

Package ‘easysurv’

May 8, 2026

Type Package

Title Simplify Survival Data Analysis and Model Fitting

Version 2.0.2

Description Inspect survival data, plot Kaplan-Meier curves, assess the proportional hazards assumption, fit parametric survival models, predict and plot survival and hazards, and export the outputs to 'Excel'. A simple interface for fitting survival models using `flexsurv::flexsurvreg()`, `flexsurv::flexsurvspline()`, `flexsurvcure::flexsurvcure()`, and `survival::survreg()`.

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URL <https://github.com/Maple-Health-Group/easysurv>,
<https://maple-health-group.github.io/easysurv/>

BugReports <https://github.com/Maple-Health-Group/easysurv/issues>

Depends R (>= 4.1.0)

Imports bshazard, censored, cli, data.table, dplyr, flexsurv,
flexsurvcure, ggplot2, ggsurvfit (>= 1.2.0), openxlsx, parsnip,
plotly, purrr, rlang, scales, stats, survival, tibble, tidyr,
usethis, utils

Suggests knitr, rmarkdown, spelling, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/Needs/website r-lib/asciicast

Config/testthat/edition 3

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

Author Niall Davison [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-9447-0825>>),
Brad Kievit [aut],
Maple Health Group, LLC [cph, fnd]

Maintainer Niall Davison <niall.davison@maplehealthgroup.com>

Repository CRAN

Date/Publication 2025-10-08 11:30:02 UTC

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easy_adtte

Formatted Copy of `ggsurvfit::adtte`

Description

Background The example simulated data set is based on large phase III clinical trials in breast cancer such as the ALTTO trial [doi:10.1200/JCO.2015.62.1797](https://doi.org/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).

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>.

Usage

easy_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

CNSDDESC Censoring description

DCTREAS Discontinuation from study reason

Source

[ggsurvfit::adtte](#)

easy_bc	<i>Formatted Copy of flexsurv::bc</i>
---------	-------------------------------------------------------

Description

This is a copy of the bc data set exported by the flexsurv package. This data set, however, has column labels assigned.

Usage

```
easy_bc
```

Format

The data set contains the following variables:

censrec 0 = Censored, 1 = Dead

rectime Time of censoring or death in days

group Prognostic group: Good, Medium, or Poor

recyrs Time of censoring or death in years

Source

[flexsurv::bc](#)

easy_lung	<i>Formatted Copy of survival::lung</i>
-----------	---------------------------------------------------------

Description

This is a copy of the lung data set exported by the survival package. This data set, however, has column labels assigned and time in months.

Usage

```
easy_lung
```

Format

The data set contains the following variables:

inst Institution code
time Survival time, months
status Censoring status, 1 = censored, 2 = dead
age Age
sex Sex, 1 = Male, 2 = Female
ph.ecog ECOG Performance Status (Physician)
ph.karno Karnofsky performance score (Physician)
pat.karno Karnofsky performance score (Patient)
meal.cal Calories consumed
wt.loss Weight loss, lbs

Source

[survival::lung](#)

fit_models

Fit Survival Models

Description

Fits survival models to the provided data using the specified engine and returns various outputs including model parameters, goodness of fit, and estimates of median survival.

Usage

```
fit_models(  
  data,  
  time,  
  event,  
  predict_by = NULL,  
  covariates = NULL,  
  dists = c("exp", "gamma", "gengamma", "gompertz", "llogis", "lnorm", "weibull"),  
  engine = "flexsurv",  
  k = c(1, 2, 3),  
  scale = "hazard",  
  add_time_0 = TRUE,  
  ...  
)
```

Arguments

data	A data frame containing the survival data.
time	The name of the column in data containing the time-to-event information.
event	The name of the column in data indicating whether the event of interest occurred.
predict_by	(Optional) The name of the column in data defining the prediction variable.
covariates	(Optional) A character vector specifying the names of covariates to be included in the model.
dists	(Optional) A character vector specifying the distribution(s) to be fitted. When the engine parameter is set to "flexsurv", options are "exp", "exponential", "gamma", "genf", "genf.orig", "gengamma", "gengamma.orig", "gompertz", "llogis", "lnorm", "lognormal", "weibull", "weibullPH". When the engine parameter is set to "flexsurvcure", options are "exp", "gamma", "gengamma", "gompertz", "llogis", "lnorm", "weibull". When the engine parameter is set to "flexsurvspline", dists are ignored in favor of k and scale parameters. When the engine parameter is set to "survival", options are "exponential", "extreme", "gaussian", "loggaussian" (same as lognormal), "logistic", "lognormal", "rayleigh", "weibull". Default is c("exp", "gamma", "gengamma", "gompertz", "llogis", "lnorm", "weibull") which applies to flexsurv-related engines.
engine	(Optional) The survival analysis engine to be used. Options are "flexsurv", "flexsurvcure", "flexsurvspline", and "survival". Default is "flexsurv". <ul style="list-style-type: none"> • "flexsurv" uses <code>flexsurv::flexsurvreg()</code>. • "flexsurvspline" uses <code>flexsurv::flexsurvspline()</code>. • "flexsurvcure" uses <code>flexsurvcure::flexsurvcure()</code>. • "survival" uses <code>survival::survreg()</code>.
k	(Optional) A numeric vector specifying the number of knots for spline-based models. Default is c(1, 2, 3) to test different numbers.
scale	(Optional) A character vector specifying the scale parameter(s) for spline-based models. Options are "hazard", "odds", and "normal". Default is "hazard".
add_time_0	Optional. Uses <code>survival::survfit0()</code> to add a starting time of 0 to the KM survfit object. This may be useful for plotting the KM at a subsequent stage (in <code>surv_plots</code>). Default is TRUE.
...	Additional arguments just to catch them and avoid errors.

Value

A list containing information about the `fit_models()` call, the distributions attempted, goodness of fit, fit averages, and cure fractions (if applicable).

Examples

```
models <- fit_models(
  data = easysurv::easy_bc,
  time = "recyrs",
  event = "censrec",
  predict_by = "group",
  covariates = "group"
)

models
```

get_km

*Generate Kaplan-Meier estimates***Description**

Calculates Kaplan-Meier estimates for survival data and returns summary statistics, plots, and additional outputs.

Usage

```
get_km(
  data,
  time,
  event,
  group = NULL,
  group_labels = NULL,
  just_km = FALSE,
  ...
)
```

Arguments

data	A data frame containing the survival data.
time	The name of the column in data containing the time-to-event information.
event	The name of the column in data indicating whether the event of interest occurred.
group	(Optional) The name of the column in data defining the grouping variable. Default is NULL.
group_labels	Optional character vector containing the names of the strata (default is NULL). Provide in a consistent order with <code>levels(as.factor(data\$group))</code> .
just_km	Logical. If TRUE, only the Kaplan-Meier estimates are returned. Default is FALSE.
...	(Optional) Parameters to pass to <code>ggsurvfit</code> .

Value

A list containing Kaplan-Meier estimates, summary statistics, and plots.

Examples

```
km_results <- get_km(
  data = easysurv::easy_bc,
  time = "recyrs",
  event = "censrec",
  group = "group",
  risktable_symbols = FALSE
)

km_results
```

get_schoenfeld

Extract Schoenfeld Residuals

Description

This function extracts Schoenfeld residuals from a fitted `cox.zph` object and formats them into a tidy data frame.

Usage

```
get_schoenfeld(fit_zph)
```

Arguments

`fit_zph` An object of class `cox.zph` produced by the `cox.zph` function, representing the Schoenfeld residuals of a Cox proportional hazards model.

Value

A tibble with the Schoenfeld residuals in long format, containing the columns:

<code>time</code>	The time variable from the Cox model.
<code>transform</code>	The transformation applied to the time variable.
<code>variable</code>	The variable names from the Cox model for which residuals are calculated.
<code>residual</code>	The Schoenfeld residuals for each variable at each time point.

Examples

```
library(survival)
test_fit <- survival::coxph(survival::Surv(time, status) ~ sex, data = lung)
test_fit_zph <- survival::cox.zph(test_fit)
get_schoenfeld(test_fit_zph)
```

inspect_surv_data	<i>Inspect Survival Data</i>
-------------------	------------------------------

Description

Quickly inspect the survival data to ensure it is in the correct format.

Usage

```
inspect_surv_data(data, time, event, group = NULL)
```

Arguments

data	A data frame containing the survival data.
time	The column name in data containing the time-to-event data.
event	The column name in data containing the event indicator data.
group	Optional. The column name in data containing the group indicator data.

Value

A list containing tibbles that summarise the first few rows of the survival data, the sample sizes, the events, and median survival.

Examples

```
inspect_surv_data(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  group = "group"  
)
```

plot.fit_models	<i>Plot method for fit_models</i>
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Description

Plot method for fit_models

Usage

```
## S3 method for class 'fit_models'
plot(
  x,
  eval_time = NULL,
  km_include = TRUE,
  subtitle_include = TRUE,
  add_plotly = FALSE,
  ...
)
```

Arguments

x	An object of class <code>fit_models</code>
eval_time	Time points at which to evaluate the survival function. Default is <code>NULL</code> .
km_include	Logical value indicating whether to include Kaplan-Meier survival data. Default is <code>TRUE</code> .
subtitle_include	Logical value indicating whether to include a subtitle in the plot. Default is <code>TRUE</code> .
add_plotly	Logical value indicating whether to add plotly interactivity. Default is <code>FALSE</code> .
...	Additional arguments

Value

A list containing predictions and plots for the survival and hazards of models in a `fit_models` object.

Examples

```
models <- fit_models(
  data = easysurv::easy_bc,
  time = "recyrs",
  event = "censrec",
  predict_by = "group",
  covariates = "group"
)

plot(models)
```

plot_cloglog

Cumulative Log Log Plot

Description

Generates a Cumulative Log Log survival curve plot using `ggsurvfit::ggsurvfit()` with customizable options.

Usage

```
plot_cloglog(
  fit,
  median_line = FALSE,
  legend_position = "top",
  plot_theme = theme_easysurv()
)
```

Arguments

fit A `survival::survfit` object representing the survival data.

median_line Logical value indicating whether to include a line representing the median survival time. Default is `FALSE`.

legend_position Position of the legend in the plot. Default is `"top"`.

plot_theme `ggplot2` theme for the plot. Default is `theme_easysurv()`.

Value

A `ggplot` object representing the cumulative log log plot.

Examples

```
library(ggsurvfit)
fit <- survfit2(Surv(time, status) ~ surg, data = df_colon)
plot_cloglog(fit)
```

<code>plot_km</code>	<i>Plot Kaplan-Meier Data</i>
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Description

Generates a Kaplan-Meier survival curve plot using `ggsurvfit::ggsurvfit()` with customizable options. This function provides sensible defaults while allowing for customization.

Usage

```
plot_km(
  fit,
  risktable = TRUE,
  risktable_symbols = TRUE,
  median_line = TRUE,
  legend_position = "top",
  plot_theme = theme_easysurv(),
  risktable_theme = theme_risktable_easysurv()
)
```

Arguments

fit	A <code>survival::survfit</code> object representing the survival data.
risktable	Logical value indicating whether to include a risk table below the plot. Default is TRUE.
risktable_symbols	Logical value indicating whether to include symbols instead of text to label risk table strata. Default is TRUE.
median_line	Logical value indicating whether to include a line representing the median survival time. Default is TRUE.
legend_position	Position of the legend in the plot. Default is "top".
plot_theme	ggplot2 theme for the plot. Default is <code>theme_easysurv()</code> .
risktable_theme	ggplot2 theme for the risk table. Default is <code>theme_risktable_easysurv()</code> .

Value

A ggplot object representing the Kaplan-Meier survival curve plot.

Examples

```
library(ggsurvfit)
fit <- survfit2(Surv(time, status) ~ surg, data = df_colon)
plot_km(fit, risktable_symbols = FALSE)
```

plot_schoenfeld

Plot Schoenfeld Residuals

Description

Plot the residuals generated by the `get_schoenfeld` function. This function creates a visual representation of Schoenfeld residuals from a Cox proportional hazards model. It allows for customization of the plot, including the addition of horizontal and smoothed lines, and styling of points and plot elements.

Usage

```
plot_schoenfeld(
  residuals,
  hline = TRUE,
  sline = TRUE,
  sline_se = TRUE,
  hline_col = "#F8766D",
  hline_size = 1,
  hline_alpha = 1,
  hline_yintercept = 0,
```

```

hline_lty = "dashed",
sline_col = "#00BFC4",
sline_size = 1,
sline_alpha = 0.2,
sline_lty = "dashed",
point_col = "black",
point_size = 1,
point_shape = 19,
point_alpha = 1,
plot_theme = ggplot2::theme_bw()
)

```

Arguments

residuals	A data frame containing the Schoenfeld residuals, typically with columns time, residual, transform, and variable.
hline	Logical. If TRUE, a horizontal line is added to the plot. Default is TRUE.
sline	Logical. If TRUE, a smooth line is added to the plot. Default is TRUE.
sline_se	Logical. If TRUE, confidence intervals are displayed around the smooth line. Default is TRUE.
hline_col	Color of the horizontal line. Default is "#F8766D" (red).
hline_size	Line width of the horizontal line. Default is 1.
hline_alpha	Transparency of the horizontal line. Default is 1.
hline_yintercept	Y-intercept for the horizontal line. Default is 0.
hline_lty	Line type for the horizontal line. Default is "dashed".
sline_col	Color of the smooth line. Default is "#00BFC4" (blue).
sline_size	Line width of the smooth line. Default is 1.
sline_alpha	Transparency of the smooth line. Default is 0.2.
sline_lty	Line type for the smooth line. Default is "dashed".
point_col	Color of the points representing residuals. Default is "black".
point_size	Size of the points representing residuals. Default is 1.
point_shape	Shape of the points representing residuals. Default is 19.
point_alpha	Transparency of the points representing residuals. Default is 1.
plot_theme	A ggplot2 theme for the plot. Default is <code>ggplot2::theme_bw()</code> .

Value

A ggplot object representing the plot of Schoenfeld residuals.

Examples

```

library(survival)
test_fit <- survival::coxph(survival::Surv(time, status) ~ sex, data = lung)
test_fit_zph <- survival::cox.zph(test_fit)
plot_schoenfeld(get_schoenfeld(test_fit_zph))

```

predict.fit_models *Predict method for fit_models*

Description

Predict method for fit_models

Usage

```
## S3 method for class 'fit_models'  
predict(object, eval_time = NULL, type = c("survival", "hazard"), ...)
```

Arguments

object	An object of class fit_models
eval_time	(Optional) A vector of evaluation time points for generating predictions. Default is NULL, which if left as NULL, generates a sequence from 0 to 5 times the maximum observed time.
type	A character vector indicating the type of predictions to generate. Default is c("survival", "hazard").
...	Additional arguments

Value

A list of predictions for each model in the fit_models object.

Examples

```
models <- fit_models(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  predict_by = "group",  
  covariates = "group"  
)  
  
predict(models)
```

predict_and_plot *Predict and Plot Fitted Models*

Description

This function generates survival and hazard predictions and plots for each model in a `fit_models` object. Optionally, interactive plotly outputs can be added for each plot.

Usage

```
predict_and_plot(  
  fit_models,  
  eval_time = NULL,  
  km_include = TRUE,  
  subtitle_include = TRUE,  
  add_plotly = FALSE  
)
```

Arguments

<code>fit_models</code>	An object returned from <code>fit_models</code> .
<code>eval_time</code>	(Optional) A vector of evaluation time points for generating predictions. Default is <code>NULL</code> , which if left as <code>NULL</code> , generates a sequence from 0 to 5 times the maximum observed time.
<code>km_include</code>	A logical indicating whether to include Kaplan-Meier estimates in the plot outputs. Default is <code>TRUE</code> .
<code>subtitle_include</code>	A logical indicating whether to include the subtitle. Default is <code>TRUE</code> . The subtitle is the name of the group.
<code>add_plotly</code>	A logical indicating whether to add interactive plotly outputs for each plot. Default is <code>FALSE</code> .

Value

A list of predictions and plots for each model in the `fit_models` object.

Examples

```
models <- fit_models(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  predict_by = "group"  
)  
  
predict_and_plot(models)
```

print.fit_models *Print methods for fit_models()*

Description

Print methods for fit_models()

Usage

```
## S3 method for class 'fit_models'  
print(x, ...)
```

Arguments

x An object of class fit_models
... Additional arguments

Value

A print summary of the fit_models object.

Examples

```
models <- fit_models(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  predict_by = "group",  
  covariates = "group"  
)  
  
models
```

print.get_km *Print methods for get_km()*

Description

Print methods for get_km()

Usage

```
## S3 method for class 'get_km'  
print(x, ...)
```

Arguments

`x` An object of class `get_km`
`...` Additional arguments

Value

The summary of the Kaplan-Meier estimates, printed via the console.

Examples

```
km_results <- get_km(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  group = "group",  
  risktable_symbols = FALSE  
)  
  
print(km_results)
```

`print.inspect_surv_data`

Print methods for inspect_surv_data()

Description

Print methods for `inspect_surv_data()`

Usage

```
## S3 method for class 'inspect_surv_data'  
print(x, ...)
```

Arguments

`x` An object of class `inspect_surv_data`
`...` Additional arguments

Value

A print summary of the `inspect_surv_data` object.

```
print.predict_and_plot
```

Print methods for predict_and_plot()

Description

Print methods for predict_and_plot()

Usage

```
## S3 method for class 'predict_and_plot'  
print(x, ...)
```

Arguments

x	An object of class predict_and_plot
...	Additional arguments

Value

A print summary of the predict_and_plot object.

Examples

```
models <- fit_models(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  predict_by = "group"  
)  
  
predict_and_plot(models)
```

```
print.test_ph
```

Print methods for test_ph()

Description

Print methods for test_ph()

Usage

```
## S3 method for class 'test_ph'  
print(x, ...)
```

Arguments

x An object of class test_ph
... Additional arguments

Value

A print summary of the test_ph object.

Examples

```
ph_results <- test_ph(  
  data = easysurv::easy_bc,  
  time = "recyrs",  
  event = "censrec",  
  group = "group"  
)  
  
ph_results
```

quick_start	<i>Launch Example Survival Analysis Script using the easy_lung Data Set</i>
-------------	-----------------------------------------------------------------------------

Description

This function launches an example script for starting survival analysis using the easysurv package. The script uses a modified version of the lung data set exported from the survival package. The code is inspired by `usethis::use_template()` but modified to work outside the context of an .RProj or package.

Usage

```
quick_start(output_file_name = NULL)
```

Arguments

output_file_name Optional. A file name to use for the script. Defaults to "easysurv_start.R" within a helper function.

Value

A new R script file with example code.

Examples

```
quick_start()
```

quick_start2	<i>Launch Example Survival Analysis Script using the easy_bc Data Set</i>
--------------	---------------------------------------------------------------------------

Description

This function launches an example script for starting survival analysis using the easysurv package. The script uses a modified version of the bc data set exported from the flexsurv package. The code is inspired by `usethis::use_template()` but modified to work outside the context of an .RProj or package.

Usage

```
quick_start2(output_file_name = NULL)
```

Arguments

`output_file_name`
Optional. A file name to use for the script. Defaults to "easysurv_start.R" within a helper function.

Value

A new R script file with example code.

Examples

```
quick_start2()
```

quick_start3	<i>Launch Example Survival Analysis Script using the easy_adtte Data Set</i>
--------------	------------------------------------------------------------------------------

Description

This function launches an example script for starting survival analysis using the easysurv package. The script uses simulated phase III breast cancer trial data available from the ggsurvfit package. The code is inspired by `usethis::use_template()` but modified to work outside the context of an .RProj or package.

Usage

```
quick_start3(output_file_name = NULL)
```

Arguments

`output_file_name`
Optional. A file name to use for the script. Defaults to "easysurv_start.R" within a helper function.

Value

A new R script file with example code.

Examples

```
quick_start3()
```

test_ph

Test Proportional Hazards Assumption

Description

Assesses the proportional hazards assumption for survival data using a Cox proportional hazards model and related tests.

Usage

```
test_ph(data, time, event, group, plot_theme = theme_easysurv())
```

Arguments

data	A data frame containing the survival data.
time	The name of the column in data containing the time-to-event information.
event	The name of the column in data indicating whether the event of interest occurred.
group	The name of the column in data defining the grouping variable.
plot_theme	The theme to be used for the plots.

Value

A list containing plots and test results related to the assessment of the proportional hazards assumption.

cloglog_plot	A plot of the log cumulative hazard function. If the lines are roughly parallel, this suggests that the proportional hazards assumption holds."
coxph_model	The coefficients from the Cox proportional hazards model. The exp(coef) column shows the hazard ratio.
survdiff	The results of the log-rank test for differences in survival curves between groups. A p-value less than 0.05 suggests that survival differences between groups are statistically significant.
coxph_test	The results of the proportional hazards assumption test. A p-value less than 0.05 suggests that the proportional hazards assumption may be violated.
schoenfeld_plot	A plot of the Schoenfeld residuals. A flat smoothed line close to zero supports the proportional hazards assumption. A non-flat smoothed line with a trend suggests the proportional hazards assumption is violated.

Examples

```
ph_results <- test_ph(
  data = easysurv::easy_bc,
  time = "recyrs",
  event = "censrec",
  group = "group"
)

ph_results
```

 theme_easysurv

Plot Theme for easysurv Survival and Hazard Plots

Description

Plot Theme for easysurv Survival and Hazard Plots

Usage

```
theme_easysurv()
```

Value

A ggplot2 theme object.

Examples

```
library(ggsurvfit)
fit <- survfit2(Surv(time, status) ~ surg, data = df_colon)
fit |> ggsurvfit() + theme_easysurv()
```

 theme_risktable_easysurv

Plot Theme for easysurv Risk Tables

Description

To be used with [ggsurvfit::add_risktable\(\)](#).

Usage

```
theme_risktable_easysurv()
```

Value

A list containing a ggplot2 theme object.

Examples

```
library(ggsurvfit)
fit <- survfit2(Surv(time, status) ~ surg, data = df_colon)
fit <- fit |> ggsurvfit() +
  theme_easysurv() +
  add_risktable(theme = theme_risktable_easysurv())
fit
```

`write_to_xl`*Export easysurv output to Excel via openxlsx*

Description

Export easysurv output to Excel via openxlsx

Usage

```
write_to_xl(wb, object)
```

Arguments

<code>wb</code>	A Workbook object containing a worksheet
<code>object</code>	The output of an easysurv command

Value

An Excel workbook with the easysurv output.

Examples

```
km_results <- get_km(
  data = easysurv::easy_bc,
  time = "recyrs",
  event = "censrec",
  group = "group",
  risktable_symbols = FALSE
)

wb <- openxlsx::createWorkbook()

## Not run:
write_to_xl(wb, km_results)
openxlsx::saveWorkbook(wb, "km_results.xlsx", overwrite = TRUE)
openxlsx::openXL("km_results.xlsx")

## End(Not run)
```

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