BiplotGUI

Features Manual

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DRAFT

Contents

Features

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
SREENSHOT	For dialogue boxes, a reference to a screenshot
REFERENCES	References to external material

Features are indented as in the table of contents. 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.

▶ 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 59. 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.

> 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
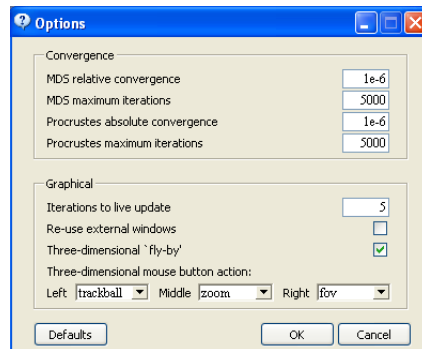
Screenshot 1: The *File → Options* dialogue box.

▷ **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 · 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

Re-use external windows

Toggles between re-using windows for external graphics, or creating new windows.

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.

DEFAULT VALUE · clear

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, 2010) 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, 2010) 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, 2010) 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 GUI settings changed during the session 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**

Lets the user 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 in their entirety. 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 are visible in their entirety. 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 that 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++
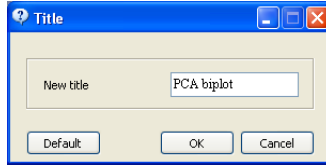
Screenshot 2: The *Format → Title* dialogue box.

▷ **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 runs counter to the spirit of biplots of the new approach. Gower and Hand (1996) call such biplots 'bad'.

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 · 2

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 dialogue box was opened, and returns to the GUI.

▷ **By group. . .**

Lets the user set graphical parameters for points, sample group means, convex hulls / alpha-bags and classification regions for a particular group, or for all groups
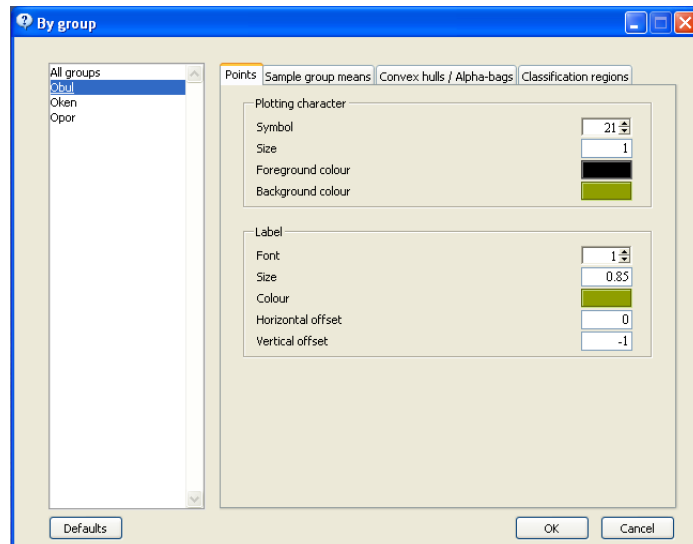
Screenshot 3: The *Points* tab of the *Format → By group* dialogue box.

simultaneously.

DETAIL · When *All groups* 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 groups. Changes to particular groups can be made by clicking the group names in the list to the left of the dialogue box. Parameter values which differ amongst groups are left blank when *All groups* is selected.

SHORTCUT · Ctrl+G

SCREENSHOT · 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
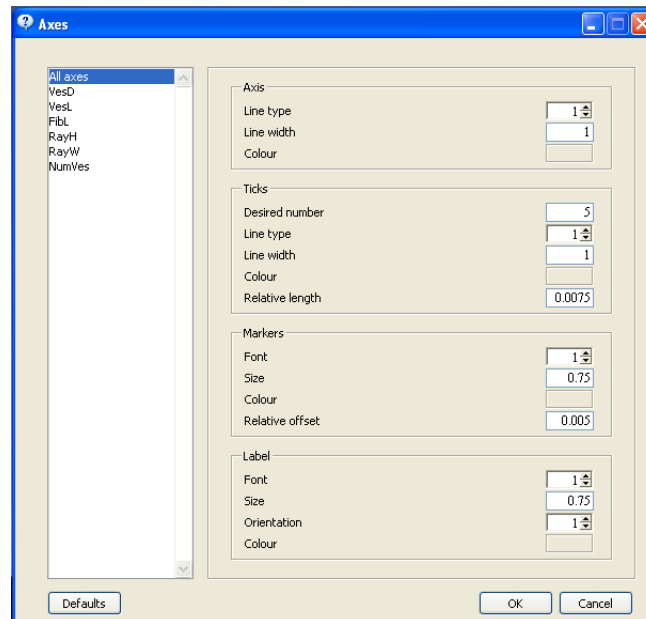
Screenshot 4: The *Format* → *Axes* dialogue box.

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. . .**

Lets the user set graphical parameters 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 · 4

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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 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 (so that the marker values increase 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
>
> **Orientation**
>
> Sets the orientation of clinging axis labels.
>
> DETAIL · Corresponds to R's `las` argument. Possible values: 0: always parallel to the biplot edge; 1: always horizontal; 2: always perpendicular to the biplot edge; 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. . .**

Lets the user set graphical parameters for variable value prediction and highlighted axes.

SCREENSHOT · 5

> **Prediction**
>
> Lets the user change the graphical parameters associated with variable value prediction.
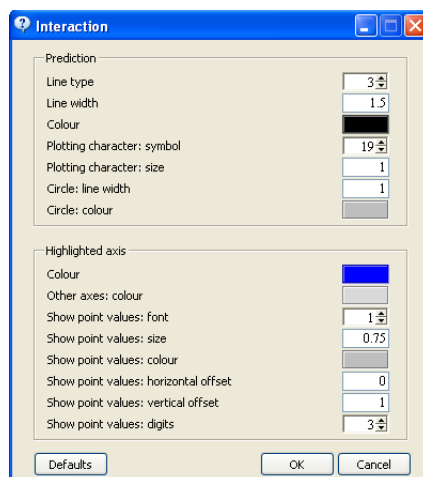
Screenshot 5: The *Format → Interaction* dialogue box.

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

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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 cirlce 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 View → 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.

<small>DEFAULT VALUE</small> · "gray75"

Show point values: horizontal offset

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

<small>DETAIL</small> · 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.

<small>DEFAULT VALUE</small> · 0

Show point values: vertical offset

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

<small>DETAIL</small> · 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.

<small>DEFAULT VALUE</small> · 1

Show point values: digits

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

<small>DETAIL</small> · Possible values: 0, . . . , 8.

<small>DEFAULT VALUE</small> · 3

Defaults

Reverts the options to their default values.

OK

Saves the options, returns to the <small>GUI</small>, and redraws the currently displayed biplot region.

Cancel

Cancels the changes made since the dialogue box was opened, and returns to the <small>GUI</small>.

▷ **Diagnostic tabs. . .**

Lets the user set graphical parameters for the graphs of the diagnostic tabs.

<small>SCREENSHOT</small> · 6

Convergence

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

Line type

Sets the line type.

<small>DETAIL</small> · Corresponds to R's `lty` argument. Possible values: 0, . . . , 6.
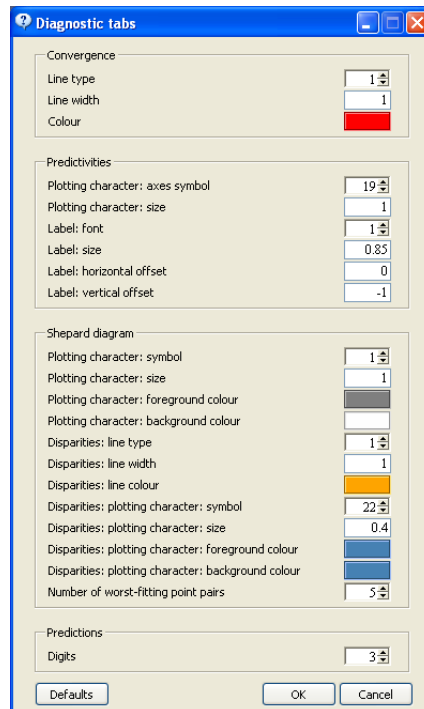
<small>DEFAULT VALUE</small> · 1

Screenshot 6: The *Format → Diagnostics* dialogue box.

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. . .**

Lets the user revert all the parameters of 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 bipot

> 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**

  Contructs 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**

  Determines 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 determine the points, while the options of the Axes menu determine the axes.

▷ **Dissimilarity metric**

Lets the user set the dissimilarity metric to be used in PCO and MDS.

DETAIL · All the dissimilarity 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 dissimilarity metric. If the axes previously selected in the Axes menu are no longer available because of the change in dissimilarity metric, the most appropriate replacement is automatically chosen.

REFERENCES · Gower and Legendre (1986), Gower and Hand (1996, Section A.5.1)

○ **Pythagoras**

The dissimilarity metric is set to Pythagoras.

DETAIL · 'Pythagoras' and 'Euclidean' are synomomous. However, to avoid confusion with the term 'Euclidean-embeddable', the term 'Pythagoras' is used rather than 'Euclidean'. Under this dissimilarity metric, the dissimilarity 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 dissimilarity metric is set to Square-root-of-Manhattan.

DETAIL · Dissimilarities under this metric are the square root of those under the Manhattan or City Block dissimilarity metric. Therefore the dissimilarity 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 dissimilarity metric is set to Clark.

DETAIL · Under this dissimilarity metric, the dissimilarity 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 dissimilarity metric is set to Mahalanobis.

DETAIL · Under this dissimilarity metric, the dissimilarity 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 the matrix with all the observations as rows.

ALTERNATIVE TO · Pythagoras, Square-root-of-Manhattan, Clark

REFERENCES · Mahalanobis (1936), Cox and Cox (2001, p. 11)

▷ **PCO**

The points are determined by PCO, with inter-sample dissimilarities calculated according to the chosen dissimilarity 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 determined by MDS, with inter-sample dissimilarities calculated according to the chosen distance metric.

REFERENCES · Cox and Cox (2001), Borg and Groenen (2005)

○ **Run**

Performs an MDS with the currently selected transformation.

DETAIL · The inter-sample disparities are taken to be the transformed inter-sample dissimilarities, calculated according to the chosen dissimilarity 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 · R

ALTERNATIVE TO · PCO

REFERENCES · Borg and Groenen (2005, Chapters 8, 9)

○ **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 dissimilarity 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, based on the chosen dissimilarity metric. In essense, 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 distances and the inter-sample

Screenshot 7: The *Points → MDS → Monotone spline transformation* dialogue box.

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, based on the chosen dissimilarity 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.
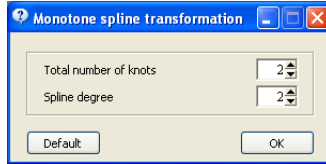
SHORTCUT · D

SCREENSHOT · 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)

○ **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.

○ **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 determine the points, while the options of the Axes menu determine the axes. The available axes depend on the choice of dissimilarity metric and the scaling technique from the Points menu.

▷ **None**

No biplot axes are shown, only points.

SHORTCUT · 0

ALTERNATIVE TO · PCA, Covariance/Correlation, CVA, Regression, Procrustes, Circular non-linear

▷ **Regression**

Shows regression biplot axes.

DETAIL · Not available when the dissimilarity 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**

Shows Procrustes biplot axes.

DETAIL · Not available when the dissimilarity 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)

▷ **Circular non-linear**

Shows circular non-linear biplot axes.

DETAIL · Only available when the points are determined by PCO, except when the dissimilarity 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 dissimilarity metric and scaling technique from the Points menu.

- **Additional**

Contains additional descriptors which can be included in the biplot.

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
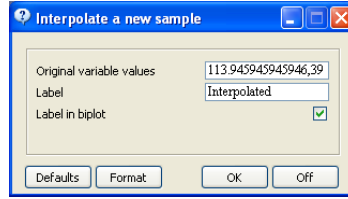
Screenshot 8: The *Additional → Interpolate → A new sample* dialogue box.

Group Mean'; CH for 'Convex Hull'; AB for 'Alpha-Bag'; TM for 'Tukey Median'; and CR for 'Classification Region'.

▷ **Interpolate**

Lets the user interpolate additional points onto the biplot.

DETAIL · Only a single new point can be interpolated at one time.

○ **A new sample. . .**

Lets the user interpolate a new sample as a point in the biplot.

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

SHORTCUT · Ctrl+N

SCREENSHOT · 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 the order of the original variables. The variable values are separated by commas, without spaces. The variable values of variables that have been dragged from the biplot into 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.

Label

The label to be used to annotate the interpolated point in the biplot or in 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.
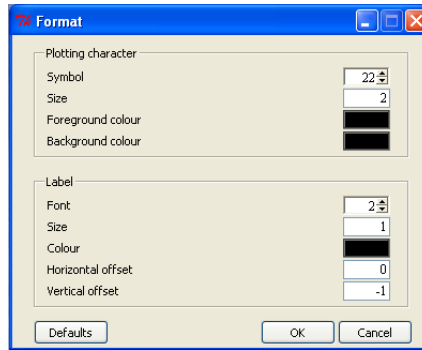
Screenshot 9: The *Additional → Interpolate → A new sample → Format* dialogue box.

OK

Saves the options, returns to the GUI, and redraws the biplot region with the interpolated point.

Off

Disables the option, and returns to the GUI, not showing the interpolated point.

Format

Lets the user set graphical parameters for interpolated samples.

SCREENSHOT · 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

Screenshot 10: The *Additional → Interpolate → Sample group means* dialogue box.
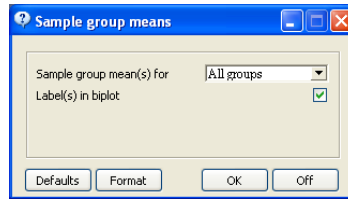

Defaults

Reverts the options to their default values.

OK

Saves the options and returns to the Additional → Interpolate → A new sample dialogue box.

Cancel

Cancels the changes made since the dialogue box was opened, and returns to the Additional → Interpolate → A new sample dialogue box.

○ **Sample group means...**

Lets the user interpolate the sample group means as points in the biplot.

DETAIL · This option is especially important in the case of 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 · 10

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

Sample group mean(s) for

Sets the group(s) of samples for which sample group means must be interpolated.

DETAIL · Possible options: All samples (the overall mean is interpolated), all groups (the mean of each group is interpolated), 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.
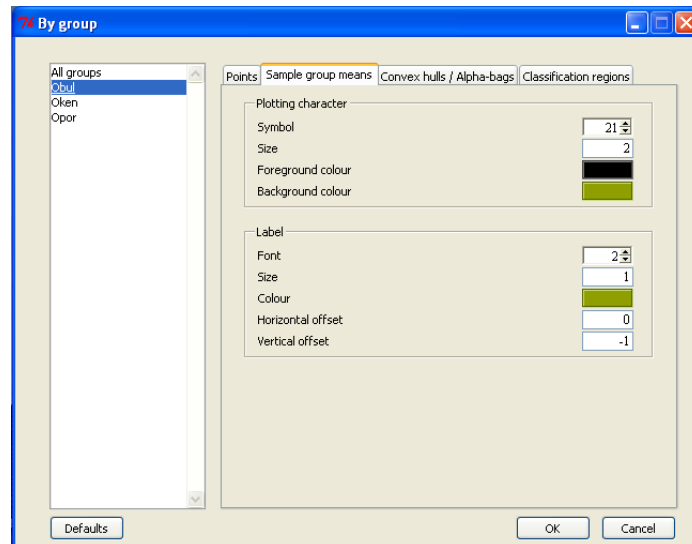
Screenshot 11: The *Additional → Interpolate → Sample group means → Format* dialogue box.
This is also the *Sample group means* tab of the *Format → By group* dialogue box

---

OK

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

Off

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

Format

Lets the user set graphical parameters for interpolated sample group means, for a particular group, or for all groups simultaneously.

SCREENSHOT · 11

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 represents 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 mean, 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 label, 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

Screenshot 12: The *Additional → Convex hulls* dialogue box.

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 Additional → Interpolate → Sample group means dialogue box.

Cancel

Cancels the changes made since the dialogue box was opened, and returns to the Additional → Interpolate → 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 of points, or around a specific group of points. If the convex hull labels are shown in the legend, the group names are preceded by the prefix CH for 'Convex Hull'.
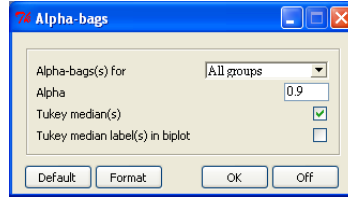
SCREENSHOT · 12

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 hull(s) must be drawn.

DETAIL · Possible options: All points (a single convex hull is drawn around all

Screenshot 13: The *Additional* → *Alpha-bags* dialogue box.

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

Discussed under Alpha-bags*.*

OK

Saves the option, returns to the GUI, and redraws the 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 of points, or around a specific group of points. Alpha-bags are closely related to bagplots which can be considered to be two-dimensional boxplots. Alpa-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 · 13

ALTERNATIVE TO · Convex hulls

REFERENCES · Rousseeuw, Ruts and Tukey (1999), Gardner (2001), Wurz, Roux, Gardner and Deacon (2003)

Alpha-bag(s) for

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

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

DEFAULT VALUE · All groups

Alpha

The value of alpha for the alpha-bag(s) 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-bag(s) as selected.

Off

Disables the option, and returns to the GUI, not showing alpha-bags.

Format

Lets the user set graphical parameters for convex hulls and alpha-bags, for a particular group, or for all groups simultaneously.

SCREENSHOT · 14

This is also the Convex hulls / Alpha-bags tab of the Format → By group dialogue box.
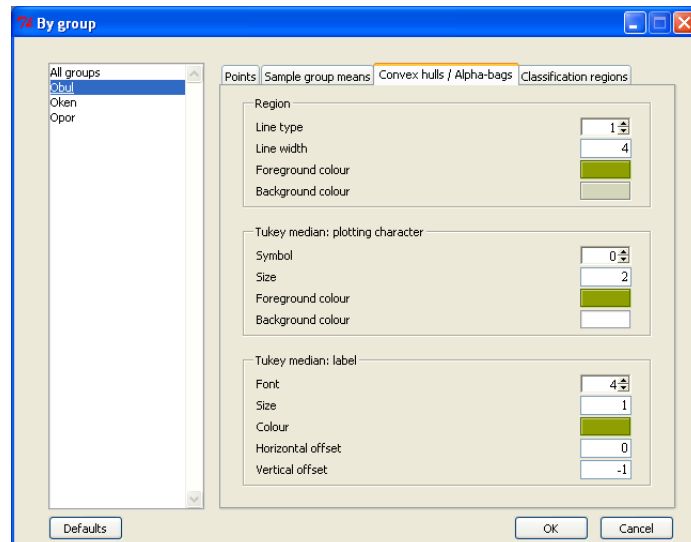
Region

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

Line type

Sets the type of line used to draw the convex hull or alpha-bag, by group.

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

DEFAULT VALUE · 1

Screenshot 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.

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 median, by group.

Symbol

Sets the symbol used to represent the Tukey median, 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 median, 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 median, 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 label, 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

41
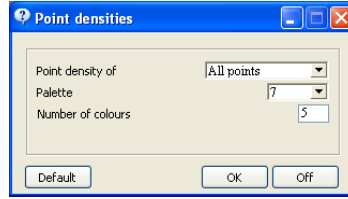
Screenshot 15: The *Additional → Point densities* dialogue box.

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

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 Additional → Convex hulls or Additional → Alpha-bags dialogue box.

Cancel

Cancels the changes made since the dialogue box was opened, and returns to the Additional → Convex hulls or Additional → Alpha-bags dialogue box.

▷ **Point densities...**

Lets the user superimpose the biplot onto a background of point density estimates.

SCREENSHOT · 15

ALTERNATIVE TO · Classification regions

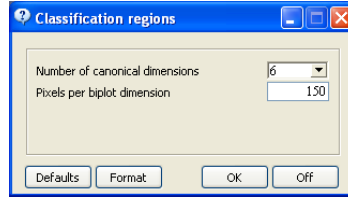REFERENCES · Wand (2009), Blasius, Eilers and Gower (2008)

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 of points.

DEFAULT VALUE · All points

Screenshot 16: The *Additional → Classification regions* dialogue box.

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 number, 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, not showing point density estimates.

▷ **Classification regions...**

Lets the user superimpose a CVA biplot onto a background of coloured classification regions.

DETAIL · Pixels are coloured in according to the closest group mean in a specified number of canonical dimensions, except when the specified number of canonical dimensions is two, in which case a Voronoi diagram gives the classification regions. If the classification region labels are shown in the legend, the group names are preceded by the prefix CR for 'Classification Region'. Only available for CVA biplots.

SCREENSHOT · 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

---
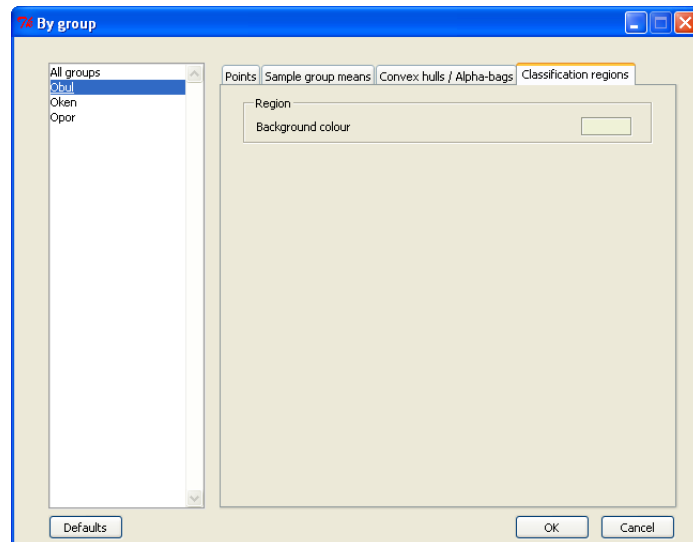
Screenshot 17: The *Additional → Classification regions → Format* dialogue box. This is also the *Classification regions* tab in the *Format → By group* dialogue box.

of groups).

DEFAULT VALUE · 2

Pixels per biplot dimension

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

DETAIL · The larger the number, the finer the image, but the more time and memory required to produce it. The smaller the number, the grainier the image.

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

Lets the user set graphical parameters for classification regions, for a particular group, or for all groups simultaneously.

SCREENSHOT · 17

> *This is also the Classification regions tab in the Format → By group dialogue box.*
>
> **Region**
>
> ***Background colour***
>
> The background colour of classification region, by group.
>
> DETAIL · Equally spaced colours from the `hcl` spectrum.
>
> **Defaults**
>
> Reverts the options to their default values.
>
> **OK**
>
> Saves the options, returns to the GUI and redraws the biplot region with classification regions.
>
> **Off**
>
> Disables the option, and returns to the GUI, not showing classification regions.

   ▷ **Clear all**

   Disables all additional descriptors.

   SHORTCUT · Ctrl+L

 • **Help**

 Some help options.

   ▷ **Vignette (in PDF)**

   Opens the package vignette.

   SHORTCUT · F1

   ▷ **Features Manual (in PDF)**

   Opens this manual.

   ▷ **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 elsewhere within the biplot 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 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 right clicking outside the biplot but inside the biplot region, and selecting Show next legend entries from the popup-menu. The keyboard shortcut is Ctrl++. Similar options are available with which to show 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 that 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 that 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**

Dynamic variable prediction is disabled.

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.

▷ **Format axes. . .**

The same as Format → Axes.

DETAIL · Not shown when there are no axes, as opposed to the axes being hidden.

▷ **Save as**

The same as File → Save as.

▷ **Copy**

The same as File → Copy.

▷ **Print. . .**

The same as File → Print.

- **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 are automatically 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 axes 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.

▷ **Format title...**

The same as Format → Title.

▷ **Show group labels in legend**

The same as View → Show group labels in legend.

▷ **Don't show axis labels**

The same as View → Don't show axis labels.

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.

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.

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.

▷ **Show next legend entries**

The same as View → Show next legend entries.

▷ **Show previous legend entries**

The same as View → Show previous legend entries.

▷ **Save as**

The same as File → Save as.

▷ **Copy**

The same as File → Copy.

▷ **Print...**

The same as File → Print.

▶ **Settings box**

Lets the user choose the action of the biplot axes, and effect data transformations.

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)

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▷ **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 effect data transformations.

DETAIL · These transformations are performed on `Data` argument of the `Biplots` function. 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 a biplot calibrated in terms of transformed variable values, the transformation has to be performed outside of the GUI and passed to the GUI via the `Data` argument.

▷ **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 substracted 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**

Shifts and scales 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 substracted 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, shifts and scales 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 version 0.0-6 of the BiplotGUI package.

• **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. Only available when the points are determined by MDS.

▷ **Pop-up menu**

Makes various options available with repspect 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. However, it applies to the graph in the tab rather than to the biplot region.

○ **Format. . .**

The same as Format → Diagnostic tabs.

○ **Save as**

The same as File → Save as. However, it it applies to the graph in the tab rather than to 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 at the bottom of the graph. To remove the space, temporarily remove the legend from the biplot and save the diagnostic graph once more.

○ **Copy**

The same as File → Copy. However, it applies to the graph in the tab rather than to 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 at the bottom of the graph. To remove the space, temporarily remove the legend from the biplot and copy the diagnostic graph once more.

○ **Print. . .**

The same as File → Print. However, it applies to the graph in the tab rather than to 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 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 at the bottom of the graph. 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 to 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 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 at the bottom of the graph, 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 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 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.

Not available for covariance/correlation biplots.

REFERENCES · Borg and Groenen (2005, Section 3.3), Gardner-Lubbe, Le Roux and Gower (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 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 biplot.

Only available for CVA biplots.

REFERENCES · Gardner-Lubbe *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 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 biplot.

Only available for PCA and CVA biplots.

REFERENCES · Gardner-Lubbe *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 (prediction - actual)/(maximum actual for variable - minimum actual for variable) ×100. Biplots are not exact but 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 to view or manipulate.

  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 selecting it and clicking Display in console. Alternatively, a quantity can be saved to the current R workspace by selecting it and clicking Save to workspace.

  REFERENCES · Gower and Hand (1996), Borg and Groenen (2005)

      ▷ **Display in console**

      Displays the quantity selected in the export tab in the R console.

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

      ▷ **Save to workspace**

      Saves the quantity selected in the export tab in the current R workspace under the name given in the list of quantities.

      DETAIL · Only available if a quantity has been selected 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 inside the kraal but not on points or 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.

  ▷ **Format axes...**

  The same as Format → Axes.

- **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 that 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 righ 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 that 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 · The 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 to constitute 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 by clicking 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 by clicking 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, 2010) for details on the choices.

• **Hide**

Hides the points and/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 after a number of iterations, taking more time. To speed up convergence, the checkbutton can be cleared. The number of iterations to the next update can be changed by clicking File → Options.

- **Stop**

  Stops the IM algorithm for MDS.

  DETAIL · Stops the iterations and proceeds with the current configuration, fitting biplot axes and all the rest. Such representations do not meet optimality criteria and may therefore be misleading. Available only while an MDS configuration is being found.

- **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.

Abbreviations

CV   canonical variate

CVA   canonical variate analysis

GUI   graphical user interface

IM   iterative majorisation

MDS   multidimensional scaling

PC   principal component

PCA   principal component analysis

PCO   principal coordinates analysis

RAE   relative absolute error

Keyboard Shortcuts

A   Shows points determined by PCO.

B   Shows points determined by MDS (identity transformation).

C   Shows points determined by MDS (monotone regression transformation).

D   Shows points determined by MDS (monotone spline transformation).

R   Shows points determined by MDS (currently selected transformation).

0   Shows no biplot axes.

1   Constructs a PCA biplot.

2   Constructs a covariance/correlation biplot.

3   Constructs a CVA 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 GUI window.

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