

SAS/STAT® 9.2 User's Guide The TREE Procedure (Book Excerpt)



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Chapter 91

The TREE Procedure

tents	
Overview: TREE Procedure	7347
Getting Started: TREE Procedure	7348
Syntax: TREE Procedure	7353
PROC TREE Statement	7353
BY Statement	7359
COPY Statement	7359
FREQ Statement	7360
HEIGHT Statement	7360
ID Statement	7360
NAME Statement	7360
PARENT Statement	7361
Details: TREE Procedure	7361
Missing Values	7361
Output Data Set	7361
Displayed Output	7362
ODS Table Names	7362
Examples: TREE Procedure	7363
Example 91.1: Mammals' Teeth	
Example 91.2: Iris Data	
References	

Overview: TREE Procedure

The TREE procedure produces a tree diagram, also known as a *dendrogram* or *phenogram*, from a data set created by the CLUSTER or VARCLUS procedure that contains the results of hierarchical clustering as a tree structure. The TREE procedure uses the data set to produce a diagram of the tree structure in the style of Johnson (1967), with the root at the top. Alternatively, the diagram can be oriented horizontally, with the root at the left. Any numeric variable in the output data set can be used to specify the heights of the clusters. PROC TREE can also create an output data set containing a variable to indicate the disjoint clusters at a specified level in the tree.

Tree diagrams are discussed in the context of cluster analysis by Duran and Odell (1974), Hartigan (1975), and Everitt (1980). Knuth (1973) provides a general treatment of tree diagrams in computer programming.

The literature on tree diagrams contains a mixture of botanical and genealogical terminology. The objects that are clustered are *leaves*. The cluster containing all objects is the *root*. A cluster containing at least two objects but not all of them is a *branch*. The general term for leaves, branches, and roots is *node*. If a cluster A is the union of clusters B and C, then A is the *parent* of B and C, and B and C are *children* of A. A leaf is thus a node with no children, and a root is a node with no parent. If every cluster has at most two children, the tree diagram is a *binary tree*. The CLUSTER procedure always produces binary trees. The VARCLUS procedure can produce tree diagrams with clusters that have many children.

Getting Started: TREE Procedure

The TREE procedure creates tree diagrams from a SAS data set containing the tree structure. You can create this type of data set with the CLUSTER or VARCLUS procedure. See Chapter 29, "The CLUSTER Procedure," and Chapter 93, "The VARCLUS Procedure," for more information.

In the following example, the VARCLUS procedure is used to divide a set of variables into hierarchical clusters and to create the SAS data set containing the tree structure. The TREE procedure then generates the tree diagrams.

The following data, from Hand et al. (1994), represent the amount of protein consumed from nine food groups for each of 25 European countries. The nine food groups are red meat (RedMeat), white meat (WhiteMeat), eggs (Eggs), milk (Milk), fish (Fish), cereal (Cereal), starch (Starch), nuts (Nuts), and fruits and vegetables (FruVeg).

The following SAS statements create the data set Protein:

```
data Protein;
  input Country $15. RedMeat WhiteMeat Eggs Milk
     Fish Cereal Starch Nuts FruVeg;
  datalines;
Albania
             10.1 1.4
                       0.5
                             8.9 0.2
                                      42.3
                                            0.6
                                                5.5
              8.9 14.0 4.3 19.9 2.1
                                      28.0
                                            3.6
Austria
                                                1.3
                                                     4 3
             13.5 9.3 4.1 17.5 4.5
                                      26.6
                                           5.7
Belgium
                       1.6
                            8.3 1.2
Bulgaria
              7.8 6.0
                                      56.7
                                            1.1
                                                3.7
                                                     4 2
Czechoslovakia 9.7 11.4
                       2.8
                            12.5
                                 2.0
                                      34.3
                                            5.0
                                                1.1
                                                     4.0
Denmark
                       3.7 25.0 9.9
             10.6 10.8
                                      21.9
                                            4.8
                                                0.7
                                                     2.4
E Germany
              8.4 11.6
                       3.7 11.1
                                 5.4 24.6
                                            6.5
                                                0.8
              9.5 4.9
                       2.7
                            33.7
                                  5.8
                                      26.3
                                            5.1
                                                1.0
                                                     1.4
Finland
             18.0
                   9.9
                       3.3
                            19.5
                                  5.7
                                      28.1
France
                                            4.8
                                                2.4
             10.2 3.0
                       2.8 17.6 5.9
                                      41.7
                                            2.2
                                                7.8
Greece
                       2.9
Hungary
              5.3 12.4
                            9.7 0.3
                                      40.1
                                           4.0
                                                5.4
                       4.7 25.8 2.2 24.0
                                                     2.9
Ireland
             13.9 10.0
                                            6.2
                                                1.6
Italy
              9.0 5.1
                       2.9 13.7 3.4 36.8 2.1
                                                4.3
                                                     6.7
Netherlands
             9.5 13.6 3.6 23.4 2.5 22.4 4.2 1.8 3.7
```

```
9.4 4.7 2.7 23.3 9.7 23.0 4.6 1.6 2.7
Norway
Poland
             6.9 10.2 2.7 19.3 3.0 36.1 5.9
                                             2.0 6.6
             6.2 3.7 1.1
                          4.9 14.2 27.0 5.9
                                             4.7 7.9
Portugal
Romania
             6.2
                 6.3
                     1.5 11.1 1.0 49.6
                                        3.1
             7.1 3.4 3.1
                          8.6
                              7.0 29.2 5.7
Spain
             9.9 7.8 3.5
                          4.7 7.5 19.5
Sweden
Switzerland 13.1 10.1 3.1 23.8 2.3 25.6 2.8
                                             2.4 4.9
            17.4 5.7 4.7 20.6
                              4.3 24.3
                                        4.7
                                             3.4
UK
USSR
            9.3 4.6 2.1 16.6 3.0 43.6
                                        6.4
           11.4 12.5 4.1 18.8 3.4 18.6
                                        5.2 1.5 3.8
W Germany
Yugoslavia
            4.4 5.0 1.2 9.5 0.6 55.9
                                            5.7 3.2
                                        3.0
;
run;
```

The data set Protein contains the character variable Country and the nine numeric variables representing the food groups. The \$15. in the INPUT statement specifies that the variable Country is a character variable with a length of 15.

The following statements cluster the variables in the data set Protein. The OUTTREE= option creates an output data set named Tree to contain the tree structure. The CENTROID option specifies the centroid clustering method, and the MAXCLUSTERS= option specifies that the largest number of clusters desired is four. The NOPRINT option suppresses the display of the output. The VAR statement specifies that all numeric variables (RedMeat—FruVeg) are used by the procedure.

```
proc varclus data=Protein outtree=Tree centroid maxclusters=4 noprint;
  var RedMeat--FruVeg;
run;
```

The output data set Tree, created by the OUTTREE= option in the previous statements, contains the following variables:

```
_NAME_ the name of the cluster

_PARENT_ the parent of the cluster

_NCL_ the number of clusters

_VAREXP_ the amount of variance explained by the cluster

_PROPOR_ the proportion of variance explained by the clusters at the current level of the tree diagram

_MINPRO_ the minimum proportion of variance explained by a cluster

_MAXEIGEN_ the maximum second eigenvalue of a cluster
```

The following statements produce tree diagrams of the clusters created by PROC VARCLUS:

```
proc tree data=tree;
proc tree data=tree lineprinter;
```

PROC TREE is invoked twice. In the first invocation, the tree diagram is presented using the default graphical output. In the second invocation, the LINEPRINTER option specifies line printer output.

Figure 91.1 displays the default graphical representation of the tree diagram.

Figure 91.1 Graphical Tree Diagram from PROC TREE

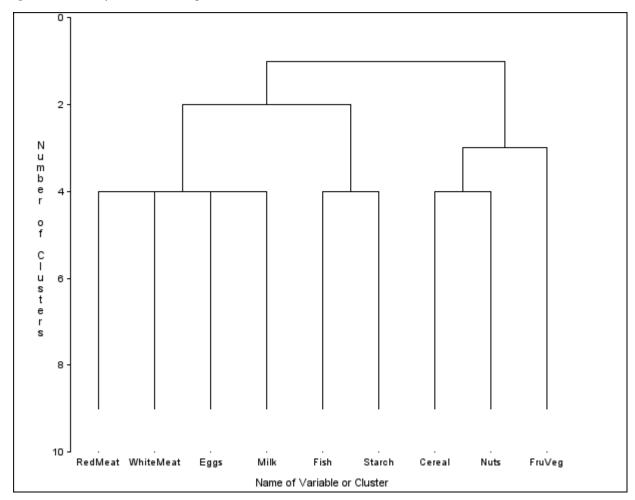


Figure 91.2 displays the same information as Figure 91.1 by using line printer output.

Figure 91.2 Line Printer Representation of the Tree Diagram

				Name	of Va	riable	or Clu	ıster		
			W							
			h							
		R	i							
		e	t				s	С		F
		d	е				t	е		r
		M	M	E	M	F	a	r	N	u
		e	е	g	i	i	r	е	u	v
		a	a	g	1	s	c	a	t	е
		t	t	s	k	h	h	1	s	g
	1	+XXXX	XXXXXX	xxxxx	XXXXXX	(XXXXX	XXXXXX	(XXXXX	XXXXX	XXXX
		XXX	XXXXXX	XXXXX	XXXXXX	XXXXXX	XXXX	XXXX	XXXXXX	XXXX
		XXX	XXXXXX	xxxxx	XXXXXX	(XXXXX	XXXX	XXXX	XXXXX	XXXX
N	2	+XXXX	XXXXXX	XXXXX	XXXXXX			XXXX	XXXXX	XXXX
u			XXXXXX				XXXX		XXXXX	
m		•	XXXXXX				XXXX		XXXXX	
b	3		XXXXXX				XXXX		XXXXX	XXXX
е		•	XXXXXX				XXXX	XXXX		•
r	_	•	XXXXXX				XXXX	XXXX		•
	4		XXXXXX	xxxxxx	XXXX	XXXX	XXXX	XXXX	XXXX	•
0		1.	•	•	•	•	•	•	•	•
f	_	1.	•	•	•	•	•	•	•	•
~	5		•	•	•	•	•	•	•	•
C 1		1.	•	•	•	•	•	•	•	•
u u	_	1.	•	•	•	•	•	•	•	•
-	ø	+.	•	•	•	•	•	•	•	•
s t		. .	•	•	•	•	•	•	•	•
e	7	+.	•	•	•	•	•	•	•	•
e r	'	T.	•	•	•	•	•	•	•	•
s		1.	•	•		•	•	•	•	•
S	8	+.	•	•	•	•	•	•	•	•
	3	T.	•	•	•	•	•	•	•	•
		1.	•	•	•	•	•	•	•	•
	9	+.	•	•		•	•	•	•	•
	_	• •	•	•	•	•	•	•	•	•

In each diagram the name of the cluster is displayed on the horizontal axis and the number of clusters is displayed on the vertical or height axis.

As you look up from the bottom of either diagram, clusters are progressively joined until a single, all-encompassing cluster is formed at the top (or root) of the tree. Clusters exist at each level of the diagram. For example, at the level where the diagram indicates three clusters, the clusters are as follows:

- Cluster 1: RedMeat WhiteMeat Eggs Milk
- Cluster 2: Fish Starch
- Cluster 3: Cereal Nuts FruVeg

As you proceed up the diagram one level, the number of clusters is two:

- Cluster 1: RedMeat WhiteMeat Eggs Milk Fish Starch
- Cluster 2: Cereal Nuts FruVeg

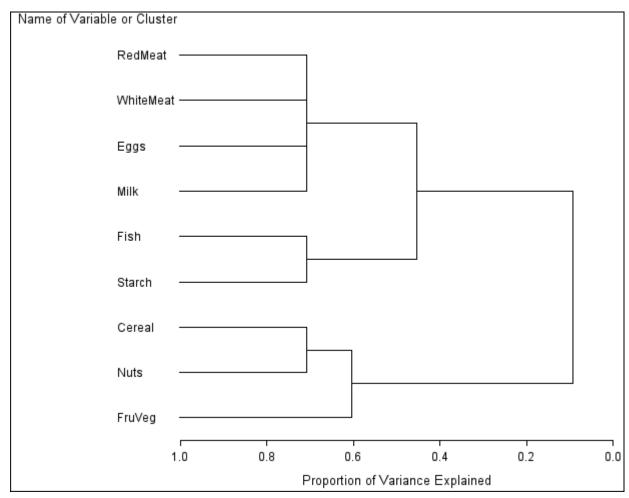
The following statements illustrate how you can specify the numeric variable defining the height of each node (cluster) in the tree:

```
axis1 order=(0 to 1 by 0.2);
proc tree data=Tree horizontal haxis=axis1;
  height _PROPOR_;
run;
```

The AXIS1 statement ORDER= option specifies the data values in the order in which they are to appear on the axis. The HORIZONTAL option in the PROC TREE statement orients the tree diagram horizontally. The HAXIS option specifies that the AXIS1 statement be used to customize the appearance of the horizontal axis. The HEIGHT statement specifies the variable _PROPOR_ (the proportion of variance explained) as the height variable.

The resulting tree diagram is shown in Figure 91.3.

Figure 91.3 Horizontal Tree Diagram with _PROPOR_ as the HEIGHT Variable



As you look from left to right in the diagram, objects and clusters are progressively joined until a single, all-encompassing cluster is formed at the right (or root) of the tree.

Clusters exist at each level of the diagram, represented by horizontal line segments. Each vertical line segment represents a point where leaves and branches are connected into progressively larger clusters.

For example, three clusters are formed at the leftmost point along the axis where three horizontal line segments exist. At that point, where a vertical line segment connects the Cereal-Nuts and FruVeg clusters, the proportion of variance explained is about 0.6 (_PROPOR_ = 0.6). At the next clustering level the variables Fish and Starch are clustered with variables RedMeat through Milk, resulting in a total of two clusters. The proportion of variance explained is about 0.45 at that point.

Syntax: TREE Procedure

The TREE procedure is invoked by the following statements:

```
PROC TREE < options > ;

NAME variables;

HEIGHT variable;

PARENT variables;

BY variables;

COPY variables;

FREQ variable;

ID variable;
```

If the input data set has been created by CLUSTER or VARCLUS, the only statement required is the PROC TREE statement. The BY, COPY, FREQ, HEIGHT, ID, NAME, and PARENT statements are described after the PROC TREE statement.

PROC TREE Statement

```
PROC TREE < options > ;
```

The PROC TREE statement starts the TREE procedure.

The options that can appear in the PROC TREE statement are summarized in Table 91.1.

Table 91.1 PROC TREE Statement Options

Option	Description
Data Sets	
DATA=	specifies input data set
DOCK=	specifies that small clusters not be counted in OUT= data
	set

Table 91.1 continued

	D 14
Option	Description
LEVEL=	defines disjoint cluster in OUT= data set
NCLUSTERS=	specifies number of clusters in OUT= data set
OUT=	specifies output data set
ROOT=	displays root of a subtree
Cluster Heights	
HEIGHT=	specifies variable for the height axis
DISSIMILAR	specifies that height values indicate dissimilarity
SIMILAR	specifies that height values indicate similarity
Horizontal Trees	
HORIZONTAL	specifies that height axis be horizontal
Sort Order	
DESCENDING	reverses sort order
SORT	sorts children by HEIGHT variable
Displayed Outpu	t
INC=	specifies increment between tick values
LINEPRINTER	displays tree by using line printer graphics
LIST	displays all nodes in tree
MAXHEIGHT=	specifies maximum value on axis
MINHEIGHT=	specifies minimum value on axis
NOPRINT	suppresses display of tree
NTICK=	specifies number of tick intervals
Graphics	
CFRAME=	specifies color of the frame
DESCRIPTION=	specifies catalog description
GOUT=	specifies catalog name
HAXIS=	customizes horizontal axis
HORDISPLAY=	displays horizontal tree with leaves on right
HPAGES=	specifies number of pages to expand tree horizontally
LINES=	specifies line color and thickness, dots at nodes
NAME=	specifies name of graph in catalog
VAXIS=	customizes vertical axis
VPAGES=	specifies number of pages to expand tree vertically
Line Printer Gra	phics
PAGES=	specifies number of pages
POS=	specifies number of column positions
SPACES=	specifies number of spaces between objects
TICKPOS=	specifies number of column positions between ticks
FILLCHAR=	specifies fill character between unjoined leaves
JOINCHAR=	specifies character displayed between joined leaves
LEAFCHAR=	specifies character representing clusters with no children
TREECHAR=	specifies character representing clusters with children

CFRAME=color

specifies a color for the frame, which is the rectangle bounded by the axes.

DATA=SAS-data-set

specifies the input data set defining the tree. If you omit the DATA= option, the most recently created SAS data set is used.

DESCENDING

DES

reverses the sorting order for the SORT option.

DESCRIPTION=entry-description

specifies a description for the graph in the GOUT= catalog. The default is "Proc Tree Graph Output."

DISSIMILAR

DIS

specifies that the values of the HEIGHT variable are dissimilarities; that is, a large height value means that the clusters are very dissimilar or far apart.

If neither the SIMILAR nor the DISSIMILAR option is specified, PROC TREE attempts to infer from the data whether the height values are similarities or dissimilarities. If PROC TREE cannot tell this from the data, it issues an error message and does not display a tree diagram.

DOCK=n

causes observations in the OUT= data set assigned to output clusters with a frequency of n or less to be given missing values for the output variables CLUSTER and CLUSNAME. If the NCLUSTERS= option is also specified, DOCK= also prevents clusters with a frequency of n or less from being counted toward the number of clusters requested by the NCLUSTERS= option. By default, DOCK=0.

FILLCHAR='c'

FC='c'

specifies the character to display between leaves that are not joined into a cluster. The character should be enclosed in single quotes. The default is a blank. The LINEPRINTER option must also be specified.

GOUT=< libref. > member-name

specifies the catalog in which the generated graph is stored. The default is WORK.GSEG.

HAXIS=AXISn

specifies that the AXISn statement used to customize the appearance of the horizontal axis.

HEIGHT=name

H=name

specifies certain conventional variables to be used for the height axis of the tree diagram. For many situations, the only option you need is the HEIGHT= option. Valid values for *name* and their meanings are as follows:

HEIGHT | H specifies the _HEIGHT_ variable.

LENGTH | L defines the height of each node as its path length from the root. This can

also be interpreted as the number of ancestors of the node.

MODE | M specifies the _MODE_ variable.

NCL | N specifies the _NCL_ (number of clusters) variable.

RSQ | R specifies the _RSQ_ variable.

See also the section "HEIGHT Statement" on page 7360, which can specify any variable in the input data set to be used for the height axis. In rare cases, you might need to specify either the DISSIMILAR option or the SIMILAR option.

HORDISPLAY=RIGHT

specifies that the graph be oriented horizontally, with the leaf nodes on the right side, when the HORIZONTAL option is also specified. By default, the leaf nodes are on the left side.

HORIZONTAL

HOR

displays the tree diagram with the height axis oriented horizontally. The leaf nodes are on the side specified in the HORDISPLAY= option. If you do not specify the HORIZONTAL option, the height axis is vertical, with the root at the top. When the tree takes up more than one page, horizontal orientation can make the tree diagram considerably easier to read.

HPAGES=n1

specifies that the original graph be enlarged to cover n1 pages. If you also specify the VPAGES=n2 option, the original graph is enlarged to cover $n1 \times n2$ graphs. For example, if HPAGES=n2 and VPAGES=n2, then the original graph is generated, followed by n2 in the horizontal direction and by a factor of n2 in the horizontal direction and by a factor of n2 in the vertical direction. The graphs are generated in left-to-right and top-to-bottom order.

INC=n

specifies the increment between tick values on the height axis. If the HEIGHT variable is _NCL_, the default is usually 1, although a different value can be specified for consistency with other options. For any other HEIGHT variable, the default is some power of 10 times 1, 2, 2.5, or 5.

JOINCHAR='c'

JC='c'

specifies the character displayed between leaves that are joined into a cluster. The character should be enclosed in single quotes. The default is 'X'. The LINEPRINTER option must also be specified.

LEAFCHAR='c'

LC='c'

specifies the character used to represent clusters having no children. The character should be enclosed in single quotes. The default is a period. The LINEPRINTER option must also be specified.

LEVEL=n

specifies the level of the tree defining disjoint clusters for the OUT= data set. The LEVEL= option also causes only clusters between the root and a height of n to be displayed. The clusters in the output data set are those that exist at a height of n on the tree diagram. For example, if the HEIGHT variable is _NCL_ (number of clusters) and LEVEL=5 is specified, then the OUT= data set contains five disjoint clusters. If the HEIGHT variable is _RSQ_ (R^2) and LEVEL=0.9 is specified, then the OUT= data set contains the smallest number of clusters that yields an R^2 of at least 0.9.

LINEPRINTER

specifies that the tree diagram be displayed using line printer graphics.

LINES=(< COLOR=color > < WIDTH=n > < DOTS >)

specifies the color and the thickness of the lines of the tree, and whether a dot is drawn at each leaf node. Note that if the frame and the lines are specified to be the same color, PROC TREE selects a different color for the lines.

LIST

lists all the nodes in the tree, displaying the height, parent, and children of each node.

MAXHEIGHT=n

MAXH=n

specifies the maximum value displayed on the height axis.

MINHEIGHT=n

MINH=n

specifies the minimum value displayed on the height axis.

NAME=name

specifies the entry name for the generated graph in the GOUT= catalog. Note that each time another graph is generated with the same name, the name is modified by appending a number to make it unique.

NCLUSTERS=n

NCL=n

N=n

specifies the number of clusters desired in the OUT= data set. The number of clusters obtained might not equal the number specified if (1) there are fewer than n leaves in the tree, (2) there are more than n unconnected trees in the data set, (3) a multiway tree does not contain a level with the specified number of clusters, or (4) the DOCK= option eliminates too many clusters.

The NCLUSTERS= option uses the _NCL_ variable to determine the order in which the clusters are formed. If there is no _NCL_ variable, the height variable (as determined by the HEIGHT statement or HEIGHT= option) is used instead.

NTICK=n

specifies the number of tick intervals on the height axis. The default depends on the values of other options.

NOPRINT

suppresses the display of the tree. Specify the NOPRINT option if you want only to create an OUT= data set.

OUT=SAS-data-set

creates an output data set containing one observation for each object in the tree or subtree being processed and variables called CLUSTER and CLUSNAME showing cluster membership at any specified level in the tree. If you specify the OUT= option, you must also specify either the NCLUSTERS= or LEVEL= option in order to define the output partition level. If you want to create a permanent SAS data set, you must specify a two-level name (see "SAS Data Files" in SAS Language Reference: Concepts).

PAGES=n

specifies the number of pages over which the tree diagram (from root to leaves) is to extend. The default is 1. The LINEPRINTER option must also be specified.

POS=n

specifies the number of column positions on the height axis. The default depends on the value of the PAGES= option, the orientation of the tree diagram, and the values specified by the PAGESIZE= and LINESIZE= options. The LINEPRINTER option must also be specified.

ROOT='name'

specifies the value of the NAME variable for the root of a subtree to be displayed if you do not want to display the entire tree. If you also specify the OUT= option, the output data set contains only objects belonging to the subtree specified by the ROOT= option.

SIMILAR

SIM

specifies that the values of the HEIGHT variable represent similarities; that is, a large height value means that the clusters are very similar or close together.

If neither the SIMILAR nor the DISSIMILAR option is specified, PROC TREE attempts to infer from the data whether the height values are similarities or dissimilarities. If PROC TREE cannot tell this from the data, it issues an error message and does not display a tree diagram.

SORT

sorts the children of each node by the HEIGHT variable, in the order of cluster formation. See the DESCENDING option on page 7355 for details.

SPACES=s

S=*s*

specifies the number of spaces between objects in the output. The default depends on the number of objects, the orientation of the tree diagram, and the values specified by the PAGE-SIZE= and LINESIZE= options. The LINEPRINTER option must also be specified.

TICKPOS=n

specifies the number of column positions per tick interval on the height axis. The default value is usually between 5 and 10, although a different value can be specified for consistency with other options.

TREECHAR='c'

TC = 'c'

specifies the character used to represent clusters with children. The character should be enclosed in single quotes. The default is 'X'. The LINEPRINTER option must also be specified.

VAXIS=AXISn

specifies that the AXISn statement be used to customize the appearance of the vertical axis.

VPAGES=n2

specifies that the original graph be enlarged to cover n2 pages. If you also specify the HPAGES=n1 option, the original graph is enlarged to cover $n1 \times n2$ pages. For example, if HPAGES=n1 option, the original graph is generated, followed by n10 years and VPAGES=n11, then the original graph is generated, followed by n12 years are graphs. In these six graphs, the original is enlarged by a factor of n12 in the horizontal direction and by a factor of n13 in the vertical direction. The graphs are generated in left-to-right and top-to-bottom order.

BY Statement

BY variables;

You can specify a BY statement with PROC TREE to obtain separate analyses on observations in groups 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 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 BY statement option NOTSORTED or DESCENDING in the BY statement for the TREE 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.

For more information about the BY statement, see SAS Language Reference: Concepts. For more information about the DATASETS procedure, see the Base SAS Procedures Guide.

COPY Statement

COPY variables;

The COPY statement specifies one or more character or numeric variables to be copied to the OUT= data set.

FREQ Statement

FREQ variable;

The FREQ statement specifies one numeric variable that tells how many clustering observations belong to the cluster. If the FREQ statement is omitted, PROC TREE uses the variable _FREQ_ to specify the number of observations per cluster. If neither the FREQ statement nor the _FREQ_ variable is present, each leaf is assumed to represent one clustering observation, and the frequency for each internal node is found by summing the frequencies of its children.

HEIGHT Statement

HEIGHT variable;

The HEIGHT statement specifies the name of a numeric variable to define the height of each node (cluster) in the tree. The height variable can also be specified by the HEIGHT= option in the PROC TREE statement. If both the HEIGHT statement and the HEIGHT= option are omitted, PROC TREE uses the variable _HEIGHT_. If the data set does not contain _HEIGHT_, PROC TREE uses the variable _NCL_. If _NCL_ is not present either, the height of each node is defined to be its path length from the root.

ID Statement

ID variable;

The ID variable is used to identify the objects (leaves) in the tree on the output. The ID variable can be a character or numeric variable of any length. If the ID statement is omitted, the variable in the NAME statement is used instead. If both the ID and NAME statements are omitted, PROC TREE uses the variable _NAME_. If the _NAME_ variable is not found in the data set, PROC TREE issues an error message and stops. The ID variable is copied to the OUT= data set.

NAME Statement

NAME variable;

The NAME statement specifies a character or numeric variable identifying the node represented by each observation. The NAME variable and the PARENT variable jointly define the tree structure. If the NAME statement is omitted, PROC TREE uses the variable _NAME_. If the _NAME_ variable is not found in the data set, PROC TREE issues an error message and stops.

PARENT Statement

PARENT variable;

The PARENT statement specifies a character or numeric variable identifying the node in the tree that is the parent of each observation. The PARENT variable must have the same formatted length as the NAME variable. If the PARENT statement is omitted, PROC TREE uses the variable _PARENT_. If the PARENT variable is not found in the data set, PROC TREE issues an error message and stops.

Details: TREE Procedure

Missing Values

An observation with a missing value for the NAME variable is omitted from processing. If the PARENT variable has a missing value but the NAME variable is present, the observation is treated as the root of a tree. A data set can contain several roots and, hence, several trees.

Missing values of the HEIGHT variable are set to upper or lower bounds determined from the nonmissing values under the assumption that the heights are monotonic with respect to the tree structure.

Missing values of the FREQ variable are inferred from nonmissing values where possible; otherwise, they are treated as zero.

Output Data Set

The OUT= data set contains one observation for each leaf in the tree or subtree being processed. The variables are as follows:

- the BY variables, if any
- the ID variable, or the NAME variable if the ID statement is not used
- the COPY variables
- a numeric variable CLUSTER taking values from 1 to c, where c is the number of disjoint clusters. The cluster to which the first observation belongs is given the number 1, the cluster to which the next observation belongs that does not belong to cluster 1 is given the number 2, and so on.

• a character variable CLUSNAME giving the value of the NAME variable of the cluster to which the observation belongs

The CLUSTER and CLUSNAME variables are missing if the corresponding leaf has a nonpositive frequency.

Displayed Output

The displayed output from the TREE procedure includes the following:

- the names of the objects in the tree
- the height axis
- the tree diagram. The leaves are displayed at the bottom of the graph. Horizontal lines connect the leaves into branches, while the topmost horizontal line indicates the root.

If the LINEPRINTER option is specified, the root (the cluster containing all the objects) is indicated by a solid line of the character specified by the TREECHAR= option (the default character is 'X'). At each level of the tree, clusters are shown by unbroken lines of the TREECHAR= symbol with the FILLCHAR= symbol (the default is a blank) separating the clusters. The LEAFCHAR= symbol (the default character is a period) represents single-member clusters.

By default, the tree diagram is oriented with the height axis vertical and the object names at the top of the diagram. If the HORIZONTAL option is specified, then the height axis is horizontal and the object names are on the left.

ODS Table Names

PROC TREE 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 91.2. For more information about ODS, see Chapter 20, "Using the Output Delivery System."

Table 91.2 ODS Tables Produced by PROC TREE

ODS Table Name	Description	Statement	Option
TreeListing	Listing of all nodes in the tree	PROC	LIST

Examples: TREE Procedure

Example 91.1: Mammals' Teeth

The following statements produce a data set containing the numbers of different kinds of teeth for a variety of mammals:

```
data teeth;
   title 'Mammals'' Teeth';
   input mammal $ 1-16 @21 (v1-v8) (1.);
   label V1='Right Top Incisors'
         V2='Right Bottom Incisors'
         V3='Right Top Canines'
         V4='Right Bottom Canines'
         V5='Right Top Premolars'
         V6='Right Bottom Premolars'
         V7='Right Top Molars'
         V8='Right Bottom Molars';
   datalines;
Brown Bat
                   23113333
Mole
                  32103333
Silver Hair Bat 23112333
                  23112233
Pigmy Bat
                  23111233
House Bat
Red Bat
                  13112233
Pika
                  21002233
Rabbit 21003233
Beaver 11002133
Groundhog 11002133
Gray Squirrel 11001133
House Mouse
                  11000033
Porcupine
                   11001133
Wolf
                  33114423
                  33114423
Bear
                  33114432
33114412
Raccoon
Marten
Weasel
                  33113312
Wolverine
                 33114412
Badger
                    33113312
River Otter
                 33114312
Sea Otter
                  32113312
                  33113211
Jaguar
Cougar
                  33113211
                  32114411
Fur Seal
Sea Lion
                  32114411
Grey Seal
                   32113322
                 21114411
Elephant Seal
Reindeer
                  04103333
Elk
                   04103333
```

```
Deer 04003333
Moose 04003333
;
run;
```

The following statements use the CLUSTER procedure to cluster the mammals by average linkage and the TREE procedure to produce a horizontal tree diagram that uses the average-linkage distance as its height axis:

```
proc cluster method=average std pseudo noeigen outtree=tree;
  id mammal;
  var v1-v8;
run;
proc tree horizontal;
run;
```

Output 91.1.1 displays the information about how the clusters are joined. For example, the cluster history shows that the observations Wolf and Bear form cluster 29, which is merged with Raccoon to form cluster 11.

Output 91.1.1 Output from PROC CLUSTER

```
Mammals' Teeth

The CLUSTER Procedure
Average Linkage Cluster Analysis

The data have been standardized to mean 0 and variance 1

Root-Mean-Square Total-Sample Standard Deviation 1

Root-Mean-Square Distance Between Observations 4
```

Output 91.1.1 continued

		Cluster Histor	ry				
						Norm	
						RMS	
NCL	Clusters	Joined	FREQ	PSF	PST2	Dist	
31	Beaver	Groundhog	2			0	
30	Gray Squirrel	Porcupine	2		•	0	
29	Wolf	Bear	2		•	0	
28	Marten	Wolverine	2			0	
27	Weasel	Badger	2		•	0	
26	Jaguar	Cougar	2			0	
25	Fur Seal	Sea Lion	2			0	
24	Reindeer	Elk	2			0	
23	Deer	Moose	2			0	
22	Pigmy Bat	Red Bat	2	281		0.2289	
21	CL28	River Otter	3	139		0.2292	
20	CL31	CL30	4	83.2		0.2357	
19	Brown Bat	Silver Hair Bat	2	76.7	•	0.2357	
18	Pika	Rabbit	2	73.2		0.2357	
17	CL27	Sea Otter	3	67.4		0.2462	
16	CL22	House Bat	3	62.9	1.7	0.2859	
15	CL21	CL17	6	47.4	6.8	0.3328	
14	CL25	Elephant Seal	3	45.0		0.3362	
13	CL19	CL16	5	40.8	3.5	0.3672	
12	CL15	Grey Seal	7	38.9	2.8	0.4078	
11	CL29	Raccoon	3	38.0		0.423	
10	CL18	CL20	6	34.5	10.3	0.4339	
9	CL12	CL26	9	30.0	7.3	0.5071	
8	CL24	CL23	4	28.7		0.5473	
7	CL9	CL14	12	25.7	7.0	0.5668	
6	CL10	House Mouse	7	28.3	4.1	0.5792	
5	CL11	CL7	15	26.8	6.9	0.6621	
4	CL13	Mole	6	31.9	7.2	0.7156	
3	CL4	CL8	10	31.0	12.7	0.8799	
2	CL3	CL6	17	27.8	16.1		
1	CL2	CL5	32		27.8	1.1938	

Output 91.1.2 shows the corresponding tree diagram.

Mammals' Teeth Name of Observation or Cluster Brown Bat Silver Hair Bat Pigmy Bat Red Bat House Bat Mole Reindeer Elk Deer Moose Pika Rabbit Beaver Groundhog Gray Squirrel Porcupine House Mouse Wolf Bear Raccoon Marten Wolverine River Otter Weasel Badger Sea Otter Grey Seal Jaguar Cougar Fur Seal Sea Lion Elephant Seal 0.0 0.1 0.2 0.3 0.4 0.5 0.6 0.7 0.8 0.9 1.0 1.1 1.2 Average Distance Between Clusters

Output 91.1.2 Tree Diagram of Mammal Teeth Clusters

As you view the diagram in Output 91.1.2 from left to right, objects and clusters are progressively joined until a single, all-encompassing cluster is formed at the right (or root) of the tree. Clusters exist at each level of the diagram, and every vertical line connects leaves and branches into progressively larger clusters. For example, the five bats form a cluster at the 0.6 level, while the next cluster consists only of the mole. The observations Reindeer, Elk, Deer, and Moose form the next cluster at the 0.6 level, the mammals Pika through House Mouse are in the fourth cluster, The observations Wolf, Bear, and Raccoon form the fifth cluster, while the last cluster contains the observations Marten through Elephant Seal.

The following statements create the same tree with line printer graphics in a vertical orientation:

```
proc tree lineprinter;
run;
```

The tree is displayed in Output 91.1.3.

Output 91.1.3 PROC TREE with the LINEPRINTER Option

```
Mammals' Teeth
          Name of Observation or Cluster
    s
    i
    1
               G
                             E
    v
               r
                             1
               а
                     R
                             e
                     i
                             р
   В
                    ₩v
                        SG
                             h
    F
               Рu
   rHi
        R
              rSos
                           FSa
      0
                    o e
                        e r
   oagRu
              oqre
                   R
                    1 r
                        a e
                         уЈС
   wimes
            RBuuc
                   a M v
                      WВ
            a e n i u M
                   caeOeaO
          DoPbadrpoWBcrrtadtSguSLS
   BBBBBoeEeoibvhriuoeotitsqteuqeie
   aaaaaleleskieoenslaoeneeeaaaaoa
   ttttterkreatrgleefrnnerlrrlrlnl
 1.5 +
Α
v
е
r
   а
   g
  е
   D
   i
   s
   t
 а
   n
С
   XXX XXXXX . XXX XXX XXX XXXXXXX . XXX . XXXXX XXXXX . XXX XXX .
   | . . . . . . XXX XXX . . XXX XXX . XXX . XXX . XXX . . XXX XXX .
В
   | . . . . . . XXX XXX . . XXX XXX . XXX . XXX . XXX . . XXX XXX .
    . . . . . XXX XXX . . XXX XXX . XXX . XXX . XXX . . XXX XXX .
е
t
```

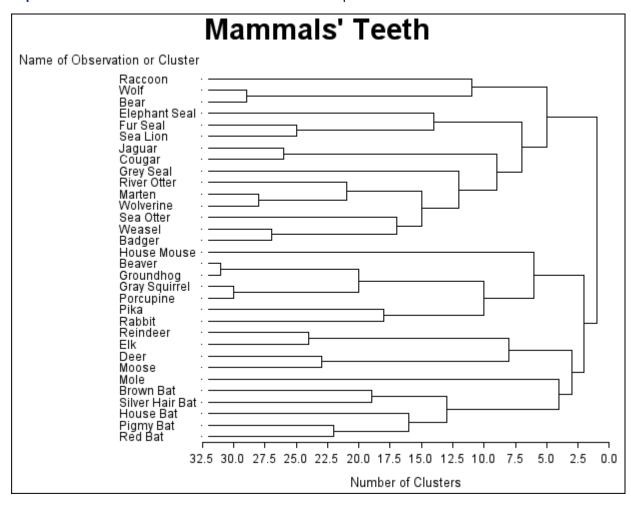
As you look up from the bottom of the diagram, objects and clusters are progressively joined until a single, all-encompassing cluster is formed at the top (or root) of the root. Clusters exist at each level of the diagram. For example, the unbroken line of Xs at the leftmost side of the 0.6 level indicates that the five bats have formed a cluster. The next cluster is represented by a period because it contains only one mammal, Mole. Reindeer, Elk, Deer, and Moose form the next cluster, indicated by Xs again. The mammals Pika through House Mouse are in the fourth cluster. The observations Wolf, Bear, and Raccoon form the fifth cluster, while the last cluster contains the observations Marten through Elephant Seal.

The next statements sort the clusters at each branch in order of formation and use the number of clusters as the height axis:

```
proc tree sort height=n horizontal;
run;
```

The resulting tree is displayed in Output 91.1.4.

Output 91.1.4 PROC TREE with SORT and HEIGHT= Options



Because the CLUSTER procedure always produces binary trees, the number of internal (root and branch) nodes in the tree is one less than the number of leaves. Therefore 31 clusters are formed from the 32 mammals in the input data set. These are represented by the 31 vertical line segments in the tree diagram, each at a different value along the horizontal axis.

As you examine the tree from left to right, the first vertical line segment is where Beaver and Groundhog are clustered and the number of clusters is 31. The next cluster is formed from Gray Squirrel and Porcupine. The third contains Wolf and Bear. Note how the tree graphically displays the clustering order information that was presented in tabular form by the CLUSTER procedure in Output 91.1.1.

The same clusters as in Output 91.1.2 and Output 91.1.3 can be seen at the six-cluster level of the tree diagram in Output 91.1.4, although the SORT and HEIGHT= options make them appear in a different order.

The following statements create these six clusters and save the result in the output data set part:

```
proc tree noprint out=part nclusters=6;
  id mammal;
  copy v1-v8;
proc sort;
  by cluster;
```

The PROC TREE statement produces no output but creates an output data set indicating the cluster to which each observation belongs at the six-cluster level in the tree. The following statements print part, with the results shown in Output 91.1.5:

```
proc print label uniform;
  id mammal;
  var v1-v8;
  format v1-v8 1.;
  by cluster;
run;
```

Output 91.1.5 PROC TREE OUT= Data Set

	Mamma.	ls' Teeth		
	CLU	STER=1		
mammal	Right Top Incisors	Right Bottom Incisors	Right Top Canines	Bottom
шашшат	Incisors	Incisors	Canines	Canines
Beaver	1	1	0	0
Groundhog	1	1	0	0
Gray Squirrel	1	1	0	0
Porcupine	1	1	0	0
Pika	2	1	0	0
Rabbit	2	1	0	0
House Mouse	1	1	0	0
		Right	Right	Right
	Right Top	Bottom	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Beaver	2	1	3	3
Groundhog	2	1	3	3
Gray Squirrel	1	1	3	3
Porcupine	1	1	3	3
Pika	2	2	3	3
Rabbit	3	2	3	3
House Mouse	0	0	3	3

Output 91.1.5 continued

	Mammal	ls' Teeth			
	CLUS	STER=2			
	=	Right	Right	Right	
	•	Bottom	_	Bottom	
mammal	Incisors	Incisors	Canines	Canines	
Wolf	3	3	1	1	
Bear	3	3	1	1	
Raccoon	3	3	1	1	
		Right	Right	Right	
	Right Top	Bottom	Top	Bottom	
mammal	Premolars	Premolars	Molars	Molars	
Wolf	4	4	2	3	
Bear	4	4	2	3	
Raccoon	4	4	3	2	
	CI III				
	CLUS	STER=3			
	Right	Right	Right	Right	
	Right Top	Right Bottom	Right Top	Right Bottom	
mamma1	Right Top	Right	Right Top	Right Bottom	
	Right Top	Right Bottom	Right Top	Right Bottom Canines	
mamma1	Right Top Incisors	Right Bottom Incisors 3 3	Right Top Canines	Right Bottom Canines	
mammal Marten	Right Top Incisors 3	Right Bottom Incisors	Right Top Canines	Right Bottom Canines	-
mammal Marten Wolverine	Right Top Incisors 3 3	Right Bottom Incisors 3 3	Right Top Canines 1 1	Right Bottom Canines 1 1	
mammal Marten Wolverine Weasel	Right Top Incisors 3 3 3 3	Right Bottom Incisors 3 3 3 Right	Right Top Canines 1 1 1 1 Right	Right Bottom Canines 1 1 1 1 Right	
mammal Marten Wolverine Weasel	Right Top Incisors 3 3 3 3	Right Bottom Incisors 3 3 3 3	Right Top Canines 1 1 1 1 Right	Right Bottom Canines 1 1 1 1 Right	
mammal Marten Wolverine Weasel	Right Top Incisors 3 3 3 3 Right Top	Right Bottom Incisors 3 3 3 Right	Right Top Canines 1 1 1 1 Right Top	Right Bottom Canines 1 1 1 1 Right Bottom	
mammal Marten Wolverine Weasel Badger	Right Top Incisors 3 3 3 3 Right Top	Right Bottom Incisors 3 3 3 Right Bottom	Right Top Canines 1 1 1 1 Right Top	Right Bottom Canines 1 1 1 1 Right Bottom	
mammal Marten Wolverine Weasel Badger mammal	Right Top Incisors 3 3 3 3 Right Top Premolars	Right Bottom Incisors 3 3 3 Right Bottom Premolars	Right Top Canines 1 1 1 1 Right Top Molars	Right Bottom Canines 1 1 1 1 Right Bottom Molars	
mammal Marten Wolverine Weasel Badger mammal Marten	Right Top Incisors 3 3 3 3 Right Top Premolars	Right Bottom Incisors 3 3 3 Right Bottom Premolars	Right Top Canines 1 1 1 1 Right Top Molars	Right Bottom Canines 1 1 1 1 Right Bottom Molars	

	Mamma.	ls' Teeth		
	CLUS	STER=3		
	(cont	tinued)		
	Right	Right	Right	Right
	Top	Bottom	Top	Bottom
mammal	Incisors	Incisors	Canines	Canines
Jaguar	3	3	1	1
Cougar	3	3	1	1
Fur Seal	3	2	1	1
Sea Lion	3	2	1	1
River Otter	3	3	1	1
Sea Otter	3	2	1	1
Elephant Seal	2	1	1	1
Grey Seal	3	2	1	1
		Right	Right	Right
	Right Top	Bottom	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Jaguar	3	2	1	1
Cougar	3	2	1	1
Fur Seal	4	4	1	1
Sea Lion	4	4	1	1
River Otter	4	3	1	2
Sea Otter	3	3	1	2
Elephant Seal	4	4	1	1
Grey Seal	3	3	2	2

Output 91.1.5 continued

	Mamma	ls' Teeth		
	CLUS	STER=4		
	Right	Right	Right	Right
	Top	Bottom	Top	Bottom
mammal	Incisors	Incisors	Canines	Canines
Reindeer	0	4	1	0
Elk	0	4	1	0
Deer	0	4	0	0
Moose	0	4	0	0
		Right	Right	Right
	Right Top	Bottom Premolars	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Reindeer	3	3	3	3
Elk	3	3	3	3
Deer	3	3	3	3
Moose	3	3	3	3
	CLUS	STER=5		
	Right	Right	Right	Right
		Bottom		
mammal	Incisors			
Pigmy Bat	2	3	1	1
Red Bat	1	3	1	1
Brown Bat	2	3	1	1
			Right	
	Right Top	Bottom	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Pigmy Bat	2	2	3	3
Red Bat	2	2	3	3
Red Bat	_	_	_	_

	Mamma	ls' Teeth		
	CLUS	STER=5		
	(cont	tinued)		
		Right		
	Top	Bottom	Top	Bottom
mammal	Incisors	Incisors	Canines	Canines
Silver Hair Bat	2	3	1	1
House Bat	2	3	1	1
		Right	Right	Right
	Right Top	Bottom	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Silver Hair Bat	2	3	3	3
House Bat	1	2	3	3
	CLUS	STER=6		
	Right	Right	Right	Right
	Top	Bottom	Top	Bottom
mammal	Incisors	Incisors	Canines	Canines
Mole	3	2	1	0
		Right	Right	Right
	Right Top	Bottom	Top	Bottom
mammal	Premolars	Premolars	Molars	Molars
Mole	3	3	3	3

Example 91.2: Iris Data

Fisher (1936)'s iris data give sepal and petal dimensions for three different species of iris. The data are clustered by kth-nearest-neighbor density linkage by using the CLUSTER procedure with K=8. Observations are identified by species (Setosa, Versicolor, or Virginica) in the tree diagram, which is oriented with the height axis horizontal. The following statements produce the results shown in Output 91.2.1 and Output 91.2.2:

```
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.';
   symbol = put(species, specname10.);
   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
65 30 52 20 3 56 25 39 11 2 65 30 55 18 3 58 27 51 19 3
68 32 59 23 3 51 33 17 05 1 57 28 45 13 2 62 34 54 23 3
77 38 67 22 3 63 33 47 16 2 67 33 57 25 3 76 30 66 21 3
49 25 45 17 3 55 35 13 02 1 67 30 52 23 3 70 32 47 14 2
64 32 45 15 2 61 28 40 13 2 48 31 16 02 1 59 30 51 18 3
55 24 38 11 2 63 25 50 19 3 64 32 53 23 3 52 34 14 02 1
49 36 14 01 1 54 30 45 15 2 79 38 64 20 3 44 32 13 02 1
67 33 57 21 3 50 35 16 06 1 58 26 40 12 2 44 30 13 02 1
77 28 67 20 3 63 27 49 18 3 47 32 16 02 1 55 26 44 12 2
50 23 33 10 2 72 32 60 18 3 48 30 14 03 1 51 38 16 02 1
61 30 49 18 3 48 34 19 02 1 50 30 16 02 1 50 32 12 02 1
61 26 56 14 3 64 28 56 21 3 43 30 11 01 1 58 40 12 02 1
51 38 19 04 1 67 31 44 14 2 62 28 48 18 3 49 30 14 02 1
51 35 14 02 1 56 30 45 15 2 58 27 41 10 2 50 34 16 04 1
46 32 14 02 1 60 29 45 15 2 57 26 35 10 2 57 44 15 04 1
50 36 14 02 1 77 30 61 23 3 63 34 56 24 3 58 27 51 19 3
57 29 42 13 2 72 30 58 16 3 54 34 15 04 1 52 41 15 01 1
71 30 59 21 3 64 31 55 18 3 60 30 48 18 3 63 29 56 18 3
49 24 33 10 2 56 27 42 13 2 57 30 42 12 2 55 42 14 02 1
49 31 15 02 1 77 26 69 23 3 60 22 50 15 3 54 39 17 04 1
66 29 46 13 2 52 27 39 14 2 60 34 45 16 2 50 34 15 02 1
44 29 14 02 1 50 20 35 10 2 55 24 37 10 2 58 27 39 12 2
47 32 13 02 1 46 31 15 02 1 69 32 57 23 3 62 29 43 13 2
74 28 61 19 3 59 30 42 15 2 51 34 15 02 1 50 35 13 03 1
56 28 49 20 3 60 22 40 10 2 73 29 63 18 3 67 25 58 18 3
49 31 15 01 1 67 31 47 15 2 63 23 44 13 2 54 37 15 02 1
56 30 41 13 2 63 25 49 15 2 61 28 47 12 2 64 29 43 13 2
51 25 30 11 2 57 28 41 13 2 65 30 58 22 3 69 31 54 21 3
54 39 13 04 1 51 35 14 03 1 72 36 61 25 3 65 32 51 20 3
61 29 47 14 2 56 29 36 13 2 69 31 49 15 2 64 27 53 19 3
68 30 55 21 3 55 25 40 13 2 48 34 16 02 1 48 30 14 01 1
45 23 13 03 1 57 25 50 20 3 57 38 17 03 1 51 38 15 03 1
```

The PAGES=1 option specifies that the tree diagram extend over one page from tree to root. Since the HORIZONTAL option is also specified, the horizontal extent of the diagram is one page. The number of vertical pages required for the diagram is dictated by the number of leaves in the tree.

The MAXH=10 limits the values displayed on the height axis to a maximum of 10. This prunes the tree diagram so that only the portion from the leaves to level 10 is displayed. You can see this pruning effect in Output 91.2.2.

Output 91.2.1 Clustering of Fisher's Iris Data

		Fish	er (1936)	Iris Data			
		The	CLUSTER P	rocedure			
		Two-Stage 1	Density Li	nkage Cluster	ring		
			K = 8				
	Root-Mean-Se	quare Total	-Sample St	andard Deviat	ion 10.	69224	
			Cluster H	listory			
				Normalized	Maximum	Density	I
				Fusion	in Each	Cluster	i
NCL	Clusters	Joined	FREQ	Density	Lesser	Greater	•
10	CL11	ОВ98	49	0.2879	0.1479	8.3678	
9	CL13	OB24	45	0.2802	0.2005	3.5156	
9			50	0 0000	0 1050	8.3678	
8	CL10	OB25	50	0.2699	0.1372	0.3076	
	CL10 CL8	OB25 OB121	51	0.2599			
8					0.1372	8.3678	
8	CT8	OB121	51	0.2586	0.1372 0.0832	8.3678 3.5156	
8 7 6	CL8	OB121 OB45	51 46	0.2586 0.1412	0.1372 0.0832 0.0605	8.3678 3.5156 3.5156	
8 7 6 5	CF6 CF8	OB121 OB45 OB39	51 46 47	0.2586 0.1412 0.107	0.1372 0.0832 0.0605 0.0541	8.3678 3.5156 3.5156 3.5156	

Output 91.2.2 Horizontal Tree for Fisher's Iris Data

				Fis	her (1	936) I:	ris Dat	a			
					Cli	ıster 1	usion	Densit	E y		
		0	_	_	_		_			8 +	
Vir	ginica										
Vir	ginica										
Vir	ginica										
Vir	ginica										
Vir	ginica										
Vir	ginica										
Vir	ginica		αх								
Vir	ginica		αх								
Vir	ginica	XXXXX	xxxxx								
Vir	ginica	XXXXX		х							
Vir	ginica	XXXXX		х							
Vir	ginica	XXXXX		хх							
Vir	ginica	xxxxx		xxxx.							
Vir	ginica	XXXXX		XXXX.							
Vir	ginica	XXXXX		xxxxx							
Vir	ginica	XXXXX		xxxxx							
Vir	ginica	XXXXX	xxxxx								
Vir	ginica	XXXXX		xxxxx			· · · · · ·				
Vir	ginica			XXXXX							
Vers	icolor			XXXXX							
Vir	ginica			XXXXX							
Vir	ginica			XXXXX							
Vir	ginica			XXXXX				. .			
Vir	ginica			XXXXX							
Vir	ginica			XXXXX							
Vir	ginica				XXXXXX						
Vir	ginica				XXXXXX						
	-			xxxxx							

Virginica	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
*** * . *	XXXXXXXXXXXXXXXX
Virginica	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
Virginica	XXXXXXXXXXXXXXXX
, 11g110d	XXXXXXXXXXXXXX
Virginica	XXXXXXXXXXXXXXX
j	XXXXXXXXXXXXX
Versicolor	xxxxxxxxxxxxx
	XXXXXXXXXXXXX
Virginica	xxxxxxxxxxxxx
	XXXXXXXXXXXX
Virginica	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
	XXXXXXXXXXXX
Virginica	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
	XXXXXXXXXXX
Virginica	XXXXXXXXXXXXX
	XXXXXXXXXXX
Virginica	XXXXXXXXXXX
*** * . *	XXXXXXXXXX
Virginica	XXXXXXXXXXX
77:ii	XXXXXXXXXX
Virginica	XXXXXXX
Virginica	XXXXXXXX
VIIginica	XXXXXXX
Virginica	XXXXXXXX
	XXXXXX
Virginica	xxxxxx
	XXXXXX
Virginica	XXXXXX
	XXXXX
Virginica	XXXXX
	XXXX
Virginica	XXXX
****	XXXX
Virginica	xxx
Virginica	XXX
VIIginica	XX
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Subject Index

```
analyzing data in groups
    TREE procedure, 7359
cluster analysis
    tree diagrams, 7347, 7348
CLUSTER procedure, see also TREE procedure
dendrogram, 7347
missing values
    TREE procedure, 7361
OUT= data sets
    TREE procedure, 7361
output data sets
    TREE procedure, 7361
output table names
    TREE procedure, 7362
phenogram, 7347
tree diagram
    binary tree, 7348
    branch, 7348
    children, 7348
    definitions, 7348
    leaves, 7348
    node, 7348
    parent, 7348
    root, 7348
tree diagrams
    cluster analysis, 7348
TREE procedure, 7347
    missing values, 7361
    OUT= data sets, 7361
    output data sets, 7361
    output table names, 7362
```

VARCLUS procedure, see also TREE procedure

Syntax Index

BY statement	LEVEL= option
TREE procedure, 7359	PROC TREE statement, 7357
	LINEPRINTER option
CFRAME= option	PROC TREE statement, 7357
PROC TREE statement, 7354	LINES= option
COPY statement	PROC TREE statement, 7357
TREE procedure, 7359	LIST option
DATA	PROC TREE statement, 7357
DATA= option	
PROC TREE statement, 7355	MAXHEIGHT= option
DESCENDING option PROC TREE statement, 7355	PROC TREE statement, 7357
DESCRIPTION= option	MINHEIGHT= option
PROC TREE statement, 7355	PROC TREE statement, 7357
DISSIMILAR option	NAME statement
PROC TREE statement, 7355	
DOCK= option	TREE procedure, 7360 NAME= option
PROC TREE statement, 7355	PROC TREE statement, 7357
TROC TREE statement, 7333	NCLUSTERS= option
FILLCHAR= option	PROC TREE statement, 7357
PROC TREE statement, 7355	NOPRINT option
FREQ statement	PROC TREE statement, 7358
TREE procedure, 7360	NTICK= option
•	PROC TREE statement, 7357
GOUT= option	TROC TREE statement, 7557
PROC TREE statement, 7355	OUT= option
HAXIS= option	PROC TREE statement, 7358
PROC TREE statement, 7355	PAGES= option
HEIGHT statement	PROC TREE statement, 7358
TREE procedure, 7360	PARENT statement
HEIGHT= option	TREE procedure, 7361
PROC TREE statement, 7355	POS= option
HORDISPLAY= option	PROC TREE statement, 7358
PROC TREE statement, 7356	PROC TREE statement, see TREE procedure
HORIZONTAL option	TROE TREE statement, see TREE procedure
PROC TREE statement, 7356	ROOT= option
HPAGES= option	PROC TREE statement, 7358
PROC TREE statement, 7356	,
	SIMILAR option
ID statement	PROC TREE statement, 7358
TREE procedure, 7360	SORT option
INC= option	PROC TREE statement, 7358
PROC TREE statement, 7356	SPACES= option
IOINGHAD	PROC TREE statement, 7358
JOINCHAR= option	THOW DOG
PROC TREE statement, 7356	TICKPOS= option
LEAFCHAR= option	PROC TREE statement, 7358
PROC TREE statement, 7356	TREE procedure

```
syntax, 7353
TREE procedure, BY statement, 7359
TREE procedure, COPY statement, 7359
TREE procedure, FREQ statement, 7360
TREE procedure, HEIGHT statement, 7360
TREE procedure, ID statement, 7360
TREE procedure, NAME statement, 7360
TREE procedure, PARENT statement, 7361
TREE procedure, PROC TREE statement, 7353
    CFRAME= option, 7354
    DATA= option, 7355
    DESCENDING option, 7355
    DESCRIPTION= option, 7355
    DISSIMILAR option, 7355
    DOCK= option, 7355
    FILLCHAR= option, 7355
    GOUT= option, 7355
    HAXIS= option, 7355
    HEIGHT= option, 7355
    HORDISPLAY= option, 7356
    HORIZONTAL option, 7356
    HPAGES= option, 7356
    INC= option, 7356
    JOINCHAR= option, 7356
    LEAFCHAR= option, 7356
    LEVEL= option, 7357
    LINEPRINTER option, 7357
    LINES= option, 7357
    LIST option, 7357
    MAXHEIGHT= option, 7357
    MINHEIGHT= option, 7357
    NAME= option, 7357
    NCLUSTERS= option, 7357
    NOPRINT option, 7358
    NTICK= option, 7357
    OUT= option, 7358
    PAGES= option, 7358
    POS= option, 7358
    ROOT= option, 7358
    SIMILAR option, 7358
    SORT option, 7358
    SPACES= option, 7358
    TICKPOS= option, 7358
    TREECHAR= option, 7359
    VAXIS= option, 7359
    VPAGES= option, 7359
TREECHAR= option
    PROC TREE statement, 7359
VAXIS= option
    PROC TREE statement, 7359
VPAGES= option
    PROC TREE statement, 7359
```

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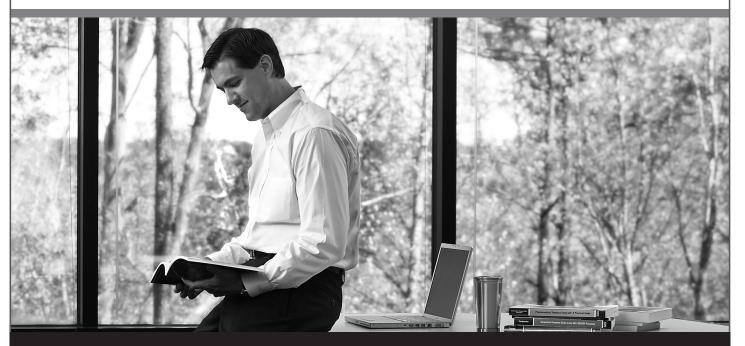
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