

Package ‘forplo’

March 31, 2021

Type Package

Title Flexible Forest Plots

Version 0.1.0

Description Simplifies the creation and customization of forest plots (alternatively called dot-and-whisker plots). Input classes accepted by 'forplo' are data.frame, matrix, lm, glm, and coxph. 'forplo' was written in base R and does not depend on other packages.

License GPL-3

Encoding UTF-8

Language en-US

Depends R (>= 3.5.0)

VignetteBuilder knitr, rmarkdown, lattice

RoxygenNote 7.1.1

Suggests knitr, rmarkdown, lattice, MASS, meta, survival

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-03-31 09:00:02 UTC

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forplo

forplo - flexible forest plots with R

Description

forplo is an R package meant to simplify the creation and customization of forest plots (alternatively called dot-and-whisker plots). Input classes accepted by forplo are `data.frame`, `matrix`, `lm`, `glm`, and `coxph`. forplo was written in base R and does not depend on other packages. For extensive examples and how to use all arguments for customization, please refer to the package vignette.

Usage

```
forplo(  
  mat,  
  em = "OR",  
  row.labels = NULL,  
  linreg = FALSE,  
  prop = FALSE,  
  pval = NULL,  
  xlim = xlimits,  
  fliprow = NULL,  
  flipbelow1 = FALSE,  
  flipsymbol = "*",  
  ci.sep = "-",  
  ci.lwd = 1.5,  
  ci.edge = TRUE,  
  font = "Calibri",  
  groups = NULL,  
  grouplabs = NULL,  
  group.space = 1,  
  group.italics = FALSE,  
  left.align = FALSE,  
  favorlabs = NULL,  
  sort = FALSE,  
  char = 20,  
  size = 1.5,  
  col = 1,  
  insig.col = "gray",  
  scaledot.by = NULL,  
  scaledot.factor = 0.75,  
  diamond = NULL,  
  diamond.col = col,  
  diamond.line = TRUE,  
  add.columns = NULL,  
  add.colnames = NULL,  
  right.bar = FALSE,  
  rightbar.ticks = 0,  
)
```

```

left.bar = TRUE,
leftbar.ticks = 0,
shade.every = NULL,
shade.col = "red",
shade.alpha = 0.05,
fill.by = NULL,
fill.colors = NULL,
margin.left = NULL,
margin.top = 0,
margin.bottom = 2,
margin.right = 10,
horiz.bar = FALSE,
title = NULL,
save = FALSE,
save.path = NULL,
save.name = NULL,
save.type = "png",
save.width = 9,
save.height = 4.5
)

```

Arguments

mat	An n*3 data.frame or matrix, or a regression model of class lm, glm or coxph.
em	Effect measure to be displayed (e.g. OR, RR, HR).
row.labels	Labels to display as variable names (character vector of length nrow(mat)).
linreg	Set to TRUE if the estimates are from a linear regression model.
prop	Set to TRUE if the estimates are proportions.
pval	A numeric or character vector of same length as nrow(mat), with p-values.
xlim	A numeric vector of length 2 indicating the limits of the x-axis.
fliprow	A numeric vector indicating which estimates should be inverted (only for ratios).
flipbelow1	Set to TRUE to invert all ratios below 1.
flipsymbol	A symbol to display besides inverted estimates. Asterisk by default.
ci.sep	The separator between confidence intervals. Dash by default.
ci.lwd	Line width for the confidence interval 'whiskers'.
ci.edge	Set to FALSE to remove the 90 degree edges at the end of the CI whiskers.
font	Controls the font family. 'Calibri' by default. Note: monospaced fonts work poorly.
groups	A numeric vector of length nrow(mat) indicating group membership of each element.
grouplabs	A character vector of equal length to the number of groups, with the labels of each group.
group.space	A single numeric value to indicate how much empty rows should be between grouped estimates.

<code>group.italics</code>	Set to TRUE to italicize the group labels.
<code>left.align</code>	Set to TRUE to left align variable and group labels.
<code>favorlabs</code>	A character vector of length 2, providing labels for underneath the x-axis (e.g. <code>c(' favors control', ' favors intervention')</code>).
<code>sort</code>	Set to TRUE to sort the rows by effect size (not compatible with groups or diamond).
<code>char</code>	Controls the character to display for the dots. Equivalent to <code>pch</code> in the base R plot function.
<code>size</code>	Controls the size of the dots. Equivalent to <code>cex</code> in the base R plot function.
<code>col</code>	Controls the color of the dots. Equivalent to <code>col</code> in the base R plot function.
<code>insig.col</code>	Controls the color of the CI whiskers when crossing the null line. Gray by default.
<code>scaledot.by</code>	Numeric vector of length <code>nrow(mat)</code> to indicate relative importance of each variable (e.g. sample size, weight).
<code>scaledot.factor</code>	Scaling factor (scalar) for <code>scaledot.by</code> , to adapt the size of all scaled dots at once.
<code>diamond</code>	Numeric vector indicating the rows that should be displayed as diamonds (e.g. for meta-analytic estimates).
<code>diamond.col</code>	Controls the color of the diamonds.
<code>diamond.line</code>	Shows a dotted vertical line through the last diamond. Set to FALSE to disable.
<code>add.columns</code>	A data.frame of <code>nrow(mat)</code> with additional columns to add to the right of the plot.
<code>add.colnames</code>	A character vector of length <code>ncol(add.columns)</code> with column labels for these columns.
<code>right.bar</code>	Set to TRUE to show a vertical bar directly to the left of the estimates.
<code>rightbar.ticks</code>	Controls the tick marks on the right axis.
<code>left.bar</code>	Set to FALSE to remove the horizontal bar on the left axis.
<code>leftbar.ticks</code>	Controls the tick marks on the left axis.
<code>shade.every</code>	Controls row shading option. A value of 1 colors every other row, a value of 2 per blocks of 2, etc. Non-integer values also allowed.
<code>shade.col</code>	Controls the default row shading color. Default is 'red'.
<code>shade.alpha</code>	Controls the transparency of the row shading color. Default is 0.05.
<code>fill.by</code>	Numeric vector of length <code>nrow(mat)</code> indicating color group membership of each element.
<code>fill.colors</code>	Character vector of length <code>unique(fill.by)</code> , with colors for each color group.
<code>margin.left</code>	Controls size of left margin.
<code>margin.top</code>	Controls size of top margin.
<code>margin.bottom</code>	Controls size of bottom margin.
<code>margin.right</code>	Controls size of right margin.
<code>horiz.bar</code>	Set to TRUE to display a horizontal bar below the plot.

<code>title</code>	Title to display above the plot. Equivalent to <code>title</code> in the base R plot function.
<code>save</code>	Set to <code>TRUE</code> to save the plot (also requires <code>save.name</code> and <code>save.path</code>) in 300 dpi resolution.
<code>save.path</code>	Indicates folder where the plot should be saved.
<code>save.name</code>	Name of the plot (should not include filetype extension).
<code>save.type</code>	Filetype of the saved plot. Default is <code>.png</code> , but also supports <code>.wmf</code> on Windows.
<code>save.width</code>	Width of the saved plot in inches. Default is 9.
<code>save.height</code>	Height of the saved plot in inches. Default is 4.5.

Value

The function plots in the user's plot window, but does not return anything.

Examples

```
##### Create some regression models #####
mod1 <- lm(Sepal.Length~Sepal.Width+Species+Petal.Width+Petal.Length,iris)

##### Example forest plots#####
# default plot for linear regression model
forplo(mod1,font='Helvetica')

# customized plot for linear regression model
forplo(mod1,
       font='Helvetica',
       row.labels=c('Sepal width','Versicolor','Virginica','Petal width','Petal length'),
       groups=c(1,2,2,3,3),
       grouplabs=c('Sepal traits','Species','Petal traits'),
       shade.every=1,
       shade.col='gray',
       left.align=TRUE,
       xlim=c(-2,2),
       title='Linear regression with grouped estimates')

## More examples are given in the vignette.
```

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