

# Package: jskm (via r-universe)

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**Title** Kaplan-Meier Plot with 'ggplot2'

**Version** 0.5.6

**Date** 2024-10-23

**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, ggpubr, survival, survey, scales, patchwork

**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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**Repository** <https://jinseob2kim.r-universe.dev>

**RemoteUrl** <https://github.com/cran/jskm>

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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,
  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 = F,
  marks = TRUE,
  shape = 3,
  med = FALSE,
  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,
    status.cmprsk = NULL,
    linewidth = 0.75,
    theme = NULL,
    nejm.infigure.ratiow = 0.6,
    nejm.infigure.ratioh = 0.5,
    nejm.infigure.ylim = c(0, 1),
    ...
)

```

## 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>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
<code>med</code>	should a median line be added to the plot? Default = F
<code>legend</code>	logical. should a legend be added to the plot?
<code>legendposition</code>	numeric. x, y position of the legend if plotted. Default= <code>c(0.85,0.8)</code>
<code>ci</code>	logical. Should confidence intervals be plotted. Default = FALSE
<code>subs</code>	= NULL,
<code>label.nrisk</code>	Numbers at risk label. Default = "Numbers at risk"
<code>size.label.nrisk</code>	Font size of label.nrisk. Default = 10

linecols	Character or Character vector. Colour brewer pallettes too 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
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 NEJM 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.ylim	y-axis limit of infigure, Default = c(0,1)
...	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)
```

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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,  
  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 = 5,  
  pval.coord = c(NULL, NULL),  
  pval.testname = F,  
  med = FALSE,  
  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,  
  cut.landmark = NULL,  
  showpercent = F,  
  linewidth = 0.75,  
  nejm.infigure.ratiow = 0.6,  
  nejm.infigure.ratioh = 0.5,  
  nejm.infigure.ylim = c(0, 1),  
  ...  
)
```

**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
<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>med</code>	should a median line be added to the plot? Default = F
<code>legend</code>	logical. should a legend be added to the plot?
<code>legendposition</code>	numeric. x, y position of the legend if plotted. Default=c(0.85,0.8)
<code>ci</code>	logical. Should confidence intervals be plotted. Default = NULL
<code>linecols</code>	Character or Character vector. Colour brewer pallettes too colour lines. Default = "Set1", "black" for black with dashed line, character vector for the customization of line colors.
<code>dashed</code>	logical. Should a variety of linetypes be used to identify lines. Default: FALSE
<code>cumhaz</code>	Show cumulative incidence function, Default: F
<code>design</code>	Data design for reactive design data, Default: NULL
<code>subs</code>	= NULL,
<code>table</code>	logical: Create a table graphic below the K-M plot, indicating at-risk numbers?
<code>label.nrisk</code>	Numbers at risk label. Default = "Numbers at risk"
<code>size.label.nrisk</code>	Font size of label.nrisk. Default = 10
<code>cut.landmark</code>	cut-off for landmark analysis, Default = NULL
<code>showpercent</code>	Shows the percentages on the right side.
<code>linewidth</code>	Line width, Default = 0.75
<code>nejm.infigure.ratiow</code>	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.ylim  
                        y-axis limit of infigure, Default = c(0,1)  
...                      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)  
dpcb <- svydesign(id = ~1, prob = ~randprob, strata = ~edema, data = subset(pbc, randomized))  
s1 <- svykm(Surv(time, status > 0) ~ sex, design = dpcb)  
svyjskm(s1)
```

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