

Package: epimixr (via r-universe)

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Title Epidemiological analysis using social mixing matrices

Version 0.1

Description Provides methods to conduct epidemiological analysis using social mixing matrices, such as calculating contact-adjusted immunity levels or age distributions of epidemics.

Depends R (>= 3.5.0)

Imports socialmixr

Suggests testthat

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Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

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

RemoteUrl <https://github.com/sbfknk/epimixr>

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adjust_immunity	<i>Estimate reproduction number from contact information and immunity profile</i>
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Description

This takes a contact survey to derive a contact matrix and rescales contacts to represent contacts with susceptibles. This is then combined with information on the basic reproduction number R_0 to calculate the effective or net reproduction number.

Usage

```
adjust_immunity(mixing_matrix, immunity, vector = FALSE)
```

Arguments

mixing_matrix	A mixing matrix, as returned by <code>socialmixr::contact_matrix</code>
immunity	immunity profile; this should be given as a vector of the same length as the number of rows/columns of the mixing matrix; each element of the vector should contain a value <1 representing the proportion of the population immune in the corresponding age group; any element set to "herd" will be set to $1-1/R_0$
vector	if TRUE, will return the eigenvector corresponding to the dominant eigenvector instead of adjusted immunity; this corresponds to the expected stable age distribution of infections in case of an outbreak

Value

a list contain vectors of adjusted immunities

Author(s)

Sebastian Funk

Examples

```
library("socialmixr")
mixing <- contact_matrix(survey = polymod, age.limits
  = c(0, 5, 10))
adjust_immunity(mixing$matrix, immunity = c(0, 0.5, 0.8))
```

epidemic_age_dist	<i>Calculates the age distribution of an epidemic</i>
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Description

calculates the age distribution in an epidemic setting using the iterative method of: J Wallinga, P Teunis, M Kretzschmar (2006) Using Data on Social Contacts to Estimate Age-specific Transmission Parameters for Respiratory-spread Infectious Agents. Am J Epidemiol 164(10), 945-946.

Usage

```
epidemic_age_dist(  
  mixing_matrix,  
  r_0,  
  immunity = 0,  
  final_size_start = 0.01,  
  tol = 1e-05  
)
```

Arguments

<code>mixing_matrix</code>	A mixing matrix or set of mixing matrices, as returned by <code>socialmixr::contact_matrix</code>
<code>r_0</code>	basic reproduction number
<code>immunity</code>	proportion immune before the epidemic
<code>final_size_start</code>	starting value for incidence
<code>tol</code>	tolerance for stopping the iteration

Value

A matrix of the final size(s) (proportion of susceptibles infected) in each age group (one row per matrix contained in `mixing`)

Examples

```
library("socialmixr")  
mixing <- contact_matrix(survey = polymod, age.limits = c(0, 5, 10))  
epidemic_age_dist(mixing$matrix, r_0 = 5, immunity = 0.50)
```

project_immunity *Project immunity from a baseline*

Description

Project immunity from a baseline via vaccination coverage rates

Usage

```
project_immunity(  
  baseline_immunity,  
  baseline_year,  
  year,  
  coverage,  
  schedule,  
  maternal_immunity,  
  efficacy  
)
```

Arguments

baseline_immunity	baseline immunity, as a named vector; the names correspond to lower limits of the age groups, and the vector itself to the corresponding levels of immunity.
baseline_year	year at which baseline immunity is taken (corresponding to a column in the coverage argument)
year	year to project to
coverage	coverage with multiple vaccine doses, given as a matrix in which each row is a dose and each (named) column a year
schedule	the ages at which vaccines are given (in years).
maternal_immunity	the proportion maternally immune.
efficacy	vaccine efficacy.

Value

a data frame of immunity levels by age group (as in baseline_immunity).

Author(s)

Sebastian Funk <sebastian.funk@lshtm.ac.uk>

Examples

```
baseline_immunity <- c(`2` = 0.85, `5` = 0.9, `10` = 0.95)
coverage <- matrix(rep(0.9, 10), nrow = 2)
colnames(coverage) <- as.character(seq(2015, 2019))
project_immunity(
  baseline_immunity, 2018, 2019, coverage = coverage,
  schedule = c(1, 2), 0.5, 0.95
)
```

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