Package ‘KMunicate’

August 26, 2023

Title KMunicate-Style Kaplan–Meier Plots
Version 0.2.4
Description Produce Kaplan–Meier plots in the style recommended following the KMunicate study by Morris et al. (2019) <doi: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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BugReports https://github.com/ellessenne/KMunicate-package/issues

Depends R (>= 2.10), survival
Imports checkmate, cowplot, ggplot2, pammtools, tidyr
Suggests broom, covr, devtools, knitr, rmarkdown, simsurv, testthat, usethis

VignetteBuilder knitr

ByteCompile true

Encoding UTF-8

Language en-GB

LazyData true

RoxygenNote 7.2.3

NeedsCompilation no

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**Repository** CRAN  
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**R topics documented:**

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### KMunicate-package

**Description**

Produce Kaplan–Meier plots in the style recommended following the KMunicate study, doi:10.1136/bmjopen2019030215.

**Author(s)**

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### brcancer

**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

```r
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**

```r
KMunicate(
  fit,  # A survfit object.
  time_scale,  # The time scale that will be used for the x-axis and for the summary tables.
  .risk_table = "KMunicate",  # This arguments define the type of risk table that is produced.
  .reverse = FALSE,  # If reverse = TRUE, then the plot uses 1 - survival probability on the y-axis. Defaults to KMunicate, where the cumulative number of events and censored are calculated. Another possibility is survfit, which will use the default numbers returned by summary.survfit (e.g. number of events and censored per interval). .risk_table can also be NULL, in which case the risk table will be omitted from the plot.
  .theme = NULL,  # These arguments define the type of plot.
  .color_scale = NULL,  # These arguments define the type of table.
  .fill_scale = NULL,  # These arguments define the type of table.
  .linetype_scale = NULL,  # These arguments define the type of table.
  .annotate = NULL,  # These arguments define the type of table.
  .xlab = "Time",  # These arguments define the type of table.
  .ylab = ifelse(.reverse, "Estimated (1 - survival)", "Estimated survival"),  # These arguments define the type of table.
  .title = NULL,  # These arguments define the type of table.
  .alpha = 0.25,  # These arguments define the type of table.
  .rel_heights = NULL,  # These arguments define the type of table.
  .ff = NULL,  # These arguments define the type of table.
  .risk_table_base_size = 11,  # These arguments define the type of table.
  .size = NULL,  # These arguments define the type of table.
  .legend_position = c(1, 1)  # These arguments define the type of table.
)
```
.theme ggplot theme used by the plot. Defaults to NULL, where the default ggplot theme will be used.
.color_scale Colour scale used for the plot. Has to be a scale_colour_* component, and defaults to NULL where the default colour scale will be used.
.fill_scale Fill scale used for the plot. Has to be a scale_fill_* component, and defaults to NULL where the default fill scale will be used.
.linetype_scale Linetype scale used for the plot. Has to be a scale_linetype_* component, and defaults to NULL where the default linetype scale will be used.
.annotate Optional annotation to be added to the plot, e.g. using ggplot2::annotate(). Defaults to NULL, where no extra annotation is added.
.xlab Label for the horizontal axis, defaults to Time.
.ylab Label for the vertical axis, defaults to Estimated survival if .reverse = FALSE, to Estimated (1 - survival) otherwise.
.title A title to be added on top of the plot. Defaults to NULL, where no title will be included.
.alpha Transparency of the point-wise confidence intervals
.rel_heights 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 cowplot::plot_grid() for more details on how to use this argument.
.ff A string used to define a base font for the plot.
.risk_table_base_size Base font size for the risk table, given in pts. Defaults to 11.
.size Thickness of each Kaplan-Meier curve. Defaults to NULL, where ggplot2’s default will be used.
.legend_position Position of the legend in the plot. Defaults to c(1, 1), which corresponds to top-right of the plot. It is also possible to pass a string, as in ggplot2, e.g. "none" to suppress the legend. N.B.: Legend justification is modified accordingly. See ggplot2::theme() 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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