

Package ‘jskm’

May 27, 2026

Title Kaplan-Meier Plot with 'ggplot2'

Version 0.6.3

Date 2026-05-27

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)

License Apache License 2.0

Encoding UTF-8

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

RoxygenNote 7.3.3

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

Author Jinseob Kim [aut, cre] (ORCID: <<https://orcid.org/0000-0002-9403-605X>>),
yoonkyoung Chun [aut],
Zarathu [cph, fnd],
sungho Choi [aut],
Mingu Jee [aut],
Wonbin Hahn [aut],
Taehong Kim [aut],
Sangho Oh [aut],
Sewon Lee [aut]

Maintainer Jinseob Kim <jinseob2kim@gmail.com>

Repository CRAN

Date/Publication 2026-05-27 11:40:02 UTC

Contents

jskm	2
svyjskm	5

Index	9
--------------	----------

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

Description

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

Usage

```
jskm(
  sfit,
  table = TRUE,
  table.censor = FALSE,
  xlabs = "Time-to-event",
  ylabs = NULL,
  xlims = c(0, max(sfit$time)),
  ylims = c(0, 1),
  surv.scale = c("percent", "default"),
  ystratalabs = NULL,
  ystrataname = "Group",
  timeby = signif(max(sfit$time)/7, 1),
  main = "",
  pval = FALSE,
  pval.size = 5,
  pval.coord = c(NULL, NULL),
  pval.testname = T,
  marks = FALSE,
  shape = 3,
  med = FALSE,
  med.decimal = 2,
  legend = TRUE,
  legendposition = c(0.85, 0.8),
  ci = FALSE,
  subs = NULL,
  label.nrisk = "No. at Risk",
  left.nrisk = TRUE,
  size.label.nrisk = 11,
  linecols = "Set1",
  dashed = FALSE,
  cumhaz = F,
  cluster.option = "None",
```

```

cluster.var = NULL,
data = NULL,
cut.landmark = NULL,
showpercent = F,
status.cmprsk = NULL,
linewidth = 1.2,
theme = NULL,
nejm.infigure.ratiow = 0.6,
nejm.infigure.ratioh = 0.5,
nejm.infigure.xlim = NULL,
nejm.infigure.ylim = c(0, 1),
surv.by = 0.1,
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
...	PARAM_DESCRIPTION

Details

DETAILS

Value

Plot

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 = NULL,
  xlims = NULL,
  ylims = c(0, 1),
  ystratalabs = NULL,
  ystrataname = "Group",
  surv.scale = c("percent", "default"),
  timeby = NULL,
  main = "",
  pval = FALSE,
  pval.size = 5,
  pval.coord = c(NULL, NULL),
  pval.testname = F,
  marks = FALSE,
```

```

hr = FALSE,
hr.size = 5,
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 = TRUE,
table.censor = F,
label.nrisk = "No. at Risk",
left.nrisk = TRUE,
size.label.nrisk = 11,
cut.landmark = NULL,
showpercent = F,
linewidth = 1.2,
nejm.infigure.ratiow = 0.6,
nejm.infigure.ratioh = 0.5,
nejm.infigure.xlim = NULL,
nejm.infigure.ylim = c(0, 1),
surv.by = 0.1,
nejm.surv.by = NULL,
...
)

```

Arguments

<code>sfit</code>	a svykm object
<code>theme</code>	Theme of the plot, Default = NULL, "nejm" for NEJM 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)
dpbc <- svydesign(id = ~1, prob = ~randprob, strata = ~edema, data = subset(pbc, randomized))
s1 <- svykm(Surv(time, status > 0) ~ sex, design = dpbc)
svyjskm(s1)
```

Index

jskm, 2

svyjskm, 5