

Package ‘ggcorrplot’

August 29, 2016

Type Package

Title Visualization of a Correlation Matrix using 'ggplot2'

Version 0.1.1

Date 2016-01-12

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>

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

RoxygenNote 5.0.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2016-01-12 23:12:53

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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)
```

```
cor_pmat(x, ...)
```

Arguments

<code>corr</code>	the correlation matrix to visualize
<code>method</code>	character, the visualization method of correlation matrix to be used. Allowed values are "square" (default), "circle".
<code>type</code>	character, "full" (default), "lower" or "upper" display.
<code>ggtheme</code>	function, <code>ggplot2</code> theme name. Default value is <code>theme_minimal</code> . Allowed values are the official <code>ggplot2</code> themes including <code>theme_gray</code> , <code>theme_bw</code> , <code>theme_minimal</code> , <code>theme_classic</code> , <code>theme_void</code> ,
<code>title</code>	character, title of the graph.
<code>show.legend</code>	logical, if TRUE the legend is displayed.
<code>legend.title</code>	a character string for the legend title. lower triangular, upper triangular or full matrix.
<code>show.diag</code>	logical, whether display the correlation coefficients on the principal diagonal.
<code>colors</code>	a vector of 3 colors for low, mid and high correlation values.
<code>outline.color</code>	the outline color of square or circle. Default value is "gray".
<code>hc.order</code>	logical value. If TRUE, correlation matrix will be hc.ordered using <code>hclust</code> function.
<code>hc.method</code>	the agglomeration method to be used in <code>hclust</code> (see <code>?hclust</code>).
<code>lab</code>	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).
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 upper 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)

# 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")
```

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