transformed Iris Data: PROC SGPLOT



**Output 22.1.4** Clustering of Transformed Iris Data: Partial Output from PROC FASTCLUS

```

Fisher (1936) Iris Data

The FASTCLUS Procedure
Replace=FULL Radius=0 Maxclusters=3 Maxiter=10 Converge=0

Cluster Summary

Cluster      Frequency      RMS Std      Maximum Distance
Deviation      from Seed
to Observation      Radius      Nearest
Exceeded      Cluster

-----
1              50          1.1016          5.2768          3
2              50          1.8880          6.8298          3
3              50          1.4138          5.3152          2

Cluster Summary

Cluster      Distance Between
Cluster Centroids
-----
1              13.2845
2              5.8580
3              5.8580

Statistics for Variables

Variable      Total STD      Within STD      R-Square      RSQ/(1-RSQ)
-----
Can1          8.04808          1.48537          0.966394          28.756658
Can2          1.90061          1.85646          0.058725          0.062389
Can3          1.43395          1.32518          0.157417          0.186826
Can4          1.28044          1.27550          0.021025          0.021477
OVER-ALL      4.24499          1.50298          0.876324          7.085666

Pseudo F Statistic = 520.80

Approximate Expected Over-All R-Squared = 0.80391

Cubic Clustering Criterion = 5.179

WARNING: The two values above are invalid for correlated variables.

Cluster Means

Cluster      Can1      Can2      Can3      Can4
-----
1      -10.67516964      0.06706906      0.27068819      0.11164209
2       8.12988211      0.52566663      0.51836499      0.14915404
3       2.54528754     -0.59273569     -0.78905317     -0.26079612

```

**Output 22.1.4** *continued*

| Cluster Standard Deviations |             |             |             |             |
|-----------------------------|-------------|-------------|-------------|-------------|
| Cluster                     | Can1        | Can2        | Can3        | Can4        |
| 1                           | 0.953761025 | 0.931943571 | 1.398456061 | 1.058217627 |
| 2                           | 1.799159552 | 2.743869556 | 1.270344142 | 1.370523175 |
| 3                           | 1.572366584 | 1.393565864 | 1.303411851 | 1.372050319 |

**Output 22.1.5** Crosstabulation of Cluster by Species for Fisher's Iris Data: PROC FREQ

| Fisher (1936) Iris Data     |         |          |          |        |  |
|-----------------------------|---------|----------|----------|--------|--|
| The FREQ Procedure          |         |          |          |        |  |
| Table of CLUSTER by Species |         |          |          |        |  |
| CLUSTER(Cluster)            | Species |          |          |        |  |
| Frequency                   |         |          |          |        |  |
| Percent                     |         |          |          |        |  |
| Row Pct                     |         |          |          |        |  |
| Col Pct                     | Setosa  | Versicol | Virginic | Total  |  |
|                             |         | or       | a        |        |  |
| -----+-----+-----+-----+    |         |          |          |        |  |
| 1                           | 50      | 0        | 0        | 50     |  |
|                             | 33.33   | 0.00     | 0.00     | 33.33  |  |
|                             | 100.00  | 0.00     | 0.00     |        |  |
|                             | 100.00  | 0.00     | 0.00     |        |  |
| -----+-----+-----+-----+    |         |          |          |        |  |
| 2                           | 0       | 2        | 48       | 50     |  |
|                             | 0.00    | 1.33     | 32.00    | 33.33  |  |
|                             | 0.00    | 4.00     | 96.00    |        |  |
|                             | 0.00    | 4.00     | 96.00    |        |  |
| -----+-----+-----+-----+    |         |          |          |        |  |
| 3                           | 0       | 48       | 2        | 50     |  |
|                             | 0.00    | 32.00    | 1.33     | 33.33  |  |
|                             | 0.00    | 96.00    | 4.00     |        |  |
|                             | 0.00    | 96.00    | 4.00     |        |  |
| -----+-----+-----+-----+    |         |          |          |        |  |
| Total                       | 50      | 50       | 50       | 150    |  |
|                             | 33.33   | 33.33    | 33.33    | 100.00 |  |

---

## References

- Art, D., Gnanadesikan, R., and Kettenring, R. (1982), "Data-Based Metrics for Cluster Analysis," *Utilitas Mathematica*, 75–99.
- Everitt, B. S. (1980), *Cluster Analysis*, Second Edition, London: Heineman Educational Books.
- Fisher, R. A. (1936), "The Use of Multiple Measurements in Taxonomic Problems," *Annals of Eugenics*, 7, 179–188.
- Hartigan, J. A. (1975), *Clustering Algorithms*, New York: John Wiley & Sons.
- Kettenring, R. (1984), "Personal Communication," .
- Mezzich, J. and Solomon, H. (1980), *Taxonomy and Behavioral Science*, New York: Academic Press.
- Puri, M. L. and Sen, P. K. (1971), *Nonparametric Methods in Multivariate Analysis*, New York: John Wiley & Sons.
- Rouncefield, M. (1995), "The Statistics of Poverty and Inequality," *Journal of Statistics Education Data Archive*, last accessed May 22, 2009.  
URL <http://www.amstat.org/publications/jse/v3n2/datasets.rouncefield.html>
- Wolfe, J. H. (1970), "Pattern Clustering by Multivariate Mixture Analysis," *Multivariate Behavioral Research*, 5, 329–350.

# Subject Index

- ACECLUS procedure
  - analyzing data in groups, 786, 803
  - between-cluster SSCP matrix, 780
  - clustering methods, 795
  - compared with other procedures, 783
  - computational resources, 801
  - controlling iterations, 782
  - decomposition of the SSCP matrix, 780
  - eigenvalues and eigenvectors, 790, 791, 796, 800, 802, 803
  - initial estimates, 782, 795
  - memory requirements, 801
  - missing values, 799
  - output data sets, 800
  - output table names, 803
  - time requirements, 802
  - within-cluster SSCP matrix, 780
- analyzing data in groups
  - ACECLUS procedure, 786
- approximate covariance estimation
  - clustering, 780
- between-cluster SSCP matrix
  - ACECLUS procedure, 780
- cluster
  - elliptical, 779
- clustering
  - approximate covariance estimation, 780
- clustering methods
  - ACECLUS procedure, 795
- computational resources
  - ACECLUS procedure, 801
- convergence criterion
  - ACECLUS procedure, 795
- decomposition of the SSCP matrix
  - ACECLUS procedure, 780
- eigenvalues and eigenvectors
  - ACECLUS procedure, 790, 791, 796, 800, 802, 803
- initial estimates
  - ACECLUS procedure, 795
- memory requirements
  - ACECLUS procedure, 801
- missing values
  - ACECLUS procedure, 799
- OUT= data sets
  - ACECLUS procedure, 800
- output data sets
  - ACECLUS procedure, 800
- output table names
  - ACECLUS procedure, 803
- pooled within-cluster covariance matrix
  - definition, 780
- time requirements
  - ACECLUS procedure, 802
- within-cluster SSCP matrix
  - ACECLUS procedure, 780





# Syntax Index

- ABSOLUTE option
  - PROC ACECLUS statement, [795](#)
- ACECLUS procedure
  - syntax, [793](#)
- ACECLUS procedure, BY statement, [798](#)
- ACECLUS procedure, FREQ statement, [799](#)
- ACECLUS procedure, PROC ACECLUS statement, [794](#)
  - ABSOLUTE option, [795](#)
  - CONVERGE= option, [795](#)
  - DATA= option, [795](#)
  - INITIAL= option, [795](#)
  - MAXITER= option, [795](#)
  - METHOD= option, [795](#)
  - METRIC= option, [796](#)
  - MPAIRS= option, [796](#)
  - N= option, [796](#)
  - NOPRINT option, [796](#)
  - OUT= option, [796](#)
  - OUTSTAT= option, [796](#)
  - P= option, [797](#)
  - PERCENT= option, [797](#)
  - PP option, [797](#)
  - PREFIX= option, [797](#)
  - PROPORTION= option, [797](#)
  - QQ option, [797](#)
  - SHORT option, [797](#)
  - SINGULAR= option, [797](#)
  - T= option, [797](#)
  - THRESHOLD= option, [797](#)
- ACECLUS procedure, VAR statement, [799](#)
- ACECLUS procedure, WEIGHT statement, [799](#)
- BY statement
  - ACECLUS procedure, [798](#)
- CONVERGE= option
  - PROC ACECLUS statement, [795](#)
- DATA= option
  - PROC ACECLUS statement, [795](#)
- INITIAL= option
  - PROC ACECLUS statement, [795](#)
- MAXITER= option
  - PROC ACECLUS statement, [795](#)
- METHOD= option
  - PROC ACECLUS statement, [795](#)
- METRIC= option
  - PROC ACECLUS statement, [796](#)
- MPAIRS= option
  - PROC ACECLUS statement, [796](#)
- N= option
  - PROC ACECLUS statement, [796](#)
- NOPRINT option
  - PROC ACECLUS statement, [796](#)
- OUT= option
  - PROC ACECLUS statement, [796](#)
- OUTSTAT= option
  - PROC ACECLUS statement, [796](#)
- P= option
  - PROC ACECLUS statement, [797](#)
- PERCENT= option
  - PROC ACECLUS statement, [797](#)
- PP option
  - PROC ACECLUS statement, [797](#)
- PREFIX= option
  - PROC ACECLUS statement, [797](#)
- PROC ACECLUS statement, *see* ACECLUS procedure
- PROPORTION= option
  - PROC ACECLUS statement, [797](#)
- QQ option
  - PROC ACECLUS statement, [797](#)
- SHORT option
  - PROC ACECLUS statement, [797](#)
- SINGULAR= option
  - PROC ACECLUS statement, [797](#)
- T= option
  - PROC ACECLUS statement, [797](#)
- THRESHOLD= option
  - PROC ACECLUS statement, [797](#)



## Your Turn

---

We welcome your feedback.

- If you have comments about this book, please send them to **`yourturn@sas.com`**. Include the full title and page numbers (if applicable).
- If you have comments about the software, please send them to **`suggest@sas.com`**.



# SAS® Publishing Delivers!

Whether you are new to the work force or an experienced professional, you need to distinguish yourself in this rapidly changing and competitive job market. SAS® Publishing provides you with a wide range of resources to help you set yourself apart. Visit us online at [support.sas.com/bookstore](http://support.sas.com/bookstore).

## SAS® Press

Need to learn the basics? Struggling with a programming problem? You'll find the expert answers that you need in example-rich books from SAS Press. Written by experienced SAS professionals from around the world, SAS Press books deliver real-world insights on a broad range of topics for all skill levels.

**[support.sas.com/saspress](http://support.sas.com/saspress)**

## SAS® Documentation

To successfully implement applications using SAS software, companies in every industry and on every continent all turn to the one source for accurate, timely, and reliable information: SAS documentation. We currently produce the following types of reference documentation to improve your work experience:

- Online help that is built into the software.
- Tutorials that are integrated into the product.
- Reference documentation delivered in HTML and PDF – **free** on the Web.
- Hard-copy books.

**[support.sas.com/publishing](http://support.sas.com/publishing)**

## SAS® Publishing News

Subscribe to SAS Publishing News to receive up-to-date information about all new SAS titles, author podcasts, and new Web site features via e-mail. Complete instructions on how to subscribe, as well as access to past issues, are available at our Web site.

**[support.sas.com/spn](http://support.sas.com/spn)**



**THE  
POWER  
TO KNOW®**

