Package: GDILM.SEIRS (via r-universe)

December 8, 2024

Title Spatial Modeling of Infectious Disease with Reinfection

Version 0.0.2

Description Geographically Dependent Individual Level Models (GDILMs)
within the Susceptible-Exposed-Infectious-Recovered-Susceptible
(SEIRS) framework are applied to model infectious disease
transmission, incorporating reinfection dynamics. This package
employs a likelihood based Monte Carlo Expectation Conditional
Maximization (MCECM) algorithm for estimating model parameters.
It also provides tools for GDILM fitting, parameter estimation,
AIC calculation on real pandemic data, and simulation studies
customized to user-defined model settings.

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Encoding UTF-8

LazyData true

Imports MASS, mvtnorm, ngspatial, stats

RoxygenNote 7.3.2

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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Depends R (>= 3.5.0)

Repository CRAN

Date/Publication 2024-12-08 00:00:10 UTC

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Datasets	*Hypothetical Datasets*

Description

The primary function, GDILM_SEIRS_Par_Est, fits the Geographically Dependent Individual Level Model (GDILM) for infectious disease transmission incorporating reinfection dynamics within the SEIRS framework, using real-world data. It can be applied to any dataset with the appropriate structure, requiring two dataframes: data and adjacency_matrix, along with the necessary parameters. For illustration purposes, we provide two hypothetical examples of data and adjacency_matrix to demonstrate the structure of the inputs. These examples will also be used to illustrate how the function works in practice.

data

A data frame with 100 rows and 12 columns.

This hypothetical dataset demonstrates the structure required for the dataframe used in this package. The dataset for use with the package should adhere to the same column format and order but can include any number of rows, with each row representing an infected individual. The example dataset includes individual-level characteristics (e.g., age, infection status) and area-level characteristics (e.g., socioeconomic status, STI rate) for 100 individuals, each associated with a postal code. This dataset will be used as input in the example for the GDILM_SEIRS_Par_Est function.

Ave_Postal_Pop Average population of each postal code

AverageAge Average age of individuals within each postal code (individual-level data)

InfectedTime Time of infection for each individual, represented as a numerical value from 1 to the end of the pandemic period

LAT Latitude of the postal code

LONG Longitude of the postal code

Label_NC_shape The region number that the postal code belongs to, here assuming the study area is divided into five subregions

MaleRate Rate of males in the population of the postal code (individual-level data)

NInfected Number of infected individuals in the postal code

SES Socioeconomic status indicator of the region to which the postal code belongs (area-level data)

STI Sexually transmitted infection rate of the region that the postal code belongs to (area-level data)

SymptomRate Rate of disease symptoms in the postal code (individual-level data), indicating whether individuals are symptomatic or asymptomatic

status 1 if the postal code is infected for the first time, and 0 if the postal code is reinfected

adjacency_matrix

A 5x5 matrix.

This hypothetical adjacency matrix is provided to illustrate the structure required for use with this package. The matrix used with the package should follow a similar format, maintaining the same layout but allowing for any number of regions. The adjacency matrix defines the neighborhood relationships between subregions in a hypothetical study area. In this example, it represents a spatial structure with five subregions, where each cell indicates the presence or absence of a connection between the corresponding subregions. The example for the GDILM_SEIRS_Par_Est function will use this matrix as input.

V1 Subregion 1: Represents the first subregion in the region under study

V2 Subregion 2: Represents the second subregion in the region under study

V3 Subregion 3: Represents the third subregion in the region under study

V4 Subregion 4: Represents the fourth subregion in the region under study

V5 Subregion 5: Represents the fifth subregion in the region under study

Value Each cell in the matrix (e.g., between subregion 1 and subregion 2) represents the connection (typically 0 or 1) between the two subregions, where 1 indicates they are neighbors and 0 indicates they are not.

GDILM_SEIRS_Par_Est *GDILM SEIRS for Real Data*

Description

This function applies the Geographically Dependent Individual Level Model (GDILM) for infectious disease transmission, incorporating reinfection dynamics within the Susceptible-Exposed-Infectious-Recovered-Susceptible (SEIRS) framework, to real data. It employs a likelihood based Monte Carlo Expectation Conditional Maximization (MCECM) algorithm for parameter estimation and AIC calculation. This function requires two dataframes, named data and adjacency_matrix, along with the necessary parameters. Detailed information on the structure of these two datasets is provided in the package.

Usage

```
GDILM_SEIRS_Par_Est(
  data,
  adjacency_matrix,
  DimCovInf,
  DimCovSus,
  DimCovSusReInf,
  tau0,
  lambda0,
  alphaS0,
  delta0,
  alphaT0,
```

```
    InfPrd,
    IncPrd,
    NIterMC,
    NIterMCECM
)
```

Arguments

data	Dataset. The dataset should exactly match the data file in the data folder, including all the columns with the same names.
adjacency_matrix	
	Adjacency matrix representing the regions in the study area (0 if no connection between regions)
DimCovInf	Dimensions of the individual infectivity covariate
DimCovSus	Dimensions of the area-level susceptibility to initial infection covariate
DimCovSusReInf	Dimensions of the area-level susceptibility to reinfection covariate
tau0	Initial value for spatial precision
lambda0	Initial value for spatial dependence
alphaS0	Initial value for the susceptibility intercept
delta0	Initial value for the spatial decay parameter
alphaT0	Initial value for the infectivity intercept
InfPrd	Infectious period that can be obtained either from the literature or by fitting an SEIRS model to the data
IncPrd	Incubation period that can be obtained either from the literature or by fitting an SEIRS model to the data
NIterMC	Number of MCMC iterations
NIterMCECM	Number of MCECM iterations

Value

alphaS Estimate of alpha S

BetaCovInf Estimate of beta vector for the individual level infection covariate

BetaCovSus Estimate of beta vector for the areal susceptibility to first infection covariate

BetaCovSusReInf Estimate of beta vector for the areal susceptibility to reinfection covariate

alphaT Estimate of alpha T

delta Estimate of delta

tau1 Estimate of tau

lambda1 Estimate of lambda

AIC AIC of the fitted GDILM SEIRS

Examples

```
data(data)
data(adjacency_matrix)
GDILM_SEIRS_Par_Est(data,adjacency_matrix,2,2,2,0.5, 0.5, 1, 2, 1, 1, 1, 20, 2)
```

GDILM_SEIRS_Sim_Par_Est

GDILM SEIRS for a Simulation Study

Description

This function conducts a simulation study for the Geographically Dependent Individual Level Model (GDILM) of infectious disease transmission, incorporating reinfection dynamics within the Susceptible-Exposed-Infectious-Recovered-Susceptible (SEIRS) framework, using a user-defined grid size. It applies a likelihood based Monte Carlo Expectation Conditional Maximization (MCECM) algorithm to estimate model parameters and compute the AIC.

Usage

```
GDILM_SEIRS_Sim_Par_Est(
  GridDim1,
  GridDim2,
  NPostPerGrid,
  MaxTimePand,
  tau0,
  lambda0,
  alphaS0,
  delta0,
  alphaT0,
  PopMin,
  PopMax,
  InfFraction,
  ReInfFraction,
  InfPrd,
  IncPrd,
  NIterMC,
  NIterMCECM
)
```

Arguments

GridDim1	First dimension of the grid
GridDim2	Second dimension of the grid
NPostPerGrid	Number of postal codes per grid cell

MaxTimePand	Last time point of the pandemic
tau0	Initial value for spatial precision
lambda0	Initial value for spatial dependence
alphaS0	Initial value for the susceptibility intercept
delta0	Initial value for the spatial decay parameter
alphaT0	Initial value for the infectivity intercept
PopMin	Minimum population per postal code
PopMax	Maximum population per postal code
InfFraction	Fraction of each grid cell's population to be infected
ReInfFraction	Fraction of each grid cell's population to be reinfected
InfPrd	Infectious period that can be obtained either from the literature or by fitting an SEIRS model to the data
IncPrd	Incubation period that can be obtained either from the literature or by fitting an SEIRS model to the data
NIterMC	Number of MCMC iterations
NIterMCECM	Number of MCECM iterations

Value

alphaS Estimate of alpha S

BetaCovInf Estimate of beta vector for the individual level infection covariate

BetaCovSus Estimate of beta vector for the areal susceptibility to first infection covariate

BetaCovSusReInf Estimate of beta vector for the areal susceptibility to reinfection covariate

alphaT Estimate of alpha T

delta Estimate of delta

tau1 Estimate of tau

lambda1 Estimate of lambda

AIC AIC of the fitted GDILM SEIRS

Examples

```
GDILM_SEIRS_Sim_Par_Est(3,3,8,30,0.7, 0.5, -1, 2.5, 0,30, 50,0.5,0.5, 2, 3, 10, 2)
```

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