

# Package ‘GDILM.SIR’

May 14, 2024

**Type** Package

**Title** Inference for Infectious Disease Transmission in SIR Framework

**Version** 0.1.0

**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

**Suggests** knitr, rmarkdown, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Imports** mvtnorm, psych, stats, MASS, maxLik, Matrix

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2024-05-14 08:23:27 UTC

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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))
```

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