Package ‘epitabulate’

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Title Tables for Epidemiological Analysis

Version 0.1.0

Description Produces tables for descriptive epidemiological analysis.
These tables include attack rates, case fatality ratios, and mortality
rates (with appropriate confidence intervals), with additional
functionality to calculate Mantel-Haenszel odds, risk, and incidence
rate ratios. The methods implemented follow standard epidemiological
approaches described in Rothman et al. (2008, ISBN:978-0-19-513554-2).
This package is part of the 'R4EPIs' project <`https://R4EPI.github.io/sitrep/`>.

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URL `https://R4EPI.github.io/epitabulate/`,
`https://github.com/R4EPI/epitabulate/`

BugReports `https://github.com/R4EPI/epitabulate/issues`

Imports binom, dplyr (>= 1.0.2), epikit (>= 0.1.2), forcats, glue,
gtsummary, MASS, purrr, rlang (>= 0.4.0), scales, stats, tibble
(>= 3.0.0), tidyr (>= 1.0.0), tidyselect (>= 1.0.0)

Suggests broom.helpers, cardx, covr, matchmaker (>= 0.1.0), testthat

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

Author Alexander Spina [aut, cre] (ORCID:
<`https://orcid.org/0000-0001-8425-1867`>),
Zhian N. Kamvar [aut] (ORCID: <`https://orcid.org/0000-0003-1458-7108`>),
Amy Gimma [aut],
Kate Doyle [ctb],
Applied Epi Incorporated [cph],
Medecins Sans Frontieres Operational Centre Amsterdam [fnd]

Maintainer Alexander Spina <`aspina@appliedepi.org`>

Repository CRAN

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Contents

`add_ar` *Add attack rate statistics to a gtsummary table*

Description

This function wraps `gtsummary::add_stat()` to calculate and display **attack rates** (cases per given population multiplier) with 95% confidence intervals, using the `epitabulate::attack_rate()` function internally.

Usage

```
add_ar(
  gts_object,
  case_var,
  population = NULL,
  multiplier = 10^4,
  drop_tblsummary_stat = FALSE
)
```

Arguments

`gts_object`	A gtsummary object created with functions such as `gtsummary::tbl_summary()`
`case_var`	A logical variable name in the data indicating case status (e.g. `TRUE` for cases).
`population`	Optional numeric vector giving the population size for the denominator. If `NULL`, the population is inferred from the data.
`multiplier`	Numeric multiplier used to scale the attack rate (e.g. `1` = proportion, `100` = percent, `10^4` = per 10,000).
`drop_tblsummary_stat`	Logical; if `TRUE`, removes the original `tbl_summary` statistic column (default = `FALSE`).

Value

A modified gtsummary object with additional columns showing the number of cases, population, attack rate, and 95% confidence interval.

`add_cfr` *Add case fatality rate (CFR) statistics to a gtsummary table*

Description

This function wraps `gtsummary::add_stat()` to calculate and display **case fatality rates** (deaths among cases) with 95% confidence intervals, using the `epitabulate::case_fatality_rate_df()` function internally.

Usage

```
add_cfr(gts_object, deaths_var)
```

Arguments

`gts_object`	A gtsummary object created with functions such as `gtsummary::tbl_summary()` or `gtsummary::tbl_cross()`.
`deaths_var`	A logical variable name in the data indicating death status (e.g. `TRUE` for death).

Value

A modified gtsummary object with additional columns showing the number of deaths, number of cases, case fatality rate, and 95% confidence interval.

`add_crosstabs` *A {gtsummary} wrapper function that takes a gtsummary univariate regression table and adds appropriate cross tabs by exposure and outcome*

Description

A {gtsummary} wrapper function that takes a gtsummary univariate regression table and adds appropriate cross tabs by exposure and outcome

Usage

```
add_crosstabs(x, wide = FALSE)
```

Arguments

`x`	Object with class `tbl_uvregression` from the gtsummary tbl_uvregression function or `tbl_cmh` from the epitabulate tbl_cmh function.
`wide`	TRUE/FALSE to specify whether would like to have the output in wide format. Results in four columns rather than two, but in a single row. This is only works for dichotomous variables (yes/no, TRUE/FALSE, male/female), others will be dropped with a warning message. (Default is FALSE)

Value

A modified `gtsummary` table object (same class as input — e.g. `"tbl_uvregression"` or `"tbl_cmh"`) containing additional cross-tabulated counts of outcomes and exposures. The structure depends on regression type:

- For logistic models: adds case and control counts.
- For Poisson models without offsets: adds total and case counts per exposure group (risk ratios).
- For Poisson models with offsets: adds total person-time and case counts per exposure group (incidence rate ratios).
- When `wide = TRUE`, dichotomous variables are reshaped to wide format with separate columns for exposed/unexposed counts.

References

Inspired by Daniel Sjoberg, see gtsummary github repo

`add_mr` *Add mortality rate statistics to a gtsummary table*

Description

This function wraps `gtsummary::add_stat()` to calculate and display **mortality rates** (deaths per given population multiplier) with 95% confidence intervals, using the `epitabulate::mortality_rate()` function internally.

Usage

```
add_mr(
  gts_object,
  deaths_var,
  population = NULL,
  multiplier = 10^4,
  drop_tblsummary_stat = FALSE
)
```

Arguments

`gts_object`	A gtsummary object created with functions such as `gtsummary::tbl_summary()` or `gtsummary::tbl_cross()`.
`deaths_var`	A logical variable name in the data indicating death status (e.g. `TRUE` for death).
`population`	Optional numeric vector giving the population size for the denominator. If `NULL`, the population is inferred from the data.
`multiplier`	Numeric multiplier used to scale the mortality rate (e.g. `1` = proportion, `100` = percent, `10^4` = per 10,000).
`drop_tblsummary_stat`	Logical; if `TRUE`, removes the original `tbl_summary` statistic column (default = `FALSE`).

Value

A modified gtsummary object with additional columns showing the number of deaths, population, mortality rate, and 95% confidence interval.

`attack_rate` *Rates and Ratios*

Description

Calculate attack rate, case fatality rate, and mortality rate

Usage

```
attack_rate(
  cases,
  population,
  conf_level = 0.95,
  multiplier = 100,
  mergeCI = FALSE,
  digits = 2
)

case_fatality_rate(
  deaths,
  population,
  conf_level = 0.95,
  multiplier = 100,
  mergeCI = FALSE,
  digits = 2
)

case_fatality_rate_df(
  x,
  deaths,
  group = NULL,
  conf_level = 0.95,
  multiplier = 100,
  mergeCI = FALSE,
  digits = 2,
  add_total = FALSE
)

mortality_rate(
  deaths,
  population,
  conf_level = 0.95,
  multiplier = 10^4,
```

```
  mergeCI = FALSE,
  digits = 2
)
```

Arguments

`cases, deaths`	number of cases or deaths in a population. For `_df` functions, this can be the name of a logical column OR an evaluated logical expression (see examples).
`population`	the number of individuals in the population.
`conf_level`	a number representing the confidence level for which to calculate the confidence interval. Defaults to 0.95, representing a 95% confidence interval using `binom::binom.wilson()`
`multiplier`	The base by which to multiply the output: • `multiplier = 1`: ratio between 0 and 1 • `multiplier = 100`: proportion • `multiplier = 10^4`: x per 10,000 people
`mergeCI`	Whether or not to put the confidence intervals in one column (default is FALSE)
`digits`	if `mergeCI = TRUE`, this determines how many digits are printed
`x`	a data frame
`group`	the bare name of a column to use for stratifying the output
`add_total`	if `group` is not NULL, then this will add a row containing the total value across all groups.

Value

a data frame with five columns that represent the numerator, denominator, rate, lower bound, and upper bound.

- `attack_rate()`: cases, population, ar, lower, upper
- `case_fatality_rate()`: deaths, population, cfr, lower, upper

`gt_remove_stat`

A gtsummary wrapper function that takes a gtsummary object and removes a column from the table body by column name

Description

A gtsummary wrapper function that takes a gtsummary object and removes a column from the table body by column name

Usage

```
gt_remove_stat(gts_object, col_name = "stat_0")
```

Arguments

`gts_object`	A data frame, passed by the gtsummary::add_stat function
`col_name`	the column name from the gtsummary object's table_body to remove

Value

a gtsummary object without the named column

`tbl_cmh` *A {gtsummary} wrapper function that takes a dataframe and produces crude, stratified and Cochran-Mantel-Haenszel estimates.*

Description

A {gtsummary} wrapper function that takes a dataframe and produces crude, stratified and Cochran-Mantel-Haenszel estimates.

Usage

```
tbl_cmh(
  data,
  case,
  exposure,
  strata,
  measure,
  obstime = NULL,
  conf.level = 0.95
)
```

Arguments

`data`	A data frame
`case`	Name of a variable as your outcome of interest
`exposure`	Names of variables as exposures of interest. Can be multiple variables using tidyselect syntax.
`strata`	Name of a variable to be used for stratifying results. This gives you a table of crude measure, measures for each strata and the mantel-haeszel adjusted measure for each exposure variable
`measure`	Specify what you would like to calculated, options are "OR", "RR" or "IRR". Default is "OR". If "OR or "RR" are specified then a woolf test for homogeneity p-value is produced. This tests whether there is a significant difference in the estimates between strata.
`obstime`	A numeric variable containing the observation time for each individual
`conf.level`	Confidence level for confidence intervals (default 0.95)

Value

A gtsummary table of class `"tbl_cmh"` (and `"gtsummary"`, `"tbl_stack"`) containing:

- Crude estimates of association (odds ratios, risk ratios, or rate ratios)
- Stratified estimates for each level of the stratification variable
- Cochran–Mantel–Haenszel (CMH) adjusted estimates with 95\
- Woolf test p-values for assessing homogeneity across strata (when applicable)

References

Inspired by Daniel Sjoberg, see gtsummary github repo

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