Package 'ggsurvfit'

August 27, 2022

Title Easy and Flexible Time-to-Event Figures

Version 0.1.0

Description Ease the creation of time-to-event (i.e. survival) endpoint
figures. The modular functions create figures ready for
publication. Each of the functions that add to or modify the figure
are written as proper 'ggplot2' geoms or stat methods, allowing
the functions from this package to be combined with any function or
customization from 'ggplot2' and other 'ggplot2' extension packages.

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URL https://github.com/ddsjoberg/ggsurvfit,
http://www.danieldsjoberg.com/ggsurvfit/

BugReports https://github.com/ddsjoberg/ggsurvfit/issues

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R **topics documented:**

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add_censor_mark   *Add Censor Marking*

Description

Add a marking on the figure to represent the time an observations was censored.

Usage

```
add_censor_mark(...)
```

Arguments

...   arguments passed to passed to ggplot2::geom_point(...) with defaults shape
                  = 3 and size = 2

Value

a ggplot2 figure

Examples

```
survfit2(Surv(time, status) ~ 1, data = df_lung) %>%
  ggsurvfit() +
  add_confidence_interval() +
  add_censor_mark()
```

---

add_confidence_interval

Add Confidence Interval

Description

Add a confidence interval represented by either a ribbon or lines.

Usage

```
add_confidence_interval(type = c("ribbon", "lines"), ...)
```

Arguments

type	string indicating the type of confidence interval to draw. Must be one of c("ribbon", "lines")
...	arguments pass to geom.

- type = 'ribbon': Defaults are ggplot2::geom_ribbon(alpha = 0.2, color = NA, ...)
- type = 'lines': Defaults are ggplot2::geom_step(linetype = "dashed", na.rm = TRUE, ...)

Value

a ggplot2 figure

Examples

```
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit() +
  add_confidence_interval()

survfit2(Surv(time, status) ~ 1, data = df_lung) %>%
  ggsurvfit() +
  add_confidence_interval(type = "lines")
```

---

add_quantile   *Add Quantile Annotation*

Description

Add quantile information annotated on to the plot.

Usage

```
add_quantile(y_value = 0.5, ...)
```

Arguments

y_value   Numeric value where the line segment will be drawn. Default is `0.5`

...   Named arguments passed to `ggplot2::geom_segment()` with default `linetype = 2`

Value

a ggplot2 figure

Examples

```
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit() +
  add_quantile(linetype = 2)

survfit2(Surv(time, status) ~ 1, data = df_lung) %>%
  ggsurvfit() +
  add_quantile(linetype = 2) +
  add_quantile(y_value = 0.9, linetype = 3)
```

---

add_risktable   *Add risk table*

Description

Add risk tables below the plot showing the number at risk, events observed, and number of censored observations.

Usage

```
add_risktable(
  times = NULL,
  risktable_stats = c("n.risk", "cum.event"),
  risktable_group = c("auto", "strata", "risktable_stats"),
  risktable_height = NULL,
  stats_label = NULL,
  combine_groups = FALSE,
  theme = theme_risktable_default(),
  ...
)
```

Arguments

times
: numeric vector of times where risk table values will be placed. Default are the times shown on the x-axis. The times passed here will not modify the tick marks shown on the figure. To modify which tick marks are shown, use `ggplot2::scale_x_continuous(breaks=)`.

risktable_stats
: character vector of statistics to show in the risk table. Must be one or more of `c("n.risk", "cum.event", "cum.censor", "n.event", "n.censor")`. Default is `c("n.risk", "cum.event")`.

  - `"n.risk"` Number of patients at risk
  - `"cum.event"` Cumulative number of observed events
  - `"cum.censor"` Cumulative number of censored observations
  - `"n.event"` Number of events in time interval
  - `"n.censor"` Number of censored observations in time interval

risktable_group
: String indicating the grouping variable for the risk tables. Default is `"auto"` and will select `"strata"` or `"risktable_stats"` based on context.

  - `"strata"` groups the risk tables per stratum when present.
  - `"risktable_stats"` groups the risk tables per risktable_stats.

risktable_height
: A numeric value between 0 and 1 indicates the proportion of the final plot the risk table will occupy.

stats_label
: named vector or list of custom labels. Names are the statistics from `risktable_stats=` and the value is the custom label.

combine_groups
: logical indicating whether to combine the statistics in the risk table across groups. Default is FALSE

theme
: A risk table theme. Default is `theme_risktable_default()`

...
: arguments passed to `ggplot2::geom_text(...)`. Pass arguments like, `size = 3` to increase the size of the statistics presented in the table.

Value

a ggplot2 figure

Competing Risks

The ggcuminc() can plot multiple competing events. The "cum.event" and "n.event" statistics are the sum of all events across outcomes *shown on the plot*.

Examples

```
library(ggplot2)

p <-
  df_lung %>%
  survfit2(Surv(time, status) ~ sex, data = .) %>%
  ggsurvfit() +
  add_censor_mark() +
  add_confidence_interval()

p + add_risktable()

p +
  add_risktable(
    risktable_stats = c("n.risk", "cum.event"),
    stats_label = list(
      cum.event = "Cumulative Observed Events",
      n.risk = "Number at Risk"
    ),
    risktable_group = "strata",
  )

p +
  add_risktable(
    risktable_stats = c("n.risk", "cum.event"),
    combine_groups = TRUE
  )
```

---

add_risktable_strata_symbol
                        Use Symbol for Strata in Risk Table

Description

Replace the stratum level names with a color symbol in the risk tables. Use this function when stratum level names are long.

Usage

```
add_risktable_strata_symbol(
  symbol = NULL,
  size = 15,
  face = "bold",
  vjust = 0.3,
```

```
   ...
 )
```

Arguments

symbol   [UTF-8 code](#) of shape to replace strata level with. Default is a rectangle (`"\U25AC"`).
                  Other common options are circle (`"\U25CF"`) and diamond (`"\U25C6"`). While
                  a symbol is the most common string to pass here, any string is acceptable.

size, face, vjust, ...
                  arguments passed to a function similar to `ggtext::element_markdown()`

Value

a ggplot2 figure

Examples

```
p <-
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit(size = 1) +
  add_confidence_interval() +
  add_risktable(risktable_group = "risktable_stats")

 p + add_risktable_strata_symbol()
 p + add_risktable_strata_symbol(symbol = "\U25CF")
```

---

adtte   *Example phase III clinical trial data set*

Description

Background The example simulated data set is based on large phase III clinical trials in breast
cancer such as the ALTTO trial <https://ascopubs.org/doi/pdf/10.1200/JCO.2015.62.1797>.
The example "trial" aims to determine if a combination of two therapies tablemab (T) plus vismab
(V) improves outcomes for metastatic human epidermal growth factor 2–positive breast cancer and
increases the pathologic complete response in the neoadjuvant setting (i.e. treatment given as a first
step to shrink a tumor before the main treatment or surgery).

Usage

```
adtte
```

Format

The data set contains the following variables:

STUDYID The study identifier. A code unique to the clinical trial

SUBJID subject identifier. Numeric ID unique to each patient

USUBJID unique subject identifier. Text ID combining study and patient IDs

AGE age at randomisation (years)

STR01 Hormone receptor status at randomisation

STR01N Hormone receptor positive (Numeric)

STR01L Hormone receptor positive (Long format)

STR02 Prior Radiotherapy at randomisation

STR02N Prior Radiotherapy at randomisation (Numeric)

STR02L Prior Radiotherapy at randomisation (Long format)

TRT01P Planned treatment assigned at randomisation

TRT01PN Planned treatment assigned at randomisation (Numeric)

PARAM Analysis parameter: Progression free survival

PARAMCD Analysis parameter code

AVAL Analysis value (time to event (years)

CNSR Censoring (0 = Event, 1 = Censored)

EVNTDESC Event description

CNSDTDSC Censoring description

DCTREAS Discontinuation from study reason

Details

The trial has four treatment arms, patients with centrally confirmed human epidermal growth factor 2-positive early breast cancer were randomly assigned to 1 year of adjuvant therapy with V, T, their sequence (T to V), or their combination (T+V) for 52 weeks.

The primary end point was progression-free survival (PFS) as defined by Cancer.gov: '"the length of time during and after the treatment of a disease, such as cancer, that a patient lives with the disease but it does not get worse. In a clinical trial, measuring the progression-free survival is one way to see how well a new treatment works"'.

A number of baseline measurements (taken at randomization) are also included such as age, hormone receptor status and prior radiotherapy treatment.

Additional details on reasons for study discontinuation and censoring event description are also included.

The data set adopts an abridged version of the CDISC ADaM ADTTE time to event data model. See here for more info on CDISC ADaM data standards https://www.cdisc.org/standards/foundational/adam and specifically the ADTTE time to event data model here https://www.cdisc.org/standards/foundational/adam/adam-basic-data-structure-bds-time-event-tte-analyses-v1-0.

Source

https://github.com/VIS-SIG/Wonderful-Wednesdays/tree/master/data/2020/2020-04-08

---

df_colon   *Formatted Copy of* survival::colon

Description

This is a copy of the colon data set exported by the survival package. This data set, however, has column labels, numeric categorical variables are now factors with assigned levels, and we only include the recurrence outcome.

Usage

    df_colon

Format

An object of class tbl_df (inherits from tbl, data.frame) with 929 rows and 14 columns.

---

df_lung   *Formatted Copy of* survival::lung

Description

This is a copy of the lung data set exported by the survival package. This data set, however, has column labels and numeric categorical variables are now factors with assigned levels.

Usage

    df_lung

Format

An object of class tbl_df (inherits from tbl, data.frame) with 228 rows and 10 columns.

---

format_p   *Format p-value*

Description

Round and format p-values

Usage

```
format_p(x, digits = 1)
```

Arguments

x   numeric vector of p-values

digits   number of digits large p-values will be rounded to. Default is 2, and must be
                  one of 1, 2, or 3.

Value

a string

Examples

```
p_vec <- c(0.00001, 0.01111, 0.0500000, 0.15, 0.99999)
format_p(p_vec)
format_p(p_vec, 2)
format_p(p_vec, 3)
```

---

ggcuminc   *Plot Cumulative Incidence*

Description

Plot a cumulative incidence object created with tidycmprsk::cuminc().

Usage

```
ggcuminc(
  x,
  outcome = NULL,
  linetype_aes = FALSE,
  theme = theme_ggsurvfit_default(),
  ...
)
```

Arguments

x	a 'survfit' object created with `survfit2()`
outcome	string indicating which outcome(s) to include in plot. Default is to include the first competing event.
linetype_aes	logical indicating whether to add `ggplot2::aes(linetype = strata)` to the `ggplot2::geom_step()` call. When strata are present, the resulting figure will be a mix a various line types for each stratum.
theme	a survfit theme. Default is `theme_ggsurvfit_default()`
...	arguments passed to `ggplot2::geom_step(...)`, e.g. `size = 2`

Value

a ggplot2 figure

Examples

```
library(tidycmprsk)

cuminc(Surv(ttdeath, death_cr) ~ trt, trial) %>%
  ggcuminc(outcome = "death from cancer") +
  add_confidence_interval() +
  add_risktable()

cuminc(Surv(ttdeath, death_cr) ~ trt, trial) %>%
  ggcuminc(outcome = c("death from cancer", "death other causes")) +
  add_risktable()
```

---

ggsurvfit   *Plot Survival Probability*

Description

Plot survival probabilities (and other transformations) using the results from `survfit2()` or `survival::survfit()`; although, we recommend the former to have the best experience with the **ggsurvfit** package.

Usage

```
ggsurvfit(
  x,
  type = "survival",
  linetype_aes = FALSE,
  theme = theme_ggsurvfit_default(),
  ...
)
```

Arguments

x   a 'survfit' object created with `survfit2()`

type   type of statistic to report. Default is `"survival"`. Must be one of the following:

type	transformation
`"survival"`	`x`
`"risk"`	`1 - x`
`"cumhaz"`	`-log(x)`

linetype_aes   logical indicating whether to add `ggplot2::aes(linetype = strata)` to the
                `ggplot2::geom_step()` call. When strata are present, the resulting figure will
                be a mix a various line types for each stratum.

theme   a survfit theme. Default is `theme_ggsurvfit_default()`

...   arguments passed to `ggplot2::geom_step(...)`, e.g. `size = 2`

Value

a ggplot2 figure

Details

This function creates a ggplot figure from the 'survfit' object. To better understand how to modify
the figure, review the simplified code used internally:

```
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  tidy_survfit() %>%
  ggplot(aes(x = time, y = estimate, y
             min = conf.low, ymax = conf.low,
             color = strata, fill = strata)) +
  geom_step()
```

Examples

```
# Default publication ready plot
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit()

# Changing statistic type
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit(type = "cumhaz")

# Configuring KM line type to vary by strata
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit(linetype_aes = TRUE)

# Customizing the plot to your needs
survfit2(Surv(time, status) ~ 1, data = df_lung) %>%
  ggsurvfit() +
```

```
  add_censor_mark() +
  add_confidence_interval() +
  add_quantile() +
  add_risktable()
```

---

ggsurvfit_build   *Build 'ggsurvfit' Object*

Description

Function takes an object created with ggsurvfit() or ggcuminc() and prepares the plot for printing. If a plot also has a risk table, this function will build the risk table plots and return them either as list of plots or combined using patchwork::wrap_plots().

Usage

```
ggsurvfit_build(x, combine_plots = FALSE)
```

Arguments

x   an object of class 'ggsurvfit' or 'ggcuminc'

combine_plots   logical indicating whether to combine the primary plot and the risk tables. When
                TRUE, plots are combined with patchwork::wrap_plots(). When FALSE and
                the plot has risk tables, they are returned in a list of gtable grobs. Default is
                FALSE.

Value

a list of ggplot2 objects or a single ggplot2 object

Examples

```
# construct plot
p <-
  survfit2(Surv(time, status) ~ surg, df_colon) %>%
  ggsurvfit() +
  add_risktable() +
  ggplot2::scale_y_continuous(limits = c(0, 1))

# build plots
built_p <- ggsurvfit_build(p)

# combine plots
patchwork::wrap_plots(
  built_p[[1]],
  built_p[[2]],
  built_p[[3]],
  ncol = 1,
  heights = c(0.70, 0.15, 0.15)
)
```

---

stepribbon   *Step ribbon statistic*

Description

Provides stairstep values for ribbon plots

Usage

```
stat_stepribbon(
  mapping = NULL,
  data = NULL,
  geom = "ribbon",
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  direction = "hv",
  ...
)
```

```
StatStepribbon
```

Arguments

mapping	Set of aesthetic mappings created by [aes()](#) or [aes_()](#). If specified and inherit.aes = TRUE (the default), it is combined with the default mapping at the top level of the plot. You must supply mapping if there is no plot mapping.
data	The data to be displayed in this layer. There are three options:
	If NULL, the default, the data is inherited from the plot data as specified in the call to [ggplot()](#).
	A data.frame, or other object, will override the plot data. All objects will be fortified to produce a data frame. See [fortify()](#) for which variables will be created.
	A function will be called with a single argument, the plot data. The return value must be a data.frame, and will be used as the layer data. A function can be created from a formula (e.g. ~ head(.x, 10)).
geom	which geom to use; defaults to "ribbon"
position	Position adjustment, either as a string, or the result of a call to a position adjustment function.
na.rm	If FALSE, the default, missing values are removed with a warning. If TRUE, missing values are silently removed.
show.legend	logical. Should this layer be included in the legends? NA, the default, includes if any aesthetics are mapped. FALSE never includes, and TRUE always includes. It can also be a named logical vector to finely select the aesthetics to display.

inherit.aes	If FALSE, overrides the default aesthetics, rather than combining with them. This is most useful for helper functions that define both data and aesthetics and shouldn't inherit behaviour from the default plot specification, e.g. borders().
direction	hv for horizontal-vertical steps, vh for vertical-horizontal steps
...	Other arguments passed on to layer(). These are often aesthetics, used to set an aesthetic to a fixed value, like colour = "red" or size = 3. They may also be parameters to the paired geom/stat.

Format

An object of class StatStepRibbon (inherits from Stat, ggproto, gg) of length 3.

Value

a ggplot2 figure

References

<https://groups.google.com/forum/?fromgroups=#!topic/ggplot2/9cFWHaH1CPs>

Examples

```
library(ggplot2)

survfit(Surv(time, status) ~ 1, data = df_lung) %>%
  survival::survfit0() %>%
  broom::tidy() %>%
  ggplot(aes(x = time, y = estimate, ymin = conf.low, ymax = conf.high)) +
  geom_step() +
  geom_ribbon(stat = "stepribbon", alpha = 0.2)
```

| survfit2 | *Create survival curves* |

Description

Simple wrapper for survival::survfit.formula() except the environment is also included in the returned object.

Use this function with all other functions in this package to ensure all elements are calculable.

Usage

```
survfit2(formula, ...)
```

Arguments

formula   a formula object, which must have a Surv object as the response on the left of
                 the ~ operator and, if desired, terms separated by + operators on the right. One
                 of the terms may be a strata object. For a single survival curve the right hand
                 side should be ~ 1.

...   Arguments passed on to survival::survfit.formula

                 data a data frame in which to interpret the variables named in the formula,
                     subset and weights arguments.

                 weights The weights must be nonnegative and it is strongly recommended that
                     they be strictly positive, since zero weights are ambiguous, compared to use
                     of the subset argument.

                 subset expression saying that only a subset of the rows of the data should be
                     used in the fit.

                 na.action a missing-data filter function, applied to the model frame, after any
                     subset argument has been used. Default is options()$na.action.

                 stype the method to be used estimation of the survival curve: 1 = direct, 2 =
                     exp(cumulative hazard).

                 ctype the method to be used for estimation of the cumulative hazard: 1 =
                     Nelson-Aalen formula, 2 = Fleming-Harrington correction for tied events.

                 id identifies individual subjects, when a given person can have multiple lines
                     of data.

                 cluster used to group observations for the infinitesimal jackknife variance es-
                     timate, defaults to the value of id.

                 robust logical, should the function compute a robust variance. For multi-state
                     survival curves this is true by default. For single state data see details,
                     below.

                 istate for multi-state models, identifies the initial state of each subject or ob-
                     servation

                 timefix process times through the aeqSurv function to eliminate potential
                     roundoff issues.

                 etype a variable giving the type of event. This has been superseded by multi-
                     state Surv objects and is deprecated; see example below.

                 error this argument is no longer used

Value

    survfit2 object

survfit2() vs survfit()

    Both functions have identical inputs, so why do we need survfit2()?

    The *only* difference between survfit2() and survival::survfit() is that the former tracks the
    environment from which the call to the function was made.

    The definition of survfit2() is unremarkably simple:

```
survfit2 <- function(formula, ...) {
  # construct survfit object
  survfit <- survival::survfit(formula, ...)

  # add the environment
  survfit$.Environment = rlang::current_env()

  # add class and return
  class(survfit) <- c("survfit2", "survfit")
  survfit
}
```

The environment is needed to ensure the survfit call can be accurately reconstructed or parsed at any point post estimation. The call is parsed when p-values are reported and when labels are created. For example, the raw variable names appear in the output of a stratified `survfit()` result, e.g. `"sex=Female"`. When using `survfit2()`, the originating data frame and formula may be parsed and the raw variable names removed.

Most functions in the package work with both `survfit2()` and `survfit()`; however, the output will be styled in a preferable format with `survfit2()`.

See Also

survival::survfit.formula()

Examples

```
# With `survfit()`
fit <- survfit(Surv(time, status) ~ sex, data = df_lung)
fit

# With `survfit2()`
fit2 <- survfit2(Surv(time, status) ~ sex, data = df_lung)
fit2

# Consistent behavior with other functions
summary(fit, times = c(10, 20))

summary(fit2, times = c(10, 20))
```

---

survfit2_p   *Calculate p-value*

Description

The function `survfit2_p()` wraps `survival::survdiff()` and returns a formatted p-value.

Usage

```
survfit2_p(x, pvalue_fun = format_p, prepend_p = TRUE, ...)
```

Arguments

x   a 'survfit2' object

pvalue_fun   function to round and style p-value with

prepend_p   prepend ″p=″ to formatted p-value

...   Arguments passed on to survival::survdiff

> subset expression indicating which subset of the rows of data should be used
> in the fit. This can be a logical vector (which is replicated to have length
> equal to the number of observations), a numeric vector indicating which
> observation numbers are to be included (or excluded if negative), or a char-
> acter vector of row names to be included. All observations are included by
> default.
>
> na.action a missing-data filter function. This is applied to the model.frame
> after any subset argument has been used. Default is options()$na.action.
>
> rho a scalar parameter that controls the type of test.
>
> timefix process times through the aeqSurv function to eliminate potential
> roundoff issues.

Value

a string

Examples

```
library(ggplot2)

sf <- survfit2(Surv(time, status) ~ sex, data = df_lung)

sf %>%
  ggsurvfit() +
  add_confidence_interval() +
  add_risktable() +
  labs(caption = glue::glue("Log-rank {survfit2_p(sf)}"))

sf %>%
  ggsurvfit() +
  add_confidence_interval() +
  add_risktable() +
  annotate("text", x = 2, y = 0.05, label = glue::glue("{survfit2_p(sf)}"))
```

Surv_CNSR   *Create a Survival Outcome from CDISC Data*

Description

The aim of `Surv_CNSR()` is to map the inconsistency in data 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()]

Examples

```
# Use the `Surv_CNSR()` function with ggsurvfit functions
survfit2(formula = Surv_CNSR() ~ STR01, data = adtte) %>%
  ggsurvfit() +
  add_confidence_interval()

# Use the `Surv_CNSR()` function with functions from other packages as well
survival::survfit(Surv_CNSR() ~ STR01, data = adtte)
survival::survreg(Surv_CNSR() ~ STR01 + AGE, data = adtte) %>%
  broom::tidy()
```

---

theme_ggsurvfit   *Survfit Plot Themes*

Description

Returns ggplot list of calls defining a theme.

Usage

```
theme_ggsurvfit_default()

theme_ggsurvfit_KMunicate()
```

Value

a ggplot2 theme

Examples

```
survfit2(Surv(time, status) ~ sex, data = df_lung) %>%
  ggsurvfit(theme = theme_ggsurvfit_default())
```

---

theme_risktable   *Risk Table Themes*

Description

Returns ggplot list of calls defining a theme meant to be applied to a risk table.

Usage

```
theme_risktable_default()

theme_risktable_boxed()
```

Value

a ggplot2 figure

Examples

```
p <- survfit2(Surv(time, status) ~ 1, data = df_lung) %>% ggsurvfit()

# default -----------------------------------
p + add_risktable(theme = theme_risktable_default())

# boxed -------------------------------------
p + add_risktable(theme = theme_risktable_boxed())

# none --------------------------------------
p + add_risktable(theme = NULL, risktable_height = 0.20)
```

---

tidy_cuminc   *Tidy a cuminc object*

Description

The tidycmprsk package exports a tidier for "cuminc" objects. This function adds on top of that and returns more information.

Usage

```
tidy_cuminc(x, times = NULL)
```

Arguments

x	a 'cuminc' object created with tidycmprsk::cuminc()
times	numeric vector of times. Default is NULL, which returns all observed times.

Value

a tibble

Examples

```
library(tidycmprsk)

cuminc(Surv(ttdeath, death_cr) ~ trt, trial) %>%
  tidy_cuminc()
```

---

tidy_survfit   *Tidy a survfit object*

Description

The broom package exports a tidier for `"survfit"` objects. This function adds on top of that and
returns more information. The function also utilizes additional information stored when the survfit
object is created with `survfit2()`. It's recommended to always use this function with `survfit2()`.

Usage

```
tidy_survfit(x, times = NULL, type = c("survival", "risk", "cumhaz"))
```

Arguments

x	a 'survfit' object created with `survfit2()`
times	numeric vector of times. Default is `NULL`, which returns all observed times.
type	type of statistic to report. Default is `"survival"`. Must be one of the following:

type	transformation
`"survival"`	x
`"risk"`	1 - x
`"cumhaz"`	-log(x)

Value

a tibble

Examples

```
survfit2(Surv(time, status) ~ factor(ph.ecog), data = df_lung) %>%
  tidy_survfit()
```

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