

Package ‘dimensio’

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Title Multivariate Data Analysis

Version 0.5.0

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Description Simple Principal Components Analysis (PCA) and (Multiple) Correspondence Analysis (CA) based on the Singular Value Decomposition (SVD). This package provides S4 classes and methods to compute, extract, summarize and visualize results of multivariate data analysis. It also includes methods for partial bootstrap validation described in Greenacre (1984) <isbn:978-0-12-299050-2> and Lebart et al. (2006) <isbn:978-2-10-049616-7>.

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URL <https://packages.tesselle.org/dimensio/>,
<https://github.com/tesselle/dimensio>

BugReports <https://github.com/tesselle/dimensio/issues>

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'bootstrap.R' 'ca.R' 'coerce.R' 'data.R'
'dimensio-deprecated.R' 'dimensio-internal.R'
'dimensio-package.R' 'get_contributions.R' 'get_coordinates.R'
'get_correlations.R' 'get_cos2.R' 'get_data.R'
'get_distances.R' 'get_eigenvalues.R' 'get_inertia.R'
'get_variance.R' 'loadings.R' 'mca.R' 'mutators.R' 'pca.R'
'predicates.R' 'predict.R' 'reexport.R' 'screeplot.R' 'show.R'
'subset.R' 'summary.R' 'svd.R' 'tidy.R' 'tools.R'

'viz_contributions.R' 'viz_coordinates.R' 'viz_cos2.R'
 'viz_ellipse.R' 'viz_hull.R' 'viz_labels.R' 'wrap_ellipses.R'
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NeedsCompilation no

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benthos

Benthos

Description

Abundances of Marine Species in Sea-Bed Samples

Usage

benthos

Format

A `data.frame` with 13 columns (sites) and 92 rows (species).

Source

<http://www.carme-n.org/?sec=data7>

See Also

Other datasets: [colours](#), [countries](#)

biplot

Biplot

Description

Biplot

Usage

```
## S4 method for signature 'CA'
biplot(
  x,
  ...,
  axes = c(1, 2),
  type = c("symetric", "rows", "columns", "contributions"),
  active = TRUE,
  sup = TRUE,
  labels = NULL,
  col.rows = c("#E69F00", "#009E73"),
  col.columns = c("#56B4E9", "#F0E442"),
  cex.rows = graphics::par("cex"),
  cex.columns = graphics::par("cex"),
  pch.rows = 16,
```

```

    pch.columns = 17,
    xlim = NULL,
    ylim = NULL,
    main = NULL,
    sub = NULL,
    legend = list(x = "topleft")
)

## S4 method for signature 'PCA'
biplot(
  x,
  ...,
  axes = c(1, 2),
  type = c("form", "covariance"),
  active = TRUE,
  sup = TRUE,
  labels = "variables",
  col.rows = c("#E69F00", "#009E73"),
  col.columns = c("#56B4E9", "#F0E442"),
  pch = 16,
  cex = 1,
  lty = 1,
  lwd = 2,
  xlim = NULL,
  ylim = NULL,
  main = NULL,
  sub = NULL,
  legend = list(x = "topleft")
)

```

Arguments

x	A <i>CA</i> , <i>MCA</i> or <i>PCA</i> object.
...	Currently not used.
axes	A length-two <i>numeric</i> vector giving the dimensions to be plotted.
type	A <i>character</i> string specifying the biplot to be plotted (see below). It must be one of "rows", "columns", "contribution" (<i>CA</i>), "form" or "covariance" (<i>PCA</i>). Any unambiguous substring can be given.
active	A <i>logical</i> scalar: should the active observations be plotted?
sup	A <i>logical</i> scalar: should the supplementary observations be plotted?
labels	A <i>character</i> vector specifying whether "rows"/"individuals" and/or "columns"/"variables" names must be drawn. Any unambiguous substring can be given.
col.rows	A length-two vector of color specification for the active and supplementary rows.
col.columns	A length-two vector of color specification for the active and supplementary columns.

xlim	A length-two numeric vector giving the x limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
ylim	A length-two numeric vector giving the y limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
main	A character string giving a main title for the plot.
sub	A character string giving a subtitle for the plot.
legend	A list of additional arguments to be passed to <code>graphics::legend()</code> ; names of the list are used as argument names. If NULL, no legend is displayed.
pch, pch.rows, pch.columns	A symbol specification.
cex, cex.rows, cex.columns	A numeric vector giving the amount by which plotting characters and symbols should be scaled relative to the default.
lty, lwd	A specification for the line type and width.

Details

A biplot is the simultaneous representation of rows and columns of a rectangular dataset. It is the generalization of a scatterplot to the case of multivariate data: it allows to visualize as much information as possible in a single graph (Greenacre 2010).

Biplots have the drawbacks of their advantages: they can quickly become difficult to read as they display a lot of information at once. It may then be preferable to visualize the results for individuals and variables separately.

Value

`biplot()` is called for its side-effects: it results in a graphic being displayed. Invisibly returns `x`.

PCA Biplots

form (row-metric-preserving) The form biplot favors the representation of the individuals: the distance between the individuals approximates the Euclidean distance between rows. In the form biplot the length of a vector approximates the quality of the representation of the variable.

covariance (column-metric-preserving) The covariance biplot favors the representation of the variables: the length of a vector approximates the standard deviation of the variable and the cosine of the angle formed by two vectors approximates the correlation between the two variables. In the covariance biplot the distance between the individuals approximates the Mahalanobis distance between rows.

CA Biplots

symetric (symetric biplot) Represents the row and column profiles simultaneously in a common space: rows and columns are in standard coordinates. Note that the the inter-distance between any row and column items is not meaningful.

rows (asymmetric biplot) Row principal biplot (row-metric-preserving) with rows in principal coordinates and columns in standard coordinates.

columns (**asymmetric biplot**) Column principal biplot (column-metric-preserving) with rows in standard coordinates and columns in principal coordinates.

contribution (**asymmetric biplot**) Contribution biplot with rows in principal coordinates and columns in standard coordinates multiplied by the square roots of their masses.

Author(s)

N. Frerebeau

References

Aitchison, J. and Greenacre, M. J. (2002). Biplots of Compositional Data. *Journal of the Royal Statistical Society: Series C (Applied Statistics)*, 51(4): 375-92. doi:10.1111/14679876.00275.

Greenacre, M. J. (2010). *Biplots in Practice*. Bilbao: Fundación BBVA.

See Also

Other plot methods: [screepplot\(\)](#), [viz_contributions\(\)](#), [viz_individuals\(\)](#), [viz_variables\(\)](#), [viz_wrap](#), [wrap](#)

Examples

```
## Replicate examples from Greenacre 2007, p. 59-68
data("countries")

## Compute principal components analysis
## All rows and all columns obtain the same weight
row_w <- rep(1 / nrow(countries), nrow(countries)) # 1/13
col_w <- rep(1 / ncol(countries), ncol(countries)) # 1/6
Y <- pca(countries, scale = FALSE, weight_row = row_w, weight_col = col_w)

## Row-metric-preserving biplot (form biplot)
biplot(Y, type = "form")

## Column-metric-preserving biplot (covariance biplot)
biplot(Y, type = "covariance")

## Replicate examples from Greenacre 2007, p. 79-88
data("benthos")

## Compute correspondence analysis
X <- ca(benthos)

## Symetric CA biplot
biplot(X, labels = "columns")

## Row principal CA biplot
biplot(X, type = "row", labels = "columns")

## Column principal CA biplot
biplot(X, type = "column", labels = "columns")
```

```
## Contribution CA biplot  
biplot(X, type = "contrib", labels = NULL)
```

boot

Partial Bootstrap Analysis

Description

Checks analysis with partial bootstrap resampling.

Usage

```
## S4 method for signature 'CA'  
bootstrap(object, n = 30)  
  
## S4 method for signature 'PCA'  
bootstrap(object, n = 30)
```

Arguments

`object` A [CA](#) or [PCA](#) object.
`n` A non-negative [integer](#) giving the number of bootstrap replications.

Value

Returns a [BootstrapCA](#) or a [BootstrapPCA](#) object.

Author(s)

N. Frerebeau

References

- Greenacre, Michael J. *Theory and Applications of Correspondence Analysis*. London: Academic Press, 1984.
- Lebart, L., Piron, M. and Morineau, A. *Statistique exploratoire multidimensionnelle: visualisation et inférence en fouille de données*. Paris: Dunod, 2006.
- Lockyear, K. (2013). Applying Bootstrapped Correspondence Analysis to Archaeological Data. *Journal of Archaeological Science*, 40(12): 4744-4753. doi:10.1016/j.jas.2012.08.035.
- Ringrose, T. J. (1992). Bootstrapping and Correspondence Analysis in Archaeology. *Journal of Archaeological Science*, 19(6): 615-629. doi:10.1016/03054403(92)90032X.

Examples

```
## Bootstrap on CA
## Data from Lebart et al. 2006, p. 170-172
data("colours")

## Compute correspondence analysis
X <- ca(colours)

## Bootstrap (30 replicates)
Y <- bootstrap(X, n = 30)

## Not run:
## Get replicated coordinates
get_replications(Y, margin = 1)
get_replications(Y, margin = 2)

## End(Not run)

## Plot with ellipses
viz_rows(Y)
viz_tolerance(Y, margin = 1, level = c(0.68, 0.95))

viz_columns(Y)
viz_tolerance(Y, margin = 2, level = c(0.68, 0.95))

## Plot with convex hulls
viz_columns(Y)
viz_hull(Y, margin = 2)

## Bootstrap on PCA
## Compute principal components analysis
data("iris")
X <- pca(iris)

## Bootstrap (30 replicates)
Y <- bootstrap(X, n = 30)

## Plot with ellipses
viz_variables(Y)
viz_tolerance(Y, margin = 2, level = c(0.68, 0.95))
```

burt

Burt Table

Description

Computes the burt table of a factor table.

Usage

```
burt(object, ...)  
  
## S4 method for signature 'data.frame'  
burt(object, exclude = NULL, abbrev = TRUE)
```

Arguments

object	A data.frame .
...	Currently not used.
exclude	A vector of values to be excluded when forming the set of levels (see factor()). If NULL (the default), will make NA an extra level.
abbrev	A logical scalar: should the column names be abbreviated? If FALSE, these are of the form 'factor_level' but if abbrev = TRUE they are just 'level' which will suffice if the factors have distinct levels.

Value

A symmetric [matrix](#).

Author(s)

N. Frerebeau

See Also

Other tools: [cdt\(\)](#)

Examples

```
## Create a factor table  
x <- data.frame(  
  A = c("a", "b", "a"),  
  B = c("x", "y", "z")  
)  
  
## Complete disjunctive table  
cdt(x)  
  
## Burt table  
burt(x)
```

ca *Correspondence Analysis*

Description

Computes a simple correspondence analysis based on the singular value decomposition.

Usage

```
ca(object, ...)  
  
## S4 method for signature 'data.frame'  
ca(object, rank = NULL, sup_row = NULL, sup_col = NULL)  
  
## S4 method for signature 'matrix'  
ca(object, rank = NULL, sup_row = NULL, sup_col = NULL)
```

Arguments

object	A $m \times p$ numeric matrix or a data.frame .
...	Currently not used.
rank	An integer value specifying the maximal number of components to be kept in the results. If NULL (the default), $\min(m, p) - 1$ components will be returned.
sup_row	A vector specifying the indices of the supplementary rows.
sup_col	A vector specifying the indices of the supplementary columns.

Value

A [CA](#) object.

Author(s)

N. Frerebeau

References

Greenacre, M. J. *Theory and Applications of Correspondence Analysis*. London: Academic Press, 1984.

Greenacre, M. J. *Correspondence Analysis in Practice*. Seconde edition. Interdisciplinary Statistics Series. Boca Raton: Chapman & Hall/CRC, 2007.

Lebart, L., Piron, M. and Morineau, A. *Statistique exploratoire multidimensionnelle: visualisation et inférence en fouille de données*. Paris: Dunod, 2006.

See Also

[svd\(\)](#)
Other multivariate analysis: [mca\(\)](#), [pca\(\)](#), [predict\(\)](#)

Examples

```
## Data from Lebart et al. 2006, p. 170-172
data("colours")

## The chi square of independence between the two variables
stats::chisq.test(colours)

## Compute correspondence analysis
X <- ca(colours)

## Plot rows
viz_rows(X, labels = TRUE)

## Plot columns
viz_columns(X, labels = TRUE)

## Get row coordinates
head(get_coordinates(X, margin = 1))

## Get column coordinates
head(get_coordinates(X, margin = 2))

## Get row distances to centroid
head(get_distances(X, margin = 1))

## Get row inertias
head(get_inertia(X, margin = 1))

## Get row contributions
head(get_contributions(X, margin = 1))

## Get eigenvalues
get_eigenvalues(X)
```

cdt

Complete Disjunctive Table

Description

Computes the complete disjunctive table of a factor table.

Usage

```
cdt(object, ...)
```

S4 method for signature 'matrix'

```
cdt(object, exclude = NULL, abbrev = TRUE)
```

S4 method for signature 'data.frame'

```
cdt(object, exclude = NULL, abbrev = TRUE)
```

Arguments

object	A data.frame .
...	Currently not used.
exclude	A vector of values to be excluded when forming the set of levels (see factor()). If NULL (the default), will make NA an extra level.
abbrev	A logical scalar: should the column names be abbreviated? If FALSE, these are of the form 'factor_level' but if abbrev = TRUE they are just 'level' which will suffice if the factors have distinct levels.

Value

A [data.frame](#).

Author(s)

N. Frerebeau

See Also

Other tools: [burt\(\)](#)

Examples

```
## Create a factor table
x <- data.frame(
  A = c("a", "b", "a"),
  B = c("x", "y", "z")
)

## Complete disjunctive table
cdt(x)

## Burt table
burt(x)
```

colours

Colours

Description

Contingency table of eye and hair colours of different individuals.

Usage

colours

Format

A `data.frame` with 4 columns (hair colours) and 4 rows (eye colours).

Source

Lebart, L., Piron, M. and Morineau, A. *Statistique exploratoire multidimensionnelle: visualisation et inférence en fouille de données*. Paris: Dunod, 2006, p. 170-172

See Also

Other datasets: [benthos](#), [countries](#)

countries

Countries

Description

Student ratings of 13 countries on six attributes.

Usage

```
countries
```

Format

A `data.frame` with 6 columns (attributes) and 13 rows (countries).

Source

Greenacre, M. J. *Biplots in Practice*. Bilbao: Fundación BBVA, 2010.

See Also

Other datasets: [benthos](#), [colours](#)

dimnames	<i>Dimnames of an Object</i>
----------	------------------------------

Description

Retrieve or set the dimnames of an object.

Usage

```
## S4 method for signature 'MultivariateAnalysis'
dim(x)

## S4 method for signature 'MultivariateAnalysis'
rownames(x, do.NULL = TRUE, prefix = "row")

## S4 method for signature 'MultivariateAnalysis'
colnames(x, do.NULL = TRUE, prefix = "col")

## S4 method for signature 'MultivariateAnalysis'
dimnames(x)
```

Arguments

x	An object from which to retrieve the row or column names (a CA or PCA object).
do.NULL	A logical scalar. If FALSE and names are NULL, names are created.
prefix	A character string specifying the prefix for created names.

Author(s)

N. Frerebeau

See Also

Other mutators: [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#), [subset\(\)](#)

get_contributions	<i>Get Contributions</i>
-------------------	--------------------------

Description

Get Contributions

Usage

```

get_contributions(x, ...)

get_correlations(x, ...)

get_cos2(x, ...)

## S4 method for signature 'MultivariateAnalysis'
get_contributions(x, margin = 1)

## S4 method for signature 'PCA'
get_correlations(x, sup_name = ".sup")

## S4 method for signature 'MultivariateAnalysis'
get_cos2(x, margin = 1, sup_name = ".sup")

```

Arguments

x	An object from which to get element(s) (a CA , MCA or PCA object).
...	Currently not used.
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
sup_name	A character string specifying the name of the column to create for supplementary points attribution (see below).

Value

- `get_contributions()` returns a [data.frame](#) of contributions to the definition of the principal dimensions.
- `get_correlations()` returns a [data.frame](#) of correlations between variables and dimensions (PCA). An extra column (named after `sup_name`) is added specifying whether an observation is a supplementary point or not.
- `get_cos2()` returns a [data.frame](#) of \cos^2 values (i.e. quality of the representation of the points on the factor map). An extra column (named after `sup_name`) is added specifying whether an observation is a supplementary point or not.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#), [subset\(\)](#)

get_coordinates	<i>Get Coordinates</i>
-----------------	------------------------

Description

Get Coordinates

Usage

```
get_coordinates(x, ...)

get_replications(x, ...)

## S4 method for signature 'MultivariateAnalysis'
get_coordinates(x, margin = 1, principal = TRUE, sup_name = ".sup")

## S4 method for signature 'MultivariateBootstrap'
get_replications(x, margin = 1)

## S4 method for signature 'BootstrapPCA'
get_replications(x)
```

Arguments

x	An object from which to get element(s) (a CA , MCA or PCA object).
...	Currently not used.
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
principal	A logical scalar: should principal coordinates be returned? If FALSE, standard coordinates are returned.
sup_name	A character string specifying the name of the column to create for supplementary points attribution (see below).

Value

- `get_coordinates()` returns a [data.frame](#) of coordinates. An extra column (named after `sup_name`) is added specifying whether an observation is a supplementary point or not.
- `get_replications()` returns an [array](#) of coordinates.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#), [subset\(\)](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE, sup_row = 5:10)

## Get row principal coordinates
head(get_coordinates(X, margin = 1, principal = TRUE))

## Get row standard coordinates
head(get_coordinates(X, margin = 1, principal = FALSE))

## Tidy principal coordinates
head(tidy(X, margin = 1))
head(tidy(X, margin = 2))

head(augment(X, margin = 1, axes = c(1, 2)))
head(augment(X, margin = 2, axes = c(1, 2)))
```

get_data

Get Original Data

Description

Get Original Data

Usage

```
get_data(x, ...)
```

S4 method for signature 'MultivariateAnalysis'

```
get_data(x)
```

Arguments

x An object from which to get element(s) (a [CA](#), [MCA](#) or [PCA](#) object).

... Currently not used.

Value

Returns a [data.frame](#) of original data.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#), [subset\(\)](#)

`get_distances`*Get Distances*

Description

Get Distances

Usage

```
get_distances(x, ...)
```

```
## S4 method for signature 'MultivariateAnalysis'  
get_distances(x, margin = 1)
```

Arguments

<code>x</code>	An object from which to get element(s) (a CA , MCA or PCA object).
<code>...</code>	Currently not used.
<code>margin</code>	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.

Value

A [numeric](#) vector of squared distance to the centroide.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#), [subset\(\)](#)

get_eigenvalues	<i>Get Eigenvalues</i>
-----------------	------------------------

Description

Get Eigenvalues

Usage

```
get_eigenvalues(x)
```

```
get_inertia(x, ...)
```

```
get_variance(x, ...)
```

```
## S4 method for signature 'MultivariateAnalysis'  
get_eigenvalues(x)
```

```
## S4 method for signature 'MultivariateAnalysis'  
get_inertia(x, margin = 1)
```

```
## S4 method for signature 'MultivariateAnalysis'  
get_variance(x, digits = 2)
```

Arguments

x	An object from which to get element(s) (a CA , MCA or PCA object).
...	Currently not used.
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
digits	An integer indicating the number of decimal places to be used.

Value

- `get_eigenvalues()` returns a [data.frame](#) with the following columns: eigenvalues, variance (percentage of variance) and cumulative (cumulative percentage of variance).
- `get_variance()` returns a [numeric](#) vector giving the percentage of explained variance of each dimension.
- `get_inertia()` returns a [numeric](#) vector.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [loadings\(\)](#), [subset\(\)](#)

loadings

Extract Loadings

Description

Extract loadings in principal components analysis.

Usage

```
## S4 method for signature 'PCA'  
loadings(x)
```

Arguments

x A [PCA](#) object.

Value

Returns variable loadings (i.e. the coefficients of the linear combination of the original variables).

Note

`loadings()` is only implemented for consistency with `[stats][stats::loadings]`.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [subset\(\)](#)

Description

Computes a multiple correspondence analysis.

Usage

```
mca(object, ...)  
  
## S4 method for signature 'data.frame'  
mca(object, rank = NULL, sup_row = NULL, sup_col = NULL, sup_quanti = NULL)  
  
## S4 method for signature 'matrix'  
mca(object, rank = NULL, sup_row = NULL, sup_col = NULL, sup_quanti = NULL)
```

Arguments

object	A $m \times p$ numeric matrix or a data.frame .
...	Currently not used.
rank	An integer value specifying the maximal number of components to be kept in the results. If NULL (the default), $\min(m, p) - 1$ components will be returned.
sup_row	A vector specifying the indices of the supplementary rows.
sup_col	A vector specifying the indices of the supplementary categorical columns.
sup_quanti	A vector specifying the indices of the supplementary quantitative columns.

Value

A [MCA](#) object.

Author(s)

N. Frerebeau

References

Lebart, L., Piron, M. and Morineau, A. *Statistique exploratoire multidimensionnelle: visualisation et inférence en fouille de données*. Paris: Dunod, 2006.

See Also

[svd\(\)](#), [cdt\(\)](#)

Other multivariate analysis: [ca\(\)](#), [pca\(\)](#), [predict\(\)](#)

Description

Computes a principal components analysis based on the singular value decomposition.

Usage

```
pca(object, ...)  
  
## S4 method for signature 'data.frame'  
pca(  
  object,  
  center = TRUE,  
  scale = TRUE,  
  rank = NULL,  
  sup_row = NULL,  
  sup_col = NULL,  
  weight_row = NULL,  
  weight_col = NULL  
)  
  
## S4 method for signature 'matrix'  
pca(  
  object,  
  center = TRUE,  
  scale = TRUE,  
  rank = NULL,  
  sup_row = NULL,  
  sup_col = NULL,  
  weight_row = NULL,  
  weight_col = NULL  
)
```

Arguments

object	A $m \times p$ numeric matrix or a data.frame .
...	Currently not used.
center	A logical scalar: should the variables be shifted to be zero centered?
scale	A logical scalar: should the variables be scaled to unit variance?
rank	An integer value specifying the maximal number of components to be kept in the results. If NULL (the default), $p - 1$ components will be returned.
sup_row	A vector specifying the indices of the supplementary rows.
sup_col	A vector specifying the indices of the supplementary columns.

weight_row	A numeric vector specifying the active row (individual) weights. If NULL (the default), uniform weights are used. Row weights are internally normalized to sum 1
weight_col	A numeric vector specifying the active column (variable) weights. If NULL (the default), uniform weights (1) are used.

Value

A **PCA** object.

Author(s)

N. Frerebeau

References

Lebart, L., Piron, M. and Morineau, A. *Statistique exploratoire multidimensionnelle: visualisation et inférence en fouille de données*. Paris: Dunod, 2006.

See Also

[svd\(\)](#)

Other multivariate analysis: [ca\(\)](#), [mca\(\)](#), [predict\(\)](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE, sup_row = sample(150, 10), sup_col = 2)

## Get row coordinates
head(get_coordinates(X, margin = 1))

## Get column coordinates
head(get_coordinates(X, margin = 2))

## Get correlations between variables and dimensions
head(get_correlations(X))

## Get eigenvalues
get_eigenvalues(X)
```

predict

Predict New Coordinates

Description

Predict the projection of new individuals/rows or variables/columns.

Usage

```
## S4 method for signature 'CA'  
predict(object, newdata, margin = 1)  
  
## S4 method for signature 'PCA'  
predict(object, newdata, margin = 1)
```

Arguments

object	A CA or PCA object.
newdata	An object of supplementary points coercible to a matrix for which to compute principal coordinates.
margin	A length-one numeric vector giving the subscript which the data will be predicted: 1 indicates individuals/rows (the default), 2 indicates variables/columns.

Value

A [data.frame](#) of coordinates.

Author(s)

N. Frerebeau

See Also

Other multivariate analysis: [ca\(\)](#), [mca\(\)](#), [pca\(\)](#)

Examples

```
## Create a matrix  
A <- matrix(data = sample(1:10, 100, TRUE), nrow = 10, ncol = 10)  
  
## Compute correspondence analysis  
X <- ca(A, sup_row = 8:10, sup_col = 7:10)  
  
## Predict new row coordinates  
Y <- matrix(data = sample(1:10, 120, TRUE), nrow = 20, ncol = 6)  
predict(X, Y, margin = 1)  
  
## Predict new column coordinates
```

```
Z <- matrix(data = sample(1:10, 140, TRUE), nrow = 7, ncol = 20)
predict(X, Z, margin = 2)
```

screepLOT

Scree Plot

Description

Plot eigenvalues (scree plot) or variances histogram.

Usage

```
## S4 method for signature 'MultivariateAnalysis'
screepLOT(
  x,
  ...,
  eigenvalues = FALSE,
  cumulative = FALSE,
  labels = TRUE,
  limit = 10,
  col = "grey90",
  border = "grey10",
  col.cumulative = "red",
  lty.cumulative = "solid",
  lwd.cumulative = 2
)
```

Arguments

<code>x</code>	A CA , MCA or PCA object.
<code>...</code>	Extra parameters to be passed to graphics::barplot() .
<code>eigenvalues</code>	A logical scalar: should the eigenvalues be plotted instead of variance/inertia?
<code>cumulative</code>	A logical scalar: should the cumulative percentages of variance be plotted?
<code>labels</code>	A logical scalar: should text labels be drawn on top of bars?
<code>limit</code>	An integer specifying the number of top elements to be displayed.
<code>col, border</code>	A character string specifying the bars infilling and border colors.
<code>col.cumulative</code>	A specification for the line color.
<code>lty.cumulative</code>	A specification for the line type.
<code>lwd.cumulative</code>	A specification for the line width.

Value

`screepLOT()` is called for its side-effects: it results in a graphic being displayed. Invisibly returns `x`.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [viz_contributions\(\)](#), [viz_individuals\(\)](#), [viz_variables\(\)](#), [viz_wrap](#), [wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Screeplot
screeplot(X)
screeplot(X, cumulative = TRUE)
```

subset

Extract Parts of an Object

Description

Operators acting on objects to extract parts.

Usage

```
## S4 method for signature 'CA,ANY,missing'
x[[i]]

## S4 method for signature 'PCA,ANY,missing'
x[[i]]
```

Arguments

x An object from which to extract element(s) or in which to replace element(s).

i A [character](#) string specifying elements to extract. Any unambiguous substring can be given (see details).

Details

If **i** is "data", returns a list with the following elements:

data A [numeric](#) matrix of raw data.

mean A [numeric](#) vector giving the variables means (PCA).

sd A **numeric** vector giving the variables standard deviations (PCA).

If *i* is "rows", returns a list with the following elements:

coord A **numeric** matrix of rows/individuals coordinates.

cos2 A **numeric** matrix of rows/individuals squared cosine.

masses A **numeric** vector giving the rows masses/individual weights.

sup A **logical** vector specifying whether a point is a supplementary observation or not.

If *i* is "columns", returns a list with the following elements:

coord A **numeric** matrix of columns/variables coordinates.

cor A **numeric** matrix of correlation between variables and the dimensions (PCA).

cos2 A **numeric** matrix of columns/variables squared cosine.

masses A **numeric** vector giving the columns masses/variable weights.

sup A **logical** vector specifying whether a point is a supplementary observation or not.

If *i* is "eigenvalues", returns a **numeric** vector of eigenvalues.

Value

A **list**.

Author(s)

N. Frerebeau

See Also

Other mutators: [dimnames\(\)](#), [get_contributions\(\)](#), [get_coordinates\(\)](#), [get_data\(\)](#), [get_distances\(\)](#), [get_eigenvalues\(\)](#), [loadings\(\)](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE, sup_row = 8:10, sup_col = 1)

## Get results for the individuals
X[["rows"]]
```

summary

Object Summaries

Description

Provides a summary of the results of a multivariate data analysis.

Usage

```
## S4 method for signature 'CA'  
summary(object, margin = 1, active = TRUE, sup = TRUE, rank = 3)  
  
## S4 method for signature 'PCA'  
summary(object, margin = 1, active = TRUE, sup = TRUE, rank = 3)
```

Arguments

object	A <i>CA</i> , <i>MCA</i> or <i>PCA</i> object.
margin	A length-one <i>numeric</i> vector giving the subscript which the data will be summarized: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
active	A <i>logical</i> scalar: should the active observations be summarized?
sup	A <i>logical</i> scalar: should the supplementary observations be summarized?
rank	An <i>integer</i> value specifying the maximal number of components to be kept in the results.

Author(s)

N. Frerebeau

See Also

Other summary: [tidy\(\)](#)

Examples

```
## Data from Lebart et al. 2006, p. 170-172  
data("colours")  
  
## Compute correspondence analysis  
X <- ca(colours)  
  
## Rows summary  
summary(X, margin = 1)  
  
## Columns summary  
summary(X, margin = 2)
```

tidy	<i>Tidy Coordinates</i>
------	-------------------------

Description

Tidy Coordinates

Usage

```
tidy(x, ...)
```

```
augment(x, ...)
```

```
## S4 method for signature 'MultivariateAnalysis'
augment(x, ..., margin = 1, axes = c(1, 2), principal = TRUE)
```

```
## S4 method for signature 'MultivariateAnalysis'
tidy(x, ..., margin = 1, principal = TRUE)
```

Arguments

x	A CA , MCA or PCA object.
...	Currently not used.
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
axes	A length-two numeric vector giving the dimensions to be for which to compute results.
principal	A logical scalar: should principal coordinates be returned? If FALSE, standard coordinates are returned.

Value

tidy() returns a long [data.frame](#) with the following columns:

label Row/column names of the original data.

component Component.

supplementary Whether an observation is active or supplementary.

coordinate Coordinates.

contribution Contributions to the definition of the components.

cos2 \cos^2 .

augment() returns a wide [data.frame](#) of the row/column coordinates along axes and the following columns:

label Row/column names of the original data.

supplementary Whether an observation is active or supplementary.

mass Weight/mass of each observation.

sum Sum of squared coordinates along axes.

contribution Joint contributions to the definition of axes.

cos2 Joint \cos^2 along axes.

Author(s)

N. Frerebeau

See Also

Other summary: [summary\(\)](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE, sup_row = 5:10)

## Get row principal coordinates
head(get_coordinates(X, margin = 1, principal = TRUE))

## Get row standard coordinates
head(get_coordinates(X, margin = 1, principal = FALSE))

## Tidy principal coordinates
head(tidy(X, margin = 1))
head(tidy(X, margin = 2))

head(augment(X, margin = 1, axes = c(1, 2)))
head(augment(X, margin = 2, axes = c(1, 2)))
```

viz_contributions

Visualize Contributions and cos2

Description

Plots contributions histogram and \cos^2 scatterplot.

Usage

```

viz_contributions(x, ...)

viz_cos2(x, ...)

## S4 method for signature 'MultivariateAnalysis'
viz_contributions(
  x,
  ...,
  margin = 2,
  axes = 1,
  sort = TRUE,
  decreasing = TRUE,
  limit = 10,
  horiz = FALSE,
  col = "grey90",
  border = "grey10"
)

## S4 method for signature 'MultivariateAnalysis'
viz_cos2(
  x,
  ...,
  margin = 2,
  axes = c(1, 2),
  active = TRUE,
  sup = TRUE,
  sort = TRUE,
  decreasing = TRUE,
  limit = 10,
  horiz = FALSE,
  col = "grey90",
  border = "grey10"
)

```

Arguments

x	A CA, MCA or PCA object.
...	Extra parameters to be passed to <code>graphics::barplot()</code> .
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
axes	A numeric vector giving the dimensions to be plotted.
sort	A logical scalar: should the data be sorted?
decreasing	A logical scalar: should the sort order be decreasing? Only used if sort is TRUE.
limit	An integer specifying the number of top elements to be displayed.

horiz	A logical scalar: should the bars be drawn horizontally with the first at the bottom?
col, border	A character string specifying the bars infilling and border colors.
active	A logical scalar: should the active observations be plotted?
sup	A logical scalar: should the supplementary observations be plotted?

Value

viz_contributions() and viz_cos2() are called for their side-effects: they result in a graphic being displayed. Invisibly return x.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [screepplot\(\)](#), [viz_individuals\(\)](#), [viz_variables\(\)](#), [viz_wrap](#), [wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Get row contributions
head(get_contributions(X, margin = 1))

## Plot contributions
viz_contributions(X)

## Plot cos2
viz_cos2(X)
```

viz_individuals

Visualize Individuals Factor Map

Description

Plots row/individual principal coordinates.

Usage

```
viz_individuals(x, ...)  
  
viz_rows(x, ...)  
  
## S4 method for signature 'MultivariateAnalysis'  
viz_rows(  
  x,  
  ...,  
  axes = c(1, 2),  
  active = TRUE,  
  sup = TRUE,  
  labels = FALSE,  
  highlight = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  main = NULL,  
  sub = NULL,  
  panel.first = NULL,  
  panel.last = NULL,  
  legend = list(x = "topleft")  
)  
  
## S4 method for signature 'BootstrapCA'  
viz_rows(x, ..., axes = c(1, 2))  
  
## S4 method for signature 'PCA'  
viz_individuals(  
  x,  
  ...,  
  axes = c(1, 2),  
  active = TRUE,  
  sup = TRUE,  
  labels = FALSE,  
  highlight = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  main = NULL,  
  sub = NULL,  
  panel.first = NULL,  
  panel.last = NULL,  
  legend = list(x = "topleft")  
)
```

Arguments

x	A CA, MCA or PCA object.
...	Further graphical parameters (see details).

axes	A length-two numeric vector giving the dimensions to be plotted.
active	A logical scalar: should the active observations be plotted?
sup	A logical scalar: should the supplementary observations be plotted?
labels	A logical scalar: should labels be drawn?
highlight	A vector specifying the information to be highlighted. If NULL (the default), no highlighting is applied. If a single character string is passed, it must be one of "observation", "mass", "sum", "contribution" or "cos2" (see augment()). Any unambiguous substring can be given.
xlim	A length-two numeric vector giving the x limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
ylim	A length-two numeric vector giving the y limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
main	A character string giving a main title for the plot.
sub	A character string giving a subtitle for the plot.
panel.first	An expression to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
panel.last	An expression to be evaluated after plotting has taken place but before the axes, title and box are added.
legend	A list of additional arguments to be passed to graphics::legend() ; names of the list are used as argument names. If NULL, no legend is displayed.

Details

Commonly used [graphical parameters](#) are:

- pch A vector of plotting characters or symbols. This can either be a single character or an integer code for one of a set of graphics symbols.
- cex A numerical vector giving the amount by which plotting characters and symbols should be scaled relative to the default.
- col The colors for lines and points. Multiple colors can be specified so that each point can be given its own color.
- bg The background color for the open plot symbols given by pch = 21 : 25.

Value

`viz_*()` is called for its side-effects: it results in a graphic being displayed. Invisibly returns `x`.

Note

Be careful: graphical parameters are silently recycled.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [screplot\(\)](#), [viz_contributions\(\)](#), [viz_variables\(\)](#), [viz_wrap](#), [wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Plot individuals
viz_individuals(X, panel.last = graphics::grid())

## Plot variables
viz_variables(X, panel.last = graphics::grid())

## Graphical parameters
## Continuous values
viz_individuals(X, highlight = iris$Petal.Length, pch = 16)
viz_individuals(X, highlight = iris$Petal.Length, pch = 16,
  col = grDevices::hcl.colors(12, "RdPu"))
viz_individuals(X, highlight = iris$Petal.Length, pch = 16,
  col = grDevices::hcl.colors(12, "RdPu"),
  cex = c(1, 2))

viz_variables(X, highlight = "contribution",
  col = grDevices::hcl.colors(12, "BluGrn", rev = TRUE),
  lwd = c(1, 5))

## Discrete values
viz_individuals(X, highlight = iris$Species, pch = 21:23)
viz_individuals(X, highlight = iris$Species, pch = 21:23,
  bg = c("#004488", "#DDAA33", "#BB5566"),
  col = "black")

viz_variables(X, highlight = c("Petal", "Petal", "Sepal", "Sepal"),
  col = c("#EE7733", "#0077BB"),
  lty = c(1, 3))
```

viz_variables

Visualize Variables Factor Map

Description

Plots column/variable principal coordinates.

Usage

```
viz_variables(x, ...)  
  
viz_columns(x, ...)  
  
## S4 method for signature 'MultivariateAnalysis'  
viz_columns(  
  x,  
  ...,  
  axes = c(1, 2),  
  active = TRUE,  
  sup = TRUE,  
  labels = FALSE,  
  highlight = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  main = NULL,  
  sub = NULL,  
  panel.first = NULL,  
  panel.last = NULL,  
  legend = list(x = "topleft")  
)  
  
## S4 method for signature 'BootstrapCA'  
viz_columns(x, ..., axes = c(1, 2))  
  
## S4 method for signature 'PCA'  
viz_variables(  
  x,  
  ...,  
  axes = c(1, 2),  
  active = TRUE,  
  sup = TRUE,  
  labels = TRUE,  
  highlight = NULL,  
  xlim = NULL,  
  ylim = NULL,  
  main = NULL,  
  sub = NULL,  
  panel.first = NULL,  
  panel.last = NULL,  
  legend = list(x = "topleft")  
)  
  
## S4 method for signature 'CA'  
viz_variables(  
  x,  
  ...,
```

```

axes = c(1, 2),
active = TRUE,
sup = TRUE,
labels = FALSE,
highlight = NULL,
xlim = NULL,
ylim = NULL,
main = NULL,
sub = NULL,
panel.first = NULL,
panel.last = NULL,
legend = list(x = "topleft")
)

## S4 method for signature 'BootstrapPCA'
viz_variables(x, ..., axes = c(1, 2))

```

Arguments

x	A CA, MCA or PCA object.
...	Further graphical parameters (see details).
axes	A length-two numeric vector giving the dimensions to be plotted.
active	A logical scalar: should the active observations be plotted?
sup	A logical scalar: should the supplementary observations be plotted?
labels	A logical scalar: should labels be drawn?
highlight	A vector specifying the information to be highlighted. If NULL (the default), no highlighting is applied. If a single character string is passed, it must be one of "observation", "mass", "sum", "contribution" or "cos2" (see augment()). Any unambiguous substring can be given.
xlim	A length-two numeric vector giving the x limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
ylim	A length-two numeric vector giving the y limits of the plot. The default value, NULL, indicates that the range of the finite values to be plotted should be used.
main	A character string giving a main title for the plot.
sub	A character string giving a subtitle for the plot.
panel.first	An expression to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids.
panel.last	An expression to be evaluated after plotting has taken place but before the axes, title and box are added.
legend	A list of additional arguments to be passed to graphics::legend() ; names of the list are used as argument names. If NULL, no legend is displayed.

Details

Commonly used [graphical parameters](#) are:

`pch` A vector of plotting characters or symbols. This can either be a single character or an integer code for one of a set of graphics symbols.

`cex` A numerical vector giving the amount by which plotting characters and symbols should be scaled relative to the default.

`lty` A vector of line types.

`lwd` A vector of line widths.

`col` The colors for lines and points. Multiple colors can be specified so that each point can be given its own color.

`bg` The background color for the open plot symbols given by `pch = 21:25`.

Value

`viz_*()` is called for its side-effects: it results in a graphic being displayed. Invisibly returns `x`.

Note

Be careful: graphical parameters are silently recycled.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [screplot\(\)](#), [viz_contributions\(\)](#), [viz_individuals\(\)](#), [viz_wrap](#), [wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Plot individuals
viz_individuals(X, panel.last = graphics::grid())

## Plot variables
viz_variables(X, panel.last = graphics::grid())

## Graphical parameters
## Continuous values
viz_individuals(X, highlight = iris$Petal.Length, pch = 16)
viz_individuals(X, highlight = iris$Petal.Length, pch = 16,
  col = grDevices::hcl.colors(12, "RdPu"))
viz_individuals(X, highlight = iris$Petal.Length, pch = 16,
```

```

        col = grDevices::hcl.colors(12, "RdPu"),
        cex = c(1, 2))

viz_variables(X, highlight = "contribution",
             col = grDevices::hcl.colors(12, "BluGrn", rev = TRUE),
             lwd = c(1, 5))

## Discrete values
viz_individuals(X, highlight = iris$Species, pch = 21:23)
viz_individuals(X, highlight = iris$Species, pch = 21:23,
              bg = c("#004488", "#DDAA33", "#BB5566"),
              col = "black")

viz_variables(X, highlight = c("Petal", "Petal", "Sepal", "Sepal"),
             col = c("#EE7733", "#0077BB"),
             lty = c(1, 3))

```

viz_wrap

Plot Envelopes

Description

Plot Envelopes

Usage

```
viz_hull(x, ...)
```

```
viz_confidence(x, ...)
```

```
viz_tolerance(x, ...)
```

```
## S4 method for signature 'MultivariateAnalysis'
```

```
viz_tolerance(x, ..., margin = 1, axes = c(1, 2), group = NULL, level = 0.95)
```

```
## S4 method for signature 'BootstrapCA'
```

```
viz_tolerance(x, ..., margin = 1, axes = c(1, 2), level = 0.95)
```

```
## S4 method for signature 'MultivariateAnalysis'
```

```
viz_confidence(x, ..., margin = 1, axes = c(1, 2), group = NULL, level = 0.95)
```

```
## S4 method for signature 'BootstrapCA'
```

```
viz_confidence(x, ..., margin = 1, axes = c(1, 2), level = 0.95)
```

```
## S4 method for signature 'MultivariateAnalysis'
```

```
viz_hull(x, ..., margin = 1, axes = c(1, 2), group = NULL)
```

```
## S4 method for signature 'BootstrapCA'
viz_hull(x, ..., margin = 1, axes = c(1, 2))
```

Arguments

x	An object from which to wrap observations (a <i>CA</i> , <i>MCA</i> or <i>PCA</i> object).
...	Further graphical parameters to be passed to <code>graphics::polygon()</code> .
margin	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
axes	A length-two numeric vector giving the dimensions to be for which to compute results.
group	A vector specifying the group an observation belongs to.
level	A numeric vector specifying the confidence/tolerance level.

Value

`viz_*`() is called for its side-effects: it results in a graphic being displayed. Invisibly returns `x`.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [screeplot\(\)](#), [viz_contributions\(\)](#), [viz_individuals\(\)](#), [viz_variables\(\)](#), [wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Convex hull coordinates
hulls <- wrap_hull(X, margin = 1, group = iris$Species)

## Confidence ellipse coordinates
conf <- wrap_confidence(X, margin = 1, group = iris$Species,
                        level = c(0.68, 0.95))

## Tolerance ellipse coordinates
conf <- wrap_confidence(X, margin = 1, group = iris$Species, level = 0.95)

## Plot with convex hulls
col <- c("#004488", "#DDAA33", "#BB5566")
viz_rows(X, highlight = iris$Species, col = col)
viz_hull(X, group = iris$Species, border = col)
```

 wrap

Wrap Observations

Description

- `wrap_hull()` computes convex hull of a set of observations.
- `wrap_confidence()` computes a confidence ellipse.
- `wrap_tolerance()` computes a tolerance ellipse.

Usage

```
wrap_hull(x, ...)
```

```
wrap_confidence(x, ...)
```

```
wrap_tolerance(x, ...)
```

```
## S4 method for signature 'MultivariateAnalysis'
wrap_confidence(x, margin = 1, axes = c(1, 2), group = NULL, level = 0.95)
```

```
## S4 method for signature 'MultivariateAnalysis'
wrap_tolerance(x, margin = 1, axes = c(1, 2), group = NULL, level = 0.95)
```

```
## S4 method for signature 'MultivariateAnalysis'
wrap_hull(x, margin = 1, axes = c(1, 2), group = NULL)
```

Arguments

<code>x</code>	An object from which to wrap observations (a CA , MCA or PCA object).
<code>...</code>	Currently not used.
<code>margin</code>	A length-one numeric vector giving the subscript which the data will be returned: 1 indicates individuals/rows (the default), 2 indicates variables/columns.
<code>axes</code>	A length-two numeric vector giving the dimensions to be for which to compute results.
<code>group</code>	A vector specifying the group an observation belongs to.
<code>level</code>	A numeric vector specifying the confidence/tolerance level.

Value

`wrap_*`() returns a [data.frame](#) of envelope x and y coordinates.

An extra column named `group` is added specifying the group an observation belongs to.

Author(s)

N. Frerebeau

See Also

Other plot methods: [biplot\(\)](#), [screeplot\(\)](#), [viz_contributions\(\)](#), [viz_individuals\(\)](#), [viz_variables\(\)](#), [viz_wrap](#)

Examples

```
## Load data
data("iris")

## Compute principal components analysis
X <- pca(iris, scale = TRUE)

## Convex hull coordinates
hulls <- wrap_hull(X, margin = 1, group = iris$Species)

## Confidence ellipse coordinates
conf <- wrap_confidence(X, margin = 1, group = iris$Species,
                        level = c(0.68, 0.95))

## Tolerance ellipse coordinates
conf <- wrap_confidence(X, margin = 1, group = iris$Species, level = 0.95)

## Plot with convex hulls
col <- c("#004488", "#DDAA33", "#BB5566")
viz_rows(X, highlight = iris$Species, col = col)
viz_hull(X, group = iris$Species, border = col)
```

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