

# Package ‘jskm’

August 10, 2023

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

**Version** 0.5.2

**Date** 2023-08-04

**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

**RoxygenNote** 7.2.3

**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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**Repository** CRAN

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## R topics documented:

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`jskm`*Creates a Kaplan-Meier plot for survfit object.*

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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$time)),  
  ylims = c(0, 1),  
  surv.scale = c("default", "percent"),  
  ystratalabs = names(sfit$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,  
  status.cmprsk = NULL,  
  linewidth = 0.75,  
  ...  
)
```

**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>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   |
| <code>linecols</code>         | Character. Colour brewer pallettes too colour lines. Default="Set1", "black" for black with dashed line.                             |
| <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>cluster.option</code>   | Cluster option for p value, Option: "None", "cluster", "frailty", Default: "None"  |
| <code>cluster.var</code>      | Cluster variable   |
| <code>data</code>             | select specific data - for reactive input, Default = NULL  |
| <code>cut.landmark</code>     | cut-off for landmark analysis, Default = NULL  |
| <code>showpercent</code>      | Shows the percentages on the right side.   |
| <code>status.cmprsk</code>    | Status value when competing risk analysis, Default = 2nd level of status variable  |
| <code>linewidth</code>        | Line width, Default = 0.75   |
| <code>...</code>              | 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`*Creates a Weighted Kaplan-Meier plot - svykm.object in survey package*

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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,
cut.landmark = NULL,
showpercent = F,
linewidth = 0.75,
...
)

```

### Arguments

|                             |   |
|-----------------------------|---|
| <code>sfit</code>           | a svykm object  |
| <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>legend</code>         | logical. should a legend be added to the plot? Default: TRUE  |
| <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. Colour brewer pallettes too colour lines. Default: 'Set1', "black" for black with dashed line. |
| <code>dashed</code>         | logical. Should a variety of linetypes be used to identify lines. Default: FALSE                          |
| <code>cumhaz</code>         | Show cumulaive 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>...</code>              | 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)
```

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