Package 'reportRmd'

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Title Tidy Presentation of Clinical Reporting

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Description Streamlined statistical reporting in 'Rmarkdown' environments. Facilitates the automated reporting of descriptive statistics, multiple univariate models, multivariable models and tables combining these outputs. Plotting functions include customisable survival curves, forest plots from logistic and ordinal regression and bivariate comparison plots.

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Contents

add_censor_marks . . . 3
add_cif_hazard_ratios . . . 4
add_confidence_bands . . . 5
add_km_hazard_ratios . . . 5
add_median_lines . . . 6
add_median_text . . . 6
add_set_time_lines . . . 7
add_set_time_text . . . 8
add_statistical_tests . . . 9
apply_scales_and_guides . . . 10
boxcoxfitRx . . . 10
calculate_and_add_median_times . . . 11
calculate_and_add_time_specific_estimates . . . 12
calculate_cif_median . . . 13
calculate_cif_timepoints . . . 13
clear_labels . . . 14
covsum . . . 15
create_base_plot . . . 17
create_cif_dataframe . . . 18
create_cif_risk_table_sfit . . . 19
create_km_dataframe . . . 19
create_risk_table . . . 20
crrRx . . . 21
ctDNA . . . 22
excelCol . . . 22
excelColLetters . . . 23
extract_grays_test . . . 24
extract_labels . . . 24
extract_package_details . . . 25
fit_cif_model . . . 26
fit_km_model . . . 26
forestplot2 . . . 27
forestplotMV . . . 28

forestplotUV 29
forestplotUVMV 31
geoR_boxcoxfit 31
ggkmcif2 32
ggkmcif2Parameters 33
ggkmcif_paste 36
hbld 36
lpvalue2 37
mvsum 38
nestTable 39
outTable 40
pembrolizumab 42
plotuv 43
predsum 45
process_cif_medians 47
process_cif_timepoints 48
process_covariate 49
replace_plot_labels 49
rm_cifsum 50
rm_compactsum 52
rm_covsum 55
rm_mvsum 59
rm_survdiff 62
rm_survsum 64
rm_survtime 66
rm_uvsum 68
rm_uv_mv 72
scrolling_table 73
set_labels 74
set_var_labels 75
validate_and_prepare_data 75

Index **77**

`add_censor_marks` *Add censor marks to KM plot*

Description

Add censor marks to KM plot

Usage

```
add_censor_marks(p, df, censor.size = 0.5, censor.stroke = 1.5, shape = "|")
```

Arguments

p	ggplot object
df	Plotting dataframe
censor.size	Size of censor marks
censor.stroke	Stroke of censor marks
shape	Shape for censor marks, defaults to "|", but can use an character or standard geom_point shapes (0-24)

---

add_cif_hazard_ratios *Add CIF Hazard Ratios to Strata Labels*

Description

Add CIF Hazard Ratios to Strata Labels

Usage

```
add_cif_hazard_ratios(
  stratalabs,
  data,
  response,
  cov,
  plot.event = 1,
  HR = FALSE,
  HR_pval = FALSE,
  HR.digits = 2,
  HR.pval.digits = 3
)
```

Arguments

stratalabs	Original strata labels
data	Input data
response	Time and status variables
cov	Covariate
plot.event	Event for CIF (must be 1 for HR calculation)
HR	Whether to include HR
HR_pval	Whether to include HR p-value
HR.digits	Number of digits for HR
HR.pval.digits	Number of digits for HR p-value

Value

Updated strata labels

add_confidence_bands *Add confidence bands to plot*

Description

Add confidence bands to plot

Usage

```
add_confidence_bands(p, df, type, event = "col", plot.event = 1)
```

Arguments

p	ggplot object
df	Plotting dataframe
type	Plot type
event	Event distinction method
plot.event	Events to plot

add_km_hazard_ratios *Add hazard ratios to strata labels*

Description

Add hazard ratios to strata labels

Usage

```
add_km_hazard_ratios(
  stratalabs,
  data,
  response,
  cov,
  type,
  plot.event = 1,
  HR = FALSE,
  HR_pval = FALSE,
  HR.digits = 2,
  HR.pval.digits = 3
)
```

Arguments

stratalabs	Original strata labels
data	Input data
response	Time and status variables
cov	Covariate
type	Model type ("KM" or "CIF")
plot.event	Event for CIF
HR	Whether to include HR
HR_pval	Whether to include HR p-value
HR.digits	Number of digits for HR
HR.pval.digits	Number of digits for HR p-value

---

add_median_lines *Add median survival lines to plot*

Description

Add median survival lines to plot

Usage

```
add_median_lines(p, median_vals, median.lsize = 1)
```

Arguments

p	ggplot object
median_vals	Median values
median.lsize	Line size for median lines

---

add_median_text *Add median survival text to plot*

Description

Add median survival text to plot

Usage

```
add_median_text(
  p,
  type,
  multiple_lines,
  median_txt,
  median.pos = NULL,
  times,
  ylim,
  median.size = 3,
  plot.event = 1,
  eventlabs = NULL
)
```

Arguments

p	ggplot object
type	Plot type
multiple_lines	Whether multiple strata
median_txt	Median text
median.pos	Position for median text
times	Time breaks
ylim	Y-axis limits
median.size	Text size
plot.event	Events being plotted
eventlabs	Event labels

---

add_set_time_lines *Add survival at set time lines to plot*

Description

Add survival at set time lines to plot

Usage

```
add_set_time_lines(p, set.surv, set.lsize = 1)
```

Arguments

p	ggplot object
set.surv	Data frame with survival at set times
set.lsize	Line size

`add_set_time_text` *Add survival at set time text to plot*

Description

Add survival at set time text to plot

Usage

```
add_set_time_text(
  p,
  type,
  multiple_lines,
  set.surv.text,
  set.pos = NULL,
  times,
  ylim,
  set.size = 3,
  plot.event = 1,
  eventlabs = NULL
)
```

Arguments

`p`	ggplot object
`type`	Plot type
`multiple_lines`	Whether multiple strata
`set.surv.text`	Survival text
`set.pos`	Position for survival text
`times`	Time breaks
`ylim`	Y-axis limits
`set.size`	Text size
`plot.event`	Events being plotted
`eventlabs`	Event labels

`add_statistical_tests` *Add statistical test results to plot*

Description

Add statistical test results to plot

Usage

```
add_statistical_tests(
  p,
  type,
  multiple_lines,
  pval_result,
  pval.pos = NULL,
  times,
  xlim,
  ylim,
  psize = 3.5,
  pval.digits = 3,
  plot.event = 1,
  eventlabs = NULL
)
```

Arguments

`p`	ggplot object
`type`	Plot type
`multiple_lines`	Whether multiple strata
`pval_result`	P-value
`pval.pos`	Position for p-value text
`times`	Time breaks
`xlim`	X-axis limits
`ylim`	Y-axis limits
`psize`	Text size for p-value
`pval.digits`	Number of digits for p-value
`plot.event`	Events being plotted
`eventlabs`	Event labels

`apply_scales_and_guides` *Apply colour and linetype scales*

Description

Apply colour and linetype scales

Usage

```
apply_scales_and_guides(
  p,
  col,
  linetype = NULL,
  stratalabs,
  eventlabs = NULL,
  multiple_lines,
  plot.event = 1,
  event = "col"
)
```

Arguments

`p`	ggplot object
`col`	colours vector
`linetype`	Line types vector
`stratalabs`	Strata labels
`eventlabs`	Event labels
`multiple_lines`	Whether multiple strata
`plot.event`	Events being plotted
`event`	How events are distinguished

`boxcoxfitRx` *fit box cox transformed linear model*

Description

Wrapper function to fit fine and gray competing risk model using function crr from package cmprsk

Usage

```
boxcoxfitRx(f, data, lambda = FALSE)
```

Arguments

f	formula for the model. Currently the formula only works by using the name of the column in a dataframe. It does not work by using $ or [] notation.
data	dataframe containing data
lambda	boolean indicating if you want to output the lamda used in the boxcox transformation. If so the function will return a list of length 2 with the model as the first element and a vector of length 2 as the second.

Value

a list containing the linear model (lm) object and, if requested, lambda

---

calculate_and_add_median_times

Calculate median survival times and add to labels

Description

Calculate median survival times and add to labels

Usage

```
calculate_and_add_median_times(
  sfit = NULL,
  fit = NULL,
  stratalabs,
  type = "KM",
  plot.event = 1,
  median.text = FALSE,
  median.CI = FALSE,
  median.digits = 3
)
```

Arguments

sfit	Survival fit object (for KM)
fit	CIF fit object
stratalabs	Strata labels
type	Model type
plot.event	Events to plot (for CIF)
median.text	Whether to add median text
median.CI	Whether to include CI
median.digits	Number of digits

`calculate_and_add_time_specific_estimates` *Calculate survival/CIF at specific time points and add to labels*

Description

Calculate survival/CIF at specific time points and add to labels

Usage

```
calculate_and_add_time_specific_estimates(
  sfit = NULL,
  fit = NULL,
  stratalabs,
  type = "KM",
  plot.event = 1,
  set.time.text = NULL,
  set.time = NULL,
  set.time.line = FALSE,
  set.time.CI = FALSE,
  set.time.digits = 3
)
```

Arguments

`sfit`	Survival fit object (for KM)
`fit`	CIF fit object
`stratalabs`	Strata labels
`type`	Model type
`plot.event`	Events to plot (for CIF)
`set.time.text`	Text label for time points
`set.time`	Time points to evaluate
`set.time.line`	boolean to specify if you want the survival added as lines to the plot at a specified point
`set.time.CI`	Whether to include CI
`set.time.digits`	Number of digits

`calculate_cif_median` *Calculate Median Time to Event for CIF*

Description

Calculate Median Time to Event for CIF

Usage

```
calculate_cif_median(fit, event_name)
```

Arguments

`fit`	CIF fit object
`event_name`	Name of the event in fit object

Value

Median time to event

`calculate_cif_timepoints` *Calculate CIF Estimates at Specific Time Points*

Description

Calculate CIF Estimates at Specific Time Points

Usage

```
calculate_cif_timepoints(
  fit,
  plot.event,
  set.time,
  set.time.CI = FALSE,
  set.time.digits = 3,
  multiple_lines = FALSE
)
```

Arguments

`fit`	CIF fit object
`plot.event`	Events to plot
`set.time`	Time points to evaluate
`set.time.CI`	Whether to include confidence intervals
`set.time.digits`	Number of digits
`multiple_lines`	Whether there are multiple strata

Value

Data frame with time-specific estimates

`clear_labels` *Clear variable labels from a data frame*

Description

This function will remove all label attributes from variables in the data.

Usage

```
clear_labels(data)
```

Arguments

`data`	the data frame to remove labels from

Details

To change or remove individual labels use set_labels or set_var_labels

Examples

```
# Set a few variable labels for ctDNA
data("ctDNA")
ctDNA <- ctDNA |> set_var_labels(
   ctdna_status="detectable ctDNA",
  cohort="A cohort label")
# Clear all variable data frames and check
clear_labels(ctDNA)
```

covsum *Get covariate summary dataframe*

Description

Returns a dataframe corresponding to a descriptive table.

Usage

```
covsum(
  data,
  covs,
  maincov = NULL,
  digits = 1,
  numobs = NULL,
  markup = FALSE,
  sanitize = FALSE,
  nicenames = TRUE,
  IQR = FALSE,
  all.stats = FALSE,
  pvalue = TRUE,
  effSize = FALSE,
  show.tests = FALSE,
  dropLevels = TRUE,
  excludeLevels = NULL,
  full = TRUE,
  digits.cat = 0,
  testcont = c("rank-sum test", "ANOVA"),
  testcat = c("Chi-squared", "Fisher"),
  include_missing = FALSE,
  percentage = c("column", "row"),
  B = 1000,
  seed = 1
)
```

Arguments

data	dataframe containing data
covs	character vector with the names of columns to include in table
maincov	covariate to stratify table by
digits	number of digits for summarizing mean data, does not affect p-values
numobs	named list overriding the number of people you expect to have the covariate
markup	boolean indicating if you want latex markup
sanitize	boolean indicating if you want to sanitize all strings to not break LaTeX
nicenames	boolean indicating if you want to replace . and _ in strings with a space

IQR	boolean indicating if you want to display the inter quantile range (Q1,Q3) as opposed to (min,max) in the summary for continuous variables
all.stats	boolean indicating if all summary statistics (Q1,Q3 + min,max on a separate line) should be displayed. Overrides IQR.
pvalue	boolean indicating if you want p-values included in the table
effSize	boolean indicating if you want effect sizes included in the table. Can only be obtained if pvalue is also requested. Effect sizes calculated include Cramer's V for categorical variables, Cohen's d, Wilcoxon r, or Eta-squared for numeric/continuous variables.
show.tests	boolean indicating if the type of statistical test and effect size used should be shown in a column beside the pvalues. Ignored if pvalue=FALSE.
dropLevels	logical, indicating if empty factor levels be dropped from the output, default is TRUE.
excludeLevels	a named list of covariate levels to exclude from statistical tests in the form list(varname =c('level1','level2')). These levels will be excluded from association tests, but not the table. This can be useful for levels where there is a logical skip (ie not missing, but not presented). Ignored if pvalue=FALSE.
full	boolean indicating if you want the full sample included in the table, ignored if maincov is NULL
digits.cat	number of digits for the proportions when summarizing categorical data (default: 0)
testcont	test of choice for continuous variables,one of *rank-sum* (default) or *ANOVA*
testcat	test of choice for categorical variables,one of *Chi-squared* (default) or *Fisher*
include_missing	Option to include NA values of maincov. NAs will not be included in statistical tests
percentage	choice of how percentages are presented ,one of *column* (default) or *row*
B	number of replicates used when a Monte Carlo approximation to Fisher's exact test is required. Defaults to 1000.
seed	integer seed set for the duration of any Monte Carlo test so that p-values are reproducible; the calling session's random state is restored afterwards. Defaults to 1. Set to NULL to leave the random state untouched, in which case p-values will vary between calls.

Details

Comparisons for categorical variables default to chi-square tests, but if there are counts of <5 then the Fisher Exact test will be used and if this is unsuccessful then a second attempt will be made computing p-values using MC simulation. If testcont='ANOVA' then the t-test with unequal variance will be used for two groups and an ANOVA will be used for three or more. The statistical test used can be displayed by specifying show.tests=TRUE.

The number of decimals places to display the statistics can be changed with digits, but this will not change the display of p-values. If more significant digits are required for p-values then use tableOnly=TRUE and format as desired.

References

Ellis, P.D. (2010) The essential guide to effect sizes: statistical power, meta-analysis, and the interpretation of research results. Cambridge: Cambridge University Press.doi:10.1017/CBO9780511761676

Lakens, D. (2013) Calculating and reporting effect sizes to facilitate cumulative science: a practical primer for t-tests and ANOVAs. Frontiers in Psychology, 4; 863:1-12. doi:10.3389/fpsyg.2013.00863

See Also

fisher.test,chisq.test, wilcox.test,kruskal.test,and anova

`create_base_plot` *Create base ggplot for survival curves*

Description

Create base ggplot for survival curves

Usage

```
create_base_plot(
  df,
  type,
  xlab = "Time",
  ylab = "Survival Probability",
  multiple_lines,
  plot.event = 1,
  event = "col",
  lsize = 0.5,
  fsize,
  col,
  linetype = NULL,
  legend.pos = "bottom",
  legend.title = NULL,
  times,
  ylim = c(0, 1),
  xlim = NULL,
  main = NULL
)
```

Arguments

df	Plotting dataframe
type	Plot type ("KM" or "CIF")
xlab	x axis label
ylab	y axis label

multiple_lines	Whether multiple strata
plot.event	Events to plot
event	How to distinguish events ("col" or "linetype")
lsize	Line size
fsize	Font size
col	colours vector
linetype	Line types vector
legend.pos	Legend position
legend.title	Legend title
times	Time breaks
ylim	Y-axis limits
xlim	X-axis limits
main	Plot title

`create_cif_dataframe` *Create CIF Plotting Data Frame*

Description

Create CIF Plotting Data Frame

Usage

```
create_cif_dataframe(
  fit,
  gsep,
  plot.event,
  stratalabs,
  conf.type = "log",
  flip.CIF = FALSE,
  eventlabs = NULL,
  cov = NULL,
  data = NULL
)
```

Arguments

fit	CIF fit object
gsep	Group separator from fit_cif_model
plot.event	Events to plot
stratalabs	Strata labels
conf.type	Confidence interval type

flip.CIF	Whether to flip the CIF curve
eventlabs	Event labels
cov	Covariate for proper factor levels
data	Original data (for factor levels)

Value

Data frame for plotting

`create_cif_risk_table_sfit` *Create Survival Fit for Risk Table in CIF*

Description

Create Survival Fit for Risk Table in CIF

Usage

```
create_cif_risk_table_sfit(data, response, cov = NULL)
```

Arguments

data	Input data
response	Time and status variables
cov	Covariate (optional)

Value

Survival fit object for risk table

`create_km_dataframe` *Create plotting dataframe for KM curves*

Description

Create plotting dataframe for KM curves

Usage

```
create_km_dataframe(sfit, stratalabs, conf.curves = FALSE, conf.type = "log")
```

Arguments

sfit	Survival fit object
stratalabs	Strata labels
conf.curves	Whether to include confidence intervals
conf.type	Confidence interval type

`create_risk_table` *Create risk table for survival plot*

Description

Create risk table for survival plot

Usage

```
create_risk_table(
  sfit,
  times,
  xlim,
  stratalabs,
  stratalabs.table = NULL,
  strataname.table = "",
  Numbers_at_risk_text = "At Risk",
  multiple_lines = TRUE,
  col = NULL,
  fsize = 12,
  nsize = 3
)
```

Arguments

sfit	Survival fit object
times	Time points for risk table
xlim	X-axis limits
stratalabs	Strata labels
stratalabs.table	Table-specific strata labels
strataname.table	Table strata name
Numbers_at_risk_text	Text for numbers at risk
multiple_lines	Whether multiple strata
col	colours for strata
fsize	Font size
nsize	Number size in table

crrRx *fit crr model*

Description

Wrapper function to fit fine and gray competing risk model using function crr from package cmprsk

Usage

```
crrRx(f, data)
```

Arguments

f	formula for the model. Currently the formula only works by using the name of the column in a dataframe. It does not work by using $ or [] notation.
data	dataframe containing data

Value

a competing risk model with the call appended to the list

See Also

cmprsk::crr

Examples

```
# From the crr help file:
set.seed(10)
ftime <- rexp(200)
fstatus <- sample(0:2,200,replace=TRUE)
cov <- matrix(runif(600),nrow=200)
dimnames(cov)[[2]] <- c('x1','x2','x3')
df <- data.frame(ftime,fstatus,cov)
m1 <- crrRx(as.formula('ftime+fstatus~x1+x2+x3'),df)
# Nicely output to report:
rm_mvsum(m1,data=df,showN = TRUE,vif=TRUE)
```

`ctDNA` *Tumour size change over time Longitudinal changes in tumour size since baseline for patients by changes in ctDNA status (clearance, decrease or increase) since baseline.*

Description

Tumour size change over time

Longitudinal changes in tumour size since baseline for patients by changes in ctDNA status (clearance, decrease or increase) since baseline.

Usage

```
data('ctDNA')
```

Format

A data frame with 270 rows and 5 variables:

id Patient ID

cohort Study Cohort

ctdna_status Change in ctDNA since baseline

time Number of weeks on treatment

size_change Percentage change in tumour measurement

Source

https://www.nature.com/articles/s43018-020-0096-5

`excelCol` *Retrieve columns number from spreadsheet columns specified as unquoted letters*

Description

Retrieve columns number from spreadsheet columns specified as unquoted letters

Usage

```
excelCol(...)
```

Arguments

`...`	unquoted excel column headers (i.e. excelCol(A,CG,AA)) separated by commas

Value

a numeric vector corresponding to columns in a spreadsheet

Examples

```
## Find the column numbers for excel columns AB, CE and BB
excelCol(AB,CE,bb)
## Get the columns between A and K and Z
excelCol(A-K,Z)
```

---

excelColLetters *Retrieve spreadsheet column letter-names from columns indices*

Description

Creates a vector of spreadsheet-style letter-names corresponding to column numbers

Usage

```
excelColLetters(columnIndices)
```

Arguments

columnIndices	vector of integer column indices

Details

This is the inverse function of excelCol

Value

a character vector corresponding to the spreadsheet column headings

Examples

```
## Find the column numbers for excel columns AB, CE and BB
colIndices <- excelCol(AB,CE,bb)
## Go back to the column names
excelColLetters(colIndices)
```

extract_grays_test *Extract Gray's test results from CIF fit*

Description

Extract Gray's test results from CIF fit

Usage

```
extract_grays_test(fit, plot.event = 1)
```

Arguments

fit	CIF fit object or dataframe with test attribute
plot.event	Events to test

extract_labels *Extract variable labels from labelled data frame*

Description

Extract variable labels from data and return a data frame with labels

Usage

```
extract_labels(data, sep = "_")
```

Arguments

data	the data frame to extract labels from
sep	character used to separate multiple labels, defaults to "_"

Details

All variable names will be returned, even those with no labels. If the label attribute has length greater than one the values will be concatenated and returned as a single string separated by sep

Examples

```
# Set a few variable labels for ctDNA
data("ctDNA")
ctDNA <- ctDNA |> set_var_labels(
   ctdna_status="detectable ctDNA",
  cohort="A cohort label")
# Extract labels
extract_labels(ctDNA)
```

`extract_package_details` *Extract Function and Package Information from Current Document*

Description

The function automatically detects the current R script file (works best in RStudio), parses the code to identify function calls, determines which packages they belong to, and creates a summary of all non-base R packages used in the script. It handles both namespace-qualified function calls (e.g., `dplyr::filter`) and regular function calls, while filtering out base R functions and control structures.

Usage

```
extract_package_details(ignore_comments = TRUE)
```

Arguments

`ignore_comments`
: Logical. If TRUE (default), ignores function calls within commented code (both R comments starting with # and HTML/XML comments). If FALSE, extracts functions from all code including commented sections.

Details

This function analyses the current file (an R script, Rmd or qmd file) to extract information about all functions called within the code, identifies their associated packages, and returns a summary of packages used with version and citation information.

Value

A data frame with the following columns:

package_name Character. Name of the package

functions_called Character. Comma-separated list of functions called from this package

package_version Character. Version number of the installed package

package_citation Character. Formatted citation for the package

Note

- Works best when run from RStudio with an active source file
- Requires that referenced packages are already loaded/installed
- Will not detect functions called through indirect methods (e.g., `do.call()`)

See Also

`getAnywhere`, `packageVersion`, `citation`

Examples

```
## Not run:
# Run this function from within an R script to analyze its dependencies
package_info <- extract_package_details()

# Include functions from commented code
package_info_all <- extract_package_details(ignore_comments = FALSE)
print(package_info)

## End(Not run)
```

`fit_cif_model` *Fit Competing Risks Model*

Description

Fit Competing Risks Model

Usage

```
fit_cif_model(data, response, cov = NULL)
```

Arguments

`data`	Input dataframe
`response`	Character vector with time and status column names
`cov`	Covariate column name (optional)

Value

List containing fit object and group separator

`fit_km_model` *Fit Kaplan-Meier survival curves*

Description

Fit Kaplan-Meier survival curves

Usage

```
fit_km_model(data, response, cov = NULL, conf.type = "log")
```

Arguments

data	Input data
response	Time and status variables
cov	Covariate (optional)
conf.type	Confidence interval type

`forestplot2` *Create a forest plot using ggplot2 (DEPRECATED)*

Description

#' @description **Deprecated**: Please use `forestplotMV()` instead.

Usage

```
forestplot2(
  model,
  conf.level = 0.95,
  orderByRisk = TRUE,
  colours = "default",
  showEst = TRUE,
  rmRef = FALSE,
  logScale = getOption("reportRmd.logScale", TRUE),
  nxTicks = 5
)
```

Arguments

model	an object output from the glm or geeglm function, must be from a logistic regression
conf.level	controls the width of the confidence interval
orderByRisk	logical, should the plot be ordered by risk
colours	can specify colours for risks less than, 1 and greater than 1.0. Default is red, black, green
showEst	logical, should the risks be displayed on the plot in text
rmRef	logical, should the reference levels be removed for the plot?
logScale	logical, should OR/RR be shown on log scale, defaults to TRUE, or reportRmd.logScale if set. See https://doi.org/10.1093/aje/kwr156 for why you may prefer a linear scale.
nxTicks	Number of tick marks supplied to the log_breaks function to produce

Details

[Deprecated]

This function will be removed in a future version.

This function will accept a log or logistic regression fit from glm or geeglm, and display the OR or RR for each variable on the appropriate log scale.

Value

a plot object

`forestplotMV` *Create a multivariable forest plot using ggplot2*

Description

This function creates forest plots from fitted regression models, with optional inclusion of unadjusted estimates. It uses m_summary for robust data extraction and properly handles factor level ordering and reference levels.

Usage

```
forestplotMV(
  model,
  data = NULL,
  include_unadjusted = FALSE,
  conf.level = 0.95,
  colours = "default",
  showEst = TRUE,
  showRef = TRUE,
  digits = getOption("reportRmd.digits", 2),
  logScale = getOption("reportRmd.logScale", TRUE),
  nxTicks = 5,
  showN = TRUE,
  showEvent = TRUE,
  xlim = NULL
)
```

Arguments

`model`	an object output from the glm or geeglm function, must be from a logistic or log-link regression
`data`	dataframe containing your data (required if include_unadjusted = TRUE)
`include_unadjusted`	logical, should unadjusted estimates be included? Default is FALSE
`conf.level`	controls the width of the confidence interval (default 0.95)

colours	can specify colours for risks less than, equal to, and greater than 1.0. Default is green, black, red
showEst	logical, should the risks be displayed on the plot in text? Default is TRUE
showRef	logical, should reference levels be shown? Default is TRUE
digits	number of digits to use displaying estimates (default 2)
logScale	logical, should OR/RR be shown on log scale? Defaults to TRUE. See https://doi.org/10.1093/aje/kwr156 for why you may prefer a linear scale
nxTicks	Number of tick marks for x-axis (default 5)
showN	Show number of observations per variable and category (default TRUE)
showEvent	Show number of events per variable and category (default TRUE)
xlim	Numeric vector of length 2 specifying x-axis limits (ex c(0.2, 5))

Value

a ggplot object

Examples

```
data("pembrolizumab")
glm_fit <- glm(orr ~ change_ctdna_group + sex + age + l_size,
               data = pembrolizumab, family = 'binomial')

# Adjusted only
forestplotMV(glm_fit, data = pembrolizumab)

# Both adjusted and unadjusted
forestplotMV(glm_fit, data = pembrolizumab, include_unadjusted = TRUE)
```

---

forestplotUV *Create a univariable forest plot using ggplot2*

Description

This function creates forest plots from univariable regression models. For new code, consider using forestplotMV() which can handle both adjusted and unadjusted estimates.

Usage

```
forestplotUV(
  response,
  covs,
  data,
  model = "glm",
  id = NULL,
  corstr = NULL,
  family = NULL,
```

```
  digits = getOption("reportRmd.digits", 2),
  conf.level = 0.95,
  colours = "default",
  showEst = TRUE,
  showRef = TRUE,
  logScale = getOption("reportRmd.logScale", TRUE),
  nxTicks = 5,
  showN = TRUE,
  showEvent = TRUE,
  xlim = NULL
)
```

Arguments

response	character vector with names of columns to use for response
covs	character vector with names of columns to use for covariates
data	dataframe containing your data
model	fitted model object (default "glm")
id	character vector which identifies clusters. Only used for geeglm
corstr	character string specifying the correlation structure. Only used for geeglm
family	description of the error distribution and link function to be used in the model
digits	number of digits to round to (default 2)
conf.level	controls the width of the confidence interval (default 0.95)
colours	can specify colours for risks less than, equal to, and greater than 1.0. Default is green, black, red
showEst	logical, should the risks be displayed on the plot in text? Default is TRUE
showRef	logical, should reference levels be shown? Default is TRUE
logScale	logical, should OR/RR be shown on log scale? Defaults to TRUE
nxTicks	Number of tick marks for x-axis (default 5)
showN	Show number of observations per variable and category (default TRUE)
showEvent	Show number of events per variable and category (default TRUE)
xlim	numeric vector of length 2 specifying x-axis limits (ex c(0.2, 5)) Confidence intervals extending beyond these limits will be shown with arrows.

Value

a ggplot object

Examples

```
data("pembrolizumab")
forestplotUV(response = "orr",
             covs = c("change_ctdna_group", "sex", "age", "l_size"),
             data = pembrolizumab, family = 'binomial')
```

forestplotUVMV *Combine univariable and multivariable forest plot (DEPRECATED)*

Description

This function is deprecated. Please use forestplotMV() with include_unadjusted = TRUE instead.

Usage

```
forestplotUVMV(UVmodel, MVmodel, ...)
```

Arguments

UVmodel	an UV model object output from the forestplotUV function
MVmodel	a MV model object output from the forestplotMV function
...	additional arguments (ignored)

geoR_boxcoxfit *Parameter Estimation for the Box-Cox Transformation*

Description

This function is copied from the geoR package which has been removed from the CRAN repository.

Usage

```
geoR_boxcoxfit(object, xmat, lambda, lambda2 = NULL, add.to.data = 0)
```

Arguments

object	a vector with the data
xmat	a matrix with covariates values. Defaults to rep(1, length(y)).
lambda	numerical value(s) for the transformation parameter lambda. Used as the initial value in the function for parameter estimation. If not provided default values are assumed. If multiple values are passed the one with highest likelihood is used as initial value.
lambda2	ogical or numerical value(s) of the additional transformation (see DETAILS below). Defaults to NULL. If TRUE this parameter is also estimated and the initial value is set to the absolute value of the minimum data. A numerical value is provided it is used as the initial value. Multiple values are allowed as for lambda.
add.to.data	a constant value to be added to the data.

Details

For more information see: https://cran.r-project.org/web/packages/geoR/index.html

ggkmcif2 *Plot KM and CIF curves with ggplot*

Description

This function will plot a KM or CIF curve with option to add the number at risk. You can specify if you want confidence bands, the hazard ratio, and pvalues, as well as the units of time used.

Usage

```
ggkmcif2(
  response,
  cov = NULL,
  data,
  pval = TRUE,
  conf.curves = FALSE,
  table = TRUE,
  xlab = "Time",
  ylab = NULL,
  col = NULL,
  times = NULL,
  type = NULL,
  plot.event = 1,
  returns = FALSE,
  ...
)
```

Arguments

response	Character vector with time and status column names
cov	Covariate column name (optional)
data	Input dataframe
pval	Whether to show p-values
conf.curves	Whether to show confidence bands
table	Whether to include risk table
xlab	X-axis label
ylab	Y-axis label
col	colours vector
times	Numeric vector of times for the x-axis
type	Plot type ("KM" or "CIF", auto-detected if NULL)
plot.event	Events to plot
returns	Whether to return list with plot and at risk table
...	Additional arguments see see ggkmcif2Parameters

Details

Note that for proper pdf output of special characters the following code needs to be included in the first chunk of the rmd knitr::opts_chunk$set(dev="cairo_pdf")

`ggkmcif2Parameters` *Additional parameters passed to ggkmcif2*

Description

This section documents the additional parameters for ggkmcif2.

Usage

```
ggkmcif2Parameters(
  HR = FALSE,
  HR_pval = FALSE,
  conf.type = "log",
  main = NULL,
  stratalabs = NULL,
  strataname,
  stratalabs.table = NULL,
  strataname.table = strataname,
  median.text = FALSE,
  median.lines = FALSE,
  median.CI = FALSE,
  set.time.text = NULL,
  set.time.line = FALSE,
  set.time = 5,
  set.time.CI = FALSE,
  censor.marks = TRUE,
  censor.size = 2,
  censor.stroke = 1.5,
  censor.symbol = "|",
  fsize,
  nsize = 3,
  lsize = 0.7,
  psize = 3.5,
  median.size = 3,
  median.pos = NULL,
  median.lsize = 1,
  set.size = 3,
  set.pos = NULL,
  set.lsize = 1,
  ylim = c(0, 1),
  linetype = NULL,
  xlim = NULL,
```

```
  legend.pos,
  legend.title = strataname,
  pval.pos = NULL,
  event = c("col", "linetype"),
  flip.CIF = FALSE,
  cut = NULL,
  eventlabs = NULL,
  event.name = NULL,
  Numbers_at_risk_text = "At risk",
  tbl.height = NULL,
  HR.digits = 2,
  HR.pval.digits = 3,
  pval.digits = 3,
  median.digits = 3,
  set.time.digits = 3,
  print.n.missing = TRUE,
  returns = FALSE
)
```

Arguments

HR	boolean to specify if you want hazard ratios included in the plot
HR_pval	boolean to specify if you want HR p-values in the plot
conf.type	One of "none"(the default), "plain", "log" , "log-log" or "logit". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve +- k *se(curve), where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)).
main	String corresponding to main title. When NULL uses Kaplan-Meier Plot s, and "Cumulative Incidence Plot for CIF"
stratalabs	string corresponding to the labels of the covariate, when NULL will use the levels of the covariate
strataname	String of the covariate name default is nicename(cov)
stratalabs.table	String corresponding to the levels of the covariate for the number at risk table, when NULL will use the levels of the covariate. Can use a string of "-" when the labels are long
strataname.table	String of the covariate name for the number at risk table default is nicename(cov
median.text	boolean to specify if you want the median values added to the legend (or as added text if there are no covariates), for KM only
median.lines	boolean to specify if you want the median values added as lines to the plot, for KM only
median.CI	boolean to specify if you want the 95\ with the median text (Only for KM)

set.time.text	string for the text to add survival at a specified time (eg. year OS)
set.time.line	boolean to specify if you want the survival added as lines to the plot at a specified point
set.time	Numeric values of the specific time of interest, default is 5 (Multiple values can be entered)
set.time.CI	boolean to specify if you want the 95\ interval with the set time text
censor.marks	logical value. If TRUE, includes censor marks (only for KM curves)
censor.size	size of censor marks, default is 3
censor.stroke	stroke of censor marks, default is 1.5
censor.symbol	either a character or a number 0-24 specifying the ggplot shape to be used as the censor symbol
fsize	font size
nsize	font size for numbers in the numbers at risk table
lsize	line size
psize	size of the pvalue
median.size	size of the median text (Only when there are no covariates)
median.pos	vector of length 2 corresponding to the median position (Only when there are no covariates)
median.lsize	line size of the median lines
set.size	size of the survival at a set time text (Only when there are no covariates)
set.pos	vector of length 2 corresponding to the survival at a set point position (Only when there are no covariates)
set.lsize	line size of the survival at set points
ylim	vector of length 2 corresponding to limits of y-axis. Default to NULL
linetype	vector of line types; default is solid for all lines
xlim	vector of length 2 corresponding to limits of x-axis. Default to NULL
legend.pos	A string corresponding to the legend position ("left","top", "right", "bottom", "none") or a numeric vector specifying the internal coordinates of the plot ie c(0.5,.0.5) for the centre of the plot.
legend.title	a string for the title of the legend, defaults to strataname
pval.pos	vector of length 2 corresponding to the p-value position
event	String specifying if the event should be mapped to the colour, or linetype when plotting both events to colour = "col", line type
flip.CIF	boolean to flip the CIF curve to start at 1
cut	numeric value indicating where to divide a continuous covariate (default is the median)
eventlabs	String corresponding to the event type names
event.name	String corresponding to the label of the event types

Numbers_at_risk_text	String for the label of the number at risk, set Numbers_at_risk_text=NULL to remove
tbl.height	Height of the at risk table, relative to plot. To set the table to half the height of the plot use tbl.height = 0.5
HR.digits	Number of digits printed of the hazard ratio
HR.pval.digits	Number of digits printed of the hazard ratio pvalue
pval.digits	Number of digits printed of the Gray's/log rank pvalue
median.digits	Number of digits printed of the median pvalue
set.time.digits	Number of digits printed of the probability at a specified time
print.n.missing	Logical, should the number of missing be shown !Needs to be checked
returns	Logical, if TRUE a list contain the plot and at risk table is returned

---

ggkmcif_paste *combine components of a call to ggkmci*

Description

[Deprecated]

`ggkmcif()` was deprecated in version 0.1.2 and will be removed in a future version.

Usage

```
ggkmcif_paste(list_gg)
```

Arguments

list_gg	A list of ggplot objects from `ggkmcif()`. (Deprecated) Please use `ggkmcif2()` instead.

---

hbld *Bold strings for HTML output*

Description

Wraps strings in HTML bold formatting using inline CSS.

Usage

```
hbld(strings)
```

Arguments

strings	Vector of strings to bold

Value

Vector of strings wrapped in HTML bold span

---

lpvalue2 *Format p-values for plot annotations*

Description

Formats p-values specifically for display in plots (e.g., survival curves). Returns formatted string with "p = " or "p < " prefix.

Usage

```
lpvalue2(x, digits)
```

Arguments

x	Numeric p-value
digits	Number of decimal places to display (default from context)

Details

Formatting rules:

- p < 10^-digits: returns "p < threshold" (e.g., "p < 0.001")
- p >= threshold: returns "p = value" rounded to specified digits

Used by: ggkmcif2() for survival curve annotations in main.R and ggkmcif3.R

Value

Character string with "p = " or "p < " prefix

Examples

```
## Not run:
lpvalue2(0.0001, 3)  # Returns: "p < 0.001"
lpvalue2(0.0456, 3)  # Returns: "p = 0.046"

## End(Not run)
```

mvsum *Get multivariate summary dataframe*

Description

Returns a dataframe with the model summary and global p-value for multi-level variables.

Usage

```
mvsum(
  model,
  data,
  digits = getOption("reportRmd.digits", 2),
  showN = TRUE,
  showEvent = TRUE,
  markup = TRUE,
  sanitize = TRUE,
  nicenames = TRUE,
  CIwidth = 0.95,
  vif = TRUE
)
```

Arguments

model	fitted model object
data	dataframe containing data
digits	number of digits to round to
showN	boolean indicating sample sizes should be shown for each comparison, can be useful for interactions
showEvent	boolean indicating if number of events should be shown. Only available for logistic.
markup	boolean indicating if you want latex markup
sanitize	boolean indicating if you want to sanitize all strings to not break LaTeX
nicenames	boolean indicating if you want to replace . and _ in strings with a space.
CIwidth	width for confidence intervals, defaults to 0.95
vif	boolean indicating if the variance inflation factor should be included. See details

Details

Global p-values are likelihood ratio tests for lm, glm and polr models. For lme models an attempt is made to re-fit the model using ML and if,successful LRT is used to obtain a global p-value. For coxph models the model is re-run without robust variances with and without each variable and a LRT is presented. If unsuccessful a Wald p-value is returned. For GEE and CRR models Wald global p-values are returned.

If the variance inflation factor is requested (VIF=TRUE) then a generalised VIF will be calculated in the same manner as the car package.

VIF for competing risk models is computed by fitting a linear model with a dependent variable comprised of the sum of the model independent variables and then calculating VIF from this linear model.

References

John Fox & Georges Monette (1992) Generalized Collinearity Diagnostics, Journal of the American Statistical Association, 87:417, 178-183, DOI: 10.1080/01621459.1992.10475190

John Fox and Sanford Weisberg (2019). An R Companion to Applied Regression, Third Edition. Thousand Oaks CA: Sage.

`nestTable` *Combine two table columns into a single column with levels of one nested within levels of the other.*

Description

This function accepts a data frame (via the data argument) and combines two columns into a single column with values from the head_col serving as headers and values of the to_col displayed underneath each header. The resulting table is then passed to outTable for printing and output, to use the grouped table as a data frame specify tableOnly=TRUE. By default the headers will be bolded and the remaining values indented.

Usage

```
nestTable(
  data,
  head_col,
  to_col,
  colHeader = "",
  caption = NULL,
  indent = TRUE,
  boldheaders = TRUE,
  hdr_prefix = "",
  hdr_suffix = "",
  digits = getOption("reportRmd.digits", 2),
  tableOnly = FALSE,
  fontsize
)
```

Arguments

`data`	dataframe
`head_col`	character value specifying the column name with the headers

to_col	character value specifying the column name to add the headers into
colHeader	character with the desired name of the first column. The default is to leave this empty for output or, for table only output to use the column name 'col1'.
caption	table caption
indent	Boolean should the original values in the to_col be indented
boldheaders	Boolean should the header column values be bolded
hdr_prefix	character value that will prefix headers
hdr_suffix	character value that will suffix headers
digits	number of digits to round numeric columns to, wither a single number or a vector corresponding to the number of numeric columns
tableOnly	boolean indicating if the table should be formatted for printing or returned as a data frame
fontsize	PDF/HTML output only, manually set the table fontsize

Details

Note that it is possible to combine multiple tables (more than two) with this function.

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

Examples

```
## Investigate models to predict baseline ctDNA and tumour size and display together
## (not clinically useful!)
data(pembrolizumab)
fit1 <- lm(baseline_ctdna~age+l_size+pdl1,data=pembrolizumab)
m1 <- rm_mvsum(fit1,tableOnly=TRUE)
m1$Response = 'ctDNA'
fit2 <- lm(l_size~age+baseline_ctdna+pdl1,data=pembrolizumab)
m2 <- rm_mvsum(fit2,tableOnly=TRUE)
m2$Response = 'Tumour Size'
nestTable(rbind(m1,m2),head_col='Response',to_col='Covariate')
```

---

outTable *Print tables to PDF/Latex HTML or Word*

Description

Output the table nicely to whatever format is appropriate. This is the output function used by the rm_* printing functions.

Usage

```
outTable(
  tab,
  row.names = NULL,
  to_indent = numeric(0),
  bold_headers = TRUE,
  rows_bold = numeric(0),
  bold_cells = NULL,
  caption = NULL,
  digits = getOption("reportRmd.digits", 2),
  align,
  applyAttributes = TRUE,
  keep.rownames = FALSE,
  nicenames = TRUE,
  fontsize,
  chunk_label,
  format = NULL,
  header_above = NULL
)
```

Arguments

tab	a table to format
row.names	a string specifying the column name to assign to the rownames. If NULL (the default) then rownames are removed.
to_indent	numeric vector indicating which rows to indent in the first column.
bold_headers	boolean indicating if the column headers should be bolded
rows_bold	numeric vector indicating which rows to bold
bold_cells	array indices indicating which cells to bold. These will be in addition to rows bolded by rows_bold.
caption	table caption
digits	number of digits to round numeric columns to, either a single number or a vector corresponding to the number of numeric columns in tab
align	string specifying column alignment, defaults to left alignment of the first column and right alignment of all other columns. The align argument accepts a single string with 'l' for left, 'c' for centre and 'r' for right, with no separations. For example, to set the left column to be centred, the middle column right-aligned and the right column left aligned use: align='crl'
applyAttributes	boolean indicating if the function should use to_indent and bold_cells formatting attributes. This will only work properly if the dimensions of the table output from rm_covsum, rm_uvsum etc haven't changed.
keep.rownames	should the row names be included in the output
nicenames	boolean indicating if you want to replace . and _ in strings with a space
fontsize	PDF/HTML output only, manually set the table fontsize

chunk_label	only used knitting to Word docs to allow cross-referencing
format	if specified ('html','latex') will override the global pandoc setting
header_above	a named numeric vector specifying an extra header row above the column names, where the names are the labels and the values are the number of columns each label should span. For example, `c(" " = 1, "Group A" = 2, "Group B" = 2)` will leave the first column blank, then span "Group A" over the next 2 columns, and "Group B" over the following 2. For HTML and PDF output the header is rendered as a true spanning row via kableExtra. For Word output the labels are prepended as the first data row of the table (pandoc markdown does not support cell merging).

Details

Entire rows can be bolded, or specific cells. Currently indentation refers to the first column only. By default, underscores in column names are converted to spaces. To disable this set nicenames to FALSE

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

---

pembrolizumab *Survival data Survival status and ctDNA levels for patients receiving pembrolizumab*

Description

Survival data

Survival status and ctDNA levels for patients receiving pembrolizumab

Usage

```
data('pembrolizumab')
```

Format

A data frame with 94 rows and 15 variables:

id Patient ID

age Age at study entry

sex Patient Sex

cohort Study Cohort

l_size Target lesion size at baseline

pdl1 PD L1 percent

tmb log of TMB

baseline_ctdna Baseline ctDNA

change_ctdna_group Did ctDNA increase or decrease from baseline to cycle 3

orr Objective Response

cbr Clinical Beneficial Response

os_status Overall survival status

os_time Overall survival time in months

pfs_status Progression free survival status

pfs_time Progression free survival time in months

Source

https://www.nature.com/articles/s43018-020-0096-5

`plotuv` *Plot multiple bivariate relationships in a single plot*

Description

This function is designed to accompany `rm_uvsum` as a means of visualising the results, and uses similar syntax.

Usage

```
plotuv(
  response,
  covs,
  data,
  showN = FALSE,
  showPoints = TRUE,
  na.rm = TRUE,
  response_title = NULL,
  return_plotlist = FALSE,
  ncol = 2,
  p_margins = c(0, 0.2, 1, 0.2),
  bpThreshold = 20,
  mixed = TRUE,
  violin = FALSE,
  position = c("dodge", "stack", "fill"),
  use_labels = TRUE
)
```

Arguments

response	character vector with names of columns to use for response
covs	character vector with names of columns to use for covariates
data	dataframe containing your data
showN	boolean indicating whether sample sizes should be shown on the plots
showPoints	boolean indicating whether individual data points should be shown when n>20 in a category
na.rm	boolean indicating whether na values should be shown or removed
response_title	character value with title of the plot
return_plotlist	boolean indicating that the list of plots should be returned instead of a plot, useful for applying changes to the plot, see details
ncol	the number of columns of plots to be display in the ggarrange call, defaults to 2
p_margins	sets the TRBL margins of the individual plots, defaults to c(0,0.2,1,.2)
bpThreshold	Default is 20, if there are fewer than 20 observations in a category then dotplots, as opposed to boxplots are shown.
mixed	should a mix of dotplots and boxplots be shown based on sample size? If false then all categories will be shown as either dotplots, or boxplots according the bpThreshold and the smallest category size
violin	Show violin plots instead of boxplots. This will override bpThreshold and mixed.
position	for categorical variables how should barplots be presented. Default is "dodge" IF stack is TRUE then n will not be shown.
use_labels	boolean, default is true if the variables have label attributes this will be shown in the plot instead of the variable names, or if there are no labels then tidy versions of the variable names will be used. If use_labels=FALSE the variable names will be used.

Details

Plots are displayed as follows: If response is continuous For a numeric predictor scatterplot For a categorical predictor: If 20+ observations available boxplot, otherwise dotplot with median line If response is a factor For a numeric predictor: If 20+ observations available boxplot, otherwise dotplot with median line For a categorical predictor barplot Response variables are shown on the ordinate (y-axis) and covariates on the abscissa (x-axis)

Variable names are replaced by their labels if available, or by tidy versions if not. Set use_labels=FALSE to use the variable names.

Value

a list containing plots for each variable in covs

See Also

`ggplot2::ggplot` and `ggpubr::ggarrange` `replace_plot_labels`

Examples

```
## Run multiple univariate analyses on the pembrolizumab dataset to predict cbr and
## then visualise the relationships.
data("pembrolizumab")
rm_uvsum(data=pembrolizumab,
response='cbr',covs=c('age','sex','l_size','baseline_ctdna'))
plotuv(data=pembrolizumab,  response='cbr',
covs=c('age','sex','l_size','baseline_ctdna'),showN=TRUE)
```

`predsum` *Summarise Performance of a Prediction Model*

Description

Standardised reporting of binary prediction model performance. Returns a data frame of metrics (point estimate + confidence interval) and optionally renders it via `reportRmd::outTable()`.

Usage

```
predsum(
  true,
  predicted,
  cutoff = NULL,
  positive = NULL,
  ci = c("clopper-pearson", "bootstrap"),
  ci_width = 0.95,
  ci_separate = FALSE,
  nboot = 2000,
  seed = 1,
  digits = 2,
  output = "epi",
  tableOnly = FALSE
)
```

Arguments

`true`	Vector of true class labels. Must be 0/1 or a two-level factor.
`predicted`	Vector of predicted values, either dichotomous (0/1) or numeric scores. If scores, `cutoff` must be supplied.
`cutoff`	Numeric cut-off applied as `predicted >= cutoff` to define the positive class. Required when `predicted` is non-binary and ignored (with a message) otherwise.
`positive`	The value of `true` treated as the positive class. Defaults to `1` when `true` is 0/1, or to the second level when `true` is a factor.
`ci`	Confidence interval method: `"clopper-pearson"` (default; Delong is used for AUC) or `"bootstrap"` (percentile).

ci_width	Nominal coverage, default 0.95.
ci_separate	logical. If FALSE (default) estimate and CI are combined in a single Value (95%CI) column. If TRUE, the output has four columns: Statistic, Estimate, lower, upper.
nboot	Number of bootstrap replicates, default 2000.
seed	integer seed set for the duration of the bootstrap so that confidence intervals are reproducible; the calling session's random state is restored afterwards. Defaults to 1. Set to NULL to leave the random state untouched, in which case intervals will vary between calls.
digits	Number of digits for rounding, default 2.
output	One of "epi" (default), "data-science", "all", or a character vector of statistic names. Recognised names (case-insensitive): prevalence, sensitivity, specificity, ppv, npv,accuracy, auc, aucpr, f1, brier, tp, fp, tn, fn, n, events, positive,cutoff. The aliases recall and precision are accepted and, when supplied, are reflected in the row labels. Preset names cannot be combined with individual statistics.
tableOnly	logical. If TRUE the data frame is returned silently; if FALSE (default) the data frame is rendered via reportRmd::outTable() and returned invisibly.

Details

Clopper-Pearson intervals are used for proportion-based metrics (prevalence, sensitivity, specificity, PPV, NPV, accuracy). AUC uses the Delong variance estimator on the logit scale. Brier score, F1 and AUC-PR have no closed-form interval and are obtained by percentile bootstrap; when ci = "clopper-pearson" this is done automatically and a message is emitted.

When predicted is dichotomous, AUC, AUC-PR, Brier and the cut-off row are omitted.

Value

A data frame of performance statistics.

References

Delong ER, Delong DM, Clarke-Pearson DL (1988). Comparing the areas under two or more correlated receiver operating characteristic curves: a nonparametric approach. *Biometrics* 44(3):837-845.

Clopper CJ, Pearson ES (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika* 26(4):404-413.

Examples

```
# Simulate true labels and model scores
set.seed(1)
n <- 300
true  <- rbinom(n, 1, 0.3)
score <- plogis(rnorm(n, mean = ifelse(true == 1, 0.9, -0.9)))

# Epidemiology-style summary from probability scores
```

```
predsum(true, score, cutoff = 0.5, tableOnly = TRUE)

# Data-science style (Recall, Precision, F1, Brier, AUC-PR)
predsum(true, score, cutoff = 0.5,
        output = "data-science", tableOnly = TRUE)

# Custom selection with separate CI columns
predsum(true, score, cutoff = 0.5,
        output = c("sensitivity", "specificity", "auc"),
        ci_separate = TRUE, tableOnly = TRUE)

# Dichotomous predictions: AUC, AUC-PR, Brier and cut-off are omitted
pred_class <- as.integer(score >= 0.5)
predsum(true, pred_class, tableOnly = TRUE)
```

`process_cif_medians` *Process CIF Median Values*

Description

Process CIF Median Values

Usage

```
process_cif_medians(
  fit,
  plot.event,
  stratalabs,
  median.lines = FALSE,
  median.text = FALSE,
  median.digits = 3,
  multiple_lines = FALSE
)
```

Arguments

`fit`	CIF fit object
`plot.event`	Events to plot
`stratalabs`	Strata labels
`median.lines`	Whether to calculate for median lines
`median.text`	Whether to add median text
`median.digits`	Number of digits for median
`multiple_lines`	Whether there are multiple strata

Value

List with updated stratalabs and median values

process_cif_timepoints *Process CIF Time-Specific Estimates*

Description

Process CIF Time-Specific Estimates

Usage

```
process_cif_timepoints(
  fit,
  plot.event,
  stratalabs,
  set.time.text = NULL,
  set.time = NULL,
  set.time.line = FALSE,
  set.time.CI = FALSE,
  set.time.digits = 3,
  multiple_lines = FALSE
)
```

Arguments

fit	CIF fit object
plot.event	Events to plot
stratalabs	Strata labels
set.time.text	Text label for time points
set.time	Time points to evaluate
set.time.line	Whether to add lines
set.time.CI	Whether to include confidence intervals
set.time.digits	Number of digits
multiple_lines	Whether there are multiple strata

Value

List with updated stratalabs and time-specific estimates

process_covariate *Process covariate variable (factor conversion, numeric cutoffs)*

Description

Process covariate variable (factor conversion, numeric cutoffs)

Usage

```
process_covariate(data, cov, cut = NULL, stratalabs = NULL)
```

Arguments

data	Input data
cov	Covariate column name
cut	Numeric cutoff for continuous variables
stratalabs	Custom strata labels

replace_plot_labels *Replace variable names with labels in ggplot*

Description

If the data stored in a ggplot object has variable labels then this will replace the variable names with the variable labels. If no labels are set then the variable names will be tidied and a nicer version used.

Usage

```
replace_plot_labels(plot)
```

Arguments

plot	output from a call to ggplot2

See Also

set_var_labels() for setting individual variable labels, set_labels() for setting variable labels using a data frame, extract_labels() for creating a data frame of all variable labels, clear_labels() for removing variable labels

Examples

```
## Not run:
data("pembrolizumab")
p <- ggplot(pembrolizumab,aes(x=change_ctdna_group,y=baseline_ctdna)) +
geom_boxplot()
replace_plot_labels(p)
pembrolizumab <- set_var_labels(pembrolizumab,
change_ctdna_group="Change in ctDNA group")
p <- ggplot(pembrolizumab,aes(x=change_ctdna_group,y=baseline_ctdna)) +
geom_boxplot()
replace_plot_labels(p)
# Can also be used with a pipe, but expression needs to be wrapped in a brace
(ggplot(pembrolizumab,aes(x=change_ctdna_group,y=baseline_ctdna)) +
geom_boxplot()) |> replace_plot_labels()

## End(Not run)
```

---

rm_cifsum *Summarize cumulative incidence by group*

Description

Displays event counts and event rates at specified time points for the entire cohort and by group. Gray's test of differences in cumulative incidence is displayed.

Usage

```
rm_cifsum(
  data,
  time,
  status,
  group = NULL,
  eventcode = 1,
  cencode = 0,
  eventtimes,
  eventtimeunit,
  eventtimeLbls = NULL,
  CIwidth = 0.95,
  unformattedp = FALSE,
  na.action = "na.omit",
  showCounts = TRUE,
  showGraystest = TRUE,
  digits = 2,
  caption = NULL,
  tableOnly = FALSE,
  nocensored = FALSE
)
```

Arguments

data	data frame containing survival data
time	string indicating survival time variable
status	string indicating the event status variable. The status variable may be numeric, character, or factor and must identify the event of interest and at least one competing event. Censoring and the event of interest are specified using cencode and eventcode.
group	string or character vector indicating the variable(s) to group observations by. If this is left as NULL (the default), summaries are provided for the entire cohort.
eventcode	value of the status variable indicating the event of interest. May be numeric, character, or factor-compatible. Default is 1.
cencode	value of the status variable indicating censoring. May be numeric, character, or factor-compatible. Default is 0.
eventtimes	numeric vector specifying when event probabilities should be calculated
eventtimeunit	unit of time to suffix to the time column label if event probabilities are requested, should be plural
eventtimeLbls	if supplied, a vector the same length as eventtimes with descriptions (useful for displaying years with data provided in months)
CIwidth	width of the event probabilities, default is 95%
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Should be used in conjunction with the digits argument.
na.action	default is to omit missing values, but can be set to throw and error using na.action='na.fail'
showCounts	boolean indicating if the event and total counts should be displayed; default is TRUE
showGraystest	boolean indicating Gray's test should be included in the final table, default is TRUE
digits	the number of digits to report in the event probabilities, default is 2.
caption	table caption for markdown output
tableOnly	should a dataframe or a formatted object be returned
nocensored	boolean indicating that the dataset genuinely contains no censored observations. If the value specified by cencode is not observed, the function will stop unless nocensored = TRUE; this provides protection against an incorrectly specified censoring value. Default is FALSE.

Value

A character vector of the event table source code, unless tableOnly=TRUE in which case a data frame is returned

Examples

```
library(survival)
data(pbc)

# Event probabilities at various time points with replacement time labels
rm_cifsum(data=pbc,time='time',status='status',
eventtimes=c(1825,3650),eventtimeLbls=c(5,10),eventtimeunit='yr')

# Event probabilities by one group
rm_cifsum(data=pbc,time='time',status='status',group='trt',
eventtimes=c(1825,3650),eventtimeunit='day')


# Event probabilities by multiple groups
rm_cifsum(data=pbc,time='time',status='status',group=c('trt','sex'),
eventtimes=c(1825,3650),eventtimeunit='day')

#'
# Character event status
pbc$status_chr <- factor(pbc$status, levels = c(0, 1, 2),
  labels = c("Censored", "Transplant", "Death"))

rm_cifsum(data = pbc, time = "time", status = "status_chr", group = "trt",
  eventcode = "Death", cencode = "Censored", eventtimes = c(1825, 3650),
  eventtimeLbls = c(5, 10), eventtimeunit = "yr")
```

---

rm_compactsum *Output a compact summary table*

Description

Outputs a table formatted for pdf, word or html output with summary statistics

Usage

```
rm_compactsum(
  data,
  xvars,
  grp,
  use_mean,
  caption = NULL,
  tableOnly = FALSE,
  covTitle = "",
  digits = 1,
  digits.cat = 0,
  nicenames = TRUE,
  iqr = TRUE,
  all.stats = FALSE,
```

```
  pvalue = TRUE,
  effSize = FALSE,
  p.adjust = "none",
  unformattedp = FALSE,
  show.sumstats = FALSE,
  show.tests = FALSE,
  full = TRUE,
  percentage = "col",
  B = 1000,
  seed = 1
)
```

Arguments

data	dataframe containing data
xvars	character vector with the names of covariates to include in table
grp	character with the name of the grouping variable
use_mean	logical indicating whether mean and standard deviation will be returned for continuous variables instead of median. Otherwise, can specify for individual variables using a character vector containing the names of covariates to return mean and sd for (if use_mean is not supplied, all covariates will have median summaries). See examples.
caption	character containing table caption (default is no caption)
tableOnly	logical, if TRUE then a dataframe is returned, otherwise a formatted printed object is returned (default is FALSE)
covTitle	character with the name of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name 'Covariate'
digits	numeric specifying the number of digits for summarizing mean data. Digits can be specified for individual variables using a named vector in the format digits=c("var1"=2,"var2"=3). If a variable is not in the vector the default will be used for it (default is 1). See examples
digits.cat	numeric specifying the number of digits for the proportions when summarizing categorical data (default is 0)
nicenames	logical indicating if you want to replace . and _ in strings . with a space
iqr	logical indicating if you want to display the interquartile range (Q1-Q3) as opposed to (min-max) in the summary for continuous variables
all.stats	logical indicating if all summary statistics (Q1, Q3 + min, max on a separate line) should be displayed. Overrides iqr
pvalue	logical indicating if you want p-values included in the table
effSize	logical indicating if you want effect sizes and their 95% confidence intervals included in the table. Effect sizes calculated include Cramer's V for categorical variables, and Cohen's d, Wilcoxon r, Epsilon-squared, or Omega-squared for numeric/continuous variables
p.adjust	p-adjustments to be performed

unformattedp	logical indicating if you would like the p-value to be returned unformatted (ie. not rounded or prefixed with '<'). Best used with tableOnly = T and outTable function. See examples
show.sumstats	logical indicating if the type of statistical summary (mean, median, etc) used should be shown.
show.tests	logical indicating if the type of statistical test and effect size (if effSize = TRUE) used should be shown in a column beside the p-values.
full	logical indicating if you want the full sample included in the table, ignored if grp is not specified
percentage	choice of how percentages are presented, either column (default) or row
B	number of replicates used when a Monte Carlo approximation to Fisher's exact test is required. Defaults to 1000.
seed	integer seed set for the duration of any Monte Carlo test so that p-values are reproducible; the calling session's random state is restored afterwards. Defaults to 1. Set to NULL to leave the random state untouched, in which case p-values will vary between calls.

Details

Comparisons for categorical variables default to chi-square tests, but if there are counts of <5 then the Fisher Exact test will be used. For grouping variables with two levels, either t-tests (mean) or wilcoxon tests (median) will be used for numerical variables. Otherwise, ANOVA (mean) or Kruskal- Wallis tests will be used. The statistical test used can be displayed by specifying show.tests = TRUE. Statistical tests and effect sizes for grp and/ or xvars with less than 2 counts in any level will not be shown.

Effect sizes are calculated as Cohen d for between group differences if the variable is summarised with the mean, otherwise Wilcoxon R if summarised with a median. Cramer's V is used for categorical variables, omega is used for differences in means among more than two groups and epsilon for differences in medians among more than two groups. Confidence intervals are calculated using bootstrapping.

tidyselect can only be used for xvars and grp arguments. Additional arguments (digits, use_mean) must be passed in using characters if variable names are used.

Value

A character vector of the table source code, unless tableOnly = TRUE in which case a data frame is returned. The output has the following attribute:

- "description", which describes what is included in the output table and the type of statistical summary for each covariate. When applicable, the types of statistical tests used will be included. If effSize = TRUE, the effect sizes for each covariate will also be mentioned.

References

Smithson, M. (2002). Noncentral Confidence Intervals for Standardized Effect Sizes. (07/140 ed., Vol. 140). SAGE Publications. doi:10.4135/9781412983761.n4

Steiger, J. H. (2004). Beyond the F Test: Effect Size Confidence Intervals and Tests of Close Fit in the Analysis of Variance and Contrast Analysis. Psychological Methods, 9(2), 164–182. doi:10.1037/1082989X.9.2.164

Kelley, T. L. (1935). An Unbiased Correlation Ratio Measure. Proceedings of the National Academy of Sciences - PNAS, 21(9), 554–559. doi:10.1073/pnas.21.9.554

Okada, K. (2013). Is Omega Squared Less Biased? A Comparison of Three Major Effect Size Indices in One-Way ANOVA. Behavior Research Methods, 40(2), 129-147.

Breslow, N. (1970). A generalized Kruskal-Wallis test for comparing K samples subject to unequal patterns of censorship. Biometrika, 57(3), 579-594.

FRITZ, C. O., MORRIS, P. E., & RICHLER, J. J. (2012). Effect Size Estimates: Current Use, Calculations, and Interpretation. Journal of Experimental Psychology. General, 141(1), 2–18. doi:10.1037/a0024338

Examples

```
data("pembrolizumab")
rm_compactsum(data = pembrolizumab, xvars = c("age",
"change_ctdna_group", "l_size", "pdl1"), grp = "sex", use_mean = "age",
digits = c("age" = 2, "l_size" = 3), digits.cat = 1, iqr = TRUE,
show.tests = TRUE)

# Other Examples (not run)
## Include the summary statistic in the variable column
#rm_compactsum(data = pembrolizumab, xvars = c("age",
#"change_ctdna_group"), grp = "sex", use_mean = "age", show.sumstats=TRUE)

## To show effect sizes
#rm_compactsum(data = pembrolizumab, xvars = c("age",
#"change_ctdna_group"), grp = "sex", use_mean = "age", digits = 2,
#effSize = TRUE, show.tests = TRUE)

## To return unformatted p-values
#rm_compactsum(data = pembrolizumab, xvars = c("l_size",
#"change_ctdna_group"), grp = "cohort", effSize = TRUE, unformattedp = TRUE)

## Using tidyselect
#pembrolizumab |> rm_compactsum(xvars = c(age, sex, pdl1), grp = cohort,
#effSize = TRUE)
```

`rm_covsum` *Add header row to table Outputs a descriptive covariate table*

Description

Returns a data frame corresponding to a descriptive table.

Usage

```
rm_covsum(
  data,
  covs = NULL,
  maincov = NULL,
  caption = NULL,
  tableOnly = FALSE,
  covTitle = "",
  digits = 1,
  digits.cat = 0,
  nicenames = TRUE,
  IQR = FALSE,
  all.stats = FALSE,
  pvalue = TRUE,
  effSize = FALSE,
  p.adjust = "none",
  unformattedp = FALSE,
  show.tests = FALSE,
  testcont = c("rank-sum test", "ANOVA"),
  testcat = c("Chi-squared", "Fisher"),
  full = TRUE,
  include_missing = FALSE,
  percentage = c("column", "row"),
  dropLevels = TRUE,
  excludeLevels = NULL,
  numobs = NULL,
  fontsize,
  chunk_label,
  xvars = NULL,
  grp = NULL,
  B = 1000,
  seed = 1
)
```

Arguments

data	dataframe containing data
covs	Covariate names to summarize. Accepts either a character vector (e.g., c("age", "sex")) or tidyselect bare names (e.g., c(age, sex)). Can also be specified using the xvars alias.
maincov	Grouping variable. Accepts either a character string (e.g., "sex") or a tidyselect bare name (e.g., sex). Can also be specified using the grp alias.
caption	character containing table caption (default is no caption)
tableOnly	Logical, if TRUE then a dataframe is returned, otherwise a formatted printed object is returned (default).
covTitle	character with the names of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name

	'Covariate'.
digits	number of digits for summarizing mean data
digits.cat	number of digits for the proportions when summarizing categorical data (default: 0)
nicenames	boolean indicating if you want to replace . and _ in strings with a space
IQR	boolean indicating if you want to display the inter quantile range (Q1,Q3) as opposed to (min,max) in the summary for continuous variables
all.stats	boolean indicating if all summary statistics (Q1,Q3 + min,max on a separate line) should be displayed. Overrides IQR.
pvalue	boolean indicating if you want p-values included in the table
effSize	boolean indicating if you want effect sizes included in the table. Can only be obtained if pvalue is also requested. Effect sizes calculated include Cramer's V for categorical variables, Cohen's d, Wilcoxon r, or Eta-squared for numeric/continuous variables.
p.adjust	p-adjustments to be performed. Uses the p.adjust function from base R
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Best used with tableOnly = T and outTable function. See examples.
show.tests	boolean indicating if the type of statistical test and effect size used should be shown in a column beside the pvalues. Ignored if pvalue=FALSE.
testcont	test of choice for continuous variables,one of *rank-sum* (default) or *ANOVA*
testcat	test of choice for categorical variables,one of *Chi-squared* (default) or *Fisher*
full	boolean indicating if you want the full sample included in the table, ignored if maincov is NULL
include_missing	Option to include NA values of maincov. NAs will not be included in statistical tests
percentage	choice of how percentages are presented, one of *column* (default) or *row*
dropLevels	logical, indicating if empty factor levels be dropped from the output, default is TRUE.
excludeLevels	a named list of covariate levels to exclude from statistical tests in the form list(varname =c('level1','level2')). These levels will be excluded from association tests, but not the table. This can be useful for levels where there is a logical skip (ie not missing, but not presented). Ignored if pvalue=FALSE.
numobs	named list overriding the number of people you expect to have the covariate
fontsize	PDF/HTML output only, manually set the table fontsize
chunk_label	only used if output is to Word to allow cross-referencing
xvars	Alias for covs. Supports tidyselect.
grp	Alias for maincov. Supports tidyselect.
B	number of replicates used when a Monte Carlo approximation to Fisher's exact test is required. Defaults to 1000.
seed	integer seed set for the duration of any Monte Carlo test so that p-values are reproducible; the calling session's random state is restored afterwards. Defaults to 1. Set to NULL to leave the random state untouched, in which case p-values will vary between calls.

Details

Comparisons for categorical variables default to chi-square tests, but if there are counts of <5 then the Fisher Exact test will be used and if this is unsuccessful then a second attempt will be made computing p-values using MC simulation. If testcont='ANOVA' then the t-test with unequal variance will be used for two groups and an ANOVA will be used for three or more. The statistical test used can be displayed by specifying show.tests=TRUE.

Effect size can be obtained when p-value is requested.

Further formatting options are available using tableOnly=TRUE and outputting the table with a call to outTable.

A newer version of this function is rm_compactsum which is more flexible and displays fewer rows of output.

Tidyselect can be used for `covs`, `maincov`, `xvars`, and `grp` arguments, allowing bare column names (e.g., `c(age, sex)`) in addition to character strings (e.g., `c("age", "sex")`).

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

References

Ellis, P.D. (2010) The essential guide to effect sizes: statistical power, meta-analysis, and the interpretation of research results. Cambridge: Cambridge University Press.doi:10.1017/CBO9780511761676

Lakens, D. (2013) Calculating and reporting effect sizes to facilitate cumulative science: a practical primer for t-tests and ANOVAs. Frontiers in Psychology, 4; 863:1-12. doi:10.3389/fpsyg.2013.00863

See Also

`covsum`,`fisher.test`, `chisq.test`, `wilcox.test`, `kruskal.test`, `anova`, and `outTable`

Examples

```
data("pembrolizumab")
rm_covsum(data=pembrolizumab, maincov = 'orr',
covs=c('age','sex','pdl1','tmb','l_size','change_ctdna_group'),
show.tests=TRUE)

# To Show Effect Sizes
rm_covsum(data=pembrolizumab, maincov = 'orr',
covs=c('age','sex'),
effSize=TRUE)

# To make custom changes or change the fontsize in PDF/HTML
tab <- rm_covsum(data=pembrolizumab,maincov = 'change_ctdna_group',
covs=c('age','sex','pdl1','tmb','l_size'),show.tests=TRUE,tableOnly = TRUE)
outTable(tab, fontsize=7)

# To return unformatted p-values
tab <- rm_covsum(data=pembrolizumab, maincov = 'orr',
```

```
covs=c('age','sex','pdl1','tmb','l_size','change_ctdna_group'),
show.tests=TRUE,unformattedp=TRUE,tableOnly=TRUE)
outTable(tab,digits=5)
outTable(tab,digits=5, applyAttributes=FALSE) # remove bold/indent
```

`rm_mvsum` *Format a regression model nicely for 'Rmarkdown'*

Description

Multivariable (or univariate) regression models are re-formatted for reporting and a global p-value is added for the evaluation of factor variables.

Usage

```
rm_mvsum(
  model,
  data,
  digits = getOption("reportRmd.digits", 2),
  covTitle = "",
  showN = TRUE,
  showEvent = TRUE,
  CIwidth = 0.95,
  vif = TRUE,
  whichp = c("levels", "global", "both"),
  caption = NULL,
  tableOnly = FALSE,
  p.adjust = "none",
  unformattedp = FALSE,
  nicenames = TRUE,
  include_unadjusted = FALSE,
  chunk_label,
  fontsize
)
```

Arguments

`model`	model fit
`data`	**[Deprecated]** data is no longer required as it is extracted from the model. This argument will be removed in the future
`digits`	number of digits to round estimates to, does not affect p-values
`covTitle`	character with the names of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name 'Covariate'.
`showN`	boolean indicating sample sizes should be shown for each comparison, can be useful for interactions

showEvent	boolean indicating if number of events should be shown. Only available for logistic.
CIwidth	width for confidence intervals, defaults to 0.95
vif	boolean indicating if the variance inflation factor should be included. See details
whichp	string indicating whether you want to display p-values for levels within categorical data ("levels"), global p values ("global"), or both ("both"). Irrelevant for continuous predictors.
caption	table caption
tableOnly	boolean indicating if unformatted table should be returned
p.adjust	p-adjustments to be performed. Uses the p.adjust function from base R
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Should be used in conjunction with the digits argument.
nicenames	boolean indicating if you want to replace . and _ in strings with a space
include_unadjusted	Logical. If TRUE, includes univariate estimates alongside multivariable estimates. Default is FALSE. The univariate models are fit on the same complete-case sample as the multivariable model, so that the two sets of estimates are directly comparable and the N column applies to both. Any p-value adjustment requested via p.adjust is applied to the multivariable p-values only. Covariates that appear only inside an interaction term are appended to the end of the table with an unadjusted estimate and no adjusted estimate.
chunk_label	Deprecated, previously used in Word to allow cross-referencing, this should now be done at the chunk level.
fontsize	PDF/HTML output only, manually set the table fontsize

Details

Global p-values are likelihood ratio tests for lm, glm and polr models. For lme models an attempt is made to re-fit the model using ML and if successful LRT is used to obtain a global p-value. For lmer models (lme4), if the lmerTest package is installed, Satterthwaite-based p-values and F-test global p-values are used; otherwise Wald z-based p-values and chi-squared LRT global p-values are returned. For glmer models (lme4), Wald z-based p-values are used with chi-squared LRT global p-values. Estimates are exponentiated for binomial (OR) and poisson/negative binomial (RR) families. For coxph models the model is re-run without robust variances with and without each variable and a LRT is presented. If unsuccessful a Wald p-value is returned. For GEE and CRR models Wald global p-values are returned. For negative binomial models a deviance test is used.

If the variance inflation factor is requested (VIF=TRUE, default) then a generalised VIF will be calculated in the same manner as the car package.

As of version 0.1.1 if global p-values are requested they will be included in the p-value column.

As of R 4.4.0 profile likelihood confidence intervals will be calculated automatically and there is no longer an option to force Wald tests.

The number of decimals places to display the statistics can be changed with digits, but this will not change the display of p-values. If more significant digits are required for p-values then use tableOnly=TRUE and format as desired.

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

References

John Fox & Georges Monette (1992) Generalized Collinearity Diagnostics, Journal of the American Statistical Association, 87:417, 178-183, doi:10.1080/01621459.1992.10475190

John Fox and Sanford Weisberg (2019). An R Companion to Applied Regression, Third Edition. Thousand Oaks CA: Sage.

Examples

```
data("pembrolizumab")
glm_fit = glm(change_ctdna_group~sex:age+baseline_ctdna+l_size,
data=pembrolizumab,family = 'binomial')
rm_mvsum(glm_fit)

#linear model with p-value adjustment
lm_fit=lm(baseline_ctdna~age+sex+l_size+tmb,data=pembrolizumab)
rm_mvsum(lm_fit,p.adjust = "bonferroni")
#Coxph
require(survival)
res.cox <- coxph(Surv(os_time, os_status) ~ sex+age+l_size+tmb, data = pembrolizumab)
rm_mvsum(res.cox, vif=TRUE)

# lmer (lme4 mixed effects model) - single random intercept

if (require(lme4)){
lmer_fit <- lme4::lmer(age ~ sex + pdl1 + (1|cohort), data = pembrolizumab)
rm_mvsum(lmer_fit)
}


# lmer with multiple random effects and global p-values

if (require(lme4) && require(geepack)){
data(dietox, package = "geepack")
dietox$Cu <- as.factor(dietox$Cu)
lmer_fit2 <- lme4::lmer(Weight ~ Cu + Time + (1|Pig) + (1|Litter), data = dietox)
rm_mvsum(lmer_fit2, whichp = "both")
}


# glmer (binomial mixed effects model) - odds ratios

if (require(lme4)){
data(cbpp, package = "lme4")
glmer_fit <- lme4::glmer(cbind(incidence, size - incidence) ~ period + (1|herd),
  data = cbpp, family = binomial)
rm_mvsum(glmer_fit)
```

```
}


# glmer.nb (negative binomial mixed effects model) - rate ratios

if (require(lme4) && require(geepack)){
data(dietox, package = "geepack")
dietox$Cu <- as.factor(dietox$Cu)
nb_fit <- lme4::glmer.nb(Weight ~ Cu + Time + (1|Pig), data = dietox)
rm_mvsum(nb_fit, whichp = "both")
}
```

`rm_survdiff` *Display event counts, expected event counts and logrank test of differences*

Description

This is a wrapper function around the survdiff function to display overall event rates and group-specific rates along with the log-rank test of a difference in survival between groups in a single table suitable for markdown output. Median survival times are included by default but can be removed setting median=FALSE

Usage

```
rm_survdiff(
  data,
  time,
  status,
  covs,
  strata,
  includeVarNames = FALSE,
  digits = 1,
  showCols = c("N", "Observed", "Expected"),
  CIwidth = 0.95,
  conf.type = "log",
  caption = NULL,
  tableOnly = FALSE,
  fontsize,
  unformattedp = FALSE
)
```

Arguments

`data`	data frame containing survival data
`time`	string indicating survival time variable
`status`	string indicating event status variable

covs	character vector indicating variables to group observations by
strata	string indicating the variable to stratify observations by
includeVarNames	boolean indicating if the variable names should be included in the output table, default is FALSE
digits	the number of digits in the survival rate
showCols	character vector indicating which of the optional columns to display, defaults to c('N','Observed','Expected')
CIwidth	width of the median survival estimates, default is 95%
conf.type	type of confidence interval see survival::survfit for details. Default is 'log'.
caption	table caption
tableOnly	should a dataframe or a formatted object be returned
fontsize	PDF/HTML output only, manually set the table fontsize
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Should be used in conjunction with the digits argument.

Value

A character vector of the survival table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also

survival::survdiff

Examples

```
#' # Differences between sex
data("pembrolizumab")
rm_survdiff(data=pembrolizumab,time='os_time',status='os_status',
covs='sex',digits=1)

# Differences between sex, stratified by cohort
rm_survdiff(data=pembrolizumab,time='os_time',status='os_status',
covs='sex',strata='cohort',digits=1)
# Differences between sex/cohort groups
rm_survdiff(data=pembrolizumab,time='os_time',status='os_status',
covs=c('sex','cohort'),digits=1)
```

rm_survsum *Summarise survival data by group*

Description

Displays event counts, median survival time and survival rates at specified times points for the entire cohort and by group. The logrank test of differences in survival curves is displayed.

Usage

```
rm_survsum(
  data,
  time,
  status,
  group = NULL,
  survtimes = NULL,
  survtimeunit = NULL,
  survtimesLbls = NULL,
  CIwidth = 0.95,
  unformattedp = FALSE,
  conf.type = "log",
  na.action = "na.omit",
  showCounts = TRUE,
  showLogrank = TRUE,
  eventProb = FALSE,
  digits = getOption("reportRmd.digits", 2),
  caption = NULL,
  tableOnly = FALSE,
  add.reverse.KM = FALSE,
  fontsize = NULL,
  cencode = 0,
  eventcode = 1,
  digits.reverse.KM = 1
)
```

Arguments

data	data frame containing survival data
time	string indicating survival time variable
status	string indicating the event status variable. The status variable may be numeric, character, or factor; censoring and event values can be specified using cencode and eventcode.
group	string or character vector indicating the variable(s) to group observations by. If this is left as NULL (the default) then summaries are provided for the entire cohort.
survtimes	numeric vector specifying when survival probabilities should be calculated.

survtimeunit	unit of time to suffix to the time column label if survival probabilities are requested, should be plural
survtimesLbls	if supplied, a vector the same length as survtimes with descriptions (useful for displaying years with data provided in months)
CIwidth	width of the survival probabilities, default is 95%
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Should be used in conjunction with the digits argument.
conf.type	type of confidence interval see survival::survfit for details. Default is 'log'.
na.action	default is to omit missing values, but can be set to throw and error using na.action='na.fail'
showCounts	boolean indicating if the at risk, events and censored columns should be output; default is TRUE
showLogrank	boolean indicating if the log-rank test statistic and p-value should be output; default is TRUE
eventProb	boolean indicating if event probabilities, rather than survival probabilities, should be displayed; default is FALSE
digits	the number of digits in the survival rate, default is 2, unless the reportRmd.digits option is set
caption	table caption for markdown output
tableOnly	should a dataframe or a formatted object be returned
add.reverse.KM	boolean indicating if median follow-up and its confidence interval should be estimated using the reverse Kaplan-Meier method and displayed in the table; default is FALSE.
fontsize	PDF/HTML output only, manually set the table fontsize
cencode	value of the status variable indicating censoring. May be numeric, character, or factor-compatible. Default is 0.
eventcode	value of the status variable indicating the event of interest. May be numeric, character, or factor-compatible. Default is 1.
digits.reverse.KM	number of digits used to display the median follow-up and confidence interval estimated using the reverse Kaplan-Meier method; default is 1.

Details

This summary table is supplied for simple group comparisons only. To examine differences in groups with stratification see rm_survdiff. To summarise differences in survival rates controlling for covariates see rm_survtime.

Value

A character vector of the survival table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also

survival::survfit

Examples

```
# Simple median survival table
data("pembrolizumab")
rm_survsum(data=pembrolizumab,time='os_time',status='os_status')

# Survival table with yearly survival rates
rm_survsum(data=pembrolizumab,time='os_time',status='os_status',
survtimes=c(12,24),survtimesLbls=1:2, survtimeunit='yr')

# Median survival by group
rm_survsum(data=pembrolizumab,time='os_time',status='os_status',group='sex')

# Survival Summary by cohort, displayed in years
rm_survsum(data=pembrolizumab,time='os_time',status='os_status',
group="cohort",survtimes=seq(12,72,12),
survtimesLbls=seq(1,6,1),
survtimeunit='years')

# Survival Summary by Sex and ctDNA group
rm_survsum(data=pembrolizumab,time='os_time',status='os_status',
group=c('sex','change_ctdna_group'),survtimes=c(12,24),survtimeunit='mo')


# Character event status and reverse Kaplan-Meier median follow-up
pembrolizumab$status_chr <- ifelse(pembrolizumab$os_status == 1, "Death",
  "Censored")
rm_survsum(data = pembrolizumab, time = "os_time", status = "status_chr",
  group = "sex", cencode = "Censored", eventcode = "Death",
  survtimes = c(12, 24), survtimeunit = "mo", add.reverse.KM = TRUE)
```

---

rm_survtime *Display survival rates and events for specified times*

Description

This is a wrapper for the survfit function to output a tidy display for reporting. Either Kaplan Meier or Cox Proportional Hazards models may be used to estimate the survival probabilities.

Usage

```
rm_survtime(
  data,
  time,
  status,
  covs = NULL,
```

```
  strata = NULL,
  type = "KM",
  survtimes,
  survtimeunit,
  strata.prefix = NULL,
  survtimesLbls = NULL,
  showCols = c("At Risk", "Events", "Censored"),
  CIwidth = 0.95,
  conf.type = "log",
  na.action = "na.omit",
  showCounts = TRUE,
  digits = getOption("reportRmd.digits", 2),
  caption = NULL,
  tableOnly = FALSE,
  fontsize
)
```

Arguments

data	data frame containing survival data
time	string indicating survival time variable
status	string indicating event status variable
covs	character vector with the names of variables to adjust for in coxph fit
strata	string indicating the variable to group observations by. If this is left as NULL (the default) then event counts and survival rates are provided for the entire cohort.
type	survival function, if no covs are specified defaults to Kaplan-Meier, otherwise the Cox PH model is fit. Use type='PH' to fit a Cox PH model with no covariates.
survtimes	numeric vector specifying when survival probabilities should be calculated.
survtimeunit	unit of time to suffix to the time column label if survival probabilities are requested, should be plural
strata.prefix	character value describing the grouping variable
survtimesLbls	if supplied, a vector the same length as survtimes with descriptions (useful for displaying years with data provided in months)
showCols	character vector specifying which of the optional columns to display, defaults to c('At Risk','Events','Censored')
CIwidth	width of the survival probabilities, default is 95%
conf.type	type of confidence interval see survival::survfit for details. Default is 'log'.
na.action	default is to omit missing values, but can be set to throw and error using na.action='na.fail'
showCounts	boolean indicating if the at risk, events and censored columns should be output, default is TRUE
digits	the number of digits in the survival rate, default is 2.
caption	table caption for markdown output
tableOnly	should a dataframe or a formatted object be returned
fontsize	PDF/HTML output only, manually set the table fontsize

Details

If covariates are supplied then a Cox proportional hazards model is fit for the entire cohort and each strata. Otherwise the default is for Kaplan-Meier estimates. Setting type = 'PH' will force a proportional hazards model.

Value

A character vector of the survival table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also

survival::survfit

Examples

```
# Kaplan-Mieir survival probabilities with time displayed in years
data("pembrolizumab")
rm_survtime(data=pembrolizumab,time='os_time',status='os_status',
strata="cohort",type='KM',survtimes=seq(12,72,12),
survtimesLbls=seq(1,6,1),
survtimeunit='years')

# Cox Proportional Hazards survivial probabilities
rm_survtime(data=pembrolizumab,time='os_time',status='os_status',
strata="cohort",type='PH',survtimes=seq(12,72,12),survtimeunit='months')

# Cox Proportional Hazards survivial probabilities controlling for age
rm_survtime(data=pembrolizumab,time='os_time',status='os_status',
covs='age',strata="cohort",survtimes=seq(12,72,12),survtimeunit='months')
```

---

rm_uvsum *Output several univariate models nicely in a single table*

Description

#'A table with the model parameters from running separate univariate models on each covariate. For factors with more than two levels a Global p-value is returned.

Usage

```
rm_uvsum(
  response,
  covs,
  data,
  digits = getOption("reportRmd.digits", 2),
  covTitle = "",
```

```
  caption = NULL,
  tableOnly = FALSE,
  removeInf = FALSE,
  p.adjust = "none",
  unformattedp = FALSE,
  whichp = c("levels", "global", "both"),
  chunk_label,
  gee = FALSE,
  id = NULL,
  corstr = NULL,
  family = NULL,
  type = NULL,
  offset = NULL,
  strata = 1,
  nicenames = TRUE,
  showN = TRUE,
  showEvent = TRUE,
  CIwidth = 0.95,
  reflevel = NULL,
  returnModels = FALSE,
  fontsize,
  forceWald = FALSE
)
```

Arguments

response	string vector with name of response
covs	character vector with the names of columns to fit univariate models to
data	dataframe containing data
digits	number of digits to round estimates and CI to. Does not affect p-values.
covTitle	character with the names of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name 'Covariate'.
caption	character containing table caption (default is no caption)
tableOnly	boolean indicating if unformatted table should be returned
removeInf	boolean indicating if infinite estimates should be removed from the table
p.adjust	p-adjustments to be performed. Uses the p.adjust function from base R
unformattedp	boolean indicating if you would like the p-value to be returned unformatted (ie not rounded or prefixed with '<'). Should be used in conjunction with the digits argument.
whichp	string indicating whether you want to display p-values for levels within categorical data ("levels"), global p values ("global"), or both ("both"). Irrelevant for continuous predictors.
chunk_label	only used if output is to Word to allow cross-referencing

gee	boolean indicating if gee models should be fit to account for correlated observations. If TRUE then the id argument must specify the column in the data which indicates the correlated clusters.
id	character naming the column that identifies clusters. Used for GEE models (gee = TRUE) and, for coxph models, to compute robust (sandwich) variances clustered on this variable
corstr	character string specifying the correlation structure. Only used for geeglm. The following are permitted: '"independence"', '"exchangeable"', '"ar1"', '"unstructured"' and '"userdefined"'
family	description of the error distribution and link function to be used in the model. Only used for geeglm
type	string indicating the type of univariate model to fit. The function will try and guess what type you want based on your response. If you want to override this you can manually specify the type. Options include "linear", "logistic", "poisson",coxph", "crr", "boxcox", "ordinal", "geeglm"
offset	string specifying the offset term to be used for Poisson or negative binomial regression. Example: offset="log(follow_up)"
strata	character vector of covariates to stratify by. Only used for coxph and crr
nicenames	boolean indicating if you want to replace . and _ in strings with a space
showN	boolean indicating if you want to show sample sizes
showEvent	boolean indicating if you want to show number of events. Only available for logistic.
CIwidth	width of confidence interval, default is 0.95
reflevel	manual specification of the reference level. Only used for ordinal regression This will allow you to see which model is not fitting if the function throws an error
returnModels	boolean indicating if a list of fitted models should be returned. If this is TRUE then the models will be returned, but the output will be suppressed. In addition to the model elements a data element will be appended to each model so that the fitted data can be examined, if necessary. See Details
fontsize	PDF/HTML output only, manually set the table fontsize
forceWald	**[Deprecated]** forceWald = TRUE is no longer supported; this function will always use profile likelihoods as per the inclusion of the MASS confidence intervals into base from from R 4.4.0

Details

Global p-values are likelihood ratio tests for lm, glm and polr models. For lme models an attempt is made to re-fit the model using ML and if,successful LRT is used to obtain a global p-value. For coxph models the model is re-run without robust variances with and without each variable and a LRT is presented. For coxph models fit with clustering (id specified) a robust Wald global p-value is returned; otherwise a LRT is used. For GEE and CRR models Wald global p-values are returned.

As of version 0.1.1 if global p-values are requested they will be included in the p-value column.

The number of decimals places to display the statistics can be changed with digits, but this will not change the display of p-values. If more significant digits are required for p-values then use tableOnly=TRUE and format as desired.

tidyselect can only be used for response and covs variables. Additional arguments must be passed in using characters

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also

lm,glm, cmprsk::crr, survival::coxph, nlme::lme, geepack::geeglm, MASS::glm.nb

Examples

```
# Examples are for demonstration and are not meaningful
# Coxph model with 90% CI
data("pembrolizumab")
rm_uvsum(response = c('os_time','os_status'),
covs=c('age','sex','baseline_ctdna','l_size','change_ctdna_group'),
data=pembrolizumab,CIwidth=.9)

# Linear model with default 95% CI
rm_uvsum(response = 'baseline_ctdna',
covs=c('age','sex','l_size','pdl1','tmb'),
data=pembrolizumab)

# Logistic model with default 95% CI
rm_uvsum(response = 'os_status',
covs=c('age','sex','l_size','pdl1','tmb'),
data=pembrolizumab,family = binomial)
# Poisson models returned as model list
mList <- rm_uvsum(response = 'baseline_ctdna',
covs=c('age','sex','l_size','pdl1','tmb'),
data=pembrolizumab, returnModels=TRUE)
#'
# GEE on correlated outcomes
data("ctDNA")
rm_uvsum(response = 'size_change',
covs=c('time','ctdna_status'),
gee=TRUE,
id='id', corstr="exchangeable",
family=gaussian("identity"),
data=ctDNA,showN=TRUE)

# Using tidyselect
pembrolizumab |> rm_uvsum(response = sex,
covs = c(age, cohort))
```

rm_uv_mv *Combine univariate and multivariable regression tables*

Description

This function will combine rm_uvsum and rm_mvsum outputs into a single table. The tableOnly argument must be set to TRUE when tables to be combined are created. The resulting table will be in the same order as the uvsum table and will contain the same columns as the uvsum and mvsum tables, but the p-values will be combined into a single column. There must be a variable overlapping between the uvsum and mvsum tables and all variables in the mvsum table must also appear in the uvsum table.

Usage

```
rm_uv_mv(
  uvsumTable,
  mvsumTable,
  covTitle = "",
  vif = FALSE,
  showN = FALSE,
  showEvent = FALSE,
  caption = NULL,
  tableOnly = FALSE,
  chunk_label,
  fontsize
)
```

Arguments

uvsumTable	Output from rm_uvsum, with tableOnly=TRUE
mvsumTable	Output from rm_mvsum, with tableOnly=TRUE
covTitle	character with the names of the covariate (predictor) column. The default is to leave this empty for output or, for table only output to use the column name 'Covariate'.
vif	boolean indicating if the variance inflation factor should be shown if present in the mvsumTable. Default is FALSE.
showN	boolean indicating if sample sizes should be displayed.
showEvent	boolean indicating if number of events (dichotomous outcomes) should be displayed.
caption	table caption
tableOnly	boolean indicating if unformatted table should be returned
chunk_label	only used if output is to Word to allow cross-referencing
fontsize	PDF/HTML output only, manually set the table fontsize

Value

A character vector of the table source code, unless tableOnly=TRUE in which case a data frame is returned

See Also

rm_uvsum,rm_mvsum

Examples

```
require(survival)
data("pembrolizumab")
uvTab <- rm_uvsum(response = c('os_time','os_status'),
covs=c('age','sex','baseline_ctdna','l_size','change_ctdna_group'),
data=pembrolizumab,tableOnly=TRUE)
mv_surv_fit <- coxph(Surv(os_time,os_status)~age+sex+
baseline_ctdna+l_size+change_ctdna_group, data=pembrolizumab)
uvTab <- rm_mvsum(mv_surv_fit)

#linear model
uvtab<-rm_uvsum(response = 'baseline_ctdna',
covs=c('age','sex','l_size','pdl1','tmb'),
data=pembrolizumab,tableOnly=TRUE)
lm_fit=lm(baseline_ctdna~age+sex+l_size+tmb,data=pembrolizumab)
mvtab<-rm_mvsum(lm_fit,tableOnly = TRUE)
rm_uv_mv(uvtab,mvtab,tableOnly=TRUE)

#logistic model
uvtab<-rm_uvsum(response = 'os_status',
covs=c('age','sex','l_size','pdl1','tmb'),
data=pembrolizumab,family = binomial,tableOnly=TRUE)
logis_fit<-glm(os_status~age+sex+l_size+pdl1+tmb,data = pembrolizumab,family = 'binomial')
mvtab<-rm_mvsum(logis_fit,tableOnly = TRUE)
rm_uv_mv(uvtab,mvtab,tableOnly=TRUE)
```

---

scrolling_table *Output a scrollable table*

Description

This function accepts the output of a aa call to knitr::kable or reportRmd::outTable and, if the output format is html, will produce a scrollable table. Otherwise a regular table will be output for pandoc/latex

Usage

```
scrolling_table(knitrTable, pixelHeight = 500)
```

Arguments

knitrTable	output from a call to knitr::kable or outTable
pixelHeight	the height of the scroll box in pixels, default is 500

Examples

```
data("pembrolizumab")
tab <- rm_covsum(data=pembrolizumab,maincov = 'change_ctdna_group',
covs=c('age','cohort','sex','pdl1','tmb','l_size'),full=FALSE)
scrolling_table(tab,pixelHeight=300)
```

---

set_labels *Set variable labels*

Description

Assign variable labels to a data.frame from a lookup table.

Usage

```
set_labels(data, names_labels)
```

Arguments

data	data frame to be labelled
names_labels	data frame with column 1 containing variable names from data and column 2 containing variable labels. Other columns will be ignored.

Details

Useful if variable labels have been imported from a data dictionary. The first column in names_labels must contain the variable name and the second column the variable label. The column names are not used.

If no label is provided then the existing label will not be changed. To remove a label set the label to NA.

See Also

set_var_labels() for setting individual variable labels, extract_labels() for creating a data frame of all variable labels, clear_labels() for removing variable labels

Examples

```
data("ctDNA")
# create data frame with labels
lbls <- data.frame(c1=c('cohort','size_change'),
c2=c('Cancer cohort','Change in tumour size'))
# set labels and return labelled data frame
set_labels(ctDNA,lbls)
```

set_var_labels *Set variable labels*

Description

Set variable labels for a data frame using name-label pairs.

Usage

```
set_var_labels(data, ...)
```

Arguments

data	data frame containing variables to be labelled
...	Name-label pairs the name gives the name of the column in the output and the label is a character vector of length one.

Details

If no label is provided for a variable then the existing label will not be changed. To remove a label set the label to NA.

See Also

`set_labels()` for setting variable labels using a data frame, `extract_labels()` for creating a data frame of all variable labels, `clear_labels()` for removing variable labels

Examples

```
# set labels using name-label pairs
# and return labelled data frame
data("ctDNA")
ctDNA |> set_var_labels(
   ctdna_status="detectable ctDNA",
  cohort="A cohort label")
```

validate_and_prepare_data *Validate and prepare input data*

Description

Validate and prepare input data

Usage

```
validate_and_prepare_data(data, response, cov = NULL, print.n.missing = TRUE)
```

Arguments

`data`	Input dataframe
`response`	Character vector with time and status column names
`cov`	Covariate column name (optional)
`print.n.missing`	Whether to print missing data message

Index

∗ **dataframe**
  covsum, 15
  mvsum, 38
  rm_covsum, 55
∗ **datasets**
  ctDNA, 22
  pembrolizumab, 42
∗ **helper**
  hbld, 36
  lpvalue2, 37
∗ **model**
  boxcoxfitRx, 10
  crrRx, 21
∗ **plot**
  forestplot2, 27
  forestplotMV, 28
  forestplotUV, 29
  plotuv, 43

add_censor_marks, 3
add_cif_hazard_ratios, 4
add_confidence_bands, 5
add_km_hazard_ratios, 5
add_median_lines, 6
add_median_text, 6
add_set_time_lines, 7
add_set_time_text, 8
add_statistical_tests, 9
anova, *17*, *58*
apply_scales_and_guides, 10

boxcoxfitRx, 10

calculate_and_add_median_times, 11
calculate_and_add_time_specific_estimates, 12
calculate_cif_median, 13
calculate_cif_timepoints, 13
chisq.test, *17*, *58*
citation, *25*
clear_labels, 14
clear_labels(), *49*, *74, 75*
cmprsk::crr, *21*, *71*
covsum, 15, *58*
create_base_plot, 17
create_cif_dataframe, 18
create_cif_risk_table_sfit, 19
create_km_dataframe, 19
create_risk_table, 20
crrRx, 21
ctDNA, 22

excelCol, 22
excelColLetters, 23
extract_grays_test, 24
extract_labels, 24
extract_labels(), *49*, *74, 75*
extract_package_details, 25

fisher.test, *17*, *58*
fit_cif_model, 26
fit_km_model, 26
forestplot2, 27
forestplotMV, 28
forestplotMV(), *27*
forestplotUV, 29
forestplotUVMV, 31

geepack::geeglm, *71*
geoR_boxcoxfit, 31
getAnywhere, *25*
ggkmcif2, 32, *33*
ggkmcif2(), *36*
ggkmcif2Parameters, *32*, 33
ggkmcif_paste, 36
ggplot2::ggplot, *44*
ggpubr::ggarrange, *44*
glm, *71*

hbld, 36

kruskal.test, *17*, *58*

lm, *71*
lpvalue2, 37

MASS::glm.nb, *71*
mvsum, 38

nestTable, 39
nlme::lme, *71*

outTable, 40, *58*

p.adjust, *57*, *60*, *69*
packageVersion, *25*
pembrolizumab, 42
plotuv, 43
predsum, 45
process_cif_medians, 47
process_cif_timepoints, 48
process_covariate, 49

replace_plot_labels, *44*, 49
rm_cifsum, 50
rm_compactsum, 52, *58*
rm_covsum, 55
rm_mvsum, 59, *73*
rm_survdiff, 62, *65*
rm_survsum, 64
rm_survtime, *65*, 66
rm_uv_mv, 72
rm_uvsum, *43*, 68, *73*

scrolling_table, 73
set_labels, 74
set_labels(), *49*, *75*
set_var_labels, 75
set_var_labels(), *49*, *74*
survival::coxph, *71*
survival::survdiff, *63*
survival::survfit, *63*, *65–68*

validate_and_prepare_data, 75

wilcox.test, *17*, *58*