

Package ‘CAbiplot’

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Type Package

Title Correspondence Analysis Biplots and Diagnostic Reports

Version 0.1.0

Description A convenience wrapper around 'FactoMineR' and 'factoextra' for running Correspondence Analysis (CA) on a numeric data table (e.g. a genotype-by-trait or contingency-style matrix) and producing a full set of publication-ready diagnostic plots: scree plot, symmetric biplot, row-only and column-only plots, row/column contribution plots, and row/column cos2 (quality-of-representation) plots. A single top-level function runs the whole pipeline, prints formatted result tables, and optionally saves every plot as a high-resolution image, mirroring a typical CA reporting workflow used in agronomy and plant-breeding studies. An example genotype-by-trait data set is included.

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ca_biplot	<i>Symmetric CA biplot (rows and columns)</i>
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Description

Symmetric CA biplot (rows and columns)

Usage

```
ca_biplot(res.ca, axes = c(1, 2), col.row = "#1F4E79",
  col.col = "#B22222", ...)
```

Arguments

- res.ca An object of class "CA" from [run_ca](#) or [CA](#).
- axes Length-2 integer vector of the dimensions to plot. Defaults to c(1, 2).
- col.row Color for row points/labels. Defaults to "#1F4E79".
- col.col Color for column points/labels. Defaults to "#B22222".
- ... Additional arguments passed to [fviz_ca_biplot](#).

Value

A ggplot object.

ca_col_plot	CA column-only plot
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Description

CA column-only plot

Usage

```
ca_col_plot(res.ca, axes = c(1, 2), col.col = "#B22222", ...)
```

Arguments

res.ca	An object of class "CA" from run_ca or CA .
axes	Length-2 integer vector of the dimensions to plot. Defaults to c(1, 2).
col.col	Color for column points/labels. Defaults to "#B22222".
...	Additional arguments passed to fviz_ca_col .

Value

A ggplot object.

ca_contrib_plot	Row or column contribution plot
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Description

Row or column contribution plot

Usage

```
ca_contrib_plot(res.ca, choice = c("row", "col"), axes = 1, top = NULL, ...)
```

Arguments

res.ca	An object of class "CA" from run_ca or CA .
choice	Either "row" or "col".
axes	Integer vector of dimension(s) to sum contributions over. Defaults to 1.
top	Number of rows/columns to display. Defaults to all of them.
...	Additional arguments passed to fviz_contrib .

Value

A ggplot object.

ca_cos2_plot	<i>Row or column cos2 (quality of representation) plot</i>
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Description

Row or column cos2 (quality of representation) plot

Usage

```
ca_cos2_plot(res.ca, choice = c("row", "col"), axes = 1:2, top = NULL, ...)
```

Arguments

res.ca	An object of class "CA" from run_ca or CA .
choice	Either "row" or "col".
axes	Integer vector of dimension(s) to sum cos2 over. Defaults to 1:2.
top	Number of rows/columns to display. Defaults to all of them.
...	Additional arguments passed to fviz_cos2 .

Value

A ggplot object.

ca_report	<i>Run a full Correspondence Analysis report</i>
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Description

End-to-end pipeline that runs Correspondence Analysis on data and produces the full battery of diagnostic plots used in the package vignette: a scree plot, a symmetric biplot, row-only and column-only plots, row and column contribution plots (dimensions 1 and 2), row and column cos2 plots, and a combined summary figure. Optionally saves every plot as a high-resolution JPEG and prints formatted result tables to the console, mirroring a typical CA reporting workflow.

Usage

```
ca_report(data, output_dir = ".", prefix = "CA", save_plots = TRUE,
  dpi = 600, verbose = TRUE)
```

Arguments

data	A numeric matrix, numeric data.frame, a path to a delimited text file, or an already-computed object of class "CA".
output_dir	Directory where plots are saved when save_plots = TRUE. Created if it does not already exist. Defaults to the current working directory.
prefix	File name prefix used for saved plots. Defaults to "CA".
save_plots	Logical; save each plot as a JPEG in output_dir? Defaults to TRUE.
dpi	Resolution (dots per inch) used when saving plots. Defaults to 600.
verbose	Logical; print formatted result tables (eigenvalues, coordinates, contributions, cos2) to the console? Defaults to TRUE.

Value

Invisibly, a list with elements:

res.ca The fitted "CA" object.

eig Eigenvalue/inertia table from [get_eigenvalue](#).

plots A named list of the individual ggplot objects (scree, biplot, row, col, contrib_row_dim1, contrib_row_dim2, contrib_col_dim1, contrib_col_dim2, cos2_row, cos2_col) plus combined, a gridExtra arrangement of the scree plot, biplot, and the two dimension-1 contribution plots.

Examples

```
geno <- get_genotype_traits()
report <- ca_report(geno, save_plots = FALSE, verbose = FALSE)
report$plots$biplot
```

ca_row_plot	<i>CA row-only plot</i>
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Description

CA row-only plot

Usage

```
ca_row_plot(res.ca, axes = c(1, 2), col.row = "#1F4E79", ...)
```

Arguments

res.ca	An object of class "CA" from run_ca or CA .
axes	Length-2 integer vector of the dimensions to plot. Defaults to c(1, 2).
col.row	Color for row points/labels. Defaults to "#1F4E79".
...	Additional arguments passed to fviz_ca_row .

Value

A ggplot object.

ca_scree_plot	<i>Scree plot of CA eigenvalues</i>
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Description

Scree plot of CA eigenvalues

Usage

```
ca_scree_plot(res.ca, ...)
```

Arguments

res.ca	An object of class "CA" from run_ca or CA .
...	Additional arguments passed to fviz_eig .

Value

A ggplot object.

get_genotype_traits	<i>Load the bundled example genotype-by-trait data set</i>
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Description

Loads the example data set shipped with the package: a table of plant genotypes (rows) evaluated across six morphological/agronomic traits (columns). This is the same data used in the package vignette and examples.

Usage

```
get_genotype_traits()
```

Value

A numeric data.frame with genotypes as row names and traits as columns.

Examples

```
geno <- get_genotype_traits()
head(geno)
```

read_ca_data	<i>Read a CA-ready numeric data table</i>
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Description

Reads a delimited text file into a numeric data.frame suitable for [CA](#). The first column is used as row names, and every remaining column is coerced to numeric.

Usage

```
read_ca_data(file, sep = ",", header = TRUE, row.names = 1,  
             check.names = FALSE)
```

Arguments

file	Path to a delimited text file (e.g. CSV).
sep	Field separator passed to read.table . Defaults to ",".
header	Logical; does the file have a header row? Defaults to TRUE.
row.names	Column to use as row names, passed to read.table . Defaults to 1 (the first column).
check.names	Logical; passed to read.table . Defaults to FALSE so that column names are kept exactly as written in the file.

Value

A numeric data.frame with row names taken from the input file.

Examples

```
file <- system.file("extdata", "genotype_traits.csv", package = "CAbiplot")  
data <- read_ca_data(file)  
head(data)
```

run_ca	<i>Run Correspondence Analysis on a numeric data table</i>
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Description

Thin, validating wrapper around [CA](#). Accepts either a numeric matrix/data.frame already in memory, or a path to a delimited text file, which is read with [read_ca_data](#).

Usage

```
run_ca(data, ...)
```

Arguments

data	A numeric matrix, numeric data.frame, or a path (character string) to a delimited text file to be read with read_ca_data .
...	Additional arguments passed on to CA (for example ncp, row.sup, col.sup).

Value

An object of class "CA" as returned by [CA](#), computed with graph = FALSE.

Examples

```
geno <- get_genotype_traits()
res.ca <- run_ca(geno)
summary(res.ca)
```

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