Simulation of Complex Systems

Homework 1: Disease Spreading

Time and place:

- Assistance: November 9, 2016, 08:00-09:45, MT14
- Assessment: November 18, 2016, 08:00-09:45, F-T7204

Computer lab: The computer lab serves two purposes: To assist with homework and assess homework. The time we have available for computer lab is limited, so it is important that you ***come prepared to the lab***, with specific questions you need to have answered. Everyone involved will appreciate the reduced queue times. You are also ***strongly encouraged*** to team up and collaborate on the problems, to ask your classmates if you are stuck at some point, and to assist classmates in need of advice. But you must write your own implementation and generate your own results!

Examination: During lab hour, presumably in groups, you should demonstrate your homework to a tutor. ***Be prepared for the assessment:*** Generate all figures and/or videos up front. There will be no time for running simulations during assessment. Check that you have answered all questions carefully. Writing down your answers beforehand will many times be helpful. ***No late assignments will be accepted.***

In this exercise we are going to implement a simple agent-based model for studying disease spreading. Agent-based models are a natural next step from the simple ODE approach, and has become an important tool in understanding disease dynamics and developing countermeasures. Before you do the exercises, make sure you read "The SIR model and the Foundations of Public Health" and have a good understanding of the SIR model. Also read the Nature opinion "Modelling to contain pandemics" by Epstein to get an appreciation of the role agent based models can play in developing policies for infectious diseases.

We will consider the three-compartment model known as SIR, where each individual is either Susceptible to the disease, Infected, or has Recovered and is immune. Infected individuals infect susceptible they meet with some rate β and recover with some rate γ. In a simple ODE or PDE-version of the model only the ratio $R_0 = \beta/\gamma$ matters for the behavior of the model. In these exercises you will examine what happens when we take into account spatial effects.

Below is a brief description of the model you will implement. The exercises are focused on examining the behaviour of this model for different parameters. In order to do these efficiently, spend some time in setting up the model properly.

- We model the movements of the agents as random walks on a square grid (lattice): Every time step each agent either sits still with some probability $1 - d$, or moves to a random neighbouring tile (use von Neumann neighbourhood) with probability d, where d sets the diffusion rate.

- Check for infection when agents of the susceptible and infected types land on the same lattice site. Every time step, each infected should have a probability β of infecting all susceptibles at its current site *and* a probability γ of recovering.

- To make the simulation scalable (we want to be able to look at 1000 agents at least), don't check the position of every agent against everyone else's (this scales as the square of the number of agents). Instead, do something along the lines of keeping a list, corresponding to the lattice, that keeps track of which susceptibles (if any) are at a given site. This scales linearly in the size of the lattice and the density of agents.

- The disease dynamics is static when the number of infected agents reaches zero. This fact can be used as a stopping criteria for the simulations.

Exercises:

1. Implement the basic model and visualize it. Start with just a single agent and make sure it performs the random walk correctly. Then test some small number of agents to check that the disease dynamics seems reasonable, and then scale it up to, e.g., a thousand agents on a 100×100–lattice. **To demonstrate**: 1) A plot of a random walk performed by a single agent; 2) A figure similar to Fig. 1 for a small number of agents; 3) A figure similar to Fig. 1 for 1000 agents on a 100×100–lattice. For each figure, include information on what parameters were used in the simulation. Explain what we see in the figures. **(6p)**

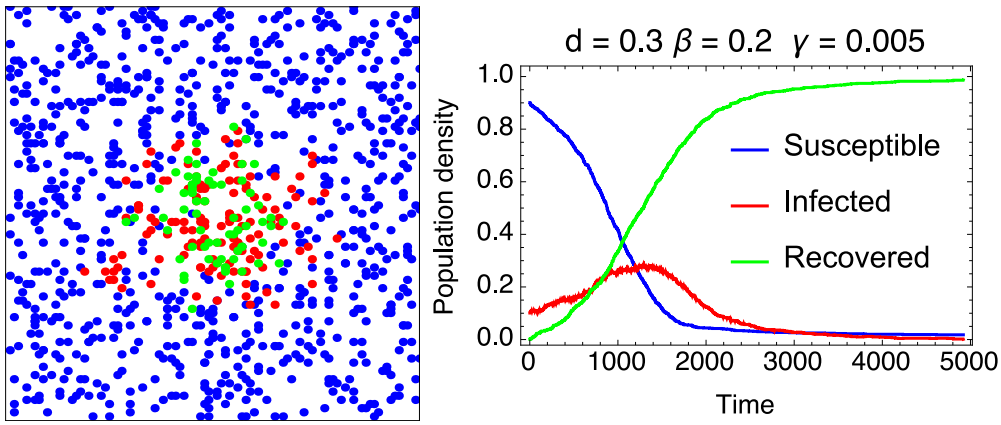

Figure 1: SIR-agents on a lattice and a plot of the proportions of individuals in each state over time.

2. Show that the model contains two regimes, i.e., that there are parameter values for which the disease spreads to a large proportion of the population and values for which it doesn't. **To demonstrate**: 1) A figure similar to Fig. 1 that demonstrates population-wide disease spreading; 2) A figure similar to Fig. 1 that demonstrates limited disease spreading; For each figure, include information on what parameters were used in the simulation. Explain what we see in the figures. **(4p)**

3. Show that, in contrast with the ODEs discussed in "The SIR model and the Foundations of Public Health", the epidemic threshold R_0 depends

on not just the ratio β/γ but on the parameters themselves. Use a small initial number of infectives ($\approx 1\%$), fix a value for β, run the model for each of several values of γ and record the final proportion of recovered $R_\infty = R(\infty)$. Plot these values as a function of β/γ, similarly to Fig. 2. You should clearly see the two regimes. It will be beneficial (and good practice) to do several runs at each setting and average the results to avoid noisy results; make sure you do this. Then repeat the process for another value of β and compare the results. **To demonstrate**: A plot comparing the two data sets, showing clearly respective thresholds. Include information on what parameters were used in the simulations and how many runs were used for averaging. Explain what we see in the figure. **(7p)**

4. Map out the whole critical line in the β-R_0-plane, i.e., repeat the above process for enough values of β that you can determine the important features of the phase diagram. **To demonstrate**: The resulting 3D phase diagram. Include information on what parameters were used in the simulations and how many runs were used for averaging. Explain what we see in the figure and argue why you obtain this result. Provide a brief discussion of how your findings relate to the ODE version of the SIR model. **(8p)**

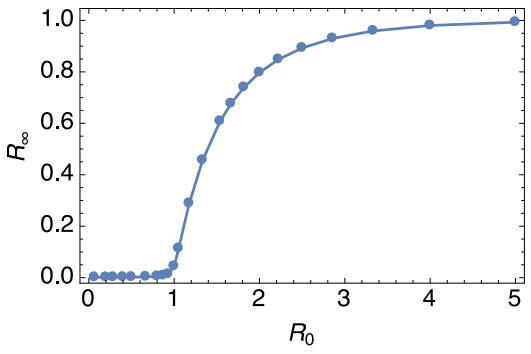

Figure 2: The epidemic threshold from an ODE version of the SIR model. The total proportion of the population afflicted by the disease, R_∞, is negligible under the critical value $R_0 = 1$ of the basic reproduction number and quickly increases towards 1 above it.