

# Package ‘jskm’

January 27, 2026

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

**Version** 0.6.0

**Date** 2026-01-27

**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** 7.3.2

**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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|                  |                                                        |
|------------------|--------------------------------------------------------|
| j <sup>skm</sup> | <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 = 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 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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