

Package: forplo (via r-universe)

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Type Package

Title Flexible Forest Plots

Version 0.2.5

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.

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Depends R (>= 3.5.0)

VignetteBuilder knitr, rmarkdown, lattice

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

NeedsCompilation no

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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 = "sans",  
  groups = NULL,  
  grouplabs = NULL,  
  group.space = 1,  
  group.italics = FALSE,  
  indent.groups = NULL,  
  left.align = FALSE,  
  favorlabs = NULL,  
  add.arrow.left = FALSE,  
  add.arrow.right = FALSE,  
  arrow.left.length = 3,  
  arrow.right.length = 3,  
  arrow.vadj = 0,  
  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,
column.spacing = 3,
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,
fill.labs = NULL,
legend = FALSE,
legend.vadj = 0,
legend.hadj = 0,
legend.spacing = 1,
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

| | |
|-------------------------|---------------------------------------------------------------------------------------------------------------------------------|
| <code>mat</code> | An $n \times 3$ data.frame or matrix, or a regression model of class <code>lm</code> , <code>glm</code> or <code>coxph</code> . |
| <code>em</code> | Effect measure to be displayed (e.g. OR, RR, HR). |
| <code>row.labels</code> | Labels to display as variable names (character vector of length <code>nrow(mat)</code>). |
| <code>linreg</code> | Set to TRUE if the estimates are from a linear regression model. |
| <code>prop</code> | Set to TRUE if the estimates are proportions. |
| <code>pval</code> | A numeric or character vector of same length as <code>nrow(mat)</code> , with p-values. |
| <code>xlim</code> | A numeric vector of length 2 indicating the limits of the x-axis. |
| <code>fliprow</code> | A numeric vector indicating which estimates should be inverted (only for ratios). |
| <code>flipbelow1</code> | Set to TRUE to invert all ratios below 1. |
| <code>flipsymbol</code> | A symbol to display besides inverted estimates. Asterisk by default. |
| <code>ci.sep</code> | The separator between confidence intervals. Dash by default. |

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| <code>ci.lwd</code> | Line width for the confidence interval 'whiskers'. |
| <code>ci.edge</code> | Set to FALSE to remove the 90 degree edges at the end of the CI whiskers. |
| <code>font</code> | Controls the font family. 'Calibri' by default. Note: monospaced fonts work poorly. |
| <code>groups</code> | A numeric vector of length <code>nrow(mat)</code> indicating group membership of each element. |
| <code>grouplabs</code> | A character vector of equal length to the number of groups, with the labels of each group. |
| <code>group.space</code> | 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>indent.groups</code> | A numeric vector indicating which groups to indent (works only when <code>left.align==TRUE</code>) |
| <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>add.arrow.left</code> | Adds an arrow pointing left underneath the x-axis. |
| <code>add.arrow.right</code> | Adds an arrow pointing right underneath the x-axis. |
| <code>arrow.left.length</code> | Controls the length of the arrow pointing left. |
| <code>arrow.right.length</code> | Controls the length of the arrow pointing right. |
| <code>arrow.vadj</code> | Allows to adjust the vertical placement of the arrows. |
| <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. |

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| <code>add.colnames</code> | A character vector of length <code>ncol(add.columns)</code> with column labels for these columns. |
| <code>column.spacing</code> | A constant that controls the horizontal spacing between added columns. |
| <code>right.bar</code> | Set to <code>TRUE</code> 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 <code>FALSE</code> 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>fill.labs</code> | Character vector of length <code>fill.colors</code> , specifying the legend labels. |
| <code>legend</code> | Set to <code>TRUE</code> to display a legend if <code>fill.colors</code> is not <code>NULL</code> . |
| <code>legend.vadj</code> | Controls the vertical placement of the legend. |
| <code>legend.hadj</code> | Controls the horizontal placement of the legend. |
| <code>legend.spacing</code> | Controls the spacing between legend items. |
| <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 <code>TRUE</code> 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)

# customized plot for linear regression model
forplo(mod1,
  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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