Package 'impactflu'

October 13, 2022

Title Quantification of Population-Level Impact of Vaccination

Version 0.1.0

Description Implements the compartment model from Tokars (2018) <doi:10.1016/j.vaccine.2018.10.026>. This enables quantification of population-wide impact of vaccination against vaccine-preventable diseases such as influenza.

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Encoding UTF-8

LazyData true

Depends R (>= 3.6.0)

RoxygenNote 7.0.2

LinkingTo Rcpp

Imports Rcpp, tibble, dplyr, rlang, glue, lubridate, magrittr

Suggests testthat (>= 2.1.0)

NeedsCompilation yes

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R topics documented:

generate_counts *Generate normal counts*

Description

Generates counts from a normal distribution density function.

Usage

```
generate_counts(init_pop_size, n_timepoints, overall_prop, mean, sd)
```

Arguments

init_pop_size	Initial population size
n_timepoints	Number of timepoints
overall_prop	Overall proportion of the population to be included in the counts over all the timepoints
mean	Mean of the normal distribution
sd	Standard deviation of the normal distribution

Value

An integer vector of counts of length n_timepoints

Examples

```
# Tokars (2018) vaccinations
vacs_tok <- generate_counts(1e6, 304, 0.55, 100, 50)
# Tokars (2018) cases
casen_tok <- generate_counts(1e6, 304, 0.12, 190, 35)
```

generate_dates *Generate dates*

Description

Generate dates given timepoint indices, start date and step unit

Usage

```
generate_dates(timepoints, start, unit)
```

Arguments

`timepoints`	Integer vector timepoint indices
`start`	Date of index 1
`unit`	"year" "month" or "day"

Value

A vector of dates the same length as `timepoints`

Examples

```
# Dates from Tokars (2018)
timepoints <- 1L:304L
dates <- generate_dates(timepoints, lubridate::ymd("2017-08-01"), "day")
```

`method1` *Analysis methods from Tokars (2018)*

Description

Method 1 was said to be as current. Method 3 was determined to be the least biased.

Usage

```
method1(init_pop_size, vaccinations, cases, ve)

method3(init_pop_size, vaccinations, cases, ve)
```

Arguments

`init_pop_size`	Integer initial population size
`vaccinations`	Integer vector counts of vaccinations
`cases`	Integer vector counts of cases
`ve`	Vector vaccine effectiveness. If length 1, assumed to not vary with time.

Value

A tibble with the following columns (method-dependent):

`cases`	Observed cases
`vaccinations`	Observed vaccinations
`ve`	Assumed vaccine effectiveness
`pvac`	Proportion of the starting population vaccinated
`vc_lag`	Vaccine coverage lagged
`pops`	Susceptible population

pflu	Infection risk
popn	Non-cases is absence of vaccination
cases_novac	Cases in absence of vaccination
avert	Expected number of vaccinations

References

Tokars JI, Rolfes MA, Foppa IM, Reed C. An evaluation and update of methods for estimating the number of influenza cases averted by vaccination in the United States. Vaccine. 2018;36(48):7331–7337. doi:10.1016/j.vaccine.2018.10.026

Examples

```
library(dplyr)

# Simulate a population
nsam <- 1e6L
ndays <- 304L
pop_tok <- sim_reference(
  init_pop_size = nsam,
  vaccinations = generate_counts(nsam, ndays, 0.55, mean = 100, sd = 50),
  cases_novac = generate_counts(nsam, ndays, 0.12, mean = 190, sd = 35),
  ve = 0.48,
  lag = 14,
  deterministic = TRUE
)

# Summarise by month
pop_tok_month <- pop_tok %>%
  mutate(
    datestamp = generate_dates(
      timepoint, lubridate::ymd("2017-08-01"), "day"
    ),
    year = lubridate::year(datestamp),
    month = lubridate::month(datestamp)
 ) %>%
 group_by(year, month) %>%
 summarise(
   vaccinations = sum(vaccinations), cases = sum(cases), ve = mean(ve)
 ) %>%
 ungroup()

# Estimate averted cases using the two different methods
m1 <- method1(
  nsam, pop_tok_month$vaccinations, pop_tok_month$cases, pop_tok_month$ve
)
m3 <- method3(
  nsam, pop_tok_month$vaccinations, pop_tok_month$cases, pop_tok_month$ve
)
sum(m1$avert)
sum(m3$avert)
```

`sim_reference` *Simulate an ideal population*

Description

Simulates an ideal population using the reference model from Tokars (2018).

Usage

```
sim_reference(
  init_pop_size,
  vaccinations,
  cases_novac,
  ve,
  lag,
  deterministic,
  seed = sample.int(.Machine$integer.max, 1)
)
```

Arguments

`init_pop_size`	Integer initial population size
`vaccinations`	Integer vector number of vaccinations at every timepoint
`cases_novac`	Integer vector number of cases at every timepoint
`ve`	Vaccine effectiveness (proportion)
`lag`	Integer lag period measured in timepoints
`deterministic`	Boolean whether to make the simulation deterministic
`seed`	Integer seed to use

Value

A tibble with the following columns:

`timepoint`	Index of timepoint
`vaccinations`	Expected number of vaccinations
`cases_novac`	Expected number of cases in absence of vaccination
`ve`	Expected vaccine effectiveness
`pflu`	Flu incidence
`cases`	Actual number of cases
`popn`	Non-cases in absence of vaccination
`pvac`	Proportion of starting population vaccinated
`b`	Number vaccinated at that time
`A`	Non-vaccinated non-cases
`B`	Vaccinated non-cases lagging
`E`	Non-vaccinated cases

References

Tokars JI, Rolfes MA, Foppa IM, Reed C. An evaluation and update of methods for estimating the number of influenza cases averted by vaccination in the United States. Vaccine. 2018;36(48):7331–7337. doi:10.1016/j.vaccine.2018.10.026

Examples

```
# Population from Tokars (2018)
nsam <- 1e6L
ndays <- 304L
pop_tok <- sim_reference(
  init_pop_size = nsam,
  vaccinations = generate_counts(nsam, ndays, 0.55, mean = 100, sd = 50),
  cases_novac = generate_counts(nsam, ndays, 0.12, mean = 190, sd = 35),
  ve = 0.48,
  lag = 14,
  deterministic = TRUE
)
head(pop_tok)
sum(pop_tok$avert)
```

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