

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.

Depends R (>= 3.4.0)

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Encoding UTF-8

Imports ggplot2 (>= 3.5.0), ggpubr, survival, survey, scales, patchwork, cmprsk, stats, ggsci

RoxygenNote 7.3.2

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

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

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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jskm	<i>Creates a Kaplan-Meier plot for survfit object.</i>
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Description

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

Usage

```
jskm(  
  sfit,  
  table = FALSE,  
  table.censor = FALSE,  
  xlabs = "Time-to-event",  
  ylabs = NULL,  
  xlims = c(0, max(sfit$time)),  
  ylims = c(0, 1),  
  surv.scale = c("default", "percent"),  
  ystratalabs = NULL,  
  ystrataname = "Strata",  
  timeby = signif(max(sfit$time)/7, 1),  
  main = "",  
  pval = FALSE,  
  pval.size = 5,  
  pval.coord = c(NULL, NULL),  
  pval.testname = T,  
  marks = TRUE,  
  shape = 3,  
  med = FALSE,  
  med.decimal = 2,  
  legend = TRUE,  
  legendposition = c(0.85, 0.8),  
  ci = FALSE,  
  subs = NULL,  
  label.nrisk = "Numbers at risk",  
  left.nrisk = FALSE,  
  size.label.nrisk = 10,  
  linecols = "Set1",  
  dashed = FALSE,  
  cumhaz = F,  
  cluster.option = "None",
```

```

cluster.var = NULL,
data = NULL,
cut.landmark = NULL,
showpercent = F,
status.cmprsk = NULL,
linewidth = 0.75,
theme = NULL,
nejm.infigure.ratiow = 0.6,
nejm.infigure.ratioh = 0.5,
nejm.infigure.xlim = NULL,
nejm.infigure.ylim = c(0, 1),
surv.by = NULL,
nejm.surv.by = NULL,
hr = FALSE,
hr.size = 5,
hr.coord = c(NULL, NULL),
hr.testname = F,
...
)

```

Arguments

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

med	should a median line be added to the plot? Default = F
med.decimal	Select the decimal to round to. Default = 2
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"
left.nrisk	Should risk label be at top left? Default = "False"
size.label.nrisk	Font size of label.nrisk. Default = 10
linecols	Character or Character vector. Colour imported from ggsci. Default = "Set1", "black" for black with dashed line, character vector for the customization of line colors.
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.
status.cmprsk	Status value when competing risk analysis, Default = 2nd level of status variable
linewidth	Line width, Default = 0.75
theme	Theme of the plot, Default = NULL, "nejm" for NEJMOA style, "jama" for JAMA style
nejm.infigure.ratiow	Ratio of infigure width to total width, Default = 0.6
nejm.infigure.ratioh	Ratio of infigure height to total height, Default = 0.5
nejm.infigure.xlim	x-axis limit of infigure, Default = NULL
nejm.infigure.ylim	y-axis limit of infigure, Default = c(0,1)
surv.by	breaks unit in y-axis, default = NULL(ggplot default)
nejm.surv.by	breaks unit in y-axis in nejm figure, default = NULL(ggplot default)
hr	logical: add the hazard ratio to the plot?
hr.size	numeric value specifying the HR text size. Default is 5.
hr.coord	numeric vector, of length 2, specifying the x and y coordinates of the p-value. Default values are NULL
hr.testname	logical: add '(Log-rank)' text to p-value. Default = F
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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

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,
  theme = NULL,
  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 = 4,
  pval.coord = c(NULL, NULL),
  pval.testname = F,
  marks = FALSE,
```

```

hr = FALSE,
hr.size = 2,
hr.coord = c(NULL, NULL),
med = FALSE,
med.decimal = 2,
legend = TRUE,
legendposition = c(0.85, 0.8),
ci = NULL,
linecols = "Set1",
dashed = FALSE,
cumhaz = F,
design = NULL,
subs = NULL,
table = F,
table.censor = F,
label.nrisk = "Numbers at risk",
left.nrisk = FALSE,
size.label.nrisk = 10,
cut.landmark = NULL,
showpercent = F,
linewidth = 0.75,
nejm.infigure.ratiow = 0.6,
nejm.infigure.ratioh = 0.5,
nejm.infigure.xlim = NULL,
nejm.infigure.ylim = c(0, 1),
surv.by = NULL,
nejm.surv.by = NULL,
...
)

```

Arguments

<code>sfit</code>	a <code>svykm</code> object
<code>theme</code>	Theme of the plot, Default = NULL, "nejm" for NEJMOA style, "jama" for JAMA style
<code>xlabs</code>	x-axis label, Default: 'Time-to-event'
<code>ylabs</code>	y-axis label.
<code>xlims</code>	numeric: list of min and max for x-axis. Default: NULL
<code>ylims</code>	numeric: list of min and max for y-axis. Default: c(0, 1)
<code>ystratalabs</code>	character list. A list of names for each strata. Default: NULL
<code>ystrataname</code>	The legend name. Default: 'Strata'
<code>surv.scale</code>	scale transformation of survival curves. Allowed values are "default" or "percent".
<code>timeby</code>	numeric: control the granularity along the time-axis; defaults to 7 time-points.
<code>main</code>	plot title, Default: ""
<code>pval</code>	logical: add the pvalue to the plot?, Default: FALSE

pval.size	numeric value specifying the p-value text size. Default is 4.
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?
hr	logical: add the Hazard Ratio to the plot?, Default: FALSE
hr.size	numeric value specifying the Hazard Ratio text size. Default is 2.
hr.coord	numeric vector, of length 2, specifying the x and y coordinates of the Hazard Ratio. Default values are NULL
med	should a median line be added to the plot? Default = F
med.decimal	Select the decimal to round to. Default = 2
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 = NULL
linecols	Character or Character vector. Colour imported from ggsci to colour lines. Default ="Set1", "black" for black with dashed line, character vector for the customization of line colors.
dashed	logical. Should a variety of linetypes be used to identify lines. Default: FALSE
cumhaz	Show cumulative incidence 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?
table.censor	logical: Add numbers of censored in table graphic
label.nrisk	Numbers at risk label. Default = "Numbers at risk"
left.nrisk	Should risk label be at top left? Default = "False"
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.
linewidth	Line width, Default = 0.75
nejm.infigure.ratiow	Ratio of infigure width to total width, Default = 0.6
nejm.infigure.ratioh	Ratio of infigure height to total height, Default = 0.5
nejm.infigure.xlim	x-axis limit of infigure, Default = NULL
nejm.infigure.ylim	y-axis limit of infigure, Default = c(0,1)
surv.by	breaks unit in y-axis, default = NULL(ggplot default)
nejm.surv.by	breaks unit in y-axis in nejm figure, default = NULL(ggplot default)
...	PARAM_DESCRIPTION

Details

DETAILS

Value

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)
dpsc <- svydesign(id = ~1, prob = ~randprob, strata = ~edema, data = subset(pbc, randomized))
s1 <- svykm(Surv(time, status > 0) ~ sex, design = dpsc)
svyjskm(s1)
```


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