

Package ‘kmrskplot’

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Type Package

Title Survival Plots

Version 1.0

Date 2016-02-08

Author Erica Wozniak

Maintainer Erica Wozniak <ewozniak@mcw.edu>

Description This package generates Kaplan-Meier curves and cumulative incidence plots for competing risks models.

Imports survival, cmprsk

License GPL-2

NeedsCompilation no

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kmrskplot-package	<i>Survival Plots</i>
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Description

This package generates Kaplan-Meier curves and cumulative incidence plots for competing risks models.

Details

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Index of help topics:

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kmrskplot-package	Survival Plots

This package outputs Kaplan-Meier plots and cumulative incidence plots for competing risks models. A table of the number of observations in the risk set at each specified time point is printed below the plot.

Author(s)

Erica Wozniak
 Maintainer: Erica Wozniak <ewozniak@mcw.edu>

See Also

[km_plot](#)

Examples

```
library(survival)

# Set up data as a survival object
# KM plot for time to death
# Censor those who receive a transplant or are indicated by the dataset as censored
pbc_km <- na.omit(pbc[, c("time", "status", "trt")])
pbc_km$status[pbc_km$status == 1] <- 0
pbc_km$status[pbc_km$status == 2] <- 1
pbc_km$SurvObj <- with(pbc_km,
  Surv(time = time,
        event = status)
)
fit <- survfit(SurvObj ~ trt,
  data = pbc_km,
  conf.type = "log-log")

# Usage note: if gridlines are extending outside the plot border, run
# "dev.off()" and then run the plotting function again.

# Default options only
km_plot(fit = fit)

# Customized pretty plot with some options
km_plot(fit = fit,
  type = "km",
  col = c("orange3", "olivedrab"),
  # Add an extra major gridline and risk table column at time 4500
  xlim_major = c(0, 1000, 2000, 3000, 4000, 4500, 5000),
  plot_title = "Primary biliary cirrhosis survival",
  plot_subtitle = "By randomized treatment status",
```

```

y_axis_label = "Survival",
x_axis_label = "Time since registration (days)",
group_names = c("D-penicillamine", "Placebo"),
risk_table_title = bquote(italic("Patients at risk:")))

# Customized retro plot with lots of options
km_plot(fit = fit,
        font_family = "mono",
        type = "1-km",
        col = c("black", "black"),
        lty = c(1, 2),
        lwd = c(2, 2),
        xlim_major = c(0, 500, 1000, 2000, 3000, 3375, 4000, 4500, 5000),
        col_grid_major = "gray80",
        col_grid_minor = "gray92",
        plot_title = bquote(bold("Death following transplant registration")),
        plot_subtitle = "Mayo Clinic 1974-1984",
        plot_title_size = 1,
        y_axis_label = bquote(bold("Cumulative incidence")),
        x_axis_label = bquote(bold("Days")),
        group_names = c("D-penicillamine", "Placebo"),
        group_order = c(2, 1),
        risk_table_title = bquote(bold(underline("RISK TABLE"))),
        extra_left_margin = 5)

```

km_plot

Kaplan-Meier Survival Plot

Description

This function generates Kaplan-Meier survival curves.

Usage

```
km_plot(fit, type, xlim_major, xlim_minor, ylim_major, ylim_minor, grid, col_grid_major, col_grid_min)
```

Arguments

fit	Fitted model object from survfit . Required.
type	Kaplan-Meier plot ("km") or complement ("1-km"). Optional; defaults to "km".
xlim_major	Vector of x-axis locations for labels and major gridlines. Optional.
xlim_minor	Vector of x-axis locations for minor gridlines. Optional.
ylim_major	Vector of y-axis locations for labels and major gridlines. Optional.
ylim_minor	Vector of y-axis locations for minor gridlines. Optional.
grid	Plot gridlines? Optional logical; defaults to TRUE.
col_grid_major	Color of major gridlines. Optional.
col_grid_minor	Color of minor gridlines. Optional.
lwd_grid_major	Line width of major gridlines. Optional.
lwd_grid_minor	Line width of minor gridlines. Optional.
conf_int	Plot confidence intervals? Optional logical; defaults to FALSE.

mark_time	Plot censoring tick marks? Optional logical; defaults to FALSE.
col	Vector of colors for plotted curves. Optional; defaults to ordered rainbow colors.
lty	Vector of line types for plotted curves. Optional; defaults to all solid.
lwd	Vector of line widths for plotted curves. Optional; defaults to 1.
plot_title	Main plot title. Optional.
plot_title_size	Text size for plot title. Optional.
plot_subtitle	Subtitle for plot. Optional.
plot_subtitle_size	Text size for plot subtitle. Optional.
x_axis_label	Label for the x-axis. Optional; defaults to "Time".
y_axis_label	Label for the y-axis. Optional; defaults to "Probability".
axis_label_size	Text size for axis labels. Optional.
extra_left_margin	Increase numeric value for added left margin padding to accomodate long labels. Optional.
font_family	Choice of "sans", "serif", "mono", or a specified font set up to work on the user's system. Optional; defaults to "serif".
print_risk_table	Print risk table beneath plot? Optional logical; defaults to TRUE.
print_group_lines	Print legend lines next to risk table? Optional logical; defaults to TRUE.
print_group_names	Print group/strata names next to risk table? Optional logical; defaults to TRUE.
risk_table_title	Header for risk table. Optional; defaults to "Total at risk".
group_names	Vector of group names to print in risk table. Optional.
group_order	Numeric vector giving order of groups to be printed in risk table. Optional.
legend	Logical indicator for printing a legend on the plot. Optional; defaults to FALSE since the information is found by default in the risk table.
legend_x_loc	X-axis coordinate or position for the legend location. Optional; defaults to "bottomleft".
legend_y_loc	Y-axis coordinate for the legend location. Optional; defaults to NULL.

Value

Returns a Kaplan-Meier plot with the requested attributes.

Author(s)

Erica Wozniak

Examples

```
library(survival)

# Set up data as a survival object
# KM plot for time to death
# Censor those who receive a transplant or are indicated by the dataset as censored
pbc_km <- na.omit(pbc[, c("time", "status", "trt")])
pbc_km$status[pbc_km$status == 1] <- 0
pbc_km$status[pbc_km$status == 2] <- 1
pbc_km$SurvObj <- with(pbc_km,
                      Surv(time = time,
                           event = status)
                      )
fit <- survfit(SurvObj ~ trt,
              data = pbc_km,
              conf.type = "log-log")

# Usage note: if gridlines are extending outside the plot border, run
# "dev.off()" and then run the plotting function again.

# Default options only
km_plot(fit = fit)

# Customized pretty plot with some options
km_plot(fit = fit,
        type = "km",
        col = c("orange3", "olivedrab"),
        # Add an extra major gridline and risk table column at time 4500
        xlim_major = c(0, 1000, 2000, 3000, 4000, 4500, 5000),
        plot_title = "Primary biliary cirrhosis survival",
        plot_subtitle = "By randomized treatment status",
        y_axis_label = "Survival",
        x_axis_label = "Time since registration (days)",
        group_names = c("D-penicillamine", "Placebo"),
        risk_table_title = bquote(italic("Patients at risk:")))

# Customized retro plot with lots of options
km_plot(fit = fit,
        font_family = "mono",
        type = "1-km",
        col = c("black", "black"),
        lty = c(1, 2),
        lwd = c(2, 2),
        xlim_major = c(0, 500, 1000, 2000, 3000, 3375, 4000, 4500, 5000),
        col_grid_major = "gray80",
        col_grid_minor = "gray92",
        plot_title = bquote(bold("Death following transplant registration")),
        plot_subtitle = "Mayo Clinic 1974-1984",
        plot_title_size = 1,
        y_axis_label = bquote(bold("Cumulative incidence")),
        x_axis_label = bquote(bold("Days")),
        group_names = c("D-penicillamine", "Placebo"),
        group_order = c(2, 1),
        risk_table_title = bquote(bold(underline("RISK TABLE"))),
        extra_left_margin = 5)
```

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