

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, vdiff (>= 1.0.0)

Encoding UTF-8

Language en-US

RoxygenNote 7.1.0

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NeedsCompilation no

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ggcorrplot	<i>Visualization of a correlation matrix using ggplot2</i>
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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 <code>melt.array</code> . If TRUE, dimnames will be left as strings instead of being converted using <code>type.convert</code> .
x	numeric matrix or data frame
...	other arguments to be passed to the function <code>cor.test</code> .

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 upper 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 coefficient
# -----
ggcorrplot(cor(mtcars),
  type = "lower",
  insig = "blank",
  lab = TRUE,
  digits = 3
)
```

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