

Package: impactflu (via r-universe)

August 28, 2024

Version 0.1.0.9000

Title Quantification of Population-Level Impact of Vaccination

Description Implements the compartment model from Tokars (2018) [<doi:10.1016/j.vaccine.2018.10.026>](https://doi.org/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 7.1.1

LinkingTo Rcpp

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

Suggests testthat (>= 2.1.0), knitr, rmarkdown

VignetteBuilder knitr

Repository <https://khvorov45.r-universe.dev>

RemoteUrl <https://github.com/khvorov45/impactflu>

RemoteRef HEAD

RemoteSha 338a68204d05e068e5be5a6213b2fb54bd22f777

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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),
  infections_novac = generate_counts(nsam, ndays, 0.12, mean = 190, sd = 35),
  ve = 0.48,
  lag = 14
)

# 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),
    infections = sum(infections),
    ve = mean(ve)
  ) %>%
  ungroup()

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

```
)
sum(m1$avert)
sum(m3$avert)
```

sim_reference	<i>Simulate an ideal population</i>
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Description

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

Usage

```
sim_reference(init_pop_size, vaccinations, infections_novac, ve, lag)
```

Arguments

init_pop_size	Integer initial population size
vaccinations	Integer vector number of vaccinations at every timepoint
infections_novac	Integer vector number of infections at every timepoint
ve	Vaccine effectiveness (proportion)
lag	Integer lag period measured in timepoints

Value

A [tibble](#) with the following columns:

timepoint	Index of timepoint
vaccinations	Expected number of vaccinations
infections_novac	Expected number of infections in absence of vaccination
ve	Expected vaccine effectiveness
pflu	Flu incidence
infections	Actual number of infections
popn	Non-cases in absence of vaccination
pvac	Proportion of starting population vaccinated
b	Number vaccinated at that time who didn't get infected later
b_og	Number vaccinated at that time
A	Non-vaccinated non-cases
C	Vaccinated susceptible
D	Vaccinated immune
E	Non-vaccinated infections cumulative total
F	Vaccinated infections cumulative total

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),
  infections_novac = generate_counts(nsam, ndays, 0.12, mean = 190, sd = 35),
  ve = 0.48,
  lag = 14
)
head(pop_tok)
sum(pop_tok$avert)
```

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