Package 'GDILM.SIR'

June 4, 2024

Title Inference for Infectious Disease Transmission in SIR Framework

Version 1.2.1

Description Model and estimate the model parameters
for the spatial model of individual-level infectious disease
transmission in Susceptible-Infected-Recovered (SIR) framework.

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Encoding UTF-8

RoxygenNote 7.3.1

LazyData true

Suggests knitr, rmarkdown, testthat (>= 3.0.0)

Config/testthat/edition 3

Imports mvtnorm, psych, stats,MASS,numDeriv,Matrix

Depends R (>= 2.10)

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-06-04 17:30:14 UTC

Contents

Area_Level_Data   *Area level data*

Description

The data which describes the sociodemographic characters (proportion of indigenous people, proportions of immigrants, proportion of low education, median household income) for 96 regions.

Usage

```
Area_Level_Data
```

Format

A data frame with 96 rows and 5 columns:

RHDA Region name

Percentage_of_immigrants percentage of immigrants in each region

Percentage_of_indigenous percentage of indigenous people in each region

Proporton_of_Low_education proportion of persons 15+ who have not graduated high school

Income median household income ...

Individual_Level_Data *Individual level data*

Description

The data which describes the Individual characteristics (gender, age group, infected status) and corresponding area details for 700 individuals.

Usage

```
Individual_Level_Data
```

Format

A data frame with 700 rows and 8 columns:

Disease_Status Disease status of the individual

Region The regioal health authority of the individual

Gender Gender of the individual

Age_Group Age group of the individual

Postal_code postal code which the individual belong to

Longitde longitude of the region

Latitude latitude of the region

Region_Number Region number assigned for each regional health authority ...

Realdata_Finalmodel   *This function is used to estimate model parameters*

Description

This function is used to estimate model parameters

Usage

```
Realdata_Finalmodel(
  ITER,
  zz,
  lambda0,
  sigma0,
  Di,
  D,
  n,
  time,
  tau,
  lambda,
  alpha0,
  q1,
  q2,
  cov1,
  cov2,
  phi,
  delta0,
  Nlabel,
  npar,
  I
)
```

Arguments

ITER	Number of iterations
zz	Number of Regions
lambda0	Spatial dependence
sigma0	precision
Di	Euclidean distance between susceptible individual and infectious individual
D	Neighborhood structure
n	total number of individuals
time	time
tau	tau
lambda	lambda ###

alpha0	intercept
q1	Number of variables corresponding to individual level data
q2	Number of variables corresponding to area level data
cov1	Individual level covariates
cov2	Area level covariates
phi	Spatial random effects
delta0	Spatial parameter
Nlabel	Label for each sample from the area
npar	number of parameters
I	Identity matrix

Value

Numerical values for estimates

Examples

```
Realdata_Finalmodel(2,4,0.2,0.5,
matrix(runif(400,min = 4,max = 20),nrow=20, byrow = TRUE),
matrix(c(0,-1,0,-1,-1,0,-1,-1,0,-1,0,-1,-1,-1,-1,0),nrow=4,byrow=TRUE),20,10,
sample(c(0,1),replace = TRUE, size = 20),rep(3,20),0.4,6,5,
matrix(runif(120, 0, 1),nrow=20,byrow=TRUE),
matrix(runif(20, 0, 1),nrow=4,byrow=TRUE),runif(4,min = 0, max = 1),2,
rep(1:4,each=5),15,diag(4))
```

Simulation_Finalmodel	*This function can use to estimate the model parameters using the initial values.*

Description

This function can use to estimate the model parameters using the initial values.

Usage

```
Simulation_Finalmodel(
  ITER,
  zz,
  lambda0,
  sigma0,
  Di,
  g,
  nSample,
  d,
```

```
    n,
    time,
    tau,
    lambda,
    alpha0,
    beta10,
    beta20,
    cov1,
    cov2,
    phi,
    delta0,
    Nlabel,
    D,
    I
)
```

Arguments

ITER	Number of iterations
zz	Number of Regions
lambda0	initial value for Spatial dependence
sigma0	initial value for the precision of spatial random effects
Di	Euclidean distance between susceptible individual and infectious individual
g	Number of rows in the lattice
nSample	Number of individuals in each cell
d	infectious time units
n	total number of individuals
time	time
tau	the set of infectious individuals at time t in the zth area
lambda	a vector containing the length of infectious period
alpha0	initial value for the intercept
beta10	initial value for the parameter corresponding to the covariate associated with susceptible individual
beta20	initial value for the parameter corresponding to the area-level covariates corresponding to area
cov1	a vector of covariates associated with susceptible individual
cov2	a vector of area-level covariates corresponding to area
phi	Spatial random effects
delta0	Spatial parameter
Nlabel	Label for each sample from the area
D	matrix reflecting neighborhood structure
I	Identity matrix

Value

the estimated values for the model parameters

Examples

```
Simulation_Finalmodel(2,4,0.2,0.5,
matrix(runif(1600,min=4,max=20),nrow=40,byrow=TRUE),2,10,3,40,10,
sample(c(0,1),replace=TRUE,size=40),rep(3,40),0.4,1,1,runif(40,0,1),
runif(4,0,1),runif(4,min=0,max=1),2,rep(1:4,each=10),
matrix(c(0,-1,0,-1,-1,0,-1,-1,0,-1,0,-1,-1,-1,-1,0),nrow=4,byrow=TRUE),
diag(4))
```

Sim_Estpar | *Calculating the estimated values for the parameters using log-likelihood function*

Description

Calculating the estimated values for the parameters using log-likelihood function

Usage

```
Sim_Estpar(
  Nlabel,
  phi,
  Di,
  alpha1,
  delta,
  lambda1,
  sigma1,
  beta1,
  beta2,
  zz,
  time,
  n,
  tau,
  lambda,
  I,
  D,
  cov1,
  cov2
)
```

Arguments

Nlabel	Label for each sample from the area
phi	Spatial random effects
Di	Euclidean distance between susceptible individual and infectious individual
alpha1	intercept
delta	Spatial parameter
lambda1	Spatial dependence
sigma1	precision of spatial random effects
beta1	the parameter corresponding to the covariate associated with susceptible individual
beta2	the parameter corresponding to the covariate associated with area
zz	Number of areas
time	Time
n	Total number of individuals
tau	the set of infectious individuals at time t in the zth area
lambda	a vector containing the length of infectious period
I	identity matrix
D	Neighborhood structure
cov1	Individual level covariates
cov2	Area level covariates

Value

a list of the solutions for the estimations of the parameters

Examples

```
Sim_Estpar(rep(1:4,each=5),runif(4,min = 0, max = 1),
matrix(runif(400,min=4,max=20),nrow=20,byrow = TRUE),0.4,3,0.2,0.5,1,1,4,10,
20,sample(c(0,1),replace = TRUE, size = 20),rep(3,20),diag(4),
matrix(c(0,-1,0,-1,-1,0,-1,-1,0,-1,0,-1,-1,-1,-1,0),nrow=4,byrow=TRUE),
runif(20, 0, 1),runif(4, 0, 1))
```

| Sim_Loglik | *This function calculates the value of the log-likelihood function* |

Description

This function calculates the value of the log-likelihood function

Usage

```
Sim_Loglik(
  Nlabel,
  phi,
  Di,
  alpha1,
  delta,
  lambda,
  sigma1,
  beta1,
  beta2,
  time,
  n,
  zz,
  tau,
  lambda1,
  I,
  D,
  cov1,
  cov2
)
```

Arguments

Nlabel	Label for each sample from the area
phi	Spatial random effects
Di	Euclidean distance between susceptible individual and infectious individual
alpha1	intercept
delta	Spatial parameter
lambda	a vector containing the length of infectious period
sigma1	precision of spatial random effects
beta1	the parameter corresponding to the covariate associated with susceptible individual
beta2	the parameter corresponding to the covariate associated with area
time	time
n	Total number of individuals

zz	Number of areas
tau	the set of infectious individuals at time t in the zth area
lambda1	Spatial dependence
I	Identity matrix
D	matrix reflecting neighborhood structure
cov1	Individual level covariates
cov2	Area level covariates

Value

a numeric value for the log-likelihood

Examples

```
Sim_Loglik(rep(1:4,each=5), runif(4,min = 0, max = 1),
matrix(runif(400,min=4,max=20),nrow=20,byrow=TRUE),0.4, 2,rep(3,20),0.5,1,1,
10,20,4,sample(c(0,1),replace = TRUE, size = 20),0.6,diag(4),
matrix(c(0,-1,0,-1,-1,0,-1,-1,0,-1,0,-1,-1,-1,-1,0),nrow=4,byrow=TRUE),
runif(20, 0, 1), runif(4, 0, 1))
```

TwoWeek	*TwoWeek*

Description

The simulated data for the date diagnosed and tau

Usage

```
TwoWeek
```

Format

A data frame with 700 rows and 2 columns:

date_diagnosed The date which the disease diagnosed

V2 the week

...

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