Package ‘GDILM.SIR’

January 20, 2025

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.

License MIT + file LICENSE

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

Author Ruwani Herath [aut, cre],
Leila Amiri [ctb],
Mahmoud Torabi [ctb]

Maintainer Ruwani Herath <`ruwanirasanjalih@gmail.com`>

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

...

Index