



Multivariate analysis

A Guide to Multivariate Analysis in Genstat® (21st Edition)

by Roger Payne.

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E-mail: info@genstat.co.uk

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Introduction

Multivariate analysis is useful when you have several different measurements on a set of n objects. In Genstat the measurements would usually be stored in separate variates, and these would have a unit for each object. The objects are often regarded as being a set of n points in p dimensions (p being the number of variates).

Many techniques, for example principal components analysis (Chapter 2) and canonical variates analysis (Chapter 3) are aimed at reducing the dimensionality. That is, they aim to find a smaller number of dimensions (usually 2 or 3) that exhibit most of the variation present in the data. This can help you determine patterns or structure in the data, as well as identify the relative importance of individual variables. Genstat has several menus for producing graphical representations, for example principal coordinates analysis (Chapter 4) and multidimensional scaling (Chapter 5). It also has facilities for modelling multivariate data, including multivariate analysis of variance (Chapter 8) and partial least squares.

Another important requirement is to take a set of units and classify them into groups based on their observed characteristics. Hierarchical cluster analysis (Chapter 6) starts with a set of groups each of which contains one of the units. These initial groups are successively merged into larger groups, according to their similarity, until there is just one group containing all the observations. Genstat also provide menus for non-hierarchical classification (Chapter 7), where the aim is to form a single grouping of the observations that optimizes some criterion such as the within-class dispersion, or the Mahalanobis squared distance between the groups, or the between-group sum of squares.

Chapter 9 describes the facilities for constructing classification trees, which allow you to predict the classification of unknown objects using multivariate observations. Regression trees, which predict the value of a response variate from multivariate observations are described in Chapter 10.

Finally, Chapter 11 describes how generalized Procrustes analysis can be used to obtain a consensus from assessors in activities such as wine tasting.

The book works through a series of straightforward examples, with frequent practicals to allow you to try the methods for yourself. The examples work mainly through the menus of Genstat *for Windows*, so there is no need for prior knowledge of the Genstat command language. Details of the commands for multivariate analysis can be found in Chapter 6 of the *Guide to the Genstat Command Language, Part 2, Statistics*.

1 Exploratory data analysis

Before you begin a multivariate analysis, it is sensible to investigate the properties of the data by looking at some plots and summary statistics.

We illustrate some of the insights that can be obtained by examining seven variables recorded in 41 towns in the USA, stored in the Spreadsheet file `Pollution.gsh` shown in Figure 1.1:

`SO2`

`Temp`

`Manuf`

`Pop`

`Wind`

`Precip`

`Days`

(For more details, see Everitt, 2005, *An R and S-PLUS Companion to Multivariate Analysis*.)

Row	Town	SO2	Temp	Manuf	Pop	Wind	Precip	Days	Label
1	Phoenix	10	-70.3	213	582	6	7.05	36	Px
2	Little Rock	13	-61	91	132	8.2	48.52	100	Lr
3	San Francisco	12	-56.7	453	716	8.7	20.66	67	Sf
4	Denver	17	-51.9	454	515	9	12.95	86	Dv
5	Hartford	56	-49.1	412	158	9	43.37	127	Hf
6	Wilmington	36	-54	80	80	9	40.25	114	Wm
7	Washington	29	-57.3	434	757	9.3	38.89	111	Ws
8	Jacksonville	14	-68.4	136	529	8.8	54.47	116	Jv
9	Miami	10	-75.5	207	335	9	59.8	128	Mi
10	Atlanta	24	-61.5	368	497	9.1	48.34	115	At
11	Chicago	110	-50.6	3344	3369	10.4	34.44	122	Ch
12	Indianapolis	28	-52.3	361	746	9.7	38.74	121	In

Figure 1.1

sulphur dioxide

temperature in degrees Fahrenheit

number of enterprises with 20+ staff

population size in thousands

average annual wind speed (miles per hour)

average annual rainfall in inches

average number of days with rain per year

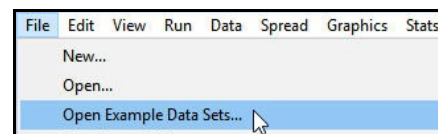


Figure 1.2

This file (and the others in this Guide) can be opened using the [Example Data Sets](#) menu (Figure 1.3). You can open this by clicking on the [Open Example Data Sets](#) option of the [File](#) menu on the menu bar (Figure 1.2)

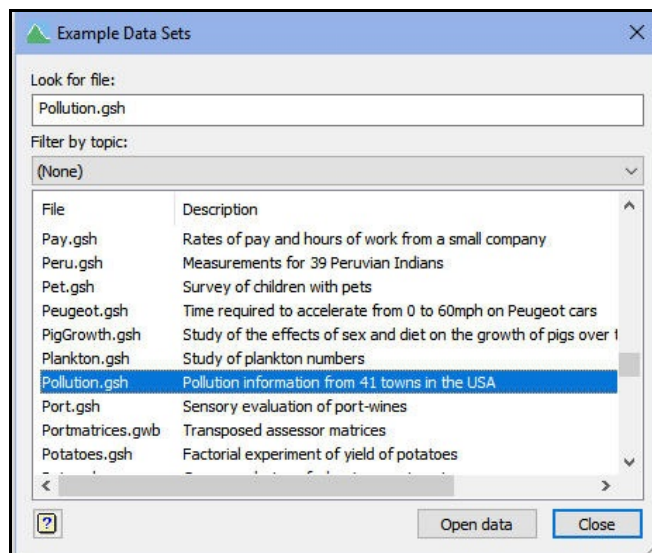


Figure 1.3

First we open the **Summary Statistics** menu by clicking on the **Summary Statistics** sub-option of the **Summary Statistics** option of the **Stats** menu on the menu bar (see Figure 1.4).

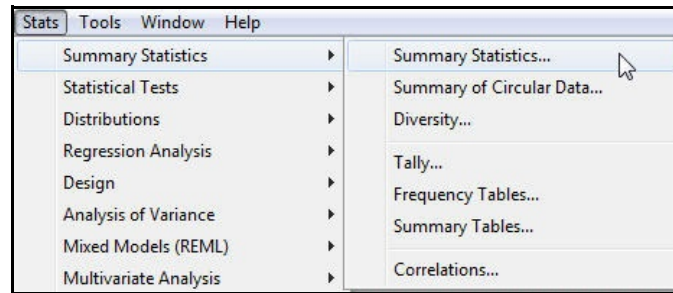


Figure 1.4

In the menu (Figure 1.5), we have entered all seven variates into the **Variates** box, selected the required summary statistics in the **Options** box, and checked the **Histogram** and **Boxplot** boxes in the **Graphics** box. The resulting output is shown below, and the plots are in Figures 1.6 - 1.19.

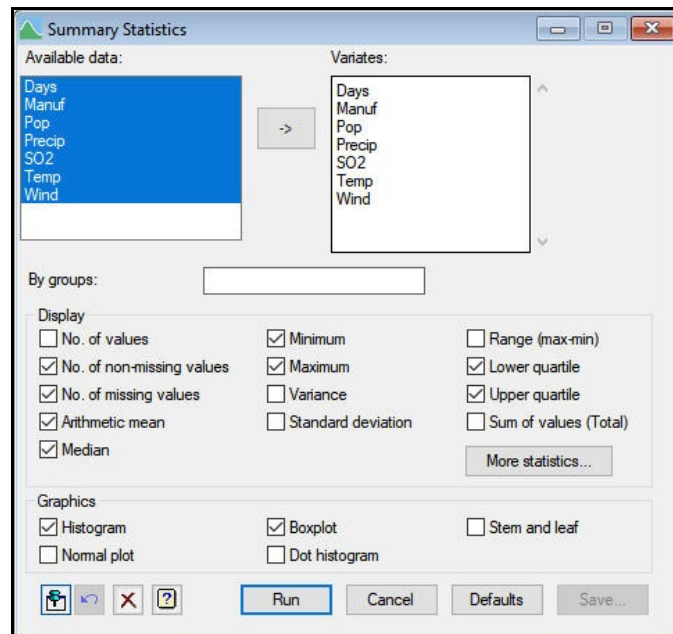


Figure 1.5

Summary statistics for Days

Number of observations = 41
 Number of missing values = 0
 Mean = 113.9
 Median = 115
 Minimum = 36
 Maximum = 166
 Lower quartile = 102.2
 Upper quartile = 128.2
 Standard deviation = 26.51

Summary statistics for Manuf

Number of observations = 41
 Number of missing values = 0
 Mean = 463.1
 Median = 347
 Minimum = 35
 Maximum = 3344

Lower quartile = 170
Upper quartile = 488.8
Standard deviation = 563.5

Summary statistics for Pop

Number of observations = 41
Number of missing values = 0
Mean = 608.6
Median = 515
Minimum = 71
Maximum = 3369
Lower quartile = 293.5
Upper quartile = 723.8
Standard deviation = 579.1

Summary statistics for Precip

Number of observations = 41
Number of missing values = 0
Mean = 36.77
Median = 38.74
Minimum = 7.05
Maximum = 59.8
Lower quartile = 30.93
Upper quartile = 43.17
Standard deviation = 11.77

Summary statistics for SO2

Number of observations = 41
Number of missing values = 0
Mean = 30.05
Median = 26
Minimum = 8
Maximum = 110
Lower quartile = 12.75
Upper quartile = 35.25
Standard deviation = 23.47

Summary statistics for Temp

Number of observations = 41
Number of missing values = 0
Mean = -55.76
Median = -54.6
Minimum = -75.5
Maximum = -43.5
Lower quartile = -59.32
Upper quartile = -50.55
Standard deviation = 7.228

Summary statistics for Wind

Number of observations = 41
Number of missing values = 0
Mean = 9.444
Median = 9.3
Minimum = 6
Maximum = 12.7
Lower quartile = 8.7
Upper quartile = 10.6
Standard deviation = 1.429

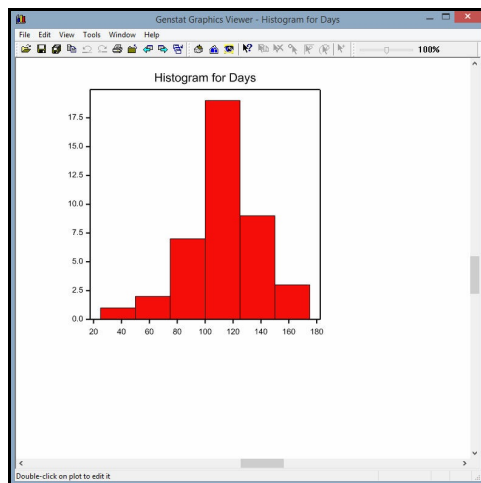


Figure 1.6

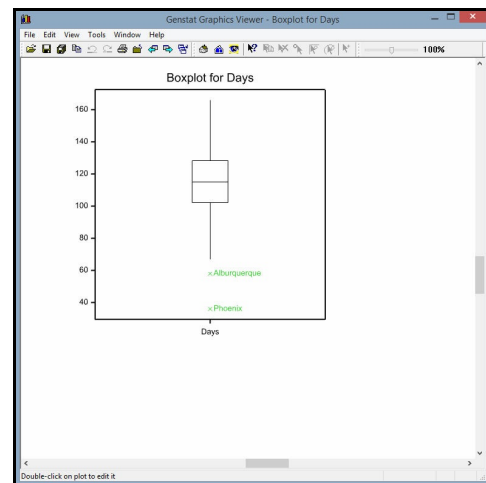


Figure 1.7

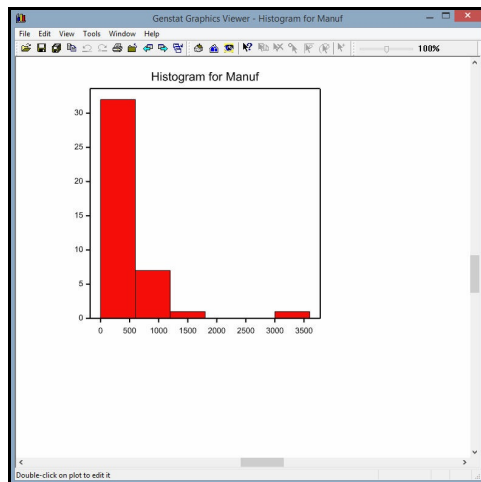


Figure 1.8

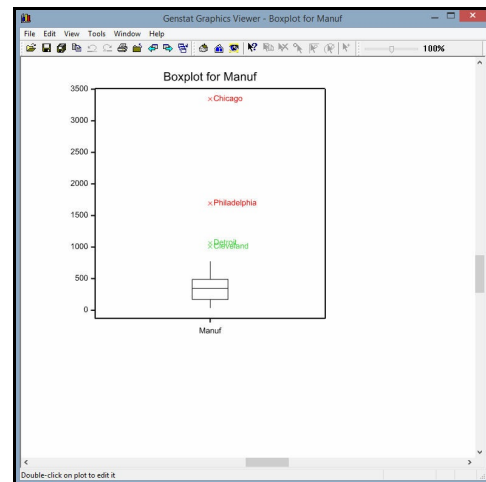


Figure 1.9

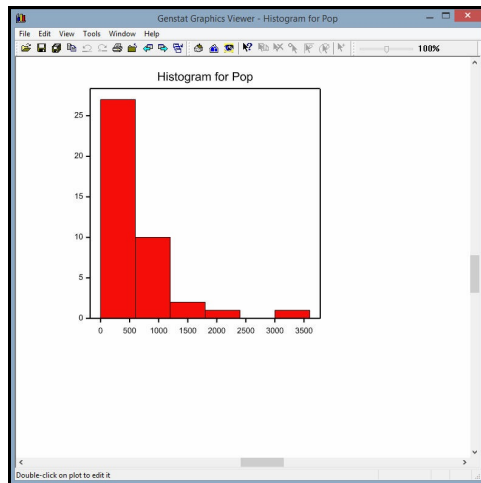


Figure 1.10

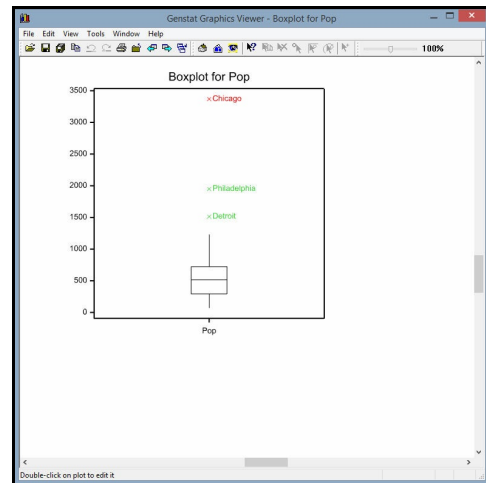


Figure 1.11

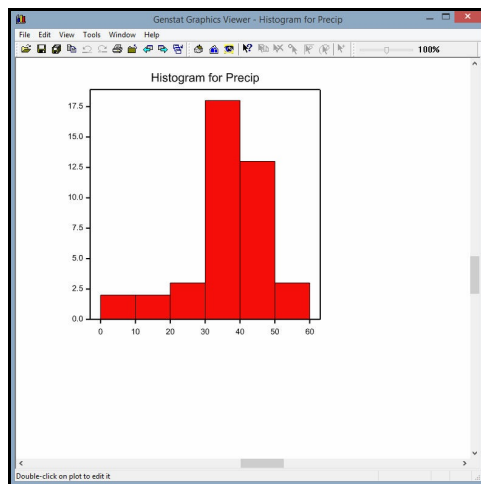


Figure 1.12

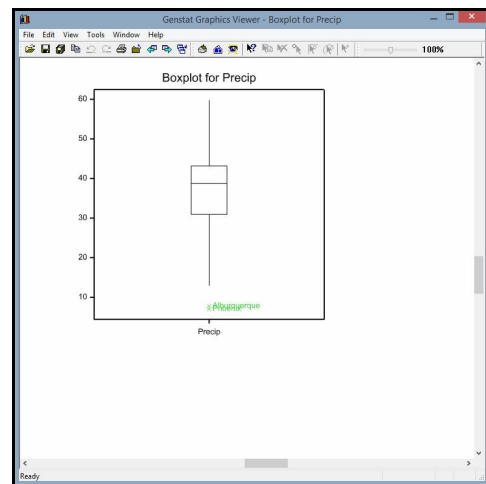


Figure 1.13

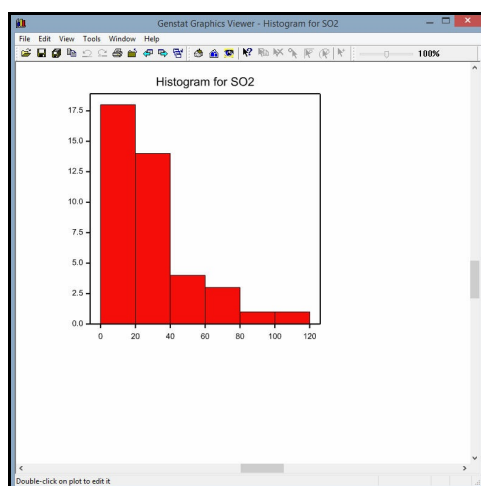


Figure 1.14

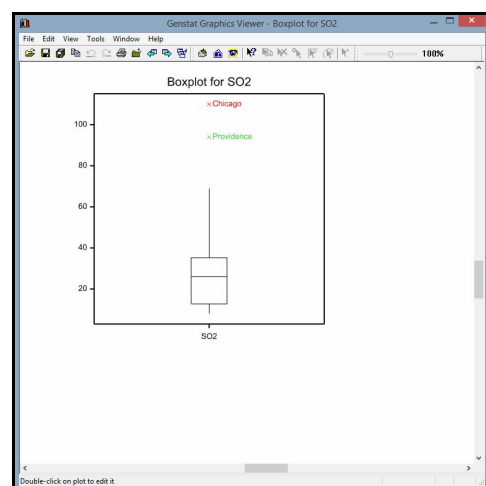


Figure 1.15

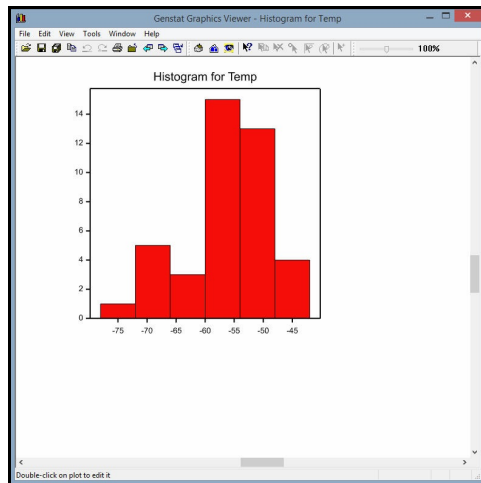


Figure 1.16

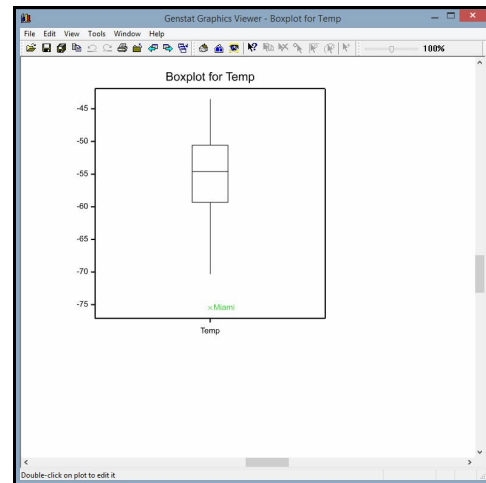


Figure 1.17

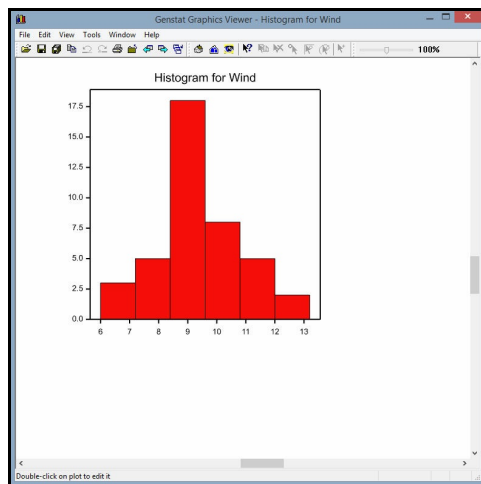


Figure 1.18

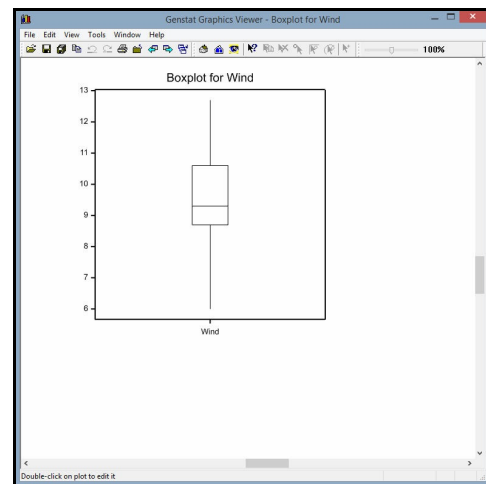


Figure 1.19

The main thing to notice in the plots and statistics show that the variables are on very different scales –and we will need to remember this in the later multivariate analyses.

To study the inter-relationships between the variates, we can select the [Scatter Plot Matrix](#) option of the [Graphics](#) menu on the menu bar. In the resulting menu (Figure 1.20), we just need to select the variates to plot and click on [Run](#). The plot is useful for showing variates that are positively and negatively correlated, extreme observations and any clusters of the units.

The pollution data are plotted in Figure 1.21).

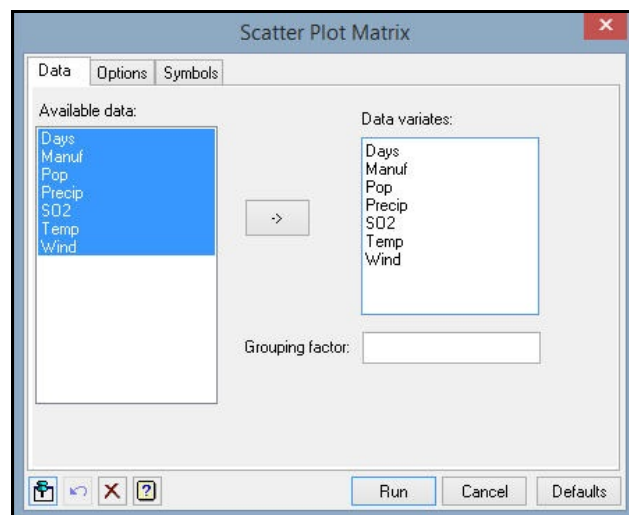


Figure 1.20

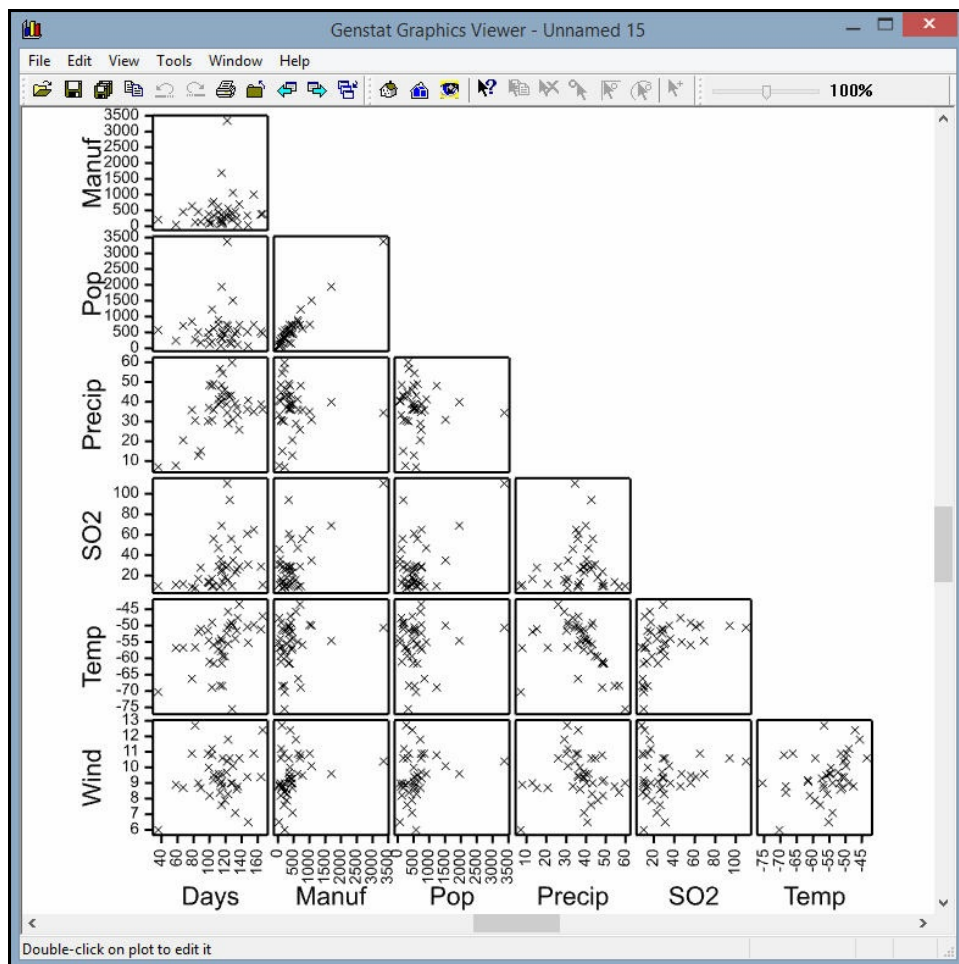


Figure 1.21

1.1 Practical

Genstat spreadsheet file [Exam.gsh](#) (Figure 1.22) contains examination marks for 88 students in the subjects Mechanics, Vectors, Algebra, Analysis and Statistics. (For details, see Mardia, Kent and Bibby, 1979, *Multivariate Analysis*, Academic Press, London.) Print summary statistics and plot graphs to study the data.

Row	Mechanics	Vectors	Algebra	Analysis	Statistics
1	72	82	67	67	81
2	63	78	80	70	81
3	75	73	71	66	81
4	55	72	63	70	68
5	63	63	65	70	63
6	53	61	72	64	73
7	51	67	65	65	68
8	59	70	68	62	56
9	62	60	58	62	70
10	64	72	60	62	45
11	52	64	60	63	54
12	55	67	59	62	44

Figure 1.22

2 Principal components analysis

A major problem with multivariate data is that there are generally too many variates for you to be able to visualise the properties and inter-relationships of the data units easily. Principal components analysis (or PCP) provides one way to overcome this “curse of dimensionality”. It aims to find linear combinations of the data variates that contain most of the variation between the units. The combinations (or *principal components*) indicate relationships between the variates, and also define planes in multi-dimensional space where the relationships between the units can be studied effectively. We shall illustrate this using the pollution data from Chapter 1.

The **Principal Components Analysis** menu (Figure 2.1) is obtained by clicking on the **Principal Components** line in the **Multivariate Analysis** section of the **Stats** menu on the menu bar. You first need to enter the data variates into the **Data to be analysed** window. Here we have chosen to enter all of the variates except **SO₂**, which we will be treating as a response variate later in this Guide.

One important issue is to decide whether to base the analysis on sums of squares and products, or variances and covariances or correlations. The first two produce essentially the same analysis (there is just a common scaling of $\sqrt{(n-1)}$ applied to the variates, to convert from sums of squares to variances). The final setting, **Correlation matrix** standardizes each variate (by subtracting its mean and dividing by its standard deviation). This can be very useful if the variates do not share a common scale and show very different amounts of variation.

In the pollution data set, the variates are not only on different scales (see Chapter 1), they are of inherently different types. So we have chosen to use the correlation matrix (which Genstat will calculate for us automatically, from the variates).

Clicking on the **Options** button produces the **Principal Components Analysis Options** menu (Figure 2.2), which controls the printed output from the analysis. We have set **Display** box to print **Latent roots** and **Loadings**, we have requested a scree plot, and we have set the **Number of dimensions** box to 6 which will give all the available latent roots and vectors. If you choose to

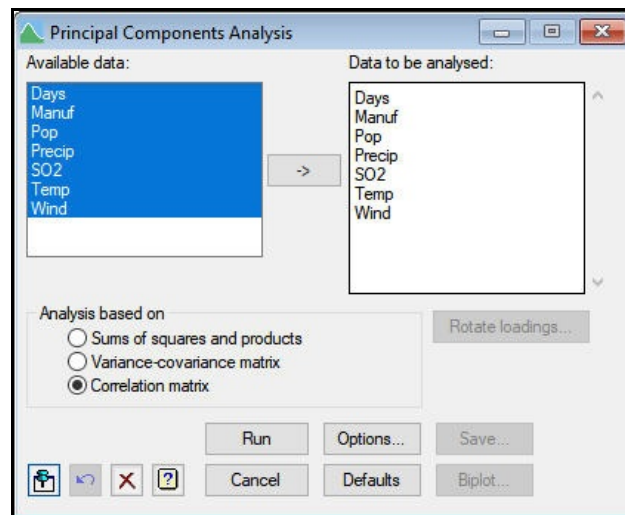


Figure 2.1

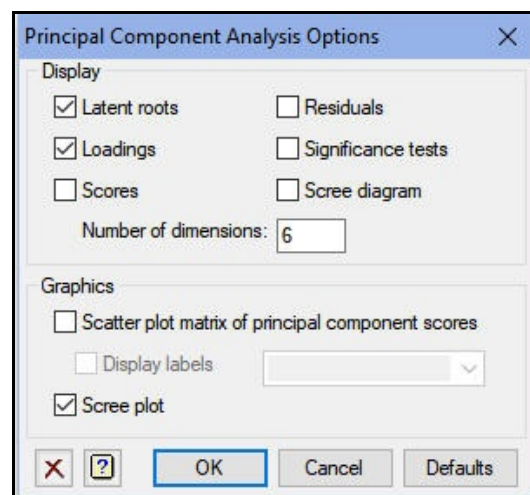


Figure 2.2

have less than the full number of dimensions, the [Residuals](#) check box can print residuals representing the information in the dimensions that have been excluded. The [Number of dimensions](#) setting also applies to results saved from the [Principal Components Save Options](#) menu, which is obtained by clicking on the [Save](#) button on the [Principal Components Analysis](#) menu.

The output is shown below.

Principal components analysis

Latent roots

1	2	3	4	5	6
2.196	1.500	1.395	0.760	0.115	0.034

Percentage variation

1	2	3	4	5	6
36.60	25.00	23.24	12.67	1.91	0.57

Trace

6.000

Latent vectors (loadings)

	1	2	3	4	5
Days	0.23792	0.70777	0.09309	0.31131	0.58000
Manuf	0.61154	-0.16806	-0.27289	0.13684	-0.10204
Pop	0.57782	-0.22245	-0.35037	0.07248	0.07807
Precip	-0.04081	0.62286	-0.50456	-0.17115	-0.56818
Temp	0.32965	0.12760	0.67169	0.30646	-0.55806
Wind	0.35384	0.13079	0.29725	-0.86943	0.11327
	6				
Days	0.02196				
Manuf	0.70297				
Pop	-0.69464				
Precip	-0.06062				
Temp	-0.13619				
Wind	0.02453				

The first principal component defines the direction in which the towns exhibit the greatest variation. The second component defines the direction with the greatest variation of the directions orthogonal to the first component. The third component defines the direction with the greatest variation of the directions orthogonal to the first two components, and so on. Here, the first component contains about 37% of the variation, and the first and second components contain about 62%.

It is often interesting to interpret the directions. Those with mainly positive or mainly negative loadings represent “averages” while those with a mixture of signs represent “comparisons”. Here, the first component is in the direction

$$0.23792 \times \text{Days} + 0.61154 \times \text{Manuf} + 0.57782 \times \text{Pop} \\ - 0.04081 \times \text{Precip} + 0.32965 \times \text{Temp} + 0.35384 \times \text{Wind}$$

and seems to represent “quality of life”. The second component is

$$0.23792 \times \text{Days} + 0.61154 \times \text{Manuf} + 0.57782 \times \text{Pop} \\ - 0.04081 \times \text{Precip} + 0.32965 \times \text{Temp} + 0.35384 \times \text{Wind}$$

and seems to be related to the wetness of the climate.

We have not printed the significance tests for equality of the final K roots as these cannot be used when the analysis is based on correlations. When the analysis is based on variances or on sums of squares, they can be useful for deciding how many roots are needed. Asymptotically (that is, as the number of units becomes large) these have chi-square distributions. However, this is not true for analyses based on correlations. To use the tests, we start by testing for equality of all the roots, then all except the first, all except the first and second, and so on, until the test is non-significant. The rationale is that, if we are to omit the final dimension, we should also omit all dimensions that are no more variable than that dimension.

An alternative, visual way of deciding how many roots are needed is to examine the scree plot. The plot for the pollution data, shown in Figure 2.3, shows the pattern that you would hope to find, with a clear jump up from the final roots (with low eigenvalues) to the earlier roots (with larger eigenvalues). This is more in line with the attitude that significance tests are not really relevant if you view principal components analysis mainly as a descriptive technique, where the aim is to find dimensions in which you can most effectively study the inter-relationships of the data units.

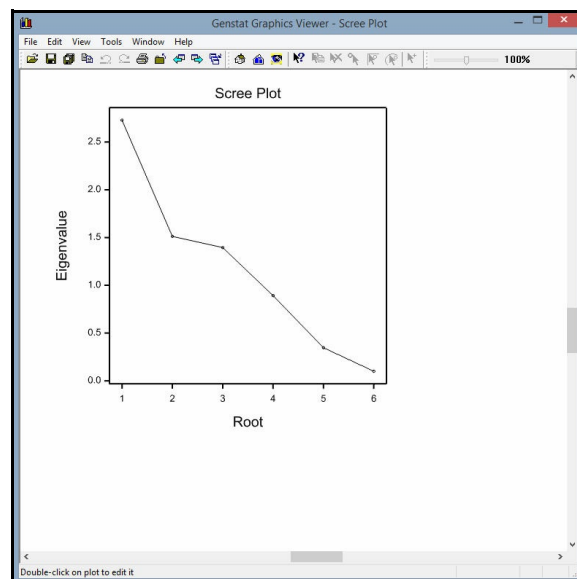


Figure 2.3

Here it seems that four principal components are needed. So, we change the number of dimensions in the [Principal Components Analysis Options](#) menu to four, check the box to plot the principal component scores, and select [Label](#) to label the points. Clicking on [OK](#) here, and then [Run](#) in the [Principal Components Analysis](#) menu, produces the plot in Figure 2.5.

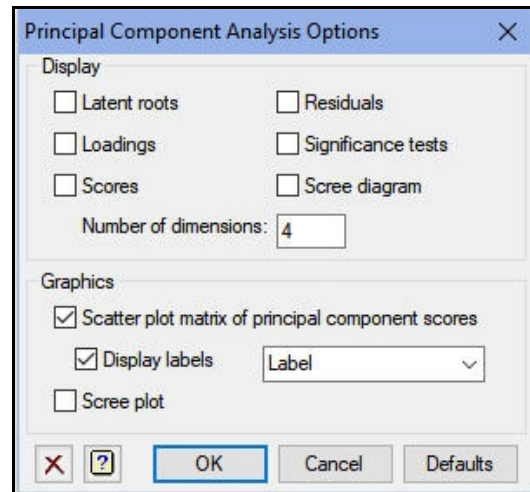


Figure 2.4

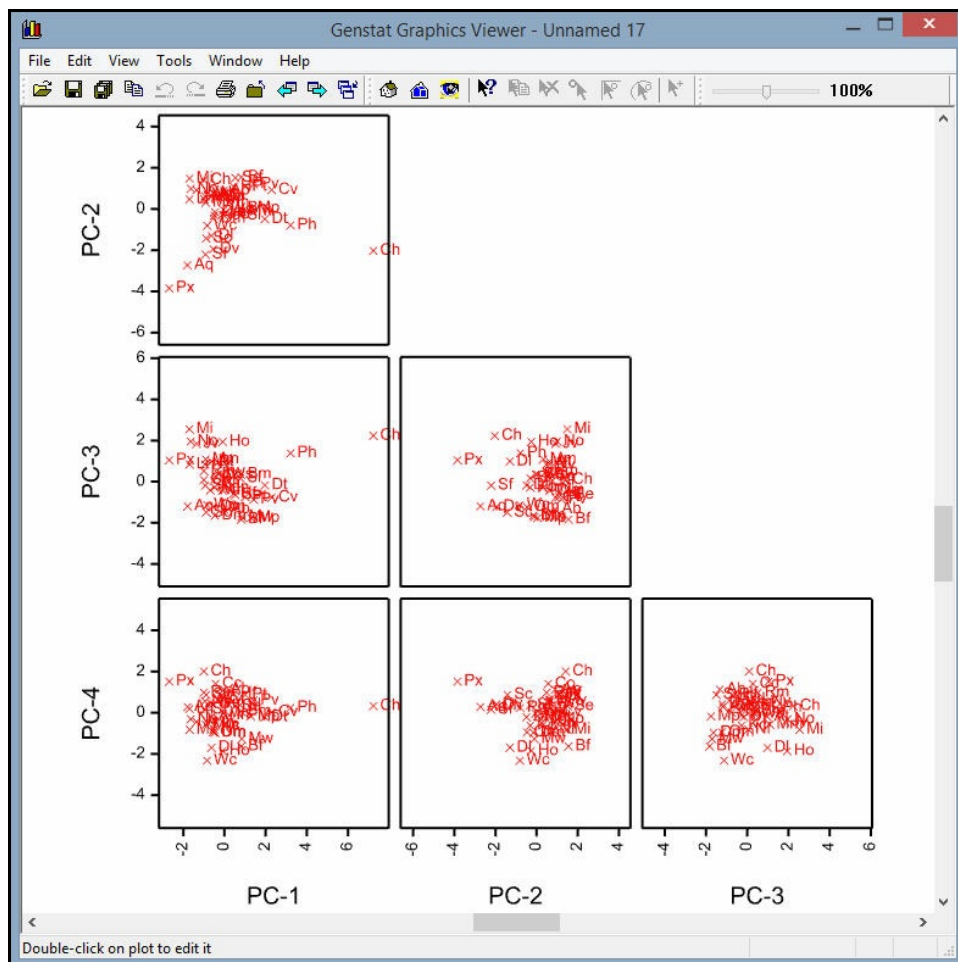


Figure 2.5

The menu uses the [PCP](#) directive, which is described in Section 6.2.1 of the *Guide to the Genstat Command Language, Part 2 Statistics*.

2.1 Principal-component biplot

Several of the multivariate analysis menus have a **Biplot** button, that becomes available once the analysis has been run. Biplots provide a convenient way of assessing the relationships between the individual observations in the analysis (here the towns), and their characteristics with respect to the variables in the data.

Clicking on the button in the **Principal Components Analysis** menu opens the menu in Figure 2.6, which has options to control the labelling of the plot, and the way in which the variables are represented. Here we enter the text vector `Label` to provide labels, and click on **Run** to produce the graph in Figure 2.7.

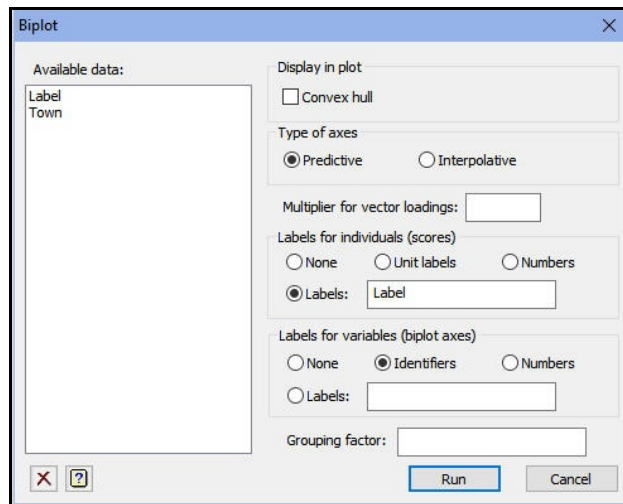


Figure 2.6

The display plots the individuals in the space defined by the first two dimensions of the multivariate analysis (from a PCP these will be the first two principal components). The plot also contains an “axis” for each variable (its *biplot* axis) that allows you to see how each individual's projection into this plane relates to its value for the variable concerned. Figure 2.7 shows the default, predictive axes. These show the values of the variables that are predicted by the projection into 2-dimensions that is defined for each point by the analysis; essentially this is done by taking an orthogonal projection of the point onto each the biplot axis. Genstat defines a *hot point* at the point for each individual. If you click on the hot point icon at the right-hand end of the Graphics Toolbar, and then click on one of the points, lines will be drawn from the point to the predictions. In Figure 2.7, we have done this for Phoenix, so you can see how this differs from the other towns. The lines can be removed again by clicking on the hot point a second time.

The angles between the biplot axes represent the correlations between the variables, and lines in opposite directions indicate negative correlation. So here we can see that temperature and wind have a strong negative correlation. The % variance of the principal components show the extent to which the plot summarizes the entire data set.

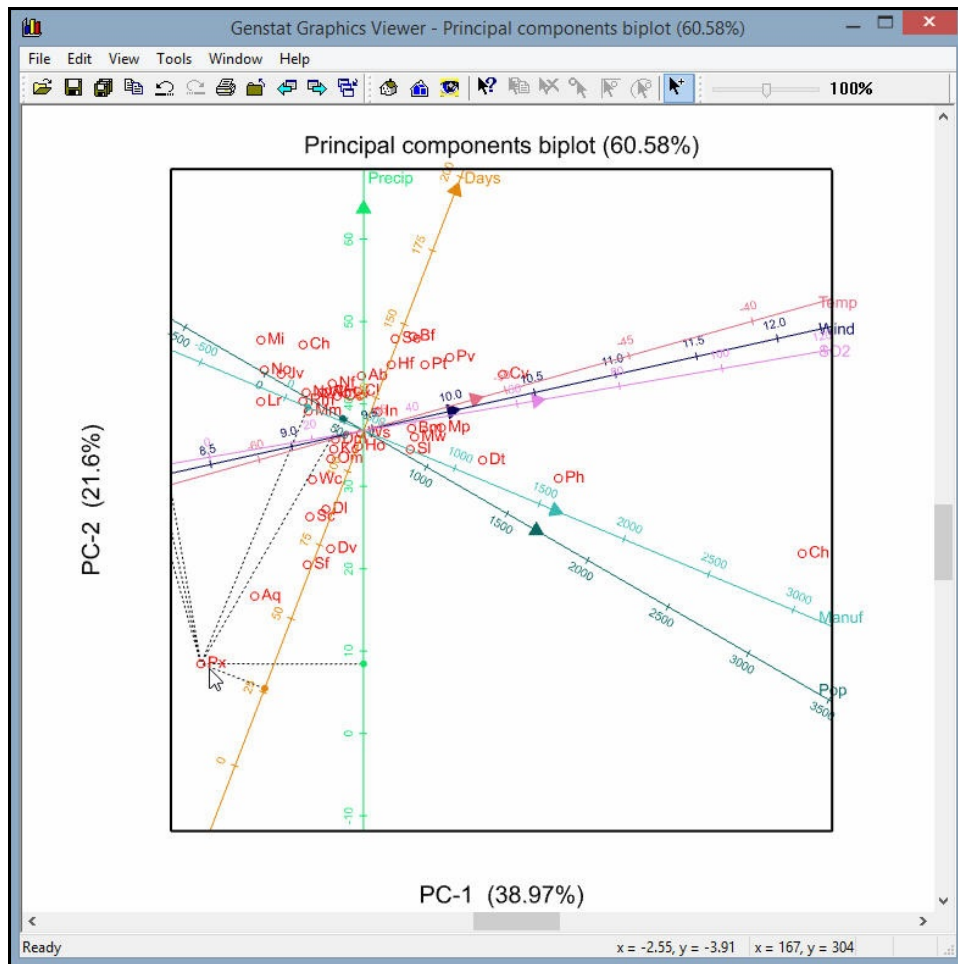


Figure 2.7

The alternative, interpolative axes show the values of the variables that would lead to a point being placed at the position of the selected point on the graph. So here the point is being predicted by the variables, rather than the variables by the point. This is done by taking the sum of a set of vectors, one in the direction of each variable, with lengths equal to the values of the variables for that point. To obtain interpolative axes, you should select the [Interpolative](#) button from the [Type of axes](#) radio buttons in the [Biplot](#) menu.

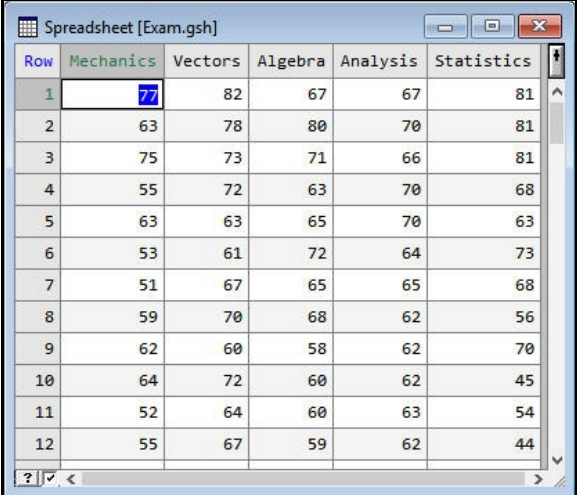
The [Biplot](#) menu uses the [DBIPLLOT](#) procedure, which is described in Section 6.16.1 of the *Guide to the Genstat Command Language, Part 2 Statistics*.

2.2 Practical

Genstat spreadsheet file `Exam.gsh` (Figure 2.8) contains examination marks for 88 students in the subjects Mechanics, Vectors, Algebra, Analysis and Statistics. (See Practical 1.1 and Mardia, Kent and Bibby, 1979, *Multivariate Analysis*, Academic Press, London.)

Perform a principal components analysis. How would you interpret the directions in which the student marks exhibit the greatest variation? How important is Statistics in distinguishing the abilities of the students?

Display a biplot from the analysis, and use the hotpoints to see how the strongest and weakest students differ from the other students.

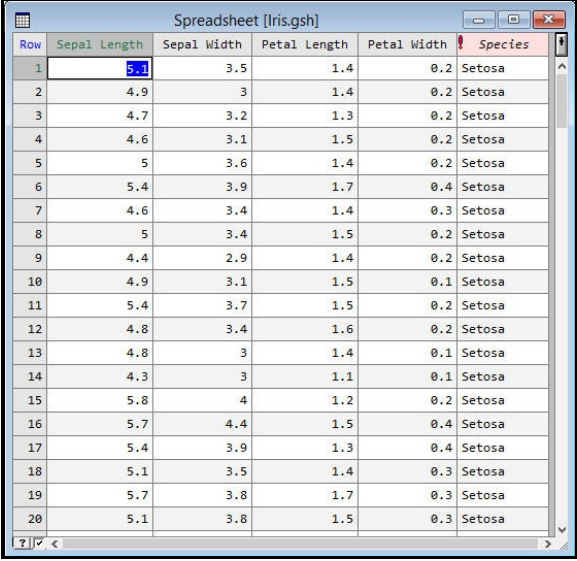


Row	Mechanics	Vectors	Algebra	Analysis	Statistics
1	77	82	67	67	81
2	63	78	80	70	81
3	75	73	71	66	81
4	55	72	63	70	68
5	63	63	65	70	63
6	53	61	72	64	73
7	51	67	65	65	68
8	59	70	68	62	56
9	62	60	58	62	70
10	64	72	60	62	45
11	52	64	60	63	54
12	55	67	59	62	44

Figure 2.8

3 Canonical variates analysis

Canonical variates analysis is appropriate when the units are classified into groups. The aim is to find linear combinations of the data variates that represent most of the variation between the groups (rather than between the individual units, as in principal components analysis; Chapter 2). We illustrate the analysis using a classic data set, Fisher's Iris Data, which consists of measurements of sepal and petal lengths and widths on iris plants of three different species. This is available in Genstat spreadsheet `Iris.gsh` (Figure 3.1).



Row	Sepal Length	Sepal Width	Petal Length	Petal Width	Species
1	5.1	3.5	1.4	0.2	Setosa
2	4.9	3	1.4	0.2	Setosa
3	4.7	3.2	1.3	0.2	Setosa
4	4.6	3.1	1.5	0.2	Setosa
5	5	3.6	1.4	0.2	Setosa
6	5.4	3.9	1.7	0.4	Setosa
7	4.6	3.4	1.4	0.3	Setosa
8	5	3.4	1.5	0.2	Setosa
9	4.4	2.9	1.4	0.2	Setosa
10	4.9	3.1	1.5	0.1	Setosa
11	5.4	3.7	1.5	0.2	Setosa
12	4.8	3.4	1.6	0.2	Setosa
13	4.8	3	1.4	0.1	Setosa
14	4.3	3	1.1	0.1	Setosa
15	5.8	4	1.2	0.2	Setosa
16	5.7	4.4	1.5	0.4	Setosa
17	5.4	3.9	1.3	0.4	Setosa
18	5.1	3.5	1.4	0.3	Setosa
19	5.7	3.8	1.7	0.3	Setosa
20	5.1	3.8	1.5	0.3	Setosa

Figure 3.1

The [Canonical Variates Analysis](#) menu (Figure 3.2) is obtained by clicking on the [Canonical Variates](#) line in the [Multivariate Analysis](#) section of the [Stats](#) menu on the menu bar. You need to enter the data variates into the [Data to be analysed](#) window, and the factor defining the groups into the [Grouping factor](#) window. Clicking on the [Options](#) button produces the [Canonical Variates Analysis Options](#) menu, which controls the printed output from the analysis.

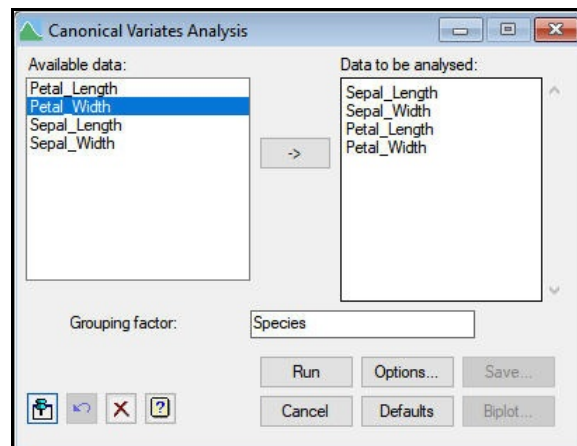


Figure 3.2

In the **Options** menu (Figure 3.3), we have set the **Display** box to print **Latent roots**, **Loadings**, **Canonical variate means** and **Distances**. The **Number of dimensions** box is set to 2, which is the maximum possible here as there are only three species of iris in the data set. If you choose to have less than the full number of dimensions, the **Residuals** check box can print residuals representing the information in the dimensions that have been excluded. The **Number of dimensions** setting also applies to results saved from the **Canonical Variates Save Options** menu, which is obtained by clicking on the **Save** button on the **Canonical Variates Analysis** menu. The **Graphics** section of the menu is set to plot the data with the first canonical variate along the x-axis, and the second along the y-axis.

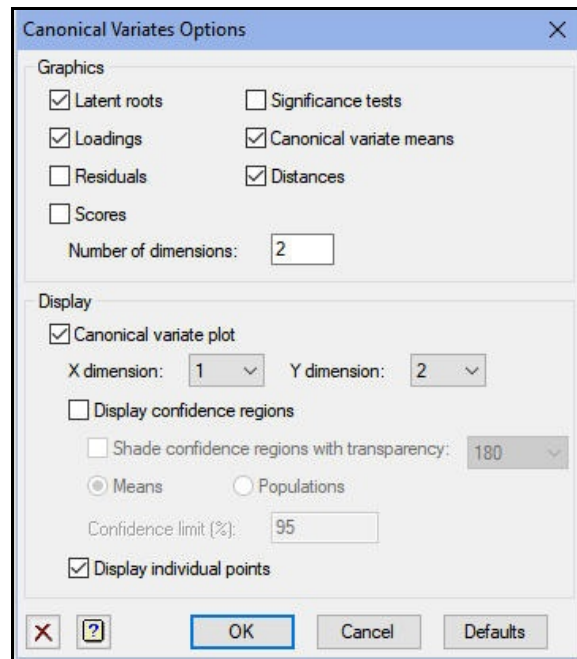


Figure 3.3

The output from the analysis is shown below.

Canonical variate analysis

Latent roots

	1	2
	32.19	0.29

Percentage variation

	1	2
	99.12	0.88

Trace

	32.48
--	-------

Latent vectors (loadings)

	1	2
1	0.829	0.024
2	1.534	2.165
3	-2.201	-0.932

4	-2.810	2.839
---	--------	-------

Canonical variate means

	1	2
1	7.608	0.215
2	-1.825	-0.728
3	-5.783	0.513

Adjustment terms

	1	2
1	-2.105	6.661

Inter-group distances

1	0.000		
2	9.480	0.000	
3	13.393	4.147	0.000
	1	2	3

The results show that 99% of the between-group variation is in the direction of the first canonical variate:

$$0.829 \times \text{Sepal-Length} + 1.534 \times \text{Sepal-Width} - 2.201 \times \text{Petal-Length} - 2.810 \times \text{Petal-Width}$$

(using the coefficients in column 1 of the latent-vectors matrix). This is confirmed by the plot in Figure 3.4.

The matrix of canonical variate means presents the coordinates (or *scores*) for each group in the direction of each canonical variate. These are adjusted so that the centroid of the points, weighted by sizes of the groups, is at the origin. The adjustment term for each canonical original variates in order to achieve this. (See *Guide to the Genstat Command Language*, Part 2 Section 6.3.1 for more details.)

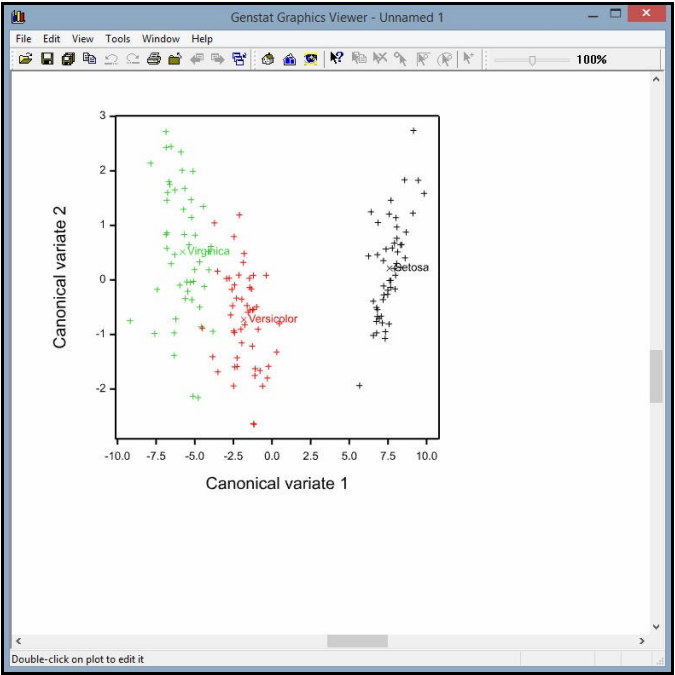
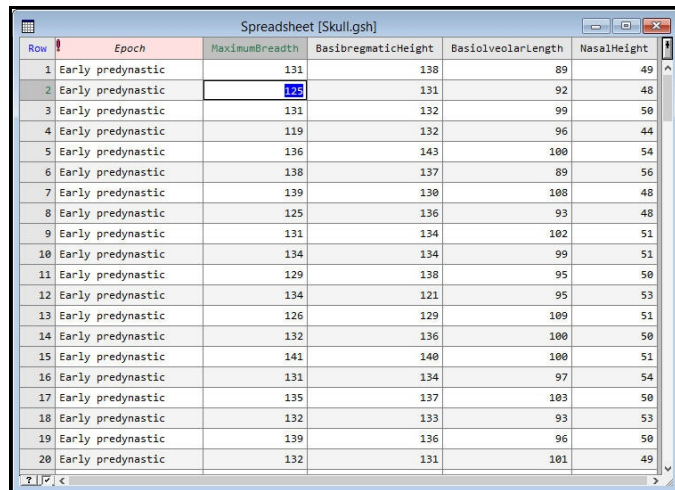


Figure 3.4

3.1 Practical

Genstat spreadsheet file `Skull.gsh` (Figure 3.5) contains data on 150 male Egyptian skulls from five different epochs (see pages 4 and 5 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London).

Perform a canonical variates analysis. Plot the first two canonical variates and study how the skulls differ between epochs.



Row	Epoch	MaximumBreadth	BasibregmaticHeight	BasioleolarLength	NasalHeight
1	Early predynastic	131	138	89	49
2	Early predynastic	125	131	92	48
3	Early predynastic	131	132	99	50
4	Early predynastic	119	132	96	44
5	Early predynastic	136	143	100	54
6	Early predynastic	138	137	89	56
7	Early predynastic	139	130	108	48
8	Early predynastic	125	136	93	48
9	Early predynastic	131	134	102	51
10	Early predynastic	134	134	99	51
11	Early predynastic	129	138	95	50
12	Early predynastic	134	121	95	53
13	Early predynastic	126	129	109	51
14	Early predynastic	132	136	100	50
15	Early predynastic	141	140	100	51
16	Early predynastic	131	134	97	54
17	Early predynastic	135	137	103	50
18	Early predynastic	132	133	93	53
19	Early predynastic	139	136	96	50
20	Early predynastic	132	131	101	49

Figure 3.5

4 Principal coordinates analysis

Principal coordinates analysis differs from principal components and canonical variates analysis in that the focus is more on the data units than the data variables. So the basic input is a symmetric matrix representing the “associations” between the data units. The menu (Figure 4.1) has radio buttons that you can use to specify how the the associations are supplied. Similarities are on a range from zero

(completely different) to one (absolutely identical). The alternative is to specify dissimilarities or distance which are zero when the two units are identical. Distances d are converted automatically to similarities s by the menu, using the transformation

$$s = -d^2$$

(See the *Guide to the Genstat Command Language*, Part 2, Section 6.10 for more information.)

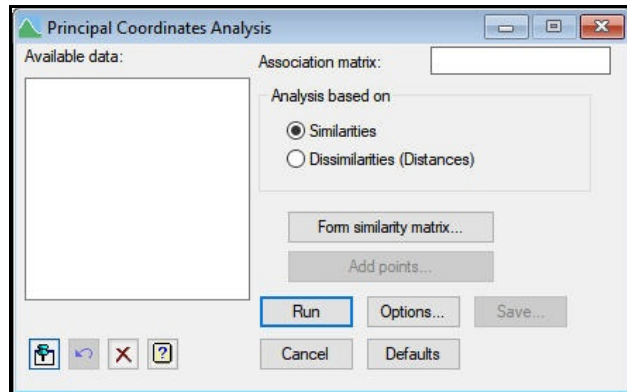


Figure 4.1

Row	Name	Hunt	Sandman	Howard	Thompson	Frelinghuysen	Forsythe	Widnall	Roe	Helstoki	Rodino	Minish	Rinaldo	Maraziti	Daniels	Patten
1	Hunt	0														
2	Sandman	8	0													
3	Howard	15	17	0												
4	Thompson	15	12	9	0											
5	Frelinghuysen	10	13	16	14	0										
6	Forsythe	9	13	12	12	8	0									
7	Widnall	7	12	15	13	9	7	0								
8	Roe	15	16	5	10	13	12	17	0							
9	Helstoki	16	17	5	8	14	11	16	4	0						
10	Rodino	14	15	6	8	12	10	15	5	3	0					
11	Minish	15	16	5	8	12	9	14	5	2	1	0				
12	Rinaldo	16	17	4	6	12	10	15	3	1	2	1	0			
13	Maraziti	7	13	11	15	10	6	10	12	13	11	12	12	0		
14	Daniels	11	12	10	10	11	6	11	7	7	4	5	6	9	0	
15	Patten	13	16	7	7	11	10	13	6	5	6	5	4	13	9	0

Figure 4.2

As an example, spreadsheet file `Voting.gsh` contains the number of times that 15 congressmen from New Jersey voted differently in 19 environmental bills (see Table 10.3 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London).

We shall analyse these as similarities, and so we first use the **Calculations** menu to convert the differences to proportions of times that they congressmen voted in the same way i.e.

$$(19 - \text{Diffvote}) / 19$$

(see Figure 4.3). We then enter the resulting symmetric matrix, *Similarity*, into the **Association matrix** box in Figure 4.1.

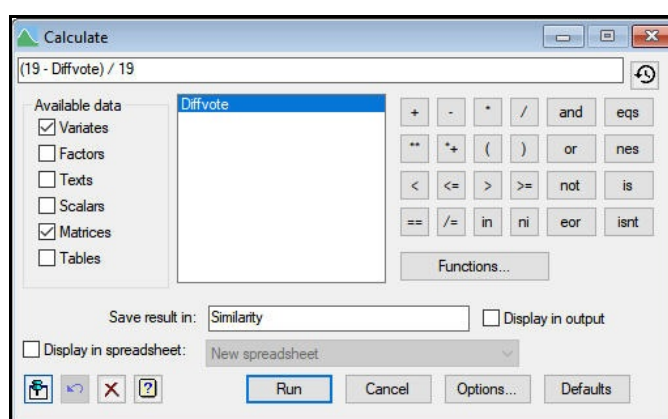


Figure 4.3

The **Principal Coordinates Analysis Options** menu (Figure 4.4) allows you to select the output to display, and specify the number of dimensions to fit. Here we have chosen to fit only two dimensions.

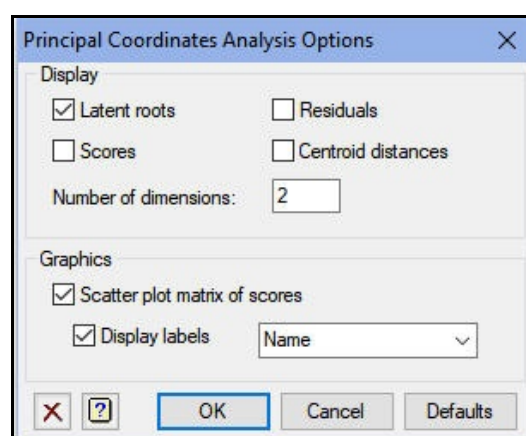


Figure 4.4

Principal coordinates analysis

Latent roots

1	2
2.824	0.972

Percentage variation

1	2
38.22	13.15

Trace

7.389

In interpreting the plot (Figure 4.5), it is interesting to note that congressmen Daniels, Helstoki, Howard, Minish, Patten, Rodino, Roe and Thompson were Democrats, while congressmen Forsythe, Frelinghuysen, Hunt, Maraziti, Rinaldo, Sandman, Widnall were Republicans.

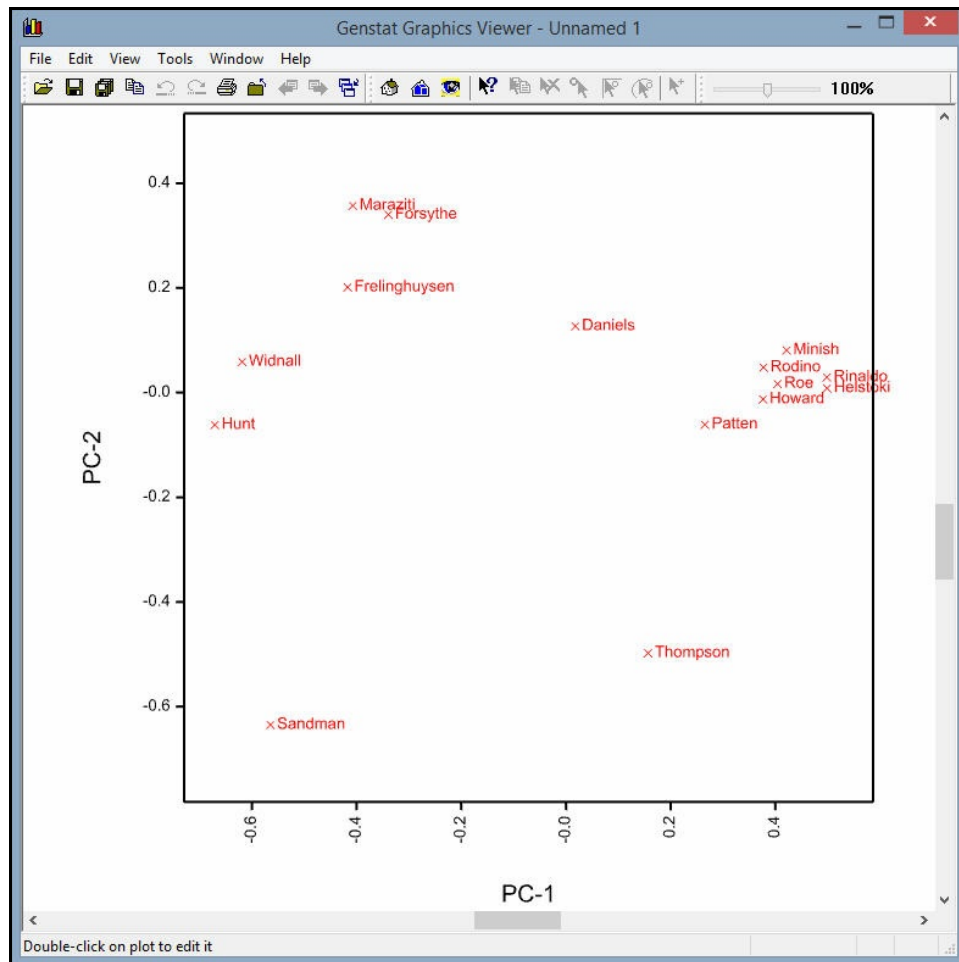


Figure 4.5

4.1 Practical

Genstat spreadsheet file `Galaxy.gsh` (Figure 4.6) contains distances between ten types of Galaxy. Use principal coordinates analysis to represent them in three dimensions.

Row	1	2	3	4	5	6	7	8	9	10
1										
2	1.36748	0								
3	1.49666	0.953939	0							
4	2.00749	1.43178	1.22882	0						
5	2.02237	1.31909	1.26095	0.824621	0					
6	2.31948	1.84662	1.77482	1.36382	1.12694	0				
7	2.65141	1.96214	1.8	1.5	1.37477	1.42127	0			
8	2.45357	2.20227	2.02731	1.73205	1.45945	1.30767	1.20416	0		
9	2.62298	2.38747	2.26274	1.92873	1.73494	1.72337	1.32288	1.06301	0	
10	2.02978	1.94165	1.96469	1.98242	1.80831	1.94165	1.87617	1.67033	1.81384	0

Figure 4.6

5 Multidimensional scaling

Multidimensional scaling operates on a symmetric matrix which is assumed to represent distances between a set of units. It aims to construct coordinates of points, in a defined number of dimensions, whose distances are approximately the same as those in the original matrix. To illustrate the analysis we will try to recreate the locations of some British towns, based on figures for the shortest distances between each of them by road. The data are in the Genstat spreadsheet `Roaddist.gsh` (Figure 5.1). This is a symmetric matrix spreadsheet (as shown by the blanks above the diagonal).

Row	Name	Aberdeen	Aberystwyth	Birmingham	Blackpool	Bournemouth	Bristol	Cardiff	Carlisle	Dover	Edinburgh	Exeter
1	Aberdeen											
2	Aberystwyth	445	0									
3	Birmingham	420	114	0								
4	Blackpool	308	153	123	0							
5	Bournemouth	564	207	147	270	0						
6	Bristol	499	125	81	204	82	0					
7	Cardiff	505	105	103	209	117	45	0				
8	Carlisle	221	224	196	87	343	277	289	0			
9	Dover	588	292	194	312	174	202	238	389	0		
10	Edinburgh	125	320	292	183	439	373	385	96	462	0	
11	Exeter	569	201	157	282	82	76	121	353	248	450	0
12	Fishguard	504	56	170	209	222	154	112	297	331	399	230
13	Fort William	149	430	392	296	539	486	485	206	596	144	560
14	Gloucester	468	102	56	174	99	35	56	247	191	349	111
15	Great Yarmouth	517	294	180	252	240	275	284	320	185	386	335
16	Harwich	535	281	167	275	187	217	246	336	125	413	279
17	Holyhead	439	111	148	141	288	206	216	231	360	333	282
18	Inverness	105	486	458	348	597	539	549	262	622	158	618
19	John O Groats	232	601	574	478	724	668	680	391	747	285	744

Figure 5.1

The **Multidimensional Scaling** menu is obtained by clicking on the **Multidimensional Scaling** line in the **Multivariate Analysis** section of the **Stats** menu. In Figure 5.2, we have entered `Distances` as the distance matrix to use, and set the required number of dimensions to 3.

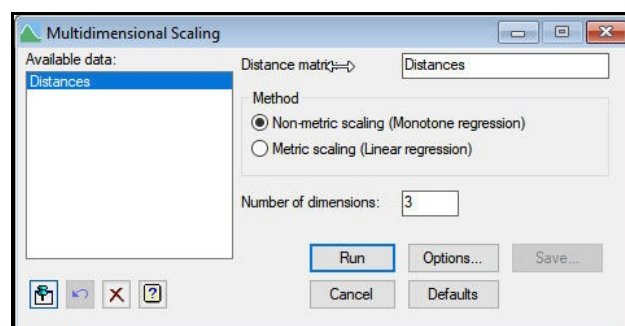


Figure 5.2

The algorithm starts with an initial configuration of points which it then modifies using a method known as *steepest descent*, until no further improvements are possible (see the *Guide to the Genstat Command Language*, Part 2 Section 6.12). To evaluate the configuration, it does a regression of the inter-point distances, calculated from the current configuration, against the supplied distances. The **Method** setting on the menu controls whether this is a “monotone regression” (which corresponds to what is known as *non-metric scaling*) or an ordinary linear regression (corresponding to *metric scaling*). It then compares the fitted

distances from the regression with the original distances using a quantity known as the *stress*.

The **Scaling** section of the **Multidimensional Scaling Options** menu (Figure 5.3) allows you to specify what to display from the analysis. Here we have asked to display the latent roots and the coordinates. It also controls whether the stress is calculated on a least-squares scale, a least-squares-squared scale or a logarithmic scale. The **Treatment of ties** section of the options menu allows you to vary the way in which tied values in the supplied distances are treated. With the **Primary** setting,

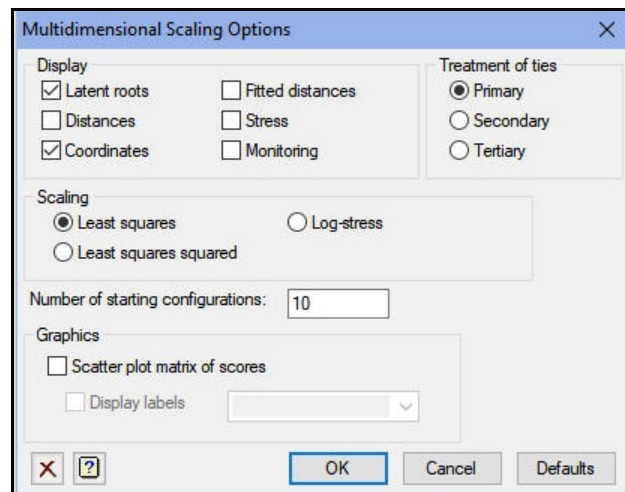


Figure 5.3

are placed on the inter-point distances corresponding to tied distances. In the **Secondary** setting, the inter-point distances corresponding to tied distances are required to be as nearly equal as possible. The **Tertiary** setting is a compromise between the primary and secondary approaches to ties: the block of ties corresponding to the smallest distance are handled by the secondary method, and the remaining blocks of ties are handled by the primary method. This is particularly useful when the supplied distance matrix contains only a distinct values. Further information is given in the *Guide to the Genstat Command Language*, Part 2 Section 6.12, which describes the **MDS** directive that is used by these menus. The directive also has some additional facilities, for example the ability to try several automatically-generated initial configurations, or to supply your own.

If we click on **OK** here, and on **Run** in the **Multidimensional Scaling** menu itself, Genstat produces the output below.

Message: Default seed for random number generator used with value 33633

Multidimensional scaling

Least-squares scaling criterion

Distances fitted using monotonic regression (non-metric MDS).
Primary treatment of ties.

Coordinates

	1	2	3
Name			
Aberdeen	-1.5498	-0.1754	-0.0455
Aberystwyth	0.3087	0.3597	-0.3365
Birmingham	0.3114	-0.0462	-0.0424

Blackpool	-0.2214	0.0591	-0.1727
Bournemouth	0.8882	-0.0407	0.2126
Bristol	0.6224	0.1741	0.0695
Cardiff	0.6422	0.3121	-0.0901
Carlisle	-0.5888	0.0634	-0.0696
Dover	0.9364	-0.7146	-0.0893
Edinburgh	-1.0006	-0.0158	0.0541
Exeter	0.8894	0.3092	0.3292
Fishguard	0.5061	0.5383	-0.4924
Fort William	-1.4431	0.3719	0.2468
Gloucester	0.5245	0.0843	0.0032
Great Yarmouth	0.3566	-0.9353	-0.0210
Harwich	0.5698	-0.7701	0.1975
Holyhead	0.1291	0.2137	-0.7365
Inverness	-1.6910	0.1129	0.2851
John O Groats	-2.2088	0.1106	0.4087
Hull	-0.1110	-0.4433	-0.1190
Lands End	1.2693	0.6009	0.6692
Lincoln	0.0800	-0.3966	0.0124
Liverpool	-0.0530	0.1262	-0.1838
Newcastle	-0.5933	-0.2389	0.0496
Plymouth	1.0069	0.4264	0.4607
Portsmouth	0.9079	-0.2205	0.1607
Sheffield	0.0046	-0.1912	-0.0319
Stranraer	-0.9726	0.2432	-0.4059
Swansea	0.6916	0.3303	-0.3322
York	-0.2118	-0.2478	0.0095

Latent roots

1	23.36
2	4.15
3	2.49

The **Multidimensional Scaling Options** menu has a check box to plot the coordinates (or scores) in a scatter-plot matrix showing all the pairs of dimensions. If you want to plot a single pair of dimensions, you first need to save the coordinates, using the **Multidimensional Scaling Save Options** menu (Figure 5.4) which is obtained by clicking on the **Save** button on the **Multidimensional Scaling** menu. Here we have asked to save the coordinates in a matrix called *Locations*, and to display these in a spreadsheet.

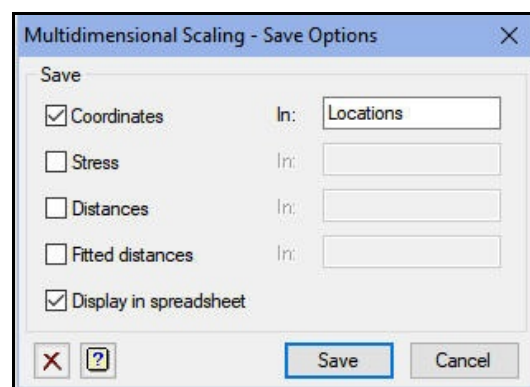


Figure 5.4

To plot the points, we need to convert the rectangular matrix spreadsheet of locations to a vector spreadsheet, by making this the active window and then selecting the **Convert** sub-option of the **Sheet** option of the **Spread** menu on the menu bar. In the resulting **Convert Sheet** menu (Figure 5.5), we change the radio button from **Matrix** to **Vector**, and click on **OK** to make the change. The columns will then become variates, probably with names **C1**, **C2** and **C3**, which can be used in the graphics menus in the usual way.

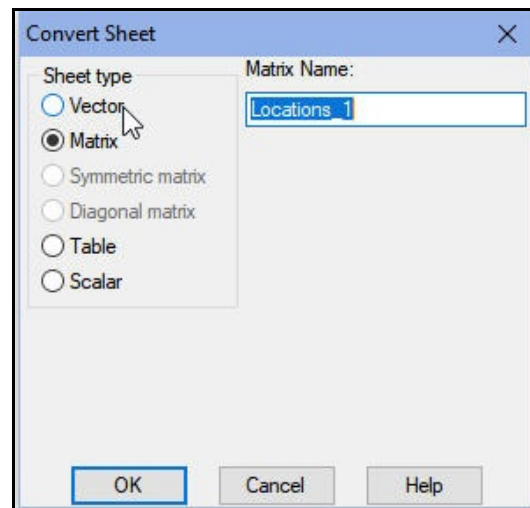


Figure 5.5

We can then plot the points using the **2D Scatter Plot** wizard in the usual way. First we use the initial **Data** menu (Figure 5.6) to select **C1** for the y-coordinates, and **C2** for the x-coordinates.

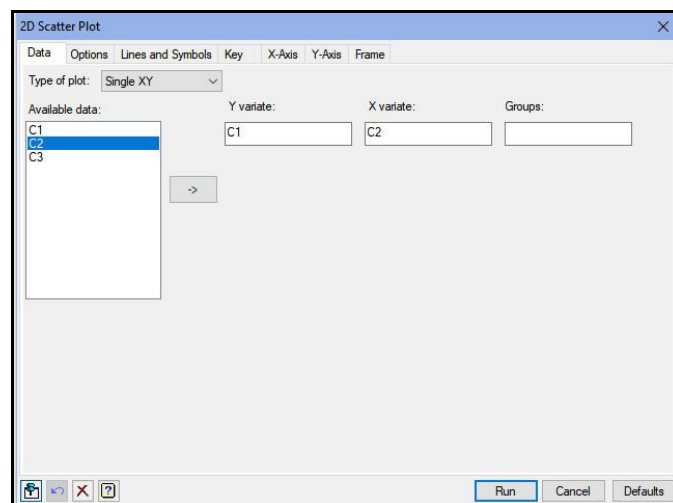


Figure 5.6

Then we select the **Lines and Symbols** tab of the **Attributes** menu (Figure 5.7), and arrange to label the points using the text **Name**. We also cancel the key on the **Options** tab.

Figure 5.8 shows the resulting plot of the first two dimensions, and Figure 5.9 shows a similar plot of the first dimension against the third dimension (showing some of the distortion in the data from a 2-dimensional solution).

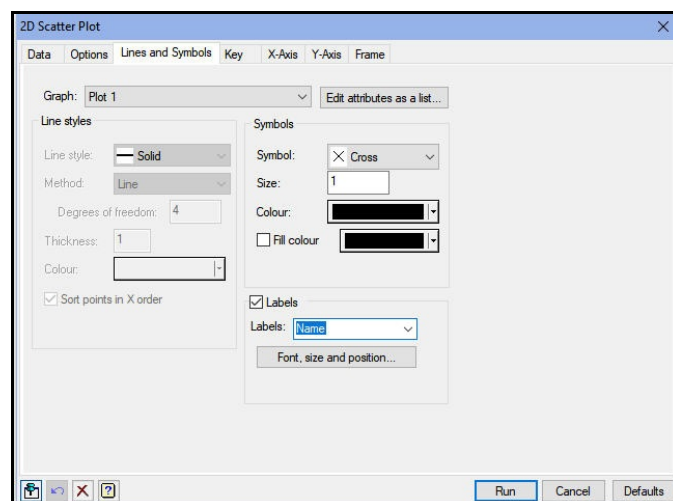


Figure 5.7

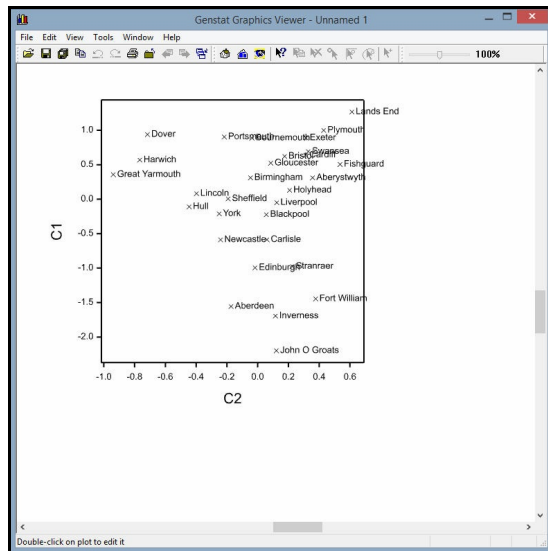


Figure 5.8

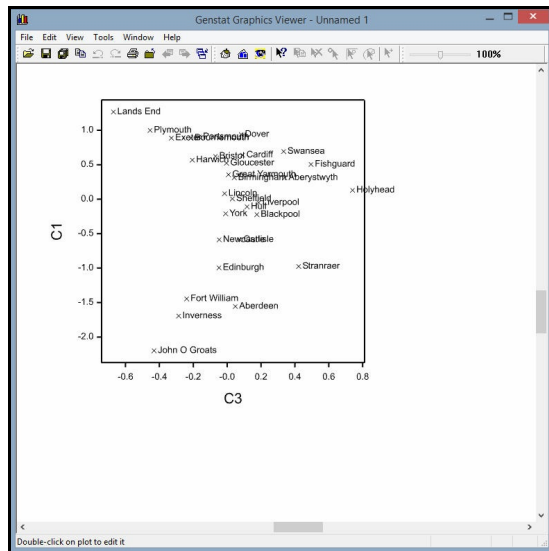


Figure 5.9

5.1 Practical

Genstat spreadsheet file `Galaxy.gsh` (Figure 5.10) contains distances between ten types of Galaxy. Use multidimensional scaling to represent them in three dimensions.

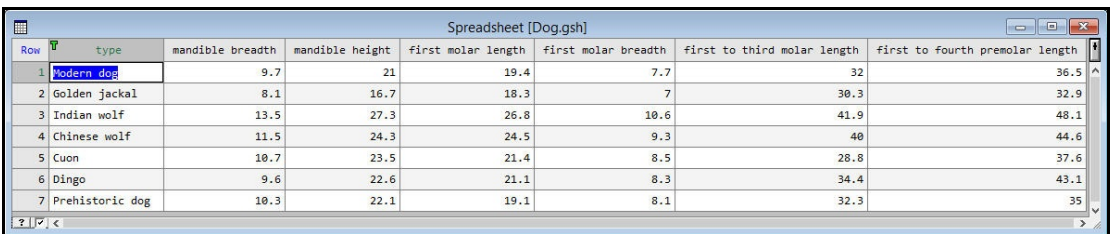
Row	1	2	3	4	5	6	7	8	9	10
1										
2	1.36748	0								
3	1.49666	0.953939	0							
4	2.00749	1.43178	1.22882	0						
5	2.02237	1.31909	1.26095	0.824621	0					
6	2.31948	1.84662	1.77482	1.36382	1.12694	0				
7	2.65141	1.96214	1.8	1.5	1.37477	1.42127	0			
8	2.45357	2.20227	2.02731	1.73205	1.45945	1.30767	1.20416	0		
9	2.62298	2.38747	2.26274	1.92873	1.73494	1.72337	1.32288	1.06301	0	
10	2.02978	1.94165	1.96469	1.98242	1.80831	1.94165	1.87617	1.67033	1.81384	0

Figure 5.10

6 Hierarchical cluster analysis

The hierarchical cluster analysis facilities in Genstat provide ways of grouping n objects into classes according to their similarity. It starts with a set of n clusters (or groups), each containing a single object. These initial clusters are successively merged into larger clusters, according to their similarity, until there is just one cluster (containing all the objects).

We shall use a set of data concerning mean mandible measurements of various types of modern and prehistoric dog (Higham, Kijngam & Manly, 1980, An analysis of prehistoric canid remains from Thailand, *Journal of Archaeological Science*, 7, 149-165). This data set is also discussed by Manly (1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London). The data are in the Genstat spreadsheet `Dog.gsh` (Figure 6.1).



Row	type	mandible breadth	mandible height	first molar length	first molar breadth	first to third molar length	first to fourth premolar length
1	Modern dog	9.7	21	19.4	7.7	32	36.5
2	Golden jackal	8.1	16.7	18.3	7	30.3	32.9
3	Indian wolf	13.5	27.3	26.8	10.6	41.9	48.1
4	Chinese wolf	11.5	24.3	24.5	9.3	40	44.6
5	Cuon	10.7	23.5	21.4	8.5	28.8	37.6
6	Dingo	9.6	22.6	21.1	8.3	34.4	43.1
7	Prehistoric dog	10.3	22.1	19.1	8.1	32.3	35

Figure 6.1

The [Hierarchical Cluster Analysis](#) menu is obtained by clicking on the [Hierarchical](#) line in the [Cluster Analysis](#) subsection in the [Multivariate Analysis](#) section of the [Stats](#) menu on the menu bar. If you have already formed a similarity matrix, or a distance matrix or a dissimilarity matrix, you can enter its name straight into the [Similarity matrix](#) field in the menu (Figure 6.2). With a distance matrix, you would usually check the [Use square root transform](#) box.

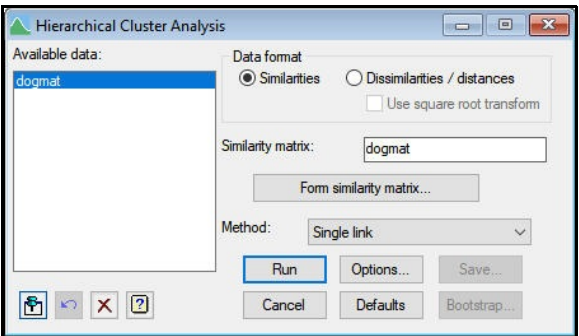


Figure 6.2

Alternatively, you can click on the [Form Similarity Matrix](#) button and use the [Form Similarity Matrix](#) menu (Figure 6.3). The names of the variates need to be entered into the [Data values](#) window, and you need to define a name (here `dogmat`) for the resulting symmetric matrix. You must also select the way in which the similarities are to be calculated from each variate.

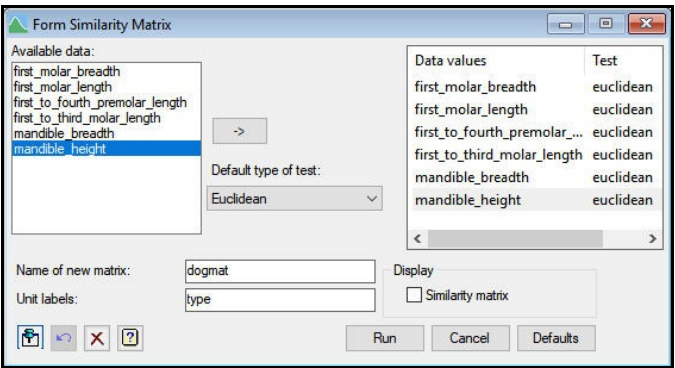


Figure 6.3

Here we have chosen the default type to be “euclidean”, which uses the geometric distance between the points representing each pair of objects. (A formal definition of this, and the other possibilities is in the *Guide to the Genstat Command Language*, Part 2, Section 6.1.2, where it describes the **METHOD** option of the **FSIMILARITY** directive, used by the menu.) You can change the types of individual data variables by double-clicking on their lines in the right-hand box. Finally, you can specify a vector (here the text called **type** from the first column of the spreadsheet) to label rows and columns of the matrix. When you click **Run**, the name of the matrix is automatically entered into the **Similarity matrix** field in the **Hierarchical Cluster Analysis** menu.

The **Method** field in the **Hierarchical Cluster Analysis** menu (Figure 6.2) contains a drop-down list box to specify the method of clustering to use. These differ according to the way in which they define the similarity between clusters containing more than one object:

Single link	defines the similarity to be the maximum similarity between any pair of objects (taken one from each cluster);
Nearest neighbour	is a synonym for Single link ;
Complete link	defines the similarity between two clusters as the minimum similarity between any pair of objects;
Furthest neighbour	is a synonym for Complete link ;
Average link	defines the similarity, between a cluster and a new cluster formed by merging two clusters, as the average of the similarities with each of the original clusters;
Group average	is similar to Average link , except that the average is over all the objects in the two merging clusters;
Median sorting	if we regard the clusters as points in a multidimensional space, when two clusters join the new cluster is represented by the midpoint of the original cluster points.

Output from the analysis is controlled by the **Hierarchical Cluster Analysis Options** menu (Figure 6.4). For the dog example, we will simply print, and plot, the dendrogram. This displays the points at which the various clusters combine, allowing you to assess the relationships between the objects. If you specify a threshold in the **Forming groups** field of the options menu, Genstat will form a factor grouping all the objects that have been combined into a single cluster at that level of similarity. You can arrange to save the factor using the **Hierarchical Cluster Analysis Save Options** menu, obtained by clicking on the **Save** button in the **Hierarchical Cluster Analysis** menu (Figure 6.2).

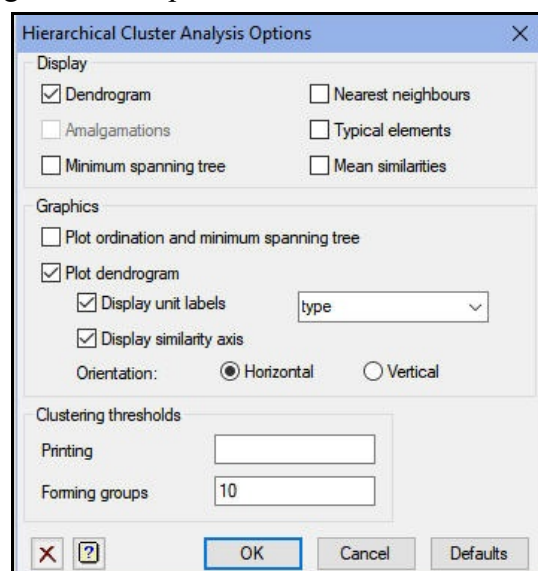


Figure 6.4

Single linkage cluster analysis

Dendrogram

```

** Levels      100.0  90.0

Modern dog      1  ..
Prehistoric dog 7  ..)
Cuon            5  ..)..
Dingo           6  .....)
Golden jackal   2  .....)
Chinese wolf    4  .....)
Indian wolf     3  .....).....

```

The dendrogram for the dogs, printed above and plotted (with better resolution) in Figure 6.5, shows that the modern and prehistoric dogs are most closely related, and that both of these are related to the Cuon and to the Dingo and Golden jackal. The Indian and Chinese wolves are related to each other more than any of the other dogs, but the similarity is not close.

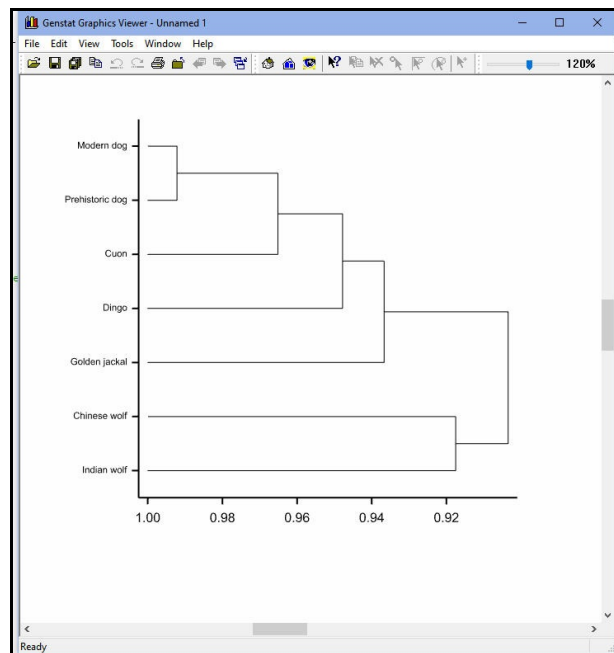


Figure 6.5

Bootstrapping provides a way to assess the reliability of the clustering. Does a cluster rely on just a few of the variables, or does it have wider support? Once you have run the cluster analysis, you can open the [Bootstrap Hierarchical Cluster Analysis](#) menu (Figure 6.6) by clicking the [Bootstrap](#) button in the [Hierarchical Cluster Analysis](#) menu. This takes a sample, with replacement, from the available variables. It forms a similarity matrix using the same settings as in the original analysis. It then does a cluster analysis, and records whether each of the original clusters is included.

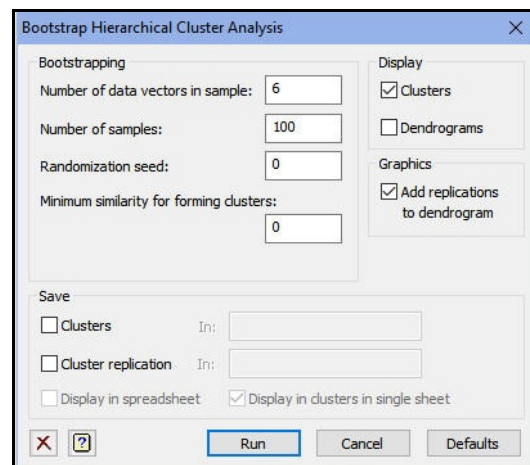


Figure 6.6

Here we have left the default, which will form samples with the same number of variables as in the original analysis (6). We shall take 100 bootstrap samples, with seed zero meaning that Genstat will choose the seed for the random numbers automatically. As we have not used any random numbers earlier in this run, Genstat will initialise the random number generator from the system clock. Different seeds will give different results. So you should remember the seed (and enter it into the [Randomization seed](#) box), if you want to redo the bootstrapping and obtain same results in future.

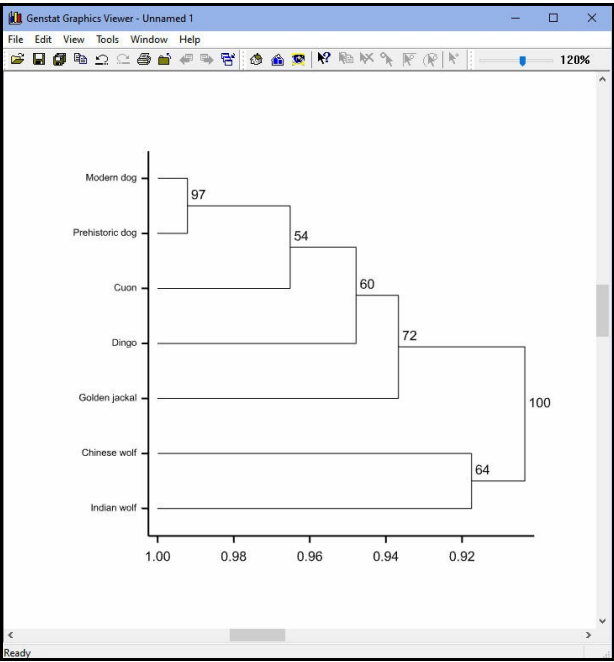


Figure 6.7

The box for the [Minimum similarity for forming clusters](#) allows you to ignore clusters that have low similarities. In our example, as all the clusters have a similarity greater than 0.9 (see Figure 6.5), it seems unnecessary to change this from the default of zero. We have chosen to print the clusters (with their replications over the samples), and to add these to the dendrogram, as shown in Figure 6.7. You can see that the cluster of modern dog with prehistoric dog occurs in almost all of the samples (97 out of 100), but the inclusion of Cuon has less support (only 54 samples).

Message: Default seed for random number generator used with value 955562

Clusters

Replication	97	64	54	60
Cluster	{ Modern dog Prehistoric dog }	{ Indian wolf Chinese wolf }	{ Modern dog Cuon Prehistoric dog }	{ Modern dog Cuon Dingo Prehistoric dog }
Replication	72	100		
Cluster	{ Modern dog Golden jackal Cuon Dingo Prehistoric dog }	{ Modern dog Golden jackal Indian wolf Chinese wolf Cuon Dingo Prehistoric dog }		

6.1 Practical

Genstat spreadsheet file `Goblet.gsh` (Figure 6.8) contains data on 25 goblets from prehistoric sites in Thailand (see page 147 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London). Perform a principal components analysis to study the relationships between the

Row	Label	MouthWidth	OverallWidth	OverallHeight	LowerStemWidth	UpperStemWidth	StemHeight
1	1	13	21	23	14	7	8
2	2	14	14	24	19	5	9
3	3	19	23	24	20	6	12
4	4	17	18	16	16	11	8
5	5	19	20	16	16	10	7
6	6	12	20	24	17	6	9
7	7	12	19	22	16	6	10
8	8	12	22	25	15	7	7
9	9	11	15	17	11	6	5
10	10	11	13	14	11	7	4
11	11	12	20	25	18	5	12
12	12	13	21	23	15	9	8

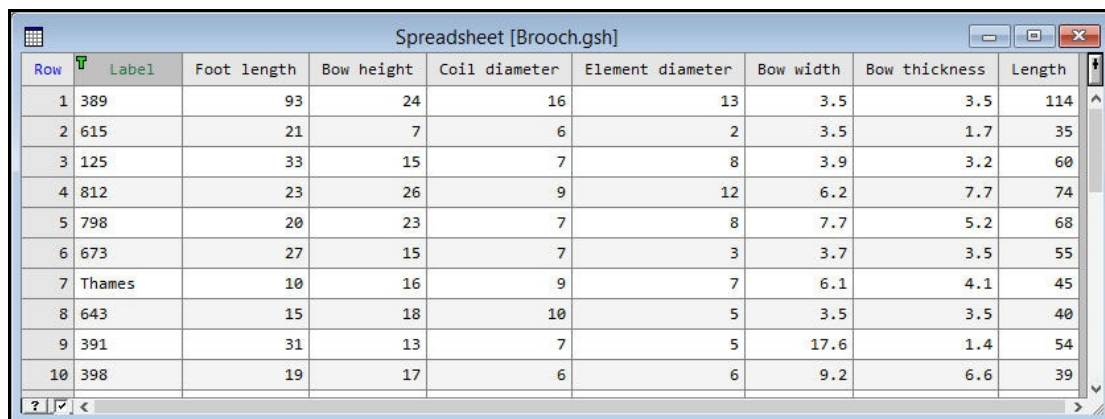
Figure 6.8

goblets. Then perform a cluster analysis of the goblets. How does the dendrogram reflect the closeness of the goblets in the principal-component plot?

7 Non-hierarchical cluster analysis

Non-hierarchical cluster analysis aims to find a single grouping of a set of n objects by optimizing a criterion, for example by maximizing the between-group sum of squares. Other criteria in Genstat include maximizing the total between-groups Mahalanobis distance, minimizing the within-class dispersion or a criterion known as *maximal predictive classification*, which is designed specifically for binary data. For full definitions, see the *Guide to the Genstat Command Language*, Part 2 Section 6.20. This form of clustering includes the technique known as *K-means clustering*, where the criterion is usually the within-class dispersion.

To illustrate the menus we shall use some measurements taken on 30 bronze brooches (Doran & Hodson, 1975, *Mathematics and Computers in Archaeology*, Edinburgh University Press, Table 9.1). These are stored in Genstat spreadsheet `Brooch.gsh` (Figure 7.1).



Row	Label	Foot length	Bow height	Coil diameter	Element diameter	Bow width	Bow thickness	Length
1	389	93	24	16	13	3.5	3.5	114
2	615	21	7	6	2	3.5	1.7	35
3	125	33	15	7	8	3.9	3.2	60
4	812	23	26	9	12	6.2	7.7	74
5	798	20	23	7	8	7.7	5.2	68
6	673	27	15	7	3	3.7	3.5	55
7	Thames	10	16	9	7	6.1	4.1	45
8	643	15	18	10	5	3.5	3.5	40
9	391	31	13	7	5	17.6	1.4	54
10	398	19	17	6	6	9.2	6.6	39

Figure 7.1

Before doing the cluster analysis, to counteract skewness in the variables, we transform each column of measurements x to $\log_{10}(x+1)$. This can be done using the [Calculate](#) menu in the usual way. Alternatively, to save time, the transformed data are available in spreadsheet `Logbrooch.gsh`.

To obtain the [Non-hierarchical Cluster Analysis](#) menu you click on the [Non-hierarchical](#) line in the [Cluster Analysis](#) subsection in the [Multivariate Analysis](#) section of the [Stats](#) menu on the menu bar.

Figure 7.2 shows the menu set to use all the measurements to form four groups using the between-group sum of squares criterion.

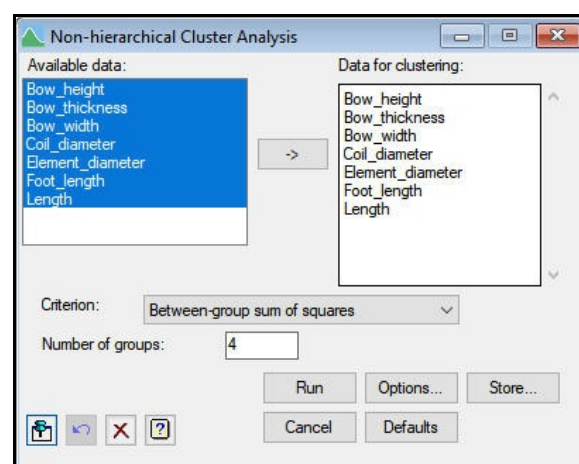


Figure 7.2

The [Non-hierarchical Cluster Analysis Options](#) menu (Figure 7.3) controls the way in which the search for the best grouping is carried out, and the output that is produced.

In Figure 7.3, we have asked Genstat to form the initial classification by finding the four objects that are furthest apart in the 7-dimensional space defined by the measurements, using these objects as the “cores” of the initial groups, and allocating the other objects to the group with the nearest core. (Note: this is feasible only if the number of groups does not exceed the number of variates.) The [Between-group interchanges](#) box controls how Genstat generates new groupings from the initial classification. Here we are allowing objects both to be swapped between groups, and to be transferred from group to group. The setting [Swap only](#) would constrain the group sizes to remain the same throughout the search (which might be useful, for example, if you wanted groups of equal sizes, and chosen the [Equal-sized groups, by unit order](#) option for the [Initial classification](#)), and the setting [Fix at initial configuration](#) makes no changes.

You can arrange to store the final classification by using the [Non-hierarchical Cluster Analysis Store Options](#) menu (Figure 7.4), which is obtained by clicking on the [Store](#) button in the [Non-hierarchical Cluster Analysis](#) menu (Figure 7.2). To save the a factor defining the groups, you check the [Grouping](#) box, and type the name of a factor into the [In](#) box.

Output from the clustering shown below.

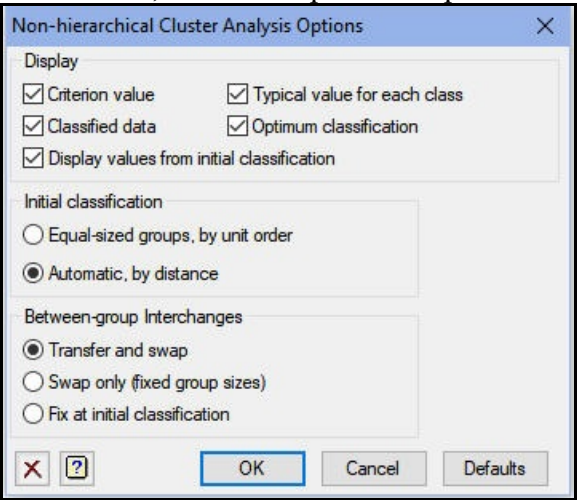


Figure 7.3

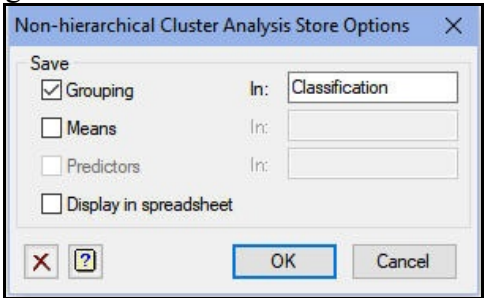


Figure 7.4

Non-hierarchical clustering

Sums of squares criterion

Initial classification

Number of classes = 4

Class contributions to criterion

1	2	3	4
0.5471	0.2434	1.4189	0.3416

Criterion value = 2.55101

Classification of units

Unit	1	2	3	4	5	6	7	8	9	10
Group	1	4	3	3	3	4	3	3	2	3
Unit	11	12	13	14	15	16	17	18	19	20
Group	1	1	2	3	3	3	3	3	2	3
Unit	21	22	23	24	25	26	27	28	29	30
Group	1	2	2	3	3	3	4	4	3	1

Class mean values

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
1	1.303	0.768	0.828	1.093
2	1.217	0.514	1.102	0.899
3	1.243	0.728	0.818	0.912
4	1.112	0.564	0.619	0.874
	Element_diameter	Foot_length	Length	
1	0.992	1.819	1.994	
2	0.756	1.402	1.710	
3	0.959	1.298	1.674	
4	0.540	1.259	1.623	

Units rearranged into class order

Group 1

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
1	1.398	0.653	0.653	1.230
11	1.380	0.833	0.919	1.079
12	1.255	0.756	0.833	1.041
21	1.204	0.724	0.724	1.114
30	1.279	0.875	1.013	1.000
	Element_diameter	Foot_length	Length	
Unit				
1	1.146	1.973	2.061	
11	1.176	1.623	1.857	
12	0.954	1.681	1.898	
21	1.079	1.978	2.111	
30	0.602	1.839	2.045	

Group 2

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
9	1.146	0.380	1.270	0.903
13	1.204	0.690	1.104	0.845
19	1.279	0.519	0.959	1.000

22	1.279	0.602	0.991	0.903
23	1.176	0.380	1.185	0.845

	Element_diameter	Foot_length	Length
Unit			
9	0.778	1.505	1.740
13	0.845	1.477	1.681
19	0.778	1.342	1.699
22	0.778	1.362	1.778
23	0.602	1.322	1.653

Group 3

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
3	1.204	0.623	0.690	0.903
4	1.431	0.940	0.857	1.000
5	1.380	0.792	0.940	0.903
7	1.230	0.708	0.851	1.000
8	1.279	0.653	0.653	1.041
10	1.255	0.881	1.009	0.845
14	1.146	0.568	0.792	0.845
15	1.204	0.763	0.756	0.778
16	1.230	0.653	0.785	0.903
17	1.204	0.681	0.813	0.903
18	1.146	0.732	0.732	0.778
20	1.255	0.556	0.544	1.041
24	1.204	0.748	0.778	0.903
25	1.362	0.869	0.892	1.000
26	1.204	0.699	0.964	1.041
29	1.146	0.778	1.025	0.699

	Element_diameter	Foot_length	Length
Unit			
3	0.954	1.531	1.785
4	1.114	1.380	1.875
5	0.954	1.322	1.839
7	0.903	1.041	1.663
8	0.778	1.204	1.613
10	0.845	1.301	1.602
14	1.041	1.380	1.623
15	1.114	1.322	1.591
16	0.954	1.255	1.653
17	0.845	1.322	1.708
18	1.041	1.322	1.568
20	0.954	1.462	1.732
24	1.146	1.362	1.681
25	1.000	1.114	1.663
26	1.000	1.447	1.732
29	0.699	1.000	1.462

Group 4

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
2	0.9031	0.4314	0.6532	0.8451
6	1.2041	0.6532	0.6721	0.9031
27	1.3010	0.6532	0.6721	0.9031
28	1.0414	0.5185	0.4771	0.8451

	Element_diameter	Foot_length	Length
--	------------------	-------------	--------

Unit			
2	0.4771	1.3424	1.5563
6	0.6021	1.4472	1.7482
27	0.6021	1.2041	1.7559
28	0.4771	1.0414	1.4314

Optimum classification

Number of classes = 4

Class contributions to criterion

1	2	3	4
0.5471	0.2434	0.9901	0.7254

Criterion value = 2.50611

Classification of units

Unit	1	2	3	4	5	6	7	8	9	10
Group	1	4	3	3	3	4	3	4	2	3
Unit	11	12	13	14	15	16	17	18	19	20
Group	1	1	2	3	3	3	3	3	2	3
Unit	21	22	23	24	25	26	27	28	29	30
Group	1	2	2	3	3	3	4	4	4	1

Class mean values

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
1	1.303	0.768	0.828	1.093
2	1.217	0.514	1.102	0.899
3	1.247	0.730	0.815	0.917
4	1.146	0.615	0.692	0.873
	Element_diameter	Foot_length	Length	
1	0.992	1.819	1.994	
2	0.756	1.402	1.710	
3	0.991	1.326	1.694	
4	0.606	1.207	1.594	

Units rearranged into class order

Group 1

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
1	1.398	0.653	0.653	1.230
11	1.380	0.833	0.919	1.079
12	1.255	0.756	0.833	1.041
21	1.204	0.724	0.724	1.114

30	1.279	0.875	1.013	1.000
	Element_diameter	Foot_length	Length	
Unit				
1	1.146	1.973	2.061	
11	1.176	1.623	1.857	
12	0.954	1.681	1.898	
21	1.079	1.978	2.111	
30	0.602	1.839	2.045	

Group 2

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
9	1.146	0.380	1.270	0.903
13	1.204	0.690	1.104	0.845
19	1.279	0.519	0.959	1.000
22	1.279	0.602	0.991	0.903
23	1.176	0.380	1.185	0.845
	Element_diameter	Foot_length	Length	
Unit				
9	0.778	1.505	1.740	
13	0.845	1.477	1.681	
19	0.778	1.342	1.699	
22	0.778	1.362	1.778	
23	0.602	1.322	1.653	

Group 3

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
3	1.204	0.623	0.690	0.903
4	1.431	0.940	0.857	1.000
5	1.380	0.792	0.940	0.903
7	1.230	0.708	0.851	1.000
10	1.255	0.881	1.009	0.845
14	1.146	0.568	0.792	0.845
15	1.204	0.763	0.756	0.778
16	1.230	0.653	0.785	0.903
17	1.204	0.681	0.813	0.903
18	1.146	0.732	0.732	0.778
20	1.255	0.556	0.544	1.041
24	1.204	0.748	0.778	0.903
25	1.362	0.869	0.892	1.000
26	1.204	0.699	0.964	1.041
	Element_diameter	Foot_length	Length	
Unit				
3	0.954	1.531	1.785	
4	1.114	1.380	1.875	
5	0.954	1.322	1.839	
7	0.903	1.041	1.663	
10	0.845	1.301	1.602	
14	1.041	1.380	1.623	
15	1.114	1.322	1.591	
16	0.954	1.255	1.653	
17	0.845	1.322	1.708	
18	1.041	1.322	1.568	
20	0.954	1.462	1.732	
24	1.146	1.362	1.681	

25	1.000	1.114	1.663
26	1.000	1.447	1.732

Group 4

	Bow_height	Bow_thickness	Bow_width	Coil_diameter
Unit				
2	0.9031	0.4314	0.6532	0.8451
6	1.2041	0.6532	0.6721	0.9031
8	1.2788	0.6532	0.6532	1.0414
27	1.3010	0.6532	0.6721	0.9031
28	1.0414	0.5185	0.4771	0.8451
29	1.1461	0.7782	1.0253	0.6990

	Element_diameter	Foot_length	Length
Unit			
2	0.4771	1.3424	1.5563
6	0.6021	1.4472	1.7482
8	0.7782	1.2041	1.6128
27	0.6021	1.2041	1.7559
28	0.4771	1.0414	1.4314
29	0.6990	1.0000	1.4624

The output gives details of the initial classification and of the final (optimal) classification, showing the criterion value, how the objects are allocated to the groups and the mean values of the measurements in each group. In this example, the initial classification has been very successful. The optimum classification differs only in that the eighth object has been transferred from group 3 to group 4, and the 29th object from group 4 to group 3.

7.1 Practical

Genstat spreadsheet file *Goblet.gsh* (Figure 7.5) contains data on 25 goblets from prehistoric sites in Thailand (see page 147 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London). Perform a non-hierarchical classification into five groups. How does this compare with the dendrogram produced in Practical 6.1?

Figure 7.5

8 Multivariate analysis of variance

Multivariate analysis of variance can be viewed as the extension of ordinary analysis of variance (as in Chapter 6) to handle several response variates at once. So, for example, instead of making assumptions of Normality for the residuals from a single response variate, we are now assuming multivariate Normality of residuals from several response variates.

We illustrate the analysis using data from an experiment to investigate sex and temperature effects on the growth of tumours in rats (see page 143 of Chatfield & Collins, 1986, *Introduction to Multivariate Analysis*, Chapman and Hall, London). Three rats of each sex were reared in each of three temperatures (4, 20 and 34). There was no blocking (i.e. this is a completely randomized design).

The weights of the rats were measured (prior to sub-cutaneous seeding of the tumours). The response variates, taken at the end of the experiment, are the tumour weight and the final weight (excluding the tumour). The data are available in spreadsheet *Tumour.gsh* (Figure 8.28).

The **MANOVA** menu (Figure 8.2) is obtained by clicking on the **MANOVA** line in the **Multivariate Analysis** section of the **Stats** menu on the menu bar.

In Figure 8.2, we have specified a treatment structure of *Sex*Temperature*, to fit the main effects of sex and temperature, and their interaction (see Section 6.6). There is no block structure but we want to treat the variate *InitialWeight* as a *covariate*

(so we check the **Covariates** box, and enter its name into the adjacent field). Covariates are included in the treatment model like variates in a linear regression. So, Genstat estimates a regression coefficient for them, and adjusts the other estimates and sums of squares to take account of their presence in the model (see *Guide to the Genstat Command Language*, Part 2 Section 4.3).

Row	Sex	Temperature	TumourWeight	FinalWeight	InitialWeight
1	Male	4	0.24	16.51	18.15
2	Male	4	0.32	19.5	18.68
3	Male	4	0.2	19.84	19.54
4	Female	4	0.16	19.49	19.15
5	Female	4	0.17	19.81	18.35
6	Female	4	0.22	19.44	20.68
7	Male	20	0.33	23.3	21.27
8	Male	20	0.45	22.3	19.57
9	Male	20	0.35	18.95	20.15
10	Female	20	0.25	22	18.87

Figure 8.1

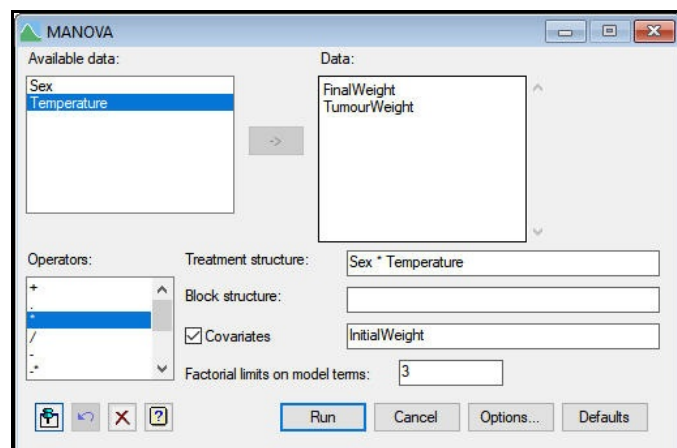


Figure 8.2

The **MANOVA Options** menu, shown in Figure 8.30, allows you to control the output from the multivariate analysis, and also to display output from the univariate anova's of the individual response variates. Here we have asked just to print the various tests from the multivariate analysis, and omitted the sums and squares and products of the treatment effects and residuals (which are involved in calculating the tests).

The output, shown below, indicates that there are sex and temperature effects, but no interaction and no effect of the covariate.

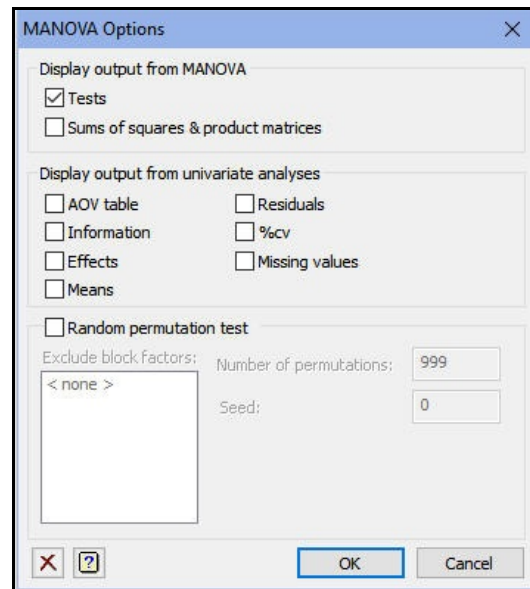


Figure 8.3

Multivariate analysis of covariance

Y-variates: FinalWt, TumourWt.

Covariate: InitWt.

Test statistics

Term	d.f.	Wilks' lambda	Rao F	n.d.f.	d.d.f.	F prob.
Sex	1	0.3485	9.35	2	10	0.005
Temperature	2	0.3269	3.75	4	20	0.020
Sex.Temperature	2	0.7830	0.65	4	20	0.633
Covariate	1	0.8219	1.08	2	10	0.375

Term	d.f.	Pillai-Bartlett trace	Roy's maximum root test	Lawley-Hotelling trace
Sex	1	0.6515	0.6515	1.8697
Temperature	2	0.8477	0.4949	1.5249
Sex.Temperature	2	0.2278	0.1605	0.2634
Covariate	1	0.1781	0.1781	0.2167

The analysis uses the **MANOVA** procedure (see *Guide to the Genstat Command Language*, Part 2 Section 6.6.1). This uses the **ANOVA** directive, which requires the design to be balanced (see Section 6.7 or *Guide to the Genstat Command Language*, Part 2 Section 4.7). For unbalanced data, you can use the **MULTIVARIATE** procedure, but this is not currently accessible through the menus.

8.1 Practical

Genstat spreadsheet file `Skull.gsh` (Figure 8.4) contains data on 150 male Egyptian skulls from five different epochs (see Practical 3.1 and pages 4 and 5 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London). Perform a multivariate analysis of variance. Are there any epoch differences?

Row	Epoch	MaximumBreadth	BasibregmaticHeight	BasioleolarLength	NasalHeight
1	Early predynastic	131	138	89	49
2	Early predynastic	125	131	92	48
3	Early predynastic	131	132	99	50
4	Early predynastic	119	132	96	44
5	Early predynastic	136	143	100	54
6	Early predynastic	138	137	89	56
7	Early predynastic	139	130	108	48
8	Early predynastic	125	136	93	48
9	Early predynastic	131	134	102	51
10	Early predynastic	134	134	99	51
11	Early predynastic	129	138	95	50
12	Early predynastic	134	121	95	53
13	Early predynastic	126	129	109	51
14	Early predynastic	132	136	100	50
15	Early predynastic	141	140	100	51
16	Early predynastic	131	134	97	54
17	Early predynastic	135	137	103	50
18	Early predynastic	132	133	93	53
19	Early predynastic	139	136	96	50
20	Early predynastic	132	131	101	49

Figure 8.4

9 Classification trees

A classification tree is a device for predicting (or identifying) the class to which an unidentified object belongs. The starting point is a sample of objects from the various classes. Measurement recorded on the sample may be either continuous (supplied in variates) or discrete (supplied in factors). Below we shall illustrate the methods using the iris data from Chapter 3, where the data were all continuous (see Figure 3.1).

The **Classification Tree** menu (Figure 9.1) is in the **Trees** sub-option of the **Multivariate Analysis** option of the **Stats** menu on the menu bar.

In Figure 9.1, we have specified **Species** as the name of the factor defining the groups to be predicted, and entered the names of all the measurements into the **X-variates** box. The **Save Tree in** box allows you to specify a name for the *tree* structure that Genstat will generate to represent the classification tree. If you do not do this, Genstat will use its own private name, but you will not find it easy to use the tree outside the menus. Here we have specified the name **IrisTree**.

The tree progressively splits the objects into subsets based on their values for the measurements. Construction starts at a node known as the *root*, which contains all of the objects. A factor or variate is chosen to use there that “best” splits the individuals into two subsets. For example, in the tree for the irises, the first division is done by seeing whether the petal lengths are less than or greater than 2.450 (see the output below). The tree is then extended to contain two new nodes, one for each of the subsets, and factors or variates are selected for use at each of these nodes to subdivide the subsets further. The process stops when either no factor or variate provides any additional information, or the subset contains individuals all from the same group, or the subset contains fewer individuals than a limit specified by the **Number of items to stop splitting** field of the **Classification Tree Options** menu (Figure 9.2). The nodes where the construction ends are known as *terminal nodes*.

Factors may have either ordered or unordered levels, according to whether or not the **X-Variable factor levels ordered** box is checked. For example, a factor called **Temperature** with levels 5, 10 and 20 would usually be treated as having ordered levels, whereas levels labelled '**London**', '**Moscow**', '**New York**', '**Ottawa**' and '**Paris**' of a factor

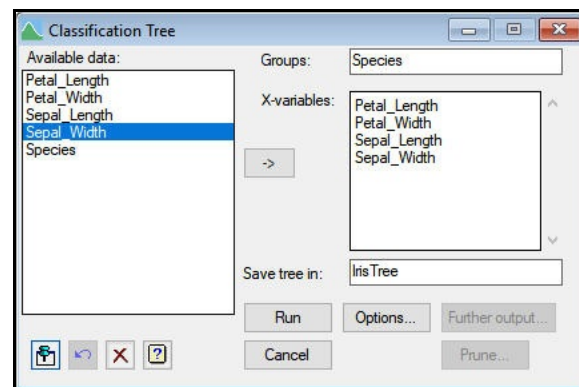


Figure 9.1

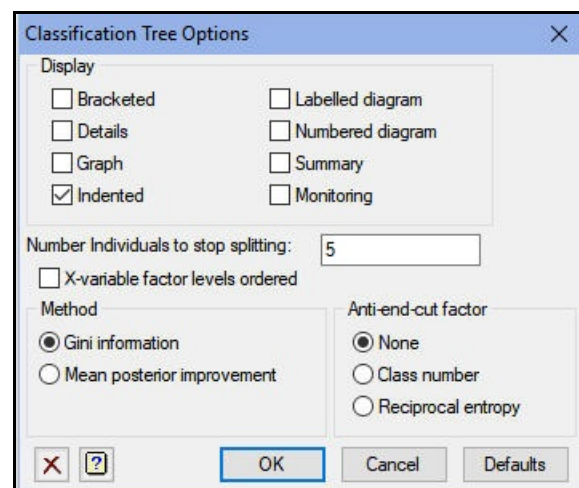


Figure 9.2

called **Town** would be regarded as unordered. For unordered factors, all possible ways of dividing the levels into two sets are tried. With variates or ordered factors with more than 2 levels, a suitable value p is found to partition the individuals into those with values less than or greater than p . The radio buttons in the **Method** and **Anti-end-cut-factor** boxes in the **Classification Tree Options** menu allow you to choose how to assess the potential splits: whether to use Gini information or mean posterior improvement, and whether to use adaptive anti-end-cut factors. Details are given in the *Guide to the Genstat Command Language*, Part 2 Section 6.21.1.

The **Display** box of the **Classification Tree Options** menu (Figure 9.2) is set to print the tree only in “indented” format. This is a representation analogous to those used to display botanical trees. In the iris output, printed below, the first variable to examine is **Petal_Length**. If this is less than 2.450, the iris specimen is identified as *Setosa*. Otherwise you progress to index 2, and examine **Petal_Width**. So, a specimen of *Versicolor* might be identified by the sequence: (1) **Petal_Length** > 2.450; (2) **Petal_Width** < 1.750; (3) **Petal_Length** > 4.950; (5) **Petal_Width** > 1.550 *Versicolor*. Notice that the same variable can be used several times as the observed characteristics are refined on the way to an identification.

```

1 Petal_Length<2.450 Setosa
1 Petal_Length>2.450 2
2 Petal_Width<1.750 3
3 Petal_Length<4.950 4
4 Petal_Width<1.650 Versicolor
4 Petal_Width>1.650 Virginica
3 Petal_Length>4.950 5
5 Petal_Width<1.550 Virginica
5 Petal_Width>1.550 Versicolor
2 Petal_Width>1.750 6
6 Petal_Length<4.850 Virginica
6 Petal_Length>4.850 Virginica

```

Generally the construction of a classification tree will result in *over-fitting*. That is, it will form a tree that keeps selecting factors or variates to subdivide the individuals beyond the point that can be justified statistically. The solution is to prune the tree to remove the uninformative sub-branches. The pruning uses *accuracy* figures, which are stored for each node of the tree. The tree also stores a *prediction* for each node, which corresponds to the group with most individuals at the node. For each node of a classification tree, the accuracy is the number of misclassified individuals at the node, divided by the total number of individuals in the data set. It thus measures the “impurity” of the subset at that node (how far it is from being homogeneous i.e. having individuals all from a single group).

You can prune the tree using the **Tree Pruning** menu (Figure 9.3), which is accessible from **Tree** subsection in the **Multivariate Analysis** section of the menu bar or by clicking on the **Prune** button on the **Classification Tree** menu. As we have loaded the menu from the **Classification Tree** menu, Genstat has filled in the name of the tree automatically.

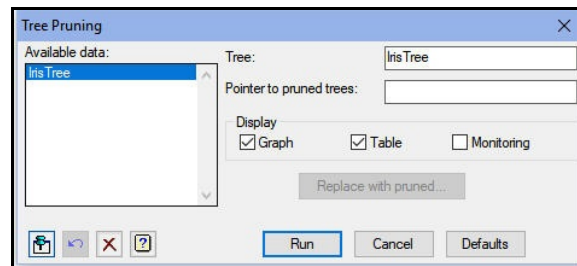


Figure 9.3

In the **Display** box, we have asked for the relationship between the impurity and the number of terminal nodes to be presented in a graph (Figure 9.4) and a table (below).

The table and graph show that the impurity of the pruned trees drops rapidly as the number of terminal nodes increases from one up to three, but then tails off more slowly. This suggests that we should prune down to three terminal nodes, but no further. This tree is the fifth in the sequence of pruned trees (count from the right of the graph, or notice the numbering in first column of the table).

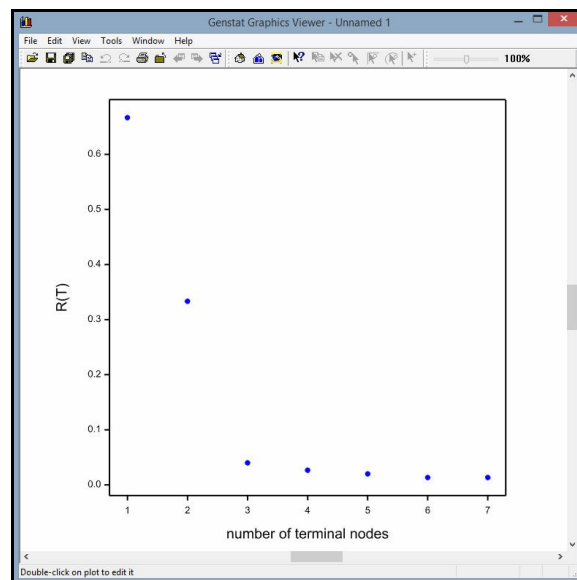


Figure 9.4

Characteristics of the pruned trees

Tree no.	RT	Number of terminal nodes
1	0.0133	7
2	0.0133	6
3	0.0200	5
4	0.0267	4
5	0.0400	3
6	0.3333	2
7	0.6667	1

By clicking the button **Replace with pruned** we can replace contents of the tree **IrisTree** with this smaller tree. We simply need to fill in the number of the tree (5) in the resulting menu (Figure 9.5), click on **OK**, and then cancel the **Tree Pruning** menu.

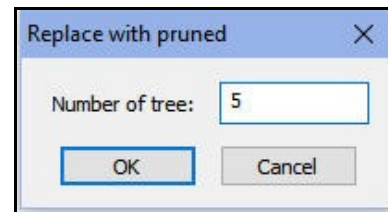


Figure 9.5

The pruned tree can be displayed using the **Classification Tree Further Output** menu (Figure 9.6), obtained by clicking on the **Further Output** button on the **Classification Tree** menu.

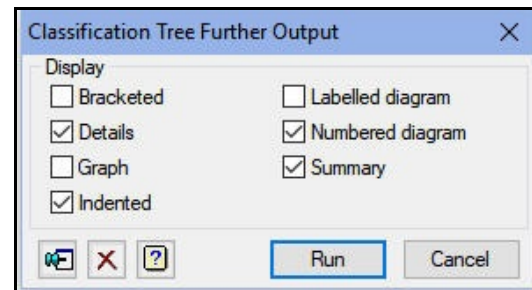


Figure 9.6

Summary of classification tree: IrisTree

Number of nodes: 5
 Number of terminal nodes: 3
 Misclassification rate: 0.040
 Variables in the tree: Petal_Length, Petal_Width.

Details of classification tree: IrisTree

- 1 Current prediction: 1.000
 Number of observations: 150
 Species Setosa Versicolor Virginica
 Proportions 0.333 0.333 0.333
 Test: Petal_Length < 2.450
 Next nodes: 23
- 2 Current prediction: 1.000
 Number of observations: 50
 Species Setosa Versicolor Virginica
 Proportions 1.000 0.000 0.000
 Conclusion: Setosa
- 3 Current prediction: 2.000
 Number of observations: 100
 Species Setosa Versicolor Virginica
 Proportions 0.000 0.500 0.500
 Test: Petal_Width < 1.750
 Next nodes: 45
- 4 Current prediction: 2.000
 Number of observations: 54
 Species Setosa Versicolor Virginica

Proportions 0.000 0.907 0.093
 Conclusion: Versicolor

5 Current prediction: 3.000
 Number of observations: 46
 Species Setosa/Versicolor/Virginica
 Proportions 0.000 0.022 0.978
 Conclusion: Virginica

1 Petal_Length<2.450 Setosa
 1 Petal_Length>2.450 2
 2 Petal_Width<1.750 Versicolor
 2 Petal_Width>1.750 Virginica

Tree diagram

```

1  2
-> 3  4
    -> 5
  
```

The initial summary, generated by the [Summary](#) check box, lists the number of nodes (5) and terminal nodes (3) in the tree, its misclassification rate and which variables it uses. The details section (from the [Details](#) check box) gives information about each node, referring to the numbering displayed in the tree diagram at the end of the output (which is generated by the [Numbered Diagram](#) check box).

Note, if possible, it is best to use “accuracy” figures that are derived from a different set or sets of data from that which was used to construct the tree. This cannot be done through the menus, but you can use the [BCVALUES](#) procedure, which is described in the *Guide to the Genstat Command Language*, Part 2 Section 6.21.3.

Another useful procedure, which also cannot be accessed currently through the menus is [BCIDENTIFY](#). This has a convenient interactive interface, that asks you to enter the information required by the tree as and when it is needed. (For details of the options and parameters that allow you to use it in batch mode, see the *Guide to the Genstat Command Language*, Part 2 Section 6.21.3). To run the procedure in this way, you merely need to set the [TREE](#) option to the name of the tree, here [IrisTree](#). If we type the command

```
BCIDENTIFY [TREE=IrisTree]
```

and execute it, for example by clicking on the [Submit Line](#) line in the [Run](#) menu on the menu bar, Genstat asks the question in Figure 9.7. (Our answer is yes.)

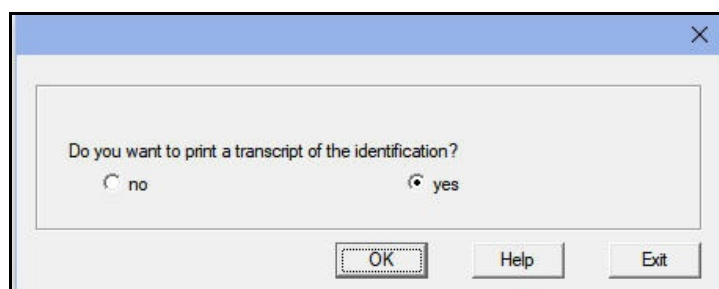


Figure 9.7

The next question is in Figure 9.8, to which we shall answer that the petal length is greater than 2.450. (Check the box and click on [OK](#).)



Figure 9.8

This generates the question in Figure 9.9, to which we shall answer that the petal width is less than 1.750.

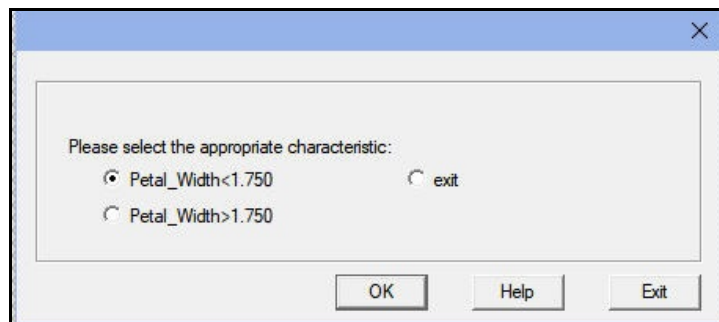


Figure 9.9

We have now reached the terminal node, and Genstat asks if we want to print the identification (Figure 9.10). It would be best to take the default suggestion, of yes, here as we have not set the option of `BCIDENTIFY` that would save the information!

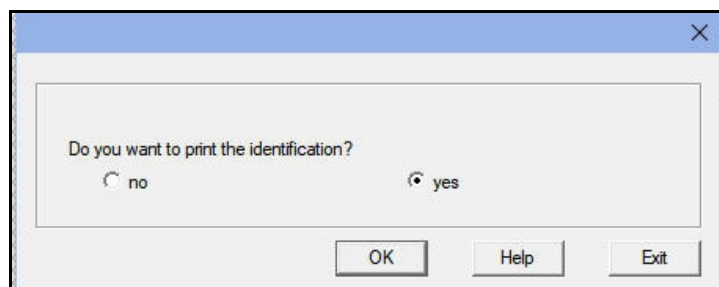


Figure 9.10

The output shows first a transcript of the questions and answers (as requested in Figure 9.7), and then the identification of *Versicolor*.

Identification using a classification tree

Observations:
Petal_Length>2.450
Petal_Width<1.750

Identification:
Versicolor

9.1 Practical

Genstat spreadsheet file `Skull.gsh` (Figure 9.11) contains data on 150 male Egyptian skulls from five different epochs (see Practical 3.1 and pages 4 and 5 of Manly, 1986, *Multivariate Statistical Methods a Primer*, Chapman & Hall, London).

Form a classification tree. Prune down to 20 terminal nodes. What is the misclassification probability?

Row	Epoch	MaximumBreadth	BasibregmaticHeight	BasioleolarLength	NasalHeight
1	Early predynastic	131	138	89	49
2	Early predynastic	125	131	92	48
3	Early predynastic	131	132	99	50
4	Early predynastic	119	132	96	44
5	Early predynastic	136	143	100	54
6	Early predynastic	138	137	89	56
7	Early predynastic	139	130	108	48
8	Early predynastic	125	136	93	48
9	Early predynastic	131	134	102	51
10	Early predynastic	134	134	99	51
11	Early predynastic	129	138	95	50
12	Early predynastic	134	121	95	53
13	Early predynastic	126	129	109	51
14	Early predynastic	132	136	100	50
15	Early predynastic	141	140	100	51
16	Early predynastic	131	134	97	54
17	Early predynastic	135	137	103	50
18	Early predynastic	132	133	93	53
19	Early predynastic	139	136	96	50
20	Early predynastic	132	131	101	49

Figure 9.11

10 Regression trees

Regression trees are very similar to classification trees, except that the attribute to predict is the value of a response variate rather than the level of a group factor. So the starting point is now a sample of observations with various values of the response. As in a classification tree, the measurements recorded on the sample may be either continuous (supplied in variates) or discrete (supplied in factors). Below we shall illustrate the methods using the pollution data from Chapters 1 and 2, where the data were all continuous (see Figure 1.1).

The **Regression Tree** menu (Figure 10.1) is a sub-option of the **Regression Analysis** option of the **Stats** menu on the menu bar. In Figure 10.1, we have specified **SO2** as the response variate, and entered the names of all the measurements into the **X-variates** box. The **Save Tree in** box allows you to specify a name for the *tree* structure that Genstat will generate to represent the classification tree. If you do not do this, Genstat will use its own private name, but you will not find it easy to use the tree outside the menus. Here we have specified the name **RegTree**.

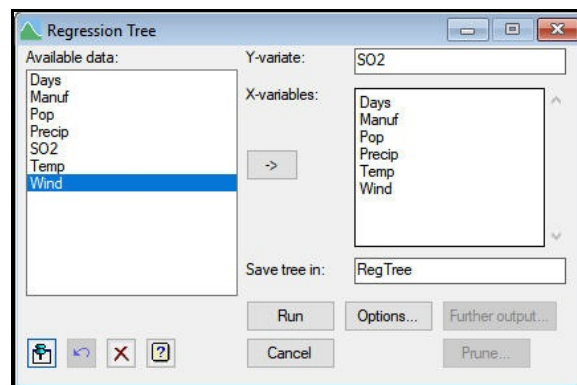


Figure 10.1

The tree progressively splits the observations into subsets based on their values for the measurements. Construction starts at a node known as the *root*, which contains all of the observations. A factor or variate is chosen to use there that “best” splits the observations into two subsets. The aim is to form subsets that have similar values for the response variate. The predicted value of the response variable at each node of the tree is the mean of its value for the subset of observations at that node. The *accuracy* of the node is the squared distance of the values of the response variate from their mean for the observations at the node, divided by the total number of observations. The potential splits at the node are assessed by their effect on the accuracy, that is the difference between the accuracy of the node and the sum of the accuracies of the two potential successor nodes. The node will become a terminal node if none of the splits provides any improvement in accuracy, or if the mean square of the observations at the node is less than a limit that can be specified in the **Regression Tree Options** menu (Figure 10.2). As in a classification tree, factors may have either ordered or unordered levels, according to whether or not the **X-Variable factor levels ordered** box is checked (see Chapter 9 for more details).

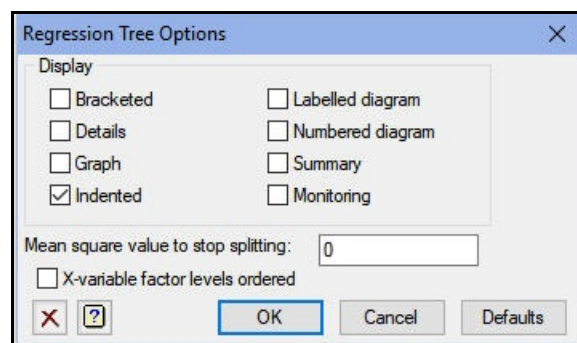


Figure 10.2

The menu also allows you to select the output to display. Here we have asked for the

tree in “indented” format (as we did earlier for the classification tree in Chapter 9). So, in the output below, the first variable to examine is *Manuf*. If this is less than 748.0, you progress to index 2, and examine *Pop*. Otherwise, you find the other line for index 1, further down the tree, which tells you to go to index 33 and form another split involving *Manuf*. The terminal nodes (at which predictions of *SO2* are made) are identified by the fact that they are followed by real numbers (with decimal points) rather than integers. So, for example, at index 5, *SO2* is predicted to be 13.

```

1 Manuf<748.0 2
2 Pop<190.0 3
3 Wind<9.800 4
4 Temp<-50.05 5
5 Temp<-58.10 13.
5 Temp>-58.10 6
6 Wind<8.850 7
7 Days<118.5 28.
7 Days>118.5 31.
6 Wind>8.850 36.
4 Temp>-50.05 8
8 Days<131.0 56.
8 Days>131.0 46.
3 Wind>9.800 94.
2 Pop>190.0 9
9 Days<108.0 10
10 Temp<-55.55 11
11 Wind<10.85 12
12 Temp<-59.20 10.
12 Temp>-59.20 13
13 Days<62.50 11.
13 Days>62.50 12.
11 Wind>10.85 14
14 Days<80.00 9.
14 Days>80.00 8.
10 Temp>-55.55 15
15 Days<101.0 16
16 Days<92.00 17.
16 Days>92.00 14.
15 Days>101.0 17.
9 Days>108.0 17
17 Temp<-59.35 18
18 Manuf<241.0 19
19 Manuf<170.0 14.
19 Manuf>170.0 20
20 Days<120.5 9.
20 Days>120.5 10.
18 Manuf>241.0 21
21 Days<117.0 24.
21 Days>117.0 18.
17 Temp>-59.35 22
22 Wind<11.20 23
23 Days<142.0 24
24 Pop<831.0 25
25 Wind<7.950 26
26 Days<123.5 26.
26 Days>123.5 23.

```

```

25 Wind>7.950 27
27 Precip<41.00 28
28 Manuf<313.5 26.
28 Manuf>313.5 29
29 Manuf<397.5 28.
29 Manuf>397.5 29.
27 Precip>41.00 30
30 Days<119.5 31.
30 Days>119.5 30.
24 Pop>831.0 47.
23 Days>142.0 31
31 Days<155.5 61.
31 Days>155.5 29.
22 Wind>11.20 32
32 Days<144.5 16.
32 Days>144.5 11.
1 Manuf>748.0 33
33 Manuf<2518 34
34 Precip<32.98 35.
34 Precip>32.98 35
35 Days<110.0 56.
35 Days>110.0 36
36 Days<135.0 69.
36 Days>135.0 65.
33 Manuf>2518 110.

```

As with classification trees (Chapter 9), the construction of a regression tree will generally result in *over-fitting*. That is, it will form a tree that keeps selecting factors or variates to subdivide the individuals beyond the point that can be justified statistically. The solution is again to prune the tree to remove the uninformative sub-branches. The pruning uses *accuracy* of the nodes of the tree, as defined above.

You can prune the tree using the **Tree Pruning** menu (Figure 10.3), which can be opened from **Tree** subsection in the **Multivariate Analysis** section of the menu bar or by clicking on the **Prune** button on the **Regression Tree** menu. As we have loaded the menu from the **Regression Tree** menu, Genstat has filled in the name of the tree automatically.

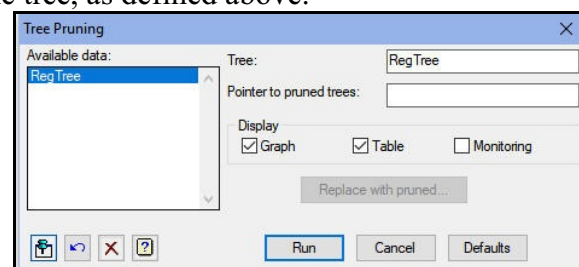


Figure 10.3

In the [Display](#) box, we have asked for the relationship between the accuracy and the number of terminal nodes to be presented in a graph (Figure 10.4) and a table (below). The table and graph show that the impurity of the pruned trees drops rapidly as the number of terminal nodes increases from one up to about ten, but then tails off more slowly. This suggests that we should prune down to ten terminal nodes, but no further. This tree is the 26th in the sequence of pruned trees.

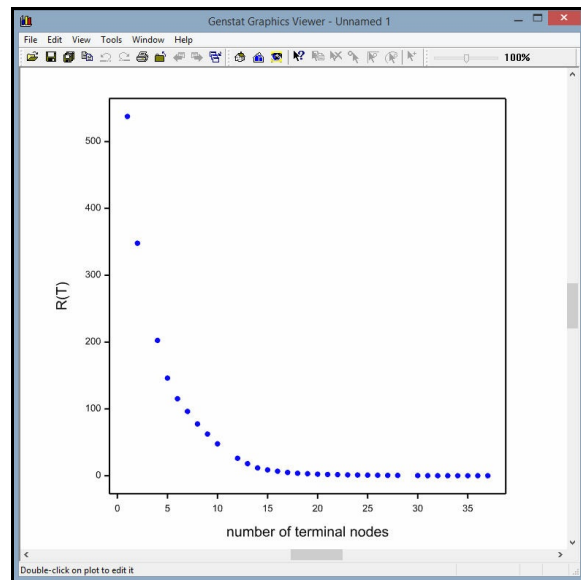


Figure 10.4

Characteristics of the pruned trees

Tree no.	RT	Number of terminal nodes
1	0.00	37
2	0.01	36
3	0.02	35
4	0.04	34
5	0.05	33
6	0.07	32
7	0.13	31
8	0.24	30
9	0.46	28
10	0.57	27
11	0.70	26
12	0.85	25
13	1.05	24
14	1.25	23
15	1.56	22
16	1.89	21
17	2.33	20
18	3.01	19
19	3.70	18
20	4.92	17
21	6.80	16
22	8.76	15
23	11.69	14
24	18.07	13
25	26.10	12
26	47.70	10
27	62.39	9
28	77.50	8

29	96.23	7
30	115.24	6
31	146.10	5
32	202.47	4
33	347.87	2
34	537.51	1

You can get the number of the tree from the index in the first column of the table, or by counting from the right of the graph, or by using the Data-info tool on the graph, as shown in Figure 10.5. To select the tool, you click on the icon with the arrow and question mark at the left-hand end of the Graphics Toolbar. The viewer will then display details of a point when you rest the pointer nearby.

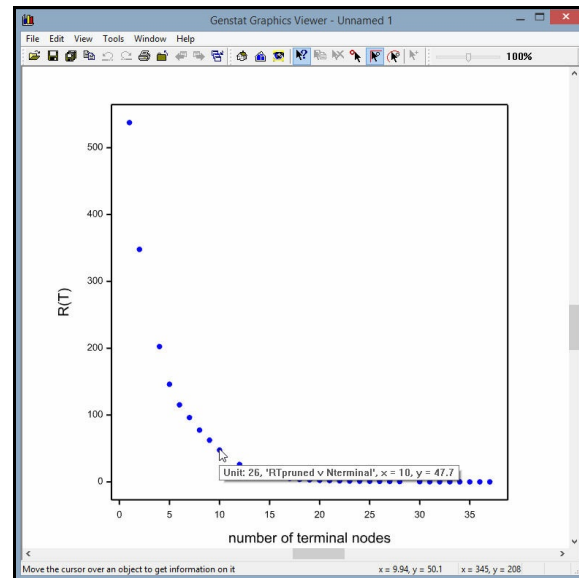


Figure 10.5

By clicking the button **Replace with pruned** we can replace contents of the tree **RegTree** with this smaller tree. We simply need to fill in the number of the tree (26) in the resulting menu (Figure 10.6), click on **OK**, and then cancel the **Tree Pruning** menu.

Figure 10.6

The pruned tree can be displayed using the **Regression Tree Further Output** menu (Figure 10.7), obtained by clicking on the **Further Output** button on the **Regression Tree** menu. Here we have asked to print the tree in indented form again, to print a summary of its properties and to display it in a graph (see Figure 10.8).

Figure 10.7

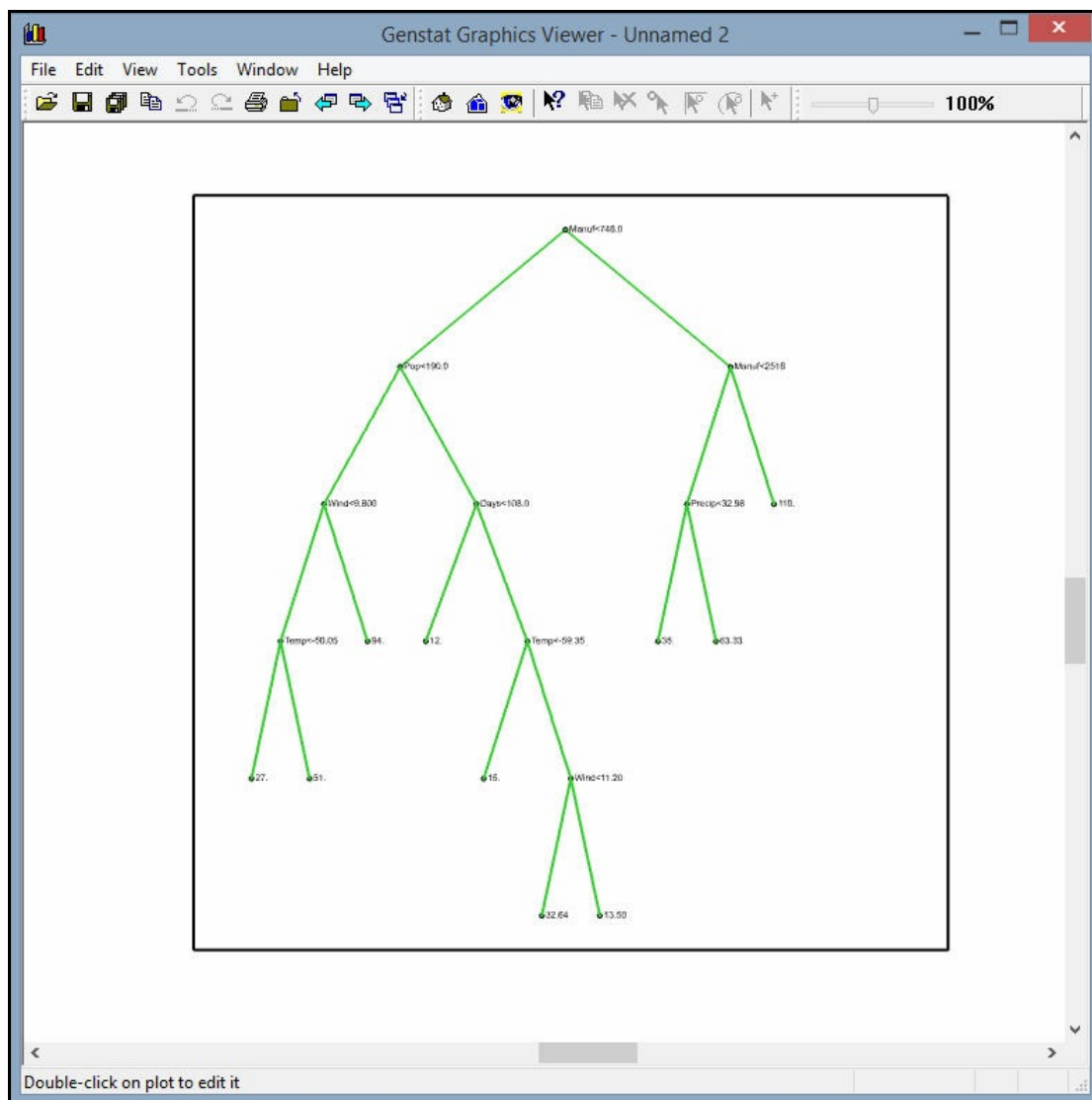
Summary of regression tree: RegTree

Number of nodes: 19
 Number of terminal nodes: 10
 Residual sum of squares: 1956
 Residual degrees of freedom: 31
 Residual mean square: 63.09
 Percentage variance accounted for: 88.55
 Variables in the tree: Manuf, Pop, Wind, Days, Precip, Temp.

```

1 Manuf<748.0 2
2 Pop<190.0 3
3 Wind<9.800 4
4 Temp<-50.05 27.
4 Temp>-50.05 51.
3 Wind>9.800 94.
2 Pop>190.0 5
5 Days<108.0 12.
5 Days>108.0 6
6 Temp<-59.35 15.
6 Temp>-59.35 7
7 Wind<11.20 32.64
7 Wind>11.20 13.50
1 Manuf>748.0 8
8 Manuf<2518 9
9 Precip<32.98 35.
9 Precip>32.98 63.33
8 Manuf>2518 110.
  
```

The initial summary, generated by the [Summary](#) check box, lists the number of nodes (19) and terminal nodes (10) in the tree, its residual sum of squares, degrees of freedom and mean square, and the variables that it uses. Note, if possible, it is best to use “accuracy” figures that are derived from a different set or sets of data from that which was used to construct the tree. This cannot be done through the menus, but you can use the [BCVALUES](#) procedure, which is described in the *Guide to the Genstat Command Language*, Part 2 Section 6.21.3.

**Figure 10.8**

10.1 Practical

Genstat spreadsheet file `Water.gsh` (Figure 10.9) contains data about the water usage of a production plant (last column of the sheet). There are also four variates that may be associated with the amount of water that has been used: the average temperature, the amount of production, the number of operating days and the number of employees. (See page 352 of *Applied Regression Analysis* by Draper & Smith, 1981, Wiley, New York.)

Form a regression tree to predict water usage from the other variates.

Row	Employ	Opdays	Product	Temp	Water
1	129	21	7.107	58.8	3.067
2	141	22	6.373	65.2	2.828
3	153	22	6.796	70.9	2.891
4	166	20	9.208	77.4	2.994
5	193	25	14.792	79.3	3.082
6	189	23	14.564	81	3.898
7	175	20	11.964	71.9	3.502
8	186	23	13.526	63.9	3.06
9	190	20	12.656	54.5	3.211
10	187	20	14.119	39.5	3.286
11	195	22	16.691	44.5	3.542
12	206	19	14.571	43.6	3.125
13	198	22	13.619	56	3.022
14	192	22	14.575	64.7	2.922
15	191	21	14.556	73	3.95
16	200	21	18.573	78.9	4.488
17	200	22	15.618	79.4	3.295

Figure 10.9

11 Generalized Procrustes analysis

Generalized Procrustes analysis allows you to produce a consensus configuration of points from several input configurations. It is often used in sensory analysis, for example of food or wine, where the input configurations will be assessments made of various attributes of the food or wine samples.

Figure 11.1 shows an example data set from an evaluation of the appearance of port-wines by Williams & Langron (1984, *Journal of*

Row	Assessor	Attribute	Sample1	Sample2	Sample3	Sample4	Sample5	Sample6	Sample7	Sample8
1	A	Ruby	7	6	8	4	4	3	2	4
2	A	Tawny	0	7	2	8	6	8	7	5
3	A	Depth	5	6	8	4	4	4	0	3
4	A	Tint	1	1	2	0	0	0	0	0
5	B	Red	7	5	7	5	5	6	5	6
6	B	Brown	0	6	2	7	7	8	4	6
7	B	Soft	5	6	5	7	6	6	10	6
8	B	Plum	8	3	5	4	4	1	3	5
9	C	Red	7	2	6	2	5	3	2	4
10	C	Blue	4	0	3	0	1	0	0	0
11	C	Brown	2	6	4	6	5	5	4	4
12	C	Intensity	6	6	7	4	6	5	3	5
13	D	Ruby	4	3	3	1	2	1	0	2
14	D	Tawny	0	6	3	6	5	5	4	6
15	D	Intensity	5	5	7	3	5	4	2	4
16	D	-	0	0	0	0	0	0	0	0
17	E	Colour	3	4	4	3	4	3	2	3
18	E	Red	8	4	6	3	4	3	2	4
19	E	Brown	0	5	3	5	4	5	4	3
20	E	-	0	0	0	0	0	0	0	0
21	F	Intensity	7	7	8	5	6	7	3	6
22	F	Red	5	1	3	1	1	0	1	1
23	F	Brown	3	8	5	6	7	7	7	6
24	F	-	0	0	0	0	0	0	0	0

Figure 11.1

the Science of Food and Agriculture, **35**, 558-568), stored in spreadsheet file `Port.gsh`. There were six assessors (labelled A-F in column 1), eight samples of port (columns `Sample1` - `Sample8`), and the attributes measured by each assessor are described in the `Attribute` column. Notice that this is an example of *free choice profiling*; the assessors were not required to observe the same attributes, but they could each define their own. The only constraint is that each assessor must be consistent in their definition of an attribute over the samples. Also, for the analysis to work, each assessor must observe the same number of attributes. However, it is valid to include a “null” attribute of zero observations for assessors that have observed too few (assessors D, E and F here).

The analysis treats the observations from each assessor as a configuration of n points (one for each sample) in p dimensions (one for each attribute), and forms a *centroid* configuration that gives a consensus view of how the assessors perceive the ports. The basic data for the analysis is a set of attribute \times sample matrices, containing the measurements made by each assessor.

These can be formed by first deleting the *Attribute* column (put the cursor into any cell in the column, then select the *Current Column* sub-option of the *Delete* option of the *Spread* menu, as shown in Figure 11.2.

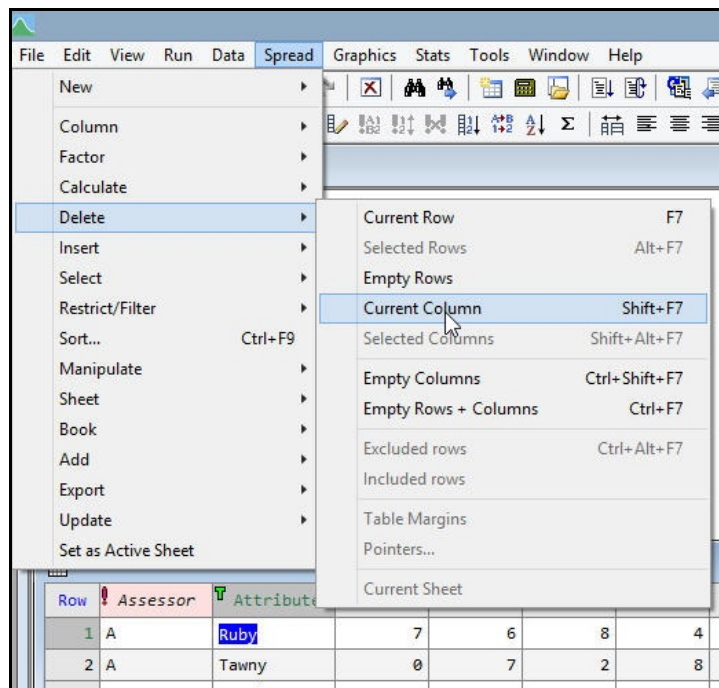


Figure 11.2

Then open the *Split/Subset Sheet* menu (Figure 11.3), by selecting the *Split/Subset* sub-option of the *Manipulate* option of the *Spread* menu. Figure 11.3 is set to split the spreadsheet into multiple sheets using all levels of the *Assessor* factor.

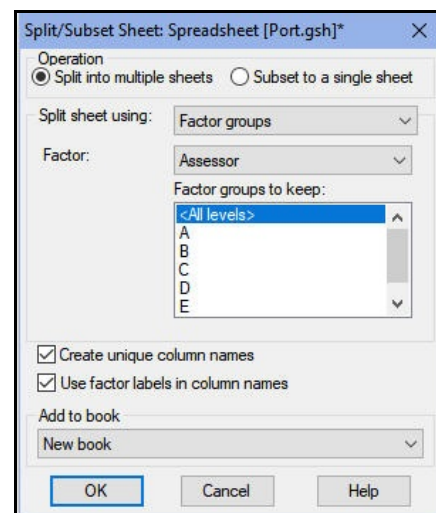


Figure 11.3

Row	Assessor A	Sample1 A	Sample2 A	Sample3 A	Sample4 A	Sample5 A	Sample6 A	Sample7 A	Sample8 A
1	A	7	6	8	4	4	3	2	4
2	A	0	7	2	8	6	8	7	5
3	A	5	6	8	4	4	4	0	3
4	A	1	1	2	0	0	0	0	0

Figure 11.4

The first of the six new spreadsheets is shown in Figure 11.4.

We need to delete the assessor column. We then convert the spreadsheet into a matrix by selecting the **Convert** sub-option of the **Sheet** option of the **Spread** menu to open the **Convert Sheet** menu. In that menu (Figure 11.5), we select Matrix as the Sheet Type, give it a name (here **M1**), and click on **OK**. We now need to transpose the spreadsheet, by selecting the **Transpose** sub-option of the **Manipulate** option of the **Spread** menu, and we can rename the transposed matrix (e.g. to **X1**) by using the Sheet Properties menu (opened by selecting the **Properties** sub-option of the **Sheet** option of the **Spread** menu). We then need to repeat the process for the other new spreadsheets, giving each transposed matrix a different name (**X2** - **X6**).

However, as spreadsheet manipulation is not the main point of this Chapter, the transposed matrices can be found in spreadsheet book *Portmatrices.gwb*, as shown in Figure 11.6. (The original data were presented in Figure 11.1 in order to display their structure more clearly.)

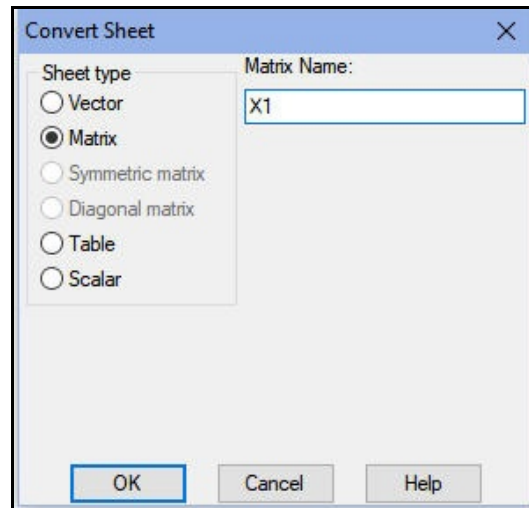


Figure 11.5

Row	1	2	3	4
1	7	0	5	1
2	6	7	6	1
3	8	2	8	2
4	4	8	4	0
5	4	6	4	0
6	3	8	4	0
7	2	7	0	0
8	4	5	3	0

Figure 11.6

The **Generalized Procrustes** menu (Figure 11.7) is opened by selecting the **Generalized Procrustes** sub-option of the **Multivariate Analysis** option of the **Stats** menu. The main task is to set the **Data to be analysed** to the matrices containing the configurations (here **X1** - **X6**).

The common centroid configuration is formed by the operations of translation to a common origin, rotation and reflection of axes, and possibly also scale changes. It is found iteratively, using either Gower's or Tenberge's method, by minimizing the sum of the

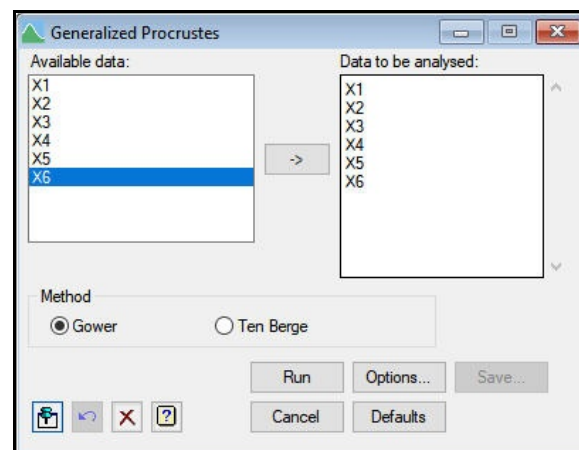


Figure 11.7

squared distances between the centroid and each individual configuration. To give a unique representation, the final centroid is defined using its principal axes.

The [Generalized Procrustes Options](#) menu (Figure 11.8) allows you to select the type of scaling to be done. *Isotropic* scaling, which scales the all the dimensions of each configuration by an equal amount, takes place during the Procrustes analysis. The alternative is to scale each configuration prior to the analysis so that the trace of each matrix is one. If this *separate* scaling is used, the subsequent residuals represent pure lack-of-fit and the scaling factors given in the results represent differences in relative size/spread of the original (centred) configurations, whereas for overall isotropic scaling the scaling factor contains components of both size and lack-of-fit.

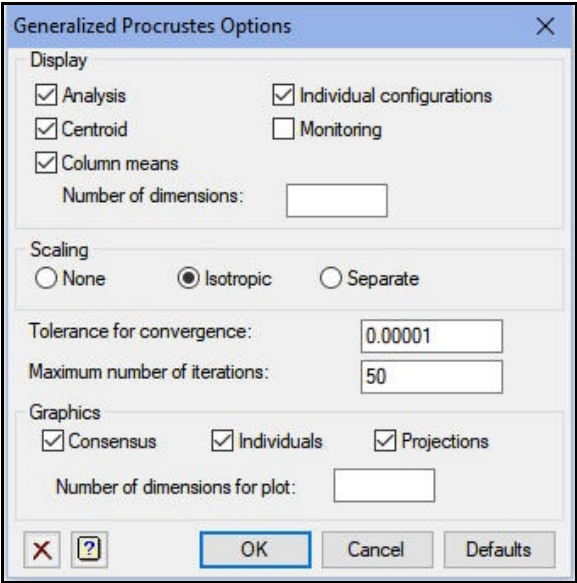


Figure 11.8

The Display boxes control the output:

- [Monitoring](#) gives monitoring information during the fitting process;
- [Column means](#) prints the column (i.e. attribute) means of the configurations;
- [Centroid](#) prints the latent roots and coordinates of the centroid configuration;
- [Individual configurations](#) prints rotations of the individual configurations to the principal axes;
- [Analysis](#) prints an analysis of variation for the configurations and entities (i.e. samples);

All of these, except monitoring, are shown in the output below.

Generalized Procrustes analysis

Isotropic scaling

Column means of the configurations

Configuration 1

1	2	3	4
4.750	5.375	4.250	0.500

Configuration 2

1	2	3	4
5.750	5.000	6.375	4.125

Configuration 3

1	2	3	4
3.875	1.000	4.500	5.250

Configuration 4

1	2	3	4
2.000	4.375	4.375	0.000

Configuration 5

1	2	3	4
3.250	4.250	3.625	0.000

Configuration 6

1	2	3	4
6.125	1.625	6.125	0.000

Rotation of centroid to principal axes

Latent roots

1	2	3	4
0.714	0.174	0.011	0.006

Percentage variance

1	2	3	4
78.88	19.25	1.22	0.65

Coordinates of the consensus configuration

	1	2	3	4
1	0.6173	-0.1389	-0.0072	0.0143
2	-0.1303	0.1879	0.0438	0.0374
3	0.3595	0.1338	0.0361	-0.0260
4	-0.2390	-0.0142	-0.0166	0.0308

5	-0.0600	0.0759	-0.0397	0.0094
6	-0.2297	0.0764	0.0040	-0.0491
7	-0.2663	-0.2994	0.0432	-0.0055
8	-0.0516	-0.0213	-0.0636	-0.0113

Final coordinates for configuration 1

Variance

1	2	3	4
0.747	0.243	0.011	0.006

Percentage variance

1	2	3	4
74.19	24.12	1.12	0.56

Coordinates

	1	2	3	4
1	0.5081	-0.0939	-0.0208	0.0072
2	-0.0224	0.2261	0.0610	0.0496
3	0.4854	0.2358	0.0555	-0.0105
4	-0.2349	0.0622	-0.0049	0.0261
5	-0.0872	-0.0149	-0.0407	-0.0158
6	-0.2734	0.0376	-0.0274	-0.0453
7	-0.3373	-0.3246	0.0151	-0.0073
8	-0.0382	-0.1282	-0.0378	-0.0041

Rotation matrix

	1	2	3	4
1	0.439	0.280	0.257	0.814
2	-0.842	0.440	0.204	0.239
3	0.283	0.852	-0.236	-0.372
4	0.137	0.044	0.915	-0.378

Final coordinates for configuration 2

Variance

1	2	3	4
0.693	0.184	0.061	0.028

Percentage variance

1	2	3	4
71.83	19.03	6.28	2.86

Coordinates

	1	2	3	4
1	0.6147	-0.1257	-0.0145	0.0315
2	-0.1278	0.0857	0.0445	0.0361
3	0.3291	0.0049	0.0878	-0.0635
4	-0.1837	0.0129	-0.0916	0.0531
5	-0.1463	0.0992	-0.0848	0.0666
6	-0.3401	0.2011	0.0508	-0.1167
7	-0.1411	-0.3280	0.1315	-0.0165
8	-0.0048	0.0498	-0.1237	0.0094

Rotation matrix

	1	2	3	4
1	0.248	0.058	-0.250	-0.934
2	-0.716	0.359	-0.599	-0.007
3	-0.393	-0.906	-0.071	-0.141
4	0.522	-0.218	-0.757	0.327

Final coordinates for configuration 3

Variance

1	2	3	4
0.817	0.144	0.025	0.021

Percentage variance

1	2	3	4
81.17	14.27	2.46	2.10

Coordinates

	1	2	3	4
1	0.6009	-0.1247	0.0045	-0.0076
2	-0.2587	0.1799	0.0926	-0.0067
3	0.3982	0.1224	0.0138	0.0217
4	-0.3332	-0.0110	0.0251	0.1044
5	0.0943	0.1167	-0.0892	0.0108
6	-0.1722	0.0182	-0.0088	-0.0231
7	-0.2808	-0.2537	0.0386	-0.0043
8	-0.0485	-0.0480	-0.0765	-0.0951

Rotation matrix

	1	2	3	4
1	0.650	0.061	-0.752	0.084
2	0.589	-0.097	0.564	0.571
3	-0.369	0.607	-0.195	0.677
4	0.307	0.787	0.278	-0.458

Final coordinates for configuration 4

Variance

1	2	3	4
0.678	0.266	0.011	0.031

Percentage variance

1	2	3	4
68.78	26.98	1.12	3.13

Coordinates

	1	2	3	4
1	0.5996	-0.1990	-0.0120	0.0479
2	-0.0664	0.2300	-0.0580	0.0902
3	0.3452	0.1843	0.0596	-0.1009
4	-0.3017	-0.0458	-0.0210	0.0291
5	-0.0285	0.1086	0.0111	-0.0246
6	-0.1461	-0.0293	0.0296	-0.0552
7	-0.2182	-0.3409	0.0304	-0.0463
8	-0.1840	0.0921	-0.0395	0.0597

Rotation matrix

	1	2	3	4
1	0.480	0.327	-0.403	0.707
2	-0.770	0.602	-0.126	0.172
3	0.421	0.728	0.261	-0.474
4	-0.016	0.020	0.868	0.496

Final coordinates for configuration 5

Variance

1	2	3	4
0.885	0.133	0.010	0.000

Percentage variance

1	2	3	4
86.10	12.91	0.98	0.02

Coordinates

	1	2	3	4
1	0.7446	-0.1389	0.0040	-0.0006
2	-0.1387	0.1825	0.0190	0.0044
3	0.2660	0.1170	0.0028	0.0054
4	-0.2672	0.0248	0.0444	-0.0030
5	-0.0515	0.0985	-0.0609	0.0062
6	-0.2672	0.0248	0.0444	-0.0030
7	-0.3085	-0.2169	-0.0101	-0.0086

8	0.0224	-0.0919	-0.0436	-0.0007
---	--------	---------	---------	---------

Rotation matrix

	1	2	3	4
1	0.092	0.734	-0.670	0.061
2	0.794	0.353	0.495	-0.009
3	-0.601	0.579	0.551	-0.013
4	-0.006	-0.034	0.052	0.998

Final coordinates for configuration 6

Variance

1	2	3	4
0.709	0.263	0.025	0.010

Percentage variance

1	2	3	4
70.41	26.14	2.46	0.99

Coordinates

	1	2	3	4
1	0.6363	-0.1511	-0.0045	0.0073
2	-0.1678	0.2228	0.1036	0.0510
3	0.3333	0.1380	-0.0030	-0.0081
4	-0.1135	-0.1284	-0.0513	-0.0249
5	-0.1407	0.0472	0.0262	0.0131
6	-0.1795	0.2060	-0.0644	-0.0509
7	-0.3116	-0.3326	0.0538	0.0497
8	-0.0565	-0.0018	-0.0605	-0.0371

Rotation matrix

	1	2	3	4
1	0.408	0.906	-0.066	-0.087
2	0.686	-0.231	0.582	0.371
3	-0.602	0.351	0.620	0.359
4	-0.003	0.045	-0.522	0.852

Analysis of variation for the configurations

	Scaling	Residual	Total
1	0.771	0.094	1.007
2	0.838	0.126	0.965
3	1.067	0.088	1.007
4	1.148	0.104	0.985
5	1.275	0.068	1.028
6	1.228	0.085	1.007

Analysis of variation for the entities

	Consensus	Residual	Total
1	2.405	0.037	2.442
2	0.334	0.072	0.406
3	0.894	0.076	0.970
4	0.351	0.077	0.428
5	0.066	0.069	0.136
6	0.366	0.097	0.463
7	0.975	0.057	1.032
8	0.044	0.080	0.123

Initial within-configuration sum of squares	463.750
Initial between-configuration sum of squares	509.875
Final residual sum of squares	0.566
Number of steps to convergence	7

The first graph (Figure 11.9) plots the positions of the eight port-wines in the consensus configuration; the default is to display the first three principal axes. This allows you to study the similarities of the port-wines, as observed overall by the assessors.

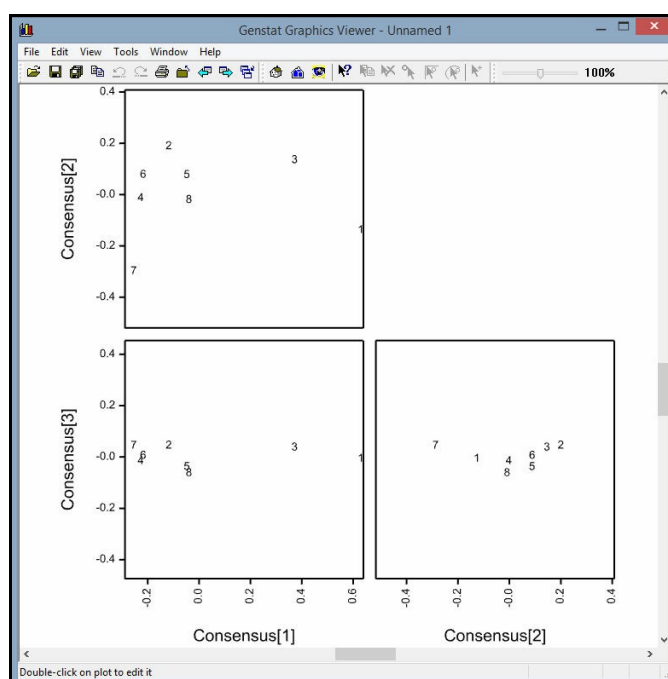


Figure 11.9

The individuals plot (Figure 11.10) is similar, but also shows how the points in each configuration are mapped to the equivalent points of the consensus. This allows you to assess the consistency of the assessors.

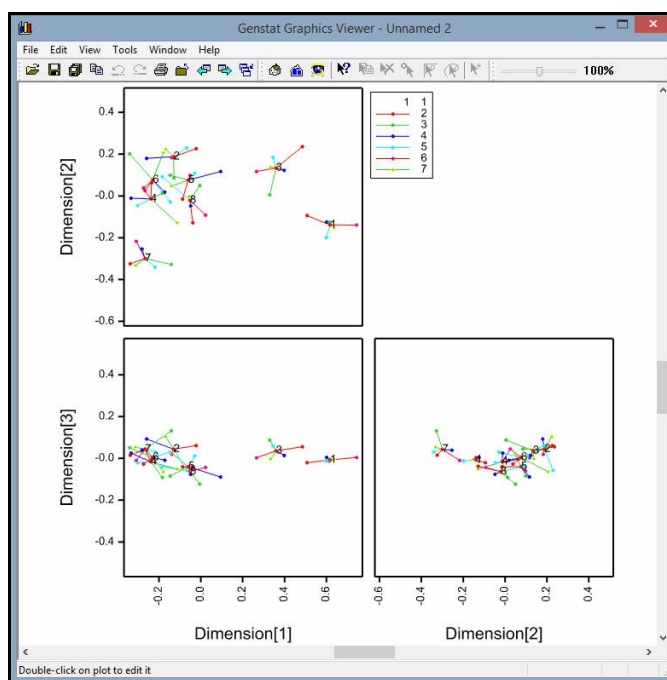


Figure 11.10

The projection plot (Figure 11.11) shows the fitted projections of the attributes, as observed by each assessor, onto the first two principal axes. A different colour is used for each attribute, taking the standard order of the Genstat pens (by default red, green, blue, cyan, mauve, yellow, brown etc.). Each line is numbered by its assessor. This shows how each of the attributes contributes to the consensus picture.

Notice that the fitted attributes (plotted in cyan) for the null attributes of assessors 4-6 are negligible. The scores fitted to these null attributes can be regarded as representing

random variation, and used as a yardstick for assessing the other scores. (However, if one of the null fitted scores were found to be noticeable, this would indicate a large Procrustes deviation between this assessor and the consensus – which might suggest that this assessor should be treated separately.)

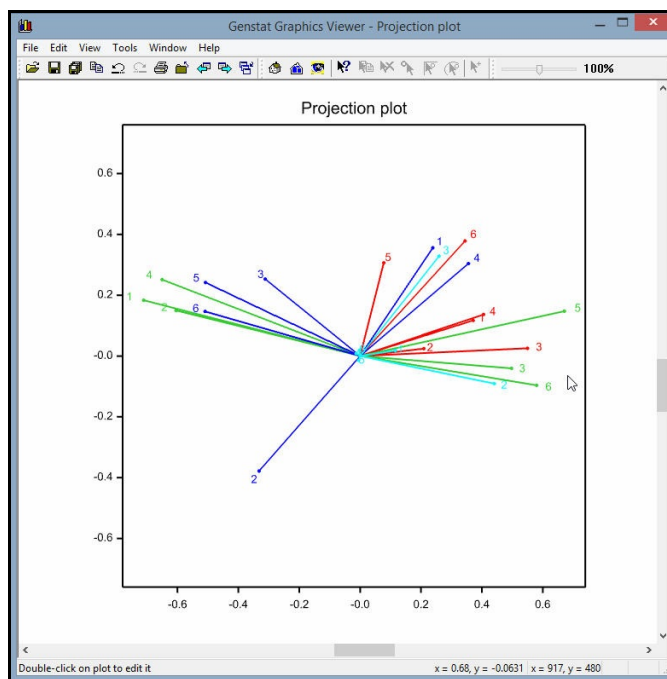


Figure 11.11

11.1 Practical

Genstat spreadsheet file `Bordeaux.gsh` contains results of a sensory assessment of aroma attributes of 24 Bordeaux wines. Do a generalized Procrustes analysis and examine a consensus plot of the first two dimensions. (Hint: use the Ten Berge method to speed convergence.) Rows 1-5 are St Estèphe wines, 6-10 are St Julien, 11-15 are Margaux, 16-20 are St Emilion, and 21-24 are regional Bordeaux wines (see the row labels of the matrices). Can you see this structure reflected in the plot?

Spreadsheet [Bordeaux.gwb] assessor 1: Matrix XB[1]

Row	Rows_	Berry	BlackCurrent	SyntheticFruit	GreenBean	BlackPepper	Soy	Spicy	Vanilla	Raisin
1	SE1	4	2	0	15	0	0	1	0	0
2	SE2	1	11	1	5	0	0	4	2	0
3	SE3	0	14	0	12	0	0	8	8	0
4	SE4	6	11	2	7	0	0	10	4	0
5	SE5	0	16	0	9	0	0	10	9	0
6	SJ1	2	11	2	5	0	0	6	5	0
7	SJ2	0	11	0	12	0	0	7	8	0
8	SJ3	0	8	0	13	0	1	2	2	0
9	SJ4	4	16	0	3	0	4	9	6	1
10	SJ5	2	12	4	4	0	0	11	9	0
11	M1	0	15	1	7	0	0	9	8	0
12	M2	5	7	2	14	0	5	4	1	0
13	M3	6	16	2	4	0	0	9	8	0
14	M4	7	9	1	4	0	0	6	6	0
15	M5	0	16	3	1	0	0	12	10	0
16	SE1	0	12	6	13	0	0	7	10	0

Figure 11.12

12 Other facilities

This chapter illustrates menus from most of the main areas of multivariate analysis provided by Genstat. Other menus are listed below with references to sections in the *Guide to the Genstat Command Language* describing the associated commands and methodology:

Discriminant analysis	Part 2 Section 6.5,
Factor analysis	Part 2 Section 6.11,
Correspondence analysis	Part 2 Section 6.13,
Canonical correlation analysis	Part 2 Section 6.9,
Redundancy analysis	Part 2 Section 6.14,
Canonical correspondence analysis	Part 2 Section 6.15,
Partial least squares regression	Part 2 Section 6.8, and
Multivariate analysis of distance	Part 2 Section 6.6.3.

Other multivariate facilities, not available through the menus, include ridge and principal-component regression (procedure `RIDGE`; Part 2 Section 6.7), analysis of skew symmetry (procedure `SKIEWSYMMETRY`; Part 2 Section 6.17), the construction of identification keys (procedure `BKEY`; Part 2 Section 6.22) and random classification forests (procedure `BCFOREST`).

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