

Package ‘EpiILM’

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Type Package

Title Spatial and Network Based Individual Level Models for Epidemics

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Description Provides tools for simulating from discrete-time individual level models for infectious disease data analysis. This epidemic model class contains spatial and contact-network based models with two disease types: Susceptible-Infectious (SI) and Susceptible-Infectious-Removed (SIR).

License GPL (>= 2)

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R topics documented:

epiBR0	2
epicurve	3
epidata	3
epidic	6
epilike	6
epimcmc	8
epispacial	10
tswv	11

Index	12
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epiBR0 *Basic reproduction number (R0)*

Description

Calculates the basic reproduction number for the specified SIR model and data set

Usage

```
epiBR0 (x = NULL, y = NULL, contact = NULL, alpha, beta, spark = NULL, infperiod,
        Sformula = NULL, tmax, niter)
```

Arguments

x	X coordinates of individuals
y	Y coordinates of individuals
contact	Contact network(s)
alpha	Susceptibility parameter(>0)
beta	Spatial parameter(s) (>0) or network parameter (s) (>0) if contact is used
spark	Sparks parameter (>=0), representing infections unexplained by other parts of the model or infections coming in from outside the observed population, default value is zero
infperiod	Length of infectious period for each individual
Sformula	An object of class formula. See formula Individual-level covariate information passable through this argument. An expression of the form $\sim \text{model}$ is interpreted as a specification that the susceptibility function, $\Omega_s(i)$ is modelled by a linear predictor specified symbolically by the model term. Such a model consists of a series of terms separated by + and - operators. If there is no covariate information, Sformula is null.
tmax	The last time point of simulation
niter	Number of epidemic simulations to calculate basic reproduction number

Value

BasicR0	The basic reproduction number value
simulated_BR0	Number of infections per simulation

epicurve *Epidemic curves*

Description

Produces graphs of various epidemic curves

Usage

```
epicurve (type, plottype, inftime, removaltime = NULL, tmin = NULL, timepoints = NULL)
```

Arguments

type	Type of compartment framework, with the choice of "SI" for Susceptible-Infectious diseases and "SIR" for Susceptible-Infectious-Removed
plottype	Plot type to be plotted, with the following choices: "complete" for plotting the number of susceptible, infected and removed individuals at each time point, "susceptible" for plotting the number of susceptible individuals at each time point, "newinfect" for plotting the number of newly infected individuals at each time point, and "totalinfect" for plotting the cumulative number of infected individuals at each time point
inftime	Times at which individuals become infected/infectious
removaltime	Time points where the individual is removed
tmin	Initial time point at which infection occurs, default value is one
timepoints	Specify time points at which the curve is plotted

epidata *Simulates epidemic for the specified model type and parameters*

Description

This function allows the user to simulate epidemics under different models and scenarios

Usage

```
epidata (type, n, tmin = NULL, tmax, alpha, beta, spark = NULL, Sformula = NULL,
         x = NULL, y = NULL, inftime = NULL, infperiod = NULL, contact = NULL)
```

Arguments

type	Type of compartment framework, with the choice of "SI" for Susceptible-Infectious diseases and "SIR" for Susceptible-Infectious-Removed
n	Population size
tmin	The time point at which simulation begins, default value is one
tmax	The last time point of simulation
alpha	Susceptibility parameter (>0)
beta	Spatial parameter(s) (>0) or network parameter (s) (>0) if contact is used
spark	Sparks parameter (>=0), representing infections unexplained by other parts of the model (eg. infections coming in from outside the observed population), default value is zero
Sformula	An object of class formula. See formula Individual-level covariate information associated with susceptibility can be passed through this argument. An expression of the form \sim model is interpreted as a specification that the susceptibility function, $\Omega_s(i)$ is modelled by a linear predictor specified symbolically by the model term. Such a model consists of a series of terms separated by + and - operators. If there is no covariate information, Sformula is null
x	X coordinates of individuals
y	Y coordinates of individuals
infptime	Times at which individuals are infected to initialize epidemic simulation
infperiod	Length of infectious period for each individual
contact	Contact network matrix (matrices)

Details

We consider following two individual level models:

Spatial model:

$$P(i, t) = 1 - \exp\{-\Omega_s(i) \sum_{j \in I(t)} d_{ij}^{-\beta} - \varepsilon\}$$

Network model:

$$P(i, t) = 1 - \exp\{-\Omega_s(i) \sum_{j \in I(t)} (\beta_1 C_{ij}^{(1)} + \dots + \beta_n C_{ij}^{(n)}) - \varepsilon\}$$

where $P(i, t)$ is the probability that susceptible individual i is infected at time point t , becoming infectious at time $t+1$; and $\Omega_s(i)$ is a susceptibility function which accommodates potential risk factors associated with susceptible individual i contracting the disease.

Value

infptime	Times at which individuals become infected/infectious
removaltime	Times at which individuals are removed

References

Deardon R, Brooks, S. P., Grenfell, B. T., Keeling, M. J., Tildesley, M. J., Savill, N. J., Shaw, D. J., Woolhouse, M. E. (2010). Inference for individual level models of infectious diseases in large populations. *Statistica Sinica*, 20, 239-261.

Rob Deardon, Xuan Fang, and Grace Pui Suze Kwong (2014). Statistical modelling of spatio-temporal infectious disease transmission in analyzing and modeling Spatial and temporal dynamics of infectious diseases, (Ed: D. Chen, B. Moulin, J. Wu), *John Wiley & Sons*. Chapter 11.

Examples

```
## Example 1: spatial SI model
# generate 100 individuals

x <- runif(100, 0, 10)

y <- runif(100, 0, 10)

covariate <- runif(100, 0, 2)

out <- epidata(type = "SI", n = 100, Sformula = ~covariate, tmax = 15,
              alpha = c(0.1, 0.3), beta = 5.0, x = x, y = y)

# Plots of epidemic progression (optional)

epispacial(type = "SI", x = x, y = y, infptime = out$infptime)

epicurve(type = "SI", infptime = out$infptime, plottype = "newinfect")

## Example 2: spatial SIR model
# generate infectious period(=3) for 100 individuals

lambda <- rep(3, 100)

epidata(type = "SIR", n = 100, tmax = 15, alpha = 0.3, beta = 5.0, infperiod = lambda,
        x = x, y = y)

## Example 3: SI network model
## Not run:
contact1 <- matrix(rbinom(1000, 1, 0.1), nrow = 100, ncol = 100)

contact2 <- matrix(rbinom(1000, 1, 0.1), nrow = 100, ncol = 100)

diag(contact1[,]) <- 0

diag(contact2[,]) <- 0

contact <- array(c(contact1, contact2), dim = c(100, 100, 2))

epidata(type = "SI", n = 100, tmax = 15, alpha = 0.3, beta = c(3.0, 5.0),
```

```

        contact = contact)

## End(Not run)

```

epidic *Deviance Information Criterion (DIC)*

Description

Computes the Deviance Information Criterion for individual level models

Usage

```
epidic (burnin, niter, LLchain, LLpostmean)
```

Arguments

burnin	Burnin period for MCMC
niter	Number of MCMC iterations
LLchain	Loglikelihood values from the MCMC output
LLpostmean	Loglikelihood value of the model with posterior mean of estimates

References

Spiegelhalter, D., Best, N., Carlin, B., Van der Linde, A. (2002). Bayesian Measures of Model Complexity and Fit. *Journal of the Royal Statistical Society. Series B (Statistical Methodology)*, 64(4), 583-639.

epilike *Calculates the log likelihood*

Description

Calculates the log likelihood for the specified individual level model and data set

Usage

```
epilike (type, x = NULL, y = NULL, infptime, infperiod = NULL, tmin = NULL, tmax, alpha,
        beta, spark = NULL, Sformula = NULL, contact = NULL)
```

Arguments

type	Type of compartment framework, with the choice of "SI" for Susceptible-Infectious diseases and "SIR" for Susceptible-Infectious-Removed
x	X coordinates of individuals
y	Y coordinates of individuals
inftime	Infection times
infperiod	Length of infectious period for each individual
tmin	The first time point at which data is observed, default value is one
tmax	The last time point at which data is observed
alpha	Susceptibility parameter(>0)
beta	Spatial parameter(s) (>0) or network parameter (s) (>0) if contact is used
spark	Sparks parameter(>=0), representing infections unexplained by other parts of the model or infections coming in from outside the observed population, default value is zero
Sformula	An object of class formula. See formula Individual-level covariate information passable through this argument. An expression of the form \sim model is interpreted as a specification that the susceptibility function, $\Omega_s(i)$ is modelled by a linear predictor specified symbolically by the model term. Such a model consists of a series of terms separated by + and - operators. If there is no covariate information, Sformula is null
contact	Contact network matrix (matrices)

References

Deardon R, Brooks, S. P., Grenfell, B. T., Keeling, M. J., Tildesley, M. J., Savill, N. J., Shaw, D. J., Woolhouse, M. E. (2010). Inference for individual level models of infectious diseases in large populations. *Statistica Sinica*, 20, 239-261.

Examples

```
## Example 1: spatial SI model
# generate 100 individuals
## Not run:
x <- runif(100, 0, 10)

y <- runif(100, 0, 10)

covariate <- runif(100, 0, 2)

out <- epidata(type = "SI", n = 100, Sformula = ~covariate, tmax = 15,
              alpha = c(0.1, 0.3), beta = 5.0, x = x, y = y)

epilike(type = "SI", x = x, y = y, inftime = out$inftime, tmax = 15,
        alpha = c(0.1, 0.3), beta = 5, Sformula = ~covariate)
```

```
## End(Not run)
## Example 2: spatial SIR model
# generate infectious period (=3) for 100 individuals
## Not run:
lambda <- rep(3, 100)

out <- epidata(type = "SIR", n = 100, tmax = 15, alpha = 0.3, beta = 5.0,
              infperiod = lambda, x = x, y = y)

epilike(type = "SIR", x = x, y = y, infperiod = lambda, inftime = out$inftime,
        tmax = 15, alpha = 0.3, beta = 5.0)

## End(Not run)
```

epimcmc

Monte Carlo Simulation

Description

Runs an MCMC algorithm for the estimation of specified model parameters

Usage

```
epimcmc (type, x = NULL, y = NULL, inftime, tmin = NULL, tmax, infperiod = NULL, niter,
        alphaini, betaini, sparkini = NULL, Sformula = NULL, contact = NULL,
        pro.var.a, pro.var.b, pro.var.sp = NULL, prioralpha, halfnorm.var.a = NULL,
        gamma.par.a = NULL, unif.range.a = NULL, priorbeta, halfnorm.var.b = NULL,
        gamma.par.b = NULL, unif.range.b = NULL, priorsp = NULL, halfnorm.var.sp = NULL,
        gamma.par.sp = NULL, unif.range.sp = NULL)
```

Arguments

type	Type of compartment framework, with the choice of "SI" for Susceptible-Infectious diseases and "SIR" for Susceptible-Infectious-Removed
x	X coordinates of individuals
y	Y coordinates of individuals
inftime	Times at which individuals are infected to initialize epidemic simulation
tmin	The first time point at which the infection occurs, default value is one
tmax	The last time point of simulation
infperiod	Length of infectious period for each individual

niter	Number of MCMC iterations
alphaini	Initial value of susceptibility parameter(s)(>0)
betaini	Initial value of spatial parameter(s) (>0) or network parameter (s) (>0) if contact is used
sparkini	Initial value of spark parameter (>=0)
Sformula	An object of class formula. See formula Individual-level covariate information associated with susceptibility can be passed through this argument. An expression of the form \sim model is interpreted as a specification that the susceptibility function, $\Omega_s(i)$ is modelled by a linear predictor specified symbolically by the model term. Such a model consists of a series of terms separated by + and - operators. If there is no covariate information, Sformula is null
contact	Contact network matrix (matrices)
pro.var.a	Proposal density variance for alpha parameter(s)
pro.var.b	Proposal density variance for beta parameter(s)
pro.var.sp	Proposal density variance for spark parameter
prioralpha	Select the prior distribution for alpha parameter(s) with the choice of "halfnormal" for positive half normal distribution, "gamma" for gamma distribution and "uniform" for uniform distribution
halfnorm.var.a	Half normal prior variance for alpha
gamma.par.a	Gamma prior: shape and scale parameters for alpha
unif.range.a	Uniform prior: Maximum and minimum range for alpha
priorbeta	Select the prior distribution for beta parameter(s) with the choice of "halfnormal" for half normal distribution, "gamma" for gamma distribution and "uniform" for uniform distribution
halfnorm.var.b	Half normal prior variance for beta
gamma.par.b	Gamma prior: shape and scale parameters for beta
unif.range.b	Uniform prior: Maximum and minimum range for beta
priorsp	Select the prior distribution for spark parameter with the choice of "halfnormal" for half normal distribution, "gamma" for gamma distribution and "uniform" for uniform distribution
halfnorm.var.sp	Half normal prior variance for spark
gamma.par.sp	Gamma prior: shape and scale parameters for spark
unif.range.sp	Uniform prior: Maximum and minimum range for spark

Details

Independent Gaussian random walks are used as the Metropolis-Hastings MCMC proposal for all parameters

Value

Estimates MCMC output
 Loglikelihood Log likelihood value of each posterior estimate

References

Rob Deardon, Xuan Fang, and Grace Pui Suze Kwong (2014). Statistical modelling of spatio-temporal infectious disease transmission in *Analyzing and Modeling Spatial and Temporal Dynamics of Infectious Diseases*, (Ed: D. Chen, B. Moulin, J. Wu), John Wiley & Sons.. Chapter 11.

See Also

[traplot](#)

Examples

```
## Example 1: spatial SI model
# generate 100 individuals
## Not run:
x <- runif(100, 0, 10)

y <- runif(100, 0, 10)

covariate <- runif(100, 0, 2)

out <- epidata(type = "SI", n = 100, Sformula = ~covariate, tmax = 15,
              alpha = c(0.1, 0.3), beta = 5.0, x = x, y = y)

mcout <- epimcmc(type = "SI", x = x, y = y, inftime = out$inftime, Sformula = ~covariate,
                tmax = 15, niter = 1000, alphaini = c(0.01, 0.01), betaini = 0.01,
                pro.var.a = c(0.01, 0.005), pro.var.b = 0.05,
                prioralpha = "halfnormal", halfnorm.var.a = c(10**5, 10**5),
                priorbeta = "halfnormal", halfnorm.var.b = 10**5)

## End(Not run)
```

epispatal

Spatial Plot

Description

Produce spatial plots of epidemic progression over time

Usage

```
epispatal (type, x, y, inftime, removaltime = NULL, time = NULL, tmin = NULL)
```

Arguments

<code>type</code>	Type of compartment framework, with the choice of "SI" for Susceptible-Infectious diseases and "SIR" for Susceptible-Infectious-Removed
<code>x</code>	X coordinates of individuals
<code>y</code>	Y coordinates of individuals
<code>inftime</code>	Times at which individuals become infected/infectious
<code>removaltime</code>	Times at which individuals are removed
<code>time</code>	Specify time points at which the spatial square is plotted
<code>tmin</code>	Initial time point at which infection occurs, default value is one

tswv

Tomato Spotted Wilt Virus data

Description

Data extracted from plots presented in Hughes et al. (1997)

Usage

```
data(tswv)
```

Format

A data frame with following variables

x X coordinate

y Y coordinate

inftime Infection times

removaltime Times at which individuals are removed

References

Hughes, G., McRoberts, N., Madden, L.V., Nelson, S. C. (1997). Validating mathematical models of plant disease progress in space and time. *IMA Journal of Mathematics Applied in Medicine and Biology*, 14, 85-112.

Index

epiBR0, [2](#)
epicurve, [3](#)
epidata, [3](#)
epidic, [6](#)
epilike, [6](#)
epimcmc, [8](#)
epispacial, [10](#)

formula, [2](#), [4](#), [7](#), [9](#)

traplot, [10](#)
tswv, [11](#)