Package ‘survivalAnalysis’

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analyse_multivariate ........................................ 2
Analyse Multivariate

Description

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

Usage

```r
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)
)
```

```r
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

An object of class "SurvivalAnalysisResult" and "SurvivalAnalysisMultivariateResult". You can use this result as a black box for further functions in this package, format or print it, retrieve
information as a data frame via `multivariate_as_data_frame` or access individual pieces via `pluck_multivariate_analysis`

See Also

`forest_plot`

Examples

```r
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**

```r
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()
)
```

```r
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 column 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

An object of class "SurvivalAnalysisResult" and "SurvivalAnalysisUnivariateResult". You can use this result as a black box for further functions in this package, format or print it, retrieve informa-
cox_as_data_frame

An unmanagable dict of mangled column name -> readable column name (as created by analyse_multivariate)

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)

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.

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=TRUE, and multivariate (analyse_multivariate) results are acceptable.

Usage

forest_plot(
  ..., 
  use_one_hot = FALSE,
  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"),
  H RsprintfFormat = "%2f",
  psprintfFormat = "%3f",
  p_lessthan_cutoff = 0.001,
  log_scale = TRUE,
  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"),
)
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 = FALSE, the HR is factor level value vs. cox reference given to survival_analysis; if use_one_hot = TRUE, 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, fac-
tor.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(endpoint, HR)

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(endpoint = order(endpoint, HR))

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

HR sprintfFormat, psprintfFormat
sprintf() format strings for hazard ratio and p value

p_less_than_cutoff The lower limit below which p value will be displayed as "less than". If p_less_than_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 = FALSE). 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.value, HR, Lower_CI, Upper_CI, p, n, subgroup_n 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

```r
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

```r
forest_plot_grid(
  ..., 
  nrow = NULL, 
  ncol = NULL, 
  byrow = TRUE, 
  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=FALSE) 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

```r
## 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

```r
## 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 = FALSE,
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  

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 = TRUE,
  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 (numeric value only in ggsurvplot)
- xscale: scaleByYear, scaleByMonth (numeric value only in ggsurvplot)
- 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=TRUE to see something)
- papersize: numeric vector of length 2, c(width, height), unit inches. kaplan_meier_plot will store a "papersize" attribute with this value which is read by save_pdf
kaplan_meier_plot

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=FALSE).

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().

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, break-ByMonth (numeric value only in ggsurvplot)
• xscale: scaleByYear, scaleByMonth (numeric value only in ggsurvplot)
• hazard.ratio (logical): display hazard ratios in addition to p value, comple-menting 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=TRUE to see something)
• papersize: numeric vector of length 2, c(width, height), unit inches. ka-plan_meier_plot will store a "papersize" attribute with this value which is read by save_pdf

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_less-than_cutoff

The lower limit below which p value will be displayed as "less than". If p_less-than_cutoff == 0.001, the a p value of 0.002 will be displayed as is, while 0.0005 will be-come "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))

multivariate_as_data_frame

Turns a multivariate analysis result to a data frame

Description

Extracts useful information into a data frame which is ready for printing or further analysis

Usage

multivariate_as_data_frame(result, factor_id_sep = ":", sort_by = NULL)
Arguments

result : An object of class "SurvivalAnalysisMultivariateResult" as returned 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.

pluck_multivariate_analysis

Access individual components of multivariate survival analysis

Description

Allows access to the `analyse_multivariate` result object.

Usage

pluck_multivariate_analysis(result, term)

Arguments

result : An object of class SurvivalAnalysisMultivariateResult as returned by `analyse_multivariate`

term : The item to be retrieved:

- "coxph" containing the result of the `coxph` function
- "summary" containing the result of the `summary` of the "coxph" result
- "summary_data_frame" containing summary as a data frame (see `multivariate_as_data_frame`)
- "p" A vector of p values for the covariates, equivalent to the "p" column of "summary_data_frame"
- "overall" A named list with human-readable labels giving information about the overall fit, including the three flavors of p values contained in "summary"

Value

object as specified by term, or NULL if not contained in result
**pluck_survival_analysis**

**Examples**

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

---

**Description**

Access individual components of univariate survival analysis.

**Usage**

```r
pluck_survival_analysis(result, term)
```

**Arguments**

- `result`: An object of class SurvivalAnalysisUnivariateResult as returned by `analyse_survival`
- `term`: The item to be retrieved:
  - "survfit" containing the result of the `survfit` function
  - "survdiff" containing the result of the `survdiff` function
  - "survfit_overall" containing the result of the `survfit` function without terms, i.e. the full group not comparing subgroups
  - "coxph" containing the result of the `coxph` function
  - "p" The log-rank p value (if by provided at least two strata)

**Value**

Object as specified by `term`, or NULL if not contained in `result`

**Examples**

```r
library(magrittr)
library(dplyr)
survival::aml %>%
  analyse_survival(vars(time, status), x) %>%
  pluck_survival_analysis("p") %>%
  print
```
print.SurvivalAnalysisMultivariateResult

Print the essentials of a SurvivalAnalysisMultivariateResult

Description

Print the essentials of a SurvivalAnalysisMultivariateResult

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 "<..."

Value

The formatted string, invisibly. #' @export

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,
survival_data_frames

documentation

time_precision = 1,
include_end_separator = FALSE,
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".

**Value**

The formatted string, invisibly.

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**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**

```r
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")
)
```
survival_essentials

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 = TRUE,
  timespan_unit = "days",
  print = TRUE
)
write_survival

Arguments

result
label
p_precision
hr_precision
time_precision
include_end_separator
include_end_separator = FALSE

timespan_unit
file
label = NULL,
p_precision = 3,
h_precision = 2,
time_precision = 1,
include_end_separator = FALSE,
timespan_unit = c("days", "months", "years")

print

Value

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

write_survival

Print the essentials of a SurvivalAnalysisUnivariateResult.

Description

Write complete textual information for one or multiple survival analysis results in a text file.

Usage

write_survival(
  ..., file,
  label = NULL,
  p_precision = 3,
  hr_precision = 2,
  time_precision = 1,
  include_end_separator = FALSE,
  timespan_unit = c("days", "months", "years")
)

Arguments

... Results generated by analyse_survival, or analyse_multivariate, or lists of such objects
file A connection, or a character string naming the file to print to. (see cat)
label A label describing the result, or a vector of the same size as results in ... (will then be mapped 1:1)
p_precision, hr_precision, time_precision

Precision with which to print floating point values

... Results generated by analyse_survival, or analyse_multivariate, or lists of such objects
file A connection, or a character string naming the file to print to. (see cat)
label A label describing the result, or a vector of the same size as results in ... (will then be mapped 1:1)
p_precision, hr_precision, time_precision

Precision with which to print floating point values
include_end_separator
  Boolean: Append "\n—\n" as separator? Comes handy if printing multiple results following each other

timespan_unit  Unit for time spans: "days", "months" or "years"

Details
  As write_survival takes potentially multiple objects, it cannot return its input in a cleanly defined way. You can still elegantly combine write_survival in a pipe followed by \texttt{kaplan_meier_plot} or \texttt{kaplan_meier_grid} for a single input object if you apply the tee pipe operator \texttt{\%T>\%} in front of write_survival.

Value
  None (invisible NULL).
Index

analyse_multivariate, 2, 7, 8, 12, 18, 20, 23
analyse_survival, 4, 7, 8, 13, 15, 16, 19, 21–23
analyze_multivariate (analyse_multivariate), 2
analyze_survival (analyse_survival), 4
arrange_ggsurvplots, 13, 16
cat, 23
cox_as_data_frame, 3, 6
coxph, 18, 19
draw_label, 10
forest_plot, 4, 7, 11
forest_plot_grid, 10, 11
format, 3, 5
format.SurvivalAnalysisMultivariateResult, 12
format.SurvivalAnalysisUnivariateResult, 12
ggsurvplot, 15, 16
ggsurvplot_to_gtable, 13
grid_layout, 14
identity_order, 14
kaplan_meier_grid, 5, 15, 24
kaplan_meier_plot, 5, 16, 24
marrangeGrob, 16
multivariate_as_data_frame, 4, 17, 18
order, 14
plot_grid, 11
pluck_multivariate_analysis, 4, 18
pluck_survival_analysis, 6, 19
print, 3, 5
print.SurvivalAnalysisMultivariateResult, 20
print.SurvivalAnalysisUnivariateResult, 20
save_pdf, 15–17
sequential_duplicates, 9
summary, 18
survdiff, 19
survfit, 19
survival_data_frames, 6, 21
survival_essentials, 22
write_survival, 23