Introduction to Computational Science
University of Amsterdam
October 2024

Project: Stochastic and Spatial Models

Due Saturday October 26 2024 @ 23:59

Introduction

In this assignment you (in teams of two people) will be exploring other ways to model infectious diseases. In the first part of the assignment you 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 you will explore spatial models (in particular networks) to study the spread of infectious diseases.

Problem 1: Gillespie's Direct Algorithm and Stochastic Hallmarks

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You will investigate the five hallmarks of stochastic SIR dynamics using an event drive SIR model:

1. variability;
2. negative co-variances;
3. increased transients;
4. stochastic resonance;
5. extinctions.

Implement Gillespies algorithm

Write some python code to implement Gillespies Algorithm (GA)[1]. You should define the events and the rates of each event for the SIR model. Keep in mind it may be insightful to compare the GA stochastic simulation with an equivalent deterministic ODE model. BONUS: You can also think about (and implement) a way to control the noise level in the GA.

Investigate Simulation Variability and Negative Co-variance

In the first experiment you should investigate how varying the model parameters changes the behaviour of the stochastic dynamics, in particular how they relate to variance between runs and how they impact negative covariance between S and I. Compare the mean of the stochastic simulations with the equivalent deterministic model output (do this for multiple settings of the model parameters).

[1] You can use first reaction, direct, or other GAs

Stochastic Resonance and Increased Transients

Show how the stochastic model can induce stochastic resonance around the equilibrium and how that resonance relates the model parameters (e.g., N, β), etc). Show some examples of increased transients away from the deterministic equilibrium - can you show which parameter values lead to the largest transients.

Extinction events and Critical Community Size

In the lectures we have discussed the possibility of extinction of the virus even when $R_0 > 1$ in closed populations. Design an experiment to show how varying R_0 impacts the extinction process. Keep in mind that in the closed system randomness will always *eventually* lead to extinction. Now look at how the extinction events are impacted by the population size. Find a way to show how the two parameters R_0 and N interact to impact the extinction process.

Problem 2: Spatial Models - Networks

In this question you are asked to develop a set of experiments to design and evaluate vaccination strategies using a network model. Using the package NDLib[2] you should assess the spread of a disease (SIR) across different types of model networks (Barabasi Albert, Watts-Strogatz, Erdos-Reyni). Finally, you will run a simulated vaccination campaign on a real contact network collected by sociopatterns (link). A modified version of this dataset can be downloaded from Canvas, the network has been converted to a static (non-temporal) form and some edges and nodes have been filtered out.

Implement SIR and Simulate

Implement SIR disease spread on the network. Think about your experimental design and which parameters of the model you will want to vary. Design code that will allow you run multiple simulations while varying the disease parameter.

Generate Networks of equivalent form

Using NetworkX generate multiple model networks with similar characteristics, again think about the parameters associated with each network generator (e.g., Number of nodes, connection probability,etc). Pick some network statistics (e.g., centrality measures, degree distributions, etc.) that are interesting to measure in terms of spreading on the network. You should generate multiple instances of each network type and then plot the network statistics (you chose) and discuss how these statistic differ between network types and for different parameter settings. You will use these generated networks in your SIR experiments in the next part.

[2]Note there are SIR Network implementations/examples that you can re-use/adapt in the library see `https://ndlib.readthedocs.io/en/latest/tutorial.html`

Simulate SIR spread on the network

Simulate epidemic spreading on the networks you generated in the previous section (NOTE: the simulations will be stochastic so think about random seeds and repitions). You can vary the fraction of initial infected, which nodes are initially infected and other disease parameters. Compare and discuss how the disease spreads in the different networks under different conditions.

Dynamic Vaccination Campaign

Finally, we will conduct vaccination experiments using the sociopatterns dataset, see Figure 1. You should design some code to load in the sociopatterns dataset (this file on canvas includes a simple edgelist and NDLib and NetworkX provide ways to import this).

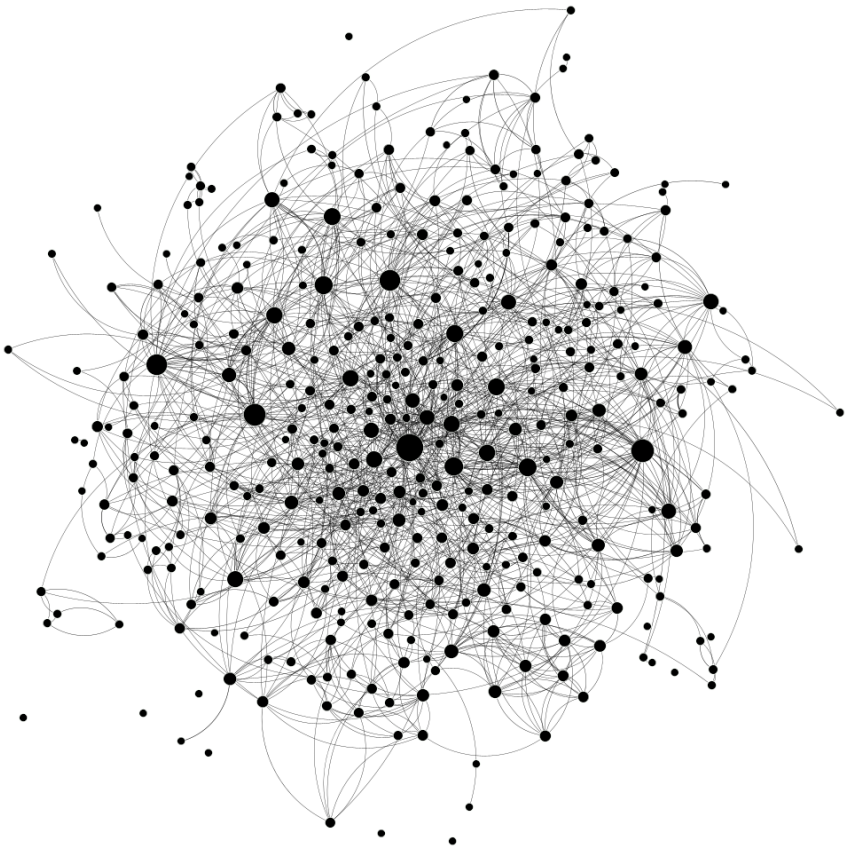

Figure 1: A view of the filtered sociopatterns data set with 374 nodes and 1265 edges. The nodes are people and edges exist if the two people spent time near each other during the conference. Note that in the original dataset edges had weights indicating how long those people were in range of one another. In this assignment we disregard the weights and assume all contacts involve equal length of contact and hence equal chance of transmission.

Now consider a scenario in which a disease is spreading on this network. You should run multiple experiments, but assume that the disease always starts with a *random* selection of 5 nodes infected.

You are to design a dynamic vaccination strategy in which you have a testing budget and a limited number of vaccinations available per iteration of the model. Assume that you have 200 tests in total, you can use a maximum number of tests per iteration (this will vary per experiment see below), you can of course use less. You can use the tests at any point during the spread and you may repeat tests on a node as often as you like. You can assume that you know the network structure, but you can only discover the disease status of a node after a test. Vaccinations can only be applied to susceptible people and that they immediately move people to the removed state. Finally, you might consider situations where the tests are not always accurate, but instead have some probability (which you can vary) of being accurate. You can also assume that people remain removed until the end of the simulation (no waning immunity).
You should compare your strategy against a simple null strategy which randomly assigns vaccinations, you should design a strategy that at least out performs the null strategy. Compare the strategies with different vaccination budgets of [1, 3, 5 and 10] per timestep and compare with different testing accuracy [0.5, 0.75, 1.0] . Finally, keep in mind that the purpose of the assignment is not to design the best strategy, but to evaluate you strategy in a systematic and scientific manner.