Package ‘forestplot’

September 3, 2021

Version 2.0.1
Title Advanced Forest Plot Using ‘grid’ Graphics
Description A forest plot that allows for
multiple confidence intervals per row,
custom fonts for each text element,
custom confidence intervals,
text mixed with expressions, and more.
The aim is to extend the use of forest plots beyond meta-analyses.
This is a more general version of the original ‘rmeta’ package’s forestplot() function and relies heavily on the ‘grid’ package.

License GPL-2

URL https://gforge.se/packages/

BugReports https://github.com/gforge/forestplot/issues

Biarch yes

Depends R (>= 3.5.0), grid, magrittr, checkmate

Suggests testthat, abind, knitr, rmarkdown, rmeta, dplyr, tidyr, rlang

Encoding UTF-8

NeedsCompilation no

VignetteBuilder knitr

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Description

The forest plot function, `forestplot`, is a more general version of the original `rmeta`-packages `forestplot` implementation. The aim is at using forest plots for more than just meta-analyses.

Details

The forestplot:
1. Allows for multiple confidence intervals per row
2. Custom fonts for each text element
3. Custom confidence intervals
4. Text mixed with expressions
5. Legends both on top/left of the plot and within the graph
6. Custom line height including auto-adapt height
7. Graph width that auto-adapts
8. Flexible arguments
9. and more

Additional functions

The `getTicks` tries to format ticks for plots in a nicer way. The major use is for exponential form where ticks are generated using the \(2^n\) since a doubling is a concept easy to grasp for less mathematical-savvy readers.
Description

As forestpot has evolved we now primarily use 'tidyverse' select style. This function helps with backward compatibility.

Usage

```r
assertAndRetrieveTidyValue(
  x,
  value,
  name = deparse(substitute(value)),
  optional = FALSE
)
```

Arguments

- `x`: The data with the potential value
- `value`: The value
- `name`: The name of the value
- `optional`: Is the value optional

Value

value with attribute

dfHRQoL  

Regression coefficients and confidence intervals from HRQoL study

Description

The data is a dataframe with the Swedish and the Danish coefficients for health related quality of life (HRQoL) 1 year after total hip arthroplasty surgery. The age is modeled as a spline and is therefore presented as a contrast.

Author(s)

Max Gordon <max@gforge.se>
Description

The forestplot is based on the rmeta-package's forestplot function. This function resolves some limitations of the original functions such as:

- Adding expressions: Allows use of expressions, e.g. expression(beta)
- Multiple bands: Using multiple confidence bands for the same label
- Autosize: Adapts to viewport (graph) size

Usage

forestplot(...)

## S3 method for class 'data.frame'
forestplot(x, mean, lower, upper, labeltext, is.summary, ...)

## Default S3 method:
forestplot(labeltext,
    mean,
    lower,
    upper,
    align,
    is.summary = FALSE,
    graph.pos = "right",
    hrzl_lines,
    clip = c(-Inf, Inf),
    xlab = "",
    zero = ifelse(xlog, 1, 0),
    graphwidth = "auto",
    colgap,
    lineHeight = "auto",
    line.margin,
    col = fpColors(),
    txt_gp = fpTxtGp(),
    xlog = FALSE,
    xticks,
    xticks.digits = 2,
    grid = FALSE,
    lwd.xaxis,
    lwd.zero,
    lwd.ci,
    lty.ci = 1,
ci.vertices,  
ci.vertices.height = 0.1,  
boxsize,  
mar = unit(rep(5, times = 4), "mm"),  
title,  
legend,  
legend_args = fpLegend(),  
n_new_page = getOption("forestplot_new_page", TRUE),  
fn.ci_norm = fpDrawNormalCI,  
fn.ci_sum = fpDrawSummaryCI,  
fn.legend,  
shapes_gp = fpShapesGp(),  
...  
)
## S3 method for class 'gforge_forestplot'
print(x, ...)
## S3 method for class 'gforge_forestplot'
plot(x, y, ...)
## S3 method for class 'grouped_df'
forestplot(x, labeltext, mean, lower, upper, legend, is.summary, ...)

Arguments

... Passed on to the fn.ci_norm and fn.ci_sum arguments
x The 'gforge_forestplot' object to be printed
mean The name of the column if using the *dplyr* select syntax - defaults to "mean", else it should be a vector or a matrix with the averages. You can also provide a 2D/3D matrix that is automatically converted to the lower/upper parameters. The values should be in exponentiated form if they follow this interpretation, e.g. use exp(mean) if you have the output from a logistic regression
lower The lower bound of the confidence interval for the forestplot, needs to be the same format as the mean.
upper The upper bound of the confidence interval for the forestplot, needs to be the same format as the mean.
labeltext A list, matrix, vector or expression with the names of each row or the name of the column if using the *dplyr* select syntax - defaults to "labeltext". Note that when using 'group_by' a separate labeltext is not allowed. The list should be wrapped in m x n number to resemble a matrix: list(list("rowname 1 col 1","rowname 2 col 1"),list("r1c2",expression(beta))). You can also provide a matrix although this cannot have expressions by design: matrix(c("rowname 1 col 1","rowname 2 col 1","r1c2","beta"),ncol = 2). Use NA:s for blank spaces and if you provide a full column with NA then that column is a empty column that adds some space. 
Note: If you do not provide the mean/lower/upper arguments the function expects the label text to be a matrix containing the label text in the rownames and then columns for mean, lower, and upper.
is.summary  A vector indicating by TRUE/FALSE if the value is a summary value which means
that it will have a different font-style
align       Vector giving alignment (l,r,c) for the table columns
graph.pos   The position of the graph element within the table of text. The position can be
1-(ncol(labeltext) + 1). You can also choose set the position to "left" or "right".
hrzl_lines  Add horizontal lines to graph. Can either be TRUE or a list of gpar. See line
section below for details.
clip        Lower and upper limits for clipping confidence intervals to arrows
xlab        x-axis label
zero        x-axis coordinate for zero line. If you provide a vector of length 2 it will print a
rectangle instead of just a line. If you provide NA the line is suppressed.
graphwidth  Width of confidence interval graph, see unit for details on how to utilize mm
etc. The default is auto, that is it uses up whatever space that is left after adjusting
for text size and legend
colgap      Sets the gap between columns, defaults to 6 mm but for relative widths. Note
that the value should be in unit, "npc".
lineheight  Height of the graph. By default this is auto and adjusts to the space that is left
after adjusting for x-axis size and legend. Sometimes it might be desirable to set
the line height to a certain height, for instance if you have several forestplots you
may want to standardize their line height, then you set this variable to a certain
height, note this should be provided as a unit object. A good option is to set the
line height to unit(2, "cm"). A third option is to set line height to "lines" and
then you get 50 % more than what the text height is as your line height
line.margin Set the margin between rows, provided in numeric or unit form. When having
multiple confidence lines per row setting the correct margin in order to visually
separate rows
col         Set the colors for all the elements. See fpColors for details
txt_gp      Set the fonts etc for all text elements. See fpTxtGp for details
xlog        If TRUE, x-axis tick marks are to follow a logarithmic scale, e.g. for logistic
regressoin (OR), survival estimates (HR), Poisson regression etc. Note: This is
an intentional break with the original forestplot function as I’ve found that
exponentiated ticks/clips/zero effect are more difficult to for non-statisticians
and there are sometimes issues with rounding the tick marks properly.
xticks      Optional user-specified x-axis tick marks. Specify NULL to use the defaults, nu-
numeric(0) to omit the x-axis. By adding a labels-attribute, attr(my_ticks,"labels")
<-. ... you can dictate the outputted text at each tick. If you specify a boolean
vector then ticks indicated with FALSE wont be printed. Note that the labels
have to be the same length as the main variable.
xticks.digits The number of digits to allow in the x-axis if this is created by default
grid        If you want a discrete gray dashed grid at the level of the ticks you can set
this parameter to TRUE. If you set the parameter to a vector of values lines will be
drawn at the corresponding positions. If you want to specify the gpar
of the lines then either directly pass a gpar object or set the gp attribute e.g.
attr(line_vector,"gp") <- gpar(lty = 2,col = "red")
lwd.xaxis  lwd for the xaxis, see gpar
lwd.zero  lwd for the vertical line that gives the no-effect line, see gpar
lwd.ci  lwd for the confidence bands, see gpar
lty.ci  lty for the confidence bands, see gpar
ci.vertices  Set this to TRUE if you want the ends of the confidence intervals to be shaped as a T. This is set default to TRUE if you have any other line type than 1 since there is a risk of a dash occurring at the very end, i.e. showing incorrectly narrow confidence interval.
ci.vertices.height  The height of the vertices. Defaults to npc units corresponding to 10% of the row height. *Note that the arrows correspond to the vertices heights.*
boxsize  Override the default box size based on precision
mar  A numerical vector of the form c(bottom, left, top, right) of the type unit
title  The title of the plot if any
legend  Legend corresponding to the number of bars
legend_args  The legend arguments as returned by the fpLegend function.
new_page  If you want the plot to appear on a new blank page then set this to TRUE, by default it is TRUE. If you want to change this behavior for all plots then set the options(forestplot_new_page = FALSE)
fn.ci_norm  You can specify exactly how the line with the box is drawn for the normal (i.e. non-summary) confidence interval by changing this parameter to your own function or some of the alternatives provided in the package. It defaults to the box function fpDrawNormalCI
fn.ci_sum  Same as previous argument but for the summary outputs and it defaults to fpDrawSummaryCI.
fn.legend  What type of function should be used for drawing the legends, this can be a list if you want different functions. It defaults to a box if you have anything else than a single function or the number of columns in the mean argument
shapes_gp  Sets graphical parameters (squares and lines widths, styles, etc.) of all shapes drawn (squares, lines, diamonds, etc.). This overrides col, lwd.xaxis, lwd.zero, lwd.ci and lty.ci.
y  Ignored

**Details**

See vignette("forestplot") for details.

**Value**

NULL

**Multiple bands**

Using multiple bands, i.e. multiple lines, per variable can be interesting when you want to compare different outcomes. E.g. if you want to compare survival specific to heart disease to overall survival for smoking it may be useful to have two bands on top of each other. Another useful implementation is to show crude and adjusted estimates as separate bands.
**Horizontal lines**

The argument *hrzl_lines* can be either TRUE or a list with *gpar* elements:

- **TRUE**: A line will be added based upon the *is.summary* rows. If the first line is a summary it
- **gpar**: The same as above but the lines will be formatted according to the *gpar* element
- **list**: The list must either be numbered, i.e. `list("2" = gpar(lty = 1))`, or have the same length as the `NROW(mean) + 1`. If the list is numbered the numbers should not exceed the `NROW(mean) + 1`. The no. *1 row designates the top*, i.e. the line above the first row, all other correspond to *the row below*. Each element in the list needs to be TRUE, NULL, or *gpar* element. The TRUE defaults to a standard line, the NULL skips a line, while *gpar* corresponds to the fully customized line. Apart from allowing standard *gpar* line descriptions, `lty`, `lwd`, `col`, and more you can also specify `gpar(columns = c(1:3, 5))` if you for instance want the line to skip a column.

**Known issues**

The x-axis does not entirely respect the margin. Autosizing boxes is not always the best option, try to set these manually as much as possible.

**API-changes from rmeta-package's forestplot**

- **xlog**: The xlog outputs the axis in log() format but the input data should be in antilog/exp format
- **col**: The corresponding function is *fpColors* for this package

**Author(s)**

Max Gordon, Thomas Lumley

**See Also**

Other forestplot functions: *fpColors()*,*fpDrawNormalCI()*,*fpLegend()*,*fpShapesGp()*

**Examples**

```r
# Simple examples of how to do a forestplot #

ask <- par(ask = TRUE)

# A basic example, create some fake data
test_data <- data.frame(
  coef = c(1.59, 1.24),
  low = c(1.4, 0.78),
  high = c(1.8, 1.55)
)
test_data %>%
```
```r
# forestplot
forestplot(labeltext = row_names,
    mean = coef,
    lower = low,
    upper = high,
    zero = 1,
    cex = 2,
    lineheight = "auto",
    xlab = "Lab axis txt")

# Print two plots side by side using the grid
# package’s layout option for viewports
grid.newpage()
pushViewport(viewport(layout = grid.layout(1, 2)))
pushViewport(viewport(layout.pos.col = 1))
test_data %>%
    forestplot(labeltext = row_names,
        mean = coef,
        lower = low,
        upper = high,
        zero = 1,
        cex = 2,
        lineheight = "auto",
        xlab = "Lab axis txt",
        new_page = FALSE)
popViewport()
pushViewport(viewport(layout.pos.col = 2))
test_data %>%
    forestplot(labeltext = row_names,
        mean = coef,
        lower = low,
        upper = high,
        zero = 1,
        cex = 2,
        lineheight = "auto",
        xlab = "Lab axis txt",
        new_page = FALSE)
popViewport(2)

# An advanced test
library(dplyr)
library(tidyr)
test_data <- data.frame(id = 1:4,
    coef1 = c(1, 1.59, 1.3, 1.24),
    coef2 = c(1, 1.7, 1.4, 1.84),
    low1 = c(1, 1.3, 1.1, 0.99),
    low2 = c(1, 1.6, 1.2, 0.7),
    high1 = c(1, 1.94, 1.6, 1.55),
    high2 = c(1, 1.8, 1.55, 1.33))

# Convert into dplyr formatted data
out_data <- test_data %>%
    pivot_longer(cols = everything() & -id) %>%
```
mutate(group = gsub("(.+)([12])$", "\"2", name),
    name = gsub("(.+)([12])$", "\"1", name)) %>%
  pivot_wider() %>%
group_by(group)

col_no <- grep("coef", colnames(test_data))
row_names <- list(
  list("Category 1", "Category 2", "Category 3", expression(Category >= 4)),
  list("ref",
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[2, col_no]), 2))
    ),
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[3, col_no]), 2))
    ),
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[4, col_no]), 2))
    )
  )
)

out_data %>%
  forestplot(mean = coef,
    lower = low,
    upper = high,
    labeltext = row_names,
    title = "Cool study",
    zero = c(0.98, 1.02),
    grid = structure(c(2^-.5, 2^.5),
      gp = gpar(col = "steelblue", lty = 2)
    ),
    boxsize = 0.25,
    col = fpColors(
      box = c("royalblue", "gold"),
      line = c("darkblue", "orange"),
      summary = c("darkblue", "red")
    ),
    xlab = "The estimates",
    new_page = TRUE,
    legend = c("Treatment", "Placebo"),
    legend_args = fpLegend(
      pos = list("topright"),
      title = "Group",
      r = unit(.1, "npc"),
      gp = gpar(col = "#CCCCCC", lwd = 1.5)
    ))

# An example of how the exponential works
test_data <- data.frame(coef = c(2.45, 0.43),
  lower = c(-Inf, -Inf),
  upper = c(Inf, Inf),
  label = c("Category 1", "Category 2", "Category 3", expression(Category >= 4)))

out_data %>%
  forestplot(mean = coef,
    lower = low,
    upper = high,
    labeltext = row_names,
    title = "Cool study",
    zero = c(0.98, 1.02),
    grid = structure(c(2^-.5, 2^.5),
      gp = gpar(col = "steelblue", lty = 2)
    ),
    boxsize = 0.25,
    col = fpColors(
      box = c("royalblue", "gold"),
      line = c("darkblue", "orange"),
      summary = c("darkblue", "red")
    ),
    xlab = "The estimates",
    new_page = TRUE,
    legend = c("Treatment", "Placebo"),
    legend_args = fpLegend(
      pos = list("topright"),
      title = "Group",
      r = unit(.1, "npc"),
      gp = gpar(col = "#CCCCCC", lwd = 1.5)
    ))
low = c(1.5, 0.25),
high = c(4, 0.75),
boxsize = c(0.25, 0.25))
row_names <- cbind(
c("Name", "Variable A", "Variable B"),
c("HR", test_data$coef)
)
test_data <- rbind(rep(NA, 3), test_data)
forestplot(
labeltext = row_names,
test_data[, c("coef", "low", "high")],
is.summary = c(TRUE, FALSE, FALSE),
boxsize = test_data$boxsize,
zero = 1,
xlog = TRUE,
col = fpColors(lines = "red", box = "darkred")
)

# An example using shapes_gp
forestplot(
labeltext = cbind(Al = c("Smith et al", "Smooth et al", "Al et al")),
mean = cbind(1:3, 1.5:3.5),
lower = cbind(0:2, 0.5:2.5),
upper = cbind(4:6, 5.5:7.5),
is.summary = c(FALSE, FALSE, TRUE),
shapes_gp = fpShapesGp(
default = gpar(lineend = "square", linejoin = "mitre", lwd = 3, col = "pink"),
box = gpar(fill = "black", col = "red"), # only one parameter
lines = list( # as many parameters as CI
gpar(lwd = 10), gpar(lwd = 5),
gpar(), gpar(),
gpar(lwd = 2), gpar(lwd = 1)
),
summary = list( # as many parameters as band per label
gpar(fill = "violet", col = "gray", lwd = 10),
gpar(fill = "orange", col = "gray", lwd = 10)
)
),
vertices = TRUE
)

par(ask = ask)
# See vignette for a more detailed description
# vignette("forestplot", package="forestplot")
Description

This function encapsulates all the colors that are used in the forestplot function. As there are plenty of color options this function gathers them all in one place.

Usage

fpColors(
  all.elements,
  box = "black",
  lines = "gray",
  summary = "black",
  zero = "lightgray",
  text = "black",
  axes = "black",
  hrz_lines = "black"
)

Arguments

all.elements  A color for all the elements. If set to NULL then it’s set to the par("fg") color
box           The color of the box indicating the estimate
lines         The color of the confidence lines
summary       The color of the summary
zero          The color of the zero line
text          The color of the text
axes          The color of the x-axis at the bottom
hrz_lines     The color of the horizontal lines

Details

Further customization of non-text elements can be performed with fpShapesGp passed as shapes_gp parameter to forestplot. The fpColors function is kept for backwards compatibility.

If you have several values per row in a forestplot you can set a color to a vector where the first value represents the first line/box, second the second line/box etc. The vectors are only valid for the box & lines options.

This function is a copy of the meta.colors function in the rmeta package.

Value

list A list with the elements:

box            the color of the box.marker
lines          the color of the lines
summary        the color of the summary
zero           the color of the zero vertical line
text           the color of the text
axes           the color of the axes
Author(s)

Max Gordon, Thomas Lumley

See Also

Other forestplot functions: forestplot(), fpDrawNormalCI(), fpLegend(), fpShapesGp()

Examples

```r
ask <- par(ask = TRUE)

# An example of how the exponential works
test_data <- data.frame(
  coef = c(2.45, 0.43),
  low = c(1.5, 0.25),
  high = c(4, 0.75),
  boxsize = c(0.5, 0.5)
)
row_names <- cbind(
  c("Name", "Variable A", "Variable B"),
  c("HR", test_data$coef)
)
test_data <- rbind(rep(NA, 3), test_data)
forestplot(
  labeltext = row_names,
  test_data[, c("coef", "low", "high")],
  is.summary = c(TRUE, FALSE, FALSE),
  boxsize = test_data$boxsize,
  zero = 1,
  xlog = TRUE,
  col = fpColors(lines = "#990000", box = "#660000", zero = "darkblue"),
  new_page = TRUE
)
par(ask = ask)
```

---

**fpDrawNormalCI**

**Draw standard confidence intervals**

**Description**

A function that is used to draw the different confidence intervals for the non-summary lines. Use the `fpDrawNormalCI` function as a template if you want to make your own funky line + marker.
Usage

```r
fpDrawNormalCI(
    lower_limit, estimate,
    upper_limit, size,
    y.offset = 0.5,
    clr.line, clr.marker,
    lwd, lty = 1,
    vertices,
    vertices.height = 0.1,
    shapes_gp = fpShapesGp(),
    shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
    ...
)
```

```r
fpDrawDiamondCI(
    lower_limit, estimate,
    upper_limit, size,
    y.offset = 0.5,
    clr.line, clr.marker,
    lwd, lty = 1,
    vertices,
    vertices.height = 0.1,
    shapes_gp = fpShapesGp(),
    shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
    ...
)
```

```r
fpDrawCircleCI(
    lower_limit, estimate,
    upper_limit, size,
    y.offset = 0.5,
    clr.line, clr.marker,
    lwd, lty = 1,
    vertices,
    vertices.height = 0.1,
    shapes_gp = fpShapesGp(),
    ...
)
```
shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
...
)

fpDrawPointCI(
  lower_limit,
  estimate,
  upper_limit,
  size,
  y.offset = 0.5,
  clr.line,
  clr.marker,
  lwd,
  lty = 1,
  vertices,
  vertices.height = 0.1,
  pch = 1,
  shapes_gp = fpShapesGp(),
  shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
...
)

fpDrawSummaryCI(
  lower_limit,
  estimate,
  upper_limit,
  size,
  col,
  y.offset = 0.5,
  shapes_gp = fpShapesGp(),
  shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
...
)

fpDrawBarCI(
  lower_limit,
  estimate,
  upper_limit,
  size,
  col,
  y.offset = 0.5,
  shapes_gp = fpShapesGp(),
  shape_coordinates = structure(c(1, 1), max.coords = c(1, 1)),
...
)
**Arguments**

- **lower_limit** The lower limit of the confidence line. A native numeric variable that can actually be outside the boundaries. If you want to see if it is outside then convert it to 'npc' and see if the value ends up more than 1 or less than 0. Here’s how you do the conversion: `convertX(unit(upper_limit,"native"),"npc",valueOnly = TRUE)` and the `convertX` together with `unit` is needed to get the right values while you need to provide the `valueOnly` as you cannot compare a unit object.

- **estimate** The estimate indicating the placement of the actual box. Note, this can also be outside bounds and is provided in a numeric format the same way as the `lower_limit`.

- **upper_limit** The upper limit of the confidence line. See `lower_limit` for details.

- **size** The actual size of the box/diamond/marker. This provided in the 'snpc' format to generate a perfect marker. Although you can provide it alternative units as well, this is useful for the legends to work nicely.

- **y.offset** If you have multiple lines they need an offset in the y-direction.

- **clr.line** The color of the line.

- **clr.marker** The color of the estimate marker

- **lwd** Line width, see `gpar`

- **lty** Line type, see `gpar`

- **vertices** Set this to TRUE if you want the ends of the confidence intervals to be shaped as a T. This is set default to TRUE if you have any other line type than 1 since there is a risk of a dash occurring at the very end, i.e. showing incorrectly narrow confidence interval.

- **vertices.height** The height hoft the vertices. Defaults to npc units corresponding to 10% of the row height.

- **shapes_gp** A set of graphical parameters of class `fpShapesGp`

- **shape_coordinates** A vector of length 2 the label (first item of the vector) and the band (second item of the vector) of the confidence interval. This is used together with `shapes_gp` to retrieve graphical parameters for that item.

- **...** Allows additional parameters for sibling functions

- **pch** Type of point see `grid.points` for details

- **col** The color of the summary object

**Value**

- **void** The function outputs the line using grid compatible functions and does not return anything.

**Author(s)**

Max Gordon, Thomas Lumley
fpDrawNormalCI

See Also

Other forestplot functions: forestplot(), fpColors(), fpLegend(), fpShapesGp()

Examples

```r
ask <- par(ask = TRUE)

test_data <- data.frame(
  coef1 = c(1, 1.59, 1.3, 1.24),
  coef2 = c(1, 1.7, 1.4, 1.04)
)

test_data$low1 <- test_data$coef1 - 1.96 * c(0, .2, .1, .15)
test_data$high1 <- test_data$coef1 + 1.96 * c(0, .2, .1, .15)

test_data$low2 <- test_data$coef2 - 1.96 * c(0, .1, .15, .2)
test_data$high2 <- test_data$coef2 + 1.96 * c(0, .1, .15, .2)

col_no <- grep("coef", colnames(test_data))
row_names <- list(
  list("Category 1", "Category 2", "Category 3", expression(Category >= 4)),
  list(
    "ref",
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[2, col_no]), 2))
    ),
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[3, col_no]), 2))
    ),
    substitute(
      expression(bar(x) == val),
      list(val = round(rowMeans(test_data[4, col_no]), 2))
    )
  )
)

coef <- with(test_data, cbind(coef1, coef2))
low <- with(test_data, cbind(low1, low2))
high <- with(test_data, cbind(high1, high2))

# Change all to diamonds
forestplot(row_names, coef, low, high,
  fn.ci_norm = fpDrawDiamondCI,
  title = "Cool study",
  zero = 1, boxsize = 0.25,
  col = fpColors(
    box = c("royalblue", "gold"),
    line = c("darkblue", "orange"),
    summary = c("darkblue", "red")
  ),
)
xlab = "The estimates",
new_page = TRUE,
legend = c("Treatment", "Placebo"),
legend_args = fpLegend(
  title = "Group",
  pos = list("topright", inset = .1),
  r = unit(.1, "snpc"),
  gp = gpar(col = "#CCCCCC", lwd = 1.5)
)
)

# Change first to diamonds
forestplot(row_names, coef, low, high,
fn.ci_norm = c(
  "fpDrawDiamondCI",
  rep("fpDrawNormalCI",
      times = nrow(coef) - 1
  )
),
title = "Cool study",
zero = 1, boxsize = 0.25,
col = fpColors(
  box = c("royalblue", "gold"),
  line = c("darkblue", "orange"),
  summary = c("darkblue", "red")
),
xlab = "The estimates",
new_page = TRUE,
legend = c("Treatment", "Placebo"),
legend_args = fpLegend(
  title = "Group",
  pos = list("topright", inset = .1),
  r = unit(.1, "snpc"),
  gp = gpar(col = "#CCCCCC", lwd = 1.5)
)
)

# You can also use a list with the actual functions
# as long as it is formatted [[row]][[column]]
# Note: if you have a non-square input then
# the software will reformat [[col]][[row]]
# to [[row]][[col]]
forestplot(row_names, coef, low, high,
fn.ci_norm = list(
  list(fpDrawDiamondCI, fpDrawCircleCI),
  list(fpDrawNormalCI, fpDrawNormalCI),
  list(fpDrawNormalCI, fpDrawCircleCI),
  list(fpDrawNormalCI, fpDrawNormalCI)
),
title = "Cool study",
zero = 1, boxsize = 0.25,
col = fpColors(
  box = c("royalblue", "gold"),
line = c("darkblue", "orange"),
summary = c("darkblue", "red")
),
xlab = "The estimates",
new_page = TRUE,
legend = c("Treatment", "Placebo"),
legend_args = fpLegend(
  title = "Group",
  pos = list("topright", inset = .1),
  r = unit(.1, "snpc"),
  gp = gpar(col = "CCCCCC", lwd = 1.5)
)
)
par(ask = ask)

fpLegend
A function for the legend used in forestplot()

Description
This function encapsulates all the legend options that are used in the forestplot function. This is in order to limit the crowding among the arguments for the forestplot call.

Usage
fpLegend(
  pos = "top",
  gp = NULL,
  r = unit(0, "snpc"),
  padding = unit(ifelse(!is.null(gp), 3, 0), "mm"),
  title = NULL
)

Arguments
pos The position of the legend, either at the "top" or the "right" unless positioned inside the plot. If you want the legend to be positioned inside the plot then you have to provide a list with the same x & y qualities as legend. For instance if you want the legend to be positioned at the top right corner then use pos = list("topright") - this is equivalent to pos = list(x = 1, y = 1). If you want to have a distance from the edge of the graph then add an inset to the list, e.g. pos = list("topright", "inset" = .1) - the inset should be either a unit element or a value between 0 and 1. The default is to have the boxes aligned vertical, if you want them to be in a line then you can specify the "align" option, e.g. pos = list("topright", "inset" = .1, "align" = "horizontal")
The `gpar` options for the legend. If you want the background color to be light grey then use `gp = gpar(fill = "lightgrey")`. If you want a border then set the `col` argument: `gp = gpar(fill = "lightgrey",col = "black")`. You can also use the `lwd` and `lty` argument as usual, `gp = gpar(lwd = 2,lty = 1)`, will result in a black border box of line type 1 and line width 2.

The box can have rounded edges, check out `grid.roundrect`. The `r` option should be a `unit` object. This is by default `unit(0,"snpc")` but you can choose any value that you want. The “`snpc`” unit is the preferred option.

The padding for the legend box, only used if box is drawn. This is the distance from the border to the text/boxes of the legend.

The title of the legend if any

Value

list Returns a list with all the elements

See Also

Other forestplot functions: `forestplot()`, `fpColors()`, `fpDrawNormalCI()`, `fpShapesGp()`

---

### Table: `fpShapesGp`

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>gp</code></td>
<td>The <code>gpar</code> options for the legend.</td>
</tr>
<tr>
<td><code>r</code></td>
<td>The box can have rounded edges.</td>
</tr>
<tr>
<td><code>padding</code></td>
<td>The padding for the legend box.</td>
</tr>
<tr>
<td><code>title</code></td>
<td>The title of the legend if any.</td>
</tr>
</tbody>
</table>

**Description**

This function encapsulates all the non-text elements that are used in the `forestplot` function. As there are plenty of shapes options this function gathers them all in one place.

**Usage**

```r
fpShapesGp(  
  default = NULL,  
  box = NULL,  
  lines = NULL,  
  vertices = NULL,  
  summary = NULL,  
  zero = NULL,  
  axes = NULL,  
  hrz_lines = NULL,  
  grid = NULL  
)
```
Arguments

- **default**: A fallback `gpar` for all unspecified attributes. If set to NULL then it defaults to legacy parameters, including the `col`, `lwd.xaxis`, `lwd.ci` and `lty.ci` parameter of `fpColors`.
- **box**: The graphical parameters (`gpar`) of the box, circle or point indicating the point estimate, i.e. the middle of the confidence interval (may be a list of `gpars`).
- **lines**: The graphical parameters (`gpar`) of the confidence lines (may be a list of `gpars`).
- **vertices**: The graphical parameters (`gpar`) of the vertices (may be a list of `gpars`). If `ci.vertices` is set to TRUE in `forestplot` vertices inherits from `lines` all its parameters but `lty` that is set to "solid" by default.
- **summary**: The graphical parameters (`gpar`) of the summary (may be a list of `gpars`).
- **zero**: The graphical parameters (`gpar`) of the zero line (may not be a list of `gpars`).
- **axes**: The graphical parameters (`gpar`) of the x-axis at the bottom (may not be a list of `gpars`).
- **hrz_lines**: The graphical parameters (`gpar`) of the horizontal lines (may not be a list of `gpars`).
- **grid**: The graphical parameters (`gpar`) of the grid (vertical lines) (may be a list of `gpars`).

Details

This function obsoletes `fpColors`.

If some, but not all parameters of a shape (e.g. box) are specified in `gpar()` such as setting `lwd` but not line color, the unspecified parameters default to the ones specified in `default`, then, default to legacy parameters of `forestplot` such as `col`.

Parameters `box`, `lines`, `vertices`, `summary` may be set as list containing several `gpars`. The length of the list must either be equal to the number of bands per label or to the number of bands multiplied by the number of labels, allowing specification of different styles for different parts of the forest plot.

The parameter `grid` can either be a single `gpar` or a list of `gpars` with as many elements as there are lines in the grid (as set by the `xticks` or `grid` arguments of `forestplot`).

Parameters `zero`, `axes`, `hrz_lines` must either be NULL or `gpar` but cannot be lists of `gpars`.

Value

A list with the elements:

- `default`: the `gpar` for default attributes
- `box`: the `gpar` or list of `gpars` of the box/marker
- `lines`: the `gpar` or list of `gpars` of the lines
- `vertices`: the `gpar` or list of `gpars` of the vertices
- `summary`: the `gpar` or list of `gpars` of the summary
- `zero`: the `gpar` of the zero vertical line
- `axes`: the `gpar` of the x-axis
- `hrz_lines`: the `gpar` of the horizontal lines
- `grid`: the `gpar` or list of `gpars` of the grid lines
Author(s)

Andre GILLIBERT

See Also

Other forestplot functions: `forestplot()`, `fpColors()`, `fpDrawNormalCI()`, `fpLegend()`

Examples

```r
ask <- par(ask = TRUE)

# An example of how fpShapesGp works

styles <- fpShapesGp(
  default = gpar(col = "pink", lwd = 2, lineend = "square", linejoin = "mitre"),
  grid = list(
    gpar(col = "blue"),
    gpar(col = "black"),
    gpar(col = "blue")
  ),
  box = list(
    gpar(fill = "black"),
    gpar(fill = "blue"),
    gpar(fill = "black"),
    gpar(fill = "blue")
  ),
  lines = gpar(lty = "dashed"),
  vertices = gpar(lwd = 5, col = "red")
)

forestplot(
  labeltext = c("Author1", "Author2", "Author3", "Author4"),
  grid = c(1, 3, 5),
  mean = 1:4, lower = 0:3, upper = 2:5,
  shapes_gp = styles
)

par(ask = ask)
```

---

**fpTxtGp**

Get font settings for forestplot

**Description**

This function generates all the `gpar()` elements for the different text elements within the graph. Elements not specified inherit their default settings from the `label` argument.

**Usage**

```r
fpTxtGp(label, summary, xlab, title, ticks, legend, legend.title, cex = 1)
```
getTicks

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>label</td>
<td>The text labels (see details below)</td>
</tr>
<tr>
<td>summary</td>
<td>The summary labels (see details below)</td>
</tr>
<tr>
<td>xlab</td>
<td>The xlab text</td>
</tr>
<tr>
<td>title</td>
<td>The plot title</td>
</tr>
<tr>
<td>ticks</td>
<td>The ticks associated with the xlab</td>
</tr>
<tr>
<td>legend</td>
<td>The legend text</td>
</tr>
<tr>
<td>legend.title</td>
<td>The legend title</td>
</tr>
<tr>
<td>cex</td>
<td>The font size</td>
</tr>
</tbody>
</table>

Value

A list of the fpTxtGp class

List arguments for label/summary

You can provide a list of elements for the label and summary in order to specify separate elements. If you provide a list in one dimension the gpar elements are assumed to follow the columns. If you provide a list of 2 dimensions the structure assumes is list[[row]][[column]] and the number of elements should correspond to the number of labels for the label argument, i.e. without the rows marked as summary elements. The same goes for summary arguments.

Examples

```r
fpTxtGp(label = gpar(fontfamily = "HersheySerif"))
```

getTicks

Ticks for plot axis

Description

Gets the ticks in a formatted version. This is since I’m not always that fond of just pretty(1:10/5). In exponential form the ticks are determined from the 2-base, meaning that you get an intuitive feeling for when the value is doubled.

Usage

```r
getTicks(low, high = low, clip = c(-Inf, Inf), exp = FALSE, digits = 0)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>low</td>
<td>lower bound, can be a single number or a vector</td>
</tr>
<tr>
<td>high</td>
<td>upper bound - optional, you can just have all data in the low variable</td>
</tr>
<tr>
<td>clip</td>
<td>if the ci are clipped</td>
</tr>
<tr>
<td>exp</td>
<td>If the value should be in exponential form (default)</td>
</tr>
<tr>
<td>digits</td>
<td>Number of digits - used in exp mode</td>
</tr>
</tbody>
</table>
Details

This function is far from perfect and I recommend specifying yourself the ticks that you want.

Value

`vector` Returns a vector with the ticks

Examples

test_data <- data.frame(
  coef = c(2, 0.5),
  low = c(1.5, 0.05),
  high = c(3, 0.75),
  boxsize = c(0.5, 0.5)
)

# Exponential form where the exponent base i 2 for easier understanding
getTicks(
  low = test_data$low,
  high = test_data$high,
  clip = c(-Inf, Inf),
  exp = TRUE
)

# Non exponential form with using pretty
getTicks(
  low = test_data$low,
  high = test_data$high,
  clip = c(-Inf, Inf),
  exp = FALSE
)

# A very simple example
getTicks(1:5 * 2.33,
  exp = FALSE
)

# A slightly more advanced exponential version
getTicks(1:10 * .33,
  digits = 2,
  exp = TRUE
)
The data is a list containing the Swedish and the Danish coefficients for health related quality of life (HRQoL) 1 year after total hip arthroplasty surgery. The age is modeled as a spline and is therefore presented as a contrast.

**Author(s)**
Max Gordon <max@gforge.se>

---

**prDefaultGp**

**Description**
Construct default parameters from arguments that may include missing arguments

**Usage**

```
prDefaultGp(col, lwd, lty)
```

**Arguments**

- `col`: Line color (or missing)
- `lwd`: Line width (or missing)
- `lty`: Line type (or missing)

**Value**

A `gpar` object containing these three attributes

---

**prGetShapeGp**

**Description**
A function to extract graphical parameters from a `fpShapesGp` object

**Usage**

```
prGetShapeGp(  
    shapes_gp,  
    coords,  
    object,  
    default = grid::gpar(),  
    nodefault = FALSE
)
```
prMergeGp

Arguments

shapes_gp An object of class `fpShapesGp` specifying all graphical parameters
coords A numeric vector of length 2, specifying the label number (first item of the vector) and the confidence band number within this label; that can be >= 2 if there are multiple confidence bands per label. Can be NULL for objects that are used only once (e.g. axes). Vector `coords` must have an R attribute `max.coords` as numeric vector of length 2 specifying the total number of labels and number of confidence bands by label for the forest plot. The first coordinate specify the label number and the second coordinate (for multi-band forest plots) specifies the band number within the label.
object One of "box", "lines", "vertices", "summary", "zero", "axes", "hrz_lines" or "grid", refering to the object for which the graphical parameters are requested.
default Default attributes to rely on when neither found in `shapes_gp$object` nor in `shapes_gp$default`
nodefault Logical. If TRUE, do not search attribute in `shapes_gp$default`

Value

An object of class `gpar`

Author(s)

Andre GILLIBERT

Description

A function to merge two sets of graphical parameters

Usage

```
prMergeGp(weak = gpar(), strong = gpar())
```

Arguments

weak A `gpar`
strong Another `gpar`, with parameters taking precedence over weak

Value

A `gpar` merging attributes of both weak and strong
**safeLoadPackage**

* Safely loads package

---

**Description**

Stops if the package doesn’t exist

**Usage**

```python
safeLoadPackage(package)
```

**Arguments**

- `package` string naming the package/name space to load.
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