Assignment 2: Stochastics, Meta-population models
Due Friday October 19 2020 @ 23:59

Introduction

In this assignment we will be exploring other ways to model infectious diseases. In the first part of the assignment we will use a stochastic discrete event model to compute the spread of an infectious disease through a population. And in the second half of the assignment we will explore spatial models to study the spread of infectious diseases.

Problem 1: Gillespie's Direct Algorithm

We have discussed the five hallmarks of stochastic SIR dynamics: variability; negative co-variances; increased transients; stochastic resonance; and extinctions. Some of those were demonstrated in the stochastic versions of the SIR ODEs (using constant or scaled noise terms) and some were shown in the context of event driven SIR.
We ask you to explore the five hallmarks in an SIR discrete event model using Gillespie's direct algorithm. Design a set of well chosen experiments to demonstrate all these aspects, also exploring the dependence on the basic parameters in the model.
Advanced topic: Try to reproduce the graphs from the book in relation to persistence and critical community size, or try to measure e.g. the first passage time. You can also consider other models, e.g. SIS, SEIR, SIRS, etc.
Hint: start with SIR without demography, then add demography, and finally add imports to the model.

Problem 2: Meta-population model

Lets start with implementing a simple meta-population model to study the spatial dynamics of a spreading infection. Start with a stochastic meta-population model with two sub-populations. Consider two large, fully susceptible populations, with $\rho_{ii} = 1$ and $\rho_{ij} < 1$. Assume the populations are of the same size, and ignore demography. What is the effect of the coupling between the two populations, are there any delays?
Now produce a meta-population of your own using more sub populations (Hint: Try using different strength of interaction between populations), and comment on the dynamics.