

Package ‘BiMaUmisc’

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Type Package

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Description Contains a function to plot publication-ready survival curves with the Kaplan-Meier method (1958) <[doi:10.2307/2281868](https://doi.org/10.2307/2281868)> and a function to format p-values, which are useful for repetitive analyses. BiMaU stands for the Biostatistics and Mathematics Research Unit at the Sant Joan de Déu - Pediatric Cancer Center Barcelona <<https://github.com/BiMaU-PCCB>>.

License GPL (>= 2)

Depends R (>= 4.1.0)

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show.p

Format p -values for display

Description

Convert p -values to a compact textual representation. The function prints decimals up to the first non-zero decimal and the following one, applying standard rounding.

Usage

```
show.p(p, add.p = FALSE)
```

Arguments

<code>p</code>	a value or vector of the p -value(s) to be shown, where $0 < p < 1$.
<code>add.p</code>	logical indicating whether the text $p=$ (or $p<$, if it applies) should be added before the p -value. The default value is FALSE.

Details

The number of decimals shown depends on the magnitude of the p -value so that two meaningful digits are displayed after the leading zeros.

Specifically:

- For $p \geq 0.1$, two decimal places are shown.
- For $0.01 \leq p < 0.1$, three decimal places are shown.
- For $0.001 \leq p < 0.01$, four decimal places are shown.
- For $0.0001 \leq p < 0.001$, five decimal places are shown.
- For $p < 0.0001$, the string " <0.0001 " is returned.

This formatting ensures that the first non-zero decimal of the p -value and the following digit are displayed, while avoiding an excessive number of leading zeros.

If `add.p = TRUE`, the prefix " $*p=$ " (or " $*p<$ " when applicable) is added to the formatted value. This will ensure the p appears in cursive when calling the function in line on R markdown documents.

Value

A character vector with the formatted p -values.

Examples

```
show.p(0.00785)
show.p(c(0.03042, 0.1579, 0.0000025))
show.p(0.00785, add.p = TRUE)
show.p(c(0.03042, 0.1579, 0.0000025), add.p = TRUE)
```

survival.plot	<i>Plot survival curves</i>
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Description

This function produces an elegant survival curve plot. It can automatically append the number-at-risk table and display the log-tank test p -value (obtained from a call to [survdif](#)). Highly customizable, it offers numerous arguments to easily modify the plot's appearance.

Usage

```
survival.plot(data, time, status, strata = 1,
              legend = TRUE, legend.pos = "bottomleft", legend.labs = NULL,
              legend.title = NULL, legend.cex = 1,
              events = FALSE, events.pos = NULL, events.text = NULL,
              mark.time = TRUE, lwd = 3,
              risk = TRUE, risk.text = TRUE, risk.labs = NULL, risk.cex = 1,
              p.value = TRUE, p.value.pos = NULL,
              units = "days", xlab = NULL, times = NULL,
              yscale = 1, ylab = NULL,
              main = "Survival curve", col = NULL, ...)
```

Arguments

<code>data</code>	name of the dataset, of class <code>data.frame</code> , containing at least 2 columns (follow up time, status indicator).
<code>time</code>	follow-up time column name. Can be specified as a character string (with quotes) or as an unquoted symbol.
<code>status</code>	status indicator column name. Can be specified as a character string (with quotes) or as an unquoted symbol.
<code>strata</code>	strata indicator column name. Can be specified as a character string (with quotes) or as an unquoted symbol. Up to four categories. Must be a factor. The default value is 1, this is, there are no groups.
<code>legend</code>	logical indicating whether a legend should be added to the plot. If <code>strata</code> is set to 1, this argument is ignored. The default value is TRUE.
<code>legend.pos</code>	this argument can be a single keyword from the list in legend , such as "bottomleft" or "topright", which places the legend on the inside of the plot frame at the given location. In this case, this argument is passed to match.arg . Otherwise, a 2-dimensional numerical vector indicating the x-y coordinates can be indicated. If <code>legend</code> is set to FALSE, this argument is ignored. The default value is "bottomleft".
<code>legend.labs</code>	a character vector of length ≥ 2 to appear as the legend labels. If <code>legend</code> is set to FALSE, this argument is ignored. The default value, NULL, indicates that the levels of <code>strata</code> are to be used as the legend labels.

<code>legend.title</code>	title for the legend. If <code>legend</code> is set to <code>FALSE</code> , this argument is ignored. The default value, <code>NULL</code> , indicates on title should be added.
<code>legend.cex</code>	legend's character expansion factor. A numerical value giving the amount by which the legend text should be magnified relative to the default. If <code>legend</code> is set to <code>FALSE</code> , this argument is ignored. The default value is 1.
<code>events</code>	logical indicating whether the number of events should be added to the text in the legend. If <code>strata</code> is set to 1, the total number of events is added directly to the plot instead. If <code>legend</code> is set to <code>FALSE</code> and <code>strata</code> is not 1, this argument is ignored. The default value is <code>FALSE</code> .
<code>events.pos</code>	2-dimensional numerical vector indicating the x-y coordinates where the number of events should be added to the plot. If <code>strata</code> is not 1 or <code>events</code> is set to <code>FALSE</code> , this argument is ignored. The default value, <code>NULL</code> , indicates that the text should be placed on the bottom-left corner.
<code>events.text</code>	a character indicating the text to display before the number of events in the plot. If <code>events</code> is set to <code>FALSE</code> , this argument is ignored. The default value, <code>NULL</code> , indicates that the text "Events" should be added when <code>strata</code> is set to 1 and the text "events" should be added when <code>strata</code> is not set to 1.
<code>mark.time</code>	logical indicating whether the curves should be marked at each censoring time. The default value is <code>TRUE</code> .
<code>lwd</code>	a number indicating the line width(s). Alternatively, when <code>strata</code> is not set to 1, an n -dimensional numerical vector can be indicated, where n is the number of levels in <code>strata</code> . The default value is 3.
<code>risk</code>	logical indicating whether the number-at-risk table should be appended to the plot. The default value is <code>TRUE</code> .
<code>risk.text</code>	logical indicating whether the legend for the number-at-risk table should display text labels. When <code>FALSE</code> , line segments are used instead. If <code>risk</code> is set to <code>FALSE</code> or <code>strata</code> is set to 1, this argument is ignored. The default value is <code>TRUE</code> .
<code>risk.labs</code>	n -dimensional character vector, where n is the number of levels in <code>strata</code> , indicating the text labels in the number-at-risk table. If <code>risk.text</code> is set to <code>FALSE</code> or <code>strata</code> is set to 1, this argument is ignored. The default value, <code>NULL</code> , indicates that the levels of <code>strata</code> should be used.
<code>risk.cex</code>	number-at-risk table's character expansion factor. A numerical value giving the amount by which the number-at-risk table text should be magnified relative to the default. If <code>risk</code> is set to <code>FALSE</code> , this argument is ignored. The default value is 1.
<code>p.value</code>	logical indicating whether the p -value obtained from a call to <code>survdif</code> with <code>rho</code> equal to 0, this is the log-rank or Mantel-Haenszel test, should be displayed in the plot. The p -value will be displayed in the format specified by the <code>show.p</code>

	function. If <code>strata</code> is set to 1, this argument is ignored. The default value is <code>TRUE</code> .
<code>p.value.pos</code>	2-dimensional numerical vector indicating the x-y coordinates where the number of events should be added to the plot. If <code>strata</code> is not 1 or <code>events</code> is set to <code>FALSE</code> , this argument is ignored. The default value, <code>NULL</code> , indicates that the text should be placed on the upper-right corner.
<code>units</code>	character indicating the time units. Options are: "days", "weeks", "months" or "years". This argument will be used to create the default label and tick-marks for the x-axis. This argument is not case-sensitive and is passed to match.arg . The default value is "days".
<code>xlab</code>	character indicating a label for the x-axis. The default value, <code>NULL</code> , indicates that indicates that the text "Time (units)" should be used, where "units" is specified by the <code>units</code> argument.
<code>times</code>	numerical vector with the time points at which tick-marks are to be drawn in the x-axis. The default value, <code>NULL</code> , indicates that a time vector will be automatically constructed based on the <code>units</code> argument: • If <code>units</code> is set to "days": from 0 to the maximum survival time rounded up to the nearest multiple of 7. • If <code>units</code> is set to "weeks": from 0 to the maximum survival time rounded up to the nearest integer. • If <code>units</code> is set to "months": from 0 to the maximum survival time rounded up to the nearest multiple of 12. • If <code>units</code> is set to "years": from 0 to the maximum survival time rounded up to the nearest integer.
<code>yscale</code>	a numeric value used to multiply the labels on the y-axis. A value of 100, for instance, would be used to give a percent scale. Notice only the labels are changed, not the actual plot coordinates. The default value is 1.
<code>ylab</code>	character indicating a label for the y-axis. The default value, <code>NULL</code> , indicates that indicates that the text "Survival" should be used. Moreover, if <code>yscale</code> is set to 1 (or 100) the text "(proportion)" or "(percentage)" will also be added.
<code>main</code>	overall title for the plot. The default value is "Survival curve".
<code>col</code>	colour palette to be used. The default value, <code>NULL</code> , indicates that a different colour should be used per level in <code>strata</code> . This is, a vector from 1 to n , where n is the number of levels in <code>strata</code> , will be used.
<code>...</code>	other graphical parameters (to be passed to plot.survfit).

Value

A customized survival curve plot displaying the requested graphical and statistical modifications.

Note

A call to `par` is used in this function. Notice that the arguments `font.axis`, `font.lab`, `cex.lab`, `las` and `xpd` are always set to 2, 2, 1.2, 1, and TRUE, respectively. Moreover, the argument `mar` is always modified and depends on the number of levels in strata as well as whether or not the number-at-risk table is appended.

For optimal resolution and layout alignment when using the function in an R file, adjust the plot window. For example, ideal dimensions are approximately 7 x 5" for 24" screens and 5.9 x 4.2" for 13" screens.

For optimal resolution and layout alignment when using the function in an R markdown file or similar, use `fig.dim = c(7, 5)` in the corresponding chunk.

Examples

```
lung <- survival::cancer
lung$time_y <- lung$time/365.25
lung$sex <- factor(lung$sex, levels = 1:2, labels = c("Male", "Female"))

# no strata
survival.plot(lung, time_y, status, units = "y")
# customizing
survival.plot(lung, time_y, status, units = "y",
              xlab = "Time since diagnosis (in years)",
              yscale = 100,
              main = "Overall survival", mark.col = "darkgray")

# 2 strata
survival.plot(lung, time_y, status, sex, units = "y")
# customizing
survival.plot(lung, time_y, status, sex,
              legend.pos = "topright", legend.title = "Sex",
              events = TRUE, risk.text = FALSE, p.value.pos = c(2.4, 0.4),
              units = "y", xlab = "Time since diagnosis (in years)",
              main = "Overall survival", col = c("darkviolet", "darkgreen"))
```

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