Package ‘jskm’

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Title Kaplan-Meier Plot with 'ggplot2'
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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.
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Description

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

Usage

```r
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, cut.landmark = NULL, showpercent = F, ...
)
```

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 p-value 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"
sizelabel.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 cumulative incidence 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
cut.landmark cut-off for landmark analysis, Default = NULL
showpercent Shows the percentages on the right side.
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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

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

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,
Arguments

svyjskm

- **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 incidence function, Default: F
  - `design`: Data design for reactive design data , Default: NULL
  - `subs`: 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
  - `cut.landmark`: cut-off for landmark analysis, Default = NULL
  - `showpercent`: Shows the percentages on the right side.
  - `...`: PARAM_DESCRIPTION
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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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