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forestplot-package Package description

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 exponentials where ticks are generated using the $2^n$ since a doubling is a concept easy to grasp for less mathematical-savvy readers.
**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**

```r
forestplot(...)
```

## Default S3 method:

```r
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(), 
  new_page = getOption("forestplot_new_page", TRUE), 
  fn.ci_norm = fpDrawNormalCI, fn.ci_sum = fpDrawSummaryCI, fn.legend, 
  ...)
```

**Arguments**

- `...`: Passed on to the `fn.ci_norm` and `fn.ci_sum` arguments
- `labeltext`: A list, matrix, vector or expression with the names of each row. The list should be wrapped in m x n number to resemble a matrix: `list(list("rowname 1 col 1", "rowname 2 col 1")
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 labeltext in the rownames and then columns for mean, lower, and upper.

- `mean`: 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
<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>lower</td>
<td>The lower bound of the confidence interval for the forestplot, needs to be the same format as the mean, i.e. matrix/vector of equal columns &amp; length</td>
</tr>
<tr>
<td>upper</td>
<td>The upper bound of the confidence interval for the forestplot, needs to be the same format as the mean, i.e. matrix/vector of equal columns &amp; length</td>
</tr>
<tr>
<td>align</td>
<td>Vector giving alignment (l,r,c) for the table columns</td>
</tr>
<tr>
<td>is.summary</td>
<td>A vector indicating by TRUE/FALSE if the value is a summary value which means that it will have a different font-style</td>
</tr>
<tr>
<td>graph.pos</td>
<td>The position of the graph element within the table of text. The position can be (1-(\text{ncol(labeltext)} + 1)). You can also choose set the position to &quot;left&quot; or &quot;right&quot;.</td>
</tr>
<tr>
<td>hrzl_lines</td>
<td>Add horizontal lines to graph. Can either be TRUE or a list of gpar. See line section below for details.</td>
</tr>
<tr>
<td>clip</td>
<td>Lower and upper limits for clipping confidence intervals to arrows</td>
</tr>
<tr>
<td>xlab</td>
<td>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 supressed.</td>
</tr>
<tr>
<td>zero</td>
<td>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, &quot;cm&quot;). A third option is to set line height to &quot;lines&quot; and then you get 50% more than what the text height is as your line height</td>
</tr>
<tr>
<td>colgap</td>
<td>Sets the gap between columns, defaults to 6 mm but for relative widths. Note that the value should be in unit(&quot;npc&quot;).</td>
</tr>
<tr>
<td>lineheight</td>
<td>Set the margin between rows, provided in numeric or unit formlar. When having multiple confidence lines per row setting the correct margin in order to visually separate rows</td>
</tr>
<tr>
<td>col</td>
<td>Set the colors for all the elements. See fpColors for details</td>
</tr>
<tr>
<td>txt_gp</td>
<td>Set the fonts etc for all text elements. See fpTxtGp for details</td>
</tr>
<tr>
<td>xlog</td>
<td>If TRUE, x-axis tick marks are to follow a logarithmic scale, e.g. for logistic regression (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.</td>
</tr>
<tr>
<td>xticks</td>
<td>Optional user-specified x-axis tick marks. Specify NULL to use the defaults, numeric(0) to omit the x-axis. By adding a labels-attribute, attr(my_ticks, &quot;labels&quot;) &lt;- ... you can dictate the outputted text at each tick. If you specify a boolean vector then ticks indicated with FALSE won't be printed. Note that the labels have to be the same length as the main variable.</td>
</tr>
</tbody>
</table>
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 hoft 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

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 `hrz1_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`

Examples

```r
ask <- par(ask=TRUE)
# A basic example, create some fake data
```
row_names <- list(list("test = 1", expression(test >= 2)))
test_data <- data.frame(coef = c(1.59, 1.24),
    low = c(1.4, 0.78),
    high = c(1.8, 1.55))

forestplot(row_names,
    test_data$coef,
    test_data$low,
    test_data$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))
forestplot(row_names,
    test_data$coef,
    test_data$low,
    test_data$high,
    zero = 1,
    cex = 2,
    lineheight = "auto",
    xlab = "Lab axis txt",
    new_page = FALSE)
popViewport()
pushViewport(viewport(layout.pos.col = 2))
forestplot(row_names,
    test_data$coef,
    test_data$low,
    test_data$high,
    zero = 1,
    cex = 2,
    lineheight = "auto",
    xlab = "Lab axis txt",
    new_page = FALSE)
popViewport(2)

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

col_no <- grep("coef", colnames(test_data))
row_names <- list(
    list("Category 1", "Category 2", "Category 3", expression(Category >= 4)),
    list("ref",
    list(...))
fpColors

A function for the color elements used in forestplot()

```r
# example of how the exponential works

# create data frame with coefficients, low, and high values
# for the example

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))

# create row names
row_names <- cbind(c("Name", "Variable A", "Variable B"),
                   c("HR", test_data$coef))

# create test data with rep(NA, 3) and test data

# plot with forestplot

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")

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**

```r
defcolors(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**

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**

- 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`
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**

```
fpDrawNormalCI(lower_limit, estimate, upper_limit, size, y.offset = 0.5,
               clr.line, clr.marker, lwd, lty = 1, vertices, vertices.height = 0.1,
               ...)  
fpDrawDiamondCI(lower_limit, estimate, upper_limit, size, y.offset = 0.5,
                clr.line, clr.marker, lwd, lty = 1, vertices, vertices.height = 0.1,
                ...)  
fpDrawCircleCI(lower_limit, estimate, upper_limit, size, y.offset = 0.5,
               clr.line, clr.marker, lwd, lty = 1, vertices, vertices.height = 0.1,
               ...)  
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, ...)  
```
fpDrawNormalCI(lower_limit, estimate, upper_limit, size, col, y.offset = 0.5, ...)

fpDrawBarCI(lower_limit, estimate, upper_limit, size, col, y.offset = 0.5, ...)

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.

...  Allows additional parameters for sibling functions

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

col  The color of the summary objectct

Value

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

Author(s)

Max Gordon, Thomas Lumley
See Also

Other forestplot functions: forestplot, fpColors, fplegend

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",
                        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)))
```
fpLegend

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 a 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")

gp
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.

r
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.

padding
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.

title
The title of the legend if any

Value

list
Returns a list with all the elements

See Also

Other forestplot functions: forestplot, fpColors, fpDrawNormalCI

fpTxtGp

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

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

Arguments

- `label`: The text labels (see details below)
- `summary`: The summary labels (see details below)
- `xlab`: The xlab text
- `title`: The plot title
- `ticks`: The ticks associated with the xlab
- `legend`: The legend text
- `legend.title`: The legend title
- `cex`: The font size

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"))
```

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

- `low`: lower bound, can be a single number or a vector
- `high`: upper bound - optional, you can just have all data in the low variable
- `clip`: if the ci are clipped
- `exp`: If the value should be in exponential form (default)
- `digits`: Number of digits - used in exp mode
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)

HRQoL

Regression coefficients and confidence intervals from HRQoL study

Description

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 modelled as a spline and is therefore presented as a contrast.

Author(s)

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