Package ‘visR’

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**Description**

Wrapper around ggplot2::annotation_custom for simplified annotation to ggplot2 plots. This function accepts a string, dataframe, data.table, tibble or customized objects of class gtable and places them on the specified location on the ggplot. The layout is fixed: bold column headers and plain body. Only the font size and type can be chosen. Both the initial plot as the individual annotation are stored as attribute component in the final object.

**Usage**

```r
add_annotation(
  gg = NULL,
  label = NULL,
  base_family = "sans",
  base_size = 11,
  xmin = -Inf,
  xmax = Inf,
  ymin = -Inf,
  ymax = Inf
)
```

**Arguments**

- `gg` Object of class ggplot.
- `label` String, dataframe, data.table, tibble used to annotate the ggplot.
- `base_family` character. Base font family
- `base_size` numeric. Base font size in pt
- `xmin` x coordinates giving horizontal location of raster in which to fit annotation.
- `xmax` x coordinates giving horizontal location of raster in which to fit annotation.
- `ymin` y coordinates giving vertical location of raster in which to fit annotation.
- `ymax` y coordinates giving vertical location of raster in which to fit annotation.

**Value**

Object of class ggplot with added annotation with an object of class gtable.

**See Also**

tableGrob annotation_custom
Examples

```r
## Estimate survival
surv_object <- visR::estimate_KM(data = adtte, strata = "TRTP")

## We want to annotate the survival KM plot with a simple string comment
visR::visr(surv_object) %>%
  visR::add_annotation(
    label = "My simple comment",
    base_family = "sans",
    base_size = 15,
    xmin = 110,
    xmax = 180,
    ymin = 0.80
  )

## Currently, care needs to be taken on the x-y values relative
## to the plot data area. Here we are plotting outside of the data area.
visR::visr(surv_object) %>%
  visR::add_annotation(
    label = "My simple comment",
    base_family = "sans",
    base_size = 15,
    xmin = 210,
    xmax = 380,
    ymin = 1.0
  )

## We may also want to annotate a KM plot with information
## from additional tests or estimates. This example we annotate
## with p-values contained in a tibble

## we calculate p-values for "Equality across strata"
lbl <- visR::get_pvalue(surv_object,
  statlist = c("test", "pvalue"),
  type = "All"
)

## display p-values
lbl

## Now annotate survival KM plot with the p-values
visR::visr(surv_object) %>%
  visR::add_annotation(
    label = lbl,
    base_family = "sans",
    base_size = 9,
    xmin = 100,
    xmax = 180,
    ymin = 0.80
  )
```
**add_CI**

*Add confidence interval (CI) to visR object*

### Description

Method to add pointwise confidence intervals to a an object created by visR through an S3 method. The method is set up to use the pipe `%>%`. There are two options to display CI’s, a "ribbon" or as "step" lines.

No default method is available at the moment.

### Usage

```r
add_CI(gg, ...)  
```

---

#### ## S3 method for class 'ggsurvfit'

```r
add_CI(gg, alpha = 0.1, style = "ribbon", linetype, ...)
```

---

#### ## S3 method for class 'ggtidycuminc'

```r
add_CI(gg, alpha = 0.1, style = "ribbon", linetype, ...)
```

### Arguments

- **gg**
  A ggplot created with visR
- **...**
  other arguments passed on to the method to modify geom_ribbon
- **alpha**
  aesthetic of ggplot2 geom_ribbon. Default is 0.1.
- **style**
  aesthetic of ggplot2 geom_ribbon. Default is "ribbon". An alternative option is "step" that uses a line to display interval bounds.
- **linetype**
  aesthetic of ggplot2 geom_ribbon.

### Value

Pointwise confidence interval overlayed on a visR ggplot

### Examples

```r
library(visR)

# Estimate KM curves by treatment group
survfit_object <- survival::survfit(data = adtte, survival::Surv(AVAL, 1 - CNSR) ~ TRTP)

## plot without confidence intervals (CI)
p <- visR::visr(survfit_object)
p

# add CI to plot with default settings
p %>% add_CI()
```
# change transparency of CI ribbon
p %>% add_CI(alpha = 0.9, style = "ribbon")

# plot CI as a step line instead of ribbon
p %>% add_CI(alpha = 0.1, style = "step")

# change linetype of CI
p %>% add_CI(style = "step", linetype = 1)

---

**add_CNSR**

*Add censoring symbols to a visR object*

**Description**

Add censoring symbols to a visR ggplot through an S3 method. The S3 method is for adding censoring symbols to a visR ggplot. The method is set up to use the pipe `%>%`.

No default method is available at the moment.

**Usage**

```
add_CNSR(gg, ...)
```

```R
## S3 method for class 'ggsurvfit'
add_CNSR(gg, shape = 3, size = 2, ...)

## S3 method for class 'ggtidycuminc'
add_CNSR(gg, shape = 3, size = 2, ...)
```

**Arguments**

| gg     | A ggplot created with visR |
| ---    | ... other arguments passed on to the method to modify geom_point |
| shape  | aesthetic of ggplot2 geom_point. Default is 3. |
| size   | aesthetic of ggplot2 geom_point. Default is 2. |

**Value**

Censoring symbols overlayed on a visR ggplot
Examples

```r
library(visR)

# Estimate KM curves by treatment group
survfit_object <- survival::survfit(data = adtte, survival::Surv(AVAL, 1 - CNSR) ~ TRTP)

## plot without confidence intervals
p <- visR::visr(survfit_object)
p

# add censoring to plot
p %>% visR::add_CNSR()

# change censor symbol shape
p %>% visR::add_CNSR(shape = 1)

# change size and shape
p %>% visR::add_CNSR(size = 4, shape = 2)
```

---

**add_highlight**

*Highlight a specific strata*

**Description**

S3 method for highlighting a specific strata by lowering the opacity of all other strata.

**Usage**

```r
add_highlight(gg, ...)
```

## S3 method for class 'ggsurvfit'

```r
add_highlight(gg = NULL, strata = NULL, bg_alpha = 0.2, ...)
```

**Arguments**

- **gg**
  - A ggplot created with visR
- **...**
  - other arguments passed on to the method
- **strata**
  - String representing the name and value of the strata to be highlighted as shown in the legend.
- **bg_alpha**
  - A numerical value between 0 and 1 that is used to decrease the opacity of all strata not chosen to be highlighted in strata. The other strata's existing alpha values are multiplied by bg_alpha to decrease their opacity, highlighting the target strata. This works on both colour and fill properties, as for example present after applying visR::add_CI().
add_quantiles

Description
Method to add quantile lines to a plot.

Usage
add_quantiles(gg, ...)

## S3 method for class 'ggsurvfit'
add_quantiles(
  gg,
  quantiles = 0.5,
  linetype = "dashed",
  linecolour = "grey50",
  alpha = 1,
  ...
)

Arguments

- **gg**: A ggplot created with visR
- **quantiles**: vector of quantiles to be displayed on the probability scale, default: 0.5
- **...**: other arguments passed on to the method to modify geom_line

Value
The input ggsurvfit object with adjusted alpha values

Examples

adtte %>%
  visR::estimate_KM(strata = "SEX") %>%
  visR::visr() %>%
  visR::add_CI(alpha = 0.4) %>%
  visR::add_highlight(strata = "M", bg_alpha = 0.2)

strata <- c("Placebo", "Xanomeline Low Dose")

adtte %>%
  visR::estimate_KM(strata = "TRTP") %>%
  visR::visr() %>%
  visR::add_CI(alpha = 0.4) %>%
  visR::add_highlight(strata = strata, bg_alpha = 0.2)
add_quantiles

linetype  string indicating the linetype as described in the aesthetics of ggplot2 `geom_line`, default: dashed (also supports "mixed" -> horizontal lines are solid, vertical ones are dashed)

linecolour string indicating the linetype as described in the aesthetics of ggplot2 `geom_line`, default: grey, (also supports "strata" -> horizontal lines are grey50, vertical ones are the same colour as the respective strata)

alpha numeric value between 0 and 1 as described in the aesthetics of ggplot2 `geom_line`, default: 1

Value

Lines indicating the quantiles overlayed on a visR ggplot

Examples

```r
library(visR)

adtte %>%
estimate_KM("SEX") %>%
  visr() %>%
  add_quantiles()

adtte %>%
estimate_KM("SEX") %>%
  visr() %>%
  add_quantiles(quantiles = c(0.25, 0.50))

adtte %>%
estimate_KM("SEX") %>%
  visr() %>%
  add_quantiles(quantiles = c(0.25, 0.50),
               linetype = "solid",
               linecolour = "grey"
               )

adtte %>%
estimate_KM("SEX") %>%
  visr() %>%
  add_quantiles(quantiles = c(0.25, 0.50),
               linetype = "mixed",
               linecolour = "strata"
               )
```
add_risktable  

Add risk tables to visR plots through an S3 method

Description

S3 method for adding risk tables to visR plots. The function has following workflow:

- The risktables are calculated using `get_risktable`
- The risktables are placed underneath visR plots using `plot_grid`
- Both the initial visR plot as the individual risktables are stored as attribute component in the final object to allow post-modification of the individual plots if desired

Usage

```r
add_risktable(gg, ...)
```

## S3 method for class 'ggsurvfit'

```r
add_risktable(
  gg,
  times = NULL,
  statlist = "n.risk",
  label = NULL,
  group = "strata",
  collapse = FALSE,
  rowgutter = 0.16,
  ...
)
```

## S3 method for class 'ggtidycuminc'

```r
add_risktable(
  gg,
  times = NULL,
  statlist = "n.risk",
  label = NULL,
  group = "strata",
  collapse = FALSE,
  rowgutter = 0.16,
  ...
)
```

Arguments

- `gg`  
  visR plot of class `ggsurvfit` or `ggtidycmprsk`
- `...`  
  other arguments passed on to the method `add_risktable`
- `times`  
  Numeric vector indicating the times at which the risk set, censored subjects, events are calculated.
### `add_risktable`

- **statlist**: Character vector indicating which summary data to present. Current choices are "n.risk", "n.event", "n.censor", "cum.event", "cum.censor". Default is "n.risk".
- **group**: String indicating the grouping variable for the risk tables. Current options are:
  - "strata": groups the risk tables per stratum. The label specifies the label within each risk table. The strata levels are used for the titles of the risk tables. This is the default.
  - "statlist": groups the risk tables per statlist. The label specifies the title for each risk table. The strata levels are used for labeling within each risk table.

- **collapse**: Boolean, indicates whether to present the data overall. Default is FALSE.

- **rowgutter**: A numeric relative value between 0 and 1 indicates the height used by the table versus the height used by the plot, as described in `cowplot::plot_grid(rel_heights=)`. The default is 0.16.

---

**Value**

Object of class `ggplot` with added risk table.

**See Also**

- `plot_grid`

**Examples**

```r
## Display 2 risk tables, 1 per statlist
adtte %>%
  visR::estimate_KM(strata = "TRTP") %>%
  visR::visr() %>%
  visR::add_risktable(
    label = c("Subjects at Risk", "Censored"),
    statlist = c("n.risk", "n.censor", "n.event"),
    group = "statlist"
  )

## Display overall risk table at selected times
adtte %>%
  visR::estimate_KM(strata = "TRTP") %>%
  visR::visr() %>%
  visR::add_risktable(
    label = c("Subjects at Risk", "Censored"),
    statlist = c("n.risk", "n.censor"),
    collapse = TRUE,
    times = c(0, 20, 40, 60)
  )
```
## Add risk set as specified times

adtte %>%
  visR::estimate_KM(strata = "TRTP") %>%
  visR::visr() %>%
  visR::add_risktable(times = c(0, 20, 40, 100, 111, 200))

---

**adtte**  
*adtte - CDISC ADaM compliant time to event data set*

### Description

ADTTE data copied from the 2013 CDISC Pilot

### Usage

adtte

### Format

A data frame with 254 rows and 26 variables:

- **STUDYID** Study Identifier
- **SITEID** Study Site Identifier
- **USUBJID** Unique Subject Identifier
- **AGE** Age
- **AGEGR1** Pooled Age Group 1
- **AGEGR1N** Pooled Age Group 1 (N)
- **RACE** Race
- **RACEN** Race (N)
- **SEX** Sex
- **TRTSDT** Date of First Exposure to Treatment
- **TRTEDT** Date of Last Exposure to Treatment
- **TRTDUR** Duration of treatment (days)
- **TRTP** Planned Treatment
- **TRTA** Actual Treatment
- **TRTAN** Actual Treatment (N)
- **PARAM** Parameter Description
- **PARAMCD** Parameter Code
- **AVAL** Analysis Value
- **STARTDT** Time to Event Origin Date for Subject
align_plots

ADT  Analysis Date
CNSR  Censor
EVNTDESC  Event or Censoring Description
SRCDOM  Source Domain
SRCVAR  Source Variable
SRCSEQ  Source Sequence Number
SAFFL  Safety Population Flag

Source


Examples

data("adtte")

align_plots  Align multiple ggplot graphs, taking into account the legend

Description

This function aligns multiple ggplot graphs by making them the same width by taking into account the legend width.

Usage

align_plots(pltlist)

Arguments

pltlist  A list of plots

Value

List of ggplot with equal width.

References

https://stackoverflow.com/questions/26159495
apply_attrition

Apply list of inclusion/exclusion criteria to a patient-level dataframe

Description

[Questioning] Apply list of inclusion/exclusion criteria to a patient-level dataframe

Usage

apply_attrition(data, criteria_conditions)

Arguments

data      data.frame. Data set to be filtered
criteria_conditions character dplyr-filter compatible conditions of the filtering criteria. These conditions will be applied to filter the input data set and obtain final analysis data set

Value

Filtered data frame
Examples

adtte_filtered <- visR::apply_attrition(adtte,
    criteria_conditions = c(
        "TRTP='Placebo'", "AGE>=75",
        "RACE='WHITE'", "SITEID=709"
    )
)

apply_theme

Applies a theme to a ggplot object.

Description

[Experimental] Takes in the styling options defined through visR::define_theme and applies them to a plot.

Usage

apply_theme(gg, visR_theme_dict = NULL)

Arguments

- **gg**: object of class ggplot
- **visR_theme_dict**: nested list containing possible font options

Value

object of class ggplot

Examples

library(visR)

theme <- visR::define_theme(
    strata = list(
        "SEX" = list(
            "F" = "red",
            "M" = "blue"
        ),
        "TRTA" = list(
            "Placebo" = "cyan",
            "Xanomeline High Dose" = "purple",
            "Xanomeline Low Dose" = "brown"
        )
    ),
    fontsizes = list(
        "title" = 14,
        "text" = 12
    )
)
define_theme

```r
"axis" = 12,
"ticks" = 10,
"legend_title" = 10,
"legend_text" = 8
),
fontfamily = "Helvetica",
grid = FALSE,
bg = "transparent",
legend_position = "top"
)

gg <- adtte %>%
visR::estimate_KM(strata = "SEX") %>%
visR::visr() %>%
visR::apply_theme(theme)

```

---

**brca_cohort**  
*Cancer survival data*

---

**Description**

Creation script in data-raw

**Usage**

```r
brca_cohort
```

**Format**

An object of class `data.frame` with 1098 rows and 10 columns.

---

**define_theme**  
*Provides a simple wrapper for themes*

---

**Description**

[**Experimental**] This function collects several lists if they are present. If absent, reasonable defaults are used. When strata are not defined in the theme, they default to grey50 and will not be presented in the legend.
**define_theme**

**Usage**

```r
define_theme(
    strata = NULL,
    fontsizes = NULL,
    fontfamily = "Helvetica",
    grid = FALSE,
    bg = "transparent",
    legend_position = NULL
)
```

**Arguments**

- **strata** named list containing the different strata and name:colour value pairs
- **fontsizes** named list containing the font sizes for different options
- **fontfamily** string with the name of a supported font
- **grid** boolean that specifies whether the major and minor grid should be drawn. The drawing of major and minor gridlines can be manipulated separately by using a boolean indicator in a named list with elements major and minor.
- **bg** string defining the colour for the background of the plot
- **legend_position** string defining the legend position. Valid options are NULL, 'top' 'bottom' 'right' 'left'

**Value**

Nested list with styling preferences for a ggplot object

**Examples**

```r
theme <- visR::define_theme(
    strata = list("SEX" = list(
            "F" = "red",
            "M" = "blue"
    )),
    fontsizes = list(
            "axis" = 12,
            "ticks" = 10,
            "legend_title" = 10,
            "legend_text" = 8
    ),
    fontfamily = "Helvetica",
    grid = list(
            "major" = FALSE,
            "minor" = FALSE
    ),
    bg = "transparent",
    legend_position = "top"
)```
estimate_cuminc  

Competing Events Cumulative Incidence

Description

Function creates a cumulative incidence object using the `tidycmprsk::cuminc()` function.

Usage

```r
estimate_cuminc(
  data = NULL,
  strata = NULL,
  CNSR = "CNSR",
  AVAL = "AVAL",
  conf.int = 0.95,
  ...
)
```

Arguments

- **data**  
  A data frame. The dataset is expected to have one record per subject per analysis parameter. Rows with missing observations included in the analysis are removed.

- **AVAL, CNSR, strata**  
  These arguments are used to construct a formula to be passed to `tidycmprsk::cuminc(formula=)`.  
  - **AVAL** Analysis value for Time-to-Event analysis. Default is "AVAL", as per CDISC ADaM guiding principles.  
  - **CNSR** Column name indicating the outcome and censoring statuses. Column must be a factor and the first level indicates censoring, the next level is the outcome of interest, and the remaining levels are the competing events. Default is "CNSR"  
  - **strata** Character vector, representing the strata for Time-to-Event analysis. When NULL, an overall analysis is performed. Default is NULL.

- **conf.int**  
  Confidence internal level. Default is 0.95. Parameter is passed to `tidycmprsk::cuminc(conf.level=)`.

- **...**  
  Additional argument passed to `tidycmprsk::cuminc()`

Value

A cumulative incidence object as explained at https://mskcc-epi-bio.github.io/tidycmprsk/reference/cuminc.html
estimate_KM

Examples

cuminc <-
visR::estimate_cuminc(
data = tidycmprsk::trial,
strata = "trt",
CNSR = "death_cr",
AVAL = "ttdeath"
)
cuminc

cuminc %>%
  visR::visr() %>%
  visR::add_CI() %>%
  visR::add_risktable(statlist = c("n.risk", "cum.event"))

---

estimate_KM  Wrapper for Kaplan-Meier Time-to-Event analysis

Description

This function is a wrapper around \texttt{survival::survfit.formula()} to perform a Kaplan-Meier analysis, assuming right-censored data. The result is an object of class \texttt{survfit} which can be used in downstream functions and methods that rely on the \texttt{survfit} class.

The function can leverage the conventions and controlled vocabulary from CDISC ADaM ADTTE data model, and also works with standard, non-CDISC datasets through the \texttt{formula} argument.

Usage

\begin{verbatim}
estimate_KM(
data = NULL,
strata = NULL,
CNSR = "CNSR",
AVAL = "AVAL",
formula = NULL,
...)
\end{verbatim}

Arguments

- \texttt{data} A data frame. The dataset is expected to have one record per subject per analysis parameter. Rows with missing observations included in the analysis are removed.
- \texttt{AVAL, CNSR, strata} These arguments are used to construct a formula to be passed to \texttt{survival::survfit(formula=Surv(AVAL, 1-CNSR)~strata)}. These arguments’ default values follow the naming conventions in CDISC.
• **AVAL** Analysis value for Time-to-Event analysis. Default is "AVAL", as per CDISC ADaM guiding principles.

• **CNSR** Censor for Time-to-Event analysis. Default is "CNSR", as per CDISC ADaM guiding principles. It is expected that CNSR = 1 for censoring and CNSR = 0 for the event of interest.

• **strata** Character vector, representing the strata for Time-to-Event analysis. When NULL, an overall analysis is performed. Default is NULL.

**formula**

[Experimental] formula with `Surv()` on RHS and stratifying variables on the LHS. Use ~1 on the LHS for unstratified estimates. This argument will be passed to `survival::survfit(formula=)`. When this argument is used, arguments AVAL, CNSR, and strata are ignored.

... additional arguments passed on to the ellipsis of the call `survival::survfit.formula(...)`. Use `?survival::survfit.formula` and `?survival::survfitCI` for more information.

**Value**

survfit object ready for downstream processing in estimation or visualization functions and methods.

**Estimation of 'survfit' object**

The `estimate_KM()` function utilizes the defaults in `survival::survfit()`:

- The Kaplan Meier estimate is estimated directly (stype = 1).
- The cumulative hazard is estimated using the Nelson-Aalen estimator (ctype = 1): \( H_{\text{tilde}} = \text{cumsum}(x\text{n.event}/x\text{n.risk}) \). The MLE (\( H_{\text{hat}}(t) = -\log(S_{\text{hat}}(t)) \)) can't be requested.
- A two-sided pointwise 0.95 confidence interval is estimated using a log transformation (conf.type = "log").

When strata are present, the returned survfit object is supplemented with the a named list of the stratum and associated label. To support full traceability, the data set name is captured in the named list and the call is captured within its corresponding environment.

**PARAM/PARAMCD and CDISC**

If the data frame includes columns PARAM/PARAMCD (part of the CDISC format), the function expects the data has been filtered on the parameter of interest.

**References**

[https://github.com/therneau/survival](https://github.com/therneau/survival)

**See Also**

`survfit.formula` `survfitCI`
get_attrition

Generate cohort attrition table

Description

[Questioning] This is an experimental function that may be developed over time. This function calculates the subjects counts excluded and included for each step of the cohort selection process.

Usage

get_attrition(data, criteria_descriptions, criteria_conditions, subject_column_name)

Arguments

data Dataframe. It is used as the input data to count the subjects that meets the criteria of interest
get_COX_HR

criteria_descriptions
character It contains the descriptions of the inclusion/exclusion criteria. Each element of the vector corresponds to the description of each criterion.

criteria_conditions
character It contains the corresponding conditions of the criteria. These conditions will be used in the table to compute the counts of the subjects.

subject_column_name
character The column name of the table that contains the subject id.

Details
criteria_descriptions and criteria_conditions need to be of same length

Value
The counts and percentages of the remaining and excluded subjects for each step of the cohort selection in a table format.

Examples
visR::get_attrition(adtte,  
criteria_descriptions =  
c(  
"1. Placebo Group", "2. Be 75 years of age or older.",  
"3. White", "4. Site 709"  
),  
criteria_conditions = c(  
"TRTP=='Var.Placebo'", "AGE>=75",  
"RACE=='Var.WHite'", "SITEID==709"  
),  
subject_column_name = "USUBJID"
)

get_COX_HR
Summary Hazard Ratio from a survival object using S3 method

Description
S3 method for extracting information regarding Hazard Ratios. The function allows the survival object's formula to be updated. No default method is available at the moment.

Usage
get_COX_HR(x, ...)

## S3 method for class 'survfit'
get_COX_HR(x, update_formula = NULL, ...)
get_pvalue

Arguments

x  An object of class survfit
... other arguments passed on to the method survival::coxph
update_formula  Template which specifies how to update the formula of the survfit object update.formula

Value

A tidied object of class coxph containing Hazard Ratios

See Also

coxph update.formula

Examples

## treatment effect
survfit_object_trt <- visR::estimate_KM(data = adtte, strata = c("TRTP"))
visR::get_COX_HR(survfit_object_trt)

## treatment and gender effect
survfit_object_trt_sex <- visR::estimate_KM(data = adtte, strata = c("TRTP", "SEX"))
visR::get_COX_HR(survfit_object_trt_sex)

## update formula of KM estimates by treatment to include "SEX" for HR estimation
visR::get_COX_HR(survfit_object_trt, update_formula = ". ~ . + SEX")

## update formula of KM estimates by treatment to include "AGE" for
## HR estimation with ties considered via the efron method
visR::get_COX_HR(survfit_object_trt, update_formula = ". ~ . + survival::strata(AGE)", ties = "efron"
)

get_pvalue  Summarize the test for equality across strata from a survival object using S3 method

Description

Wrapper around survival::survdiff that tests the null hypothesis of equality across strata.

Usage

get_pvalue(
survfit_object,
ptype = "All",
rho = NULL,
statlist = c("test", "Chisq", "df", "pvalue"),
...
)

get_pvalue

Arguments

survfit_object An object of class survfit

ptype Character vector containing the type of p-value desired. Current options are "Log-Rank" "Wilcoxon" "Tarone-Ware" "Custom" "All". "Custom" allows the user to specify the weights on the Kaplan-Meier estimates using the argument rho. The default is "All" displaying all types possible. When rho is specified in context of "All", also a custom p-value is displayed.

rho a scalar parameter that controls the type of test.

statlist Character vector containing the desired information to be displayed. The order of the arguments determines the order in which they are displayed in the final result. Default is the test name ("test"), Chi-squared test statistic ("Chisq"), degrees of freedom ("df") and p-value ("pvalue").

... other arguments passed on to the method

Value

A data frame with summary measures for the Test of Equality Across Strata

See Also

survdiff

Examples

## general examples
survfit_object <- visR::estimate_KM(data = adtte, strata = "TRTP")
visR::get_pvalue(survfit_object)
visR::get_pvalue(survfit_object, ptype = "All")

## examples to obtain specific tests
visR::get_pvalue(survfit_object, ptype = "Log-Rank")
visR::get_pvalue(survfit_object, ptype = "Wilcoxon")
visR::get_pvalue(survfit_object, ptype = "Tarone-Ware")

## Custom example - obtain Harrington and Fleming test
visR::get_pvalue(survfit_object, ptype = "Custom", rho = 1)

## Get specific information and statistics
visR::get_pvalue(survfit_object, ptype = "Log-Rank", statlist = c("test", "Chisq", "df", "pvalue"))
visR::get_pvalue(survfit_object, ptype = "Wilcoxon", statlist = c("pvalue"))
get_quantile

Wrapper around quantile methods

Description

S3 method for extracting quantiles. No default method is available at the moment.

Usage

get_quantile(x, ...)

## S3 method for class 'survfit'
get_quantile(
  x,
  ...,
  probs = c(0.25, 0.5, 0.75),
  conf.int = TRUE,
  tolerance = sqrt(.Machine$double.eps)
)

Arguments

x

An object of class survfit

...  
other arguments passed on to the method

probs  
probabilities Default = c(0.25, 0.50, 0.75)

conf.int  
should lower and upper confidence limits be returned?

tolerance  
tolerance for checking that the survival curve exactly equals one of the quantiles

Value

A data frame with quantiles of the object

See Also

quantile.survfit

Examples

## Kaplan-Meier estimates
survfit_object <- visR::estimate_KM(data = adtte, strata = c("TRTP"))

## visR quantiles
visR::get_quantile(survfit_object)

## survival quantiles
quantile(survfit_object)
get_risktable

Obtain risk tables for tables and plots

Description
Create a risk table from an object using an S3 method. Currently, no default method is defined.

Usage
get_risktable(x, ...)

## S3 method for class 'survfit'
get_risktable(
  x,
  times = NULL,
  statlist = "n.risk",
  label = NULL,
  group = c("strata", "statlist"),
  collapse = FALSE,
  ...
)

## S3 method for class 'tidycuminc'
get_risktable(
  x,
  times = pretty(x$tidy$time, 10),
  statlist = "n.risk",
  label = NULL,
  group = c("strata", "statlist"),
  collapse = FALSE,
  ...
)

Arguments

x
an object of class survfit or tidycuminc

... other arguments passed on to the method
times Numeric vector indicating the times at which the risk set, censored subjects, events are calculated.

statlist Character vector indicating which summary data to present. Current choices are "n.risk" "n.event" "n.censor", "cum.event", "cum.censor". Default is "n.risk".


group String indicating the grouping variable for the risk tables. Current options are:
• "strata": groups the risk tables per stratum. The label specifies the label within each risk table. The strata levels are used for the titles of the risk tables. This is the default
• "statlist": groups the risk tables per statlist. The label specifies the title for each risk table. The strata levels are used for labeling within each risk table.

Default is "strata".

collapse  Boolean, indicates whether to present the data overall. Default is FALSE.

Value
return list of attributes the form the risk table i.e. number of patients at risk per strata

See Also

summary.survfit

generate

get_summary(x, ...)

## S3 method for class 'survfit'
get_summary(
x, 
statlist = c("strata", "records", "events", "median", "LCL", "UCL", "CI"),
...)

Arguments

x  An object of class survfit

...  other arguments passed on to the method

statlist  Character vector containing the desired information to be displayed. The order of the arguments determines the order in which they are displayed in the final result. Default is the strata ("strata"), number of subjects ("records"), number of events ("events"), the median survival time ("median"), the Confidence Interval ("CI"), the Lower Confidence Limit ("UCL") and the Upper Confidence Limit ("UCL").
Value

list of summary statistics from survfit object
A data frame with summary measures from a survfit object

Examples

```
survfit_object <- survival::survfit(data = adtte, survival::Surv(AVAL, 1 - CNSR) ~ TRTP)
get_summary(survfit_object)
```

get_tableone

---

Calculate summary statistics

Description

**[Questioning]** S3 method for creating a table of summary statistics. The summary statistics can be used for presentation in tables such as table one or baseline and demography tables.

The summary statistics estimated are conditional on the variable type: continuous, binary, categorical, etc.

By default the following summary stats are calculated:

- Numeric variables: mean, min, 25th-percentile, median, 75th-percentile, maximum, standard deviation
- Factor variables: proportion of each factor level in the overall dataset
- Default: number of unique values and number of missing values

Usage

```
get_tableone(
  data,
  strata = NULL,
  overall = TRUE,
  summary_function = summarize_short
)
```

```
## Default S3 method:
get_tableone(
  data,
  strata = NULL,
  overall = TRUE,
  summary_function = summarize_short
)
```
get_tableone

Arguments

data  The dataset to summarize as dataframe or tibble
strata  Stratifying/Grouping variable name(s) as character vector. If NULL, only overall results are returned
overall  If TRUE, the summary statistics for the overall dataset are also calculated
summary_function  A function defining summary statistics for numeric and categorical values

Details

It is possible to provide your own summary function. Please have a loot at summary for inspiration.

Value

object of class tableone. That is a list of data specified summaries for all input variables.

Note

All columns in the table will be summarized. If only some columns shall be used, please select only those variables prior to creating the summary table by using dplyr::select()

Examples

# Example using the ovarian data set
survival::ovarian %>%
dplyr::select(-fustat) %>%
dplyr::mutate(
age_group = factor(
dplyr::case_when(
age <= 50 ~ "<= 50 years",
age <= 60 ~ "<= 60 years",
age <= 70 ~ "<= 70 years",
TRUE ~ "> 70 years"
)
),
rx = factor(rx),
ecog.ps = factor(ecog.ps)
) %>%
dplyr::select(age, age_group, everything()) %>%
visR::get_tableone()

# Examples using ADaM data
# display patients in an analysis set
adtte %>%
dplyr::filter(SAFFL == "Y") %>%
dplyr::select(TRTA) %>%
visR::get_tableone()
```r
## display overall summaries for demog
dtte %>%
  dplyr::filter(SAFFL == "Y") %>%
  dplyr::select(AGE, AGEGR1, SEX, RACE) %>%
  visR::get_tableone()

## By actual treatment
adtte %>%
  dplyr::filter(SAFFL == "Y") %>%
  dplyr::select(AGE, AGEGR1, SEX, RACE, TRTA) %>%
  visR::get_tableone(strata = "TRTA")

## By actual treatment, without overall
adtte %>%
  dplyr::filter(SAFFL == "Y") %>%
  dplyr::select(AGE, AGEGR1, SEX, EVNTDESC, TRTA) %>%
  visR::get_tableone(strata = "TRTA", overall = FALSE)
```

---

**legendopts**

*Translates options for legend into a list that can be passed to ggplot2*

**Description**

This function takes the legend position and orientation, defined by the user and puts them into a list for ggplot2.

**Usage**

`legendopts(legend_position = "right", legend_orientation = NULL)`

**Arguments**

- `legend_position`
  - Default = "right".

- `legend_orientation`
  - Default = NULL.

**Value**

List of legend options for ggplot2.
**render**

*Render a data.frame, risktable, or tableone object as a table*

---

**Description**

[Questioning] Render a previously created data.frame, tibble or tableone object to html, rtf or latex

**Usage**

```r
render(
  data,
  title = "",
  datasource,
  footnote = "",
  output_format = "html",
  engine = "gt",
  download_format = c("copy", "csv", "excel")
)
```

**Arguments**

- **data**  
  Input data.frame or tibble to visualize

- **title**  
  Specify the title as a text string to be displayed in the rendered table. Default is no title.

- **datasource**  
  String specifying the data source underlying the data set. Default is no title.

- **footnote**  
  String specifying additional information to be displayed as a footnote alongside the data source and specifications of statistical tests.

- **output_format**  
  Type of output that is returned, can be "html" or "latex". Default is "html".

- **engine**  
  If "html" is selected as output_format, one can chose between using kable, gt and DT as engine to render the output table. Default is "gt".

- **download_format**  
  Options formats generated for downloading the data. Default is a list "c('copy', 'csv', 'excel')".

**Value**

A table data structure with possible interactive functionality depending on the choice of the engine.
summarize_long Calculate summary statistics from a vector

Description

[Questioning] Calculates several summary statistics. The summary statistics depend on the vector class.

Usage

summarize_long(x)

## S3 method for class 'factor'
summarize_long(x)

## S3 method for class 'integer'
summarize_long(x)

## S3 method for class 'numeric'
summarize_long(x)

## Default S3 method:
summarize_long(x)

Arguments

x an object

Value

A summarized version of the input.

summarize_short Create abbreviated variable summary for table1

Description

[Questioning] This function creates summaries combines multiple summary measures in a single formatted string. Create variable summary for numeric variables. Calculates mean (standard deviation), median (IQR), min-max range and N/% missing elements for a numeric vector.

Create variable summary for integer variables Calculates mean (standard deviation), median (IQR), min-max range and N/% missing elements for a integer vector.
Usage

summarize_short(x)

## S3 method for class 'factor'
summarize_short(x)

## S3 method for class 'numeric'
summarize_short(x)

## S3 method for class 'integer'
summarize_short(x)

## Default S3 method:
summarize_short(x)

Arguments

x  a vector to be summarized

Value

A summarized less detailed version of the input.

Surv_CNSR  Create a Survival Object from CDISC Data

Description

[Experimental]

The aim of Surv_CNSR() is to map the inconsistency in convention between the survival package and CDISC ADaM ADTTE data model.

The function creates a survival object (e.g. survival::Surv()) that uses CDISC ADaM ADTTE coding conventions and converts the arguments to the status/event variable convention used in the survival package.

The AVAL and CNSR arguments are passed to survival::Surv(time = AVAL, event = 1 - CNSR, type = "right", origin = 0).

Usage

Surv_CNSR(AVAL, CNSR)

Arguments

AVAL  The follow-up time. The follow-up time is assumed to originate from zero. When no argument is passed, the default value is a column/vector named AVAL.

CNSR  The censoring indicator where 1=censored and 0=death/event. When no argument is passed, the default value is a column/vector named CNSR.
Value

Object of class 'Surv'

Details

The Surv_CNSR() function creates a survival object utilizing the expected data structure in the CDISC ADaM ADTTE data model, mapping the CDISC ADaM ADTTE coding conventions with the expected status/event variable convention used in the survival package—specifically, the coding convention used for the status/event indicator. The survival package expects the status/event indicator in the following format: 0=alive, 1=dead. Other accepted choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). A final but risky option is to omit the indicator variable, in which case all subjects are assumed to have an event.

The CDISC ADaM ADTTE data model adopts a different coding convention for the event/status indicator. Using this convention, the event/status variable is named 'CNSR' and uses the following coding: censor = 1, status/event = 0.

See Also

survival::Surv(), estimate_KM()

Examples

```r
# Use the `Surv_CNSR()` function with visR functions
adtte %>%
  visR::estimate_KM(formula = visR::Surv_CNSR() ~ SEX)

# Use the `Surv_CNSR()` function with functions from other packages as well
survival::survfit(visR::Surv_CNSR() ~ SEX, data = adtte)
survival::survreg(visR::Surv_CNSR() ~ SEX + AGE, data = adtte) %>%
  broom::tidy()
```

Description

[Questioning] Wrapper function to produce a summary table (i.e. Table One). Create and render a summary table for a dataset. A typical example of a summary table are "table one", the first table in an applied medical research manuscript.

Calculate summary statistics and present them in a formatted table

Usage

tableone(
  data,
  title,
  datasource,
  ...)
Arguments

- **data**: The dataframe or tibble to visualize
- **title**: Table title to include in the rendered table. Input is a text string.
- **datasource**: String specifying the datasource underlying the data set
- **footnote**: Table footnote to include in the rendered table. Input is a text string.
- **strata**: Character vector with column names to use for stratification in the summary table. Default: NULL, which indicates no stratification.
- **overall**: If TRUE, the summary statistics for the overall dataset are also calculated
- **summary_function**: A function defining summary statistics for numeric and categorical values. Pre-implemented functions are `summarize_long` and `summarize_short`
  ...
  Pass options to render_table

Value

A table-like data structure, possibly interactive depending on the choice of the engine

Example Output

Examples

```r
# metadata for table
t1_title <- "Cohort Summary"
t1_ds <- "ADaM Interim Dataset for Time-to-Event Analysis"
t1_fn <- "My table one footnote"

## table by treatment - without overall and render with GT
tbl_gt <-
adtte %>%
dplyr::filter(SAFFL == "Y") %>%
dplyr::select(AGE, AGEGR1, SEX, EVNTDESC, TRTA) %>%
visR::tableone(
strata = "TRTA",
overall = FALSE,
title = t1_title,
datasource = t1_ds,
footnote = t1_fn,
...)
```
engine = "gt"
)

## table by treatment - without overall and render with DT
tbl_DT <-
  adtte %>%
dplyr::filter(SAFFL == "Y") %>%
dplyr::select(AGE, AGEGR1, SEX, EVNTDESC, TRTA) %>%
visR::tableone(
  strata = "TRTA",
  overall = FALSE,
  title = t1_title,
  datasource = t1_ds,
  footnote = t1_fn,
  engine = "DT"
)

## table by treatment - without overall and render with kable
tbl_kable_html <-
  adtte %>%
dplyr::filter(SAFFL == "Y") %>%
dplyr::select(AGE, AGEGR1, SEX, EVNTDESC, TRTA) %>%
visR::tableone(
  strata = "TRTA",
  overall = FALSE,
  title = t1_title,
  datasource = t1_ds,
  footnote = t1_fn,
  engine = "kable"
)

## table by treatment - without overall and render with kable as
## a latex table format rather than html
tbl_kable_latex <-
  adtte %>%
dplyr::filter(SAFFL == "Y") %>%
dplyr::select(AGE, AGEGR1, SEX, EVNTDESC, TRTA) %>%
visR::tableone(
  strata = "TRTA",
  overall = FALSE,
  title = t1_title,
  datasource = t1_ds,
  footnote = t1_fn,
  output_format = "latex",
  engine = "kable"
)

the_lhs Find the "lhs" in the pipeline
**tidyme**

Description

This function finds the left-hand sided symbol in a magrittr pipe and returns it as a character.

Usage

the_lhs()

Value

Left-hand sided symbol as string in the magrittr pipe.

References

https://github.com/tidyverse/magrittr/issues/115#issuecomment-173894787

Examples

```r
blah <- function(x) the_lhs()
adte %>%
  blah()
```

**tidyme**

*Extended tidy cleaning of selected objects using S3 method*

Description

S3 method for extended tidying of selected model outputs. Note that the visR method retains the original nomenclature of the objects, and adds the one of broom::tidy to ensure compatibility with tidy workflows. The default method relies on broom::tidy to return a tidied object.

Usage

tidyme(x, ...)

## Default S3 method:
tidyme(x, ...)

## S3 method for class 'survfit'
tidyme(x, ...)

Arguments

x An S3 object

... other arguments passed on to the method
Value

Data frame containing all list elements of the S3 object as columns. The column 'strata' is a factor to ensure that the strata are sorted in agreement with the order in the survfit object.

See Also

tidy

Examples

```r
## Extended tidying for a survfit object
surv_object <- visR::estimate_KM(data = adtte, strata = "TRTA")
tidied <- visR::tidyme(surv_object)

## Tidyme for non-included classes
data <- cars
lm_object <- stats::lm(data = cars, speed ~ dist)
lm_tidied <- visR::tidyme(lm_object)
lm_tidied
```

visr

Plot a supported S3 object

Description

S3 method for creating plots directly from objects using ggplot2, similar to the base R plot() function.

[Questioning] S3 function to draw a Consort flow diagram chart.

Usage

```r
visr(x, ...)
```

## Default S3 method:
```r
visr(x, ...)
```

## S3 method for class 'survfit'
```r
visr(
  x = NULL,
  x_label = NULL,
  y_label = NULL,
  x_units = NULL,
  x_ticks = NULL,
  y_ticks = NULL,
  fun = "surv",
)```
legend_position = "right",
...
)

## S3 method for class 'attrition'
visr(
x,
description_column_name = "Criteria",
value_column_name = "Remaining N",
complement_column_name = "",
box_width = 50,
font_size = 12,
fill = "white",
border = "black",
...
)

## S3 method for class 'tidycuminc'
visr(
x = NULL,
x_label = "Time",
y_label = "Cumulative Incidence",
x_units = NULL,
x_ticks = pretty(x$tidy$time, 10),
y_ticks = pretty(c(0, 1), 5),
legend_position = "right",
...
)

Arguments

x
Object of class survfit, attritiontable, or tidycuminc

... other arguments passed on to the method

x_label
character Label for the x-axis. When not specified, the function will look for "PARAM" or "PARAMCD" information in the original data set (CDISC standards). If no "PARAM"/"PARAMCD" information is available, the default x-axis label is "Time".

y_label
character Label for the y-axis. When not specified, the default will do a proposal, depending on the fun argument.

x_units
Unit to be added to the x_label (x_label (x_unit)). Default is NULL.

x_ticks
Ticks for the x-axis. When not specified, the default will do a proposal.

y_ticks
Ticks for the y-axis. When not specified, the default will do a proposal based on the fun argument.

fun
Function that represents the scale of the estimate. The current options are:

- surv is the survival probability. This is the default.
- log is log of the survival probability
• event is the failure probability
• cloglog is log(-log(survival probability))
• pct is survival as a percentage
• logpct is log survival as a percentage
• cumhaz is the cumulative hazard

legend_position
Specifies the legend position in the plot. Character values allowed are "top" "left" "bottom" "right". Numeric coordinates are also allowed. Default is "right".

description_column_name
character Name of the column containing the inclusion descriptions

description_column_name
character Name of the column containing the inclusion descriptions

value_column_name
character Name of the column containing the remaining sample counts

complement_column_name
character Optional: Name of the column containing the exclusion descriptions

box_width
character The box width for each box in the flow chart

font_size
character The fontsize in pt

fill
The color (string or hexcode) to use to fill the boxes in the flowchart

border
The color (string or hexcode) to use for the borders of the boxes in the flowchart

Value
Object of class ggplot and ggsurvplot for survfit objects.

See Also

ggplot

Examples

# fit KM
km_fit <- survival::survfit(survival::Surv(AVAL, 1 - CNSR) ~ TRTP, data = adtte)

# plot curves using survival plot function
plot(km_fit)

# plot same curves using visr::visr plotting function
visR::visr(km_fit)

# estimate KM using visR wrapper
survfit_object <- visR::estimate_KM(data = adtte, strata = "TRTP")

# Plot survival probability
visR::visr(survfit_object, fun = "surv")

# Plot survival percentage
visR::visr(survfit_object, fun = "pct")
# Plot cumulative hazard
visr::visr(survfit_object, fun = "cloglog")

## Create attrition
attrition <- visr::get_attrition(adtte,
criteria_descriptions = c(
  "1. Not in Placebo Group",
  "2. Be 75 years of age or older.",
  "3. White",
  "4. Female"
),
criteria_conditions = c(
  "TRTP != 'Placebo'",
  "AGE >= 75",
  "RACE=='WHITE'",
  "SEX=='F'"
),
subject_column_name = "USUBJID"
)

## Draw a CONSORT attrition chart without specifying extra text for the complement
attrition %>%
  visr("Criteria", "Remaining N")

## Add detailed complement descriptions to the "exclusion" part of the CONSORT diagram
# Step 1. Add new column to attrition dataframe
attrition$Complement <- c(
  "NA",
  "Placebo Group",
  "Younger than 75 years",
  "Non-White",
  "Male"
)

# Step 2. Define the name of the column in the call to the plotting function
attrition %>%
  visr("Criteria", "Remaining N", "Complement")

## Styling the CONSORT flowchart
# Change the fill and outline of the boxes in the flowchart
attrition %>%
  visr("Criteria", "Remaining N", "Complement", fill = "lightblue", border = "grey")

## Adjust the font size in the boxes
attrition %>%
  visr("Criteria", "Remaining N", font_size = 10)
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