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# BiplotGUI

Interactive Biplots in R

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# Preface

This manual documents the features of version 0.0-2 of the **BiplotGUI** package, the first release on CRAN. **BiplotGUI** makes it easy for users to construct and interact with biplots in R.

[Chapter 1](#) gives an overview of biplots and introduces the new package. The [setup](#) of the package and some [known issues](#) are also discussed. [Chapter 2](#) introduces the main features of the package through the exploration of three data sets, while all the features of the graphical user interface ([GUI](#)) are documented in full in [Chapter 3](#). An appendix summarises the [history](#) of the package.

While the statistical output provided by the **BiplotGUI** has been checked for accuracy, the [GUI](#) itself occasionally gives console warnings or even crashes. It's quick to simply restart the [GUI](#). If the behaviour is replicable, please contact me at the address below with the details. Otherwise, visit <http://biplotgui.r-forge.r-project.org/> for more information, for help, to report bugs, or to contribute to the package.

The **BiplotGUI** package was written as part of my Masters degree at Stellenbosch University in South Africa. I would like to thank my two supervisors, Prof Niël le Roux and Dr Sugnet Gardner-Lubbe, for their continued support. I would also like to thank Prof Patrick Groenen, whose suggestions inadvertently gave rise to the project.

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# List of Keyboard Shortcuts

A	Shows points determined by <a href="#">PCO</a> .
B	Shows points determined by metric <a href="#">MDS</a> (identity transformation).
C	Shows points determined by non-metric <a href="#">MDS</a> (monotone regression).
D	Shows points determined by semi-metric <a href="#">MDS</a> (monotone spline transformation).
0	No biplot axes.
1	Constructs a <a href="#">PCA</a> biplot.
2	Constructs a covariance/correlation biplot.
3	Constructs a <a href="#">CVA</a> biplot.
4	Shows regression biplot axes.
5	Shows Procrustes biplot axes.
6	Shows circular non-linear biplot axes.
Ctrl+N	Interpolates a new sample.
Ctrl+L	Clears all additional descriptors from the biplot.
F11	Shows the currently displayed biplot region in an external window.
F12	Shows the currently displayed biplot in 3D in an external window.
Ctrl++	Shows the next set of legend entries.
Ctrl+-	Shows the previous set of legend entries.
Ctrl+G	Allows many graphical parameters to be set for the different groups of points.
Ctrl+A	Allows many graphical parameters to be set for the different biplot axes.
Ctrl+R	Reverts all the graphical parameters to their default values.
Ctrl+S	Saves the currently displayed biplot region in the currently selected file format.
Ctrl+C	Copies the currently displayed biplot region to the clipboard.
Ctrl+P	Prints the currently displayed biplot region.
F1	Enables pop-up help messages for the components of the main <a href="#">GUI</a> window.



# List of Abbreviations

ANOVA	analysis of variance
AOD	analysis of distance
CA	correspondence analysis
CCA	canonical correspondence analysis
CCO	canonical correlation analysis
CLP	category level point
CV	canonical variate
CVA	canonical variate analysis
GDP	gross domestic product
GUI	graphical user interface
IM	iterative majorisation
JCA	joint correspondence analysis
MCA	multiple correspondence analysis
MDS	multidimensional scaling
MRAE	mean relative absolute error
PC	principal component
PCA	principal component analysis
PCO	principal coordinates analysis
PPP	purchasing price parity
RAE	relative absolute error
RDA	redundancy analysis
RRR	reduced rank regression

# Chapter 1

## Introduction

### 1.1 Overview

In this section we give a brief overview of biplots, existing biplot software, and the statistical programming language and environment R. In [Section 1.2](#) we set out the main aims of the BiplotGUI package, while its most important features are showcased in [Chapter 2](#) through the exploration of three data sets. The present version of the package is 0.0-2.

The style of the article is intentionally non-mathematical. However, detailed references are provided for those who wish to gain a fuller understanding of the underlying theory. This approach allows the focus to lie firmly with the package and its features.

#### 1.1.1 Biplots

The biplot was first introduced by [Gabriel](#) in [1971](#). Since then many types of biplots have been developed. In this section, some of the most prominent are highlighted and placed within context. The discussion spans five parts. In the first, the traditional approach to biplots receives attention. Parts two, three and four slot broadly into [Gower and Hand's \(1996\)](#) new approach to biplots. Part two considers biplots of samples (observations) and numerical variables, part three broadens the discussion to include well-known graphical techniques for categorical variables, while part four focuses on biplots of samples and both numerical and categorical variables. The fifth part summarises schematically, and some final remarks are made.

#### The traditional approach

[Gabriel's 1971](#) biplot is now most commonly known as the classical biplot. The classical biplot is used to represent the elements of a matrix graphically, usually in two dimensions, although it is also possible to draw a biplot in three dimensions. The representation consists of two sets of vectors. The first set is used to represent the rows of the matrix, while the second set is used to represent the columns of the matrix. The  $(ij)$ th element of the matrix is approximated by the inner product of the  $i$ th vector for rows and the  $j$ th vector for columns. The absolute value of this inner product may be visually appraised as the length of the  $i$ th vector for rows multiplied by the length of the projection of the  $j$ th vector for columns onto it. It may also be appraised as the length of the  $j$ th vector for columns multiplied by the length of the projection of the  $i$ th vector for rows onto it. If the angle between the two vectors is obtuse, the approximated value is taken to be negative, while zero matrix entries are represented by pairs of near-orthogonal vectors. For a two-dimensional biplot, the representation is exact if the matrix is of rank two

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<sup>1</sup>This chapter and the next are adapted from work submitted for publication by La Grange, Le Roux and Gardner-Lubbe.

at most, while for matrices of rank three or higher, the best rank-two matrix approximation may be found, which in turn may be represented exactly in a two-dimensional biplot. The prefix *bi* in ‘biplot’ refers to the simultaneous representation of both the rows and the columns of the matrix, rather than the dimensionality of the representation. The approximation of matrix entries by inner products characterises biplots of the traditional approach, but other quantities may also be approximated within the same biplots.

When the matrix in question is a data matrix of samples by variables, it is the samples and the variables which are represented as vectors. To easily differentiate between the two sets of objects, the samples are often represented as points rather than vectors. [Gabriel \(1971, Section 3\)](#) focuses on two special cases of the classical biplot, which is not unique. In the first, the Pythagorean distances between the points approximate the [Mahalanobis \(1936\)](#) distances between the samples, and the variable variances, covariances and correlations are also approximated. [Greenacre \(1984\)](#) calls this biplot the covariance biplot or the correlation biplot if the variables are first standardised to have unit variances. In the second special case, the points are the same as those in the scatter plot of the scores of the first two principal components (PCs), and it is the usual Pythagorean distances between the samples which are approximated. The visual appraisal of variances, covariances and correlations is no longer valid in this biplot, except in a broad sense. In this assignment, as in [Gower and Hand \(1996\)](#), the biplot of the second special case is referred to as the principal component analysis (PCA) biplot. However, in the literature, covariance/correlation biplots are often called PCA biplots.

Besides data matrices, other matrices of interest in multivariate statistics may be biplotted. [Underhill’s \(1990\)](#) coefficient of variation biplot approximates the coefficients of variation of variables. When the samples are grouped, the points in [Gabriel’s \(1972\)](#) canonical variate analysis (CVA) biplot coincide with the first two canonical variates (CVs), bringing them into relation to the original variables. In canonical correlation analysis (CCO), two groups of variables are measured on a common set of samples. Biplots for CCO ([Haber and Gabriel, 1976](#); [ter Braak, 1990](#); [Graffelman, 2005](#)) approximate either the within-group or between-group correlations, or both. Biplots for reduced rank regression (RRR) ([ter Braak, 1990](#); [ter Braak and Looman, 1994](#)), also known as redundancy analysis (RDA), are closely related to those of CCO. Although no longer data matrices which are decomposed, data matrices remain the points of departure.

Bi-additive biplots ([Bradu and Gabriel, 1978](#)) also fall within the traditional approach to biplots. These biplots are drawn of two-way tables of numerical data rather than data matrices to provide diagnostic tools for bi-additive models. Other, more complicated models have also had biplots developed for them, amongst others by [Gower \(1990\)](#).

## A new approach

While the traditional approach to biplots is based on the inner product approximation of matrix entries, the new approach—first formulated by [Gower \(1995\)](#) and strongly advocated by [Gower and Hand \(1996\)](#)—sees the biplot as the multivariate analogue of the scatter plot. Here the vectors that represent the variables are extended through the display space to become biplot axes. The biplot axes are calibrated with convenient, representative markers. Under the new approach, the  $(ij)$ th matrix entry is approximated simply by the value on the  $j$ th biplot axis onto which the point representing the  $i$ th sample orthogonally projects. Biplot axes used in this way are said to be *predictive*. Predictive biplot axes do not in general coincide with *interpolative* biplot axes which are used to graphically position new samples within an existing representation. In order to represent more variables than there are dimensions in a biplot, biplot axes are not in general orthogonal as scatter plot axes are.

Under the new approach, various mechanisms exist with which to position the points in biplots, and similarly, various mechanisms exist with which to position the biplot axes, be

they predictive or interpolative. In fact, the choice of mechanisms define the types of biplots. For certain types of biplots, the mechanism used are entirely dependent on one another.

For certain types of biplots, the exclusive pairs of point and sample mechanisms are used, in effect forming.

So far example, many existing multivariate techniques provide incidental representations of the samples of a data matrix in a few dimensions. These techniques include PCA (Pearson, 1901; Hotelling, 1933), CVA (Hotelling, 1935, 1936) and the analysis of distance (AOD) (Gower and Krzanowski, 1999), a distance-based generalisation of the analysis of variance (ANOVA). For each technique, a matching mechanism provides the appropriate biplot axes to give the PCA biplot (Gower and Hand, 1996, Chapter 2), CVA biplot (Gower and Hand, 1996, Sections 5.2–5.4, 5.6) and the AOD biplot (Krzanowski, 2004; Gardner, Le Roux, Rypstra and Swart, 2005), respectively. Similar comments apply to the covariance/correlation biplot (Gardner, 2001, Section 2.3.2).

For some biplots, the two mechanisms do not lock in as closely. Scaling techniques such as principal coordinates analysis (PCO) (Schoenberg, 1935; Gower, 1966)—also known as classical scaling—and various forms of multidimensional scaling (MDS) (eg Cox and Cox, 2001; Borg and Groenen, 2005), exist precisely as a way of representing high-dimensional samples as points in a few dimensions. For these representations of the samples, approximate biplot axes may be provided for by either the regression method (Kruskal and Wish, 1978) or the Procrustes method to give the regression and Procrustes biplots respectively (Gower and Hand, 1996, Chapter 3). At both junctures—the representation of the samples as points, and the representation of the variables as axes—the mechanisms are interchangeable.

All the biplots considered up to this point have been linear: in the traditional approach the variables were represented as vectors, in the new approach the variables are represented as linear axes. Gower and Harding (1988) generalise the linear biplot axes of the new approach to calibrated, interpolative non-linear biplot trajectories. Gower (1995) introduces the predictive circular non-linear biplot, while Gower and Ngouenet (2005) introduce the predictive orthogonal non-linear biplot. The points in these biplots are determined by PCO. When the distance metric is Pythagorean, the non-linear biplots reduce to the PCA biplot. For convenience, non-linear biplot trajectories are also often simply referred to as biplot axes. These biplot axes, however, are not drawn through the entire display space as linear biplot axes are.

This assignment and the BiplotGUI package are based on the new approach to biplots as advocated by Gower and Hand (1996). This approach may be extended beyond data matrices of samples in numerical variables to incorporate categorical variables, either exclusively or in conjunction with numerical variables. These two scenarios are considered in the next two parts of the discussion.

### More broadly

Although not technically a biplot in the traditional sense, correspondence analysis (CA) (Hirshfield, 1935; Benzécri, 1973; Greenacre, 1984), a technique which operates on two-way contingency tables, fits neatly within the new approach to biplots. Instead of the simultaneous representation of both the samples and the numerical variables of a data matrix, the levels of two categorical variables are represented simultaneously. Rather than biplot axes, category level points (CLPs) are drawn, one for each category level. Other methods for the simultaneous display of categorical variables include canonical correspondence analysis (CCA) (ter Braak, 1986, 1994), multiple correspondence analysis (MCA) (Benzécri, 1969, 1973) and joint correspondence analysis (JCA) (Greenacre, 1988, 1991). A good reference is Greenacre (2007). MCA is closely related to PCA and may be used to represent the samples and the levels of multiple categorical variables simultaneously. JCA is also used to represent multiple

categorical variables, and it reduces to [CA](#) when there are only two categorical variables.

### Mixed data

Having discussed biplots of samples in numerical variables and biplots of categorical variables, it remains to consider biplots of samples in both numerical and categorical variables. [Gower \(1992\)](#) defines such a biplot, the generalised biplot. This biplot represents the samples as points, the numerical variables as potentially non-linear biplot axes, and the levels of the categorical variables as [CLPs](#). Both prediction and interpolation are defined. When there are only numerical variables, this biplot reduces to the non-linear biplots of before, while for categorical variables only, the biplot reduces to [MCA](#).

### Taken together

To summarise, [Figure 1.1](#) shows a schematic representation of the biplots which have been discussed. Three branches extend from the centre of the figure. The first, extending towards the top, shows those biplots for which the source of data is a data matrix of samples in numerical variables. Some of these biplots have their points and axes determined jointly; for others different mechanisms are used interchangeably. Towards the bottom left of the representation, the biplots for categorical variables are shown. The sources of data for these biplots include contingency tables, matrices of samples by indicator variables, and, as is the case for bi-additive biplots, tables of numerical data. Towards the bottom right of the figure, the generalised biplot is shown. This biplot incorporates both numerical and categorical variables, and also represents the samples.

The representation in ?? is an imperfect one; it may very well have been arranged differently. However, it provides a useful map to the different biplot types. Many of the biplots shown are closely related and some of the links between them will be highlighted in ?? of the assignment.

Some final remarks:

- The new approach to biplots offers a significant advantage over the traditional approach: information on the original variables is incorporated directly onto the representation making such biplots more intuitive.
- A disadvantage of the new approach, however, is that the biplot may become cluttered ([Gabriel, 2002](#)). [Gower \(2004, p. 713\)](#) responds to such criticism as follows:

*Gabriel (2002) may have some justification in saying that this ‘proliferation of axes and scales then clutters up the display’. Nevertheless, it reflects reality, and what one needs is a convenient way of incorporating scale information, not of ignoring it. One would discourage the publication of graphs and charts that did not have appropriate scale information; the situation is no different for biplots.*

- [Graffelman and van Eeuwijk \(2005\)](#) take a different approach to the calibration of biplot axes. Their calibrations are neither necessarily predictive nor interpolative. However, their technique may be used on many traditional biplots as well as on [CA](#). [Greenacre \(1993\)](#) also calibrates [CA](#).
- Books on biplots include [Gower and Hand \(1996\)](#); [Yan and Kang \(2003\)](#), for breeders, geneticists and agronomists; and [Jongman, ter Braak and van Tongeren \(1995\)](#), for ecologists.
- Many other developments have taken place in the area of biplots; this overview touches only on some of the most prominent.

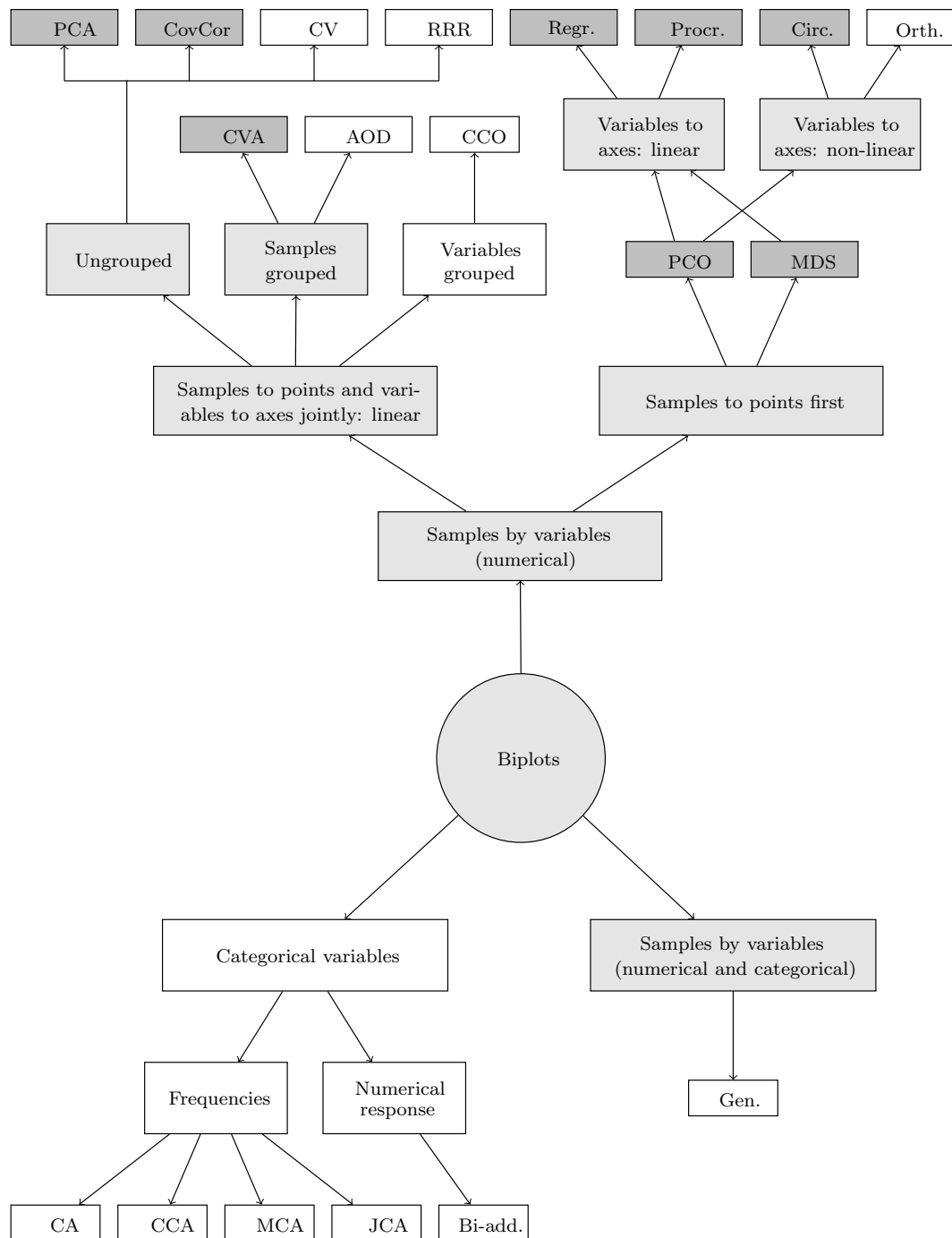


Figure 1.1. A schematic representation of the different types of biplots. The techniques which are currently supported by the **BiplotGUI** package and which are discussed in the assignment, are shown in dark grey. The outstanding techniques include the [AOD](#), orthogonal non-linear and generalised biplots.

### 1.1.2 Applications

It is especially [Yan and Kang's \(2003\)](#) adaptation, the GGE biplot, which is often been used in practice. This biplot has become a standard tool amongst crop scientists. A recent example of its use is in [Singh, Huerta-Espino, Sharma, Joshi and Trethowan \(2007\)](#). The biplots described earlier have also been applied widely. The following are some interesting examples.

**Crop science** [Vanoli, Zerbini, Grassi, Rizzolo, Forni, Cubeddu, Pifferi, Spinelli and Torricelli \(2006\)](#) use PCA biplots to study the properties of apples which have been stored for six months.

**Decision theory** [Losa, van den Honert and Joubert \(2001\)](#) use the covariance biplot as a tool for conflict resolution.

**Ecology** [Botes, McGeoch and van Rensburg \(2006\)](#) use RRR biplots to study elephant- and human-induced changes to dung beetle assemblages.

**Economics** [Lee and Choi \(2006\)](#) use JCA to relate current jobs, desirable jobs and good jobs in South Korea.

**Food science** [Adhikari, Heymann and Huff \(2003\)](#) use CVA biplots to study the textural characteristics of low-fat, full-fat and smoked cheeses.

**Forestry** [Erdman, Floren, Linsenmair, Scheu and Maraun \(2006\)](#) make use of CCA to show that forest age has little effect on oribatid mites on the bark of trees.

**Literature** [Sapiro \(2002\)](#) uses MCA to study French literature during the German Occupation (1940–1944).

**Marine biology** [Munday, Jones and Caley \(1997\)](#) use CCO biplots to study coral-dwelling gobies.

**Medical science** [Hol, Molster and Gjerdet \(2008\)](#) use a covariance biplot to help determine whether the galvanic combination of titanium and stainless steel should be avoided in surgical implants. [Gabriel and Mather \(1986\)](#) use a PCO biplot in an exploratory data analysis of the 1951–1982 summer rainfall around Nelspruit, South Africa. This period includes ten years of cloud seeding.

**Psychology** [Wright and Sladden \(2003\)](#) use CA to illustrate an own gender bias and the importance of hair in face recognition.

**Soil science** [Rooney, Kennedy, Deering, Gleeson and Clipson \(2006\)](#) use CCA to show the effect of sheep urine on bacterial communities in an acidic grassland soil.

**Sports science** [Dawkins \(1989\)](#) uses correlation biplots to compare the athletic records of different nations.

The coefficient of variation biplot has been applied less often; [Underhill \(1990\)](#) gives an example. So too the bi-additive biplot, at least in its original incarnation, although there are many derivatives.

All the examples cited thusfar have been of biplots of the traditional approach or of categorical variables. This is not surprising considering the dearth of software for biplots with calibrated axes under the new approach (see the next section). Nevertheless, a considerable number have been published. [Le Roux and Gardner \(2005\)](#), for example, showcase many examples of biplots with calibrated linear axes from fields such as archaeology, agriculture, antiques, education, financial management, mineralogy and process control. Other recently published examples include PCA/CVA biplots in chemistry ([Alves, Cunha, Amaral, Pereira and Oliveira, 2005](#)), an AOD biplot in morphology ([Gardner and Le Roux, 2006](#)), PCA biplots in mineralogy ([Jemwa and Aldrich, 2006](#)) and a CVA biplot in cephalometry ([Naidoo, Harris, Swanevelder and Lombard, 2006](#)). Applications of the other new-approach biplots have been



sparse. Gower and Hand (1996) give an example of the regression and Procrustes biplots, as well as of the non-linear and generalised biplots, of which further examples may be found in Gower and Harding (1988), Gower (1992) and Gower and Ngouenet (2005).

### 1.1.3 Other biplot software

Many statistical packages can be used to produce at least the simplest of biplots of the traditional approach. These include the major statistical packages Minitab (Minitab Inc, 2007), SPSS (SPSS Inc, 2007), STATA (StataCorp LP, 2007), STATISTICA (StatSoft Inc, 2007) and various products from SAS (2008). However, functionality is often limited, and results hard to obtain. Greater functionality is provided by the three dedicated biplot programs XLS-Biplot (Udina, 2005a,b), GGEbiplot (Yan and Kang, 2006) and BiPlot (Lipkovich and Smith, 2002a,b). XLS-Biplot is based on XLisp-Stat (Tierney, 1990) and has many useful features including a related web-server which can be used to construct biplots online. GGEbiplot is aimed mainly at agronomists, crop scientists and geneticists. It supplements the book by Yan and Kang (2003). BiPlot is an add-on for Excel, and although therefore potentially widely useful, it unfortunately has some minor but serious shortcomings (see Udina, 2005b).

The Genstat package (VSN International Ltd, 2007) can be used to calculate the coordinates of the elements of a biplot. These can then be drawn using a procedure from an add-on library. Other packages, offering some traditional biplot functionality, include Manet (Hofmann, 2000), for Macintosh only, and ViSta (Young, 2001). Some packages are aimed at ecologists—brodgar (Highland Statistics Ltd, 2007) with R, Canoco (Plant Research International, 2002) with CanoDraw (Smilauer, 2003), MVSP (Kovach Computing Services, 2008) and PC-ORD (MjM Software Design, 2007)—while the Excel add-on BrandMap (WRC Research Systems Inc, 2007) is aimed at marketers. All the software mentioned are for purchase, except XLS-Biplot, BiPlot, Manet and ViSta which are available free of charge. So too is R.

### 1.1.4 R

R (R Development Core Team, 2008) is a free statistical programming language and environment capable of producing high-quality graphics. Initiated by Ihaka and Gentleman (1996), it has become ‘the *de facto* standard for statistical computing’ (Greenacre, 2007, p. 213). It is an open-source implementation of the S programming language, available for download for all the major platforms from the R Project homepage at <http://www.r-project.org>. The R core is updated regularly with minor version revisions released roughly every six months. The current version (as of June 2008) is R 2.7.1. Updates are relatively painless. R is easily extensible: a large number of user-written packages is available for download from repositories such as CRAN and BioConductor. These repositories can be accessed via the R Project homepage. As R has increased in popularity, so too has the number of books devoted to it. Recent general-topic books on R include Braun and Murdoch (2007), Chambers (2007) and Spector (2008). The book by Murrel (2005) deals specifically with graphics in R. Many more resources are freely available from the R Project homepage.

As far as biplots are concerned, the `biplot` method in R can be used to produce two variations of Gabriel’s (1971) classical biplot. The classical biplot is most similar to the covariance/correlation biplot described earlier. Packages with support for traditional biplots include `ade4` (Dray and Dufour, 2007, 2008), `ade4TkGUI` (Thioulouse and Dray, 2007a,b) and `vegan` (Oksanen, Kindt, Legendre, O’Hara, Simpson, Stevens and Wagner, 2008). In addition, the `calibrate` package (Graffelman, 2007) can be used to calibrate both scatter plot and biplot axes as described by Graffelman and van Eeuwijk (2005). In general, however, these calibrations do not correspond to those of Gower and Hand (1996).



As opposed to the many solutions for biplots of the traditional approach listed in this section and in the previous one, software for biplots of the new approach has not been readily available. To produce biplots of the new approach, users have had to do their own programming in a suitable environment (for example, [Gardner, 2001](#)). To many potential users, such a task represents a major obstacle.

## 1.2 A new package

The primary aim with the **BiplotGUI** package is to make it easy to construct biplots of the kind advocated by [Gower and Hand \(1996\)](#) – biplots in which samples are represented as points and variables are represented as calibrated axes. The package goes beyond this, however, allowing users to interact with the data through the biplots which are produced. Naturally, the graphical output should be of a high quality and easily customisable. Its characteristics make R the ideal environment for the development of such a package.

The main features of the package can be summarised as follows:

- The package has a graphical user interface (**GUI**), making it easy to use even to the those new to R.
- Different types of biplots are supported: **PCA**, covariance/correlation, **CVA**, regression, Procrustes and circular non-linear.
- The points in regression and Procrustes biplots are determined by a separate scaling technique: **PCO** and various forms of **MDS** are available. In circular non-linear biplots, the points are fixed by **PCO**.
- Various distance metrics and data transformations are available.
- New samples can be interpolated onto existing biplots, and sample group means can be incorporated.
- Additional descriptors can be shown: convex hulls, alpha-bags, point densities and classification regions.
- Various diagnostic graphs are easily accessible: graphs of convergence; point, group and axis predictivities; and Shepard diagrams.
- The package is highly interactive with support for dynamic variable value prediction, point and axis drag and drop, zooming, and the exploration of biplots in 3D.
- Biplots can be finely tailored. Amongst the elements that can be customised are titles, labels, legends, and more than 80 well-organised graphical parameters.
- Data can be imported from R objects or Excel files. Graphs can be saved to eight file formats. An array of context-specific numerical quantities are available for export back to R for further manipulation.
- The package is free and open-source. Therefore the source code is available to all users, making it easy for others to adapt it, and to include new developments.

Many of these features are showcased in [Chapter 2](#), and all of them are documented in [Chapter 3](#)

## 1.3 Setup

R can be downloaded from CRAN via the R Project homepage at <http://www.r-project.org> for any of the three major platforms: Linux, MacOS X and Windows. **BiplotGUI** version 0.0-2 requires at least R 2.7.

At present, the package is intended to be run under Windows. To run, BiplotGUI requires a number of other packages to be installed.

The *essential* packages are

- MASS ([Venables and Ripley, 2002](#))
- tcltk ([R Development Core Team, 2008](#))
- tcltk2 ([Grosjean, 2008](#))
- tkrplot ([Tierney, 2008](#))

The first two of these should already be in place after a basic installation of R.

The *recommended* packages are

- KernSmooth ([Wand, 2008](#)), for the estimation of point densities
- rgl ([Adler and Murdoch, 2008](#)), for the creation of dynamic 3D biplots
- vcd ([Meyer, Zeileis and Hornik, 2008](#)), for the colours to be used in the representation of point densities
- xlsReadWrite ([Suter, Treetron and Switzerland, 2006](#)), for the import of data from Excel

BiplotGUI runs marginally better when the R console is set to SDI mode rather than the default MDI mode.

## 1.4 Known issues

- The graphs in [diagnostic tabs](#) occasionally do not show when the tabs are opened. Click to another tab and back.
- Interpolative circular non-linear biplots do not always initialise correctly in 3D. If this happens, first display a 3D predictive circular non-linear biplot.
- Extensive use of the [GUI](#) leads to memory leaks. If the system becomes noticeably slower, close the R console after saving, and re-open.

Avoid performing actions—besides changing the diagnostic tabs—while the progress bar shows the [GUI](#) to be busy.

# Chapter 2

## Exploring

### 2.1 Introduction

In the next three sections, the most important features of the `BiplotGUI` package are illustrated through the exploration of three data sets. Further features are highlighted in [Section 2.5](#). A systematic account of all features is given in [Chapter 3](#).

### 2.2 Countries

In this section, a country-comparative data set is used to show how the `GUI` is initialised, how its features are laid out, and how it can be used to explore multivariate data.

[Table 2.1](#) gives measurements of eight variables for the countries with the 15 largest economies (by purchasing price parity (`PPP`) gross domestic product (`GDP`)) in 2007. These data have been derived largely from the 2007 CIA World Factbook ([Agency, 2007](#)) and are for illustrative purposes only. The variables are: `PPP GDP` per capita in US dollars (`GDP`); HIV/Aids prevalence as a percentage of the population (`HIV.Aids`); life expectancy in years (`Life exp.`); military spending as a percentage of `GDP` (`Mil.`); oil consumption in barrels per annum per capita (`Oil cons.`); population in millions (`Pop.`); number of fixed line telephones per capita (`Tel.`); and percentage unemployed (`Unempl.`). The aim is to represent these data in two or three dimensions so that a single, multivariate visual impression may be obtained, with the calibrated biplot axes incorporating information on the original variables.

#### 2.2.1 Getting started

To load the `BiplotGUI` package into R, the following command is entered at the R prompt, followed as usual by the enter key:

```
library(BiplotGUI)
```

It is assumed, by this stage, that the `BiplotGUI` package has already been set up as described in [Section 1.3](#).

If the user is acquainted with R, the data to be passed to the `GUI` may be entered at the keyboard or be imported into R and saved as a matrix or a data frame. The countries data have already been included in the package as a data frame, and may be viewed from within R by typing the commands

```
data(Countries)
Countries
```

at the R prompt. To initialise the `GUI` with the countries data, the command

```
Biplots(Data = Countries)
```

Table 2.1. The countries data set. Eight variables measured on the countries with the 15 largest economies ([PPP GDP](#)) in 2007; countries listed in alphabetical order.

Country	GDP	HIV.Aids	Life exp.	Mil.	Oil cons.	Pop.	Tel.	Unempl.
Brazil	8710	0.7	72.2	2.6	4.0	190	204.2	9.6
Canada	35 370	0.3	80.3	1.1	25.1	33	622.3	6.4
China	7724	0.1	72.9	4.3	1.8	1322	278.4	4.2
France	29 852	0.4	80.6	2.6	11.3	64	543.5	8.7
Germany	31 941	0.1	79.0	1.5	11.7	82	657.8	7.1
India	3685	0.9	68.6	2.5	0.8	1130	44.0	7.8
Indonesia	4041	0.1	70.2	3.0	1.8	235	63.2	12.5
Italy	30 199	0.5	79.9	1.8	11.8	58	430.8	7.0
Japan	33 100	0.1	82.0	0.8	16.0	127	432.8	4.1
Mexico	10 570	0.3	75.6	0.5	6.6	109	182.7	3.2
Russia	12 350	1.1	65.9	2.7	6.5	141	283.6	6.6
S Korea	24 386	0.1	77.2	2.7	16.0	49	547.8	3.3
Spain	27 418	0.7	79.8	1.2	14.2	40	454.5	8.1
UK	31 723	0.2	78.7	2.4	11.0	61	552.9	2.9
USA	43 369	0.6	78.0	4.1	25.1	301	571.2	4.8

is entered. Alternatively, a data set may be saved as an Excel 1997-2003 file, with its samples as rows and its variables as columns. If the countries data were to have been saved in the working directory as an Excel file named ‘Countries.xls’, an equivalent call would have been

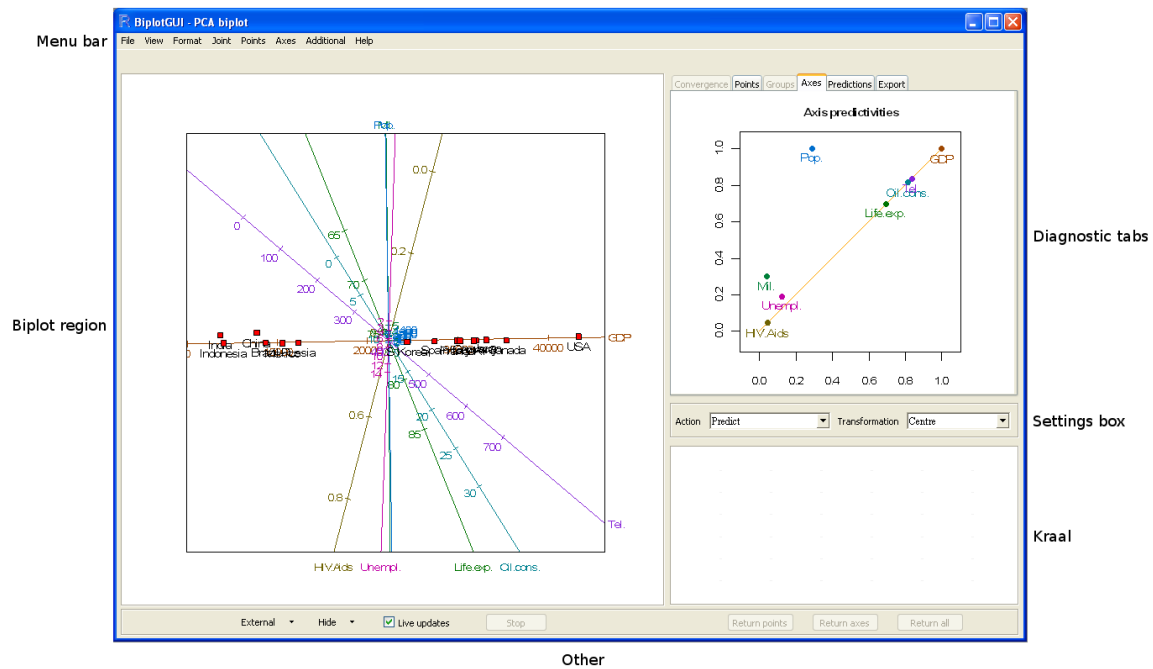
```
Biplots(excel = "Countries.xls")
```

Either of the previous two instructions launches the [GUI](#) and no further R commands are necessary for this data set.

### 2.2.2 The layout

[Screenshot 2.1](#) shows the layout of the [GUI](#) after it has launched. Six regions are indicated:

- **The menu bar**, in addition to the [settings box](#), contains the most important options. The three most important drop-down menus are [Joint](#), [Points](#) and [Axes](#). The biplots listed under Joint have both their points and axes determined according to a single, joint mechanism. The other biplots have their points determined from the Points menu and their axes determined from the Axes menu.
- **The biplot region** is where the [biplot](#) and optional [title](#) and [legend](#) are displayed. This space is responsive to mouse clicks and motion.
- **The settings box** may be used to set the [action](#) of the biplot axes, either [predictive](#), [centroid interpolative](#) or [vector sum interpolative](#). Various data [transformations](#) may be effected.
- **The diagnostics tabs** show output related to the currently displayed biplot. The [convergence tab](#) shows a graph of convergence; the [points](#), [groups](#) and [axes](#) tabs show context-specific graphs of goodness-of-fit for points, groups and axes, respectively; the [predictions tab](#) shows dynamically predicted variable values; while the [export tab](#) allows various objects to be exported to R.
- **The kraal** is where points and axes may be kept, temporarily removing them from consideration.
- **Other**. The options in this region can be used to show the currently displayed biplot in an external window (in [two](#) or [three](#) dimensions), to control the [biplot region](#) or to



Screenshot 2.1: The BiplotGUI window as it initially appears. A predictive PCA biplot of the countries data is shown towards the left; a graph of axis predictivities towards the top right.

control the kraal. While the GUI is busy, a progress bar is shown towards the left of this area.

Clicking [Help](#) → [Show pop-up help](#) activates pop-up help messages which appear as the mouse cursor is hovered over the components of the main GUI window.

### 2.2.3 Go!

A PCA biplot with predictive axes is shown by default. For the countries data, this is the biplot shown towards the left of the screenshot in [Screenshot 2.1](#). As should be the case for all biplots, a unit aspect ratio is used to ensure that distances within the biplot are properly represented. In this biplot, the points representing the countries lie ordered along a virtually straight line. In fact, the imagined line corresponds very closely to the biplot axis for GDP, and importantly, the line is almost horizontal. The reason for this becomes clear by looking at the GDP column of the countries data set. The values of GDP are orders larger than those of the other variables. Therefore, that linear combination of the variables that has the largest possible variation (the first principal component) is heavily weighted towards GDP. In effect, GDP drowns out the other variables. To avoid this, the Centre, scale transformation is chosen from the available transformations in the settings box. This transformation independently transforms each variable to have unit variance and automatically updates the biplot to the one shown in [Figure 2.1](#). Irrespective of the chosen transformation, the biplot axes are always calibrated in terms of the original variable values. The first principal component in this new figure still ranks the countries from least to most wealthy, in some more complicated sense. The developed countries of the West, together with Japan and newly-industrialised South Korea, cluster in the south-east quadrant. Brazil, Russia and Indonesia lie more towards the west, with Mexico straddling the divide. India, and especially China, lie further away.

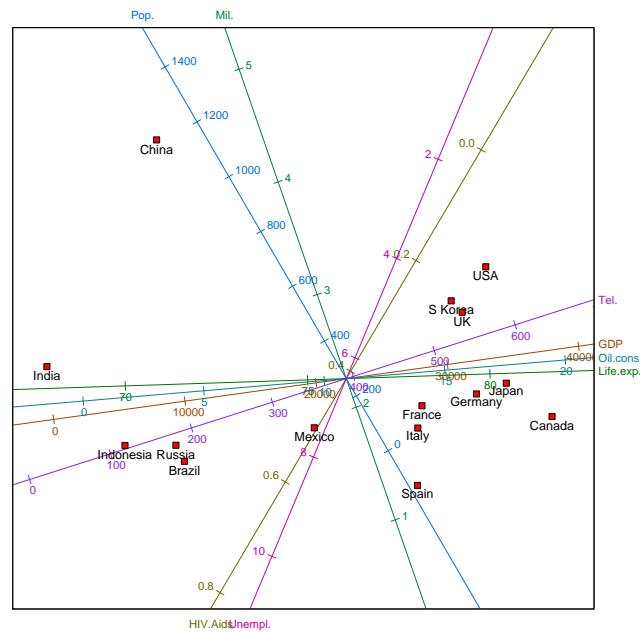


Figure 2.1. A predictive PCA biplot of the centred, scaled countries data

While the relative positions of the points are interesting, biplots come into their own when the points are related to their original variable values through the axes. By right clicking inside the predictive linear biplot and selecting [Predict cursor positions](#) from the pop-up menu, an array of orthogonally projecting lines emanates from and follows the cursor as it moves over the biplot. If [Predict points closest to cursor positions](#) is selected instead, the lines project from the point closest to the cursor as it moves, rather than from the cursor itself. So for example, [Figure 2.2](#) was created by hovering the cursor closer to the point for China than to any other point. These orthogonally projecting lines intersect the axes at the positions at which the optimal approximations to the original variables values are to be read off. It can be seen from the image that China scores relatively low on all the variables except population and military spending. As the cursor moves, these predictions are also given numerically, in real time, in the [predictions tab](#). Dynamic prediction is disabled by right clicking inside the biplot and selecting [Don't predict](#) from the pop-up menu. (Some numerical predictions follow below.)

With many variables, a biplot may become crowded. A particular axis can be highlighted by right clicking it and selecting [Highlight](#) from the pop-up menu. Doing so greys the other axes and displays the true variable values of the highlighted axis above the corresponding points by default. The displays in the [diagnostic tabs](#) are shaded accordingly and orthogonal projections are drawn to the highlighted axis only. An example is shown in [Figure 2.3](#), where [GDP](#) is highlighted and China is predicted.

The question of course, is how good the biplot approximation is. This depends on both the points and the axes. As for the points, the ‘quality’ of the PCA approximation is found by clicking to the [export tab](#). For the countries data, 69.3% of the variation in the samples is accounted for by the first two principal components. Point and axis predictivities ([Gower, Le Roux and Gardner-Lubbe, 2008](#)) may also be calculated. Diagrams of these are available in the [points](#) and [axes](#) tabs, respectively. Those for the countries data are shown in [Figure 2.4](#). They were saved by right clicking them in the GUI and making use of the [Save as](#) options in

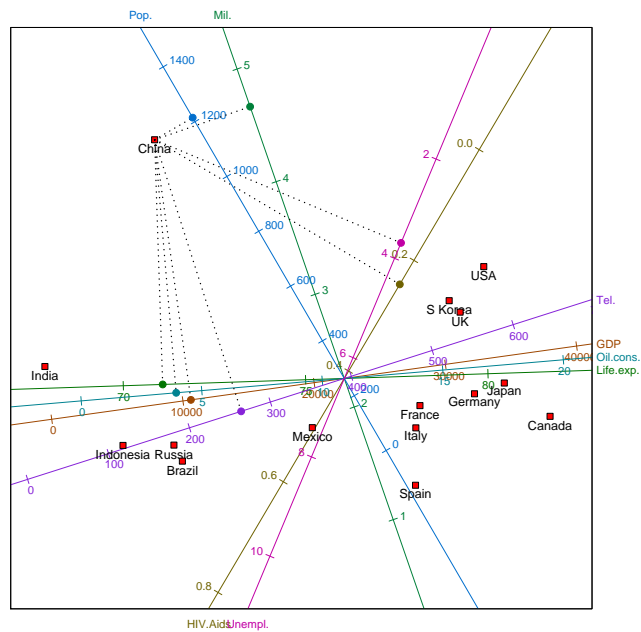


Figure 2.2. A predictive PCA biplot of the centred, scaled countries data with China projected onto all the biplot axes.

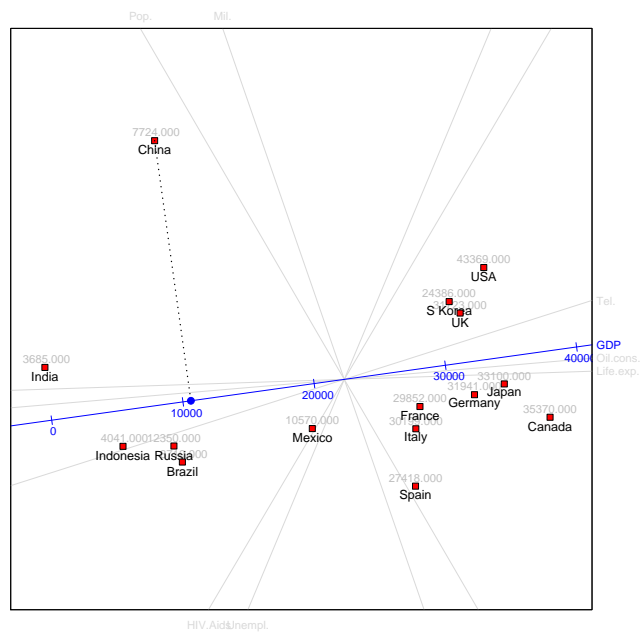


Figure 2.3. A predictive PCA biplot of the centred, scaled countries data with GDP highlighted and China projected.

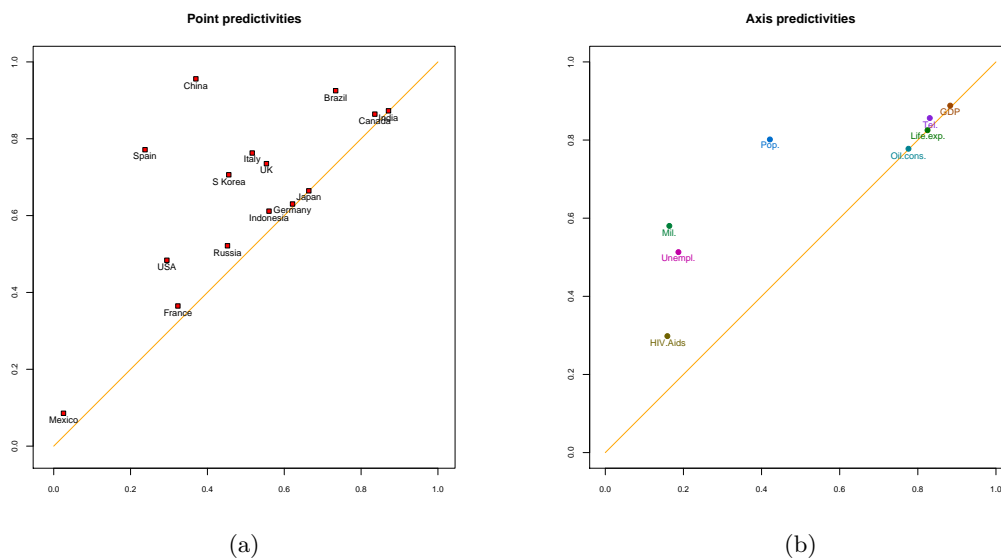


Figure 2.4. In (a), PCA point predictivities of the centred, scaled countries data. In (b), PCA axis predictivities of the centred, scaled countries data.

the pop-up menus which appear. Points or axes further to the right in these diagrams are better represented in the first (or horizontal) biplot dimension. The closer to the top of the diagram, the better the point or axis is represented overall. India, Canada and Brazil are therefore relatively well represented in the first dimension. Japan, Germany and Indonesia are represented reasonably in the first dimension, but poorly in the second. France, the United States and Russia are poorly represented overall, and Mexico extremely poorly. China is the best represented country overall. The axes may be similarly interpreted. Predictivities are also available numerically from the [export tab](#).

Another measure of the goodness of the approximation is the relative absolute error (RAE), which may be calculated for any sample on any variable. The RAE is defined to be the absolute difference between the predicted and actual values, expressed as a percentage of the range (max – min) of the particular variable. For GDP, for example, the following output is obtained for the countries data from the [export tab](#):

GDP			
	Prediction	Actual	RelAbsErr%
Brazil	9330.3	8710	1.6
Canada	37282.7	35370	4.8
China	10606.7	7724	7.3
France	27669.1	29852	5.5
Germany	31869.4	31941	0.2
India	40.2	3685	9.2
Indonesia	5054.5	4041	2.6
Italy	27130.3	30199	7.7
Japan	34209.8	33100	2.8
Mexico	19392.0	10570	22.2
Russia	8865.5	12350	8.8
S Korea	30946.1	24386	16.5
Spain	26507.7	27418	2.3
UK	31644.7	31723	0.2
USA	33889.0	43369	23.9



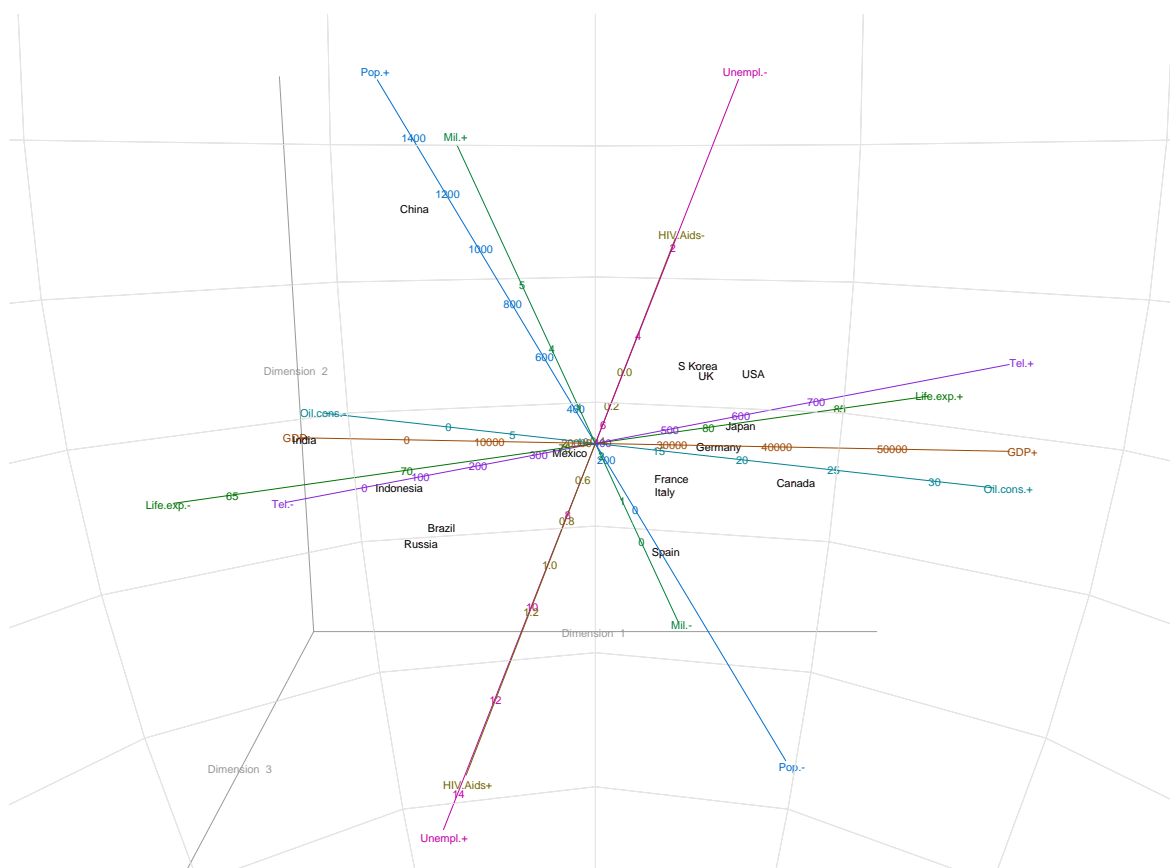


Figure 2.5. The predictive PCA biplot of the centred, scaled countries data, in three dimensions. This figure corresponds to the two-dimensional biplot in Figure 2.1.

Although the United States, Mexico and South Korea predict poorly on the GDP axis, the overall configuration is optimal. By taking means over the samples, mean relative absolute errors (MRAEs) may be obtained for the different variables. From the export tab these are:

GDP	HIV.Aids	Life.exp.	Mil.	Oil.cons.	Pop.	Tel.	Unempl.
7.7	20.1	9.8	14.4	11.2	11.3	8.8	15.1

These error rates reinforce what is conveyed by the axis predictivities: that HIV/Aids prevalence, unemployment and military spending are relatively poorly represented, the other variables better. MRAEs are useful as a measure of the loss of information in biplots since they can be calculated for any type of biplot. Predictivities are defined only when certain orthogonal decompositions exist (Gower *et al.*, 2008), as they do in the case of PCA, CVA and AOD (Krzanowski, 2004; Gardner *et al.*, 2005) biplots.

For a biplot to be usable in printed form, it must necessarily be two-dimensional. However, assisted by a computer, a user may easily interact with a biplot in three dimensions. Three-dimensional, non-MDS biplots may be obtained by clicking the External menu button at the bottom left of the GUI and then selecting the In 3D option. Alternatively, the F12 shortcut key shown alongside the option can be used. Doing so renders the three-dimensional version of the currently displayed two-dimensional biplot in an external window. This feature makes use of the rgl package (Adler and Murdoch, 2008) and allows the biplot to be rotated and enlarged dynamically. Figure 2.5 shows the three-dimensional predictive PCA biplot of the countries data that corresponds to the two-dimensional version shown in Figure 2.1. A further

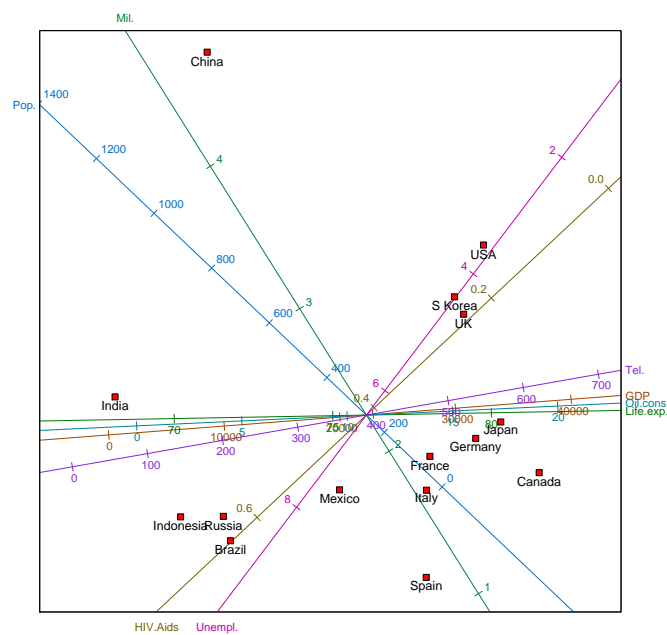


Figure 2.6. A predictive correlation biplot of the centred, scaled countries data.

12.9% of the total variation in the samples is accounted for in the additional dimension. A 360 degree ‘fly-by’ of the biplot is given by default as the window opens.

A PCA approximation results from the projection of samples onto the plane of best fit. In a covariance biplot ([Joint](#) → [Covariance/Correlation](#)), these ‘scores’ are adjusted so that the cosines of the angles between the biplot axes approximate the correlations between the corresponding variables. The correlation biplot is the same as the covariance biplot, but with the variables first transformed to have unit variances (via the [settings](#) box in the usual manner). The correlation biplot of the countries data is shown in [Figure 2.6](#). Three groups of variables are seen to be highly positively correlated (the angles between them are small):

- life expectancy, oil consumption, [GDP](#), the number of telephone lines;
- HIV/Aids prevalence, unemployment;
- population, military spending.

Notice that the labels of the axes are attached to those ends of the axes that have the higher calibrations. This is the default option for all linear biplots. Alternatively, the axis labels may be given in a [legend underneath the biplot](#), or [no axis labels](#) may be given whatsoever. These and similar options may be set via the [View](#) menu. Notice also that the option [Joint](#) → [CVA](#) is disabled, as canonical variate analysis requires the specification of group membership. This has not been provided in the case of the countries data, but will be for the antique furniture data in [Section 2.3](#).

As opposed to dimension reduction by projection, in [MDS](#) the points are chosen so that the squared differences between the inter-sample *disparities* and the inter-point *distances* are explicitly minimised. The [Points](#) → [MDS](#) menu provides various options. These include taking the inter-sample disparities to be the inter-sample *dissimilarities* themselves (the [identity transformation](#)); retaining merely the order of the inter-sample dissimilarities by optimally

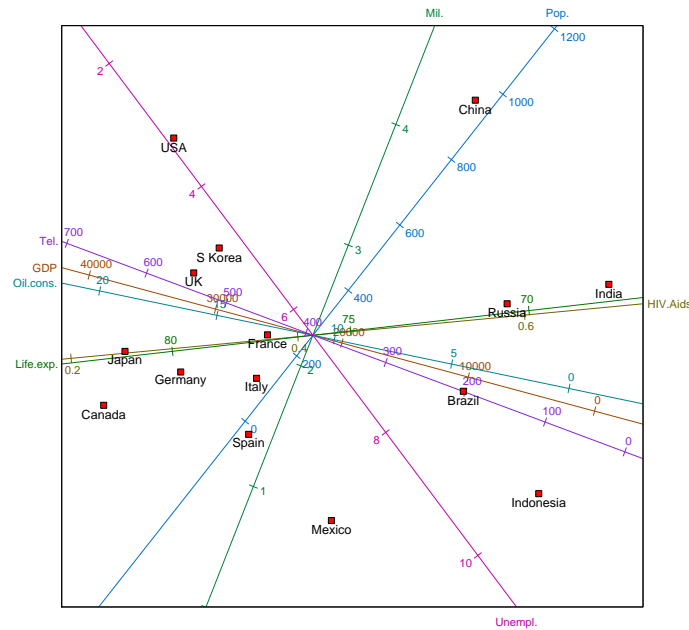


Figure 2.7. A predictive regression biplot for the metric MDS representation of the centred, scaled countries data. The MDS representation is in terms of its principal axes.

transforming them into disparities ([monotone regression](#), [Kruskal, 1964](#)); or monotonically smoothing the inter-sample dissimilarities into disparities (the [monotone spline transformation](#), [Ramsey, 1982, 1988](#)). Therefore metric, non-metric and semi-metric MDS representations are available. The inter-sample dissimilarities are calculated according to the chosen distance metric. Four such metrics are currently available from the [Points → Distance metric](#) menu: [Pythagoras](#) distance, [Square-root-of-Manhattan](#) distance, [Clark](#) distance and [Mahalanobis](#) distance. Inter-point distances are always Pythagorean. An iterative majorisation ([IM](#)) algorithm ([De Leeuw, 1977](#); [De Leeuw and Heiser, 1980](#)) is used to find the MDS solutions; for the implementations, see [Borg and Groenen \(2005, Chapters 8, 9\)](#). The [IM](#) algorithm converges uniformly, and usually leads to a local minimum, although in theory a saddle-point cannot be ruled out.

[Figure 2.7](#) shows a metric MDS of the countries data, expressed in terms of its principal axes, with approximate regression biplot axes superimposed (from [Points → MDS → In terms of principal axes](#), thereafter [Points → MDS → Identity transformation](#)). The default distance metric, Pythagoras distance, is retained. In this representation, the relative distances between the points are directly related to the corresponding dissimilarities between the countries. The United Kingdom and South Korea, therefore, are more similar to one another than they are to the other countries with respect to the eight variables. As the algorithm converges, updates of the configuration are shown in the [biplot region](#), together with updates of the graphs in the [diagnostic tabs](#). The [Live updates](#) option, however, may be disabled to increase the speed at which the algorithm runs. A graph of the stress values over iterations is given in the [convergence ta](#). In this instance, from the [export tab](#), convergence is reached after 96 iterations, with a final stress value of 45.8. A Shepard diagram ([Borg and Groenen, 2005, Section 3.3](#); [Shepard, 1962](#)) can be found in the [points tab](#) and is shown in [Figure 2.8](#). Each circle in the Shepard diagram represents a pair of samples. The horizontal axis indicates the inter-sample dissimilarity; the vertical axis indicates the corresponding inter-point distance.

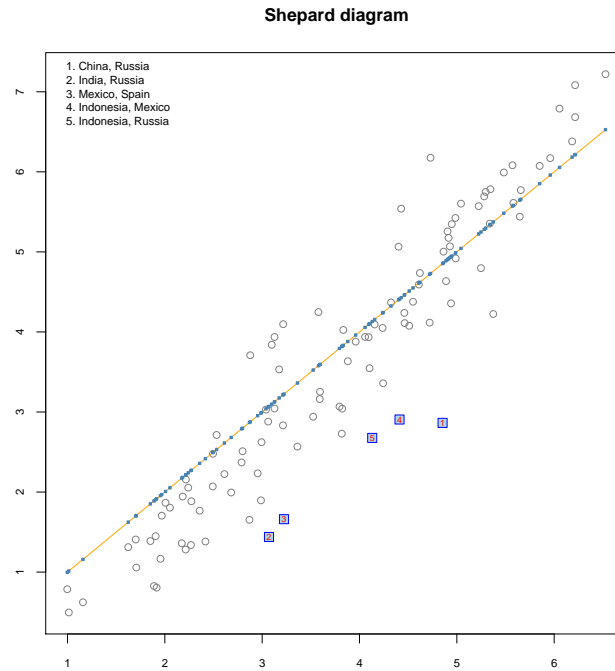


Figure 2.8. A Shepard diagram corresponding to the regression biplot of Figure 2.6.

The blue dots on the yellow line (which generalises to a step function or a curve) indicate the disparities. Thus the closer the circles are to the line (or step function or curve), the better the overall fit. The five worst-fitting point pairs are identified in the top left corner of the diagram. The dissimilarity between China and Russia, therefore, is most poorly approximated by the points. The [Points → MDS → Random initial configuration](#) option forces the algorithm to start from a random configuration at each run. Otherwise, the last [PCO](#) or [MDS](#) solution is taken to be the new initial configuration, as is the case for Figure 2.9.

To conclude with the countries data, suppose that we feel that China is in many ways atypical and that we would like to see what the effect would be of removing it from consideration. To do so we need simply ‘drag’ the point representing China from the biplot into the [kraal](#). We may also right click the point representing China and select [Send to kraal](#) from the pop-up menu. The [biplot region](#) is then automatically updated as if China were never part of the data set. The updated biplot is given in Figure 2.9. Russia’s position relative to the other countries seems to have been most greatly affected. There has also been a re-alignment amongst the axes, most notably the axes for HIV/Aids, population and unemployment. Axes may also be removed to the [kraal](#). Points and axes which have been removed to the kraal may be dragged back onto the biplot, or the kraal may be emptied of its [points only](#), its [axes only](#), or of both its [points and axes](#) simultaneously by making use of the buttons below it, or by right clicking inside it and selecting the desired option from the [pop-up menu](#). At any stage, the points and/or axes of any representation may be hidden by clicking on the options in the [hide](#) menu button at the bottom of the window. Figure 2.10 is the same as Figure 2.9 but with the biplot axes hidden as described.

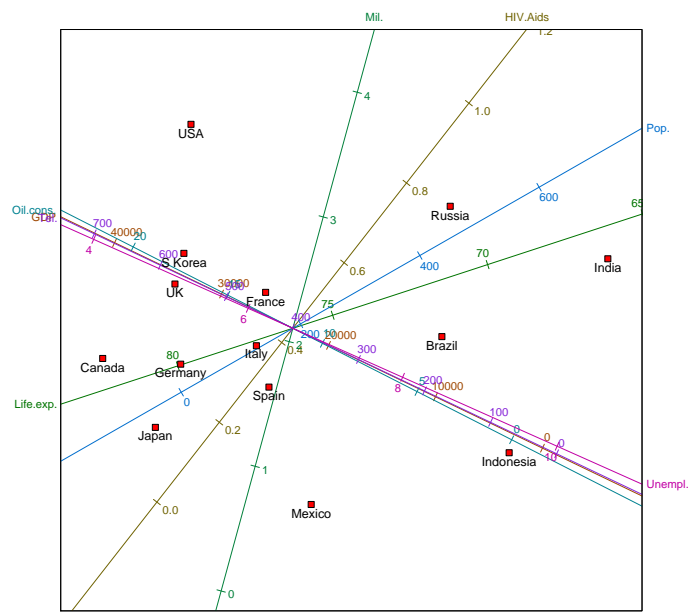


Figure 2.9. A predictive regression biplot for the metric MDS representation of the centred, scaled country data, but with China removed.

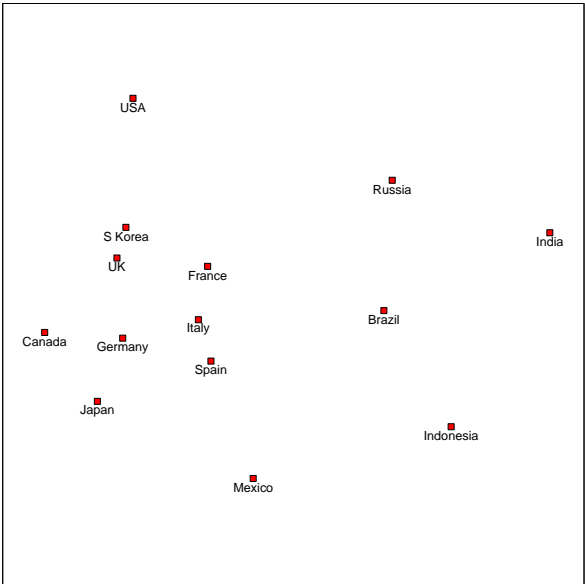


Figure 2.10. The metric MDS of the centred, scaled data with China removed.

## 2.3 Antique furniture

It is often of great interest to collectors, auctioneers and cultural historians to be able to correctly identify the type of wood used to make antique furniture. In the period between 1652 and 1900, wood from both the indigenous *Ocotea bullata* ('Stinkwood'), and the imported *Ocotea porosa* ('Imbuia'), were used to make Old-Cape furniture in South Africa. Being from the same genus and family (*Lauraceae*), it is often difficult to distinguish between the two types of wood based solely on a traditional analysis of colour, smell, and other observable characteristics. [Burden, Gardner, Le Roux and Swart \(2001\)](#) and [Le Roux and Gardner \(2005\)](#) make use of **CVA** biplots of anatomical measurements to distinguish between the species. A third species, *Ocotea kenyensis*, is also included in the analyses. The microscopically measured variables are: tangential vessel diameter in  $\mu\text{m}$  (VesD); vessel element length in  $\mu\text{m}$  (VesL); fibre length in  $\mu\text{m}$  (FibL); ray height in  $\mu\text{m}$  (RayH); ray width in  $\mu\text{m}$  (RayW); and the number of vessels per  $\text{mm}^2$  (NumVes). The 37 observations are the mean values over fifty repeat-measurements made on 20 samples of *Ocotea bullata*, 10 of *Ocotea porosa*, and 7 of *Ocotea kenyensis*. The data are included in the **BiplotGUI** package as the data frame **AntiqueFurniture**, of which the first column contains the group specifications. The data may be viewed from within R by entering the following instructions at the R prompt of the R console:

```
data(AntiqueFurniture)
AntiqueFurniture
```

To initialise the **GUI** with the antique furniture data, the following command may be entered at the R prompt:

```
Biplots(Data = AntiqueFurniture[, -1], groups = AntiqueFurniture[, 1])
```

In other words, the data consist of all the columns of **AntiqueFurniture** except the first, while the group specifications are precisely the contents of the first column. Alternatively, if the data were saved as an Excel 1997–2003 file 'AntiqueFurniture.xls', with the group specifications given in, say, the first column, the call

```
Biplots(excel = "AntiqueFurniture.xls", ExcelGroupsCol = 1)
```

could have been made instead.

As was mentioned earlier, upon initialisation of the **GUI**, a predictive **PCA** biplot is shown by default. To show a **CVA** biplot instead, the user simply needs to click **Joint → CVA**. This option is now available since, in the call to the **Biplots** function, groups were defined. The predictive **CVA** biplot of the antique furniture data is shown in [Figure 2.11](#). The positions of the points are determined by the first two **CVs** – those linear combinations of the original variables that maximally separate the group means, subject to certain restrictions ([Krzanowski, 2000](#), Section 11.1). The group means themselves are shown as larger but corresponding symbols (activated by clicking **Additional → Interpolate → Sample group means**, retaining the default options). Since there is more than one group, an optional **legend** is included below the **biplot** by default. The mechanism for prediction is the same as before and is illustrated in the case of sample 29.

[Figure 2.12](#) shows the same biplot, now overlain onto a two-dimensional density estimate of the points. The density estimate is obtained by clicking **Additional → Point densities** and accepting the default options (amongst other things, for the point densities to be estimated for all points, as opposed to certain groups of points only). The point densities are calculated using the default arguments to the **bkde2D** function of the **KernSmooth** package ([Wand, 2008](#)). Similar biplots can be found in [Blasius, Eilers and Gower \(2008\)](#).

Sometimes it is helpful to zoom into or out of portions of a biplot. This is done by right clicking on a focal point inside the biplot, and selecting the **Zoom in** or **Zoom out** option from the pop-up menu which then appears. [Figure 2.13](#) shows the **CVA** biplot of antique furniture,

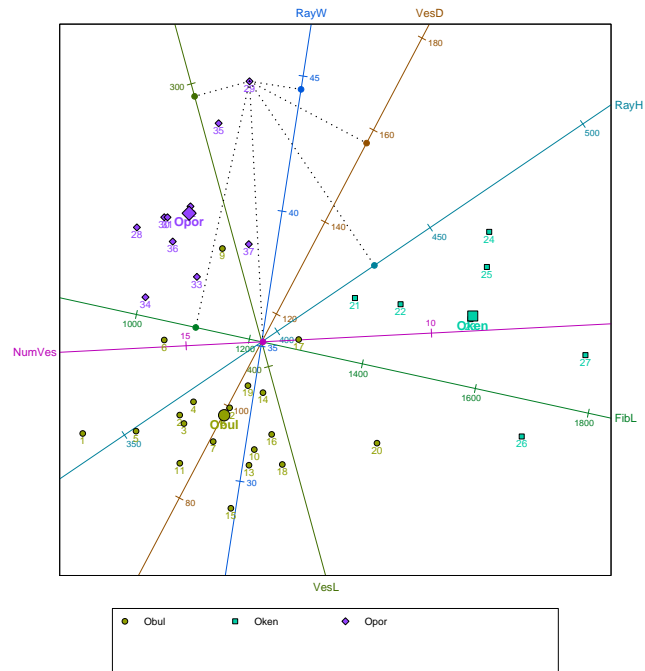


Figure 2.11. A predictive CVA biplot of the antique furniture data with sample 29 projected onto all the biplot axes. The group means are also shown.

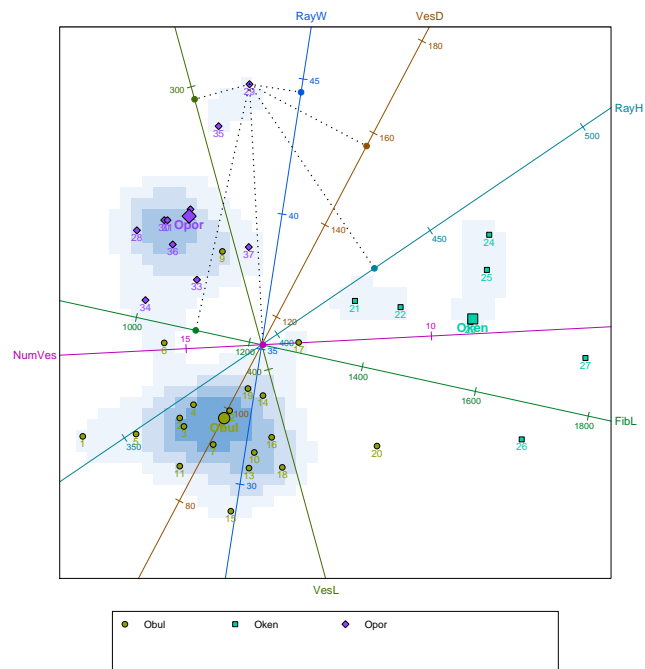


Figure 2.12. As in Figure 2.11, but with the biplot overlay onto the two-dimensional density estimate of the points.

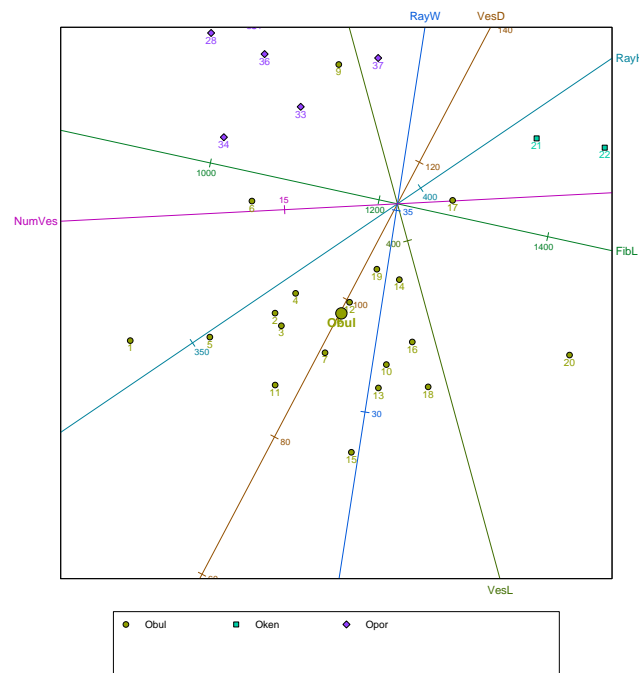


Figure 2.13. The same biplot as in Figures 2.12 and 2.13, but zoomed in around the mean of the species *Ocotea bulluta*.

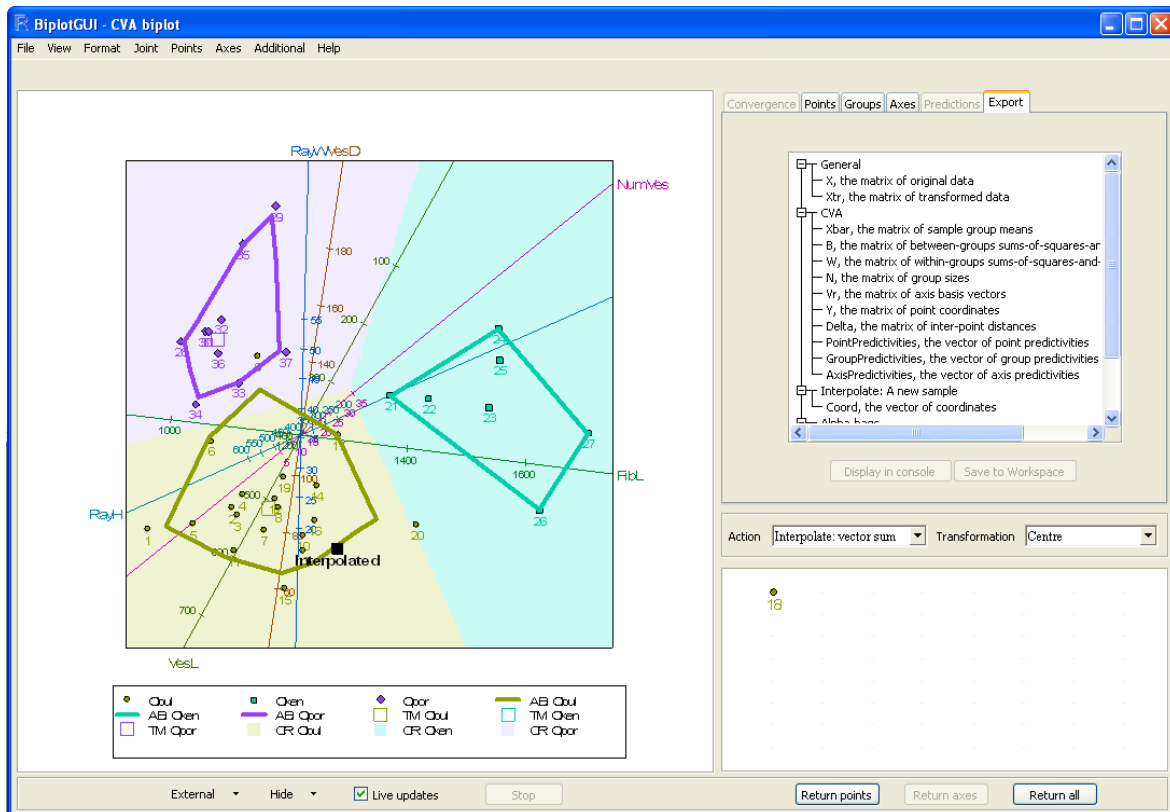
enlarged around the mean of the species *Ocotea bulluta*. The original view can be restored by clicking [Zoom in](#) in the same pop-up menu.

To the left of [Screenshot 2.2](#), a [CVA](#) biplot of the antique furniture data appears. From the [settings box](#), it can be seen that the axes are not [predictive](#); in fact they are [vector sum interpolative](#). Also, the data have not been [transformed](#), except for the obligatory centring of the columns to have zero means. In any case, [CVA](#) biplots are unaffected by the scaling of the variables to have unit variance.

Sample 18 has been dragged from the [biplot](#) into the [kraal](#). It has therefore not been taken into account in the construction of the biplot. However, using its variable values, it has subsequently been interpolated onto the biplot towards the bottom of the image ([Additional → Interpolate → A New Sample](#)). This is the most appropriate position for the sample in the existing biplot. It is reassuring that the positions assigned to sample 18 in [Figure 2.11](#) and [Screenshot 2.2](#) correspond so closely. This need not have been the case. Also notice that, notwithstanding the removal of sample 18, the calibrations and *directions* of the predictive and interpolative biplot axes differ. This is in general the case for [CVA](#) biplots.

The biplot in [Screenshot 2.2](#) also sports colour-coded classification regions. These are the regions in the display space plane closest to the respective group means in a specified number of canonical dimensions, here the maximum number possible for the particular data set, six. The classification regions are included by selecting [Classification regions](#) from the [Additional](#) menu. They may be used for the classification of interpolated samples. For more on the links between biplots and discrimination, see [Gardner and Le Roux \(2005\)](#). Furthermore, by clicking [Additional → Alpha-bags](#), alpha-bags ([Gardner, 2001](#); [Aldrich, Gardner and Le Roux, 2004](#)) and Tukey medians have been superimposed for the species *Ocotea bullata* and *Ocotea porosa* (there are too few samples for an alpha-bag for *Ocotea kenyensis* to be constructed; with an appropriate warning, a convex-hull is displayed instead). Alpha-bags are closely related to the bagplots of [Rousseeuw, Ruts and Tukey \(1999\)](#) and enclose regions that contain





Screenshot 2.2: A vector sum interpolative CVA biplot of the antique furniture data is shown towards the left, with sample 18 removed to the kraal. Sample 18 has then been interpolated to give its implied position. Classification regions are shown, as well as 90% alpha-bags for the species *Ocotea bullata* and *Ocotea porosa*. A convex hull surrounds the points of the species *Ocotea kenyensis*. The export tab is shown top right.

approximately the inner 100% of samples, here 90% of the samples for the two species separately. The alpha-bags and convex hull do not overlap. This emphasises the high degree of separation between the species. For CVA biplots, group predictivities (Gower *et al.*, 2008) may also be calculated, in addition to the point and axis predictivities discussed earlier. A diagram of these is available in the groups tab. Finally, Screenshot 2.2 also shows the export tab. As has been explained, various objects are available for export from this tab, and these objects may be either displayed in the R console or be saved to the current R workspace. The list of available objects depends on what is shown in the biplot.

## 2.4 Fighter aircraft

Measurements of four variables on 22 types of fighter aircraft were extracted by Cook and Weisberg (1982) from a report by Stanley and Miller (1979). Following Gower and Hand (1996), only the first 21 of these aircraft are included in the data and biplots below. The four variables are: specific power, proportional to power per unit weight (SPR); flight range factor (RGF); payload as a fraction of gross weight (PLF); and sustained load factor (SLF). These data can be found in the `FighterAircraft` data frame included in the BiplotGUI package. The GUI is initialised in the same way it was for the countries data in Section 2.2.1.

Figure 2.14 shows a regression biplot of the fighter aircraft data with the points determined by PCO and the inter-sample dissimilarities calculated according to the Square-root-of-

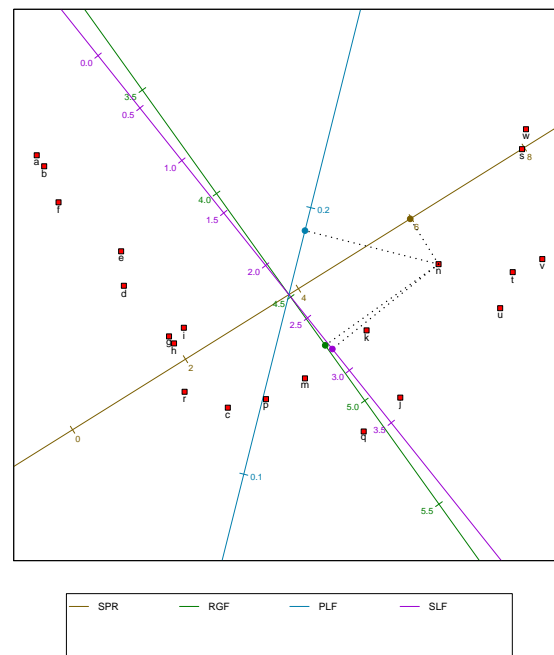


Figure 2.14. A predictive regression biplot of the fighter aircraft data, with points determined by [PCO](#) based on the Square-root-of-Manhattan distance metric. The orthogonal prediction of the variables values of aircraft ‘n’ is shown.

Manhattan distance metric. The figure is obtained by clicking [Points](#) → [Distance metric](#) → [Square-root-of-Manhattan](#) and then [Axes](#) → [Regression](#). Making use of orthogonal projection, the variable values for aircraft ‘n’ are predicted to be 7.342, 4.95, 0.202 and 3.25, respectively. These can be compared to the actual values, 5.855, 4.53, 0.172 and 2.50. [Figure 2.15](#) shows the corresponding circular non-linear biplot (obtained by clicking [Axes](#) → [Circular non-linear](#)). Here prediction is performed by completing the circle which has, as diagonal, the line stretching from the origin of the biplot to the point to be predicted. The predicted values are read off at the points at which the circle intersects the axes ([Gower and Hand, 1996](#), Section 6.3.2). If a particular axis is intersected at more than one position, the position closest to the point being predicted is used. If an axis isn’t intersected at all, no prediction for the corresponding variable can be made. For aircraft ‘n’, the valid points of intersection are shown in the figure as small, filled circles on the circumference of the larger circle. From the [predictions](#) or [export](#) tabs, the circular non-linear predictions for aircraft ‘n’ are 6.090, 4.54, 0.174 and 2.90, respectively (these values depend on how finely the non-linear axes are constructed; by default 20 positions are taken into account from each calibrated marker to the next). Except for the fourth variable, the non-linear predictions are very close to the actual values. The non-linear biplot axes represent an appreciable improvement over the approximate linear axes in this case. This need not have been so.

## 2.5 Further features

There are two main ways in which graphs can be customised. Basic customisation can be performed using the options of the [View](#) menu, while the [Format](#) menu options can be used to alter a large number of graphical parameters.

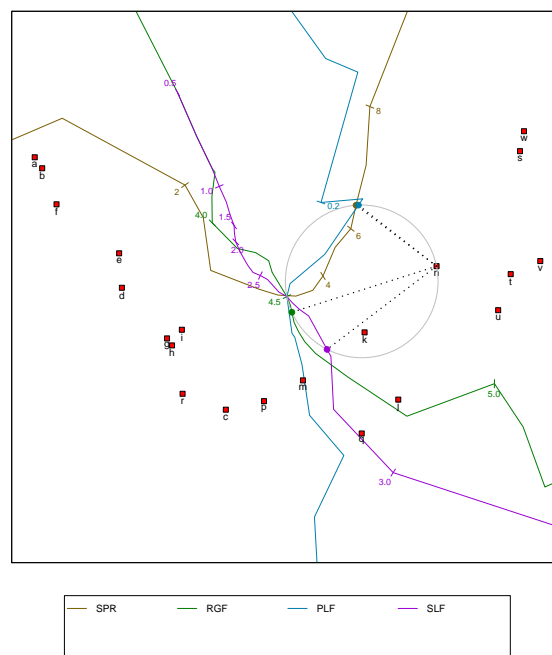


Figure 2.15. A predictive circular non-linear biplot of the fighter aircraft data, with points determined by [PCO](#) based on the Square-root-of-Manhattan distance metric. The circular prediction of the variable values of aircraft ‘n’ is shown.

[Figure 2.16](#) shows the same predictive [PCA](#) biplot of the countries data as was shown in [Figure 2.1](#). However, the biplot in [Figure 2.16](#) has been modified by changing the defaults of the [View](#) menu. The [Show title](#) option places a [title](#) above the biplot; by default the title reflects the type of biplot, but it may be changed with the [Format](#) → [Title](#) option. Furthermore, the point labels have been disabled by deselecting [Show point labels](#). Instead of showing the axis labels around the edges of the biplot as in [Figure 2.1](#), the labels in [Figure 2.16](#) are shown in a [legend](#) ([Show axis labels in legend](#)). The [Calibrate display space axes](#) option calibrates the two dimensions of the biplot, but this is generally undesirable in biplots of the new approach ([Gower and Hand, 1996](#), Section 2.6).

The [Format](#) menu allows virtually all the graphical parameters used internally by the package to be altered. The biplot in [Figure 2.17](#) serves as an example. This biplot is the same as the one in [Figure 2.11](#), but with some of the default graphical parameters changed. The [By group](#) option allows the graphical parameters which relate to points, sample group means, convex hulls / alpha-bags and classification regions to be set for all groups simultaneously, or for a single group at a time. [Screenshot 2.3](#) shows the dialogue box as it appears when customising the points of the species *Ocotea bullata*. The parameter values appear as they have been set for [Figure 2.17](#). The [Axes](#) option similarly allows the graphical parameters for axes to be set, simultaneously for all axes or individually. [Screenshot 2.4](#) shows the dialogue box of the graphical parameters for the axis ‘RayW’, again with the parameters as they have been set for [Figure 2.17](#). The graphical parameters used in variable value prediction and in the highlighting of axes can also be modified by clicking [Format](#) → [Interaction](#), while diagnostic tab customisation may be performed by clicking the [Diagnostic tabs](#) option. The [Reset all](#) option reverts all the graphical parameters back to their default values. In all, more than 80 different graphical parameters may be set, often-times differently for different groups or axes. All these parameters are documented in detail in [Chapter 3](#).

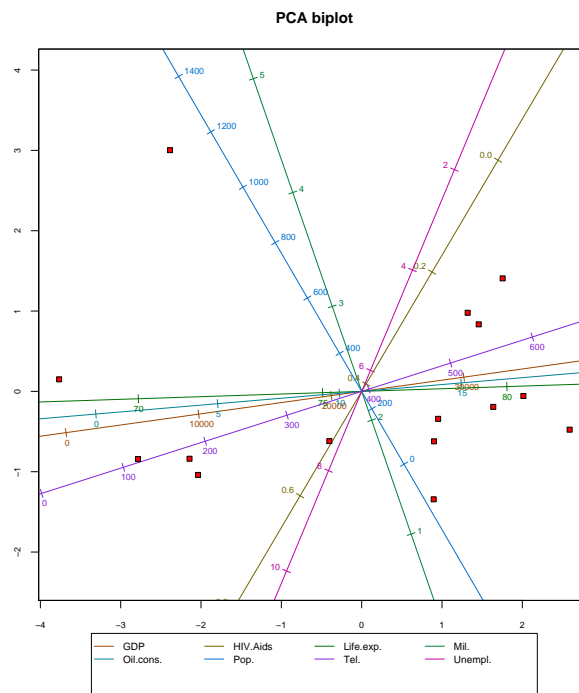


Figure 2.16. A modified version of the biplot given in Figure 2.1: a predictive PCA biplot of the countries data with a title, hidden point labels, axis labels in a legend, and the axes of the display space calibrated.

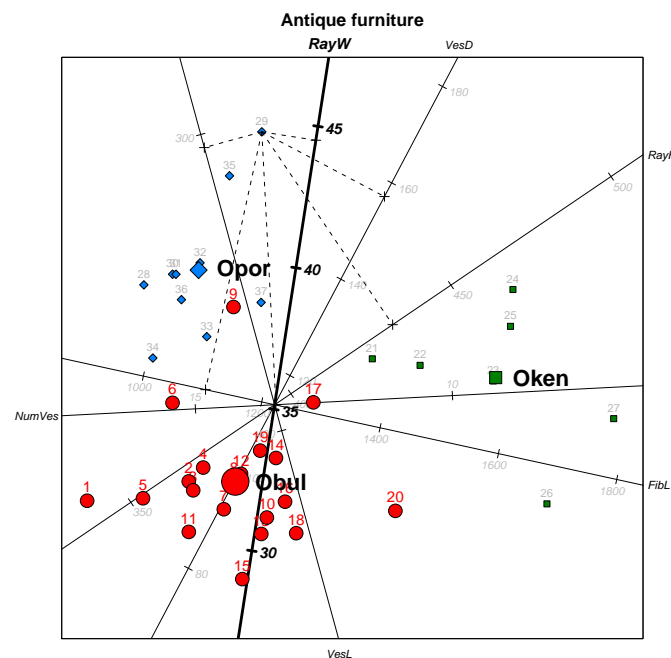
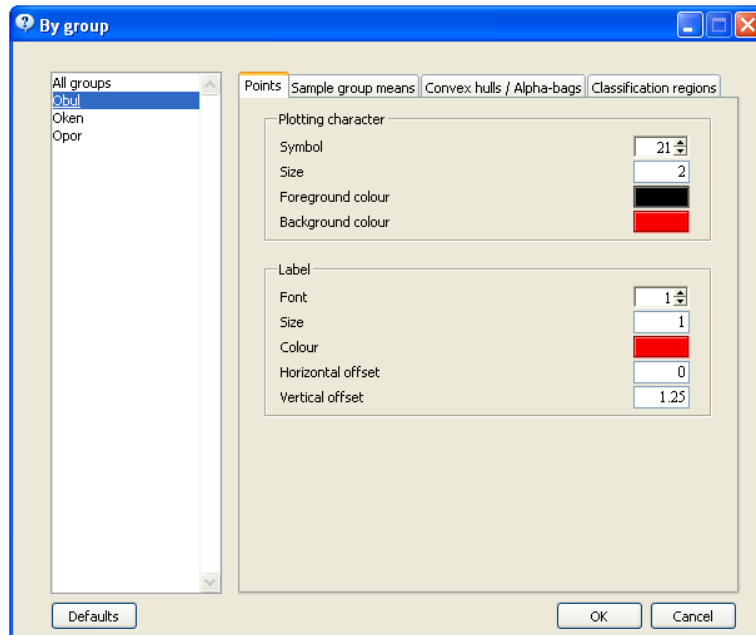
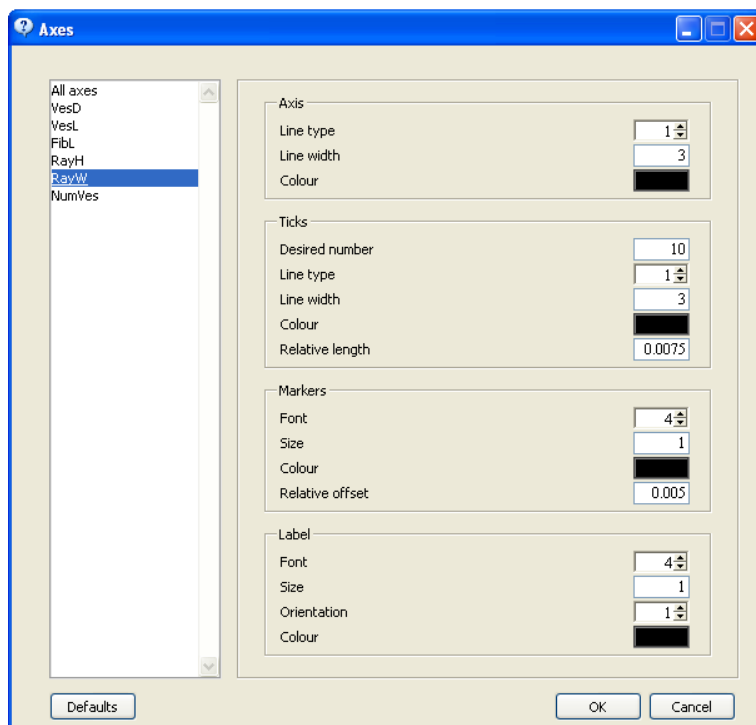


Figure 2.17. A modified version of the biplot given in Figure 2.11: a predictive CVA biplot of the antique furniture data with sample 29 projected onto all the biplot axes; the group means are shown.



Screenshot 2.3: The *Format* → *By group* dialogue box as it appears for the biplot in [Figure 2.17](#).



Screenshot 2.4: The *Format* → *Axes* dialogue box as it appears for the biplot in [Figure 2.17](#).

Naturally users would want to export the graphs produced using the **BiplotGUI** package. Biplots and diagnostic tab graphs can be saved in various file formats: [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg](#) (50%, 75% and 100% quality) and [PicTeX](#). Any graph can be saved by right clicking it and navigating the Save as menu. The biplot region may also be saved via the [File](#) → [Save as](#) menu. While the images shown onscreen are by necessity Metafile images, the images that appear in this article were saved in the PDF file format. Together with Postscript, such images are of the highest quality. [Copy](#) and [print](#) options are also available.

# Chapter 3

## Detail

In this chapter, the features of the **BiplotGUI** package are documented, starting with some general comments in [Section 3.1](#). The structure of the **GUI** can be seen from [Section 3.2](#). This section also serves as a table of contents to [Section 3.3](#), where the features are presented. Known issues are listed in [Section 1.4](#).

### 3.1 General

While more than one instance of the **GUI** may be opened simultaneously from within the same R console (by issuing additional calls to **Biplots**), this often results in a console warning as the **GUIs** are closed. It is safe to use the console for other commands while running an instance of the **GUI**. **GUIs** can be run simultaneously from different instances of R.

For more information on **Biplots**, the single function of the package, see the R help file for it by entering `?Biplots` at the R prompt of the R console. This chapter focuses on the features of the **GUI** itself.

### 3.2 List of Features

Menu bar . . . . .	32	Clip around points
File . . . . .	33	Clip around points and axes
Save as		Show point labels
PDF...		Show point values
Postscript...		Show group labels in legend
Metafile...		Don't show axis labels
Bmp...		Show clinging axis labels
Png...		Show axis labels in legend
Jpeg		Show Additional labels in legend
50% quality...		Show next legend entries
75% quality...		Show previous legend entries
100% quality...		Calibrate display space axes
PicTeX...		Format . . . . .
Copy		Title...
Print...		By group...
Options...		Axes...
Exit		Interaction...
View . . . . .	37	Diagnostic tabs...
Show title		Reset all...

Joint . . . . .	50	Zoom out	
PCA		Reset zoom	
Covariance/Correlation		Don't predict	
CVA		Predict cursor positions	
Points . . . . .	51	Predict points closest to cursor po-	
Distance metric		sitions	
Pythagoras		Remove axis highlight	
Square-root-of-Manhattan		Format by group...	
Clark		Format axes...	
Mahalanobis		Save as	
PCO		...	
MDS		Copy	
Random initial configuration		Print...	
Identity transformation		Point pop-up menu . . . . .	69
Monotone regression		Send to kraal	
Monotone spline transforma-		Format...	
tion...		Axis pop-up menu . . . . .	70
Primary approach to ties		Highlight	
Secondary approach to ties		Send to kraal	
In terms of principal axes		Format...	
Axes . . . . .	54	Outer pop-up menu . . . . .	70
None		Show title	
Regression		Format title...	
Procrustes		Show group labels in legend	
Circular non-linear		Don't show axis labels	
Default		Show clinging axis labels	
Additional . . . . .	55	Show axis labels in legend	
Interpolate		Show Additional labels in legend	
A new sample...		Show next legend entries	
Sample group means...		Show previous legend entries	
Convex hulls...		Save as	
Alpha-bags...		...	
Point densities...		Copy	
Classification regions...		Print...	
Clear all		Settings box . . . . .	71
Help . . . . .	67	Action . . . . .	71
Manual (in PDF)		Predict	
Homepage		Interpolate: centroid	
Show pop-up help		Interpolate: vector sum	
About...		Transformation . . . . .	71
Biplot region . . . . .	67	Centre	
Title . . . . .	68	Centre, scale	
Biplot . . . . .	68	Unitise, centre	
Legend . . . . .	68	Log, centre	
Inner pop-up menu . . . . .	68	Log, centre, scale	
Zoom in		Log, unitise, centre	
		Diagnostic tabs . . . . .	72



Convergence . . . . .	73	Return axes	
Pop-up menu		Return all	
Show title		Format by group...	
Format...		Format axes...	
Save as			
...		Kraal point pop-up menu . . . . .	76
Copy		Return to biplot	
Print...		Format...	
External		Kraal axis pop-up menu . . . . .	76
Points . . . . .	74	Return to biplot	
Pop-up menu		Format...	
Groups . . . . .	74	Other . . . . .	76
Pop-up menu		Progress bar . . . . .	76
...		External . . . . .	77
Axes . . . . .	74	As is	
Pop-up menu		In 3D	
...		Hide . . . . .	77
Predictions . . . . .	75	Points	
Export . . . . .	75	Axes	
Display in console		Live updates . . . . .	77
Save to workspace		Stop . . . . .	77
Kraal . . . . .	75	Return points . . . . .	77
Kraal pop-up menu . . . . .	76	Return axes . . . . .	78
Return points		Return all . . . . .	78

### 3.3 Features

In this section, the features of the BiplotGUI are systematically documented. [Section 3.2](#) serves as a table of contents. Features are indented as in [Section 3.2](#). The symbols used, from the outer-most to inner-most levels of indentation, are ►, ●, ▷, ○ and ◇, respectively. Information on the options in dialogue boxes is given in framed sections. After an introductory sentence, each feature is discussed under standard headings. These headings are listed below, together with a short description of each. Headings appear only when applicable.

DETAIL	More detailed information on the feature
DEFAULT VALUE	For graphical parameters, the default value
SHORTCUT	A keyboard shortcut to the feature
ALTERNATIVE TO	Mutually exclusive features
SCREENSHOT	For dialogue boxes, a reference to a screenshot
REFERENCES	References to external material

#### ► Menu bar

The primary interface of the [GUI](#).

DETAIL · The menu bar is located at the top of the [GUI](#). It consists of a number of drop-down menus, each with a number of entries. Entries may have sub-entries. The entries of menus are arranged around common themes of action. The [Joint](#) menu is for biplots with a joint mechanism for determining the positions of both points and axes. For other biplots, the [Points](#)

menu determines the positions of the points while the [Axes](#) menu determines the positions of the axes. Many entries contained in the menu bar can also be accessed from the pop-up menus which appear when various parts of graphs are right clicked.

**SHORTCUTS** · Often-used entries have dedicated keyboard shortcuts displayed to their right. These keyboard shortcuts are listed on page [vi](#). Menu bar entries may also be accessed via the keyboard by pressing the Alt key together with the underlined letter in the name of the corresponding drop-down menu, followed by the sequence of underlined letters in the path to the entry.

- **File**

Contains export and other options.

**DETAIL** · The File menu lets the user [save](#), [copy](#) or [print](#) the currently displayed [biplot region](#). In addition, general [options](#) may be set, or the user may [exit](#) the GUI.

- ▷ **Save as**

Lets the user save the currently displayed [biplot region](#) in a number of widely-used file formats.

**DETAIL** · Depending on how the GUI has been resized onscreen, the proportions within a saved biplot region may differ from what is shown onscreen. To ensure consistency, saved biplot regions always have both their width and height set to 20.32 centimeters (8 inches). The [PDF](#) and [Postscript](#) file formats offer the highest quality, better even than that shown onscreen.

**SHORTCUT** · Ctrl+S. Saves the currently displayed biplot region in the currently selected file format.

- **PDF...**

Saves the currently displayed [biplot region](#) as a PDF file.

**DETAIL** · Together with [Postscript](#), the PDF file format offers the highest quality.

**ALTERNATIVE TO** · [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the PDF file.

- **Postscript...**

Saves the currently displayed [biplot region](#) as a Postscript file (.ps).

**DETAIL** · Together with [PDF](#), the Postscript file format offers the highest quality.

**ALTERNATIVE TO** · [PDF](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the Postscript file.

- **Metafile...**

Saves the currently displayed [biplot region](#) as a Windows Metafile (.wmf).

**ALTERNATIVE TO** · [PDF](#), [Postscript](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the Windows Metafile.

- **Bmp...**

Saves the currently displayed [biplot region](#) as a bitmap (.bmp).

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the bitmap file.

- **Png...**

Saves the currently displayed [biplot region](#) as a png file.

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the png file.

- **Jpeg**

Lets the user save the currently displayed [biplot region](#) as a Jpeg file (.jpg, .jpeg).

- ◇ **50% quality...**

Saves the currently displayed [biplot region](#) as a Jpeg file at 50% quality.

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the 50% quality Jpeg file.

- ◇ **75% quality...**

Saves the currently displayed [biplot region](#) as a Jpeg file at 75% quality.

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 100% quality](#), [PicTeX](#)

A standard dialogue box appears which lets the user specify the name and location of the 75% quality Jpeg file.

- ◇ **100% quality...**

Saves the currently displayed [biplot region](#) as a Jpeg file at 100% quality.

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [PicTeX](#)

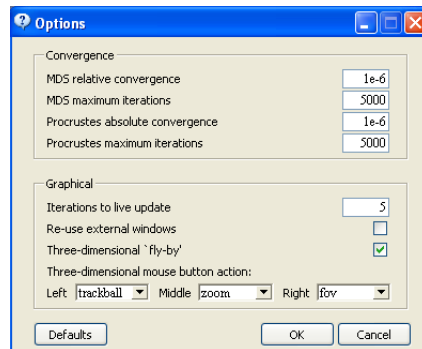
A standard dialogue box appears which lets the user specify the name and location of the 100% quality Jpeg file.

- **PicTeX...**

Saves the currently displayed [biplot region](#) in the PicTeX format (.tex).

ALTERNATIVE TO · [PDF](#), [Postscript](#), [Metafile](#), [Bmp](#), [Png](#), [Jpeg 50% quality](#), [Jpeg 75% quality](#), [Jpeg 100% quality](#)

REFERENCES · See the R help file of the `pictex` function for the limitations of the conversion to this format.

Screenshot 3.1: The *File* → *Options* dialogue box.

A standard dialogue box appears which lets the user specify the name and location of the PicTeX file.

▷ **Copy**

Copies the currently displayed [biplot region](#) to the clipboard as a Windows Metafile.

DETAIL · Depending on how the [GUI](#) has been resized onscreen, the proportions within a copied biplot region may differ from what is shown onscreen. To ensure consistency, copied biplot regions always have both their width and height set to 20.32 centimeters (8 inches). Biplots saved as [PDF](#) or [Postscript](#) files are of a higher quality than those copied to the clipboard.

SHORTCUT · Ctrl+C

▷ **Print...**

Prints the currently displayed [biplot region](#).

DETAIL · Depending on how the [GUI](#) has been resized onscreen, the proportions within a printed biplot region may differ from what is shown onscreen. To ensure consistency, printed biplot regions always have both their width and height set to 20.32 centimeters (8 inches).

SHORTCUT · Ctrl+P

A standard dialogue box appears which lets the user set various options before printing.

▷ **Options...**

Lets the user set various general options.

SCREENSHOT · [3.1](#)

**Convergence**

Lets the user set various convergence criteria.

***MDS relative convergence***

If still running, the [IM](#) algorithm for [MDS](#) stops when the *proportional* decrease in stress becomes smaller than this value.

DEFAULT VALUE ·  $10^{-6}$

REFERENCES · [Borg and Groenen \(2005, pp. 191–192, 204–205\)](#)

***MDS maximum iterations***

If still running, the **IM** algorithm for **MDS** stops when the number of iterations reaches this value.

DEFAULT VALUE · 5000

REFERENCES · [Borg and Groenen \(2005, pp. 191–192, 204–205\)](#)

***Procrustes absolute convergence***

If still running, the Procrustes algorithm for interpolative biplots stops when the absolute decrease in stress first becomes smaller than this value.

DEFAULT VALUE ·  $10^{-6}$

REFERENCES · [Gower and Hand \(1996, Section A.10.2\)](#), [Gower and Dijksterhuis \(2004, p. 57\)](#)

***Procrustes maximum iterations***

If still running, the Procrustes algorithm for interpolative biplots stops when the number of iterations reaches this value.

DEFAULT VALUE · 5000

REFERENCES · [Gower and Hand \(1996, Section A.10.2\)](#), [Gower and Dijksterhuis \(2004, p. 57\)](#)

**Graphical**

Lets the user set general graphical options.

***Iterations to live update***

The **biplot region** and relevant graphs in the **diagnostic tabs** are updated after this number of **MDS** iterations, and multiples of it.

DETAIL · The smaller the value of this option, the smoother the transitions in the graphs; the larger the value of this option, the smaller the time to convergence. Irrespective of the value of this option, the biplot region and the relevant graphs in the diagnostic tabs are only updated during **MDS** convergence if **Live updates** is checked below the biplot region.

DEFAULT VALUE · 5

***Reuse external windows***

Toggles between using the same or new windows for external graphics.

DETAIL · If checked, the same window is used to display any two-dimensional external graphs that are produced. Such graphs can be created by clicking **External → As is** below the **biplot region**, or by right clicking the graphs of the **diagnostic tabs** and selecting **External** from the pop-up menu. If clear, new windows are used to show any additional two-dimensional graphs, retaining previous external graphs, if any. Similar comments hold for three-dimensional external biplots created by clicking **External → In 3D** below the biplot region. The windows of the two- and three-dimensional graphs operate independently.

DEFAULT VALUE · clear

***Three-dimensional ‘fly-by’***

Toggles between including an initial ‘fly-by’ in three-dimensional biplots, or not including one.

DEFAULT VALUE · checked

***Three-dimensional mouse button action: left***

The action of the left mouse button in three-dimensional biplots.

DEFAULT VALUE · trackball

REFERENCES · See the R help file of the **par3d** function of the **rgl** package ([Adler and Murdoch, 2008](#)) for details on the choices.

***Three-dimensional mouse button action: middle***

The action of the middle mouse button in three-dimensional biplots.

DEFAULT VALUE · zoom

REFERENCES · See the R help file of the `par3d` function of the `rgl` package ([Adler and Murdoch, 2008](#)) for details on the choices.

***Three-dimensional mouse button action: right***

The action of the right mouse button in three-dimensional biplots.

DEFAULT VALUE · fov

REFERENCES · See the R help file of the `par3d` function of the `rgl` package ([Adler and Murdoch, 2008](#)) for details on the choices.

**Defaults**

Reverts the options to their default values.

**OK**

Saves the options and returns to the [GUI](#).

**Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

▷ **Exit**

Lets the user exit the [GUI](#).

DETAIL · Upon exiting, all actions performed and changes made in the [GUI](#) are lost. The user is returned to the R prompt of the R console.

A standard dialogue box appears which asks the user to confirm whether or not to exit the [GUI](#).

• **View**

Allows the users to customise the [biplot region](#).

▷ **Show title**

Shows a [title](#) above the [biplot](#).

DETAIL · The biplot retains the same size and relative position, irrespective of whether or not a title is shown.

▷ **Clip around points**

Sets the [biplot](#) borders around the points, ignoring the axes.

DETAIL · If selected, the biplot borders are set just large enough to show all the points and their [labels](#). [Non-linear](#) axes may not be visible in their entirety.

ALTERNATIVE TO · [Clip around points and axes](#)

▷ **Clip around points and axes**

Sets the [biplot](#) borders around the points and axes.

DETAIL · If selected, the biplot borders are set large enough to show all the points, their [labels](#), and the axes in their entirety. Available only for [non-linear](#) axes and when the axes are not [hidden](#).

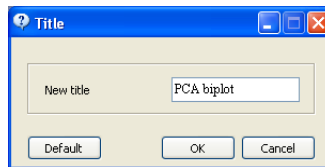
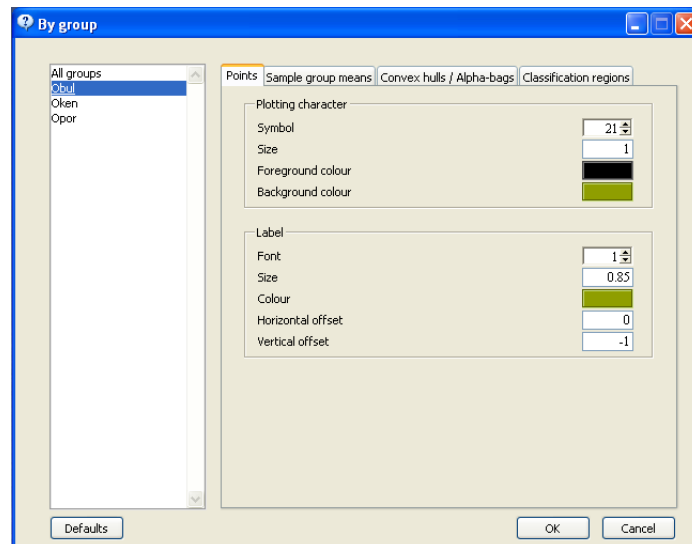
ALTERNATIVE TO · [Clip around points](#)

▷ **Show point labels**

Shows the point labels in the [biplot](#).

DETAIL · If selected, the biplot borders are enlarged so that all the point labels fit. Not available when the points are [hidden](#).

- ▷ **Show point values**  
Shows the variable values of a highlighted axis alongside the corresponding points in the [biplot](#).  
DETAIL · Only available when an axis has been [highlighted](#).
- ▷ **Show group labels in legend**  
Shows the group labels in the [legend](#).  
DETAIL · Not available when there is only one group of samples, or when the points are [hidden](#).
- ▷ **Don't show axis labels**  
Suppresses the axis labels.  
DETAIL · Not available if there are [no axes](#), or when the axes are [hidden](#).  
ALTERNATIVE TO · [Show clinging axis labels](#), [Show axis labels in legend](#)
- ▷ **Show clinging axis labels**  
Shows the axis labels at those edges of the axes with the higher calibrations.  
DETAIL · Available only for linear axes when the axes are not [hidden](#).  
ALTERNATIVE TO · [Don't show axis labels](#), [Show axis labels in legend](#)
- ▷ **Show axis labels in legend**  
Shows the axis labels in the legend.  
DETAIL · Not available if there are [no axes](#), or when the axes are [hidden](#).  
ALTERNATIVE TO · [Don't show axis labels](#), [Show clinging axis labels](#)
- ▷ **Show Additional labels in legend**  
Shows the labels of descriptors from the [Additional](#) menu in the [legend](#).
- ▷ **Show next legend entries**  
Shows the succeeding set of 16 [legend](#) entries, if any, in the legend.  
DETAIL · The legend can contain up to a maximum of 16 entries at once. This option updates the legend to show the succeeding set of at most 16 entries. The option does not show the first set of entries after the last set. Not available when there are no succeeding entries, or when no legend is shown.  
SHORTCUT · Ctrl++
- ▷ **Show previous legend entries**  
Shows the preceding set of 16 [legend](#) entries, if any, in the legend.  
DETAIL · The legend can contain up to a maximum of 16 entries at once. This option updates the legend to show the preceding set of 16 entries. The option does not show the last set of entries before the first set. Not available when there are no preceding entries, or when no legend is shown.  
SHORTCUT · Ctrl+-
- ▷ **Calibrate display space axes**  
Calibrates the two [biplot](#) dimensions.  
DETAIL · This is counter to the spirit of biplots of the new approach.  
REFERENCES · [Gower and Hand \(1996, Section 2.6\)](#)
- **Format**  
Lets the user customise the internally used graphical parameters.
  - ▷ **Title...**  
Lets the user change the [title](#).  
DETAIL · The title is shown only if [View](#) → [Show title](#) is selected.  
SCREENSHOT · [3.2](#)

Screenshot 3.2: The *Format* → *Title* dialog box.Screenshot 3.3: The *Points* tab of the *Format* → *By group* dialog box.***New title***

The new [title](#).

DEFAULT VALUE · Depends on the currently displayed biplot; can be seen from the title bar of the [GUI](#).

**Default**

Reverts the option to its default value.

**OK**

Saves the [title](#), returns to the [GUI](#), and redraws the [biplot region](#).

**Cancel**

Cancels the changes made since the dialog box was opened, and returns to the [GUI](#).

▷ **By group...**

Allows graphical parameters for [points](#), [sample group means](#), [convex hulls](#) / [alpha-bags](#), and [classification regions](#) to be set for a particular group, or for all groups simultaneously.

DETAIL · When *All groups* is selected from the list to the left of the dialog box, changes made to the parameter values to the right of the dialog box affect all groups. Changes to particular groups can be made by clicking the group names in the list to the left of the dialog box. Parameter values which differ amongst groups are left blank when *All groups* is selected.

SHORTCUT · Ctrl+G

SCREENSHOT · [3.3](#)



*Only the Points tab is discussed here. The other tabs are discussed together with the options of the [Additional](#) menu.*

### **Plotting character**

Lets the user change the graphical parameters of the points that represent the samples, by group.

#### ***Symbol***

Sets the symbol used to represent the points, by group.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · If there is only one group, 22. Otherwise the values are recycled by group with the values 21 to 25.

#### ***Size***

Sets the size of the points, by group.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger points. Possible values: positive real numbers.

DEFAULT VALUE · 1

#### ***Foreground colour***

Sets the exterior colour of the points, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

#### ***Background colour***

Sets the interior colour of the points, by group.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "red". Otherwise equally spaced colours from the `hcl` spectrum.

### **Label**

Lets the user change the graphical parameters of the point labels, by group.

#### ***Font***

Sets the font of the point labels, by group.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 1

#### ***Size***

Sets the size of the point labels, by group.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 0.85

#### ***Colour***

Sets the colour of the point labels, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "black". Otherwise equally spaced colours from the `hcl` spectrum.

#### ***Horizontal offset***

Sets the horizontal offset of the point labels from the corresponding points, by group.

DETAIL · The point labels are shifted horizontally from the corresponding

points with this multiple of the width of the letter ‘x’ (in the selected font size). Positive values shift the labels to the right; negative values shift the labels to the left.

DEFAULT VALUE · 0

### ***Vertical offset***

Sets the vertical offset of the point labels from the corresponding points, by group.

DETAIL · The point labels are shifted vertically from the corresponding points with this multiple of the height of the letter ‘x’ (in the selected font size). Positive values shift the labels towards the top; negative values shift the labels towards the bottom.

DEFAULT VALUE · -1

### **Defaults**

Reverts the options of all the tabs of the dialogue box to their default values.

### **OK**

Saves the options of all the tabs of the dialogue box, returns to the [GUI](#), redraws the currently displayed [biplot region](#) and other graphs if necessary.

### **Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

## ▷ **Axes...**

Allows graphical parameters for axes to be set for a particular axis, or for all axes simultaneously.

DETAIL · When *All axes* is selected from the list to the left of the dialogue box, changes made to the parameter values to the right of the dialogue box affect all axes. Changes to particular axes can be made by clicking the variable names from the list to the left of the dialogue box. Parameter values which differ amongst axes are left blank when *All axes* is selected.

SHORTCUT · Ctrl+A

SCREENSHOT · [3.4](#)

### **Axis**

Lets the user change the graphical parameters associated with the axis that represents the variable.

#### ***Line type***

Sets the type of line used to draw the axis.

DETAIL · Corresponds to R’s `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 1

#### ***Line width***

Sets the width of the axis.

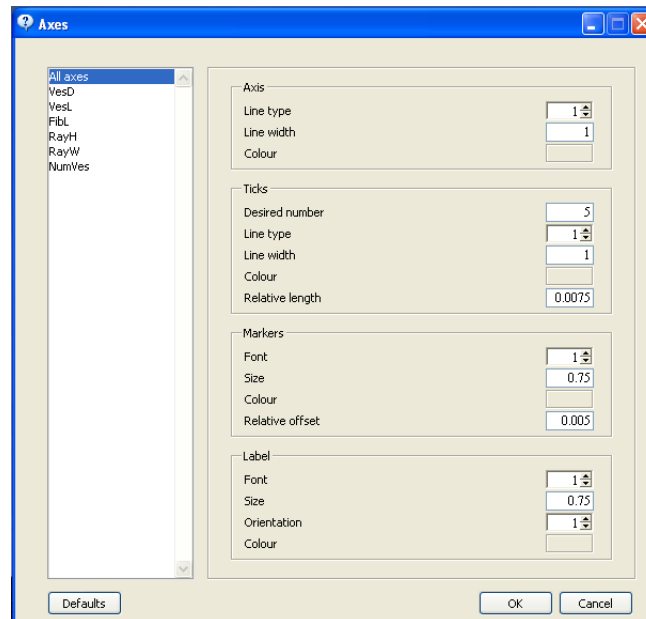
DETAIL · Corresponds to R’s `lwd` argument. Larger values result in wider axes. Possible values: positive real numbers.

DEFAULT VALUE · 1

#### ***Colour***

Sets the colour of the axis.

DETAIL · Corresponds to R’s `col` argument. Can be changed by clicking the

Screenshot 3.4: The *Format* → *Axes* dialogue box.

colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · Equally spaced colours from the `hcl` spectrum.

### Ticks

Lets the user change graphical parameters associated with the ticks of the axis.

DETAIL · The ticks, together with the markers, calibrate the axis. The ticks are the short lines orthogonal to the axis, alongside which the markers (the numbers) are given. For non-linear axes, the slopes of the ticks are approximated numerically.

### *Desired number*

Sets the desired number of ticks on the axis.

DETAIL · Corresponds to the argument `n` of R's `pretty` function. This number is not strictly adhered to; it is only approximate.

DEFAULT VALUE · 5

REFERENCES · See the R help file of the `pretty` function.

### *Line type*

Sets the type of line used to draw the ticks on the axis.

DETAIL · Corresponds to R's `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 1

### *Line width*

Sets the width of the ticks of the axis.

DETAIL · Corresponds to R's `lwd` argument. Larger values result in wider ticks. Possible values: positive real numbers.

DEFAULT VALUE · 1

### *Colour*

Sets the colour of the ticks of the axis.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the

colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · The same as the default colour of the axis.

### ***Relative length***

Sets the relative length of the ticks of the axis.

DETAIL · The length of the ticks is twice this fraction of the width of the [biplot](#).

DEFAULT VALUE · 0.0075

### **Markers**

Lets the user change graphical parameters associated with the markers of the axis.

DETAIL · The markers, together with the ticks, calibrate the axis. The markers are the numbers, in terms of the original variable values, given alongside the ticks (the short lines orthogonal to the axis). The markers are positioned on that side of the axis that would place them below the axis if the axis were to be rotated to be horizontal (with the marker values increasing from left to right).

### ***Font***

Sets the font of the markers of the axis.

DETAIL · Corresponds to R's **font** argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 1

### ***Size***

Sets the size of the markers of the axis.

DETAIL · Corresponds to R's **cex** argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 0.75

### ***Colour***

Sets the colour of the markers of the axis.

DETAIL · Corresponds to R's **col** argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · The same as the default colour of the axis.

### ***Relative offset***

Sets the relative offset of the markers from the corresponding ticks of the axis.

DETAIL · The markers are shifted this fraction of the width of the [biplot](#) from the edge of the corresponding ticks.

DEFAULT VALUE · 0.005.

### **Label**

Lets the user change the graphical parameters of the axis label.

### ***Font***

Sets the font of the axis label.

DETAIL · Corresponds to R's **font** argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

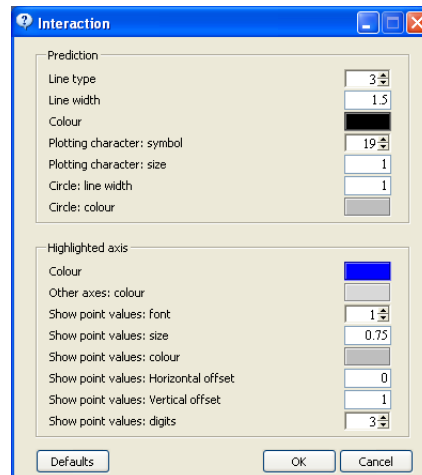
DEFAULT VALUE · 1

### ***Size***

Sets the size of the axis label.

DETAIL · Corresponds to R's **cex** argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 0.75



Screenshot 3.5: The *Format* → *Interaction* dialogue box.

### **Orientation**

Sets the orientation of clinging axis labels.

DETAIL · Corresponds to R's `las` argument. Possible values: 0: always parallel to the [biplot](#) dimension; 1: always horizontal; 2: always perpendicular to the biplot dimension; 3: always vertical.

DEFAULT VALUE · 1

### **Colour**

Sets the colour of the axis label.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · The same as the default colour of the axis.

### **Defaults**

Reverts the options to their default values.

### **OK**

Saves the options, returns to the [GUI](#), redraws the currently displayed [biplot region](#) and other graphs if necessary.

### **Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

## ▷ **Interaction...**

Allows graphical parameters for variable value prediction and highlighted axes to be set.

SCREENSHOT · [3.5](#)

### **Prediction**

Lets the user change the graphical parameters associated with variable value prediction.

#### **Line type**

Sets the line type used for projection.

DETAIL · Corresponds to R's `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 3

***Line width***

Sets the width of the projection lines.

DETAIL · Corresponds to R's `lwd` argument. Larger values result in wider ticks.  
Possible values: positive real numbers.

DEFAULT VALUE · 1.5

***Colour***

Sets the colour of the projection lines.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

***Plotting character: symbol***

Sets the symbol used to represent the projected points on the axes.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · 19

***Plotting character: size***

Sets the size of the projected points on the axes.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger points. Possible values: positive real numbers.

DEFAULT VALUE · 1

***Circle: line width***

Sets the width of the circle used in circular projection in the circular non-linear biplot.

DETAIL · Corresponds to R's `lwd` argument. Larger values result in wider ticks.  
Possible values: positive real numbers.

DEFAULT VALUE · 1

***Circle: colour***

Sets the colour of the circle used in circular projection in the circular non-linear biplot.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "gray75"

***Highlighted axis***

Lets the user change the graphical parameters associated with highlighted axes.

DETAIL · The graphical parameters prefixed with 'Show point values' are for the customisation of the variable values which are shown when an axis is highlighted and [Show point values](#) is selected.

***Colour***

Sets the colour of the highlighted axis.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "blue"

***Other axes: colour***

Sets the colour of the non-highlighted axes.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "gray85"

**Show point values: font**

Sets the font of the point values.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 1

**Show point values: size**

Sets the size of the point values.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 0.75

**Show point values: colour**

Sets the colour of the point values.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "gray75"

**Show point values: horizontal offset**

Sets the horizontal offset of the point values from the corresponding points.

DETAIL · The point values are shifted horizontally from the corresponding points with this multiple of the width of the letter 'x' (in the selected font size). Positive values shift the values to the right; negative values shift the values to the left.

DEFAULT VALUE · 0

**Show point values: vertical offset**

Sets the vertical offset of the point values from the corresponding points.

DETAIL · The point values are shifted vertically from the corresponding points with this multiple of the height of the letter 'x' (in the selected font size). Positive values shift the values towards the top; negative values shift the values towards the bottom.

DEFAULT VALUE · 1

**Show point values: digits**

Sets the number of decimal places to show in the point values.

DETAIL · Possible values: 0, ..., 8.

DEFAULT VALUE · 3

**Defaults**

Reverts the options to their default values.

**OK**

Saves the options, returns to the [GUI](#), and redraws the currently displayed [biplot region](#).

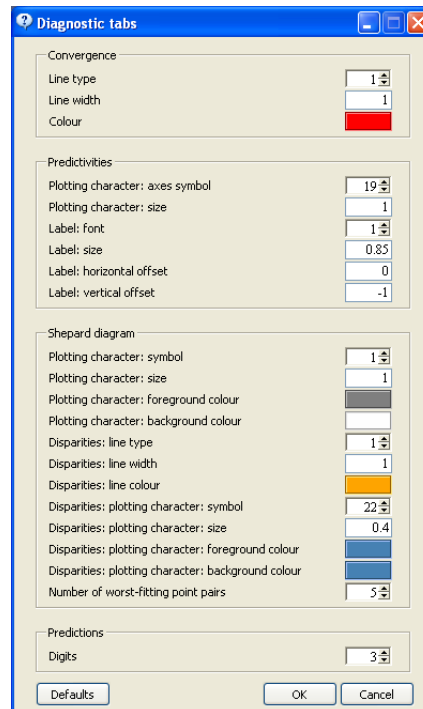
**Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

▷ **Diagnostic tabs...**

Allows graphical parameters of the graphs of the [diagnostic tabs](#) to be set.

SCREENSHOT · [3.6](#)



Screenshot 3.6: The *Format* → *Diagnostics* dialogue box.

### Convergence

Lets the user change the graphical parameters of the graph of the convergence tab.

#### ***Line type***

Sets the line type.

DETAIL · Corresponds to R's `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 1

#### ***Line width***

Sets the line width.

DETAIL · Corresponds to R's `lwd` argument. Possible values: positive real numbers.

DEFAULT VALUE · 1

#### ***Colour***

Sets the line colour.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "red"

### Predictivities

Lets the user change the graphical parameters of the points, groups and axes predictivities graphs of the points, group and axes tabs, respectively.

#### ***Plotting character: axes symbol***

Sets the symbol used to represent axes in the axes tab.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · 19



***Plotting character: size***

Sets the size of the plotting characters.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger plotting characters. Possible values: positive real numbers.

DEFAULT VALUE · 1

***Label: font***

Sets the font of the labels.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 1

***Label: size***

Sets the size of the labels.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 0.85

***Label: horizontal offset***

Sets the horizontal offset of the labels from the corresponding plotting characters.

DETAIL · The labels are shifted horizontally from the corresponding plotting characters with this multiple of the width of the letter 'x' (in the selected font size). Positive values shift the labels to the right; negative values shift the labels to the left.

DEFAULT VALUE · 0

***Label: vertical offset***

Sets the vertical offset of the labels from the corresponding plotting characters.

DETAIL · The labels are shifted vertically from the corresponding plotting characters with this multiple of the height of the letter 'x' (in the selected font size). Positive values shift the labels towards the top; negative values shift the labels towards the bottom.

DEFAULT VALUE · -1

**Shepard diagram**

Lets the user change the graphical parameters of the Shepard diagram of the points tab.

***Plotting character: symbol***

Sets the symbol used to represent the inter-point distances.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · 1

***Plotting character: size***

Sets the size of the plotting character used for inter-point distances.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger plotting characters. Possible values: positive real numbers.

DEFAULT VALUE · 1

***Plotting character: foreground colour***

Sets the exterior colour of the plotting character used for inter-point distances.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "gray50"

***Plotting character: background colour***

Sets the interior colour of the plotting character used for inter-point distances.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "white"

***Disparities: line type***

Sets the line type used for inter-sample disparities.

DETAIL · Corresponds to R's `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 1

***Disparities: line width***

Sets the width of the line used for inter-sample disparities.

DETAIL · Corresponds to R's `lwd` argument. Larger values result in a wider line. Possible values: positive real numbers.

DEFAULT VALUE · 1

***Disparities: line colour***

Sets the colour of the line used for inter-sample disparities.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "orange"

***Disparities: plotting character: symbol***

Sets the symbol used to represent the inter-sample disparities.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · 22

***Disparities: plotting character: size***

Sets the size of the plotting character used for inter-samples disparities.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger plotting characters. Possible values: positive real numbers.

DEFAULT VALUE · 0.4

***Disparities: plotting character: foreground colour***

Sets the exterior colour of the plotting character used for inter-samples disparities.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "steelblue"

***Disparities: plotting character: background colour***

Sets the interior colour of the plotting character used for inter-samples disparities.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "steelblue"

***Number of worst-fitting point pairs***

Sets the number of worst-fitting point pairs to show at the top left of the Shepard diagram.

DETAIL · The degree of misfit between a pair of points is quantified as the difference between the inter-point distance and the corresponding inter-sample disparity. Therefore as the vertical distance from the plotting character that

represents the inter-point distance to the line representing the inter-sample disparities.

DEFAULT VALUE · 5

### **Predictions**

Lets the user change the settings associated with the predictions tab.

#### ***Digits***

Sets the number of decimal places to show in the variable value predictions of the predictions tab.

DETAIL · Possible values: 0, . . . , 8.

DEFAULT VALUE · 3

### **Defaults**

Reverts the options to their default values.

### **OK**

Saves the options, returns to the [GUI](#), and redraws the the graphs of the [diagnostic tabs](#).

### **Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

#### ▷ **Reset all. . .**

Reverts all the parameters that can be changed in the Format menu to their default values.

SHORTCUT · Ctrl+R

A standard dialogue box appears asking the user to confirm whether or not to reset the graphical parameters of the Format menu.

DETAIL · Upon confirmation, the graphical parameters are reset and the biplot region and the graphs of the [diagnostic tabs](#) are redrawn.

### • **Joint**

For the construction of joint-mechanism biplots.

DETAIL · The biplots of this menu have both their points and axes determined according to a single, joint mechanism. Other biplots have their points determined from the [Points](#) menu and their axes determined from the [Axes](#) menu.

#### ▷ **PCA**

Constructs a [PCA](#) biplot.

DETAIL · The points correspond to the scores of the first two [PCs](#).

SHORTCUT · 1

ALTERNATIVE TO · [Covariance/Correlation](#), [CVA](#), [None](#), [Regression](#), [Procrustes](#), [Circular non-linear](#)

REFERENCES · [Gower and Hand \(1996, Chapter 2\)](#)

#### ▷ **Covariance/Correlation**

Constructs a covariance/correlation biplot.

DETAIL · If the data are only centred, a covariance biplot is produced. If the data are centred and scaled, a correlation biplot is produced.

SHORTCUT · 2

ALTERNATIVE TO · [PCA](#), [CVA](#), [None](#), [Regression](#), [Procrustes](#), [Circular non-linear](#)

REFERENCES · [Gabriel \(1971\)](#), [Greenacre \(1984\)](#), [Gardner \(2001, Section 2.3.2\)](#),

[Gower and Hand \(1996, Section 11.5.1\)](#)

▷ **CVA**

Constructs a [CVA](#) biplot.

DETAIL · The points correspond to the first two [CVs](#). The group means can be included by clicking [Additional](#) → [Interpolate](#) → [Sample group means](#). [CVA](#) biplots are invariant to the scaling of data to have unit variances. Only available when there is more than one group.

SHORTCUT · 3

ALTERNATIVE TO · [PCA](#), [Covariance/Correlation](#), [None](#), [Regression](#), [Procrustes](#), [Circular non-linear](#)

REFERENCES · [Gower and Hand \(1996, Chapter 5 except Section 5.5\)](#)

• **Points**

Fixes the positions of the points of those biplots which have their axes determined from the [Axes](#) menu.

DETAIL · As opposed to the biplots of the [Joint](#) menu, the [Points](#) and [Axes](#) menus are used together. The options of the [Points](#) menu fix the points, while the options of the [Axes](#) menu fix the axes.

▷ **Distance metric**

Sets the distance metric to be used in [PCO](#) and [MDS](#).

DETAIL · All the distance metrics that are available are Euclidean-embeddable. Therefore points exist in Euclidean space which have the same distances between them in Pythagorean distance as the samples have between them in the Euclidean-embeddable distance metric. If the axes previously selected in the [Axes](#) menu are no longer available because of the change in distance metric, the most appropriate replacement is automatically chosen.

REFERENCES · [Gower and Legendre \(1986\)](#), [Gower and Hand \(1996, Section A.5.1\)](#)

◦ **Pythagoras**

The distance metric is set to Pythagoras distance.

DETAIL · ‘Pythagoras distance’ and ‘Euclidean distance’ are synonymous. However, to avoid confusion with the class of ‘Euclidean-embeddable’ distances, the terminology ‘Pythagoras distance’ is used instead. Under this distance metric, the distance between a vector  $\mathbf{x} : p \times 1$  and a vector  $\mathbf{y} : p \times 1$  is given by  $((\mathbf{x} - \mathbf{y})'(\mathbf{x} - \mathbf{y}))^{1/2}$ .

ALTERNATIVE TO · [Square-root-of-Manhattan](#), [Clark](#), [Mahalanobis](#)

REFERENCES · [Loomis \(1968\)](#), [Cox and Cox \(2001, p. 11\)](#), [Borg and Groenen \(2005, p. 122\)](#)

◦ **Square-root-of-Manhattan**

The distance metric is set to Square-root-of-Manhattan distance.

DETAIL · Distances under this metric are the square root of those under the Manhattan or City Block distance metric. Therefore the distance between a vector  $\mathbf{x} : p \times 1$  and a vector  $\mathbf{y} : p \times 1$  is given by  $(\sum_{i=1}^p |x_i - y_i|)^{1/2}$ .

ALTERNATIVE TO · [Pythagoras](#), [Clark](#), [Mahalanobis](#)

REFERENCES · [Gower and Harding \(1988\)](#), [Gower and Hand \(1996, p. 103\)](#), [Cox and Cox \(2001, p. 11\)](#), [Borg and Groenen \(2005, p. 122\)](#)

◦ **Clark**

The distance metric is set to Clark distance.

DETAIL · Under this distance metric, the distance between a vector  $\mathbf{x} : p \times 1$

and a vector  $\mathbf{y} : p \times 1$  is given by  $\sum_{i=1}^p \left( \frac{x_i - y_i}{x_i + y_i} \right)^2$ .

ALTERNATIVE TO · [Pythagoras](#), [Square-root-of-Manhattan](#), [Mahalanobis](#)

REFERENCES · [Clark \(1952\)](#), [Gower and Ngouenet \(2005\)](#)

- **Mahalanobis**

The distance metric is set to Mahalanobis distance.

DETAIL · Under this distance metric, the distance between a vector  $\mathbf{x} : p \times 1$  and a vector  $\mathbf{y} : p \times 1$  is given by  $((\mathbf{x} - \mathbf{y})' \mathbf{S}^{-1} (\mathbf{x} - \mathbf{y}))^{1/2}$  where  $\mathbf{S}$  is the covariance matrix of all the vectors of observations. Mahalanobis distance is also known as ‘statistical distance’.

ALTERNATIVE TO · [Pythagoras](#), [Square-root-of-Manhattan](#), [Clark](#)

REFERENCES · [Mahalanobis \(1936\)](#), [Cox and Cox \(2001, p. 11\)](#)

- ▷ **PCO**

The points are fixed by [PCO](#), with inter-sample dissimilarities calculated according to the chosen distance metric.

DETAIL · The coordinates of the points are taken to be the first two principal coordinates. [PCO](#) is also known as ‘classical scaling’.

SHORTCUT · A

ALTERNATIVE TO · [MDS Identity transformation](#), [MDS Monotone regression](#), [MDS Monotone spline transformation](#).

REFERENCES · [Gower \(1966\)](#), [Gower and Hand \(1996, Section A.5.2\)](#), [Cox and Cox \(2001, Section 2.2\)](#), [Borg and Groenen \(2005, Chapter 12\)](#)

- ▷ **MDS**

The points are fixed by [MDS](#), with inter-sample dissimilarities calculated according to the chosen distance metric.

REFERENCES · [Cox and Cox \(2001\)](#), [Borg and Groenen \(2005\)](#)

- **Random initial configuration**

The next [MDS](#) algorithm will start from a random initial configuration.

DETAIL · If selected, the initial [MDS](#) configuration is taken to have points uniformly distributed over  $[-1, 1]$  in both dimensions. If not selected, the initial configuration is taken to be the previous configuration of points. Useful to avoid local minima.

- **Identity transformation**

Performs an [MDS](#) with the identity transformation.

DETAIL · The inter-sample disparities are taken to be the inter-sample dissimilarities, calculated according to the chosen distance metric. Using an [IM](#) algorithm, the points are chosen so that stress, the sum of squared differences between the inter-point distances and the inter-sample disparities, is minimised.

SHORTCUT · B

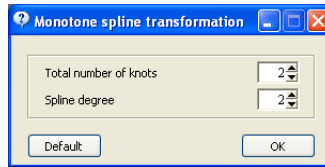
ALTERNATIVE TO · [PCO](#), [Monotone regression](#), [Monotone spline transformation](#)

REFERENCES · [Borg and Groenen \(2005, Section 8.6\)](#)

- **Monotone regression**

Performs a non-metric [MDS](#).

DETAIL · The inter-sample disparities are calculated by the up-and-down-blocks algorithm from the inter-sample dissimilarities. In essence, merely the order of the inter-sample dissimilarities is preserved. Using an [IM](#) algorithm, the points are chosen so that stress, the sum of squared differences between the inter-point



Screenshot 3.7: The *Points* → *MDS* → *Monotone spline transformation* dialogue box.

distances and the inter-sample disparities, is minimised. The [Primary approach to ties](#) or the [Secondary approach to ties](#) can be used.

SHORTCUT · C

ALTERNATIVE TO · [PCO](#), [Identity transformation](#), [Monotone spline transformation](#),

REFERENCES · [Borg and Groenen \(2005, Sections 9.1, 9.2\)](#)

◦ **Monotone spline transformation...**

Performs an [MDS](#) with a monotone spline transformation

DETAIL · The inter-sample dissimilarities are smoothed using monotone splines to obtain the inter-sample disparities. Using an [IM](#) algorithm, the points are chosen so that stress, the sum of squared differences between the inter-point distances and the inter-sample disparities, is minimised.

SHORTCUT · D

SCREENSHOT · [3.7](#)

ALTERNATIVE TO · [PCO](#), [Identity transformation](#), [Monotone regression](#)

REFERENCES · [Borg and Groenen \(2005, Sections 9.1, 9.6\)](#)

Lets the user select the spline transformation.

***Total number of knots***

The total number of spline knots, including the two exterior knots.

DETAIL · Between each successive pair of knots, a polynomial of degree *Spline degree* is fit.

DEFAULT VALUE · 2

REFERENCES · [Borg and Groenen \(2005, Section 9.6\)](#)

***Spline degree***

The degree of the polynomial of the spline transformation.

DETAIL · Between each successive pair of knots, a polynomial of degree *Spline degree* is fit.

DEFAULT VALUE · 2

REFERENCES · [Borg and Groenen \(2005, Section 9.6\)](#)

**Default**

Reverts the options to their default values.

**OK**

Saves the options, returns to the [GUI](#), and starts the [MDS](#) iteration process.

**Cancel**

Cancels the changes made since the dialogue box was opened, and returns to the [GUI](#).

◦ **Primary approach to ties**

If selected, equality in dissimilarities need not translate to equality in disparities

in monotone regression.

DETAIL · Only available when [Monotone regression](#) is selected.

ALTERNATIVE TO · [Secondary approach to ties](#)

REFERENCES · [Borg and Groenen \(2005, Section 9.4\)](#)

- **Secondary approach to ties**

If selected, equality in dissimilarities implies equality in disparities in monotone regression.

DETAIL · Only available when [Monotone regression](#) is selected.

ALTERNATIVE TO · [Primary approach to ties](#)

REFERENCES · [Borg and Groenen \(2005, Section 9.4\)](#)

- **In terms of principal axes**

If selected, newly converged [MDS](#) configurations are rotated to be in terms of their principal axes.

DETAIL · Since scaling techniques are invariant to rotation (amongst other things), expressing [MDS](#) solutions in terms of their principal axes can make different configurations more comparable.

REFERENCES · [Borg and Groenen \(2005, Section 24.1\)](#)

- **Axes**

Determines the axes to be shown along with the points determined from the [Points](#) menu.

DETAIL · As opposed to the biplots of the [Joint](#) menu, the [Points](#) and [Axes](#) menus are used together. The options of the [Points](#) menu fix the points, while the options of the [Axes](#) menu fix the axes. The available axes depend on the choice of distance metric and the scaling technique from the [Points](#) menu.

- ▷ **None**

No biplot axes are displayed, only points.

SHORTCUT · 0

ALTERNATIVE TO · [PCA](#), [Covariance/Correlation](#), [CVA](#), [Regression](#), [Procrustes](#), [Circular non-linear](#)

- ▷ **Regression**

Regression biplot axes are shown.

DETAIL · Not available when the distance metric is Mahalanobis and the scaling technique is [PCO](#).

SHORTCUT · 4

ALTERNATIVE TO · [PCA](#), [Covariance/Correlation](#), [CVA](#), [None](#), [Procrustes](#), [Circular non-linear](#)

REFERENCES · [Gower and Hand \(1996, Sections 3.3.2, 3.4.3\)](#), [Cox and Cox \(2001, Section 3.7\)](#)

- ▷ **Procrustes**

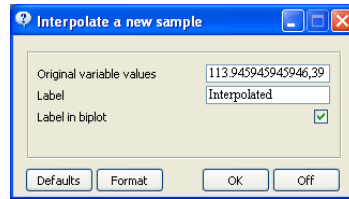
Procrustes biplot axes are shown.

DETAIL · Not available when the distance metric is Mahalanobis and the scaling technique is [PCO](#).

SHORTCUT · 5

ALTERNATIVE TO · [PCA](#), [Covariance/Correlation](#), [CVA](#), [None](#), [Regression](#), [Circular non-linear](#)

REFERENCES · [Gower and Hand \(1996, Sections 3.3.1, 3.4.2, A.10.2\)](#), [Gower and Dijksterhuis \(2004, p. 57\)](#)



Screenshot 3.8: The *Additional* → *Interpolate* → *A new sample* dialogue box.

▷ **Circular non-linear**

Circular non-linear biplot axes are shown.

DETAIL · Only available when the points are determined by [PCO](#), except when the distance metric is Mahalanobis.

SHORTCUT · 6

ALTERNATIVE TO · [PCA](#), [Covariance/Correlation](#), [CVA](#), [None](#), [Regression](#), [Procrustes](#)

REFERENCES · [Gower and Harding \(1988\)](#), [Gower and Hand \(1996, Chapter 6\)](#), [Gower and Ngouenet \(2005\)](#)

▷ **Default**

Selects the default biplot type from the Axes menu.

DETAIL · The default biplot type depends on the choice of distance metric and scaling technique from the [Points](#) menu.

• **Additional**

Additional descriptors can be included in [biplots](#).

DETAIL · When the entries of the [Additional](#) menu appear in the [legend](#), the group names are preceded by short prefixes. The prefixes are as follows: SGM for Sample Group Mean; CH for Convex Hull; AB for Alpha-Bag; TM for Tukey Median; and CR for Classification Region.

▷ **Interpolate**

Allows for the interpolation of additional points onto [biplots](#).

◦ **A new sample...**

Allows a new sample to be interpolated onto the currently displayed [biplot](#).

DETAIL · Not available if there are no axes (as opposed to the axes being hidden).

SHORTCUT · Ctrl+N

SCREENSHOT · [3.8](#)

REFERENCES · [Gower and Hand \(1996, Sections 2.3, 6.3.1\)](#)

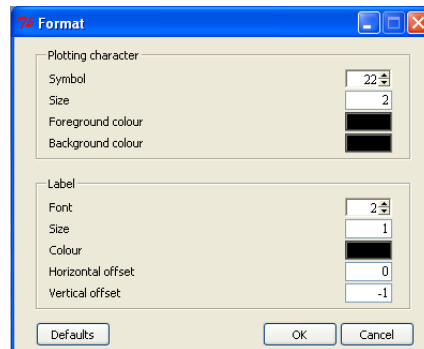
***Original variable values***

The variable values of the sample which is to be interpolated.

DETAIL · The variable values are given in terms of the units of the original variables, and in that order. The variable values are separated by commas, without spaces. The variable values of variables that have been dragged to the [kraal](#) are not entered. If axes are dragged back onto the [biplot](#) from the [kraal](#), the option is disabled.

DEFAULT VALUE · The mean values of the non-[kraal](#) variables.





Screenshot 3.9: The *Additional* → *Interpolate* → *A new sample* → *Format* dialogue box.

### ***Label***

The label to be used to indicate the interpolated point in the [biplot](#) or the [legend](#).

DEFAULT VALUE · Interpolated

### ***Label in biplot***

If checked, shows the interpolated point's label in the [biplot](#) itself. Otherwise the label is shown in the [legend](#).

DEFAULT VALUE · checked

### **Defaults**

Reverts the options to their default values.

### **Format**

*See the next framed section.*

### **OK**

Saves the options, returns to the [GUI](#), and redraws the currently displayed [biplot region](#) with the interpolated point.

### **Off**

Disables the option, and returns to the [GUI](#), not showing the interpolated point.

## **Format**

Allows various relevant graphical parameters to be customised.

SCREENSHOT · [3.9](#)

### **Plotting character**

Lets the user change the graphical parameters of the of the interpolated point.

### ***Symbol***

Sets the symbol used to represent the interpolated point.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · 22

### ***Size***

Sets the size of the interpolated point.

DETAIL · Corresponds to R's `cex` argument. A larger value results in a larger point. Possible values: positive real numbers.

DEFAULT VALUE · 2

***Foreground colour***

Sets the exterior colour of the interpolated point.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

***Background colour***

Sets the interior colour of the interpolated point.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

***Label***

Lets the user change the graphical parameters of the interpolated point label.

***Font***

Sets the font of the interpolated point label.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 2

***Size***

Sets the size of the interpolated point label.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 1

***Colour***

Sets the colour of the interpolated point label.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

***Horizontal offset***

Sets the horizontal offset of the interpolated point label from the interpolated point.

DETAIL · The interpolated point label is shifted horizontally from the interpolated point with this multiple of the width of the letter 'x' (in the selected font size). Positive values shift the label to the right; negative values shift the label to the left.

DEFAULT VALUE · 0

***Vertical offset***

Sets the vertical offset of the interpolated point label from the interpolated point.

DETAIL · The interpolated point label is shifted vertically from the interpolated point with this multiple of the height of the letter 'x' (in the selected font size). Positive values shift the label towards the top; negative values shift the label towards the bottom.

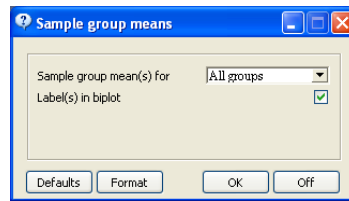
DEFAULT VALUE · -1

***Defaults***

Reverts the options to their default values.

***OK***

Saves the options and returns to the [A new sample](#) dialogue box.



Screenshot 3.10: The *Additional* → *Interpolate* → *Sample group means* dialogue box.

### Cancel

Cancels the changes made since the dialogue box was opened, and returns to the [A new sample](#) dialogue box.

### o Sample group means...

Interpolates one or more of the sample group means as points.

DETAIL · This option is especially important for [CVA](#) biplots, where the optimality criterion is in terms of separation of the group means. If the sample group mean labels are shown in the [legend](#), the group names are preceded by the prefix SGM for ‘Sample Group Mean’. Not available if there are no axes (as opposed to the axes being hidden).

SCREENSHOT · [3.10](#)

REFERENCES · [Gower and Hand \(1996, Sections 2.3, 6.3.1\)](#)

### *Sample group mean(s) for*

Sets the group(s) of points for which sample group means must be displayed.

DETAIL · Possible options: All samples (the single overall mean is shown), all groups (the mean of each group is shown), or a specific group.

DEFAULT VALUE · All groups

### *Label(s) in biplot*

If checked, shows the sample group mean labels in the [biplot](#) itself. Otherwise the labels are shown in the [legend](#).

DEFAULT VALUE · checked

### Defaults

Reverts the options to their default values.

### Format

*See the next framed region.*

### OK

Saves the options, returns to the [GUI](#), and redraws the currently displayed [biplot region](#) with the sample group mean(s).

### Off

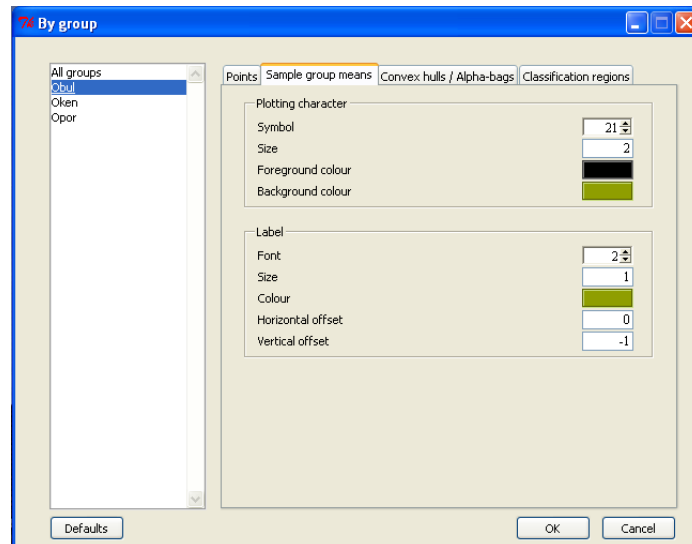
Disables the option, and returns to the [GUI](#), not showing sample group mean(s).

### Format

Allows various graphical parameters to be set by group.

DETAIL · The same dialogue box can be obtained from the *Sample group means* tab of the [Format](#) → [By group](#) dialogue box.

SCREENSHOT · [3.11](#)



Screenshot 3.11: The *Additional* → *Interpolate* → *Sample group means* → *Format* dialogue box. This is also the *Sample group means* tab of the *Format* → *By group* dialogue box

### Plotting character

Lets the user change the graphical parameters of the point that represent the sample group mean, by group.

#### **Symbol**

Sets the symbol used to represent the sample group mean, by group.

DETAIL · Corresponds to R's `pch` argument. Possible values: NA, 0, ..., 25.

DEFAULT VALUE · If there is only one group, 22. Otherwise the values are recycled by group with the values 21 to 25.

#### **Size**

Sets the size of the point that represents the sample group mean, by group.

DETAIL · Corresponds to R's `cex` argument. A larger value results in a larger point. Possible values: positive real numbers.

DEFAULT VALUE · 2

#### **Foreground colour**

Sets the exterior colour of the point that represents the sample group mean, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · "black"

#### **Background colour**

Sets the interior colour of the sample group means, by group.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "red". Otherwise equally spaced colours from the `hcl` spectrum.

#### **Label**

Lets the user change the graphical parameters of the sample group mean labels, by group.

**Font**

Sets the font of the sample group mean label, by group.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 2

**Size**

Sets the size of the sample group mean label, by group.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 1

**Colour**

Sets the colour of the sample group mean label, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "black". Otherwise equally spaced colours from the `hcl` spectrum.

**Horizontal offset**

Sets the horizontal offset of the sample group mean label from the corresponding sample group mean, by group.

DETAIL · The sample group mean label is shifted horizontally from the sample group mean with this multiple of the width of the letter 'x' (in the selected font size). Positive values shift the labels to the right; negative values shift the labels to the left.

DEFAULT VALUE · 0

**Vertical offset**

Sets the vertical offset of the sample group mean label from the corresponding sample group mean, by group.

DETAIL · The sample group mean label is shifted vertically from the sample group mean with this multiple of the height of the letter 'x' (in the selected font size). Positive values shift the label towards the top; negative values shift the label towards the bottom.

DEFAULT VALUE · -1

**Defaults**

Reverts the options of all the tabs of the dialogue box to their default values.

**OK**

Saves the options of all the tabs of the dialogue box, and returns to the [Sample group means](#) dialogue box.

**Cancel**

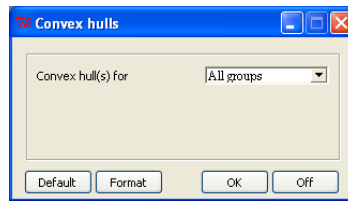
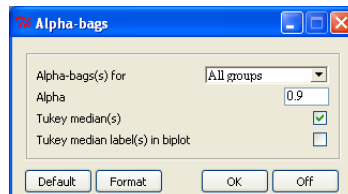
Cancels the changes made since the dialogue box was opened, and returns to the [Sample group means](#) dialogue box.

▷ **Convex hulls...**

Lets the user superimpose convex hulls around one or more of the groups of points.

DETAIL · Convex hulls may be drawn around all the points, around each group, or around a specific group. If the convex hull labels are shown in the [legend](#), the group names are preceded by the prefix CH for 'Convex Hull'.

SCREENSHOT · [3.12](#)

Screenshot 3.12: The *Additional* → *Convex hulls* dialogue box.Screenshot 3.13: The *Additional* → *Alpha-bags* dialogue box.

ALTERNATIVE TO · [Alpha-bags](#)

REFERENCES · See the R help file of the `chull` function.

### ***Convex hull(s) for***

The group(s) of points for which convex hulls must be drawn.

DETAIL · Possible options: All points (a single convex hull is drawn around all points), All groups (a convex hull is drawn around each group), or a specific group.

DEFAULT VALUE · All groups

### **Defaults**

Reverts the options to their default values.

### **Format**

*The same dialogue box can be obtained from the Convex hulls / Alpha-bags tab of the [Format](#) → [By group](#) dialogue box. Discussed under [Alpha-bags](#).*

### **OK**

Saves the option, returns to the [GUI](#), and redraws the currently displayed [biplot region](#) with the convex hull(s).

### **Off**

Disables the option, and returns to the [GUI](#), not showing convex hulls.

## ▷ **Alpha-bags...**

Lets the user superimpose alpha-bags around one or more of the groups of points.

DETAIL · Alpha-bags may be drawn around all the points, around each group, or around a specific group. Alpha-bags are closely related to bagplots which can be considered to be two-dimensional boxplots. Alpha-bags enclose approximately the inner  $100\alpha\%$  of the points of a group. If the alpha-bag labels are shown in the [legend](#), the group names are preceded by the prefix AB for ‘Alpha-Bag’. If the Tukey median labels are shown in the legend, the group names are preceded by the prefix TM for ‘Tukey Median’.

SCREENSHOT · [3.13](#)

ALTERNATIVE TO · [Convex hulls](#)

REFERENCES · [Rousseeuw \*et al.\* \(1999\)](#), [Gardner \(2001\)](#), [Wurz, Le Roux, Gardner and Deacon \(2003\)](#)

### ***Alpha-bag(s) for***

The group(s) of points for which alpha-bags must be drawn.

DETAIL · Possible options: All points (a single alpha-bag is drawn around all points), All groups (an alpha-bag is drawn around each group), or a specific group.

DEFAULT VALUE · All groups

### ***Alpha***

The value of alpha for the alpha-bags to be shown.

DETAIL · Approximately the inner 100 $\alpha$ % of the points of the group are enclosed in an alpha-bag.

DEFAULT VALUE · 0.9

### ***Tukey median(s)***

If checked, the tukey median(s) of the groups are also shown.

DEFAULT VALUE · checked

REFERENCES · [Rousseeuw \*et al.\* \(1999\)](#), [Gardner \(2001\)](#)

### ***Tukey median label(s) in biplot***

If checked and Tukey median(s) are shown, the Tukey median labels are shown in the [biplot](#), rather than in the [legend](#).

DETAIL · Approximately the inner 100 $\alpha$ % of the points of the group are enclosed in an alpha-bag.

DEFAULT VALUE · clear

### **Defaults**

Reverts the options to their default values.

### **Format**

*See the next framed section.*

### **OK**

Saves the options, returns to the [GUI](#) and redraws the [biplot region](#) with the alpha-bags as chosen.

### **Off**

Disables the option, and returns to the [GUI](#), without alpha-bags.

### **Format**

Allows various graphical parameters to be set by group.

DETAIL · The same dialogue box can be obtained from the *Convex hulls / Alpha-bags* tab of the [Format → By group](#) dialogue box. The dialogue box is the same for convex hulls.

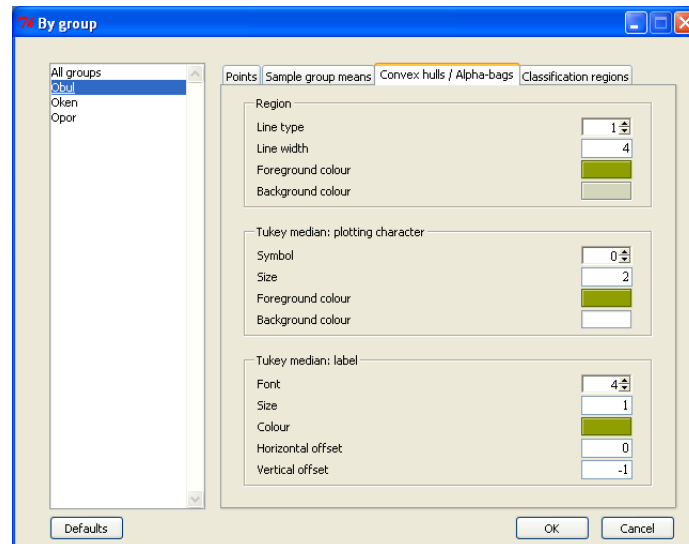
SCREENSHOT · [3.14](#)

### **Region**

Lets the user change graphical parameters associated with convex hulls or alpha-bags.

### ***Line type***

Sets the type of line used to draw a convex hull or alpha-bag around a group



Screenshot 3.14: The *Additional* → *Convex hulls / Alpha-bags* → *Format* dialogue box. This is also the *Convex hulls / Alpha-bags* tab of the *Format* → *By group* dialogue box.

of points, by group.

DETAIL · Corresponds to R's `lty` argument. Possible values: 0, ..., 6.

DEFAULT VALUE · 1

### ***Line width***

Sets the width of the convex hull or alpha-bag, by group.

DETAIL · Corresponds to R's `lwd` argument. Larger values result in wider border for convex hulls and alpha-bags. Possible values: positive real numbers.

DEFAULT VALUE · 4

### ***Foreground colour***

Sets the exterior colour of the convex hull or alpha-bag, by group.

DETAIL · Corresponds to R's `col` argument.

DEFAULT VALUE · If there is only one group, `#919191`. Otherwise equally spaced colours from the `hcl` spectrum.

### ***Background colour***

Sets the interior colour of the convex hull or alpha-bag, by group.

DETAIL · Corresponds to R's `bg` argument.

DEFAULT VALUE · If there is only one group, `#D4D4D4`. Otherwise equally spaced colours from the `hcl` spectrum.

### **Tukey median: Plotting character**

Lets the user change the graphical parameters of the Tukey medians, by group.

#### ***Symbol***

Sets the symbol used to represent the Tukey medians, by group.

DETAIL · Corresponds to R's `pch` argument. Possible values: `NA`, 0, ..., 25.

DEFAULT VALUE · 0

#### ***Size***

Sets the size of the Tukey medians, by group.

DETAIL · Corresponds to R's `cex` argument. A larger value results in a larger



point. Possible values: positive real numbers.

DEFAULT VALUE · 2

### ***Foreground colour***

Sets the exterior colour of the Tukey medians, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "red". Otherwise equally spaced colours from the `hcl` spectrum.

### ***Background colour***

Sets the interior colour of the Tukey medians, by group.

DETAIL · Corresponds to R's `bg` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · NA

### **Tukey median: label**

Lets the user change the graphical parameters of the Tukey median labels, by group.

#### ***Font***

Sets the font of the Tukey median label, by group.

DETAIL · Corresponds to R's `font` argument. Possible values: 1: regular; 2: bold; 3: italic; 4: bold italic.

DEFAULT VALUE · 4

#### ***Size***

Sets the size of the Tukey median label, by group.

DETAIL · Corresponds to R's `cex` argument. Larger values result in larger text. Possible values: positive real numbers.

DEFAULT VALUE · 1

#### ***Colour***

Sets the colour of the Tukey median label, by group.

DETAIL · Corresponds to R's `col` argument. Can be changed by clicking the colour, producing a standard colour selection dialogue box.

DEFAULT VALUE · If there is only one group, "black". Otherwise equally spaced colours from the `hcl` spectrum.

#### ***Horizontal offset***

Sets the horizontal offset of the Tukey median label from the corresponding Tukey median, by group.

DETAIL · The Tukey median label is shifted horizontally from the Tukey median with this multiple of the width of the letter 'x' (in the selected font size). Positive values shift the labels to the right; negative values shift the labels to the left.

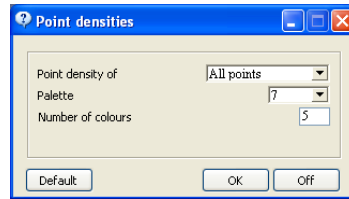
DEFAULT VALUE · 0

#### ***Vertical offset***

Sets the vertical offset of the Tukey median label from the corresponding Tukey median.

DETAIL · The Tukey median label is shifted vertically from the Tukey median with this multiple of the height of the letter 'x' (in the selected font size). Positive values shift the label towards the top; negative values shift the label towards the bottom.

DEFAULT VALUE · -1



Screenshot 3.15: The *Additional* → *Point densities* dialogue box.

### Defaults

Reverts the options of all the tabs of the dialogue box to their default values.

### OK

Saves the options of all the tabs of the dialogue box, and returns to the [Alpha-bags](#) dialogue box.

### Cancel

Cancels the changes made since the dialogue box was opened, and returns to the [Alpha-bags](#) dialogue box.

## ▷ Point densities...

Lets the user have point density estimates as a background to the [biplot](#).

SCREENSHOT · [3.15](#)

ALTERNATIVE TO · [Classification regions](#)

REFERENCES · [Wand \(2008\)](#), [Blasius et al. \(2008\)](#)

### *Point density of*

Sets the group of points on which the point densities are to be based.

DETAIL · Possible options: All points, or a specific group.

DEFAULT VALUE · All points

### *Palette*

The colour palette in which the point densities are represented.

DETAIL · Possible options: Terrain, Heat, 1, ..., 8

DEFAULT VALUE · 7

### *Number of colours*

The number of distinct colours to include in the palette.

DETAIL · The higher the number, the smoother the image. The lower the image, the easier to distinguish between different levels.

DEFAULT VALUE · 5

### Defaults

Reverts the options to their default values.

### OK

Saves the options, returns to the [GUI](#) and redraws the [biplot region](#) with the point density estimates as chosen.

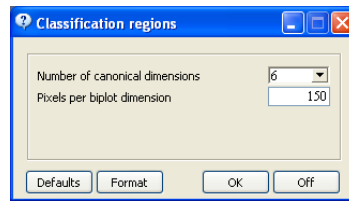
### Off

Disables the option, and returns to the [GUI](#), without point density estimates.

## ▷ Classification regions...

Draws classification regions in the background to a [CVA](#) biplot.

DETAIL · Pixels are coloured in according to the closest group mean in a specified



Screenshot 3.16: The *Additional* → *Classification regions* dialogue box.

number of canonical dimensions. If the classification region labels are shown in the [legend](#), the group names are preceded by the prefix CR for ‘Classification Region’. The option is only available for [CVA](#) biplots.

SCREENSHOT · [3.16](#)

ALTERNATIVE TO · [Point densities](#)

REFERENCES · [Gower and Hand \(1996, Section 7.3.2\)](#), [Gardner and Le Roux \(2005\)](#)

### ***Number of canonical dimensions***

The number of canonical dimensions in which classification are to be made.

DETAIL · From 1, . . . , min(the number of variables, one less than the number of groups).

DEFAULT VALUE · The maximum value.

### ***Pixels per biplot dimension***

This number of pixels squared are classified into one of the groups and colour-coded.

DETAIL · The larger the number, the finer the image, but the longer the time taken to produce the image and the more memory required. The smaller the number, the quicker the image is produced, but the grainier the image becomes.

DEFAULT VALUE · 150

### **Default**

Reverts the option to its default value.

### **Format**

*See the next framed region.*

### **OK**

Saves the options, returns to the [GUI](#) and redraws the [biplot region](#) with the classification regions shown.

### **Off**

Disables the option, and returns to the [GUI](#), without classification regions.

### **Format**

Allows various graphical parameters to be set by group.

DETAIL · The same dialogue box can be obtained from the *Classification regions* tab of the [Format](#) → [By group](#) dialogue box.

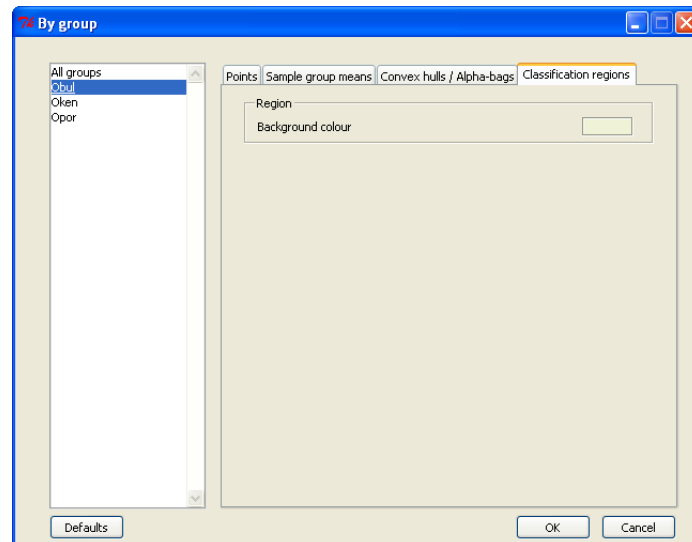
SCREENSHOT · [3.17](#)

### **Region**

#### ***Background colour***

The background colour of the group’s classification region.

DETAIL · Equally spaced colours from the [hcl](#) spectrum.



Screenshot 3.17: The *Additional* → *Classification regions* → *Format* dialogue box. This is also the *Classification regions* tab in the *Format* → *By group* dialogue box.

- ▷ **Clear all**  
Disables all additional descriptors.  
SHORTCUT · Ctrl+L

A standard dialogue box appears. If the user confirms, all the additional descriptors are disabled. Otherwise, the user is returned to the GUI with no changes made.

- **Help**

Some help options.

- ▷ **Manual (in PDF)**  
Opens this manual if possible in Windows.  
SHORTCUT · F1
- ▷ **Homepage**  
Opens the package homepage at <http://biplotgui.r-forge.r-project.org/> if an Internet connection is available.
- ▷ **Show pop-up help**  
If selected, pop-up help is shown as the mouse cursor is hovered over the major elements of the main view of the GUI.
- ▷ **About...**  
Shows information about the author, version and license.

- **Biplot region**

Contains the [biplot](#), optional [title](#), and optional [legend](#).

DETAIL · The biplot region is located towards the left of the GUI. The biplot itself is positioned at the centre of the biplot region. An optional title is shown above the biplot when [View](#) → [Show title](#) is selected. An optional legend may be shown below the biplot.

The biplot region is responsive to mouse clicks and motion. Different pop-up menus appear when right clicking [inside the biplot](#), [on a point](#), [on an axis](#), or [outside the biplot](#).

Depending on how the GUI has been resized onscreen, the proportions within the biplot region onscreen may differ from the proportions in biplot regions that have been [saved](#),

copied, printed or shown in external windows. To ensure consistency, saved and copied biplot regions always have both their width and height set to 20.32 centimeters (8 inches). Two-dimensional external-window biplot regions always have both their width and height set to 17.78 centimeters (7 inches). This is the default size of R graphs.

- **Title**

Provides a [title](#) to the [biplot](#).

DETAIL · The title is only shown if [View](#) → [Show title](#) is selected. The default title depends on the currently displayed biplot. The biplot retains the same size and relative position, irrespective of whether or not a title is shown.

- **Biplot**

A graph that displays samples as points, and variables as calibrated axes.

DETAIL · This is the graph of main interest. Right clicking on a point, on an axis, or on white space produces pop-up menus. Points and axes may be dragged from the biplot into the [kraal](#), and be dragged back onto the biplot from the [kraal](#).

REFERENCES · [Gabriel \(1971\)](#), [Gower and Hand \(1996\)](#)

- **Legend**

A legend to the elements which appear in the [biplot](#).

DETAIL · If necessary, a [legend](#) is provided below the biplot. The legend can identify point groups, axes, an interpolated point, sample group means, convex hulls, alpha-bags, Tukey medians and classification regions, in that order. All these elements can separately be included or excluded from the legend. The legend can contain a maximum of 16 entries at any one time. If there are more than 16 entries, only the first 16 are shown initially. The succeeding set of entries can be shown by clicking [View](#) → [Show next legend entries](#) or right clicking inside the biplot region but outside of the biplot, and choosing the [Show next legend entries](#) option. The keyboard shortcut is Ctrl++. Similar options are available for the preceding entries. All legend entries are restricted to be 14 characters long.

When the entries of the Additional menu appear in the legend, the group names are preceded by short prefixes. The prefixes are as follows: SGM for Sample Group Mean; CH for Convex Hull; AB for Alpha-Bag; TM for Tukey Median; CR for Classification Region.

- **Inner pop-up menu**

Provides access to biplot options.

DETAIL · This pop-up menu appears when the user right clicks inside the [biplot](#) (as opposed to the [biplot region](#)), but not on a point or on an axis.

- ▷ **Zoom in**

Zooms in around the right clicked position.

DETAIL · The biplot is enlarged and the focus is shifted so that the position which was right clicked to produce the pop-up menu appears at the centre of the biplot.

- ▷ **Zoom out**

Zooms out from the right clicked position.

DETAIL · The biplot is reduced in size and the focus is shifted so that the position which was right clicked to produce the pop-up menu appears at the centre of the [biplot](#).

- ▷ **Reset zoom**

Resets the [biplot](#) to its original zoom factor.

- ▷ **Don't predict**  
 No dynamic variable value prediction takes place.  
 DETAIL · Not shown if there are no axes (as opposed to the axes being hidden).  
 ALTERNATIVE TO · [Predict cursor positions](#), [Predict points closest to cursor positions](#)
- ▷ **Predict cursor positions**  
 The variable values of the point under the cursor position are dynamically predicted.  
 DETAIL · For linear biplots, the orthogonal projections onto the biplot axes are shown. For non-linear biplots, circular projections are shown. The predicted variable values themselves are shown in the [predictions tab](#). Not available when the axes are hidden, or if the biplot is interpolative rather than predictive. Not shown when there are no axes.  
 ALTERNATIVE TO · [Don't predict](#), [Predict points closest to cursor positions](#)  
 REFERENCES · ([Gower and Hand, 1996](#), Sections 2.3, 6.3.2)
- ▷ **Predict points closest to cursor positions**  
 The variable values of the point closest to the cursor position are dynamically predicted.  
 DETAIL · For linear biplots, orthogonal projections onto the biplot axes are shown. For non-linear biplots, circular projections are shown. The predicted variable values themselves are shown in the [Predictions tab](#). Not available when the points are hidden, the axes are hidden, or if the biplot is interpolative rather than predictive. Not shown when there are no axes.  
 ALTERNATIVE TO · [Don't predict](#), [Predict cursor positions](#)  
 REFERENCES · ([Gower and Hand, 1996](#), Sections 2.3, 6.3.2)
- ▷ **Remove axis highlight**  
 If an axis has been highlighted, this option removes the highlight.  
 DETAIL · Only available if an axis has been highlighted. Axes are highlighted by right clicking them and selecting [Highlight](#) from the pop-up menu. Not shown when there are no axes (as opposed to the axes being hidden).
- ▷ **Format by group...**  
*The same as [Format](#) → [By group](#) in the [menu bar](#).*
- ▷ **Format axes...**  
*The same as [Format](#) → [Axes](#) in the [menu bar](#).*  
 DETAIL · Not shown when there are no axes (as opposed to the axes being hidden).
- ▷ **Save as**  
*The same as [File](#) → [Save as](#) in the [menu bar](#)*
- ▷ **Copy**  
*The same as [File](#) → [Copy](#) in the [menu bar](#)*
- ▷ **Print...**  
*The same as [File](#) → [Print](#) in the [menu bar](#)*
- **Point pop-up menu**  
 Provides access to options associated with points.  
 DETAIL · This pop-up menu appears when the user right clicks a point inside the [biplot](#). A point or axis is under the mouse if the mouse cursor changes from an arrow to a hand.
  - ▷ **Send to kraal**  
 Sends the point which was right clicked to the [kraal](#).  
 DETAIL · Sending a point to the [kraal](#) temporarily removes it from consideration. The [biplot region](#) and [diagnostic tabs](#) will automatically be updated. Points and axes may also be dragged from the [biplot](#) to the [kraal](#).

- ▷ **Format...**  
Opens the *Points* tab of the [Format → By group](#) dialogue box at the group of the point that was right clicked.
- **Axis pop-up menu**  
Provides access to options associated with axes.  
DETAIL · This pop-up menu appears when the user right clicks an axis inside the [biplot](#). A point or axis is under the mouse if the mouse cursor changes from an arrow to a hand.
  - ▷ **Highlight**  
Highlights the axis which was right clicked.  
DETAIL · This option highlights the axis which was right clicked by greying the other axes in the [biplot region](#) and [diagnostic tabs](#). By default, the variable values of the highlighted axis are also then shown in the [biplot](#). An axis highlight may be removed by right clicking inside the biplot and selecting [Remove axis highlight](#) from the pop-up menu. The highlight is automatically removed if the highlighted axis is moved to the [kraal](#).
  - ▷ **Send to kraal**  
Sends the axis which was right clicked to the [kraal](#).  
DETAIL · Sending an axis to the [kraal](#) temporarily removes it from consideration. The [biplot region](#) and [diagnostic tabs](#) are automatically updated. At least three axis must be left in the [biplot](#).
  - ▷ **Format...**  
Opens the [Format → Axes](#) dialogue box at the axis that was right clicked.
- **Outer pop-up menu**  
Provides access to biplot options.
  - ▷ **Show title**  
*The same as [View → Show title in the menu bar](#)*
  - ▷ **Format title...**  
*The same as [Format → Title in the menu bar](#)*
  - ▷ **Show group labels in legend**  
*The same as [View → Show group labels in legend in the menu bar](#).*
  - ▷ **Don't show axis labels**  
*The same as [View → Don't show axis labels in the menu bar](#).*  
DETAIL · Not shown when there are no axes (as opposed to the axes being hidden).
  - ▷ **Show clinging axis labels**  
*The same as [View → Show clinging axis labels in the menu bar](#).*  
DETAIL · Not shown when there are no axes (as opposed to the axes being hidden).
  - ▷ **Show axis labels in legend**  
*The same as [View → Show axis labels in legend in the menu bar](#).*  
DETAIL · Not shown when there are no axes (as opposed to the axes being hidden).
  - ▷ **Show Additional labels in legend**  
*The same as [View → Show Additional labels in legend in the menu bar](#)*
  - ▷ **Show next legend entries**  
*The same as [View → Show next legend entries in the menu bar](#).*
  - ▷ **Show previous legend entries**  
*The same as [View → Show previous legend entries in the menu bar](#).*
  - ▷ **Save as**  
*The same as [File → Save as in the menu bar](#).*

▷ **Copy**

The same as *File → Copy* in the *menu bar*.

▷ **Print...**

The same as *File → Print* in the *menu bar*.

► **Settings box**

Allows the action of the biplot axes to specified, and data transformations to be effected.

DETAIL · The settings box is located towards the centre right of the [GUI](#).

• **Action**

Lets the user choose the action of the biplot axes.

DETAIL · Disabled when there are no axes, or the axes are hidden.

▷ **Predict**

A predictive biplot is shown.

DETAIL · Predictive biplot axes are positioned and calibrated to optimally predict variable values from the positions of points in a biplot.

ALTERNATIVE TO · [Interpolate: centroid](#), [Interpolate: vector sum](#)

REFERENCES · ([Gower and Hand, 1996](#), Sections 2.3, 6.3.2)

▷ **Interpolate: centroid**

A centroid interpolative biplot is shown.

DETAIL · Centroid interpolative biplot axes are positioned and calibrated to allow for interpolation of new samples onto an existing biplot by finding a centroid.

ALTERNATIVE TO · [Predict](#), [Interpolate: vector sum](#)

REFERENCES · [Gower and Hand \(1996, Section 5.3\)](#)

▷ **Interpolate: vector sum**

A vector sum interpolative biplot is shown.

DETAIL · Vector sum interpolative biplot axes are positioned and calibrated to allow for interpolation of new samples onto an existing biplot by finding a vector sum.

ALTERNATIVE TO · [Predict](#), [Interpolate: centroid](#)

REFERENCES · ([Gower and Hand, 1996](#), Sections 2.3, 6.3.1)

• **Transformation**

Lets the user choose from various data transformations.

DETAIL · These transformations are performed on the data passed to the `BiplotGUI` through the `Biplots` function (the `Data` argument). Data are always centred to have zero column means. Log-transformations are only available if all the non-[kraal](#) variable values of the non-[kraal](#) points are strictly positive. Irrespective of the transformation, the biplot axes are always calibrated in terms of the original variable values. In order to have biplot calibrated in terms of transformed variable values, the transformation must be performed outside of the `BiplotGUI` package in R, and passed to the `BiplotGUI` package.

▷ **Centre**

Transforms the data to have zero column means.

DETAIL · The mean of each column is subtracted from the elements of that column. The data are always centred to have zero column means.

ALTERNATIVE TO · [Centre, scale](#); [Unitise, centre](#); [Log, centre](#); [Log, centre, scale](#); [Log, unitise, centre](#)



▷ **Centre, scale**

Transforms the data to have zero column means, and then scales the data so that each column has unit variance.

DETAIL · The mean of each column is first subtracted from the elements of that column. Each column is then divided by its standard deviation.

ALTERNATIVE TO · [Centre](#); [Unitise, centre](#); [Log, centre](#); [Log, centre, scale](#); [Log, unitise, centre](#)

▷ **Unitise, centre**

Scales and shifts each column to have minimum value 0 and maximum value 1; thereafter centres to have zero column means.

DETAIL · The minimum of each column is subtracted from the elements of that column, the answers divided by the range of the (original) column.

ALTERNATIVE TO · [Centre](#); [Centre, scale](#); [Log, centre](#); [Log, centre, scale](#); [Log, unitise, centre](#)

▷ **Log, centre**

Takes natural logarithms, then transforms the data to have zero column means.

DETAIL · Natural logarithms are taken of all elements. Thereafter the mean of each column is subtracted from the elements of that column. Only available if all the non-[kraal](#) variable values of the non-[kraal](#) points are strictly positive.

ALTERNATIVE TO · [Centre](#); [Centre, scale](#); [Unitise, centre](#); [Log, centre, scale](#); [Log, unitise, centre](#)

▷ **Log, centre, scale**

Takes natural logarithms, transforms to have zero column means, then scales so that each column has unit variance.

DETAIL · Natural logarithms are taken of all elements. Thereafter the mean of each column is first subtracted from the elements of that column. Each column is then divided by its standard deviation. Only available if all the non-[kraal](#) variable values of the non-[kraal](#) points are strictly positive.

ALTERNATIVE TO · [Centre](#); [Centre, scale](#); [Unitise, centre](#); [Log, centre](#); [Log, unitise, centre](#)

▷ **Log, unitise, centre**

Takes natural logarithms, scales and shifts each column to have minimum value 0 and maximum value 1; thereafter centres to have zero column means.

DETAIL · Natural logarithms are taken of all elements. Thereafter the minimum of each column is subtracted from the elements of that column, the answers divided by the range of the (post-log) column. Only available if all the non-[kraal](#) variable values of the non-[kraal](#) points are strictly positive.

ALTERNATIVE TO · [Centre](#); [Centre, scale](#); [Unitise, centre](#); [Log, centre](#); [Log, centre, scale](#);

► **Diagnostic tabs**

Consists of tabs for diagnostic graphs, dynamic variable value predictions, and quantities for export back to R.

DETAIL · The diagnostic tabs are located towards the top right of the [GUI](#).

*Note: A known issue affects the diagnostic tabs of the [BiplotGUI](#) package. After a new biplot has been drawn, the graphs of the diagnostic tabs do not always display when the tabs are changed to them. The graphs can be seen by clicking to other tabs and back.*

- **Convergence**

If the points are determined by [MDS](#), a graph of stress values over iterations is shown.

DETAIL · If [Live updates](#) is checked, the graph is updated live. The tab is only available when the points are determined by [MDS](#).

- ▷ **Pop-up menu**

Makes various options available with respect to the graph of the convergence tab.

DETAIL · The convergence pop-up menu is obtained by right clicking the graph in the convergence tab.

- **Show title**

*The same as [View → Show title](#) in the [menu bar](#). However, it applies to the graph in the tab rather than the [biplot region](#).*

- **Format...**

*The same as [Format → Diagnostic tabs](#) in the [menu bar](#).*

- **Save as**

*The same as [File → Save as](#) in the [menu bar](#). However, it applies to the graph in the tab rather than the [biplot region](#).*

DETAIL · Diagnostic graphs are saved with the same proportions that would be used if the currently displayed biplot region were to be saved. This ensures that the graphs can be used alongside one another. Specifically, if the biplot region has a [legend](#), in the saved version of diagnostic graphs, an equivalent open space will be left. To remove the space, temporarily remove the legend from the biplot and save the diagnostic graph once more.

- **Copy**

*The same as [File → Copy](#) in the [menu bar](#). However, it applies to the graph in the tab rather than the [biplot region](#).*

DETAIL · Diagnostic graphs are copied with the same proportions that would be used if the currently displayed biplot region were to be copied. This ensures that the graphs can be used alongside one another. Specifically, if the biplot region has a [legend](#), in the copied version of diagnostic graphs, an equivalent open space will be left. To remove the space, temporarily remove the legend from the biplot and copy the diagnostic graph once more.

- **Print...**

*The same as [File → Print](#) in the [menu bar](#). However, it applies to the graph in the tab rather than the [biplot region](#).*

DETAIL · Diagnostic graphs are printed with the same proportions that would be used if the currently displayed biplot region were to be printed. This ensures that the graphs can be professionally used alongside one another. Specifically, if the biplot region has a [legend](#), in the printed version of diagnostic graphs, an equivalent open space will be left. To remove the space, temporarily remove the legend from the biplot and print the diagnostic graph once more.

- **External**

*The same as [External → As is below the biplot region](#). However, it applies to the graph in the tab rather than the [biplot region](#).*

DETAIL · External diagnostic graphs have the same proportions that would be used if the currently displayed [biplot](#) were to be placed in an external window. This ensures that the graphs can be professionally used alongside one another. Specifically, if the biplot has a [legend](#), in the diagnostic graph will have an equivalent open space. To remove the space, temporarily remove the legend and choose the External option for the diagnostic graph once more.

- **Points**

Shows graphs of goodness of fit of the points.

DETAIL · For [PCA](#) and [CVA](#) biplots, graphs of point predictivities are shown. The first axis shows the point predictivities in the first [biplot](#) dimension. Therefore, the closer a point is to the right of the graph, the better it is represented in the first dimension of the currently displayed biplot. The distance above the diagonal line represents the contribution of the second biplot dimension. Therefore, the second axis of the point predictivities graph shows the point predictivities of the first two biplot dimensions jointly. The closer a point is to the top of the graph, the better represented it is in the two dimensions of the currently displayed biplot.

When the points in a biplot are based either on [PCO](#) or [MDS](#), a Shepard diagram is shown in this tab. In a Shepard diagram, inter-sample dissimilarities are shown on the x-axis. On the y-axis, inter-point disparities are shown on the line, while inter-point distances are shown as points. The closer the inter-point distances are to the inter-point disparities, the better the fit. By default, the five worst-fitting point pairs are identified. A Shepard diagram is only shown if there are fewer than 250 non-kraal samples.

For covariance/correlation biplots, the tab is disabled.

REFERENCES · [Borg and Groenen \(2005, Section 3.3\)](#), [Gower et al. \(2008\)](#)

- ▷ **Pop-up menu**

*The same as the [convergence pop-up menu](#). However, it acts on the graphs of the [points tab](#).*

- **Groups**

Shows graphs of goodness of fit of the groups.

DETAIL · For [CVA](#) biplots, graphs of group predictivities are shown. The first axis shows the group predictivities in the first [biplot](#) dimension. Therefore, the closer a point is to the right of the graph, the better represented the corresponding group is in the first dimension of the currently displayed biplot. The distance above the diagonal line represents the contribution of the second biplot dimension. Therefore, the second axis of the group predictivities graph shows the group predictivities of the first two biplot dimensions jointly. The closer a point is to the top of the graph, the better represented the corresponding group is in the two dimensions of the currently displayed biplot.

In other cases, the tab is disabled.

REFERENCES · [Gower et al. \(2008\)](#)

- ▷ **Pop-up menu**

*The same as the [convergence pop-up menu](#). However, it acts on the graph of the [groups tab](#).*

- **Axes**

Shows graphs of goodness of fit of the axes.

DETAIL · For [PCA](#) and [CVA](#) biplots, graphs of axis predictivities are shown. The first axis shows the axis predictivities in the first [biplot](#) dimension. Therefore, the closer a point is to the right of the graph, the better represented the corresponding axis is in the first dimension of the currently displayed biplot. The distance above the diagonal line represents the contribution of the second biplot dimension. Therefore, the second axis of the axis predictivities graph shows the axis predictivities of the first two biplot dimensions jointly. The closer a point is to the top of the graph, the better represented the corresponding axis is in the two dimensions of the currently displayed biplot.

In other cases, the tab is disabled.

REFERENCES · [Gower et al. \(2008\)](#)

▷ **Pop-up menu**

*The same as the [convergence pop-up menu](#). However, it acts on the graph of the [axes tab](#).*

• **Predictions**

The tab in which live variable value predictions are shown.

DETAIL · Dynamic variable value prediction is enabled by right clicking inside the [biplot](#) and choosing either [Predict cursor positions](#) or [Predict points closest to cursor positions](#) from the pop-up menu. If [Predict cursor positions](#) is chosen, the second column of the table in the predictions tab contains the variable value predictions corresponding to the position of the mouse cursor as it moves over the biplot. If [Predict points closest to cursor positions](#) is chosen, the variable values of the point closest to the mouse cursor as it moves over the biplot, are predicted. In this case, the third column contains the actual variable values of the points. The fourth column contains the [RAE](#), which is calculated as  $(\text{prediction} - \text{actual}) / (\text{maximum actual for variable} - \text{minimum actual for variable}) \times 100$ . Biplots are not exact, but are optimal.

Not available when there are no axes, the axes are hidden, or the biplot is interpolative rather than predictive.

REFERENCES · [Gower and Hand \(1996, Sections 2.3, 6.3.2\)](#)

• **Export**

Allows various quantities to be exported back to R for further manipulation or inspection.

DETAIL · Depending on the representation in the [biplot region](#), various quantities are available for export back to R. A quantity can be displayed in the R console by clicking it and clicking the [Display in console](#) button. Alternatively, a quantity can be saved to the current R workspace by clicking it and clicking the [Save to workspace](#) button.

REFERENCES · [Gower and Hand \(1996\)](#), [Borg and Groenen \(2005\)](#)

▷ **Display in console**

Displays the quantity highlighted in the predictions tab in the R console.

DETAIL · Only available if a quantity has been highlighted in the export tab.

▷ **Save to workspace**

Saves the quantity highlighted in the predictions tab in the current R workspace under the number given in the list of quantities.

DETAIL · Only available if a quantity has been highlighted in the export tab.

► **Kraal**

Points and axes may be dragged to the kraal, temporarily removing them from consideration.

DETAIL · The kraal is located towards the bottom right of the [GUI](#). A point or axis can be removed to the kraal by first hovering the mouse cursor over it so that the cursor changes from an arrow to a hand, and then dragging the point or axis beyond the [biplot](#) borders. Alternatively, the point or axis can be right clicked, and [Send to kraal](#) selected from the pop-up menu. The [biplot region](#) and [diagnostic tabs](#) are then automatically updated as if the corresponding sample or variable were never part of the data set; the point or axis itself appears in the kraal. Many points and axes can simultaneously be kept in the kraal, but at least three axes must remain in the biplot.

The kraal itself is responsive to mouse clicks and motion. Different pop-up menus appear when right clicking [inside the kraal](#), [on a point](#), or [on an axis](#). Points and axes may be dragged around in the kraal over a grid of possible positions, or back onto the biplot. Alternatively, the buttons below the kraal may be used to send back the [points only](#), the [axes only](#), or both the [points and axes](#).

- **Kraal pop-up menu**

Shows options associated with the [kraal](#).

DETAIL · The [kraal](#) pop-up menu is obtained by right clicking the [kraal](#), excluding points and axes in the [kraal](#).

- ▷ **Return points**

Returns all the points in the [kraal](#) to the [biplot](#) and updates the biplot and the [diagnostic tabs](#).

DETAIL · Not available when there are no points in the [kraal](#).

- ▷ **Return axes**

Returns all the axes in the [kraal](#) to the [biplot](#) and updates the biplot and the [diagnostic tabs](#).

DETAIL · Not available when there are no axes in the [kraal](#).

- ▷ **Return all**

Returns all the points and axes in the [kraal](#) to the [biplot](#) and updates the biplot and [diagnostic tabs](#).

DETAIL · Not available when there are no points or axes in the [kraal](#).

- ▷ **Format by group...**

The same as [Format → By group](#) in the [menu bar](#).

- ▷ **Format axes...**

The same as [Format → Axes](#) in the [menu bar](#).

- **Kraal point pop-up menu**

Shows options associated with a point in the [kraal](#).

DETAIL · The [kraal](#) point pop-up menu is obtained by right clicking a point in the [kraal](#). When the mouse cursor is above a point or axis, the cursor changes from an arrow to a hand.

- ▷ **Return to biplot**

Returns the right clicked point to the [biplot](#) and updates the biplot and [diagnostic tabs](#).

- ▷ **Format...**

Opens the points tab of the [Format → By group](#) dialogue box at the group of the point that was right clicked.

- **Kraal axis pop-up menu**

Shows options associated with an axis in the [kraal](#).

DETAIL · The [kraal](#) axis pop-up menu is obtained by right clicking an axis in the [kraal](#). When the mouse cursor is above a point or axis, the cursor changes from an arrow to a hand.

- ▷ **Return to biplot**

Returns the right clicked axis to the [biplot](#) and updates the biplot and [diagnostic tabs](#).

- ▷ **Format...**

Opens the [Format → Axes](#) dialogue box at the axis that was right clicked.

- ▶ **Other**

Contains miscellaneous features.

DETAIL · These features are located in the strip at the bottom of the [GUI](#).

- **Progress bar**

Shows the progress while performing an action.

DETAIL · A progress bar appears at the bottom left of the screen while an action is being

performed. While the [GUI](#) is busy, no new actions should be initiated. Changing tabs is not considered an action.

- **External**

Options to display the currently displayed [biplot region](#) in an external window.

DETAIL · Whether external windows are re-used or not can be set in [File → Options](#).

- ▷ **As is**

Shows the currently displayed [biplot region](#) in an external R graph.

DETAIL · Depending on how the [GUI](#) has been resized onscreen, the proportions within an external [biplot region](#) may differ from what is shown onscreen. To ensure consistency, external biplot regions always have both their width and height set to 17.78 centimeters (7 inches). This is the default size of R graphs.

SHORTCUT · F11

- ▷ **In 3D**

Creates a three-dimensional version of the currently displayed [biplot](#) which can be dynamically navigated.

DETAIL · This option is only available for non-MDS representations so that the first two dimensions of the three-dimensional biplot corresponds to the two-dimensional biplot shown in the [GUI](#). Various options can be set in [File → Options](#). By default the left mouse button acts as a trackball for navigation, the middle mouse button allows zooming in and out, and the right mouse button sets the field of view. Not all options from the [View](#) menu or graphical parameters from the [Format](#) menu transfer to the three-dimensional biplots.

SHORTCUT · F12

REFERENCES · See the R help file of the `par3d` function of the `rgl` package ([Adler and Murdoch, 2008](#)) for details on the choices.

- **Hide**

Hides either the points or the axes of a biplot.

- ▷ **Points**

Hides the points of the [biplot](#).

- ▷ **Axes**

Hides the axes of the [biplot](#).

DETAIL · Not available when there are no axes.

- **Live updates**

Toggles between showing live updates of [MDS](#) convergence (both in the [biplot](#) and [diagnostic tabs](#)), and merely showing the graphs for the final, converged configuration.

DETAIL · It can be informative to see the [MDS](#) configuration converges. However, if checked, the [biplot region](#) and Shepard diagram is redrawn at each update, taking more time. To speed up convergence, the checkbox can be cleared. The number of iterations to the next update can be changed in [File → Options](#).

- **Stop**

Stops an [MDS](#) convergence.

DETAIL · Available while an [MDS](#) configuration is being found. Clicking it stops the iterations and proceeds with the current configuration, fitting biplot axes and all the rest. Users should be aware that such representations do not meet the optimality criteria and may therefore be misleading.

- **Return points**

Returns all the points in the [kraal](#) to the [biplot](#) and updates the biplot and the [diagnostic tabs](#).

DETAIL · Not available when there are no points in the [kraal](#).

- **Return axes**

Returns all the axes in the [kraal](#) to the [biplot](#) and updates the biplot and the [diagnostic tabs](#).

DETAIL · Not available when there are no axes in the [kraal](#).

- **Return all**

Returns all the points and axes in the [kraal](#) to the [biplot](#) and updates the biplot and [diagnostic tabs](#).

DETAIL · Not available when there are no points or axes in the [kraal](#).

# Appendix A

## History

### A.1 Version 0.0-1

29 JULY 2008. The first release. Contains support for

- Biplots: [PCA](#), covariance/correlation, [CVA](#), regression, Procrustes, circular non-linear
- Interpolation and prediction
- Scaling techniques: [PCO](#), metric [MDS](#) (identity transformation), non-metric [MDS](#) (monotone regression), semi-metric [MDS](#) (monotone spline transformation)
- Data transformations: centre; centre, scale; unitise, centre; log, centre; log, centre, scale; log, unitise, centre
- Distance metrics: Pythagoras, Square-root-of-Manhattan, Clark, Mahalanobis
- Additional descriptors: convex hulls, alpha-bags, point densities, classification regions
- Export of intermediate quantities back to R
- Diagnostic graphs: convergence; point, group and axis predictivities; Shepard diagrams
- Interactivity: variable value prediction, zooming, point and axis drag-and-drop; 3D biplots
- Customisation of graphs
- Import of data from Excel 1997–2003 files

### A.2 Version 0.0-2

4 AUGUST 2008. The first CRAN release.

- The [Help → Homepage](#) option is added
- The `CountryData` data set is renamed the `Countries` data set
- Changes are made to the package help files, including correcting the units of the GDP variable of the `Countries` data set. The variable measures ‘[PPP GDP](#) per capita in US dollars’ rather than ‘[PPP GDP](#) in trillions of US dollars’ as previously stated. However, the countries are still those with the 15 highest [PPP GDPs](#) in US dollars during 2007 without adjusting for population size.
- The manual is updated, and two new chapters included



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