Chapter 10

Disease Spreading

Disease spreading in a population is affected by a number of parameters like human activity, personal space, and the impact of the specific virus or bacterium. Infectious diseases often spread in a society through individuals' contact. This can take place through direct contact, via a sneeze or cough, or by exchange of body liquids. The dynamics of an infectious disease depends on mobility, infection probability and the recovery speed. The SIR (susceptible-infected-recovered) model, introduced by Sir Ronald Ross and several others [1], evaluates this phenomenon mathematically with a series of ordinary differential equations (ODE) that connect these variables. Lots of studies have followed building on this theory since its introduction in order to understand various aspects of disease spreading using simple ODE approaches. However, agent-based models are a natural next step from the simple ODE approach. They have become an important tool in understanding disease dynamics and developing countermeasures. In this exercise, we are going to use the basic principles of the SIR model in order to numerically simulate the spreading of diseases in a finite space environment using agent-based modelling. This exercise is self explanatory, but for further reading you can refer to "The SIR model and the Foundations of Public Health" [1] and "Modelling to contain pandemics" [2] 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 (S) to the disease, Infected (I), or has Recovered (R) and is immune. Infected individuals infect the susceptible they meet with rate β and recover with rate γ. In a simple ODE or PDE-version of the model only the ratio $k = \beta/\gamma$ matters for its behaviour 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.

- 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 susceptible agents (if any) are at a given site. This scales linearly with 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 criterium 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 (6 points)**: 1) A plot of a random walk performed by a single agent; 2) A figure similar to Fig. 10.1 for a small number of agents; 3) A figure similar to Fig. 10.1 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.

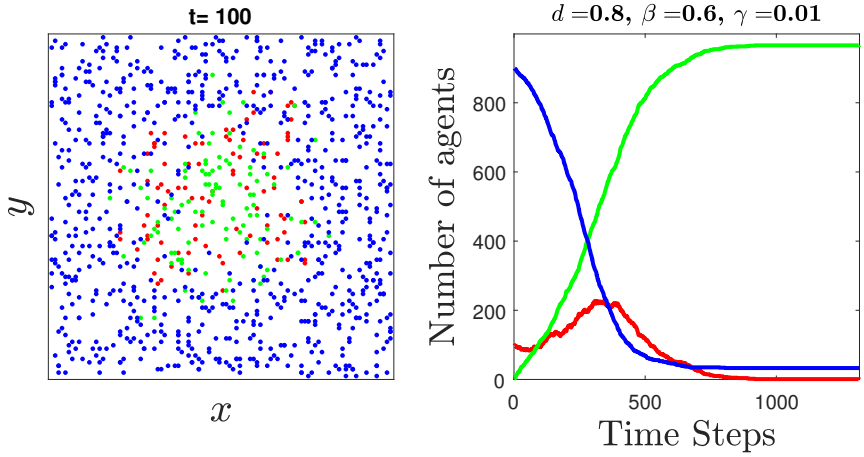

Figure 10.1: **Modelling disease spreading on a square lattice.** (a) Screenshot of SIR-agents on a lattice after 100 time steps and (b) a plot of the proportions of susceptible (blue), infected (red) and recovered (green) individuals in each state over time.

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 (4 points)**: 1) A figure similar to Fig. 10.1 that demonstrates population-wide disease spreading; 2) A figure similar to Fig. 10.1 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.

3. Show that, in contrast with the ODEs discussed in "The SIR model and the Foundations of Public Health" [1], the epidemic threshold depends on not just the ratio $k(\beta/\gamma)$ but on the parameters themselves. Use a small initial number of infective agents ($\approx 1\%$), 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. 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 (7 points)**: A plot comparing the two data sets, showing clearly the 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.

4. Map out the whole critical line in the β-k-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 (8 points)**: 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 you 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.

Bibliography

[1] H. H. Weiss, "The sir model and the foundations of public health," *Materials matematics*, pp. 0001–17, 2013.

[2] J. M. Epstein, "Modelling to contain pandemics," *Nature*, vol. 460, no. 7256, p. 687, 2009.