# Package ‘survSAKK’

May 15, 2025

**Type** Package

**Title** Create Publication Ready Kaplan-Meier Plots

**Version** 1.3.2

**Description** Incorporate various statistics and layout customization options to enhance the efficiency and adaptability of the Kaplan-Meier plots.

**License** GPL (>= 2)

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**URL** https://sakk-statistics.github.io/survSAKK/

**BugReports** https://github.com/SAKK-Statistics/survSAKK/issues

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Imports** graphics, grDevices, survival

**Config/testthat/edition** 3

**Depends** R (>= 2.10)

**LazyData** true

**NeedsCompilation** no

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**Repository** CRAN

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# Contents

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## `esophagus` *SAKK Esophagus Cancer Data*

### Description

This anonymized data contains survival data from patients with resectable esophageal carcinoma to compare the outcomes of two treatment regimens: Neoadjuvant chemotherapy followed by chemoradiation and surgery with and without cetuximab.

### Usage

`esophagus`

### Format

A data frame with 297 patients and 6 variables:

**arm** Treatment Arm.

**OS.time** Overall survival time in years.

**OS.event** Overall survival status (0 = censored, 1 = event).

**hist** Histological type of the tumor.

**PFS.time** Progression-free survival time in years.

**PFS.event** Progression-free survival status (0 = censored, 1 = event).

### Source

SAKK Competence Center, Switzerland

### References

Ruhstaller, T., Thuss-Patience, P., Hayoz, S., Schacher, S., Knorrenschild, J. R., Schnider, A., ... & Stahl, M. (2018). Neoadjuvant chemotherapy followed by chemoradiation and surgery with and without cetuximab in patients with resectable esophageal cancer: a randomized, open-label, phase III trial (SAKK 75/08). Annals of oncology, 29(6), 1386-1393.

## `surv.plot` *Publication Ready Kaplan-Meier Estimator*

### Description

Provide an open-source, user-friendly tool designed to enhance the creation and customization of Kaplan-Meier plots and incorporating various statistics and layout customization options using `surv.plot(fit, ...)`.

### Arguments

| | |
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| `fit` | An object of class survival::survfit containing survival data. |
| `ties` | String specifying the method for tie handling. If there are no tied death times all the methods are equivalent. Options: "efron", "breslow", "exact". Default: "efron" |
| `reference.arm` | A character string specifying the reference arm for comparison. |
| `time.unit` | A character string specifying the time unit which was used to create the `fit` object. *Note:* `time.unit` will not convert the time of the `fit` object.<br>Option include: `"day"`, `"week"`, `"month"`,`"year"`. |
| `y.unit` | A character string specifying the unit of the y-axis.<br>Option include: `"probability"`, `"percent"`. |
| `censoring.mark` | A logical parameter indicating whether censoring events should be marked on the survival curves. Default is `TRUE`. |
| `censoring.cex` | A numeric value specifying the size of the marks for censored patients. Default is `1.3`. |
| `conf.int` | A numeric value controlling the confidence interval on survival curves. Default is `0.95`, corresponding to a 95% confidence interval. Values between `0` and `1` represent the desired confidence interval. If set to `0`, no confidence intervals are displayed. |
| `conf.band` | A logical parameter indicating whether to display the confidence band on the survival curves. Default is `TRUE`. |
| `conf.band.col` | A colour which is used for the confidence band. Can accept a single colour value or a vector of colours. |
| `conf.band.transparent` | A numeric value between `0` and `1` controlling the transparency of the confidence band. Default is `0.25`. |
| `conf.line.lty` | A strings specifying the line type of the confidence lines.<br>Options include: `"blank"`, `"solid"`, `"dashed"`, `"dotted"`, `"dotdash"`, `"longdash"`, `"twodash"`. Default is `"blank"`. |
| `conf.line.lwd` | A numeric value specifying the width of the confidence lines. |
| `conf.type` | Transformation type for the confidence interval.<br>Options include: `"log"`, `"log-log"`, `"plain"`, `"logit"`, `"arcsin"`. Default is `log-log`. |

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| `grid` | A logical parameter specifying whether to draw a grid. Default is `FALSE`. |
| `col` | A colour which is used for the survival curves. Can accept a single colour value or a vector of colours. |
| `main` | Title of the plot. |
| `sub` | Subtitle of the plot. Note: A subtitle is only displayed if no risk table is shown. |
| `letter` | A letter to be displayed on the top to the left of the figure (for example if several plots are displayed in one figure). |
| `letter.cex` | The size of `letter` which is displayed on the top to the left. |
| `letter.pos.x` | The X-axis position of `letter` (corresponds to `adj` in `mtext`). Default is -0.35 |
| `letter.pos.y` | The Y-axis position of `letter` (corresponds to `line` in `mtext`). Default is 1. |
| `xlab` | X-axis label. |
| `ylab` | Y-axis label. |
| `xticks` | A numeric vector specifying the ticks of the x-axis.<br>Can be specified as `seq(from = , to = , by = )`.<br>• `from`: starting value<br>• `to`: end value<br>• `by`: number; increment of the sequence |
| `yticks` | A numeric vector specifying the ticks of the y-axis.<br>Can be specified as `seq(from = , to = , by = )`.<br>• `from`: starting value<br>• `to`: end value<br>• `by`: number; increment of the sequence<br>*Note*: It should always be specified as probability. |
| `xlab.pos` | Defines the margin line where the X-axis label (xlab) is displayed, starting at 0 and counting outwards. Default is 1.5. |
| `ylab.pos` | Defines the margin line the Y-axis label (ylab) is displayed, starting at 0 counting outwards. Default is 3. |
| `xlab.cex` | A numeric value specifying the size of the X-axis label. |
| `ylab.cex` | A numeric value specifying the size of the Y-axis label. |
| `cex` | A numeric value specifying the size of all all text elements (labels, annotations, etc.). |
| `axis.cex` | A numeric value specifying the size of the axis elements. |
| `bty` | Determines the style of the box drawn around the plot.<br>Options include: `"n"` ,`"o"`,`"c"`,`"u"`. Default is `"n"`. |
| `lty` | A string specifying the line type of of the curve(s).<br>Options include: `"blank"`, `"solid"`, `"dashed"`, `"dotted"`, `"dotdash"`, `"longdash"`, `"twodash"`. |
| `lwd` | A numeric value specifying the width of the line. |
| `legend` | A logical parameter specifying whether to display legend. By default, the legend is displayed if there is more than one arm. |

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| `legend.position` | Position of the legend.<br>Options include: "c(x,y)", "bottomright", "bottom", "bottomleft", "left"‘, |
| `legend.name` | A vector of character string specifying of the name(s) of the arm(s). |
| `legend.cex` | A numeric value specifying the size of the legend text. |
| `legend.text.font` | Font style of the legend text. Possible values:<br>• `1` normal<br>• `2` bold<br>• `3` italic<br>• `4` bold and italic |
| `legend.title` | Title of the legend. |
| `legend.title.cex` | A numeric value specifying the size of the legend title. |
| `segment.type` | A numeric value specifying the layout of the segment. Possible values:<br>• `1` full width<br>• `2` half width<br>• `3` vertical and horizontal segment (default) |
| `segment.timepoint` | A single value or a vector of fixed time points to be drawn as segment(s). |
| `segment.quantile` | A single value or a vector of fixed quantile to be drawn as segment(s). Example: 0.5 corresponds to median. |
| `segment.main` | Title of the segment text. |
| `segment.confint` | A logical parameter specifying whether to display the confidence interval for the segment. Default: TRUE |
| `segment.annotation` | Position of the segment annotation. If several quantiles or time points are chosen then the position can only be set to `"left"`, `"right"`, `"top"` or `"bottom"`.<br>Options include: `c(x,y)`, `"bottom"`, `"bottomleft"`, `"left"`, `"right"`, `"top"`, `"none"`. |
| `segment.annotation.offset` | The offset used in function `text()` for adding the annotation if several time points or quantiles are added. |
| `segment.annotation.two.lines` | A logical parameter to force that the annotation is displayed on two lines. This parameter only has an effect if there is only one arm. Default: FALSE |
| `segment.annotation.col` | A colour which is used for the segment annotation. Can accept a single colour value or a vector of colours. |
| `segment.annotation.space` | Spacing between the text in units of y-coordinates. |

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| `segment.col` | A colour which is used for the segment. Can accept a single colour value. |
| `segment.lty` | A strings specifying the line type of the segment(s).<br>Options include: `"blank"`, `"solid"`, `"dashed"`, `"dotted"`, `"dotdash"`, `"longdash"`, `"twodash"`. |
| `segment.lwd` | A numeric value specifying the width of the segment line. |
| `segment.cex` | A numeric value specifying the size of the segment text size. |
| `segment.font` | A numeric value specifying the font face. Possible values:<br>• `1` plain<br>• `2` bold<br>• `3` italic<br>• `4` bold-italic |
| `segment.main.font` | A numeric value specifying the font face for the segment text. Possible values:<br>• `1` plain<br>• `2` bold<br>• `3` italic<br>• `4` bold-italic |
| `stat.fit` | An object of class survival::survfit containing survival data. Used for calculation of statistics, allowing to add stratification factors.<br>*Note:* If not specified the `fit` object will be used for the `stat`. |
| `stat` | Statistics displayed in the plot.<br>Options:<br>• `"logrank"` gives the p value of the conducted logrank test using `survdiff{survival}`. To tests if there is a difference between two or more survival curves.<br>• `"coxph"` gives the hazard ratio (HR) and its CI (default: 95% CI)of the conducted Cox proportional hazards regression using `coxph{survival}`. *Note*: This option only works if there are two arms.<br>• `"coxph_logrank"` combines the hazard ratio (HR), its CI (default: 95% CI) and the logrank test. *Note:* This option only works if there are two arms.<br>• `'none'` no statistic is displayed (default).<br>Note: Confidence interval can be adjusted with the argument `stat.conf.int`. |
| `stat.position` | Position where the `stat` should be displayed.<br>Options include: `c(x,y)`,"`bottomleft"`, `"left"`, `"right"`, `"top"`, `"topright"`,`"bottomright"`, `"none"`. |
| `stat.conf.int` | A numeric value controlling the confidence interval on the `stat` (hazard ratio). Default is `0.95`, corresponds to a 95% confidence interval. Values between `0` and `1` represent the desired confidence interval. |
| `stat.col` | A colour which is used for the statistics text. Can accept a single colour value or a vector of colours. |
| `stat.cex` | A numeric value specifying the size of the ‘statistics text size. |
| `stat.font` | The font face of the statistics Possible values: |

- `1` plain
- `2` bold
- `3` italic
- `4` bold-italic

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| `risktable` | A logical parameter indicating whether to draw risk table. Default is `TRUE`. |
| `risktable.censoring` | A logical parameter indicating whether to display number of censored patients. Default is `FALSE`. |
| `risktable.pos` | Defines on which margin line of the xlab is displayed, starting at 0 counting outwards. Default is at line `3`. |
| `risktable.name` | Names of the arms for the risk table. |
| `risktable.cex` | A numeric value specifying the size of the risk table text size. |
| `risktable.col` | A coulour which is used for the risk table. Can accept a single colour value or a vector of colours. Default is `black`.<br>*Note:* If `risktable.col` = `TRUE` then the colours of the curves are used. |
| `risktable.title` | Title of risk table. |
| `risktable.title.font` | Font style of the risk table. Possible values:<br>• `1` normal<br>• `2` bold<br>• `3` italic<br>• `4` bold and italic |
| `risktable.title.col` | A colour which is used for the risk table title. Can accept a single colour value. |
| `risktable.title.position` | A numeric value specifying the position of the title on the x-axis. |
| `risktable.title.cex` | A numeric value specifying the size of the risk table title size. |
| `risktable.name.cex` | A numeric value specifying the size of the risk table legend name size. |
| `risktable.name.font` | Font style of the risk table legend name(s). Possible values:<br>• `1` normal<br>• `2` bold<br>• `3` italic<br>• `4` bold and italic |
| `risktable.name.col` | A colour which is used for the risk table name. Can accept a single colour value. |
| `risktable.name.position` | A numeric value specifying the position of the legend name(s) on the x-axis. |
| `margin.bottom` | Specifies the bottom margin of the plotting area in line units. Default is `5`. |

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| `margin.left` | Specifies the left margin of the plotting area in line units. Default is `6` (with risktable) or `4` (without risktable). |
| `margin.top` | Specifies the top margin of the plotting area in line units. Default is `3`. |
| `margin.right` | Specifies the right margin of the plotting area in line units. Default is `2`. |
| `theme` | Built-in layout options. Options include: ("none", "SAKK", "Lancet", "JCO", "WCLC", "ESMO") |

## Details

The survSAKK R package provides the `surv.plot()` function, facilitating Kaplan-Meier survival analysis. Designed with user-friendliness and efficiency in mind. Offering robust tool for analysing survival data. It utilises the functionalities of `survival::survfit()`.

For a comprehensive manual visit: `https://sakk-statistics.github.io/survSAKK/articles/surv.plot.html`

## Value

Kaplan-Meier curves of the input `fit`, incorporating various statistics and layout option(s).

## Author(s)

Vithersan Somasundaram and Katrin Gysel

## References

Therneau T (2024). A Package for Survival Analysis in R. R package version 3.5-8, `https://CRAN.R-project.org/package=survival`.

Terry M. Therneau, Patricia M. Grambsch (2000). Modeling Survival Data: Extending the Cox Model. Springer, New York. ISBN 0-387-98784-3.

## See Also

- `survival::survfit()` which this function wraps.

## Examples

```
 require(survival)
 require(survSAKK)

# Create survival object
 fit <- survfit(Surv(lung$time/365.25*12, status) ~ sex, data = lung)

# Generate survival plots
 surv.plot(fit = fit,
   time.unit = "month",
   legend.name =  c("male", "female"))
```

# Index