Package ‘vaccineff’

November 29, 2024

Title Estimate Vaccine Effectiveness Based on Different Study Designs

Version 1.0.0

Description Provides tools for estimating vaccine effectiveness and related metrics. The 'vaccineff_data' class manages key features for preparing, visualizing, and organizing cohort data, as well as estimating vaccine effectiveness. The results and model performance are assessed using the 'vaccineff' class.

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URL `https://github.com/epiverse-trace/vaccineff`, `https://epiverse-trace.github.io/vaccineff/`

BugReports `https://github.com/epiverse-trace/vaccineff/issues`

Depends R (>= 4.0.0)

Imports checkmate, ggplot2, linelist, MatchIt, rlang, scales, stats, survival

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

VignetteBuilder knitr

Config/Needs/website epiverse-trace/epiversetheme

Config/testthat/edition 3

Encoding UTF-8

Language en-US

LazyData true

RoxygenNote 7.3.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-11-29 09:30:02 UTC

Contents

`cohortdata` *Cohort data on vaccineff*

Description

Subset of data from an anonymised, real-world dataset produced as part of the early stage of the immunization program against COVID-19 in Bogota, Colombia between February 2021 and December 2021. Cohort dataset contains registers of homologous schemes for two different brands for adults aged 50 years or older. This cohort received two doses of a vaccine aimed at reducing the risk of death. All the registers were anonymised and de-identified to preserve the privacy of data. The dataset includes disaggregated information on the first and second vaccine doses (vaccine_date1, vaccine_date2, vaccine1, and vaccine2) for each participant and relevant demographic details (sex and age). Additionally, the dataset includes the dates of two outcomes: death associated with COVID-19 (death_date) and death from other causes (death_other_causes).

Usage

```
cohortdata
```

Format

`cohortdata`:

id	Anonymous ID of the individual
sex	Sex F/M
age	Age (50-100)
death_date	Registered death by COVID-19
death_other_causes	Registered death by other causes
vaccine_date_1	Registered date of the first dose
vaccine_date_2	Registered date of the second dose
vaccine_1	Brand of the first dose
vaccine_2	Brand of the second dose

Examples

```
cohortdata
```

`estimate_vaccineff` *Estimate Vaccine Effectiveness (VE)*

Description

This function provides methods for estimating VE. It relies on the Kaplan-Meier estimator and the Cox model for proportional hazards from the `{survival}` package. Currently, the default method is VE = 1 - HR, where HR is the Hazard Ratio calculated using the Cox model. The proportional hazards assumption is tested using the Schoenfeld test, with the p-value provided in the results. Log-log plots are also generated using the Kaplan-Meier estimator for a visual test of the proportional hazards hypothesis. The function uses column names provided in the tags `outcome_status_col`, `time_to_event_col`, and `vaccine_status_col` of the `linelist` object and status names from `make_vaccineff_data`. The return is an `S3 class` object with the VE (CI95%), results from the Cox model, and the Kaplan-Meier estimator. This object is compatible with `summary` and `plot` methods.

Usage

```
estimate_vaccineff(vaccineff_data, at)
```

Arguments

`vaccineff_data`	Object of the class `vaccineff_data` with vaccineff data.
`at`	Number of days at which VE is estimated from the beginning of the follow-up period.

Value

Object of the class `vaccineff`: a list with results from the estimation of VE. `ve`: `data.frame` with VE(CI95%) `cox_model`: `survival` object with Cox model results `kaplan_meier`: `survival` object with Kaplan-Meier estimator

Examples

```
# Load example data
data("cohortdata")

# Create `vaccineff_data`
vaccineff_data <- make_vaccineff_data(data_set = cohortdata,
  outcome_date_col = "death_date",
  censoring_date_col = "death_other_causes",
  vacc_date_col = "vaccine_date_2",
  vaccinated_status = "v",
  unvaccinated_status = "u",
  immunization_delay = 15,
  end_cohort = as.Date("2021-12-31"),
  match = TRUE,
  exact = c("age", "sex"),
  nearest = NULL
)

# Estimate the Vaccine Effectiveness (VE)
ve <- estimate_vaccineff(vaccineff_data, 90)

# Print summary of VE
summary(ve)

# Generate loglog plot to check proportional hazards
plot(ve, type = "loglog")

# Generate Survival plot
plot(ve, type = "surv", percentage = FALSE, cumulative = FALSE)
```

`get_age_group` *Construct age-group variable from age column*

Description

This method splits an age interval from `min_val` to `max_val` into intervals of size `step`. If the method finds ages greater or equal than `max_val` it assigns the string `">max_val"`. By default `min_val` is set to 0, however it can be assigned by convenience. If the method finds ages lower or equal than `min_val` it assigns the string `"<min_val-1"`. The function warns when (max_val - min_val) is not an integer multiple of step. In that case the last interval is truncated to the upper value closest to max_val for which (closest_upper - min_val) is multiple of step.

Usage

```
get_age_group(data_set, col_age, max_val, min_val = 0, step)
```

Arguments

`data_set`	`data.frame` with at least a column containing the age information
`col_age`	Name of the column containing the age information
`max_val`	Maximum value of age interval to split
`min_val`	Minimum value of age interval to split
`step`	Step used to split the age interval

Value

Column of type `factor` with the same length as the number of rows in `data_set`, with levels corresponding to age bins between `min_val` and `max_val`. Ages above `max_val` are represented as `>max_val`.

Examples

```
# load data provided with the package
data(cohortdata)

# assign age groups as a column of the `data.frame`
cohortdata$age_group <- get_age_group(
  data_set = cohortdata,
  col_age = "age",
  max_val = 80,
  step = 10
)

# view the `data.frame` with new column
head(cohortdata)
```

`make_vaccineff_data` *Construct* `vaccineff_data` *Object*

Description

This function constructs an S3 object of the class `vaccineff_data` that contains all the relevant information for the study. to estimate the effectiveness.

Usage

```
make_vaccineff_data(
  data_set,
  outcome_date_col,
  censoring_date_col = NULL,
  vacc_date_col,
  vacc_name_col = NULL,
  vaccinated_status = "v",
  unvaccinated_status = "u",
```

```
  immunization_delay = 0,
  end_cohort,
  match = FALSE,
  exact = NULL,
  nearest = NULL,
  take_first = FALSE,
  t0_follow_up = NULL
)
```

Arguments

`data_set`	`data.frame` with cohort information.
`outcome_date_col`	Name of the column that contains the outcome dates.
`censoring_date_col`	Name of the column that contains the censoring date. NULL by default.
`vacc_date_col`	Name of the column(s) that contain the vaccine dates.
`vacc_name_col`	Name of the column(s) that contain custom vaccine names for the vaccines (e.g. brand name, type of vaccine). If provided, must be of the same length as `vacc_date_col`.
`vaccinated_status`	Status assigned to the vaccinated population. Default is `v`.
`unvaccinated_status`	Status assigned to the unvaccinated population. Default is `u`.
`immunization_delay`	Characteristic time in days before the patient is considered immune. Default is 0.
`end_cohort`	End date of the study.
`match`	`TRUE`: cohort matching is performed. Default is `FALSE`
`exact`	Name(s) of column(s) for `exact` matching. Default is `NULL`.
`nearest`	Named vector with name(s) of column(s) for `nearest` matching and caliper(s) for each variable (e.g., `nearest = c("characteristic1" = n1, "characteristic2" = n2)`, where `n1` and `n2` are the calipers). Default is `NULL`.
`take_first`	`FALSE`: takes the latest vaccine date. `TRUE`: takes the earliest vaccine date.
`t0_follow_up`	Column with the initial dates of the follow-up period. This column is only used if `match = FALSE`. If not provided, the follow-up period starts at `start_cohort`. Default is NULL.

Value

An S3 object of class `vaccineff_data` with all the information and characteristics of the study. `data.frames` are converted into an object of class `linelist` to easily handle with the data.

Examples

```
# Load example data
data("cohortdata")

# Create `vaccineff_data`
vaccineff_data <- make_vaccineff_data(data_set = cohortdata,
  outcome_date_col = "death_date",
  censoring_date_col = "death_other_causes",
  vacc_date_col = "vaccine_date_2",
  vaccinated_status = "v",
  unvaccinated_status = "u",
  immunization_delay = 15,
  end_cohort = as.Date("2021-12-31"),
  match = TRUE,
  exact = c("age", "sex"),
  nearest = NULL
)

# Print summary of data
summary(vaccineff_data)

# Plot vaccine coverage
plot(vaccineff_data)
```

`plot.vaccineff` *Function for Extracting Vaccine Effectiveness Plot*

Description

This function creates plots from an object of class `vaccineff`. It returns a Log-Log plot when `type = "loglog"`, or a Survival curve when `type = "surv"`. Survival plots can be shown as cumulative incidence (`cumulative = TRUE`), and using percentages (`percentage = TRUE`).

Usage

```
## S3 method for class 'vaccineff'
plot(
  x,
  type = c("loglog", "surv"),
  cumulative = FALSE,
  percentage = FALSE,
  ...
)
```

Arguments

`x`	Object of class `vaccineff`.

`type`	Type of plot. Options are `loglog` and `surv`.
`cumulative`	If `TRUE`, the survival curve is shown as cumulative incidence.
`percentage`	If `TRUE`, results are shown on a percentage scale.
`...`	Additional arguments passed to other functions.

Value

Plot extracted from `vaccineff`.

`plot.vaccineff_data` *Function for Extracting Vaccineff Data Plot*

Description

This function returns a plot of the vaccine coverage or the cumulative coverage (if cumulative = TRUE). The return is a 2-axis `ggplot2` element with the number of vaccines per date on the left axis and the coverage per date on the right axis. When a matching routine is performed, the left axis also accounts for the doses of the matched cohort.

Usage

```
## S3 method for class 'vaccineff_data'
plot(x, date_interval = NULL, cumulative = FALSE, ...)
```

Arguments

`x`	Object of class `vaccineff_data`.
`date_interval`	If NULL, the function calculates the coverage interval
`cumulative`	If `TRUE`, returns the cumulative number of doses over the time window.
`...`	Additional arguments passed to other functions.

Value

Plot extracted from `vaccineff`.

`print.summary_vaccineff`
Print summary of VE Results

Description

Print summary of `vaccineff` object.

Usage

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

Arguments

`x`	Object of the class `summary.vaccineff`.
`...`	Additional arguments passed to other functions.

Value

None

`print.summary_vaccineff_data`
Print Summary of Vaccineff Data

Description

Summarizes the results of `make_vaccineff_data`.

Usage

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

Arguments

`x`	Object of the class `summary.vaccineff_data`.
`...`	Additional arguments passed to other functions.

Value

None

`summary.vaccineff` *Summarize VE Results*

Description

Summarizes the results of `vaccineff`.

Usage

```
## S3 method for class 'vaccineff'
summary(object, ...)
```

Arguments

`object`	Object of the class `vaccineff`.
`...`	Additional arguments passed to other functions.

Value

Summary of the results from `estimate_vaccineff`.

`summary.vaccineff_data` *Summarize Vaccineff Data*

Description

Summarizes the results of `make_vaccineff_data`.

Usage

```
## S3 method for class 'vaccineff_data'
summary(object, warnings_log = FALSE, ...)
```

Arguments

`object`	Object of the class `vaccineff_data`.
`warnings_log`	If `TRUE`, prints the warnings log.
`...`	Additional arguments passed to other functions.

Value

Summary of the results from vaccineff data

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