

Package ‘survsup’

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Title Plotting Survival Curves with Numbers at Risk Table

Version 0.0.2

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Description Implements functions to plot survival curves. Provides the capability to add numbers at risk tables, and allows for using the pipe operator to create more complex plots.

Depends R (>= 3.3.0)

License GPL-2

Encoding UTF-8

URL <http://github.com/dlindholm/survsup>

BugReports <http://github.com/dlindholm/survsup/issues>

LazyData true

Imports stats, utils, survival, dplyr, ggplot2, broom, colorspace,
gridExtra

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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R topics documented:

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| | |
|------|--|
| cat4 | <i>Convenience function for four-category color scheme</i> |
|------|--|

Description

Convenience function to change the color scheme to four colors: Green, blue, red, and yellow; i.e. like the ski slopes but with yellow instead of black.

Usage

```
cat4(g, reverse = FALSE)
```

Arguments

| | |
|---------|--|
| g | ggplot object containing a Kaplan-Meier plot |
| reverse | should the order of the colors be reversed? |

Value

Returns a ggplot object

Author(s)

Daniel Lindholm

Examples

```
library(survival)
library(dplyr)
veteran %>%
  survfit(Surv(time, status) ~ celltype, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  cat4(reverse = TRUE)
```

| | |
|-------------|--|
| hcl_rainbow | <i>Convenience function for the rainbow_hcl color scheme</i> |
|-------------|--|

Description

Convenience function to change the color scheme to the rainbow_hcl scheme provided by the colorspace package. The function will detect how many strata are available and will pick that many colors from rainbow_hcl.

Usage

```
hcl_rainbow(g, reverse = FALSE, c = 50, l = 70, start = 0,
  end = 360 * (n - 1)/n)
```

Arguments

| | |
|----------------------|--|
| <code>g</code> | ggplot object containing a Kaplan-Meier plot |
| <code>reverse</code> | should the order of the colors be reversed? |
| <code>c</code> | chroma |
| <code>l</code> | luminance |
| <code>start</code> | the hue at which the rainbow begins |
| <code>end</code> | the hue at which the rainbow ends |

Value

Returns a ggplot object

Author(s)

Daniel Lindholm

Examples

```
library(survival)
library(dplyr)
veteran %>%
  survfit(Surv(time, status) ~ celltype, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  hcl_rainbow()
```

 nar

Add a numbers at risk table to a Kaplan-Meier plot

Description

Creates a numbers at risk table based on a ggplot object created by the `plot_survfit` function. It will add a table in the lower part of the plot, with numbers where the X axis tick marks are situated.

Usage

```
nar(g, size = NA, x_offset = 0.02, y_offset = 0.05,
    forced_height = NULL, flip = FALSE, separator = TRUE,
    sep_lwd = 0.2, sep_color = "grey70")
```

Arguments

| | |
|-----------------------|---|
| <code>g</code> | a ggplot object to which a numbers at risk table should be added. |
| <code>size</code> | a numeric value indicating the font size of the NAR table |
| <code>x_offset</code> | a constant indicating how much padding should be placed to the left of the NAR table (a multiple of the plot size in the X dimension) |

| | |
|----------------------------|--|
| <code>y_offset</code> | a constant indicating how much each line in the NAR table should be offset (as a multiple of both the plotting space size and the row number) |
| <code>forced_height</code> | a constant that, if provided, will force the NAR table to be of a certain height. This represents a multiple of the plot size in the Y dimension. This overrides the <code>y_offset</code> setting. Useful when you wish to plot multiple plots along side each other where the number of strata differs, as this setting will ensure that the sizes of the NAR tables are constant. |
| <code>flip</code> | a logical scalar indicating wheter the order in rows of the NAR table should be flipped or not. |
| <code>separator</code> | a logical scalar indicating whether a line that separates the plot from the NAR table should be put in place |
| <code>sep_lwd</code> | what width should that line have? |
| <code>sep_color</code> | which color should we use for that line? |

Value

Returns a ggplot object

Author(s)

Daniel Lindholm

Examples

```
library(survsup); library(ggplot2); library(dplyr); library(survival)

retinopathy %>%
  survfit(Surv(futime, status) ~ trt, data = .) %>%
  plot_survfit() %>%
  nar()

# Without table flip:
flchain %>%
  survfit(Surv(futime, death) ~ sex, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  nar()

# With table flip:
flchain %>%
  survfit(Surv(futime, death) ~ sex, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  nar(flip = TRUE)
```

| | |
|--------------|------------------------------|
| plot_survfit | <i>Plot a survfit object</i> |
|--------------|------------------------------|

Description

Creates a Kaplan-Meier plot based on a survfit object

Usage

```
plot_survfit(fit, lwd = 1, xmax = NULL, xbreaks = NULL,
  ylim = NULL, ci = FALSE, cuminc = TRUE, y_percent = TRUE,
  split_legend_labels = TRUE, legend.title = NA,
  legend.position = "top")
```

Arguments

| | |
|---------------------|--|
| fit | A survfit object that we should plot |
| lwd | Line width |
| xmax | What is the upper limit of the X axis? The default will plot all data. |
| xbreaks | A numeric vector. Where should the breaks in the X axis be? The default will give ggplot's default breaks. |
| ylim | A numeric vector of length 2. Which are the Y axis limits? |
| ci | A logical scalar. Should confidence intervals be plotted? |
| cuminc | A logical scalar. Should cumulative incidence be plotted (default), or should be survival be plotted instead (cuminc = FALSE)? |
| y_percent | A logical scalar. Should the Y axis display percentages? |
| split_legend_labels | A logical scalar. Should the legends labels be split, i.e. removing the "<variable_name>=" for each stratum? |
| legend.title | What title should the legend have? By default it will take the value that was split if split_legend_labels was used; otherwise it will take the value "strata" |
| legend.position | Where should the legend be drawn? Possible answers are: "top", "bottom", "left", "right"; or if you want to skip putting a legend on the plot: "none" |

Value

Returns a ggplot object

Author(s)

Daniel Lindholm

Examples

```

library(survsup); library(ggplot2); library(dplyr); library(survival)

retinopathy %>%
  survfit(Surv(futime, status) ~ trt, data = .) %>%
  plot_survfit()

retinopathy %>%
  survfit(Surv(futime, status) ~ trt, data = .) %>%
  plot_survfit(ci = TRUE, cuminc = FALSE)

# Since a ggplot object is returned,
# you can tweak as you wish
# (in this case with multiple labels):
mgus2 %>%
  survfit(Surv(futime, death) ~ sex, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  nar(flip = TRUE) %>%
  hcl_rainbow()+ # <--- Notice + sign here!
  labs(title = "This is an excessively long title",
        subtitle = "This is a subtitle",
        x = "Time (days)",
        y = "Survival (%)",
        caption = "(This is a demo)")

```

 skislopes

Convenience function for skislope color scheme

Description

Convenience function to change the color scheme to four colors: Green, blue, red, and black; i.e. as ski slopes are classified.

Usage

```
skislopes(g, reverse = FALSE)
```

Arguments

| | |
|----------------------|--|
| <code>g</code> | ggplot object containing a Kaplan-Meier plot |
| <code>reverse</code> | should the order of the colors be reversed? |

Value

Returns a ggplot object

Author(s)

Daniel Lindholm

Examples

```
## Not run:
library(survival)
library(dplyr)
veteran %>%
  survfit(Surv(time, status) ~ celltype, data = .) %>%
  plot_survfit(cuminc = FALSE) %>%
  skislopes(reverse = TRUE)

## End(Not run)
```

theme_km

Custom ggplot theme that make Kaplan-Meier curves look nice

Description

Custom theme, based upon the theme_bw theme in ggplot2

Usage

```
theme_km(base_size = 11, base_family = "",
         base_line_size = base_size/22, base_rect_size = base_size/22)
```

Arguments

base_size base font size
base_family base font family
base_line_size base size for line elements
base_rect_size base size for rect elements

Examples

```
library(survsup); library(ggplot2)
p <- ggplot(mtcars) + geom_point(aes(x = wt, y = mpg,
  colour = factor(gear))) + facet_wrap(~am)

p + theme_km()
```

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