

Package ‘SeasEpi’

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Title Spatiotemporal Modeling of Seasonal Infectious Disease

Version 0.0.2

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.

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Imports MASS, mvtnorm, ngspatial, stats

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Suggests testthat (>= 3.0.0)

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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.

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