Package 'spread'

August 20, 2019

Title Infectious Disease Spread Models

Version 2019.8.5

Description A stochastic SEIIaR (susceptible, exposed, infectious, infectious asymptomatic, recovered) metapopulation model that including commuting. Each location has a local infection system, while the locations are connected by people who commute each day. The model differentiates between day and night. During the day you can infect/be infected in the location where you work, while during the night you can infect/be infected in the location where you live. It is the same commuters who travel back and forth each day. At the start of a day, all commuters are sent to their work location, where they mix for 12 hours. The commuters are then sent to their respective home locations, where they mix for 12 hours. The model is loosely based upon a published model by Engebretsen (2019) <doi:10.1371/journal.pcbi.1006879>.

Depends R (>= 3.5.0)

Imports Rcpp (>= 0.9.4), RcppProgress (>= 0.1), data.table, fhidata, stringr, readxl, zoo

Suggests testthat, knitr, ggplot2, glue, rmarkdown

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

LinkingTo Rcpp, RcppProgress

VignetteBuilder knitr

SystemRequirements C++11

NeedsCompilation yes

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Repository CRAN

Date/Publication 2019-08-20 15:50:02 UTC

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R topics documented:

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commuter	*commuter*

Description

This model is a stochastic SEIIaR (susceptible, exposed, infectious, infectious asymptomatic, recovered) metapopulation model that including commuting.

Usage

```
commuter(seiiar = spread::norway_seiiar_oslo_2017,
  commuters = spread::norway_commuters_2017, r0 = NULL, beta = NULL,
  latent_period = 1.9, infectious_period = 3, asymptomatic_prob = 0,
  asymptomatic_relative_infectiousness = 0, days_simulation = 7 * 8,
  N = 1)
```

Arguments

seiiar	Data frame containing 'location_code', 'S', 'E', 'I', 'Ia', and 'R' for the entire population
commuters	Data frame comtaining 'from', 'to', 'n' for the number of people who travel
r0	Float, basic reproduction number
beta	Float, infection parameter, 0.6
latent_period	Float, 1.9
infectious_period	
	Float, 3
asymptomatic_prob	
	Float, Proportion/probability of asymptomatic given infectious
asymptomatic_relative_infectiousness	
	Float, Relative infectiousness of asymptomatic infectious
days_simulation	
	Int, Number of days to simulate
N	Int = 1 int, Number of repetitions

Details

Each location has a local infection system, while the locations are connected by people who commute each day. The model differentiates between day and night. During the day you can infect/be infected in the location where you work, while during the night you can infect/be infected in the location where you live. It is the same commuters who travel back and forth each day. At the start of a day, all commuters are sent to their work location, where they mix for 12 hours. The commuters are then sent to their respective home locations, where they mix for 12 hours.

The model is loosely based upon a published model by Engebretsen (2019) doi: 10.1371/journal.pcbi.1006879.

For more information, look at vignette("commuter_model","spread")

Examples

```
spread::commuter(
  seiiar = spread::norway_seiiar_measles_oslo_2017,
  commuters = spread::norway_commuters_2017,
  r0 = 14,
  latent_period = 8,
  infectious_period = 5,
  asymptomatic_prob = 0,
  asymptomatic_relative_infectiousness = 0,
  days_simulation = 7*9,
  N = 1
)
```

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commuter_cpp   *commuter*

Description

commuter

Usage

```
commuter_cpp(seiiar_home, seiiar_commuters, beta, a, gamma,
  asymptomaticProb, asymptomaticRelativeInfectiousness, N = 1L,
  M = 56L)
```

Arguments

seiiar_home   Data frame

seiiar_commuters

               Data frame

beta   Float, infection parameter, 0.6

a   Float, 1/latent period, 1/1.9

gamma   Float, 1/infectious period, 1/3

asymptomaticProb

     Float, Proportion/probability of asymptomatic given infectious

asymptomaticRelativeInfectiousness

     Float, Relative infectiousness of asymptomatic infectious

N   Int = 1 int, Number of repetitions

M   Int, Number of days

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convert_blank_seiiar_with_vax

Convert blank seiiar with vax

Description

Takes a fully susceptible population and proportion of people vaccinated per location code and allocates an appropriate amount of people to recovered. For more information, look at `vignette("including_vax","spread")`.

Usage

```
convert_blank_seiiar_with_vax(seiiar, vax)
```

Arguments

seiiar   SEIIAR data.table representing a fully susceptible population

vax   data.table containing proportion of people vaccinated per location code

Examples

```
vax_measles <- fhidata::norway_childhood_vax[
  year==2016 &
  stringr::str_detect(location_code,"^municip") &
  vax=="measles",
  c("location_code","proportion")
]

norway_seiiar_measles_noinfected_2017 <- spread::convert_blank_seiiar_with_vax(
  seiiar = spread::norway_seiiar_noinfected_2017,
  vax = vax_measles
)
```

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norway_commuters_2017 *Daily number of commuters from/to municipalities in Norway in 2017*

Description

Daily number of commuters from/to municipalities in Norway in 2017

Usage

```
norway_commuters_2017
```

Format

from Location code.

to Location name.

n Number of people.

Source

---

norway_seiiar_measles_noinfected_2017

SEIIaR data.frame for Norway with no one infected and real measles susceptibility.

Description

Measles vaccination coverate rates for 16 year olds in the 5 year average from 2014 to 2018 were used as the proportion of recovered people.

Usage

```
norway_seiiar_measles_noinfected_2017
```

Format

location_code Location code.

S Number of susceptible people.

E Number of exposed people.

I Number of infectious and symptomatic people.

Ia Number of infectious and asymptomatic people.

R Number of recovered people.

Source

<http://khs.fhi.no/webview/>

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norway_seiiar_measles_oslo_2017

SEIIaR data.frame for Norway with 10 people infected in Oslo and real measles susceptibility.

Description

Measles vaccination coverate rates for 16 year olds in the 5 year average from 2014 to 2018 were used as the proportion of recovered people.

Usage

```
norway_seiiar_measles_oslo_2017
```

Format

location_code Location code.

S Number of susceptible people.

E Number of exposed people.

I Number of infectious and symptomatic people.

Ia Number of infectious and asymptomatic people.

R Number of recovered people.

Source

<http://khs.fhi.no/webview/>

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norway_seiiar_noinfected_2017

SEIIaR data.frame for Norway with no one infected and everyone susceptible.

Description

SEIIaR data.frame for Norway with no one infected and everyone susceptible.

Usage

```
norway_seiiar_noinfected_2017
```

Format

location_code Location code.

S Number of susceptible people.

E Number of exposed people.

I Number of infectious and symptomatic people.

Ia Number of infectious and asymptomatic people.

R Number of recovered people.

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norway_seiiar_oslo_2017

SEIIaR data.frame for Norway with 10 people infected in Oslo and everyone susceptible.

Description

SEIIaR data.frame for Norway with 10 people infected in Oslo and everyone susceptible.

Usage

norway_seiiar_oslo_2017

Format

location_code Location code.

S Number of susceptible people.

E Number of exposed people.

I Number of infectious and symptomatic people.

Ia Number of infectious and asymptomatic people.

R Number of recovered people.

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