Package ‘survivalAnalysis’

April 17, 2020

Type Package

Title High-Level Interface for Survival Analysis and Associated Plots

Version 0.1.2

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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.

Cox (1972) <JSTOR:2985181>
Peto & Peto (1972) <JSTOR:2344317>.

License GPL-3

Encoding UTF-8

LazyData true

Depends R (>= 3.3.0)

Imports grDevices, graphics, stats, utils, survival, dplyr (>= 0.8.0), forcats, magrittr, purrr, stringr, tibble, tidyr, gridExtra, ggplot2 (>= 2.2.1), scales, survminer (> 0.4.0), cowplot, tidytidbits

RoxygenNote 7.1.0

Suggests knitr, rmarkdown, tidyverse

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

Date/Publication 2020-04-17 12:40:02 UTC
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`analyse_multivariate`  
*Multivariate analysis (Cox Regression)*

**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,
```
analyse_multivariate

```r
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"
analyse_survival

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()

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.
analyse_survival

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

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

```r
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**

```r
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.
**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**

```r
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)
)
```

```r
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_lesssthan_cutoff = 0.001,
log_scale = T,
HR_x_breaks = seq(0, 10),
HR_x_limits = NULL,
factor_id_sep = ":",
a_r_m = 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, 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=T.

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

HRsprintfFormat, p sprintfFormat

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.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()
```

---

**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 = 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()
ggsurvplot_to_gtable

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()
**grid_layout**

*Grid layouting*

**Description**

Creates a grid layout \( n_{row} \times n_{col} \) for \( n \) items.

**Usage**

\[
grid_layout(n, rows = \text{NULL}, cols = \text{NULL})
\]

**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**

\[
identity_order(x, \ldots)
\]

**Arguments**

- \( x \): a vector
- \( \ldots \): Effectively ignored

**Value**

An integer vector
**kaplan_meier_grid**

A grid of kaplan meier plots

**Description**

A grid of kaplan meier plots

**Usage**

```r
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 (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=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 (numeric value only in ggsurvplot)
print.SurvivalAnalysisMultivariateResult

### Description

Print the essentials of a `SurvivalAnalysisMultivariateResult`

### Usage

```r
## 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 "<..."

Description

Print the essentials of a SurvivalAnalysisUnivariateResult

Usage

```r
## 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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