Package 'survivalAnalysis'

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Type Package

Title High-Level Interface for Survival Analysis and Associated Plots

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Author Marcel Wiesweg [aut, cre]

Maintainer Marcel Wiesweg <marcel.wiesweg@uk-essen.de>

Description A high-level interface to perform survival analysis,
including Kaplan-Meier analysis and log-rank tests and Cox regression.
Aims at providing a clear and elegant syntax, support for use in a pipeline, structured output and plotting.
Builds upon the 'survminer' package for Kaplan-Meier plots and provides
a customizable implementation for forest plots.
Kaplan & Meier (1958) <doi:10.1080/01621459.1958.10501452>
Cox (1972) <JSTOR:2985181>
Peto & Peto (1972) <doi:10.2307/2344317>.

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 3.3.0)

Imports grDevices, graphics, stats, utils, survival, rlang, dplyr,
forcats, magrittr, purrr, stringr, tibble, tidyr, gridExtra,
ggplot2 (>= 2.2.1), scales, survminer (> 0.4.0), cowplot,
tidytidbits

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Suggests knitr, rmarkdown, tidyverse

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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R topics documented:

`analyse_multivariate` *Multivariate analysis (Cox Regression)*

Description

Performs Cox regression on right-censored data using a multiple covariates.

Usage

```
analyse_multivariate(data, time_status, covariates, strata = NULL,
  covariate_name_dict = NULL, covariate_label_dict = NULL,
  reference_level_dict = NULL, sort_frame_by = vars(HR))

analyze_multivariate(data, time_status, covariates, strata = NULL,
  covariate_name_dict = NULL, covariate_label_dict = NULL,
  reference_level_dict = NULL, sort_frame_by = vars(HR))
```

Arguments

`data`	A data frame containing the time/status information and, if used, the covariate.
`time_status`	A vector of length 2 giving the time and status fields. It is recommended to use vars() and symbolic column names or code that is tidily-evaluated on `data`. You can also pass a character vector with the column names or a numeric vector with column indices.

`covariates` The covariates. Pass symbolic columns names or code that is tidily-evaluated on `data`. Column names or column indices are also possible. In any case, factors with appropriate labels will be generated which in all printouts. You can use `covariate_name_dict` and `covariate_label_dict` to rename these factors and their levels.

`strata` Strata (optional). Same format as covariates. For each strata level (if multiple fields, unique combinations of levels) a separate baseline hazard is fit.

`covariate_name_dict`
A dictionary (named list or vector) of old->new covariate names

`covariate_label_dict`
A dictionary (named list or vector) of old->new covariate value level labels

`reference_level_dict`
For categorical variables, the Cox regression uses pseudo variables for each level relative to a reference category, resulting in n-1 variables for n levels of a categorical covariate. Hazard ratios will be relative to the reference level, which is defined as having hazard ratio 1.0. Per default, the reference level is the first factor level. You can specify a different level by passing a named vector: factor name -> value of reference level. Note that this is independent of covariate_label_dict, i.e. specify the factor level as it is in `data`#'

`sort_frame_by` A vars() list of one or more symbolic column names. The result contains a data frame of the cox regression results (`cox_as_data_frame`). This frame contains the variables "Lower_CI", "HR", "Upper_CI", "Inv_Lower_CI", "Inv_HR", "Inv_Upper_CI", "p". You can specify by which variables the frame should be sorted. Default: Hazard Ratio.

Details

This method builds upon the `survival` package and returns a comprehensive result object for survival analysis containing the coxph results. A `format`/`print` method is provided that prints the essential statistics.

Value

A named list which is an object of class "SurvivalAnalysisResult" and "SurvivalAnalysisMultivariateResult"

See Also

forest_plot

Examples

```
library(magrittr)
library(dplyr)
survival::colon %>%
   analyse_multivariate(vars(time, status),
                        vars(rx, sex, age, obstruct, perfor, nodes, differ, extent)) %>%
   print()
```

`analyse_survival` *Univariate survival analysis*

Description

Performs survival analysis on right-censored data using a single covariate, or no covariate.

Usage

```
analyse_survival(data, time_status, by, by_label_map = NULL,
  by_order_vector = NULL, cox_reference_level = NULL,
  p_adjust_method = "none", plot_args = list())

analyze_survival(data, time_status, by, by_label_map = NULL,
  by_order_vector = NULL, cox_reference_level = NULL,
  p_adjust_method = "none", plot_args = list())
```

Arguments

`data`	A data frame containing the time/status information and, if used, the covariate.
`time_status`	A vector of length 2 giving the time and status fields. It is recommended to use vars() and symbolic column names or code that is tidily-evaluated on `data`. You can also pass a character vector with the column names or a numeric vector with column indices.
`by`	The term by which survival curves will be separated. Pass `NULL` or omit to generate a single curve and only descriptive statistics. Pass symbolic columns names or code that is tidily-evaluated on `data` to generate more than one curve, and the appropriate statistics to compare the curves. A column name or column index is also possible. In any case, the parameter will be used to create a factor with appropriate labels. This factor will appear in all printouts and plots. You can use `by_label_map` and `by_order_vector` to rename and reorder this factor.
`by_label_map`	A dictionary (named list or vector) of old->new labels of the factor created using `by`. The factor will be renamed accordingly, and also reordered by the order of the vector.
`by_order_vector`	A vector of the labels of the factor created using `by`, after renaming them based on `by_label_map` (so specify the "new" level). The factor will be ordered according to the order of this vector. It need not contain all elements, only those found will be reorder at the top.
`cox_reference_level`	The result will include a univariate Cox regression. Use this parameter to specify the level of the factor generated using `by` that you want to use a the reference level (Hazard ratios will be relative to the reference level, which is defined as having hazard ratio 1.0) Note that the given string applies after all renaming has been done, so specify the "new" level.

p_adjust_method
: If there are more than two levels in the by factor, the result will include the return value of pairwise_survdiff, which performs p adjustment. You can specify the desired method here. Note that other p values are not corrected, this is beyond the scope of this method.

plot_args
: Named list of arguments that will be stored for later use in plotting methods, such as kaplan_meier_plot. There they will take precedence over arguments given to that method. This is useful when plotting multiple results with a set of default arguments, of which some such as title or axis scale differ per-plot.

Details

This method builds upon the `survival` package and returns a comprehensive result object for survival analysis containing the survfit, survdiff and coxph results. A `format`/`print` method is provided that prints the essential statistics. Kaplan-Meier plots are readily generated using the `kaplan_meier_plot` or `kaplan_meier_grid` functions.

Value

A named list which is an object of class "SurvivalAnalysisResult" and "SurvivalAnalysisUnivariateResult"

Examples

```
library(magrittr)
library(dplyr)
survival::aml %>%
  analyse_survival(vars(time, status), x) %>%
  print
```

---

cox_as_data_frame *Turns a coxph result to a data frame*

Description

Extracts useful information from a coxph/summary.coxph into a data frame which is ready for printing or further analysis

Usage

```
cox_as_data_frame(coxphsummary, unmangle_dict = NULL,
  factor_id_sep = ":", sort_by = NULL)
```

Arguments

coxphsummary	The summary.coxph or coxph result object
unmangle_dict	An unmangle dict of mangled column name -> readable column name (as created by analyse_multivariate)
factor_id_sep	The frame contains one column "factor.id" which is a composite of covariate name and, if categorical, the factor level (one line for each factor level except for the reference level)
sort_by	A vars() list of one or more symbolic column names. This frame contains the variables "Lower_CI", "HR", "Upper_CI", "Inv_Lower_CI", "Inv_HR", "Inv_Upper_CI", "p". You can choose to sort by any combination. Use desc() to sort a variable in descending order.

Value

A tibble.

---

forest_plot *Forest plots for survival analysis.*

Description

Creates a forest plot from SurvivalAnalysisResult objects. Both univariate (analyse_survival) results, typically with use_one_hot=T, and multivariate (analyse_multivariate) results are acceptable.

Usage

```
forest_plot(..., use_one_hot = F, factor_labeller = identity,
  endpoint_labeller = identity, orderer = identity_order,
  categorizer = NULL, relative_widths = c(1, 1, 1),
  ggtheme = theme_bw(), labels_displayed = c("endpoint", "factor"),
  label_headers = c(endpoint = "Endpoint", factor = "Subgroup", n = "n"),
  values_displayed = c("HR", "CI", "p"), value_headers = c(HR = "HR",
  CI = "CI", p = "p", n = "n", subgroup_n = "n"),
  HRsprintfFormat = "%.2f", psprintfFormat = "%.3f",
  p_lessthan_cutoff = 0.001, log_scale = T, HR_x_breaks = seq(0, 10),
  HR_x_limits = NULL, factor_id_sep = ":", na_rm = TRUE,
  title = NULL, title_relative_height = 0.1,
  title_label_args = list(), base_papersize = dinA(4))

forest_plot.df(.df, factor_labeller = identity,
  endpoint_labeller = identity, orderer = identity_order,
  categorizer = NULL, relative_widths = c(1, 1, 1),
  ggtheme = theme_bw(), labels_displayed = c("endpoint", "factor"),
  label_headers = c(endpoint = "Endpoint", factor = "Subgroup", n = "n"),
  values_displayed = c("HR", "CI", "p"), value_headers = c(HR = "HR",
```

```
  CI = "CI", p = "p", n = "n", subgroup_n = "n"),
  HRsprintfFormat = "%.2f", psprintfFormat = "%.3f",
  p_lessthan_cutoff = 0.001, log_scale = T, HR_x_breaks = seq(0, 10),
  HR_x_limits = NULL, factor_id_sep = ":", na_rm = TRUE,
  title = NULL, title_relative_height = 0.1,
  title_label_args = list(), base_papersize = dinA(4))
```

Arguments

`...` The SurvivalAnalysisResult objects. You can also pass one list of such objects, or use explicit splicing (!!! operator). If not `use_one_hot`, also a list of coxph objects, or a mix is acceptable.

`use_one_hot` If not use_one_hot (default), will take univariate or multivariate results and plot hazard ratios against the reference level (as provided to the `analyse_survival` or `analyse_multivariate` function, or, per default, the first factor level), resulting in k-1 values for k levels. If use_one_hot == TRUE, will only accept univariate results from `analyse_survival` and plot HRs of one factor level vs. remaining cohort, resulting in k values for k levels.

`factor_labeller, endpoint_labeller`
Either

- A function which returns labels for the input: First argument, a vector of either (factor.ids) or (endpoints), resp. If the function takes ... or two arguments, as second argument a data frame with (at least) the columns survivalResult, endpoint, factor.id, factor.name, factor.value, HR, Lower_CI, Upper_CI, p, n, where survivalResult is the corresponding result object passed to forest_plot; Note the function must be vectorized, if you have a non-vectorized function taking single arguments, you may want to have a look at purrr::map_chr or purrr::pmap_chr.
- a dictionaryish list, looks up by (endpoints) or (factor.ids). The factor.id value: For continous factors, the factor name (column name in data frame); For categorical factors, factor name, factor_id_sep, and the factor level value. (note: If use_one_hot = F, the HR is factor level value vs. cox reference given to survival_analysis; if use_one_hot = T, the HR is the factor level value vs. remaining population)

`orderer` A function which returns an integer ordering vector for the input:

- if the supplied function takes exactly one argument, a data frame with (at least) the columns survivalResult, endpoint, factor.id, factor.name, factor.value, HR, Lower_CI, Upper_CI, p, n, subgroup_n where survivalResult is the corresponding result object passed to forest_plot;
- or, if the function takes more than one argument, or its arguments include ..., the nine vectors (endpoint, factor.name, factor.value, HR, Lower_CI, Upper_CI, p, n, subgroup_n): a vector of endpoints (as given to Surv(endpoint, ...) in coxph), a vector of factors (as given to the right hand side of the coxph formula), and numeric vectors of the HR, lower CI, upper CI, p-value
- You can create a function from ordered vectors via orderer_function_from_sorted_vectors, or call order() with one or more of these vectors.

- Alternatively, you can provide a quosure of code, or a right-hand side formula; it will be executed such that the above nine vectors are available as symbols.

Example:

- `orderer = quo(order(endpoint, HR))`
- equivalent to `orderer = ~order(endpoint, HR)`
- equivalent to `orderer = function(df) df %$% order(endpoint, HR)`
- equivalent to `orderer = function(df) { order(df$endpoint, df$HR) }`
- equivalent to `orderer = function(endpoint, factor.name, factor.value, HR, ...) order(`

`categorizer` A function which returns one logical value if a breaking line should be inserted _above_ the input: Same semantics as for orderer. !Please note!: The order of the data is not yet ordered as per your orderer! If you do calculations depending on order, first order with your own orderer function. A proper implementation is easy using `sequential_duplicates`, for example `categorizer=~!sequential_duplicates(endpoin`

`relative_widths`
relation of the width of the plots, labels, plot, values. Default is 1:1:1.

`ggtheme` ggplot2 theme to use

`labels_displayed`
Combination of "endpoint", "factor", "n", determining what is shown on the left-hand table and in which order.

`label_headers` Named vector with name=<allowed values of labels_displayed>, value=<your heading>.

`values_displayed`
Combination of "HR", "CI", "p", "subgroup_n", determining what is shown on the right-hand table and in which order. Note: subgroup_n is only applicable if oneHot=T.

`value_headers` Named vector with name=<allowed values of values_displayed>, value=<your heading>.

`HRsprintfFormat, psprintfFormat`
sprintf() format strings for hazard ratio and p value

`p_lessthan_cutoff`
The lower limit below which p value will be displayed as "less than". If p_lessthan_cutoff == 0.001, the a p value of 0.002 will be displayed as is, while 0.0005 will become "p < 0.001".

`log_scale` Plot on log scale, which is quite common and gives symmetric length for the CI bars. Note that HRs of 0 (did not converge) will not be plotted in this case.

`HR_x_breaks` Breaks of the x scale for plotting HR and CI

`HR_x_limits` Limits of the x scale for plotting HR and CI. Default (HR_x_lim = NULL) depends on log_scale and existing limits. Pass NA to use the existing minimum and maximum values without interference. Pass a vector of size 2 to specify (min, max) manually

`factor_id_sep` Allows you to customize the separator of the factor id, the documentation of factor_labeller.

`na_rm` Only used in the multivariate case (use_one_hot = F). Should null coefficients (NA/0/Inf) be removed?

`title, title_relative_height, title_label_args` A title on top of the plot, taking a fraction of title_relative_height of the returned plot. The title is drawn using draw_label; you can specify any arguments to this function by giving title_label_args Per default, font attributes are taken from the "title" entry from the given ggtheme, and the label is drawn centered as per draw_label defaults.

`base_papersize` numeric vector of length 2, c(width, height), unit inches. forest_plot will store a suggested "papersize" attribute in the return value, computed from base_papersize and the number of entries in the plot (in particular, the height will be adjusted) The attribute is read by save_pdf. It will also store a "forestplot_entries" attribute which you can use for your own calculations.

`.df` Data frame containing the columns `survivalResult, endpoint, factor.id, factor.name, factor.` giving the information that is to be presented in the forest plot

`df` For the variant taking a data frame: A data frame which must contain (at least) the columns: endpoint, factor.id, factor.name, factor.value, HR, Lower_CI, Upper_CI, p, n, subgroup_n

Details

The plot has a left column containing the labels (covariate name, levels for categorical variables, optionally subgroup size), the actual line plot in the middle column, and a right column to display the hazard ratios and their confidence intervals. A rich set of parameters allows full customizability to create publication-ready plots.

Value

A ggplot2 plot object

Functions

- `forest_plot.df`: Creates a forest plot from the given data frame

See Also

forest_plot_grid

Examples

```
library(magrittr)
library(dplyr)
survival::colon %>%
   analyse_multivariate(vars(time, status),
                        vars(rx, sex, age, obstruct, perfor, nodes, differ, extent)) %>%
   forest_plot()
```

forest_plot_grid *Create a grid of forest plots*

Description

Makes use of the stored layout information in a forest_plot plot to create grids of plots.

Usage

```
forest_plot_grid(..., nrow = NULL, ncol = NULL, byrow = T,
  plot_grid_args = list())
```

Arguments

...	Pass individual plots returned by forest_plot, or lists of such plots (bare lists will be spliced).
nrow, ncol	Specify the grid (one is sufficient, uses auto layout if both are null)
byrow	If the plots are given in by-row, or by-column (byrow=F) order
plot_grid_args	Additional arguments to the plot_grid function which is used to create the grid.

Value

Return value of plot_grid

format.SurvivalAnalysisMultivariateResult *Formats a SurvivalAnalysisMultivariateResult for printing*

Description

Formats a SurvivalAnalysisMultivariateResult for printing

Usage

```
## S3 method for class 'SurvivalAnalysisMultivariateResult'
format(x, ...,
  p_precision = 3, hr_precision = 2, p_less_than_cutoff = 0.001)
```

Arguments

x	The result generated by analyse_multivariate
...	Further arguments passed from other methods.
p_precision, hr_precision	Precision with which to print floating point values
p_less_than_cutoff	Cut-off for small p values. Values smaller than this will be displayed like "<..."

Value

A formatted string, ready for output with cat()

`format.SurvivalAnalysisUnivariateResult` *Formats a SurvivalAnalysisUnivariateResult for printing*

Description

Formats a SurvivalAnalysisUnivariateResult for printing

Usage

```
## S3 method for class 'SurvivalAnalysisUnivariateResult'
format(x, ..., label = NULL,
  p_precision = 3, hr_precision = 2, p_less_than_cutoff = 0.001,
  time_precision = 1, include_end_separator = F,
  timespan_unit = c("days", "months", "years"))
```

Arguments

`x`	The result generated by `analyse_survival`
`...`	Further arguments passed from other methods.
`label`	A label describing the result
`p_precision, hr_precision, time_precision`	Precision with which to print floating point values
`p_less_than_cutoff`	Cut-off for small p values. Values smaller than this will be displayed like "<..."
`include_end_separator`	Append "\n—\n"? Comes handy if printing multiple results following each other
`timespan_unit`	Unit for time spans: "days", "months" or "years".

Value

A formatted string, ready for output with cat()

ggsurvplot_to_gtable *Build a gtable representation from a ggsurvplot object*

Description

Build a gtable representation from a ggsurvplot object

Usage

```
ggsurvplot_to_gtable(ggsurv_obj, surv.plot.height = NULL,
  risk.table.height = NULL, ncensor.plot.height = NULL)
```

Arguments

ggsurv_obj	The ggsurvplot object
surv.plot.height, risk.table.height, ncensor.plot.height	Layout parameters, see arrange_ggsurvplots

Value

A gtable object

grid_layout *Grid layouting*

Description

Creates a grid layout nrow x ncol for n items.

Usage

```
grid_layout(n, rows = NULL, cols = NULL)
```

Arguments

n	Number of items in grid
rows, cols	Pass one of rows or cols, or none, in which case auto layout is used.

Value

A numeric vector of length 2: rows, cols

Examples

```
grid_layout(24, cols=4)
grid_layout(24)
grid_layout(24, rows=2)
```

identity_order *Ordering function: identity order*

Description

This can be used in a place where a function with a signature like `order` is required. It simply retains the original order.

Usage

```
identity_order(x, ...)
```

Arguments

x	a vector
...	Effectively ignored

Value

An integer vector

kaplan_meier_grid *A grid of kaplan meier plots*

Description

A grid of kaplan meier plots

Usage

```
kaplan_meier_grid(..., nrow = NULL, ncol = NULL,
  layout_matrix = NULL, byrow = T, mapped_plot_args = list(),
  paperwidth = NULL, paperheight = NULL,
  size_per_plot = dinAWidth(5), title = NA, surv.plot.height = NULL,
  risk.table.height = NULL, ncensor.plot.height = NULL,
  p_lessthan_cutoff = 0.001)
```

Arguments

...	One or many SurvivalAnalysisResult objects as returned by `analyse_survival` and arguments that will be passed to ggsurvplot. Bare lists will be spliced. If using lists, the same argument may be contained in multiple lists; in this case, the last occurrence is used, i.e. you can first pass a list with default arguments, and then override some of them. In addition to all arguments supported by `ggsurvplot`, these arguments and shortcuts can be used additionally:

- break.time.by: breakByYear, breakByHalfYear, breakByQuarterYear, breakByMonth
- hazard.ratio (logical): display hazard ratios in addition to p value, complementing pval=T
- xlab: {.OS,.PFS,.TTF,.DFS}.{years,months,days}
- table.layout: clean, displays risk table only with color code and number, no grid, axes or labels. (do not forget risk.table=T to see something)

`nrow, ncol` Determines the layout by giving nrow and/or ncol, if missing, uses an auto layout.

`layout_matrix` Optionally specify a layout matrix, which is passed to `gridExtra::marrangeGrob`

`byrow` If no layout_matrix is specified and there are multiple rows: How should the plots by layout? The order of the plots can be by-row (default) or by-col (set byrow=F).

`mapped_plot_args` Optionally, if given n objects to plot, a named list of vectors of size n. The name is an argument names passed to ggsurvplot. The elements of the vector will be mapped 1:1 to each object. This allows to perform batch plotting where only few arguments differ (e.g. titles A, B, C...) between the plots. Please note that only object that need plotting (survival_analysis results) are considered, not those that are already plotted (kaplan_meier_plot results)

`paperwidth, paperheight, size_per_plot` You can specify the size per plot, or the full paper width and height. size_per_plot may be a number (width == height) or two-dimensional, width and height. The resulting paper size will be stored as a papersize attribute that is e.g. read by `tidytidbits::save_pdf`

`title, surv.plot.height, risk.table.height, ncensor.plot.height` Passed to `arrange_ggsurvplots`

`p_lessthan_cutoff` The lower limit below which p value will be displayed as "less than". If p_lessthan_cutoff == 0.001, the a p value of 0.002 will be displayed as is, while 0.0005 will become "p < 0.001".

Value

An object of class arrangelist, which can be printed or saved to pdf with ggsave().

`kaplan_meier_plot` *Kaplan Meier plots from survival results.*

Description

Uses `ggsurvplot` from the survminer package to create publication-ready plots.

Usage

```
kaplan_meier_plot(..., mapped_plot_args = list(),
  p_lessthan_cutoff = 0.001)
```

Arguments

`...` One or many SurvivalAnalysisResult objects as returned by `analyse_survival` and arguments that will be passed to ggsurvplot. Bare lists will be spliced. If using lists, the same argument may be contained in multiple lists; in this case, the last occurrence is used, i.e. you can first pass a list with default arguments, and then override some of them. In addition to all arguments supported by `ggsurvplot`, these arguments and shortcuts can be used additionally:

- break.time.by: breakByYear, breakByHalfYear, breakByQuarterYear, breakByMonth
- hazard.ratio (logical): display hazard ratios in addition to p value, complementing pval=T
- xlab: {.OS,.PFS,.TTF,.DFS}.{years,months,days}
- table.layout: clean, displays risk table only with color code and number, no grid, axes or labels. (do not forget risk.table=T to see something)

`mapped_plot_args` Optionally, if given n objects to plot, a named list of vectors of size n. The name is an argument names passed to ggsurvplot. The elements of the vector will be mapped 1:1 to each object. This allows to perform batch plotting where only few arguments differ (e.g. titles A, B, C...) between the plots.

`p_lessthan_cutoff` The lower limit below which p value will be displayed as "less than". If p_lessthan_cutoff == 0.001, the a p value of 0.002 will be displayed as is, while 0.0005 will become "p < 0.001".

Value

If given one result to plot, one ggsurvplot object; if given more than one result, a list of ggsurvplot objects.

Examples

```
library(magrittr)
library(dplyr)
survival::aml %>%
  analyse_survival(vars(time, status), x) %>%
  kaplan_meier_plot(break.time.by="breakByMonth",
                    xlab=".OS.months",
                    risk.table=TRUE,
                    ggtheme=ggplot2::theme_bw(10))
```

print.SurvivalAnalysisMultivariateResult

Print the essentials of a SurvivalAnalySurvivalAnalysisMultivariateResult

Description

Print the essentials of a SurvivalAnalySurvivalAnalysisMultivariateResult

Usage

```
## S3 method for class 'SurvivalAnalysisMultivariateResult'
print(x, ...,
  p_precision = 3, hr_precision = 2, p_less_than_cutoff = 0.001)
```

Arguments

x	The result generated by analyse_multivariate
...	Further arguments passed from other methods.
p_precision	Precision with which to print floating point values
hr_precision	Precision with which to print floating point values
p_less_than_cutoff	Cut-off for small p values. Values smaller than this will be displayed like "<..."

print.SurvivalAnalysisUnivariateResult

Print the essentials of a SurvivalAnalysisUnivariateResult

Description

Print the essentials of a SurvivalAnalysisUnivariateResult

Usage

```
## S3 method for class 'SurvivalAnalysisUnivariateResult'
print(x, ..., label = NULL,
  p_precision = 3, hr_precision = 2, time_precision = 1,
  include_end_separator = F, timespan_unit = c("days", "months",
  "years"))
```

Arguments

x	The result generated by analyse_survival
...	Further arguments passed from other methods.
label	A label describing the result
p_precision	Precision with which to print floating point values
hr_precision	Precision with which to print floating point values
time_precision	Precision with which to print floating point values
include_end_separator	Append "\n—\n"? Comes handy if printing multiple results following each other
timespan_unit	Unit for time spans: "days", "months" or "years".

---

survival_data_frames *Extract results from univariate survival analysis structured as data frames*

Description

Extract results from univariate survival analysis structured as data frames

Usage

```
survival_data_frames(result, format_numbers = TRUE, p_precision = 3,
  hr_precision = 2, p_less_than_cutoff = 0.001, time_precision = 1,
  timespan_unit = c("days", "months", "years"))
```

Arguments

result	The result generated by analyse_survival
format_numbers	If true, all numbers will be formatted for printing according to the following options and will be returned as strings
p_precision, hr_precision, time_precision	Precision with which to print floating point values
p_less_than_cutoff	Cut-off for small p values. Values smaller than this will be displayed like "<..."
timespan_unit	Unit for time spans: "days", "months" or "years".

Value

A named list list of data frame objects:

- cohortMetadata: information about the full cohort
- if there are strata (analysis performed "by" a covariate):
  - strataMetadata: information about each stratum
  - hazardRatios: hazard ratios for combinations of strata
  - only if there are more than two strata:
    - pairwisePValues: Matrix of pairwise (uncorrected) p values

`survival_essentials` *Convenience formatting and printing of result*

Description

Takes the given result, formats and prints it

Usage

```
survival_essentials(result, label = NULL, p_precision = 3,
  hr_precision = 2, time_precision = 1, include_end_separator = T,
  timespan_unit = "days", print = T)
```

Arguments

`result`	The result generated by `analyse_survival`
`label`	Optional label to include
`p_precision`	Precision with which to print floating point values
`hr_precision`	Precision with which to print floating point values
`time_precision`	Precision with which to print floating point values
`include_end_separator`	Append "\n—\n"? Comes handy if printing multiple results following each other
`timespan_unit`	Unit for time spans: "days", "months" or "years".
`print`	Print string to console

Value

The formatted string, invisibly. Ready for output with cat or saving to a file.

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