Package 'ggcorrplot'

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Type Package

Title Visualization of a Correlation Matrix using 'ggplot2'

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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.

License GPL-2

LazyData TRUE

Depends ggplot2

Imports reshape2, stats

Suggests knitr

URL http://www.sthda.com/english/wiki/ggcorrplot

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

RoxygenNote 6.0.1

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.

Compute the matrix of correlation 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 = FALSE,
  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)

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	logical, whether display the correlation coefficients on the principal diagonal.
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').
`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.col = "white")

# Types of correlogram layout
```

```
# -------------------------------
# Get the lower triangle
ggcorrplot(corr,
  hc.order = TRUE, type = "lower",
  outline.col = "white"
)
# Get the upeper triangle
ggcorrplot(corr,
  hc.order = TRUE, type = "upper",
  outline.col = "white"
)

# Change colors and theme
# -------------------------------
# Argument colors
ggcorrplot(corr,
  hc.order = TRUE, type = "lower",
  outline.col = "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"
)
```

Index