

Package ‘EpiILMCT’

March 28, 2018

Title Continuous Time Distance-Based and Network-Based Individual Level Models for Epidemics

Version 1.1.2

Date 2018-03-27

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Description Provides tools for simulating from continuous-time individual level models of disease transmission, and carrying out infectious disease data analyses with the same models. The epidemic models considered are distance-based and contact network-based models within Susceptible-Infectious-Removed (SIR) or Susceptible-Infectious-Notified-Removed (SINR) compartmental frameworks.

Depends graphics (≥ 3.0), grDevices, methods (≥ 3.0), stats (≥ 3.0), utils (≥ 2.0), coda, R ($\geq 3.2.0$)

License GPL (≥ 2)

NeedsCompilation yes

Repository CRAN

Date/Publication 2018-03-28 08:17:58 UTC

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contactnet	<i>Generate binary adjacency contact networks</i>
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Description

This function allows the user to generate binary contact network adjacency matrices from spatial (power-law and cauchy) and random network models.

Usage

```
contactnet(type, location=NULL, beta, alpha=NULL, plot=FALSE)
```

Arguments

type	Type of contact network model, with the choice of “powerlaw” for the power-law model, “Cauchy” for the Cauchy model, and “random” for randomly generated contact network from a Bernoulli distribution with parameter beta.
location	A matrix of XY coordinates of individuals.
beta	Spatial parameter of the spatial contact network model or the probability parameter of the random network model (>0).
alpha	Scale parameter of the power-law contact network model (>0). Default value is 1.
plot	If plot set to TRUE, a graphical representation of the generated contact network is produced. The default is FALSE.

Details

The contact networks considered here are undirected and binary, so that $c_{ij} = c_{ji}$ for $i \neq j; i, j = 1, \dots, N$, and each element of the contact network is defined as $c_{ij} = 1$ if a connection exist between individuals i and j , and 0 otherwise. Here, we consider spatial networks with connections more likely to be present between two individuals close together than far apart, or random contact networks.

For spatial contact networks, there are two options of specifying the model for the probability of connections between individuals. We use a generalized version of the power-law contact network model of Bifulchi et al. (2013) for the first option, in which the probability of a connection between individuals i and j is given by:

$$p(c_{ij} = 1) = 1 - e^{-\alpha(d_{ij}^{-\beta})}, \quad \alpha, \beta > 0,$$

where d_{ij} is the Euclidean distance between individuals i and j ; β is the spatial parameter; and α is the scale parameter.

The second option is a Cauchy model as used in Jewell et al., (2009). The probability of a connection between individuals i and j is given by:

$$p(c_{ij} = 1) = 1 - e^{-\beta/(d_{ij}^2 + \beta^2)}, \quad \beta > 0,$$

where d_{ij} is the Euclidean distance between individual i and j ; and β is the spatial parameter.

The final option is a random contact network in which the probability of a connection is generated from a Bernoulli distribution with probability equal to β .

Value

Binary contact network adjacency matrix

References

Jewell, C. P., Kypraios, T., Neal, P., and Roberts, G. O. (2009). Bayesian analysis for emerging infectious diseases. *Bayesian Analysis*, 4(3):465-496.

Bifulchi, N., Deardon, R., and Feng, Z. (2013). Spatial approximations of network-based individual level infectious disease models. *Spatial and Spatio-temporal Epidemiology*, 6:59-70.

Examples

```
set.seed(66)
loc<- matrix(cbind(runif(50,0,10),runif(50,0,10)),ncol=2,nrow=50)
net1<- contactnet(type="powerlaw",location=loc,beta=1.5,alpha=0.5,
  plot=TRUE)
net2<- contactnet(type="Cauchy",location=loc,beta=0.5,plot=TRUE)
net3<- contactnet(type="random",location=loc,beta=0.08,plot=TRUE)
```

datagen	<i>Generate epidemics from distance-based and/or network-based continuous-time ILMs.</i>
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Description

Generate epidemics from distance-based and/or network-based ILMs.

Usage

```
datagen(type, kerneltype, kernelmatrix, distancekernel = NULL, initialepi = NULL,
  tmax = NULL, suspar = NULL, transpar = NULL, powersus = NULL, powertrans = NULL,
  kernel.par = NULL, spark = NULL, gamma = NULL, delta, suscov = NULL,
  transcov = NULL, seedval = NULL)
```

Arguments

type	Type of the compartmental framework, with the choice of “SIR” for Susceptible-Infectious-Removed and “SINR” for Susceptible-Infectious-Notified-Removed.
kerneltype	Type of kernel function with choice of “distance” for a distance-based ILM, “network” for a contact network-based ILM and “both” for a combination of network- and distance-based ILM.
kernelmatrix	A matrix of distances between individuals when kerneltype is set to “distance”. A matrix of incidence (0 or 1) or weights $[0, \infty)$ representing contact network when kerneltype is set to “network”. A list of two matrices (1: distance matrix, 2: contact network matrix) when kerneltype is set to “both”.
distancekernel	The spatial kernel type when kerneltype is set to “distance” or “both”. Choices are “powerlaw” for a power-law distance kernel or “Cauchy” for a Cauchy distance kernel.
initialepi	The epidemic data of the initial n_{ini} infected individuals. When type is set to “SIR”, it is an $n_{ini} \times 4$ matrix representing the id numbers of the individuals, removal times, infectious periods, and infection times. When type is set to “SINR”, it is an $n_{ini} \times 6$ matrix representing the id numbers of the individuals, removal times, delay periods, notification times, incubation periods, and infection times. The default is that one randomly chosen individual is infected with infection time set to zero.
tmax	The time at which the epidemic simulation ends. If not set the simulation is run until the epidemic dies out or all individuals are infected and then enter the removed state.
suspar	Parameter(s) for the susceptibility function (>0). Default value(s) is 1.
transpar	Parameter(s) for the transmissibility function (>0). Default value(s) is 1.
powersus	The power parameter(s) of the susceptibility function (>0). Default value(s) is 1.
powertrans	The power parameter(s) of the transmissibility function (>0). Default value(s) is 1.
kernel.par	A scalar spatial parameter when kerneltype is set to “distance” (>0), or a vector of the spatial and network effect parameters when kerneltype is set to “both” (>0). Default = NULL means that it is not required in the case when the kerneltype is set to “network”.
spark	Spark parameter (≥ 0), representing random infections that are unexplained by other parts of the model. Default value is zero.
gamma	The notification effect parameter for SINR model. The default value is 1.
delta	A vector of the shape and rate parameters of the gamma-distributed infectious period (SIR) or a 2×2 matrix of the shape and rate parameters of the gamma-distributed incubation and delay periods (SINR). Note that an exponential distribution can be assigned as it is a special case of the gamma distribution where the shape parameter is equal to one.
suscov	Covariate matrix of the susceptibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.

transcov	Covariate matrix of the transmissibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.
seedval	An integer initialized seed value to fix the (Fortran) random number generator used in the simulation procedure. A random seed value is used as a default.

Details

We consider the simulation of epidemics from continuous-time ILMs in the following way. Each infected individual has an infection life history defined by their time of infection and the length of time spent in the infectious state. We are assuming that infection events follow a non-homogenous Poisson process, so that the time to the next infected individual, given that the last infection occurred at time t , is given by the minimum $W_j \sim \text{Exp}(\lambda_{jt})$, where W_j represents the “waiting time” for susceptible individual j becoming infected.

Under both SIR and SINR ILMs option, an epidemic is simulated using the specified model starting with a randomly chosen infected individual k at time I_1 , or as specified via the `initialepi` option. Under the SIR model, the rate of infection of each susceptible individual j at time $t \in \mathbb{R}^+$ follows the framework of Deardon et al. (2010):

$$\lambda_{jt} = \left[\Omega_S(j) \sum_{i \in \mathcal{I}(t)} \Omega_T(i) \kappa(i, j) \right] + \epsilon(j, t),$$

where $\mathcal{I}(t)$ is the set of infectious individual at time t . Under the SINR model, the rate of infection of each susceptible individual j at time t follows Jewell et al. (2009):

$$\lambda_{jt} = \left[\Omega_S(j) \sum_{i \in \mathcal{N}^-(t)} \Omega_T(i) \kappa(i, j) + \gamma \left(\Omega_S(j) \sum_{i \in \mathcal{N}^+(t)} \Omega_T(i) \kappa(i, j) \right) \right] + \epsilon(j, t),$$

where $\mathcal{N}^-(t)$ is the set of infectious individual at time t who have been infected but have not reached the notified state; $\mathcal{N}^+(t)$ is the set of infectious individual at time t who have been infected and reached the notified state; γ is the notification effect parameter usually allowing for infectious risk reduction after notification (Jewell et al., 2009); $\Omega_S(j)$ is a function of risk factors associated with susceptible individual j (i.e., susceptibility); and $\Omega_T(i)$ is a function of risk factors associated with infectious individual i (i.e., transmissibility). The $\Omega_S(j)$ and $\Omega_T(i)$ are defined as:

$$\Omega_S(j) = \mathbf{S}\mathbf{X}_j^\phi; \text{ and } \Omega_T(i) = \mathbf{T}\mathbf{Z}_i^\xi,$$

where \mathbf{S} and \mathbf{T} are the parameters vectors of the susceptibility and transmissibility functions, respectively; \mathbf{X} and \mathbf{Z} are the susceptibility and transmissibility risk factor matrices, respectively; and ϕ and ξ are vectors of the power parameters of the susceptibility and transmissibility functions, respectively. These power parameters allow for nonlinear relationships between the susceptibility and transmissibility risk factors and the infection rate (Deardon et al., 2010).

The infection kernel $\kappa(i, j)$ allows for distance (spatial) and/or contact network-based mechanisms. In distance-based models, the kernel function $\kappa(i, j)$ is a power-law or Cauchy function of distance. In network-based models, the kernel function $\kappa(i, j)$ is the contact network elements (binary c_{ij}) or

weighted (w_{ij}). In both distance-network-based models, the kernel function $\kappa(i, j)$ is represented by two terms: (1) spatial function, and (2) the contact network.

The optional kernel function formulas are as follows:

- **Distance-based ILMs:**

- Power-law spatial kernel: $\kappa(i, j) = d_{ij}^{-\beta}$
- Cauchy spatial kernel: $\kappa(i, j) = \frac{\beta}{d_{ij}^2 + \beta^2}$

- **Network-based ILMs:**

- $\kappa(i, j) = c_{ij}$ for binary contact network or,
- $\kappa(i, j) = w_{ij}$ for weighted contact network.

- **Both distance- and network-based ILMs:**

- With power-law spatial kernel:
 - * $\kappa(i, j) = d_{ij}^{-\beta_1} + \beta_2 c_{ij}$ with binary contact network or,
 - * $\kappa(i, j) = d_{ij}^{-\beta_1} + \beta_2 w_{ij}$ with weighted contact network.
- With Cauchy spatial kernel:
 - * $\kappa(i, j) = \frac{\beta_1}{(d_{ij}^2 + \beta_1^2)} + \beta_2 c_{ij}$ with binary contact network or,
 - * $\kappa(i, j) = \frac{\beta_1}{(d_{ij}^2 + \beta_1^2)} + \beta_2 w_{ij}$ with weighted contact network.

At time I_s , the waiting time until being infected is assigned for each susceptible individual j from $W_j \sim Exp(\lambda_{jI_s})$. The individual with minimum W is chosen as the next infected individual, and assigned infection time $I_{s+1} = I_s + \min(W_j)$. Under SIR model, this newly-infected individual is also assigned an infectious period D_j generated from the infectious period (exponential or gamma) distribution $f(D_j; \delta)$. Thus, its removal time becomes $R_{s+1} = I_{s+1} + D_j$. Under SINR model, each infected individual is assigned an incubation period defining the time from infection to notification, and a delay period defining the time from notification to removal. Thus, this newly-infected individual is assigned an incubation and delay period $D_j^{(inc)}$ and $D_j^{(delay)}$, generated from the (exponential or gamma) incubation and delay periods distributions $f(D_j^{(inc)}; \delta^{(inc)})$ and $f(D_j^{(delay)}; \delta^{(delay)})$, respectively. Thus, its notification and removal times become $N_{s+1} = I_{s+1} + D_j^{(inc)}$ and $R_{s+1} = N_{s+1} + D_j^{(delay)}$, respectively. The process is repeated until no infectives remain in the population, or until $I_{s+1} > tmax$ if it is specified.

The distance matrix can be obtained using the `dist` function from the `stats` package if the XY coordinates of individuals are given.

Value

Under an SIR ILM, the function `datagen()` returns a matrix with four columns representing the id numbers of the individuals, removal times, infectious periods, and infection times, respectively. Under an SINR ILM, the `datagen()` function returns a matrix with six columns: the id numbers of the individuals, removal times, delay periods, notification times, incubation periods, and infection times. Uninfected individuals are assigned infinity values (∞) for both their removal and infection times.

References

Jewell, C. P., Kypraios, T., Neal, P., and Roberts, G. O. (2009). Bayesian analysis for emerging infectious diseases. *Bayesian Analysis*, 4(3):465-496.

Deardon, R., Brooks, S. P., Grenfell, B. T., Keeling, M. J., Tildesley, M. J., Savill, N. J., Shaw, D. J., and Woolhouse, M. E. (2010). Inference for individual-level models of infectious diseases in large populations. *Statistica Sinica*, 20(1):239.

See Also

[loglikelihoodepiILM](#), [contactnet](#), [epiplot](#).

Examples

```
## Individual locations
N<-50
xx<-cbind(runif(N,0,10),runif(N,0,10))
## Euclidean distance matrix:
d3<-as.matrix(dist(xx,method="euclidean"))
## The susceptible covariate:
covsust<-cbind(rep(1,N),rbinom(N,1,0.5))
## The contact network with power-law model of parameter values as beta=1.8 and alpha=1:
net<-contactnet(type="powerlaw",location=xx,beta=1.8,alpha=1,plot=TRUE)
## Distance-based SIR-ILMs
## Epidemic is generated with parameter values as
## alpha_s(1)=0.8, alpha_s(2)=0.5 and beta=2
## The infectious period is generated from gamma(1,2) which is equivalent to Exp(2).
epi1<-datagen(type="SIR", kerneltype = "distance", kernelmatrix = d3 ,
              distancekernel = "powerlaw",suspar = c(0.8,0.5), kernel.par = 2,
              delta = c(1,2),suscov = covsust)
## Network-based SIR-ILMs
## Epidemic is generated with parameter values as
## alpha_s(1)=0.8 and alpha_s(2)=0.5
## The infectious period is generated from gamma(1,2) which is equivalent to Exp(2).
epi2<-datagen(type="SIR", kerneltype = "network", kernelmatrix = net, suspar = c(0.8,0.5),
              delta = c(1,2), suscov = covsust)
## Distance-based SINR-ILMs
## Epidemic is generated with parameter values as
## alpha_s(1)=0.08, alpha_s(2)=0.5 and beta=2
## The incubation and delay periods are generated from gamma(1,2) which is equivalent to Exp(2).
epi3<-datagen(type="SINR", kerneltype = "distance", kernelmatrix = d3, distancekernel = "powerlaw",
              suspar = c(0.08,0.5), kernel.par = 2, delta = matrix(c(1,1,2,2),ncol=2,nrow=2),
              suscov = covsust)
## Network-based SINR-ILMs
## Epidemic is generated with parameter values as
## alpha_s(1)=0.8 and alpha_s(2)=0.5
## The incubation and delay periods are generated from gamma(1,2) which is equivalent to Exp(2).
epi4<-datagen(type="SINR", kerneltype = "network", kernelmatrix = net, suspar = c(0.8,0.5),
              delta = matrix(c(1,1,2,2),ncol=2,nrow=2), suscov = covsust)
## Network-based SINR-ILMs
## Epidemic is generated with parameter values as
## alpha_s(1)=0.08, alpha_s(2)=0.5, beta_1 = 2 and beta_2 = 0.5
```

```
## The incubation and delay periods are generated from gamma(1,2) which is equivalent to Exp(2).
epi5<-datagen(type="SINR", kerneltype = "both", kernelmatrix = list(d3,net),
distancekernel = "powerlaw",suspar = c(0.08,0.5),kernel.par = c(2,0.5),
delta = matrix(c(1,1,2,2),ncol=2,nrow=2), suscov = covsust)
```

epictmcmc	<i>Markov Chain Monte Carlo-based tool for analyzing (SIR/SINR) distance-based/network-based individual-level disease data.</i>
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Description

Runs a Bayesian data augmented MCMC algorithm for fitting specified models (SIR or SINR) with three possible assumptions regarding the data set: 1. a completely observed epidemic; 2. unknown infection times but known removal times; or 3. unknown removal and infection times but known notification times (SINR only).

Usage

```
epictmcmc(epidat, type, kerneltype, kernelmatrix, distancekernel = NULL, datatype,
blockupdate = NULL, nsim, sus.par = NULL, trans.par = NULL, power.sus = NULL,
power.trans = NULL, kernel.par = NULL, spark.par = NULL, delta = NULL, gamma.par = NULL,
suscov = NULL, transcov = NULL, periodproposal = NULL, seedval = NULL )
```

Arguments

epidat	Epidemic data. Output from datagen or input a data frame in the same format.
type	Type of the compartmental framework, with the choice of “SIR” for Susceptible-Infectious-Removed and “SINR” for Susceptible-Infectious-Notified-Removed.
kerneltype	Type of kernel function with choice of “distance” for distance-based ILM, “network” for contact network-based ILM and “both” for a combination of network- and distance-based ILM.
kernelmatrix	A matrix of distances between individuals when kerneltype is set to “distance”. A matrix of edge incidence (0 or 1) or edge weights $[0, \infty)$ representing the contact network when kerneltype is set to “network”. A list of two matrices (1: distance matrix, 2: contact network matrix) when kerneltype is set to “both”.
distancekernel	The spatial kernel type when kerneltype is set to “distance” or “both”. Choices are “powerlaw” for a power-law distance kernel or “Cauchy” for a Cauchy distance kernel.

datatype	The ILM data set is analyzed based on three possible assumptions. The possible assumptions are “known epidemic” for completely observed epidemic; “known removal” times for observing only the removal times for SIR model or removal and notified times for SINR model; or “unknown removal” times for observing only the notified times which is applicable only to the SINR model.
blockupdate	A vector of the number of the initially observed infection times and the size of blocks for updating the infection times/infectious periods (SIR model), or infection times/incubation periods and removal times/delay periods (SINR model). The default is observing only the first infection time and performing the MCMC updating infection time parameters via single parameter updates.
nsim	The number of MCMC iterations.
sus.par	A $n_s \times 5$ matrix of arguments for updating the parameters of the susceptibility function (>0), where n_s is the number of susceptibility parameters. Default = NULL means the model does not include these parameters. See details for description of required arguments.
trans.par	A $n_t \times 5$ matrix of arguments for updating the parameters of the transmissibility function (>0), where n_t is the number of transmissibility parameters. Default = NULL means the model does not include these parameters. See details for description of required arguments.
power.sus	A $n_s \times 5$ matrix of arguments for updating the power parameters of the susceptibility function (>0), where n_s is the number of susceptibility parameters. Default = NULL means the model does not include these parameters. See details for description of required arguments.
power.trans	A $n_t \times 5$ matrix of arguments for updating the power parameters of the transmissibility function (>0), where n_t is the number of transmissibility parameters. Default = NULL means the model does not include these parameters. See details for description of required arguments.
kernel.par	A vector of arguments for updating the spatial parameter of the distance-based kernel when kerneltype is set to “distance” (>0). A 2×5 matrix of arguments for updating the spatial and network effect parameters when kerneltype is set to “both” (>0). Default = NULL means the model does not include these parameters (Network-based ILMs). See details for description of required arguments.
spark.par	A vector of arguments for updating the spark parameter (≥ 0). It should be defined if kerneltype is set to “network” with datatype= “known removal” or “unknown removal”. Default = NULL means the model does not include this parameter. See details for description of required arguments.
delta	A vector of arguments for updating the infectious periods for SIR model, or a 2×4 matrix of arguments for updating the incubation and delay periods for SINR model (>0). Default = NULL means these parameters do not need to be updated, especially when datatype is set to “known epidemic”. Note that when type=“SINR” with datatype=“known removal”, the user should just input a vector of arguments for updating the incubation period. The arguments for updating each rate are the known shape and initial value of the rate of the (infectious, incubation or delay) period distribution, the shape and rate parameters of the gamma prior distribution for the rate parameter.

gamma.par	A vector of arguments for updating the notification effect parameter (SINR). The default value(s) is 1, and this means no need to update the parameter. See details for description of required arguments.
suscov	Covariate matrix of the susceptibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.
transcov	Covariate matrix of the transmissibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.
periodproposal	A vector/matrix of the proposal distribution parameters of the independence sampler for updating the infectious period (SIR model), or the incubation and/or delay periods (SINR model). Here, we set the proposal distribution to gamma distribution. It is required when datatype is set to “known removal” or “unknown removal”. Default = NULL means the parameters of the gamma proposal distribution are the known shape and updated rate values based on the argument delta.
seedval	An integer initialized seed value to fix the (Fortran) random number generator used in the MCMC procedure. A random seed value is used as a default.

Details

Bayesian MCMC is performed to estimate the model parameters and latent variables using data augmentation method. When the datatype is set to “known removal” or “unknown removal”, we assume the infectious periods (SIR model) or the incubation and/or delay periods (SINR model) to follow a gamma distribution with known shape and unknown rate parameters. We assign a gamma prior distribution for the rate parameter with shape a and rate b . This leads the rate parameter(s) to have a gamma conditional distribution.

Under the SIR model:

$$\delta|\theta, \mathbf{I}, \mathbf{R} \sim \Gamma(m + a_\delta, M + b_\delta),$$

where δ is the rate of the infectious period distribution; m is the number of infected individuals; $M = \sum_{i=1}^m (R_i - I_i)$; and a_δ and b_δ are the prior parameters for the infectious period rate.

Under the SINR model:

$$\delta^{(inc)}|\theta, \mathbf{I}, \mathbf{N}, \mathbf{R} \sim \Gamma(m + a_{\delta^{(inc)}}, M_{inc} + b_{\delta^{(inc)}}),$$

where $\delta^{(inc)}$ is the rate of the incubation period distribution; $M_{inc} = \sum_{i=1}^m (N_i - I_i)$; and $a_{\delta^{(inc)}}$ and $b_{\delta^{(inc)}}$ are the prior parameters for the incubation period rate, and

$$\delta^{(delay)}|\theta, \mathbf{I}, \mathbf{N}, \mathbf{R} \sim \Gamma(m + a_{\delta^{(delay)}}, M_{delay} + b_{\delta^{(delay)}}),$$

where $\delta^{(delay)}$ is the rate parameter of the delay period distribution; $M_{delay} = \sum_{i=1}^m (R_i - N_i)$; and $a_{\delta^{(delay)}}$ and $b_{\delta^{(delay)}}$ are the prior parameters for the delay period rate.

A Gibbs update (i.e., sampling from the conditional posterior distribution) is then used for the infectious period (SIR model) or the incubation and/or delay period rates (SINR model). An independence sampler is used for updating the infection times and infectious periods (SIR model), and

the infection and/or removal times, and the incubation and/or delay periods. To do so under the SIR model, we update each infection time I_i by proposing infectious period D_i^* from a proposal distribution with tuning parameter, such that $D_i \sim f(\cdot)$. Then, the new infection time is just the difference between the fixed known removal time and the new infectious period of the i^{th} individual. Each infection time/infectious period is updated in this way in turn. The same procedure is applied for updating the missing event times and incubation and delay periods for the SINR model, with their corresponding parameters.

Other model parameters (`sus.par`, `trans.par`, `power.sus`, `power.trans`, `kernel.par`, `spark.par` and `gamma.par`) are updated in turn using a random-walk Metropolis Hastings algorithm with normal proposal. The normal proposals must be tuned, via the proposal variance, by the user to achieve good mixing properties. To update each parameter, the user must input the following arguments in order: initial value, prior distribution ("gamma", "half normal" (positive half-normal) or "uniform"), a vector of the prior distribution parameters, and the proposal variance.

Note that, setting the variance of the normal proposal distribution to zero fixes a parameter at its initial value. This option allows the user to fix such a parameter in the MCMC procedure while updating others.

Value

Returns an object of class `epictmcmc` that contains:

compart.framework: the compartmental framework model used in the analysis.

kernel.type: the used `kernel.type` in the function.

data.assumption: the assumed event times datatype.

parameter.samples: the MCMC output of the updated model parameters.

log.posterior: the log posterior densities.

acceptance.rate: the acceptance rates for updates of each parameter.

number.iteration: the number of iterations.

number.parameter: the number of the unknown model parameters.

infection.times.samples: the updated infection times when `datatype` is set to "known removal".

Average.infectious.periods: the average infectious period when `type` is set to "SIR" and `datatype` is set to "known removal".

removal.times.samples: the updated removal times when `datatype` is set to "unknown removal".

Average.incubation.periods: the average incubation period when `type` is set to "SINR" and `datatype` is set to either "known removal" or "unknown removal".

Average.delay.periods: the average delay period when `type` is set to "SINR" and `datatype` is set to "unknown removal".

See Also

[print.epictmcmc](#), [summary.epictmcmc](#), [plot.epictmcmc](#), [datagen](#), [loglikelihoodepiILM](#).

Examples

```

## Not run:
## distance-based SIR continuous-time ILMs ##
data(SpatialData)
## performing the MCMC-tool for analyzing the fully observed spatial data
## under the SIR distance-based continuous ILM:
mcmcrs2 <- epictmcmc(epidat = SpatialData$epi, type = "SIR", kerneltype = "distance",
kernelmatrix = SpatialData$dis,
distancekernel = "powerlaw", datatype = "known epidemic", nsim = 10000,
sus.par = c(2, "gamma", 1, 0.01, 0.5),
kernel.par = c(2, "gamma", 1, 0.01, 0.5), seedval = 524837)

## performing the MCMC-tool for analyzing the partially observed spatial data
## (unknown infection times) under the SIR distance-based continuous ILM:
mcmcrs22 <- epictmcmc(epidat = SpatialData$epi, type = "SIR", kerneltype = "distance",
kernelmatrix = SpatialData$dis, distancekernel = "powerlaw",
datatype = "known removal", nsim = 50000, sus.par = c(2, "gamma", 1, 0.01, 0.8),
kernel.par = c(2, "gamma", 1, 0.01, 0.5), delta = c(1, 2, 4, 2), seedval = 524837)

## distance-based and network-based SIR ILMs ##
data(SpatialNetData)
## performing the MCMC-tool for analyzing the fully observed spatial and network data
## under the SIR distance-based and network-based continuous-time ILM:
mcmcrs3 <- epictmcmc(epidat = SpatialNetData$epi, type = "SIR", kerneltype = "both",
kernelmatrix = list(SpatialNetData$dis, SpatialNetData$net),
distancekernel = "powerlaw", datatype = "known epidemic", nsim = 10000,
sus.par = matrix(c(0.08, 0.2, "gamma", "gamma", 1, 1, 0.01, 0.01, 0.1, 0.5), ncol = 5, nrow = 2),
kernel.par = matrix(c(5, 0.5, "gamma", "gamma", 1, 1, 0.01, 0.01, 0.5, 1), ncol = 5, nrow = 2),
suscov = SpatialNetData$cov, seedval = 524837)

## network-based SIR ILMs ##
data(NetworkData)
## performing the MCMC-tool for analyzing the fully observed network data
## under the SIR network-based continuous-time ILM:
mcmcrs4 <- epictmcmc(epidat = NetworkData$epi, type = "SIR", kerneltype = "network",
kernelmatrix = NetworkData$net, datatype = "known epidemic", nsim = 10000,
sus.par = matrix(c(0.08, 0.5, "gamma", "gamma", 1, 1, 1, 1, 0.1, 0.5), ncol = 5, nrow = 2),
suscov = NetworkData$cov, seedval = 524837)

## network-based SINR ILMs ##
data(NetworkDataSINR)
## performing the MCMC-tool for analyzing the fully observed network data
## under the SINR network-based continuous-time ILM:
mcmcrs5 <- epictmcmc(epidat = NetworkDataSINR$epi, type = "SINR", kerneltype = "network",
kernelmatrix = NetworkDataSINR$net, datatype = "known epidemic", nsim = 10000,
sus.par = matrix(c(0.08, 0.2, "gamma", "gamma", 1, 1, 0.01, 0.01, 0.05, 0.5), ncol = 5, nrow = 2),
suscov = NetworkDataSINR$cov, seedval = 524837)

## End(Not run)

```

epiplot *Epidemic summary plots*

Description

Provides different plots summarizing epidemic

Usage

```
epiplot(type, kerneltype, epidat, location, network = NULL, plottype = NULL,
time.index = NULL)
```

Arguments

type	Type of the compartmental framework, with the choice of “SIR” for Susceptible-Infectious-Removed and “SINR” for Susceptible-Infectious-Notified-Removed.
kerneltype	The kernel type of the ILMs: “distance”, “network” or “both”.
epidat	Epidemic data. Output from datagen or input a data frame in the same format.
location	A matrix or data frame of XY coordinates of individuals.
network	Contact network matrix. It is required when kerneltype is set to “network”.
plottype	History or propagation plots of the epidemic.
time.index	Used for obtaining propagation plots at specific infection time points rather than at every infection time. A plot at the first time point is included in any chosen set of infection time points. The default is to provide propagation plot at every infection time point. It is not required when plottype is set to “history”.

Details

If plottype is set to “history”, the function produces epidemic curves of infection and removal times (SIR model), or infection, notification, and removal times (SINR model). If it is set to “propagation”, the function produces plots of the propagation of epidemic over time based on the setting option of the argument kerneltype. With the network kernel, the function plots all the connections between individuals (in gray) and overlays these with the epidemic pathway direction over time. With the distance kernel, the function plots the epidemic dispersion over time. It shows the changes in the individual status that related to the chosen compartmental framework in type.

Value

plot

See Also

[contactnet](#), [datagen](#).

Examples

```
## network-based SIR ILMs:
data(NetworkData)
epiplot(type="SIR",kerneltype="network",epidat=NetworkData$epi,
location=NetworkData$loc,network=NetworkData$net,
plottype="propagation",time.index=seq(1,33,by=6))
epiplot(type="SIR",kerneltype="network",epidat=NetworkData$epi,
location=NetworkData$loc,network=NetworkData$net,
plottype="history")
## network-based SINR ILMs:
data(NetworkDataSINR)
epiplot(type="SINR",kerneltype="network",epidat=NetworkDataSINR$epi,
location=NetworkDataSINR$loc,network=NetworkDataSINR$net,
plottype="propagation",time.index=seq(1,34,by=6))
epiplot(type="SINR",kerneltype="network",epidat=NetworkDataSINR$epi,
location=NetworkDataSINR$loc,network=NetworkDataSINR$net,
plottype="history")
## distance-based SIR ILMs:
data(SpatialData)
epiplot(type="SIR",kerneltype="distance",epidat=SpatialData$epi,
location=SpatialData$loc,plottype="propagation",
time.index=seq(1,33,by=6))
epiplot(type="SIR",kerneltype="distance",epidat=SpatialData$epi,
location=SpatialData$loc,plottype="history")
## distance and network-based SIR ILMs:
data(SpatialNetData)
epiplot(type="SIR",kerneltype="both",epidat=SpatialNetData$epi,
location=SpatialNetData$loc,network= SpatialNetData $net,
plottype="propagation",time.index=seq(1,21,by=6))
epiplot(type="SIR",kerneltype="both",epidat=SpatialNetData$epi,
location=SpatialNetData$loc,network= SpatialNetData $net,
plottype="history")
```

loglikelihoodepiILM *Calculates the log likelihood*

Description

Calculates the log likelihood for the specific compartmental framework of the continuous-time ILMs.

Usage

```
loglikelihoodepiILM(type, epidat, kerneltype, kernelmatrix, distancekernel = NULL,
suspar = NULL, powersus = NULL, transpar = NULL, powertrans = NULL,
kernel.par = NULL, spark = NULL, gamma = NULL, delta = NULL,
```

suscov = NULL, transcov = NULL)

Arguments

type	Type of the compartmental framework, with the choice of “SIR” for Susceptible-Infectious-Removed and “SINR” for Susceptible-Infectious-Notified-Removed.
epidat	Epidemic data. Output from datagen or input a data frame in the same format.
kerneltype	Type of kernel function with choice of “distance” for a distance-based ILM, “network” for a contact network-based ILM and “both” for a combination of network- and distance-based ILM.
kernelmatrix	A matrix of distances between individuals when kerneltype is set to “distance”. A matrix of edge incidence (0 or 1) or edge weights $[0, \infty)$ representing contact network when kerneltype is set to “network”. A list of two matrices (1: distance matrix, 2: contact network matrix) when kerneltype is set to “both”.
distancekernel	The spatial kernel type when kerneltype is set to “distance” or “both”. Choices are “powerlaw” for a power-law distance kernel or “Cauchy” for a Cauchy distance kernel.
suspar	Parameter(s) for the susceptibility function (>0).
powersus	The power parameter(s) of the susceptibility function (>0). Default value(s) is 1.
transpar	Parameter(s) for the transmissibility function (>0).
powertrans	The power parameter(s) of the transmissibility function (>0). Default value(s) is 1.
kernel.par	A scalar spatial parameter for the distance-based kernel (>0), or a vector of the spatial and network effect parameters of the network and distance-based kernel (both). It is not required when the kerneltype is set to “network”.
spark	Spark parameter (≥ 0), representing random infections that are unexplained by other parts of the model. Default value is zero.
gamma	The notification effect parameter for SINR model. The default value is 1.
delta	A vector of the shape and rate parameters of the gamma-distributed infectious period (SIR) or a 2×2 matrix of the shape and rate parameters of the gamma-distributed incubation and delay periods (SINR).
suscov	Covariate matrix of the susceptibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.
transcov	Covariate matrix of the transmissibility function, representing each covariate in a column. If intercept exists or in the case of no covariates, the first column is set to unity.

Details

We label the m infected individuals $i = 1, 2, \dots, m$ corresponding to their infection (I_i) and removal (R_i) times; whereas the $N - m$ individuals who remain uninfected are labeled $i = m + 1, m + 2, \dots, N$ with $I_i = R_i = \infty$. We then denote infection and removal time vectors

for the population as $\mathbf{I} = \{I_1, \dots, I_m\}$ and $\mathbf{R} = \{R_1, \dots, R_m\}$, respectively. We assume that infectious periods follow a gamma distribution with shape and rate δ . The likelihood of the general SIR continuous-time ILMs is then given as follows:

$$\begin{aligned} L(\mathbf{I}, \mathbf{R}|\theta) &= \prod_{j=2}^m \left(\epsilon + \sum_{i: I_i < I_j \leq R_i} \lambda_{ij}^- \right) \\ &\times \exp \left\{ - \sum_{i=1}^m \left(\sum_{j=1}^N ((R_i \wedge I_j) - (I_i \wedge I_j)) \lambda_{ij}^- \right) \right\} \\ &\times \exp \left(-\epsilon \sum_{i=1}^N [(t_{obs} \wedge I_i) - I_1] \right) \prod_{i=1}^m f(D_i; \delta) \end{aligned}$$

where θ is the vector of unknown parameters; $f(\cdot; \delta)$ indicates the density of the infectious period distribution; and D_i is the infectious period of infected individual i defined as $D_i = R_i - I_i$. The likelihood of the general SINR continuous-time ILMs is given by:

$$\begin{aligned} L(\mathbf{I}, \mathbf{N}, \mathbf{R}|\theta) &= \prod_{j=2}^m \left(\epsilon + \sum_{i: I_i < I_j \leq N_i} \lambda_{ij}^- + \sum_{i: N_i < I_j \leq R_i} \lambda_{ij}^+ \right) \\ &\times \exp \left\{ - \sum_{i=1}^{n_I} \left(\sum_{j=1}^N ((t_{obs} \wedge N_i \wedge I_j) - (I_i \wedge I_j)) \lambda_{ij}^- \right) \right\} \\ &\times \exp \left\{ - \sum_{i=1}^{n_N} \left(\sum_{j=1}^N ((t_{obs} \wedge R_i \wedge I_j) - (I_i \wedge I_j)) - ((t_{obs} \wedge N_i \wedge I_j) - (I_i \wedge I_j)) \lambda_{ij}^+ \right) \right\} \\ &\times \exp \left(-\epsilon \sum_{i=1}^N [(t_{obs} \wedge I_i) - I_1] \right) \\ &\times \prod_{i=1}^m f(D_i^{(inc)}; \delta^{(inc)}) \prod_{i=1}^m f(D_i^{(delay)}; \delta^{(delay)}) \end{aligned}$$

where D_i^{inc} and D_i^{delay} are the incubation and delay periods such that $D_i^{inc} = N_i - I_i$ and $D_i^{delay} = R_i - N_i$, and

$$\lambda_{ij}^- = \Omega_S(j) \Omega_T(i) \kappa(i, j),$$

for $i \in I(t), j \in S(t)$, and

$$\lambda_{ij}^+ = \gamma(\Omega_S(j) \Omega_T(i) \kappa(i, j)),$$

for $i \in N(t), j \in S(t)$.

Note, λ_{ij}^+ is used only under the SINR model.

Value

Returns the log likelihood value.

See Also

[contactnet](#), [datagen](#), [epictmcmc](#).

NetworkData

*Simulated epidemic data set from a network-based SIR ILM***Description**

This is a simulated epidemic data set of population size = 50 individuals that was generated using network-based SIR individual-level model (ILM) with a contact network that was generated using the power-law model with parameters $\beta = 1.8$ and $\alpha = 1$. The model has one binary susceptible covariate and the infectivity rate is given by:

$$\lambda_{jt} = (\alpha_0 + \alpha_1 z_j) \sum_{i \in I_t} c_{ij}$$

The infectious period is assumed to follow gamma distribution $\Gamma(4, \delta)$. The epidemic was simulated with the following parameter values: $\alpha_0 = 0.08$, $\alpha_1 = 0.5$ and $\delta = 2$.

The data set file contains the XY coordinates of individuals, the contact network matrix, the covariate matrix and the simulated epidemic data.

Usage

```
data(NetworkData)
```

Format

A list of the simulated data:

loc The XY coordinates of individuals.

cov A matrix of two columns represents the unity intercept and the binary covariate z .

net The undirected binary contact network matrix.

epi The simulated epidemic with four columns as: the id numbers of individuals, removal times, infectious periods, and infection times.

NetworkDataSINR

*Simulated epidemic data set from a network-based SINR ILM***Description**

This is a simulated epidemic data set of population size = 50 individuals that was generated using network-based SINR individual-level model (ILM) with a contact network that was generated using the power-law model with parameters $\beta = 1.8$ and $\alpha = 1$. The model has one binary susceptible covariate and the infectivity rate is given by:

$$\lambda_{jt} = (\alpha_0 + \alpha_1 z_j) \sum_{i \in I_t} c_{ij}$$

The incubation period is assumed to follow gamma distribution $\Gamma(4, \delta^{(inc)})$, and the delay period is assumed to follow exponential distribution $\delta^{(delay)}$. The epidemic was simulated with the following parameter values: $\alpha_0 = 0.08$, $\alpha_1 = 2$, $\delta^{(inc)} = 2$ and $\delta^{(delay)} = 2$.

The data set file contains the XY coordinates of individuals, the contact network matrix, the covariate matrix and the simulated epidemic data.

Usage

```
NetworkDataSINR
```

Format

A list of the simulated data:

loc The XY coordinates of individuals.

net The undirected binary contact network matrix.

cov A matrix of two columns represents the unity intercept and the binary covariate z.

epi The simulated epidemic with six columns as: the id numbers of individuals, removal times, delay periods, notification times, incubation periods, and infection times.

plot.epictmcmc	<i>Plot the output of epictmcmc object</i>
----------------	--

Description

plot.epictmcmc is an S3 method that plots the output of an S3 object of class epictmcmc.

Usage

```
## S3 method for class 'epictmcmc'
plot(x, epidat, start = NULL, end = NULL, thin = NULL,
      ask = TRUE, trace = TRUE, density = TRUE, auto.layout = TRUE, ...)
```

Arguments

x an S3 object of class epictmcmc (i.e. the output of the epictmcmc function).

epidat Epidemic data in the format of [datagen](#) output.

start, end, thin options for creating [mcmc](#) object.

ask, trace, density, auto.layout options for [plot.mcmc](#).

... additional arguments that are passed to the generic plot function.

Value

Trace and density plots of the posterior distribution of the model parameters. Additionally, in the case of unobserved event times, a plot of the average posterior and 95% percentile intervals of the inferred event times are produced in new plot window.

See Also

[epictmcmc](#), [print.epictmcmc](#), [summary.epictmcmc](#), [mcmc](#), [plot.mcmc](#).

print.epictmcmc	<i>Prints the contents of an epictmcmc object to the console</i>
-----------------	--

Description

print.epictmcmc is an S3 method that prints the content of an S3 object of class epictmcmc to the console.

Usage

```
## S3 method for class 'epictmcmc'  
print(x, digits = 6, ...)
```

Arguments

x	an S3 object of class epictmcmc (i.e. the output of the epictmcmc function).
digits	the number of printed digits of the estimates. Default value is 6.
...	additional arguments that are passed to the generic print function

Value

Formatted output of a epictmcmc object.

See Also

[epictmcmc](#), [summary.epictmcmc](#), [plot.epictmcmc](#).

 SpatialData

Simulated epidemic data set from a distance-based SIR ILM

Description

This is a simulated epidemic data set of population size = 50 individuals that was generated using simple distance-based SIR individual-level model (ILM) with power-law distance kernel. The infectivity rate is given by:

$$\lambda_{jt} = \alpha \sum_{i \in I_t} d_{ij}^{-\beta}$$

The infectious period is assumed to follow exponential distribution with rate λ . The epidemic was simulated with the following parameter values: $\alpha = 1.5$, $\beta = 3$ and $\delta = 2$.

The data set file contains the XY coordinates of individuals, the Euclidean distance matrix, and the simulated epidemic data set.

Usage

SpatialData

Format

A list of the simulated data:

loc The XY coordinates of individuals.

dis The Euclidean distance matrix.

epi The simulated epidemic with four columns as: the id numbers of individuals, removal times, infectious periods, and infection times.

 SpatialNetData

Simulated epidemic data set from a distance and network-based SIR ILM

Description

This is a simulated epidemic data set of population size = 50 individuals that was generated using distance and network-based SIR individual-level model (ILM) with power-law distance kernel. The model has one binary susceptible covariate and the infectivity rate is given by:

$$\lambda_{jt} = (\alpha_0 + \alpha_1 z_j) \sum_{i \in I_t} d_{ij}^{-\beta_1} + \beta_2 c_{ij}$$

The infectious period is assumed to follow exponential distribution with rate δ . The epidemic was simulated with the following parameter values: $\alpha_0 = 0.008$, $\alpha_1 = 0.2$, $\beta_1 = 2$, $\beta_2 = 0.5$ and $\delta = 2$.

The data set file contains the XY coordinates of individuals, the Euclidean distance matrix, the undirected binary contact network matrix, the covariate matrix and the simulated epidemic data set.

Usage

SpatialNetData

Format

A list of the simulated data:

loc The XY coordinates of individuals.

dis The Euclidean distance matrix.

net The undirected binary contact network matrix.

cov A matrix of two columns represents the unity intercept and the binary covariate z.

epi The simulated epidemic with four columns as: the id numbers of individuals, removal times, infectious periods, and infection times.

summary.epictmcmc *Summary method for epictmcmc objects*

Description

Summarize a `epictmcmc` object and return an object of class `summary.epictmcmc`.

Usage

```
## S3 method for class 'epictmcmc'
summary(object, digits = NULL, start = NULL, end = NULL, thin = NULL, ...)
## S3 method for class 'summary.epictmcmc'
print(x, digits = NULL, start = NULL, end = NULL, thin = NULL, ...)
```

Arguments

`x`, `object` an S3 object of class `epictmcmc` (i.e. the output of the `epictmcmc` function).
`digits` the number of printed digits of the estimates. Default value is 6.
`start`, `end`, `thin` options for creating `mcmc` object.
`...` potential further arguments (require by generic).

See Also

`epictmcmc`, `print.epictmcmc`, `plot.epictmcmc`.

tswv

Tomato Spotted Wilt Virus data

Description

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

Usage

tswv

Format

A list of data frames as follows:

loc The XY coordinates of plants.

tswvsir The tswv data in the format of 4 columns: id numbers of plants, removal times, infectious periods, and infection times.

tswvsinr The tswv data in the format of 6 columns: id numbers of plants, removal times, delay periods, notification times, incubation periods, and infection times.

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.

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