Package ‘jskm’

October 13, 2022

Title  Kaplan-Meier Plot with 'ggplot2'
Version  0.4.3
Date  2021-10-09
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, gridExtra, survival, survey, scales
RoxygenNote  7.1.1
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:

  jskm ................................................................. 2
  svyjskm ......................................................... 4

Index  7
Description

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

Usage

```r
jskm(
  sfit,
  table = FALSE,
  xlabs = "Time-to-event",
  ylabs = "Survival probability",
  xlimits = c(0, max(sfit$time)),
  ylimits = c(0, 1),
  surv.scale = c("default", "percent"),
  ystratalabs = names(sfit$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,
  ...
)
```

Arguments

- `sfit` a survfit object
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>table</code></td>
<td>logical: Create a table graphic below the K-M plot, indicating at-risk numbers?</td>
</tr>
<tr>
<td><code>xlabs</code></td>
<td>x-axis label</td>
</tr>
<tr>
<td><code>ylabs</code></td>
<td>y-axis label</td>
</tr>
<tr>
<td><code>xlims</code></td>
<td>numeric: list of min and max for x-axis. Default = c(0,max(sfit$time))</td>
</tr>
<tr>
<td><code>ylims</code></td>
<td>numeric: list of min and max for y-axis. Default = c(0,1)</td>
</tr>
<tr>
<td><code>surv.scale</code></td>
<td>scale transformation of survival curves. Allowed values are &quot;default&quot; or &quot;percent&quot;.</td>
</tr>
<tr>
<td><code>ystratalabs</code></td>
<td>character list. A list of names for each strata. Default = names(sfit$strata)</td>
</tr>
<tr>
<td><code>ystrataname</code></td>
<td>The legend name. Default = &quot;Strata&quot;</td>
</tr>
<tr>
<td><code>timeby</code></td>
<td>numeric: control the granularity along the time-axis; defaults to 7 time-points. Default = signif(max(sfit$time)/7, 1)</td>
</tr>
<tr>
<td><code>main</code></td>
<td>plot title</td>
</tr>
<tr>
<td><code>pval</code></td>
<td>logical: add the pvalue to the plot?</td>
</tr>
<tr>
<td><code>pval.size</code></td>
<td>numeric value specifying the p-value text size. Default is 5.</td>
</tr>
<tr>
<td><code>pval.coord</code></td>
<td>numeric vector, of length 2, specifying the x and y coordinates of the p-value. Default values are NULL</td>
</tr>
<tr>
<td><code>pval.testname</code></td>
<td>logical: add '(Log-rank)' text to p-value. Default = F</td>
</tr>
<tr>
<td><code>marks</code></td>
<td>logical: should censoring marks be added?</td>
</tr>
<tr>
<td><code>shape</code></td>
<td>what shape should the censoring marks be, default is a vertical line</td>
</tr>
<tr>
<td><code>legend</code></td>
<td>logical. should a legend be added to the plot?</td>
</tr>
<tr>
<td><code>legendposition</code></td>
<td>numeric. x, y position of the legend if plotted. Default= c(0.85,0.8)</td>
</tr>
<tr>
<td><code>ci</code></td>
<td>logical. Should confidence intervals be plotted. Default = FALSE</td>
</tr>
<tr>
<td><code>subs</code></td>
<td>= NULL,</td>
</tr>
<tr>
<td><code>label.nrisk</code></td>
<td>Numbers at risk label. Default = &quot;Numbers at risk&quot;</td>
</tr>
<tr>
<td><code>size.label.nrisk</code></td>
<td>Font size of label.nrisk. Default = 10</td>
</tr>
<tr>
<td><code>linecols</code></td>
<td>Character. Colour brewer pallettes too colour lines. Default = &quot;Set1&quot;, &quot;black&quot; for black with dashed line.</td>
</tr>
<tr>
<td><code>dashed</code></td>
<td>logical. Should a variety of linetypes be used to identify lines. Default = FALSE</td>
</tr>
<tr>
<td><code>cumhaz</code></td>
<td>Show cumulative incidence function, Default: F</td>
</tr>
<tr>
<td><code>cluster.option</code></td>
<td>Cluster option for p value, Option: &quot;None&quot;, &quot;cluster&quot;, &quot;frailty&quot;, Default: &quot;None&quot;</td>
</tr>
<tr>
<td><code>cluster.var</code></td>
<td>Cluster variable</td>
</tr>
<tr>
<td><code>data</code></td>
<td>select specific data - for reactive input, Default = NULL</td>
</tr>
<tr>
<td><code>cut.landmark</code></td>
<td>cut-off for landmark analysis, Default = NULL</td>
</tr>
<tr>
<td><code>showpercent</code></td>
<td>Shows the percentages on the right side.</td>
</tr>
</tbody>
</table>

**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

```r
library(survival)
data(colon)
fit <- survfit(Surv(time,status)~rx, data=colon)
jskm(fit, timeby=500)
```

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svyjskm

### Description

Creates a Weighted Kaplan-Meier plot - svykm.object in survey package

### Usage

```r
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,
)```

Arguments

sfit a svykm object
xlabs x-axis label, Default: 'Time-to-event'
ylabs y-axis label.
xlims numeric: list of min and max for x-axis. Default: NULL
ylims numeric: list of min and max for y-axis. Default: c(0, 1)
ystratalabs character list. A list of names for each strata. Default: NULL
ystrataname The legend name. Default: 'Strata'
surv.scale scale transformation of survival curves. Allowed values are "default" or "percent".
timeby numeric: control the granularity along the time-axis; defaults to 7 time-points.
main plot title, Default: "
pval logical: add the pvalue to the plot?, Default: FALSE
pval.size numeric value specifying the p-value text size. Default is 5.
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
legend logical. should a legend be added to the plot? Default: TRUE
legendposition numeric. x, y position of the legend if plotted. Default: c(0.85, 0.8)
linecols Character. Colour brewer pallettes too colour lines. Default: 'Set1', "black" for black with dashed line.
dashed logical. Should a variety of linetypes be used to identify lines. Default: FALSE
cumhaz Show cumulaive 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?
label.nrisk Numbers at risk label. Default = "Numbers at risk"
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.
... PARAM_DESCRIPTION
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, 4