Package: SeasEpi (via r-universe)

May 20, 2026

Title Spatiotemporal Modeling of Seasonal Infectious Disease

Version 0.0.3

Description Spatiotemporal individual-level model of seasonal infectious disease transmission within the Susceptible-Exposed-Infectious-Recovered-Susceptible (SEIRS) framework are applied to model seasonal infectious disease transmission. This package employs a likelihood based Monte Carlo Expectation Conditional Maximization (MCECM) algorithm for estimating model parameters. In addition to model fitting and parameter estimation, the package offers functions for calculating AIC using real pandemic data and conducting simulation studies customized to user-specified model configurations.

License MIT + file LICENSE

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

Author Amin Abed [aut, cre, cph] (ORCID: <`https://orcid.org/0000-0002-7381-4721`>), Mahmoud Torabi [ths], Zeinab Mashreghi [ths]

Maintainer Amin Abed <`abeda@myumanitoba.ca`>

Depends R (>= 3.5.0)

Repository https://amin-abed.r-universe.dev

Date/Publication 2025-11-02 23:00:02 UTC

RemoteUrl https://github.com/cran/SeasEpi

RemoteRef HEAD

RemoteSha 0f18d27bcf0f9ea2ed76ee9918812f78c12728f6

Contents

`Datasets` *Hypothetical Datasets*

Description

The main function, `SeasEpi_Par_Est`, applies the spatiotemporal individual-level model of seasonal infectious disease transmission within the SEIRS framework to a hypothetical dataset. It is compatible with any dataset that follows the required format, which includes two dataframes: `data` and `adjacency_matrix`, along with relevant parameter inputs. To demonstrate the expected input structure and the function's practical use, we provide two hypothetical examples of `data` and `adjacency_matrix`.

`data`

A data frame with 100 rows and 11 columns.

This sample dataset illustrates the required structure for the dataframe used with this package. While the number of rows can vary, each row must represent a single infected individual, and the column names and order must follow the specified format. The example includes individual-level attributes (e.g., age, infection status) as well as area-level information (e.g., socioeconomic status) for 100 individuals, each linked to a postal code. This dataset will serve as input in the example demonstrating the `SeasEpi_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 `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 `SeasEpi_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.

`SeasEpi_Par_Est` *SeasEpi for Real Data*

Description

This function applies the spatiotemporal individual-level model of seasonal infectious disease transmission 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

```
SeasEpi_Par_Est(
  data,
  adjacency_matrix,
  DimCovInf,
  DimCovSus,
  tau0,
  lambda0,
  alphaS0,
  delta0,
  alphaT0,
  InfPrd,
  IncPrd,
```

```
  NIterMC,
  NIterMCECM,
  zeta10,
  zeta20,
  T_cycle
)
```

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
`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
`zeta10`	Initial value for the amplitude of the seasonal oscillation parameter (sin part)
`zeta20`	Initial value for the phase of the seasonal oscillation parameter (cos part)
`T_cycle`	The duration of a complete seasonal cycle (e.g., 12 months for an annual cycle)

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

`alphaT` Estimate of alpha T

`delta` Estimate of delta

`zeta1` Estimate of zeta1

`zeta2` Estimate of zeta2

`tau1` Estimate of tau

`lambda1` Estimate of lambda

`AIC` AIC of the fitted GDILM SEIRS

Examples

```
data(data)
data(adjacency_matrix)
SeasEpi_Par_Est(data,adjacency_matrix,2,2,0.5, 0.5, 1, 0.1, 1, 1, 1, 20, 2,0.2,0.2,5)
```

`SeasEpi_Sim_Par_Est` *SeasEpi for a Simulation Study*

Description

This function conducts a simulation study for spatiotemporal individual-level model of seasonal infectious disease transmission 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

```
SeasEpi_Sim_Par_Est(
  GridDim1,
  GridDim2,
  NPostPerGrid,
  MaxTimePand,
  tau0,
  lambda0,
  alphaS0,
  delta0,
  alphaT0,
  PopMin,
  PopMax,
  InfFraction,
  InfPrd,
  IncPrd,
  NIterMC,
  NIterMCECM,
  zeta10,
  zeta20,
  T_cycle
)
```

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
`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
`zeta10`	Initial value for the amplitude of the seasonal oscillation parameter (sin part)
`zeta20`	Initial value for the phase of the seasonal oscillation parameter (cos part)
`T_cycle`	The duration of a complete seasonal cycle (e.g., 12 months for an annual cycle)

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

`alphaT` Estimate of alpha T

`delta` Estimate of delta

`zeta1` Estimate of zeta1

`zeta2` Estimate of zeta2

`tau1` Estimate of tau

`lambda1` Estimate of lambda

`AIC` AIC of the fitted GDILM SEIRS

Examples

```
SeasEpi_Sim_Par_Est(5,5,10,30,0.7, 0.7, -1, 0.1, 0,40, 50,0.6, 5, 5, 10, 3,0.2,0.2,5)
```

Index