

Package ‘KMunicate’

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Title KMunicate-Style Kaplan–Meier Plots

Version 0.2.5

Description Produce Kaplan–Meier plots in the style recommended following the KMunicate study by Morris et al. (2019) <[doi:10.1136/bmjopen-2019-030215](https://doi.org/10.1136/bmjopen-2019-030215)>. The KMunicate style consists of Kaplan–Meier curves with confidence intervals to quantify uncertainty and an extended risk table (per treatment arm) depicting the number of study subjects at risk, events, and censored observations over time. The resulting plots are built using 'ggplot2' and can be further customised to a certain extent, including themes, fonts, and colour scales.

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URL <https://ellessenne.github.io/KMunicate-package/>,
<https://github.com/ellessenne/KMunicate-package>

BugReports <https://github.com/ellessenne/KMunicate-package/issues>

Depends R (>= 2.10), survival

Imports checkmate, cowplot, ggplot2, pammttools, tidyr

Suggests broom, covr, devtools, knitr, rmarkdown, simsurv, testthat,
usethis

VignetteBuilder knitr

ByteCompile true

Encoding UTF-8

Language en-GB

LazyData true

RoxygenNote 7.3.1

NeedsCompilation no

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brcancer	<i>German Breast Cancer Study Data</i>
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Description

German breast cancer study data, imported from Stata 16.

Usage

brcancer

Format

A data frame with 686 rows and 14 variables:

- id A numeric vector;
- hormon Hormonal therapy;
- x1 Age, in years;
- x2 Menopausal status;
- x3 Tumour size, mm;
- x4 Tumour grade;
- x5 Number of positive nodes;
- x6 Progesterone receptor, fmol;
- rectime Recurrence-free survival time, days;
- censrec Censoring indicator;
- x4a Tumour grade ≥ 2 ;
- x4b Tumour grade $= 3$;
- x5e $\exp(-0.12 * x5)$.

References

<http://www.stata-press.com/data/r16/brcancer.dta>

Examples

```
data("brcancer", package = "KMunicate")
```

cancer2

Patient Survival in Drug Trial

Description

Patient survival in drug trial data, imported from Stata 16.

Usage

```
cancer2
```

Format

A data frame with 48 rows and 4 variables:

- studytime Months to death or end of follow-up;
- died Event indicator variable, died = 1 if a patient died;
- drug Drug type, with drug = 1 being placebo;
- age Age of a patient at baseline.

Note

The dataset is named cancer2 to avoid name collision with the cancer dataset from the survival package.

References

<http://www.stata-press.com/data/r16/cancer.dta>

Examples

```
data("cancer2", package = "KMunicate")
```

Description

Produce Kaplan–Meier plots in the style recommended following the KMunicate study by TP Morris *et al.* ([doi:10.1136/bmjopen2019030215](https://doi.org/10.1136/bmjopen2019030215)).

Usage

```
KMunicate(
  fit,
  time_scale,
  .risk_table = "KMunicate",
  .reverse = FALSE,
  .theme = NULL,
  .color_scale = NULL,
  .fill_scale = NULL,
  .linetype_scale = NULL,
  .annotate = NULL,
  .xlab = "Time",
  .ylab = ifelse(.reverse, "Estimated (1 - survival)", "Estimated survival"),
  .title = NULL,
  .alpha = 0.25,
  .rel_heights = NULL,
  .ff = NULL,
  .risk_table_base_size = 11,
  .size = NULL,
  .legend_position = c(1, 1)
)
```

Arguments

<code>fit</code>	A <code>survfit</code> object.
<code>time_scale</code>	The time scale that will be used for the x-axis and for the summary tables.
<code>.risk_table</code>	This arguments define the type of risk table that is produced.
<code>.reverse</code>	If <code>reverse = TRUE</code> , then the plot uses 1 - survival probability on the y-axis. Defaults to <code>KMunicate</code> , where the cumulative number of events and censored are calculated. Another possibility is <code>survfit</code> , which will use the default numbers returned by <code>summary.survfit</code> (e.g. number of events and censored per interval). <code>.risk_table</code> can also be <code>NULL</code> , in which case the risk table will be omitted from the plot.
<code>.theme</code>	ggplot theme used by the plot. Defaults to <code>NULL</code> , where the default ggplot theme will be used.
<code>.color_scale</code>	Colour scale used for the plot. Has to be a <code>scale_colour_*</code> component, and defaults to <code>NULL</code> where the default colour scale will be used.

<code>.fill_scale</code>	Fill scale used for the plot. Has to be a <code>scale_fill_*</code> component, and defaults to NULL where the default fill scale will be used.
<code>.linetype_scale</code>	Linetype scale used for the plot. Has to be a <code>scale_linetype_*</code> component, and defaults to NULL where the default linetype scale will be used.
<code>.annotate</code>	Optional annotation to be added to the plot, e.g. using <code>ggplot2::annotate()</code> . Defaults to NULL, where no extra annotation is added.
<code>.xlab</code>	Label for the horizontal axis, defaults to <i>Time</i> .
<code>.ylab</code>	Label for the vertical axis, defaults to <i>Estimated survival</i> if <code>.reverse = FALSE</code> , to <i>Estimated (1 - survival)</i> otherwise.
<code>.title</code>	A title to be added on top of the plot. Defaults to NULL, where no title will be included.
<code>.alpha</code>	Transparency of the point-wise confidence intervals
<code>.rel_heights</code>	Override default relative heights of plots and tables. Must be a numeric vector of length equal 1 + 1 per each arm in the Kaplan-Meier plot. See <code>cowplot::plot_grid()</code> for more details on how to use this argument.
<code>.ff</code>	A string used to define a base font for the plot.
<code>.risk_table_base_size</code>	Base font size for the risk table, given in pts. Defaults to 11.
<code>.size</code>	Thickness of each Kaplan-Meier curve. Defaults to NULL, where <code>ggplot2</code> 's default will be used.
<code>.legend_position</code>	Position of the legend in the plot. Defaults to <code>c(1, 1)</code> , which corresponds to <i>top-right</i> of the plot. It is also possible to pass a string, as in <code>ggplot2</code> , e.g. "none" to suppress the legend. N.B.: Legend justification is modified accordingly. See <code>ggplot2::theme()</code> for more details on how to place the legend of the plot.

Value

A KMunicate-style `ggplot` object.

Examples

```
library(survival)
data("cancer2", package = "KMunicate")
KM <- survfit(Surv(studytime, died) ~ drug, data = cancer2)
time_scale <- seq(0, max(cancer2$studytime), by = 7)
KMunicate(fit = KM, time_scale = time_scale)
```

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