Diffusion Processes on Complex Networks - Lab

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1 Assignment 5

1. SIR model In 1927, W. O Kermack and A. G. McKendrick created a model in which they considered a fixed population with three compartments: susceptible S, infected I and removed R. Analogous to the principles of reaction kinetics, they assumed that encounters between infected and susceptible individuals occur at a rate proportional to their respective numbers in the population. The rate of new infections can thus be defined as βSI, where β is a parameter for infectivity. Moreover, infected individuals were assumed to recover with a constant probability at any time, which translates into a constant per capita recovery rate that we denote with r and thus an overall rate of recovery rI. The model may be translated into the following set of differential equations:

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta SI \\ \frac{dI(t)}{dt} &= \beta SI - rI \\ \frac{dR(t)}{dt} &= \beta rI \end{aligned} \tag{1}$$

A key parameter in epidemiology is the basic reproductive ratio R_0. It is defined as the average number of secondary cases transmitted by a single infected individual that is placed into a fully susceptible population. R_0 tells us something about the initial rate of spread of the disease. If $R_0 > 1$, there will be an epidemic and if $R_0 < 1$, the introduced infected will recover (or die) without being able to replace themselves by new infections. In the above model it is pretty easy to derive R_0. The disease-free state corresponds to $S = N$, $I = 0$ and $R = 0$. If one infected individual appears in the population, there will be an epidemic if and only if $dI(t)/dt > 0$. By replacing S with N in the above equations this yields $\beta N/r > 1$. Thus we take:

$$R_0 = \frac{\beta N}{r} \tag{2}$$

(a) Check the formula for R_0 by solving the model numerically for different sets of parameters. Fix N, and vary β and r. Choose your values such as to have combinations with both $R_0 > 1$ and $R_0 < 1$. Run the model for each parameter combination, plot the time evolution of each compartment and record whether there was an epidemic or not.

(b) Notice that the basic SIR model can be reduced to a two-dimensional system, because the variable for recovered individuals does not appear in the equations of the other two variables. The reduced SI system is thus given by

$$\begin{aligned} \frac{dS(t)}{dt} &= -\beta SI \\ \frac{dI(t)}{dt} &= \beta SI - rI \end{aligned} \tag{3}$$

Phase portraits provide a powerful tool to visualize the dynamics of ODE systems. For a fixed set of parameters, draw a phase portrait with trajectories corresponding to different initial conditions. (Hint: cuiver command in the matplotlib library)

(c) For different combinations of r and β determine the total number of individuals infected during an epidemic and then calculate R_0 for each parameter set. Plot the total number of infections as a function of R_0.

2. SIR model on a network. You are given a graph representing the contact network. So an edge between the nodes v and w means that if v becomes infected at some point, the disease has the potential to spread directly to w. Each node may go through the Susceptible-Infectious-Removed cycle. The progress of the epidemic is controlled by the contact network structure and an additional quantity: the probability of contagion p (for the sake of simplicity we assume that the length of the infection is exactly one time step). You should simulate the dynamics synchronously as follows (one Monte Carlo steps corresponds to a loop over all nodes in the network):

- Initialize all nodes as susceptible.
- Select a single node at random to begin the infection.
- While there are any infected nodes do:
  - For each infected node u in the previous step: * For each susceptible neighbor v of u with probability p set it to infected on the next step,

- Set u to recovered on the next step.

(a) Simulate the model on: (a) a 2D lattice, (b) a random graph, (c) a Watts-Strogatz graph and (d) a Barabasi-Albert graph. Keep the number of nodes low, e.g. equal to 100 (performance issues).

(b) Record the fraction of infected nodes in the network at each time point for three different values of p. Because the SIR dynamics is stochastic, you will want to simulate each infection multiple times with the same starting node. Plot the average of this runs over time for each value of p.

(c) Discuss how the infection curves compare to the behavior seen in the ODE model.

(d) Now select at least 20 different values of p. Simulate the SIR dynamics on the network starting with a random node. Measure the total proportion of the network that becomes infected, the time to clear infection and the time to the largest number of infected nodes. Be sure to simulate the infection enough times (each run starting from a different randomly chosen starting node) that you can reasonably estimate the mean of each of these measures. For each measure plot it as a function of p. Make one plot for each measure, including a separate line (labeled appropriately) for each network.

(e) What each of the above measures tells you about the different networks?

(f) For each network of size $N = 30$, visualize a single run of the infection spreading in form of an animated gif or an avi file.

3. SIR model on a network (continued) Repeat the above simulation in the asynchronous update scheme. In other words, for every Monte Carlo step do the following:

   Do as many times as the number of nodes:

   - Pick a node u at random. If the node is infected:
     - For each susceptible neighbor v of u with probability p set it to infected on the next step.
     - Set u to recovered on the next step.

   (a) analyze the impact of the updating scheme on the final outcome of the model.