Package 'biplotEZ'

November 28, 2023

Title EZ-to-Use Biplots

Version 1.2.0

Description Provides users with an EZ-to-use platform for representing data
with biplots. Currently principal component analysis (PCA) and canonical variate
analysis (CVA) biplots are included. This is accompanied by various formatting
options for the samples and axes. Alpha-bags and concentration ellipses
are included for visual enhancements and interpretation. For an extensive
discussion on the topic, see Gower, J.C., Lubbe, S. and le Roux, N.J.
(2011, ISBN: 978-0-470-01255-0) Understanding Biplots. Wiley: Chichester.

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NeedsCompilation no

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R topics documented:

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alpha.bags   *Create alpha bags*

Description

This function produces α-bags, which is a useful graphical summary of the scatter plot. The alpha-bag refers to a contour which contains $\alpha\%$ of the observations.

Usage

```
alpha.bags(bp, alpha = 0.95, which = NULL, col = bp$sample$col[which], lty = 1,
lwd = 1, max = 2500, trace = TRUE)
```

Arguments

bp	an object of class `biplot`.
alpha	value between 0 and 1 to determine coverage of bag (α), with default `0.95`.
which	the selection of groups or classes to be fitted with α-bags.
col	vector of colours for the α-bags. Multiple α bags for one group will be displayed in the same colour.
lty	vector of line types for the α-bags. The same line type will be used per value of α.
lwd	vector of line widths for the α-bags. The same line width will be used per value of α.
max	maximum number of samples to include in α-bag calculations, with default 2500. If more samples are in the group, a random sample of size max is taken for the computations.
trace	logical, indicating progress of computation.

Value

A list with the following components is available:

`alpha.bags`	list of coordinates for the α-bags for each group.
`col`	vector of colours for the α-bags.
`lty`	vector of line types for the α-bags.
`lwd`	vector of line widths for the α-bags.

References

Gower, J., Gardner-Lubbe, S. & Le Roux, N. (2011, ISBN: 978-0-470-01255-0) *Understanding Biplots.* Chichester, England: John Wiley & Sons Ltd.

Examples

```
biplot (iris[,1:4]) |> PCA(group.aes=iris[,5]) |> alpha.bags(alpha=0.95) |> plot()
biplot (iris[,1:4],group.aes=iris[,5]) |> PCA() |> alpha.bags(alpha=0.95) |> plot()
```

---

axes   *Aesthetics for biplot axes*

Description

This function allows formatting changes to axes.

Usage

```
axes(bp, X.names=colnames(bp$X), which = 1:bp$p, col = grey(0.7),
lwd = 1, lty = 1, label.dir = "Orthog", label.col = col, label.cex = 0.75,
 label.line = 0.1, ticks = 5, tick.col = col, tick.size = 1, tick.label = TRUE,
 tick.label.col = tick.col, tick.label.cex = 0.6, tick.label.side = "left",
 tick.label.offset = 0.5, tick.label.pos = 1, predict.col = col, predict.lwd = lwd,
  predict.lty = lty, ax.names = X.names, orthogx = 0, orthogy = 0)
```

Arguments

`bp`	an object of class `biplot`.
`X.names`	refers to the column names of bp to specify which axes to label.
`which`	vector of columns to be displayed in the biplot, with default `1:bp$p`.
`col`	axis colour, with default `grey(0.7)`.
`lwd`	axis line width, with default `1`.
`lty`	axis line type, with default `1`.
`label.dir`	direction of axis label, with default `Orthog`.
`label.col`	axis label colour, with default, `col`.

`label.cex`	axis label expansion, with default `0.75`.
`label.line`	axis label written on which margin line, with default `0.1`.
`ticks`	number of tick marks per axis, with default 5.
`tick.col`	tick mark colour, with default `col`.
`tick.size`	tick mark size, with default 1.
`tick.label`	logical, whether axes should be labelled or not, with default `TRUE`.
`tick.label.col`	tick mark label colour, with default `tick.col`.
`tick.label.cex`	tick mark label expansion, with default `0.6`.
`tick.label.side`	side of the tick mark label, with default `left`.
`tick.label.offset`	tick mark label offset, with default `0.5`.
`tick.label.pos`	side of the tick mark label, with default `below`.
`predict.col`	predicted samples colour, with default `col`.
`predict.lwd`	predicted samples line width, with default `lwd`.
`predict.lty`	predicted samples line type, with default `lty`.
`ax.names`	vector of size p containing user defined names for the variables.
`orthogx`	the horizontal translation, with default `0`.
`orthogy`	the vertical translation with default `0`.

Value

A list with the following components is available:

`which`	vector of the columns displayed as axes.
`col`	vector of axis colours.
`lwd`	vector of axis line widths.
`lty`	vector of axis line types.
`label.dir`	direction of the axis labels.
`label.col`	vector of axis label colours.
`label.cex`	vector of axis labels expansions.
`label.line`	vector of axis label margin lines from axes.
`ticks`	vector representing the number of tick marks per axis.
`tick.col`	vector of tick mark colours.
`tick.size`	vector of tick mark sizes.
`tick.label`	vector of logical values indicating whether axes are labelled.
`tick.label.col`	vector of tick mark label colours.
`tick.label.cex`	vector of tick mark label expansions.
`tick.label.side`	vector of the side of tick mark labels.

tick.label.offset

        vector of tick mark label offsets.

tick.label.pos   vector of the side of tick mark labels.

predict.col   vector of colours for the predicted samples.

predict.lty   vector of line types for the predicted samples.

predict.lwd   vector of line widths for the predicted samples.

names   vector of variable names defined by the user.

orthogx   vector of the horisontal translations for each axis.

orthogy   vector of the vertical translations for each axis.

Examples

```
biplot(iris[,1:4]) |> PCA() |> axes(col="purple") |> plot()
biplot(iris[,1:4]) |> PCA() |> samples(col="purple",pch=15) |> axes() |> plot()
```

---

    biplot   *First step to create a new biplot with* **biplotEZ**

Description

This function produces a list of elements to be used when producing a biplot, which provides a useful data analysis tool and allows the visual appraisal of the structure of large data matrices. Biplots are the multivariate analogue of scatter plots. They approximate the multivariate distribution of a sample in a few dimensions and they superimpose on this display representations of the variables on which the samples are measured.

Usage

```
biplot(data, classes = NULL, group.aes = NULL, center = TRUE, scaled = FALSE,
Title = NULL)
```

Arguments

data   a dataframe or matrix containing all variables the user wants to analyse.

classes   vector identifying class membership.

group.aes   vector identifying groups for aesthetic formatting.

center   logical, indicating whether data should be column centered, with default TRUE.

scaled   logical, indicating whether data should be standardized to unit column variances, with default FALSE.

Title   title of the biplot to be rendered, enter text in " ".

Value

A list with the following components is available:

X	matrix of the centered and scaled numeric variables.
Xcat	data frame of the categorical variables.
raw.X	original data.
center	TRUE or FALSE, whether X is centered.
scaled	TRUE or FALSE, wether X is scaled.
means	vector of means for each numeric variable.
sd	vector of standard deviations for each numeric variable.
group.aes	vector of category levels for the grouping variable. This is to be used for colour, pch and cex specifications.
Title	title of the biplot to be rendered

References

Gabriel, K.R. (1971) The biplot graphic display of matrices with application to principal component analysis. *Biometrika.* 58(3):453–467. Gower, J., Gardner-Lubbe, S. & Le Roux, N. (2011, ISBN: 978-0-470-01255-0) *Understanding Biplots.* Chichester, England: John Wiley & Sons Ltd. Gower, J.C. & Hand, D.J.(1996, ISBN: 0-412-71630-5) *Biplots.* London: Chapman & Hall.

Examples

```
biplot(data = iris)
# create a PCA biplot
biplot(data = iris) |> PCA() |> plot()
```

CVA   *Canonical Variate Analysis (CVA) method*

Description

This function produces a list of elements to be used for CVA biplot construction.

Usage

```
CVA(bp, dim.biplot = c(2, 1, 3), e.vects = 1:ncol(bp$X),
         classes=bp$classes, weightedCVA = "weighted", show.class.means = TRUE)
```

Arguments

bp	object of class `biplot` obtained from preceding function `biplot()`.
dim.biplot	dimension of the biplot. Only values 1, 2 and 3 are accepted, with default 2.
e.vects	which eigenvectors (canonical variates) to extract, with default `1:dim.biplot`.
classes	vector of the same length as the number of rows in the data matrix with the class indicator for the samples.
weightedCVA	the default is "weighted", specifying a weighted CVA to be performed. Other possible values are "unweightedI" and "unweightedCent".
show.class.means	logical, indicating whether to plot the class means on the biplot.

Value

Object of class CVA with the following elements:

X	matrix of the centered and scaled numeric variables.
Xcat	matrix of the categorical variables.
raw.X	original data.
na.action	vector of observations that have been removed.
center	TRUE or FALSE, whether X is centred.
scaled	TRUE or FALSE, whether X is scaled.
means	mean of each numerical variable.
sd	standard deviation of each numerical variable.
n	number of observations.
p	number of variables.
group.aes	vector of the same length as the number of rows in the data matrix for differentiated aesthetics for samples.
g.names	descriptive name to be used for group labels.
g	number of groups.
Title	title of the biplot to be rendered.
Gmat	indicator matrix for class membership.
Xmeans	matrix of class means.
Z	matrix with each row containing the details of the point to be plotted (i.e. coordinates).
Zmeans	matrix of canonical means.
Lmat	matrix for transformation to the canonical space.
eigenvalues	vector of eigenvalues of the two-sided eigenvalue problem.
Cmat	Centring matrix based on different choices of weighting. For "weighted", Cmat is a diagonal matrix with the class sizes, for "unweightedI", Cmat is an indicator matrix and for "unweightedCent", Cmat is the usual centring matrix.
Bmat	Between class sums of squares and cross products matrix.

Wmat	Within class sums of squares and corss products matrix.
e.vects	vector indicating which canonical variates are plotted in the biplot.
ax.one.unit	one unit in the positive direction of each biplot axis.
class.means	logical value, indicating whether the class means should be plotted in the biplot.
Zmeans	matrix of the class mean coordinates to be plotted in the biplot.

Examples

```
biplot(iris[,1:4]) |> CVA(classes=iris[,5])
# create a CVA biplot
biplot(iris[,1:4]) |> CVA(classes=iris[,5]) |> plot()
```

CVA.biplot   *CVA biplot*

Description

Performs calculations for a CVA biplot.

Usage

```
## S3 method for class 'biplot'
CVA(
  bp,
  dim.biplot = c(2, 1, 3),
  e.vects = 1:ncol(bp$X),
  classes = bp$classes,
  weightedCVA = "weighted",
  show.class.means = TRUE
)
```

Arguments

bp	object of class `biplot` obtained from preceding function `biplot()`.
dim.biplot	dimension of the biplot. Only values 1, 2 and 3 are accepted, with default 2.
e.vects	which eigenvectors (canonical variates) to extract, with default `1:dim.biplot`.
classes	vector of the same length as the number of rows in the data matrix with the class indicator for the samples.
weightedCVA	the default is "weighted", specifying a weighted CVA to be performed. Other possible values are "unweightedI" and "unweightedCent".
show.class.means	
	logical, indicating whether to plot the class means on the biplot.

Value

an object of class CVA, inherits from class biplot.

Examples

```
biplot(iris[,1:4]) |> CVA(classes=iris[,5])
```

---

ellipses	*Concentration ellipses (κ-ellipses)*

Description

This function produces κ-ellipses, which is a useful geometrical description of the data points about the sample mean.

Usage

```
ellipses(bp, df=2, kappa = NULL, which = NULL,
alpha = 0.95, col = bp$sample$col[which], lty = 1, lwd = 1,
alpha.transparency = 0.5, trace = TRUE)
```

Arguments

bp	an object of class `biplot`.
df	degrees of freedom, with default 2.
kappa	value to construct κ-ellipse (the value of κ).
which	the selection of the group for ellipse construction.
alpha	size of α-bag, with default `0.95`.
col	colour of ellipse. Multiple κ-ellipse for one group will be displayed in the same colour.
lty	line type of ellipse. The same line type will be used per value of κ.
lwd	line width of ellipse. The same line width will be used per value of κ.
alpha.transparency	
	level of opacity, with default `0.5`.
trace	logical, indicating progress of computation.

Value

A list with the following components is available:

conc.ellipses	list of coordinates for the κ-ellipses for each group.
col	vector of colours for the κ-ellipses.
lty	vector of line types for the κ-ellipses.
lwd	vector of line widths for the κ-ellipses.
alpha	vector of α values.

References

Gower, J., Gardner-Lubbe, S. & Le Roux, N. (2011, ISBN: 978-0-470-01255-0) *Understanding Biplots.* Chichester, England: John Wiley & Sons Ltd.

Examples

```
biplot (iris[,1:4]) |> PCA(group.aes=iris[,5]) |> ellipses(kappa=2) |> plot()
```

---

fit.measures	*Compute measures of fit for biplot.*

Description

Compute measures of fit for biplot.

Usage

```
fit.measures(bp)
```

Arguments

bp   an object of class `biplot`.

Value

An object of class `biplot`. The object is augmented with additional items, depending on the type of biplot object.

quality   overall quality of fit.

adequacy   adequacy of representation of variables.

For an object of class PCA:

axis.predictivity
                fit measure of each individual axis.
sample.predictivity
                fit measure for each individual sample.

For an object of class CVA:

axis.predictivity
                fit measure of each individual axis.
class.predictivity
                fit measure for each class mean.
within.class.axis.predictivity
                fit measure for each axis based on values expressed as deviations from their class means.
within.class.sample.predictivity
                fit measure for each sample expressed as deviation from its class mean.

Examples

```
out <- biplot (iris[,1:4]) |> PCA() |> fit.measures()
summary(out)
```

---

interpolate	*Interpolation of new samples*

Description

Interpolation of new samples

Usage

```
interpolate(bp, newdata)
```

Arguments

bp	an object of class `biplot` obtained from preceding function `biplot()`.
newdata	a new data set, similar in structure to the data set supplied to `biplot()` containing supplementary data points to be added on the biplot.

Value

Object of class PCA with the following elements:

X	matrix of the centered and scaled numeric variables.
Xcat	matrix of the categorical variables.
raw.X	original data.
na.action	vector of observations that have been removed.
center	TRUE or FALSE, whether X is centred.
scaled	TRUE or FALSE, whether X is scaled.
means	mean of each numerical variable.
sd	standard deviation of each numerical variable.
n	number of observations.
p	number of variables.
group.aes	vector of the same length as the number of rows in the data matrix for differentiated aesthetics for samples.
g.names	descriptive name to be used for group labels.
g	number of groups.
Title	title of the biplot to be rendered
Z	matrix with each row containing the details of the point to be plotted (i.e. coordinates).

Lmat	matrix for transformation to the principal components.
e.vects	vector indicating which principal components are plotted in the biplot.
ax.one.unit	one unit in the positive direction of each biplot axis.
Xnew.raw	newdata numerical variables.
Xnew	matrix of the centered and scaled new numeric variables.
Xnew.cat	matrix of the new categorical variables.
Znew	matrix of the coordinates of the newdata in the biplot.

Examples

```
biplot(data = iris[1:145,]) |> PCA() |> interpolate(newdata = iris[146:150,]) |> plot()
```

---

legend.type	*Legend type*

Description

This function enables the user to format the legend and make a required selection to display.

Usage

```
legend.type(bp, samples = FALSE, means = FALSE, bags = FALSE, ellipses = FALSE,
new = FALSE, ...)
```

Arguments

bp	an object of class biplot.
samples	logical, indicating whether legend should be printed for samples, with default FALSE.
means	logical, indicating whether legend should be printed for means, with default FLASE.
bags	logical, indicating whether legend should be printed for bags, with default FALSE.
ellipses	logical, indicating whether legend should be printed for concentration ellipses, with default FALSE.
new	logical, indicating whether the legend should appear in a new window, with default FALSE.
...	additional arguments to be sent to legend().

Value

A list with the following components is available:

samples	TRUE or FALSE, whether legend for samples are provided.
means	TRUE or FALSE, whether legend for class means are provided.
bags	TRUE or FALSE, whether legend for alpha-bags are provided.
ellipses	TRUE or FALSE, whether legend for kappa-ellipses are provided.
new	TRUE or FALSE, whether legend appears on new plot.

Examples

```
biplot (iris[,1:4], Title="Test biplot") |> PCA(group.aes = iris[,5]) |>
    legend.type(samples=TRUE) |> plot()
```

---

means	*Aesthetics for biplot class / group means*

Description

This function allows formatting changes to class means or group means.

Usage

```
means (bp,  which = NULL, col = NULL, pch = 1, cex = 1, label = FALSE,
label.col = NULL,label.cex = 0.75, label.side = "bottom", label.offset = 0.5)
```

Arguments

bp	an object of class biplot.
which	vector of which means to display, with default bp$g.
col	mean colour, with default to sample colour.
pch	mean plotting character, with default o.
cex	mean character expansion, with default 1.
label	logical, whether means should be labelled or not, with default TRUE.
label.col	vector of length g with the colour of the labels, defaulting to the colour of the means.
label.cex	label text expansion, with default 0.75.
label.side	side of the plotting character where label appears, with default bottom. Note that unlike the argument pos in text(), options are "bottom", "left", "top", "right" and not 1, 2, 3, 4.
label.offset	offset of the label from the mean point. See ?text for a detailed explanation of the argument offset.

Details

The number of classes or groups (defined by group.aes) is indicated as g. If an argument is not of length g, recycling is used.

Value

A list with the following components is available:

which	which means to display.
col	colour of the means.
pch	plotting character of the means.
cex	expansion of the plotting character of the means.
label	logical, whether means should be labelled.
label.col	colour of the label.
label.cex	expansion of the label.
label.side	side at which to plot the label of means.
label.offset	offset of the label from the mean point.

Examples

```
biplot(iris[,1:4]) |> PCA() |>
        means(col = "purple", pch = 15, cex = 2) |> plot()
```

---

newsamples   *Aesthetics for supplementary (new) biplot samples*

Description

This function allows formatting changes to new samples.

Usage

```
newsamples (bp,  col = "darkorange1", pch = 1, cex = 1, label = FALSE,
label.col = NULL,label.cex = 0.75, label.side = "bottom", label.offset = 0.5,
connected = FALSE, connect.col = "black", connect.lty=1, connect.lwd=1)
```

Arguments

bp	an object of class biplot.
col	new sample colour, with default darkorange1.
pch	new sample plotting character, with default o.
cex	new sample character expansion, with default 1.
label	logical, whether samples should be labelled or not, with default FALSE.

label.col	vector of length number of new samples with the colour of the labels, defaulting to the colour of the sample points.
label.cex	label text expansion, with default 0.75.
label.side	side of the plotting character where label appears, with default bottom. Note that unlike the argument pos in text(), options are "bottom", "left", "top", "right" and not 1, 2, 3, 4.
label.offset	offset of the label from the data point. See ?text for a detailed explanation of the argument offset.
connected	logical, whether samples are connected in order of rows of data matrix, with default FALSE.
connect.col	colour of the connecting line, with default black.
connect.lty	line type of the connecting line, with default 1.
connect.lwd	line width of the connecting line, with default 1.

Value

A list with the following components is available:

col	colour of the samples.
pch	plotting character of the samples.
cex	expansion of the plotting character of the samples.
label	TRUE or FALSE, whether samples should be labelled.
label.col	colour of the label.
label.cex	expansion of the label.
label.side	side at which to plot the label of samples.
label.offset	offset of the label from the data point.
connected	TRUE or FALSE, whether samples should be connected in row order of X.
connect.col	colour of the connecting line.
connect.lty	line type of the connecting line.
connect.lwd	line width of the connecting line.

Examples

```
biplot(data = iris[1:145,]) |> PCA() |> samples(col = "grey") |>
interpolate(newdata = iris[146:150,]) |> newsamples(col = rainbow(6), pch=15) |> plot()
```

PCA   *Principal Component Analysis (PCA) method*

Description

This function produces a list of elements to be used for PCA biplot construction.

Usage

```
PCA(bp, dim.biplot = c(2, 1, 3), e.vects = 1:ncol(bp$X),
group.aes = NULL, show.group.means = FALSE, correlation.biplot = FALSE)
```

Arguments

bp	an object of class `biplot` obtained from preceding function `biplot()`.
dim.biplot	dimension of the biplot. Only values 1, 2 and 3 are accepted, with default 2.
e.vects	which eigenvectors (principal components) to extract, with default `1:dim.biplot`.
group.aes	vector of the same length as the number of rows in the data matrix for differentiated aesthetics for samples.
show.group.means	logical, indicating whether group means should be plotted in the biplot.
correlation.biplot	logical, if `FALSE`, the distances between sample points are optimally approximated in the biplot. If `TRUE`, the correlations between variables are optimally approximated by the cosine of the angles between axes. Default is `FALSE`.

Value

Object of class PCA with the following elements:

X	matrix of the centered and scaled numeric variables.
Xcat	matrix of the categorical variables.
raw.X	original data.
na.action	vector of observations that have been removed.
center	TRUE or FALSE, whether X is centred.
scaled	TRUE or FALSE, whether X is scaled.
means	mean of each numerical variable.
sd	standard deviation of each numerical variable.
n	number of observations.
p	number of variables.
group.aes	vector of the same length as the number of rows in the data matrix for differentiated aesthetics for samples.
g.names	descriptive name to be used for group labels.

g	number of groups.
Title	title of the biplot to be rendered
Z	matrix with each row containing the details of the point to be plotted (i.e. coordinates).
Lmat	matrix for transformation to the principal components.
eigenvalues	vector of eigenvalues of the covariance matrix of X.
e.vects	vector indicating which principal components are plotted in the biplot.
ax.one.unit	one unit in the positive direction of each biplot axis.
class.means	logical, indicating whether group means should be plotted in the biplot.
Zmeans	matrix of class mean coordinates to be plotted in the biplot.

References

Gabriel, K.R. (1971) The biplot graphic display of matrices with application to principal component analysis. *Biometrika.* 58(3):453–467.

Examples

```
biplot(iris[,1:4]) |> PCA()
# create a PCA biplot
biplot(data = iris) |> PCA() |> plot()
```

PCA.biplot	*PCA biplot*

Description

Performs calculations for a PCA biplot.

Usage

```
## S3 method for class 'biplot'
PCA(
  bp,
  dim.biplot = c(2, 1, 3),
  e.vects = 1:ncol(bp$X),
  group.aes = NULL,
  show.group.means = FALSE,
  correlation.biplot = FALSE
)
```

Arguments

`bp`	an object of class `biplot` obtained from preceding function `biplot()`.
`dim.biplot`	dimension of the biplot. Only values 1, 2 and 3 are accepted, with default 2.
`e.vects`	which eigenvectors (principal components) to extract, with default `1:dim.biplot`.
`group.aes`	vector of the same length as the number of rows in the data matrix for differentiated aesthetics for samples.
`show.group.means`	
	logical, indicating whether group means should be plotted in the biplot.
`correlation.biplot`	
	logical, if `FALSE`, the distances between sample points are optimally approximated in the biplot. If `TRUE`, the correlations between variables are optimally approximated by the cosine of the angles between axes. Default is `FALSE`.

Value

an object of class PCA, inherits from class biplot.

Examples

```
biplot(iris[,1:4]) |> PCA()
# create a PCA biplot
biplot(data = iris) |> PCA() |> plot()
```

---

plot.biplot   *Generic Plotting function of objects of class biplot*

Description

Generic Plotting function of objects of class biplot

Usage

```
## S3 method for class 'biplot'
plot(
  x,
  exp.factor = 1.2,
  axis.predictivity = NULL,
  sample.predictivity = NULL,
  ...
)
```

Arguments

x	An object of class `biplot`.
exp.factor	factor to expand plotting area beyond samples.
axis.predictivity	
	either logical or a numeric value between 0 and 1. If it is a numeric value, this value is used as threshold so that only axes with axis predictivity larger than the threshold is displayed. If `axis.predictivity = TRUE`, the axis color is 'diluted' in proportion with the axis predictivity.
sample.predictivity	
	either a logical or a numeric value between 0 and 1. If it is a numeric value, this value is used as threshold so that only samples with sample predictivity larger than the threshold is displayed. if `sample.predictivity = TRUE`, the sample size is shrinked in proportion with the sample predictivity.
...	additional arguments.

Value

An object of class `biplot`.

Examples

```
biplot (iris[,1:4]) |> PCA() |> plot()
```

---

print.biplot	*Generic print function of objects of class biplot*

Description

Generic print function of objects of class biplot

Usage

```
## S3 method for class 'biplot'
print(x, ...)
```

Arguments

x	an object of class `biplot`.
...	additional arguments.

Value

no return value, called for side effects.

Examples

```
out <- biplot (iris[,1:4]) |> PCA()
out
```

---

samples   *Aesthetics for biplot samples*

Description

This function allows formatting changes to samples.

Usage

```
samples (bp,  which = 1:bp$g, col = ez.col, pch = 3, cex = 1, label = FALSE,
label.col = NULL,label.cex = 0.75, label.side = "bottom", label.offset = 0.5,
connected = FALSE, connect.col = "black", connect.lty = 1, connect.lwd = 1)
```

Arguments

bp	an object of class `biplot`.
which	vector of which groups of samples to display, with default bp$g.
col	sample colour, with default `blue`.
pch	sample plotting character, with default +.
cex	sample character expansion, with default 1.
label	logical, whether samples should be labelled or not, with default FALSE.
label.col	vector of length number of samples with the colour of the labels, defaulting to the colour of the sample points.
label.cex	label text expansion, with default 0.75.
label.side	side of the plotting character where label appears, with default `bottom`. Note that unlike the argument pos in `text()`, options are "bottom", "left", "top", "right" and not 1, 2, 3, 4.
label.offset	offset of the label from the data point. See ?text for a detailed explanation of the argument `offset`.
connected	logical, whether samples are connected in order of rows of data matrix, with default FALSE.
connect.col	colour of the connecting line, with default `black`.
connect.lty	line type of the connecting line, with default 1.
connect.lwd	line width of the connecting line, with default 1.

Details

The arguments `which`, `col`, `pch` and `cex` are based on the specification of `group.aes` or `classes`. If no groups are specified, a single colour, plotting character and / or character expansion is expected. If g groups are specified, vectors of length g is expected, or values are recycled to length g.

The arguments `label`, `label.cex`, `label.side` and `label.offset` are based on the sample size n. A single value will be recycled n times or a vector of length n is expected.

Value

A list with the following components is available:

which	which means to display.
col	colour of the samples.
pch	plotting character of the samples.
cex	expansion of the plotting character of the samples.
label	TRUE or FALSE, whether samples should be labelled.
label.col	colour of the label.
label.cex	expansion of the label.
label.side	side at which to plot the label of samples.
label.offset	offset of the label from the data point.
connected	TRUE or FALSE, whether samples should be connected in row order of X.
connect.col	colour of the connecting line.
connect.lty	line type of the connecting line.
connect.lwd	line width of the connecting line.

Examples

```
biplot(iris[,1:4]) |> PCA() |> samples(col="purple",pch=15) |> plot()
```

---

summary.biplot	*Generic summary function of objects of class biplot*

Description

Generic summary function of objects of class biplot

Usage

```
## S3 method for class 'biplot'
summary(
  object,
  adequacy = TRUE,
  axis.predictivity = TRUE,
  sample.predictivity = TRUE,
  class.predictivity = TRUE,
  within.class.axis.predictivity = TRUE,
  within.class.sample.predictivity = TRUE,
  ...
)
```

Arguments

`object`	an object of class `biplot`.
`adequacy`	logical, whether variable adequacies should be reported.
`axis.predictivity`	
	logical, whether axis predictivities should be reported.
`sample.predictivity`	
	logical, whether sample predictivities should be reported.
`class.predictivity`	
	logical, whether class predictivities should be reported (only applicable to objects of class CVA).
`within.class.axis.predictivity`	
	logical, whether within class axis predictivity should be reported(only applicable to objects of class CVA).
`within.class.sample.predictivity`	
	logical, whether within class sample predictivity should be reported(only applicable to objects of class CVA).
`...`	additional arguments.

Value

no return value, called for side effects.

Examples

```
out <- biplot (iris[,1:4]) |> PCA() |> fit.measures()
summary(out)
```

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