Package 'facilityepimath'

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Title Analyze Mathematical Models of Healthcare Facility Transmission

Version 0.1.0

Description Calculate useful quantities for a user-defined differential equation model of infectious disease transmission among individuals in a healthcare facility. Input rates of transition between states of individuals with and without the disease-causing organism, distributions of states at facility admission, relative infectivity of transmissible states, and the facility length of stay distribution. Calculate the model equilibrium and the basic facility reproduction number, as described in Toth et al. (2025) <doi:10.1101/2025.02.21.25322698>.

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Encoding UTF-8

RoxygenNote 7.3.2

URL https://github.com/EpiForeSITE/facilityepimath

BugReports https://github.com/EpiForeSITE/facilityepimath/issues

Imports MASS

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

VignetteBuilder knitr

NeedsCompilation no

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equilib

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equilib

Calculate the equilibrium of a linear facility model

Description

Calculate the equilibrium of a linear facility model

Usage

equilib(M, init, mgf = NULL)

Arguments

М	A matrix of state transition rates between facility patient states
init	A vector of admission state probabilities to each state
mgf	The moment generating function characterizing a time-of-stay-dependent re- moval hazard

Value

A vector with the proportion of patients in each state at equilibrium

Examples

```
M <- rbind(c(-0.06,0.03,0),c(0.06,-0.08,0),c(0,0.05,0))
init <- c(0.95,0.05,0)
mgf <- function(x, deriv=0) MGFgamma(x, rate = 0.05, shape = 2.5, deriv)
equilib(M, init, mgf)</pre>
```

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facilityeq

Description

Calculate the equilibrium of a facility transmission model

Usage

facilityeq(S, C, A, R, transm, init, mgf = NULL)

Arguments

S	A matrix of state transition rates between and removal from the susceptible states in the absence of colonized individuals
С	A matrix of state transition rates between and removal from the colonized states
A	A matrix describing transitions from susceptible to colonized states at acquisition
R	A matrix of recovery rates: state transition rates from colonized to susceptible states
transm	A vector of transmission rates from each colonized state
init	A vector of admission state probabilities to each state
mgf	The moment generating function characterizing a time-of-stay-dependent re- moval hazard

Value

A vector with the proportion of patients in each state at equilibrium; the vector contains the equilibrium S states followed by C states

```
S <- 0
C <- rbind(c(-0.38,0),c(0.08,0))
A <- rbind(1,0)
R <- cbind(0.3,0)
transm <- c(0.1,0.05)
init <- c(0.99,0.01,0)
mgf <- function(x, deriv=0) MGFgamma(x, rate=0.2, shape=3, deriv)
facilityeq(S, C, A, R, transm, init, mgf)
```

facilityR0

Description

Calculate basic reproduction number R0

Usage

facilityR0(S, C, A, transm, initS, mgf = NULL)

Arguments

S	A matrix of state transition rates between and removal from the susceptible states in the absence of colonized individuals
С	A matrix of state transition rates between and removal from the colonized states
A	A matrix describing transitions from susceptible to colonized states at acquisition
transm	A vector of transmission rates from each colonized state
initS	A vector of admission state probabilities to each susceptible state
mgf	The moment generating function characterizing the time-of-stay-dependent re- moval hazard

Value

A number (R0)

```
S <- rbind(c(-1,2),c(1,-2))
C <- rbind(c(-1.1,0),c(0.1,-0.9))
A <- rbind(c(1,0),c(0,2))
transm <- c(0.4,0.6)
initS <- c(0.9,0.1)
mgf <- function(x, deriv=0) MGFgamma(x, rate=0.01, shape=3.1, deriv)
facilityR0(S,C,A,transm,initS,mgf)
```

meanlengthofstay Calculate the mean length of stay for a linear facility model

Description

Calculate the mean length of stay for a linear facility model

Usage

```
meanlengthofstay(M, init, mgf)
```

Arguments

М	A matrix of state transition rates between facility patient states
init	A vector of admission state probabilities to each state
mgf	The moment generating function characterizing a time-of-stay-dependent re- moval hazard

Value

The mean length of stay

Examples

```
M <- rbind(c(-1.1,2),c(1,-2.2))
init <- c(0.9,0.1)
mgf <- function(x, deriv=0) MGFgamma(x, rate=0.2, shape=3, deriv)
meanlengthofstay(M, init, mgf)</pre>
```

MGFexponential	Evaluate the moment generating function (MGF) of the exponential
	distribution or a derivative of the MGF

Description

Evaluate the moment generating function (MGF) of the exponential distribution or a derivative of the MGF

Usage

MGFexponential(x, rate, deriv = 0)

Arguments

Х	The value at which to evaluate the MGF
rate	The rate parameter value of the exponential distribution
deriv	An integer, the number of derivatives of the MGF to apply

Value

The number resulting from the function evaluation

Examples

```
# MGF of an exponential distribution, evaluated at -0.1:
MGFexponential(-0.1, rate = 0.05)
# Second moment of the distribution (second derivative evaluated at zero):
MGFexponential(0, rate = 0.05, deriv = 2)
```

MGFgamma	Evaluate the moment generating function (MGF) of the gamma distri-
	bution or a derivative of the MGF

Description

Evaluate the moment generating function (MGF) of the gamma distribution or a derivative of the MGF

Usage

```
MGFgamma(x, rate, shape, deriv = 0)
```

Arguments

х	The value at which to evaluate the MGF
rate	The rate parameter value of the gamma distribution
shape	The shape parameter values of the gamma distribution
deriv	An integer, the number of derivatives of the MGF to apply

Value

The number resulting from the function evaluation

```
# MGF of a gamma distributions, evaluated at -0.1:
MGFgamma(-0.1, rate = 0.7, shape = 3)
# Second moment of the distribution (second derivative evaluated at zero):
MGFgamma(0, rate = 0.7, shape = 3, deriv = 2)
```

MGFmixedgamma

Evaluate the moment generating function (MGF) of the mixed gamma distribution or a derivative of the MGF

Description

Evaluate the moment generating function (MGF) of the mixed gamma distribution or a derivative of the MGF

Usage

```
MGFmixedgamma(x, prob, rate, shape, deriv = 0)
```

Arguments

x Tl	he value at which to evaluate the MGF
prob A	vector of probabilities of following each gamma distribution in the mixture
rate A	vector of rate parameter values for each gamma distribution in the mixture
shape A	vector of shape parameter values for each gamma distribution in the mixture
deriv A	n integer, the number of derivatives of the MGF to apply

Value

The number resulting from the function evaluation

```
# MGF of a 40/60 mixture of two gamma distributions, evaluated at -0.1:
MGFmixedgamma(-0.1, prob = c(0.4, 0.6), rate = c(0.4, 0.7), shape = c(0.5, 3))
# Second moment of the distribution (second derivative evaluated at zero):
MGFmixedgamma(0, prob = c(0.4, 0.6), rate = c(0.4, 0.7), shape = c(0.5, 3), deriv = 2)
```

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