

Extended SEIR model Edit Manage topics -0- 32 commits № 1 branch 🗇 **0** packages O releases **Q** contributors ₫ View license Branch: master ▼ New pull request Create new file Upload files Find file Clone or download ▼ Jim Duggan and Jim Duggan Uploading model structure diagram Latest commit 9371751 1 hour ago Adding dplyr:: to filter call for explain() 2 hours ago Uploading model structure diagram ata-raw 1 hour ago Updates for first relase 17 hours ago ata data Uploading model structure diagram inst 1 hour ago Update polymod location 2 hours ago man man tests Updates for first relase 17 hours ago .DS_Store Adding test data 4 days ago Rbuildignore **Update README** 2 hours ago a.gitignore Initial Update 6 days ago **DESCRIPTION** Adding explain() method 5 hours ago **LICENSE** Update 5 days ago **NAMESPACE** Update polymod location 2 hours ago README.md Test Picture 1 hour ago release-comments.md Updating first example 9 hours ago seirR.Rproj Initial Update 6 days ago **■ README.md**

seirR

This package contains a SEIR model to model the spread of an infectious disease. The model is a population-level model. The package is best used in conjunction with R's tidyverse tools such as **dplyr** and **ggplot2**.

Current Version 0.0.0.1

html_document

default

output

pdf_document

default

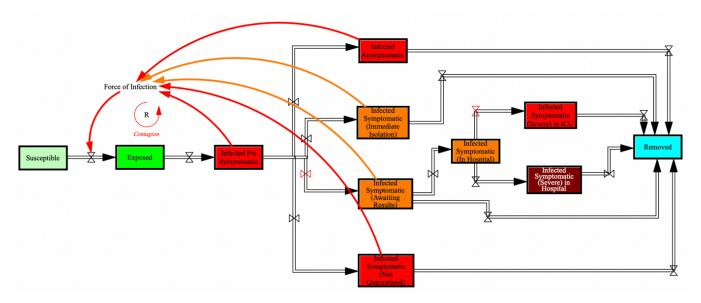
This package is currently undergoing testing and has not yet been released. See version history below for a record of changes and version

Installation

To install, obtain the authorisation key from the repo owner, and type the following command:

install_github("JimDuggan/seirR",auth="THE_KEY_GOES_HERE")

Model Overview



Examples

The following are three examples of how to use the model (and data)

- Running a model
- Exploring the data set
- Running a sensitivity analysis
- Explain Feature

Version History

Version 0.0.0.1

- Release date: April 2nd 2020
- First beta version. Contains a population level SEIR model based on agreed structure.