

Package ‘SIRmcmc’

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Title Compartmental Susceptible-Infectious-Recovered (SIR) Model of Community and Household Infection

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Description We build an Susceptible-Infectious-Recovered (SIR) model where the rate of infection is the sum of the household rate and the community rate. We estimate the posterior distribution of the parameters using the Metropolis algorithm. Further details may be found in: F Scott Dahlgren, Ivo M Foppa, Melissa S Stockwell, Celibell Y Vargas, Philip LaRussa, Carrie Reed (2021) ``Household transmission of influenza A and B within a prospective cohort during the 2013-2014 and 2014-2015 seasons" <doi:10.1002/sim.9181>.

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R topics documented:

community.attack.rate	2
hh.transmission	2
hh.transmission.epsilon	3
household.transmission	3
MCMC.date	7
prior	8
secondary.attack.rate	8
unifprior	9

Index**11**

community.attack.rate *Compute the community attack rate*

Description

Computes the community attack rate for a cohort using the value of a call to [household.transmission](#).

Usage

```
community.attack.rate(SIRmcmc, probs=c(0.5, 0.025, 0.975))
```

Arguments

SIRmcmc	The value of a call to household.transmission .
probs	A numeric vector of the quantiles of the posterior distribution. The default is the median and the central 95% credible region.

Details

Computes the posterior probability distribution of the community attack rate from the Metropolis algorithm. Returns quantiles of the distribution specified in the probs argument.

Value

An array of community attack rates. The first dimension is the value of epsilon in SIRmcmc. The second dimension is the posterior probability in the probs argument

hh.transmission *Simulated data under the SIR.*

Description

Simulated data under the SIR model, without covariates.

Usage

```
data("hh.transmission")
```

Format

A data frame with 1000 observations on the following 3 variables.

household A numeric vector of household IDs.

onset Date of onset for cases

transmission A factor with levels Community Household None representing source of infection.

`hh.transmission.epsilon`*Simulated data under SIR, with covariates.*

Description

Simulated data under the SIR model with a high risk and low risk group. The first 1000 observations are identical to the data `hh.transmission`.

Usage

```
data("hh.transmission.epsilon")
```

Format

A data frame with 2000 observations on the following 4 variables.

`household` A numeric vector of household IDs.

`onset` Date of onset for cases.

`transmission` A factor with levels Community Household None representing source of infection.

`epsilon` A numeric vector of the value of epsilon used to simulate the data.

`household.transmission`*Estimate parameters from SIR model*

Description

Use the Metropolis algorithm to estimate parameters from the SIR compartmental model

Usage

```
household.transmission(onset.date, household.index, covariate = NULL,  
  followup.time, iterations,  
  delta = c(0.1,0.3,0.4,0.1), plot.chain = TRUE,  
  index = 1, start.date = NULL, prior = unifprior,  
  constant.hazard = FALSE,...)
```

Arguments

<code>onset.date</code>	A vector of onset dates. If <code>onset.date</code> is a character vector, then it will be coerced to dates using <code>as.Date</code> . NA values are interpreted as remaining susceptible at the end of followup.
<code>household.index</code>	A vector identifying households, which should be the same length as the <code>onset.date</code> argument.
<code>covariate</code>	A vector identifying covariate patterns. If given, then it is interpreted as a factor. A value for <code>epsilon</code> will be given for each level of covariate. If NULL, then <code>epsilon</code> is not estimated.
<code>followup.time</code>	An integer for the followup time in days.
<code>iterations</code>	An integer for the number of iterations of the Metropolis algorithm.
<code>delta</code>	A vector of length 4 for tuning the acceptance rate of the Metropolis algorithm. The order is (1) alpha, (2) beta, (3) gamma, and (4) epsilon.
<code>plot.chain</code>	A boolean of whether to plot the value of the chain vs the iterate.
<code>index</code>	An integer for the index date. Probabilities are conditional on the index date. Any coordinates of <code>onset.date</code> equal to <code>index</code> will have a likelihood of 1. If you want unconditional probabilities, then <code>index</code> should be less than <code>start.date</code> .
<code>start.date</code>	Should be the same format as <code>onset.date</code> . Specifies the start of the followup period.
<code>prior</code>	A function to compute the prior probability of alpha, beta, gamma, and epsilon. Any user written function must take the arguments alpha, beta, gamma, epsilon, and esteps. Builtin functions are <code>unifprior</code> and <code>prior</code> . <code>unifprior</code> is uniform on (0.01,1000).
<code>constant.hazard</code>	If FALSE, then the algorithm computes a time dependent hazard for the cohort and the hazard from the community is proportional to the hazard in the cohort. If TRUE, then the algorithm assumes a constant hazard from the community.
<code>...</code>	Arguments to be passed to the function in the prior argument.

Details

If no covariates are supplied, only the model parameters alpha, beta, and gamma are estimated using a stepwise Metropolis algorithm. The model parameters are drawn from a uniform distribution on (0.1,1). The first step proposes a new alpha using `rnorm` and the mixing parameter `delta[1]`. The second and third steps are similar for beta and gamma. If covariates are supplied, the additional parameters, collectively called `epsilon`, are also estimated.

The algorithm assumes followup begins on `start.date` and lasts for `followup.time` days. Any coordinate of `onset.date` equal to `index` does not contribute to the likelihood.

Two priors are builtin: `prior` and `unifprior`. User defined prior functions must take the arguments alpha, beta, gamma, epsilon, and esteps.

Value

An object of the class `SIRmcmc`.

See Also[prior.unifprior](#)**Examples**

```

##A trivial example-----
library(graphics)
onset<-sample(c(seq(1,10),rep(Inf,20)),size=500,replace=TRUE)
hh<-sample(seq(1,300),size=500,replace=TRUE)
chain<-household.transmission(onset.date = onset, household.index = hh,
                             followup.time = 10, iterations = 100)
community.attack.rate(SIRmcmc=chain)
secondary.attack.rate(household.size=3,SIRmcmc=chain)

##An example with household transmission-----
library(graphics)
data(hh.transmission)
set.seed(1)
iterations<-100
T<-30
delta<-c(0.1,0.6,0.8)
index<-0
##Find the MCMC estimates of alpha, beta, and gamma
chain<-household.transmission(
  onset.date=hh.transmission$onset,
  household.index=hh.transmission$household,
  covariate=NULL,
  followup.time=T,
  iterations=iterations,
  delta=delta,
  prior=unifprior,
  index=index
)
#Tabulate true type of transmission
hh.table<-table(
  table(
    is.finite(MCMC.date(hh.transmission$onset)),
    hh.transmission$household)["TRUE",]
)
##Calculate the true SAR
truth.table<-table(hh.transmission$transmission)
truth<-unname(truth.table["Household"]/sum(hh.table[2:3]))
cat("\n\nTrue Value of SAR\n\n")
print(truth)
##Find point and 95% central creditable intervals for MCMC SAR
cat("\n\nMCMC Estimate of SAR\n\n")
secondary.attack.rate(household.size=2,SIRmcmc=chain)
days<-NULL
for(d in c(seq(1:5))){
  days<-c(days,as.character(d))
  a<-sum(table(tapply(X=hh.transmission$onset,INDEX=hh.transmission$household,FUN=diff))[days])
}

```

```

cat(
  paste0(
    "\n\n",
    d,
    " Day Counting Estimate of SAR\n\n"
  )
)
##Find point and 95% confidence intervals for normal approx to SAR
print(
  a/sum(hh.table[2:3])+c(p=0, LB=-1, UB=1) *
  qnorm(p=0.975) *
  sqrt(a*(hh.table[2]+hh.table[3]-a)/(hh.table[2]+hh.table[3])^3)
)
}

##An example with rate ratios-----
## Not run:
library(graphics)
data(hh.transmission.epsilon)
set.seed(1)
iterations<-100
T<-30
delta<-c(0.1,0.1,0.1,0.1)
index<-0
##Find the MCMC estimates of alpha, beta, gamma, and epsilon
chain<-household.transmission(
  onset.date=hh.transmission.epsilon$onset,
  household.index=hh.transmission.epsilon$household,
  covariate=hh.transmission.epsilon$epsilon,
  followup.time=T,
  iterations=iterations,
  delta=delta,
  prior=unifprior,
  index=index
)

##Find point and 95% central creditable intervals for MCMC SAR
cat("\n\nMCMC Estimate of SAR\n\n")
print(secondary.attack.rate(household.size=2, SIRmcmc=chain))
for(e in c(1,5)){
  hh.table<-table(table(
    is.finite(MCMC.date(hh.transmission.epsilon$onset)),
    hh.transmission.epsilon$household,
    hh.transmission.epsilon$epsilon) ["TRUE", , as.character(e)])
  ##Tabulate true type of transmission
  truth.table<-table(
    hh.transmission.epsilon$transmission[which(
      hh.transmission.epsilon$epsilon==e
    )])
  ##Calculate the true SAR
  truth<-unname(truth.table["Household"]/sum(hh.table[2:3]))
  cat("\n\nTrue Value of SAR\n\n")
}

```

```

print(truth)
days<-NULL
for(d in c(seq(1:5))){
  days<-c(days,as.character(d))
  a<-sum(table(tapply(
    X=hh.transmission.epsilon$onset[which(hh.transmission.epsilon$epsilon==e)],
    INDEX=hh.transmission.epsilon$household[which(hh.transmission.epsilon$epsilon==e)],
    FUN=diff)))[days])
  ##Find point and 95% confidence intervals for normal approx to SAR
  cat(paste0(
    "\n\n",
    d,
    " Day Counting Estimate of SAR\n\n"
  ))
  print(
    a/sum(hh.table[2:3])+c(p=0, LB=-1, UB=1)
    * qnorm(p=0.975)
    * sqrt(a*(hh.table[2]+hh.table[3]-a)/(hh.table[2]+hh.table[3])^3)
  )
}
}

## End(Not run)

```

MCMC.date

Convert dates to a list of extended natural numbers.

Description

Converts dates to a list of numbers representing the number of days from the start of followup until the start of the infectious period.

Usage

```
MCMC.date(dates, start.date=NULL)
```

Arguments

dates	A list of dates. May be of character, numeric, or date class.
start.date	The start date of follow up

Details

Coverrts dates to days of followup until the start of the infectious period. Missing data are set to infinity and are assumed susceptible during followup.

Value

A list of extended natural numbers.

prior *Compute prior probability of parameters*

Description

Compute the prior probability of alpha, beta, gamma, and epsilon

Usage

```
prior(alpha, beta, gamma, epsilon, esteps, params = list(alpha =
  list(location = 0, scale = 2), beta = list(shape = 0.01, rate = 0.01),
  gamma = list(shape = 0.01, rate = 0.01),
  epsilon = list(location = 0, scale = 2)))
```

Arguments

alpha	A number. The logarithm of alpha follows a logistic distribution.
beta	A number. beta follows a gammadistribution.
gamma	A number. gamma follows a gamma distribution.
epsilon	A number. The logarithm of epsilon follows a logistic distribution.
esteps	A number in (0,1). Used for logic as to whether to compute the prior probability of epsilon (1) or not (0).
params	A list of parameters for the prior distributions.

Value

A probability of the model parameters under the prior distributions.

See Also

[dlogis](#) [dgamma](#) [household.transmission](#)

secondary.attack.rate *Compute the secondary attack rate*

Description

Using the value of a call to [household.transmission](#), computes the secondary attack rate for households.

Usage

```
secondary.attack.rate(household.size, SIRmcmc, probs=c(0.5, 0.025, 0.975))
```


Arguments

household.size	A numeric vector containing the number of people in a household.
SIRmcmc	The value of a call to <code>household.transmission</code> .
probs	A numeric vector of the quantiles of the posterior distribution. The default is the median and the central 95% credible region.

Details

Computes the posterior probability distribution of the secondary attack rate from the Metropolis algorithm. Returns quantiles of the distribution specified in the `probs` argument.

Value

An array with secondary attack rates.

The first dimension of the array is the household size.

The second dimension of the array is the quantiles of the posterior distribution in the `probs` argument.

The third dimension of the array is the value of `epsilon` in `SIRmcmc`.

unifprior

A uniform prior on the model parameters

Description

Compute a uniform prior on `alpha`, `beta`, `gamma`, and `epsilon`

Usage

```
unifprior(alpha, beta, gamma, epsilon, esteps, UB = 1000, LB = 0.01)
```

Arguments

alpha	A number compared to the upper bound <code>UB</code> and the lower bound <code>LB</code> .
beta	A number compared to the upper bound <code>UB</code> and the lower bound <code>LB</code> .
gamma	A number compared to the upper bound <code>UB</code> and the lower bound <code>LB</code> .
epsilon	A number compared to the upper bound <code>UB</code> and the lower bound <code>LB</code> .
esteps	A number in (0,1). Used for logic as to whether to compute the prior probability of <code>epsilon</code> (1) or not (0).
UB	A number used as an upper bound on the model parameters.
LB	A number used as a lower bound on the model parameters.

Value

If all the model parameters are between the lower bound and the upper bound, then `unifprior` returns 1. Otherwise, `unifprior` returns 0.

See Also

[dlogis dgamma household.transmission prior](#)

Index

as.Date, [4](#)

community.attack.rate, [2](#)

dgamma, [8](#), [10](#)

dlogis, [8](#), [10](#)

hh.transmission, [2](#)

hh.transmission.epsilon, [3](#)

household.transmission, [2](#), [3](#), [8–10](#)

MCMC.date, [7](#)

prior, [4](#), [5](#), [8](#), [10](#)

secondary.attack.rate, [8](#)

unifprior, [4](#), [5](#), [9](#)