Package: GABB (via r-universe)

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Title Facilitation of Data Preparation and Plotting Procedures for RDA and PCA Analyses

Version 0.3.8

Description Help to the occasional R user for synthesis and enhanced graphical visualization of redundancy analysis (RDA) and principal component analysis (PCA) methods and objects. Inputs are : data frame, RDA (package 'vegan') and PCA (package 'FactoMineR') objects. Outputs are : synthesized results of RDA, displayed in console and saved in tables ; displayed and saved objects of PCA graphic visualization of individuals and variables projections with multiple graphic parameters.

Encoding UTF-8

RoxygenNote 7.3.1

Language en

Suggests FactoMineR, testthat (>= 3.0.0)

Config/testthat/edition 3

Imports dplyr, egg (>= 0.4.5), ggforce, ggplot2, ggrepel, ggplotify, ggpubr, tidyr, Hotelling, pheatmap, stats, vegan, utils

NeedsCompilation no

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Contents

`check_data_for_RDA` *check_data_for_RDA function*

Description

This function check if the factor variables used for RDA fit the required conditions. Results are grouped and conclusions go / no go are displayed in the console and saved in a table. This function is mainly derived from the explanations of Maxime Herve `https://www.maximeherve.com/r-et-statistiques`

Usage

```
check_data_for_RDA(data_quant, initial_data, factor_names)
```

Arguments

`data_quant`	Data frame of numeric values, generally transformed and scalled
`initial_data`	Initial data frame, including both numeric and factor columns
`factor_names`	Character vector of considered factor variables/columns : c("Variable1", "Variable2")

Value

Outputs are saved in a data frame and conclusions are displayed in console.

Examples

```
check_data_for_RDA(mtcars[,1:7], mtcars, c("gear","carb"))
```

`PCA_RDA_graphics` *PCA_RDA_graphics function This function facilitate the user creation of PCA (! from FactoMineR package !) enhanced graphics with multiple options. Individuals and variables graphics are possible. With or without variable cor, cos, contrib.. correlation to dimensions. RDA outputs are displayable as table under graphics.*

Description

PCA_RDA_graphics function This function facilitate the user creation of PCA (! from FactoMineR package !) enhanced graphics with multiple options. Individuals and variables graphics are possible. With or without variable cor, cos, contrib.. correlation to dimensions. RDA outputs are displayable as table under graphics.

Usage

```
PCA_RDA_graphics(
  complete.data.set,
  factor.names,
  sample.column,
  PCA.object,
  Var.quanti.supp,
  Display.quanti.supp,
  Dim.a,
  Dim.b,
  Barycenter,
  Segments,
  Barycenter.min.size,
  Ind.min.size,
  Segment.line.type,
  Segment.line.size,
  Segment.line.col,
  Ellipse.IC,
  IC.x,
  Ellipse.sd,
  sd.x,
  Ellipse.transparency,
  Barycenter.Ellipse.Fac1,
  Barycenter.Ellipse.Fac2,
  Barycenter.Ellipse.Fac3,
  factor.colors,
  color.palette,
  factor.shapes,
  factor.sizes,
  Barycenter.factor.col,
  Barycenter.factor.size,
  Barycenter.factor.shape,
  factor.col.border.ellipse,
  ellipse.line.type,
  Var.circle,
  Var.circle.size,
  Var.selected,
  Var.label.size,
  Var.label.repel,
  col.arrow.var.PCA,
  col.text.var.PCA,
  col.arrow.var.supp.PCA,
  col.circle.var.PCA,
  Biplot.PCA,
  width.PCA.ind.graph,
  width.PCA.var.graph,
  width.heat.map.graph,
  Spacing.HM.circle,
```

```
  Heat.map.graph,
  Type.heat.map.graph,
  var.parameter.heat.map,
  Dims.heat.map,
  Display.cell.values.heat.map,
  Top.var.heat.map.Dim.a,
  Top.var.heat.map.Dim.b,
  Multi.dim.combination,
  width.cell.heat.map,
  height.cell.heat.map,
  Cluster.col.heat.map,
  Cluster.row.heat.map,
  RDA.object,
  nbperms,
  RDA.table.graph,
  RDA.table.graph.height,
  Size.RDA.table.graph,
  Get.generated.data.frame
)
```

Arguments

`complete.data.set`	Original complete data set used for the PCA, with quantitative and qualitative/factor columns.
`factor.names`	Character vector regrouping names of considered factor variables of PCA.
`sample.column`	Numeric or name (character) of the individual sample column. Default is data frame row names.
`PCA.object`	The PCA object, built from package FactoMineR. PCA.object <- FactoMineR::PCA(mtcars_quant, scale.unit = T, ncp = 5, graph = F).
`Var.quanti.supp`	Character vector of column name of supplementary quantitative variables for PCA.
`Display.quanti.supp`	TRUE or FALSE. Display supplementary quantitative variable on PCA var and Heat map graphs.
`Dim.a`	Numeric value (1 ; 2 ...) of the first PCA dimension selected for graphic outputs.
`Dim.b`	Numeric value (1 ; 2 ...) of the first PCA dimension selected for graphic outputs.
`Barycenter`	TRUE or FALSE. TRUE : Calculate and Display the barycenter of individuals for Barycenter.Ellipse.Fac1 and/or .2 and/or .3.
`Segments`	TRUE or FALSE. TRUE : Display the linking segments between individuals and barycenters.
`Barycenter.min.size`	Numeric. Minimum size of barycenter point projections. Ignore if Barycenter = FALSE.
`Ind.min.size`	Numeric. Minimum size of individuals point projections.

`Segment.line.type`	Numeric. Type of segment lines (see ggplot2 line type). Ignore if Segments = FALSE.
`Segment.line.size`	Numeric. Minimum size of segment lines. Ignore if Segments = FALSE.
`Segment.line.col`	Character. Set the color of segments. Default = azure4.
`Ellipse.IC`	TRUE or FALSE. TRUE : Calculate and Display Ellipse of mean confidence interval of individuals for Barycenter.Ellipse.Fac1 and/or .2 and/or .3. Default is 95% mean confidence interval.
`IC.x`	0 to 100. Set the value of mean confidence interval of Ellipse.IC parameter. Default is 95.
`Ellipse.sd`	TRUE or FALSE. TRUE : Calculate and Display Ellipse of mean standard deviation of individuals for Barycenter.Ellipse.Fac1 and/or .2 and/or .3. Default is 95% mean confidence interval.
`sd.x`	Numeric. Set the value of the multiplication factor of sd (x*sd) for Ellipse.sd parameter. Default is 1.
`Ellipse.transparency`	Set the transparency level of the ellipse, ranging from 0 to 1. Default is 0.1.
`Barycenter.Ellipse.Fac1`	Character. Name of 1st factor/data frame column for Barycenter / Ellipses calculation.
`Barycenter.Ellipse.Fac2`	Character. Name of 2nd factor/data frame column for Barycenter / Ellipses calculation.
`Barycenter.Ellipse.Fac3`	Character. Name of 3rd factor/data frame column for Barycenter / Ellipses calculation.
`factor.colors`	Character. Name of the factor/column considered for individuals colors.
`color.palette`	Vector of characters of desired colors.
`factor.shapes`	Character. Name of the factor/column considered for individual and barycenter shapes.
`factor.sizes`	Character. Name of the factor/column considered for individual and barycenter colors.
`Barycenter.factor.col`	Character. Name of the factor/column considered for barycenter colors.
`Barycenter.factor.size`	Character. Name of the factor/column considered for barycenter size.
`Barycenter.factor.shape`	Character. Name of the factor/column considered for barycenter shape.
`factor.col.border.ellipse`	Character. Name of the factor/column considered for ellipse border colors.
`ellipse.line.type`	Numeric. R line type for ellipse borders.

`Var.circle`	TRUE or FALSE. TRUE = Display the PCA variable circle projection.
`Var.circle.size`	Numeric. Value for increasing the size of Var.circle graphic.
`Var.selected`	Character vector of selected variables for the PCA plot. Default = all variables.
`Var.label.size`	Numeric. Value for increasing the size of Var.circle graphic labels.
`Var.label.repel`	TRUE or FALSE. For PCA variables graphic, force variable labels to repel.
`col.arrow.var.PCA`	Character. Set the color of arrows for PCA variable plot. Default = gray20.
`col.text.var.PCA`	Character. Set the color of text for PCA variable plot. Default = gray20.
`col.arrow.var.supp.PCA`	Character. Set the color of arrows and text for PCA supplementary variable plot. Default = cadetblue.
`col.circle.var.PCA`	Character. Set the color of the PCA variable circle. Default = gray20.
`Biplot.PCA`	TRUE or FALSE. TRUE = Biplot of PCA individuals and variables graphics. Default is set to FALSE.
`width.PCA.ind.graph`	Numeric. Width ratio for PCA individuals graphic.
`width.PCA.var.graph`	Numeric. Width ratio for PCA variables graphic.
`width.heat.map.graph`	Numeric. Width ratio for Heat map variables graphic.
`Spacing.HM.circle`	Numeric. Width ratio for spacing x axis of circle heat map variables graphic. Default is 0.06.
`Heat.map.graph`	TRUE or FALSE. TRUE = Display the heat map of variable X parameter correlation to dimension.
`Type.heat.map.graph`	Character. Define the type of heat map to display : "square" or "circle". Default = "square".
`var.parameter.heat.map`	Character. Parameter selected for the heat map correlation of Variable parameter to dimensions. values : "cor", "cos2", "coor","contrib". Default = "cor".
`Dims.heat.map`	Numeric. Numeric vector c(1,2) of dimensions considered for the variable parameter correlation.
`Display.cell.values.heat.map`	TRUE or FALSE. TRUE = Display the rounded value of correlations within heat map cells.
`Top.var.heat.map.Dim.a`	Numeric. Number of variables to plot in heat maps and PCA variable projection for Dim a. Default = all.
`Top.var.heat.map.Dim.b`	Numeric. Number of variables to plot in heat maps and PCA variable projection for Dim b. Default = all.

`Multi.dim.combination`	TRUE or FALSE. TRUE = display 10 plots of PCA ind and variables dims combination (1,2 ; 1,3...).
`width.cell.heat.map`	Numeric. Width for Heat map cells. Default set to default pheat.map.
`height.cell.heat.map`	Numeric. Width for Heat map cells. Default set to default pheat.map.
`Cluster.col.heat.map`	TRUE or FALSE. TRUE = cluster heat.map columns / dimensions.
`Cluster.row.heat.map`	TRUE or FALSE. TRUE = cluster heat.map rows / quantitative variables.
`RDA.object`	The RDA object, built from package vegan. RDA.object <- vegan::rda(mtcars_quant, scale.unit = T, ncp = 5, graph = F).
`nbperms`	Numeric number of permutations used by the RDA.anova function. Default is 1000.
`RDA.table.graph`	TRUE or FALSE. TRUE = Display the RDA outputs table under PCA graphics.
`RDA.table.graph.height`	Numeric. Set the ratio of RDA table graphic height. Default is set to 1.
`Size.RDA.table.graph`	Numeric. Set the ratio of RDA table graphic size. Default is set to 7.
`Get.generated.data.frame`	TRUE or FALSE. TRUE = save the generated data frames for graphic constructions. Default = FALSE.

Value

Several graphics

Examples

```
library(FactoMineR)
my.PCA <- FactoMineR::PCA(mtcars[,1:7], scale.unit = FALSE, ncp = 5, graph = FALSE)
PCA_RDA_graphics(complete.data.set = mtcars, factor.names = c("vs", "gear"), PCA.object = my.PCA)
```

`prep_data` *prep_data function*

Description

This function helps user to transform and scale quantitative defined data (columns identitified from a given dataset) for better PCA and RDA outputs.

Usage

```
prep_data(data, quantitative_columns, transform_data_method, scale_data)
```

Arguments

`data`	A data frame with at least one numeric column
`quantitative_columns`	Numeric vector of numeric columns position : c(1,2,4)
`transform_data_method`	Method of quantitative data transformation : "log", "sqrt4", "clr", "none"
`scale_data`	TRUE or FALSE. TRUE => scaling of quantitative columns

Value

The transformed/scaled quantitative data frame

Examples

```
prep_data(mtcars, c(1:7), "log", TRUE)
```

`RDA_outputs_synthesis` *RDA_outputs_synthesis function*

Description

This function facilitate output analysis of vegan package RDA.

Usage

```
RDA_outputs_synthesis(RDA, RDA.synth, RDA.anova, nbperms, RDA.Table)
```

Arguments

`RDA`	The RDA object : RDA <- vegan::rda(mtcars_quant~gear+carb,data=mtcars)
`RDA.synth`	TRUE or FALSE. If TRUE, displays the RDA model's global variance partitioning. Default is TRUE.
`RDA.anova`	TRUE or FALSE. If TRUE, prints the results of the vegan function anova.cca, displaying the variance partitioning by terms in the RDA model. Default is TRUE.
`nbperms`	Numeric number of permutations used by the RDA.anova function. Default is 1000.
`RDA.Table`	TRUE or FALSE. TRUE : calculate and display the variance percentage of considered factor / total unconstrained variance. Default : TRUE.

Value

Results can be displayed in the console. Outputs are saved in data frame.

Examples

```
library(vegan)
my.RDA <- vegan::rda(mtcars[,1:7]~vs+am+gear, data=mtcars)
RDA_outputs_synthesis(RDA = my.RDA, RDA.synth = TRUE, RDA.anova = FALSE, RDA.Table = TRUE)
```

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