

Package ‘jskm’

May 17, 2020

Title Kaplan-Meier Plot with 'ggplot2'

Version 0.3.9

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Description The function 'jskm()' creates publication quality Kaplan-Meier plot with at risk tables below. 'svyjskm()' provides plot for weighted Kaplan-Meier estimator.

Depends R (>= 3.4.0)

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Encoding UTF-8

LazyData true

Imports ggplot2, gridExtra, plyr, survival, survey, scales

RoxygenNote 6.1.1

URL <https://github.com/jinseob2kim/jskm>

BugReports <https://github.com/jinseob2kim/jstable/issues>

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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 jskm

Creates a Kaplan-Meier plot for survfit object.

Description

Creates a Kaplan-Meier plot with at risk tables below for survfit object.

Usage

```
jskm(sfit, table = FALSE, xlabs = "Time-to-event",
     ylabs = "Survival probability", xlims = c(0, max(sfit$time)),
     ylims = c(0, 1), surv.scale = c("default", "percent"),
     ystratalabs = names(sfit$strata), ystrataname = "Strata",
     timeby = signif(max(sfit$time)/7, 1), main = "", pval = FALSE,
     pval.size = 5, pval.coord = c(NULL, NULL), pval.testname = F,
     marks = TRUE, shape = 3, legend = TRUE, legendposition = c(0.85,
     0.8), ci = FALSE, subs = NULL, label.nrisk = "Numbers at risk",
     size.label.nrisk = 10, linecols = "Set1", dashed = FALSE,
     cumhaz = F, cluster.option = "None", cluster.var = NULL,
     data = NULL, ...)
```

Arguments

sfit	a survfit object
table	logical: Create a table graphic below the K-M plot, indicating at-risk numbers?
xlabs	x-axis label
ylabs	y-axis label
xlims	numeric: list of min and max for x-axis. Default = c(0,max(sfit\$time))
ylims	numeric: list of min and max for y-axis. Default = c(0,1)
surv.scale	scale transformation of survival curves. Allowed values are "default" or "percent".
ystratalabs	character list. A list of names for each strata. Default = names(sfit\$strata)
ystrataname	The legend name. Default = "Strata"
timeby	numeric: control the granularity along the time-axis; defaults to 7 time-points. Default = signif(max(sfit\$time)/7, 1)
main	plot title
pval	logical: add the pvalue to the plot?
pval.size	numeric value specifying the p-value text size. Default is 5.
pval.coord	numeric vector, of length 2, specifying the x and y coordinates of the p-value. Default values are NULL
pval.testname	logical: add '(Log-rank)' text to p-value. Default = F
marks	logical: should censoring marks be added?

shape	what shape should the censoring marks be, default is a vertical line
legend	logical. should a legend be added to the plot?
legendposition	numeric. x, y position of the legend if plotted. Default=c(0.85,0.8)
ci	logical. Should confidence intervals be plotted. Default = FALSE
subs	= NULL,
label.nrisk	Numbers at risk label. Default = "Numbers at risk"
size.label.nrisk	Font size of label.nrisk. Default = 10
linecols	Character. Colour brewer pallettes too colour lines. Default ="Set1", "black" for black with dashed line.
dashed	logical. Should a variety of linetypes be used to identify lines. Default = FALSE
cumhaz	Show cumulaive hazard function, Default: F
cluster.option	Cluster option for p value, Option: "None", "cluster", "frailty", Default: "None"
cluster.var	Cluster variable
data	select specific data - for reactive input. Default = NULL
...	PARAM_DESCRIPTION

Details

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Author(s)

Jinseob Kim, but heavily modified version of a script created by Michael Way. <https://github.com/michaelway/ggkm/> I have packaged this function, added functions to namespace and included a range of new parameters.

Examples

```
library(survival)
data(colon)
fit <- survfit(Surv(time,status)~rx, data=colon)
jskm(fit, timeby=500)
```

svyjskm	<i>Creates a Weighted Kaplan-Meier plot - svykm.object in survey package</i>
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Description

Creates a Weighted Kaplan-Meier plot - svykm.object in survey package

Usage

```
svyjskm(sfit, xlabs = "Time-to-event", ylabs = "Survival probability",
        xlims = NULL, ylims = c(0, 1), ystratalabs = NULL,
        ystrataname = NULL, surv.scale = c("default", "percent"),
        timeby = NULL, main = "", pval = FALSE, pval.size = 5,
        pval.coord = c(NULL, NULL), pval.testname = F, legend = TRUE,
        legendposition = c(0.85, 0.8), ci = NULL, linecols = "Set1",
        dashed = FALSE, cumhaz = F, design = NULL, subs = NULL,
        table = F, label.nrisk = "Numbers at risk", size.label.nrisk = 10,
        ...)
```

Arguments

sfit	a svykm object
xlabs	x-axis label, Default: 'Time-to-event'
ylabs	y-axis label.
xlims	numeric: list of min and max for x-axis. Default: NULL
ylims	numeric: list of min and max for y-axis. Default: c(0, 1)
ystratalabs	character list. A list of names for each strata. Default: NULL
ystrataname	The legend name. Default: 'Strata'
surv.scale	scale transformation of survival curves. Allowed values are "default" or "percent".
timeby	numeric: control the granularity along the time-axis; defaults to 7 time-points.
main	plot title, Default: ""
pval	logical: add the pvalue to the plot?, Default: FALSE
pval.size	numeric value specifying the p-value text size. Default is 5.
pval.coord	numeric vector, of length 2, specifying the x and y coordinates of the p-value. Default values are NULL
pval.testname	logical: add '(Log-rank)' text to p-value. Default = F
legend	logical. should a legend be added to the plot? Default: TRUE
legendposition	numeric. x, y position of the legend if plotted. Default: c(0.85, 0.8)
ci	logical. Should confidence intervals be plotted. Default = NULL

linecols	Character. Colour brewer pallettes too colour lines. Default: 'Set1', "black" for black with dashed line.
dashed	logical. Should a variety of linetypes be used to identify lines. Default: FALSE
cumhaz	Show cumulaive hazard function, Default: F
design	Data design for reactive design data , Default: NULL
subs	= NULL,
table	logical: Create a table graphic below the K-M plot, indicating at-risk numbers?
label.nrisk	Numbers at risk label. Default = "Numbers at risk"
size.label.nrisk	Font size of label.nrisk. Default = 10
...	PARAM_DESCRIPTION

Details

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plot

Examples

```

library(survey)
data(pbc, package="survival")
pbc$randomized <- with(pbc, !is.na(trt) & trt>0)
biasmodel <- glm(randomized~age*edema,data=pbc)
pbc$randprob <- fitted(biasmodel)
dpbc <- svydesign(id=~1, prob=~randprob, strata=~edema, data=subset(pbc,randomized))
s1 <- svykm(Surv(time,status>0)~sex, design=dpbc)
svyjskm(s1)

```

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