Package ‘ggcorrplot’

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Type Package

Title Visualization of a Correlation Matrix using 'ggplot2'

Version 0.1.4.1

Description The 'ggcorrplot' package can be used to visualize easily a correlation matrix using 'ggplot2'. It provides a solution for reordering the correlation matrix and displays the significance level on the plot. It also includes a function for computing a matrix of correlation p-values.

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URL `http://www.sthda.com/english/wiki/ggcorrplot-visualization-of-a-correlation-matrix-using-ggplot2`

BugReports `https://github.com/kassambara/ggcorrplot/issues`

Depends R (>= 3.3), ggplot2 (>= 3.3.6)

Imports reshape2, stats

Suggests testthat (>= 3.0.0), knitr, spelling, vdiffr (>= 1.0.0)

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NeedsCompilation no

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R topics documented:

`ggcorrplot` *Visualization of a correlation matrix using ggplot2*

Description

- ggcorrplot(): A graphical display of a correlation matrix using ggplot2.
- cor_pmat(): Compute a correlation matrix p-values.

Usage

```
ggcorrplot(
  corr,
  method = c("square", "circle"),
  type = c("full", "lower", "upper"),
  ggtheme = ggplot2::theme_minimal,
  title = "",
  show.legend = TRUE,
  legend.title = "Corr",
  show.diag = NULL,
  colors = c("blue", "white", "red"),
  outline.color = "gray",
  hc.order = FALSE,
  hc.method = "complete",
  lab = FALSE,
  lab_col = "black",
  lab_size = 4,
  p.mat = NULL,
  sig.level = 0.05,
  insig = c("pch", "blank"),
  pch = 4,
  pch.col = "black",
  pch.cex = 5,
  tl.cex = 12,
  tl.col = "black",
  tl.srt = 45,
  digits = 2,
  as.is = FALSE
)

cor_pmat(x, ...)
```

Arguments

`corr`	the correlation matrix to visualize
`method`	character, the visualization method of correlation matrix to be used. Allowed values are "square" (default), "circle".

`type`	character, "full" (default), "lower" or "upper" display.
`ggtheme`	ggplot2 function or theme object. Default value is ‘theme_minimal‘. Allowed values are the official ggplot2 themes including theme_gray, theme_bw, theme_minimal, theme_classic, theme_void, ... Theme objects are also allowed (e.g., ‘theme_classic()‘).
`title`	character, title of the graph.
`show.legend`	logical, if TRUE the legend is displayed.
`legend.title`	a character string for the legend title. lower triangular, upper triangular or full matrix.
`show.diag`	NULL or logical, whether display the correlation coefficients on the principal diagonal. If `NULL`, the default is to show diagonal correlation for `type = "full"` and to remove it when `type` is one of "upper" or "lower".
`colors`	a vector of 3 colors for low, mid and high correlation values.
`outline.color`	the outline color of square or circle. Default value is "gray".
`hc.order`	logical value. If TRUE, correlation matrix will be hc.ordered using hclust function.
`hc.method`	the agglomeration method to be used in hclust (see ?hclust).
`lab`	logical value. If TRUE, add correlation coefficient on the plot.
`lab_col, lab_size`	size and color to be used for the correlation coefficient labels. used when lab = TRUE.
`p.mat`	matrix of p-value. If NULL, arguments sig.level, insig, pch, pch.col, pch.cex is invalid.
`sig.level`	significant level, if the p-value in p-mat is bigger than sig.level, then the corresponding correlation coefficient is regarded as insignificant.
`insig`	character, specialized insignificant correlation coefficients, "pch" (default), "blank". If "blank", wipe away the corresponding glyphs; if "pch", add characters (see pch for details) on corresponding glyphs.
`pch`	add character on the glyphs of insignificant correlation coefficients (only valid when insig is "pch"). Default value is 4.
`pch.col, pch.cex`	the color and the cex (size) of pch (only valid when insig is "pch").
`tl.cex, tl.col, tl.srt`	the size, the color and the string rotation of text label (variable names).
`digits`	Decides the number of decimal digits to be displayed (Default: ‘2‘).
`as.is`	A logical passed to `melt.array`. If `TRUE`, dimnames will be left as strings instead of being converted using `type.convert`.
`x`	numeric matrix or data frame
`...`	other arguments to be passed to the function cor.test.

Value

- ggcorrplot(): Returns a ggplot2
- cor_pmat(): Returns a matrix containing the p-values of correlations

Examples

```
# Compute a correlation matrix
data(mtcars)
corr <- round(cor(mtcars), 1)
corr

# Compute a matrix of correlation p-values
p.mat <- cor_pmat(mtcars)
p.mat

# Visualize the correlation matrix
# --------------------------------
# method = "square" or "circle"
ggcorrplot(corr)
ggcorrplot(corr, method = "circle")

# Reordering the correlation matrix
# --------------------------------
# using hierarchical clustering
ggcorrplot(corr, hc.order = TRUE, outline.color = "white")

# Types of correlogram layout
# --------------------------------
# Get the lower triangle
ggcorrplot(corr,
  hc.order = TRUE, type = "lower",
  outline.color = "white"
)
# Get the upeper triangle
ggcorrplot(corr,
  hc.order = TRUE, type = "upper",
  outline.color = "white"
)

# Change colors and theme
# --------------------------------
# Argument colors
ggcorrplot(corr,
  hc.order = TRUE, type = "lower",
  outline.color = "white",
  ggtheme = ggplot2::theme_gray,
  colors = c("#6D9EC1", "white", "#E46726")
)

# Add correlation coefficients
# --------------------------------
# argument lab = TRUE
ggcorrplot(corr,
  hc.order = TRUE, type = "lower",
  lab = TRUE,
  ggtheme = ggplot2::theme_dark(),
)
```

```
# Add correlation significance level
# --------------------------------
# Argument p.mat
# Barring the no significant coefficient
ggcorrplot(corr,
  hc.order = TRUE,
  type = "lower", p.mat = p.mat
)
# Leave blank on no significant coefficient
ggcorrplot(corr,
  p.mat = p.mat, hc.order = TRUE,
  type = "lower", insig = "blank"
)

# Changing number of digits for correlation coeffcient
# --------------------------------
ggcorrplot(cor(mtcars),
  type = "lower",
  insig = "blank",
  lab = TRUE,
  digits = 3
)
```

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