

FRTN30 Network Dynamics

Assignment 4

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In this hand-in, we will learn the network-structure characteristics and disease-dynamics parameters of the pandemic in Sweden 2009.

1 Preliminary parts

In this task, we will simulate an epidemic on a given graph and generate a random graph with preferential attachment.

1.1 Epidemic on a known graph

We will simulate an epidemic on a symmetric k -regular undirected graph with node set $\mathcal{V} = \{1, \dots, n\}$. The graph has $n = 500$ nodes and $k = 4$ nodes.

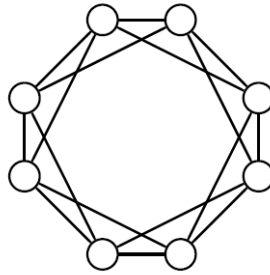


Figure 1: Symmetric k -regular graph

The epidemic is simulated using a discrete-time version of the SIR epidemic model. The probability of one susceptible node being infected by its neighbors is $1 - (1 - \beta)^m$ where β is the probability of infection and m is the number of infected neighbors.

We simulate the epidemic for 15 weeks with 100 iterations. At the beginning of each iteration, 10 infected nodes are selected at random from the node set \mathcal{V} .

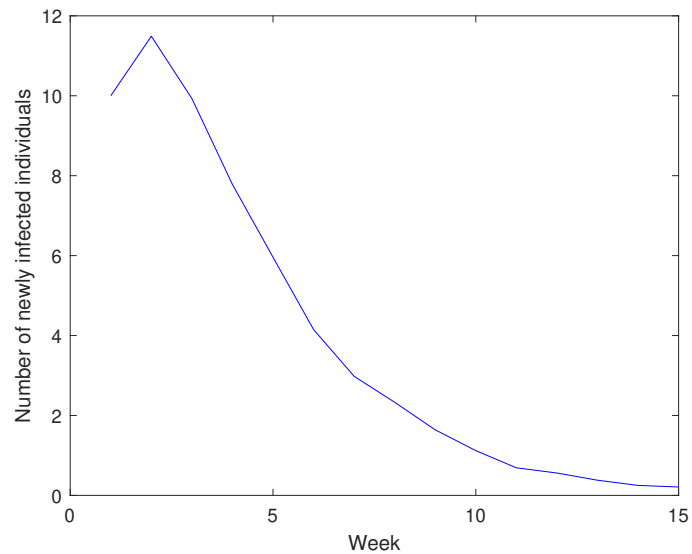


Figure 2: Newly infected individuals

Since each infected node is connected to $k = 4$ nodes, the total number of neighbors for the 10 infected nodes would be $10 * 4 = 40$. Therefore, with 10 infected nodes, each having 40 neighbors, and with $\beta = 0.3$, the expected number of newly infected individuals in the second week would be approximately $40 * 0.3 = 12$. It seems reasonable with our simulation.

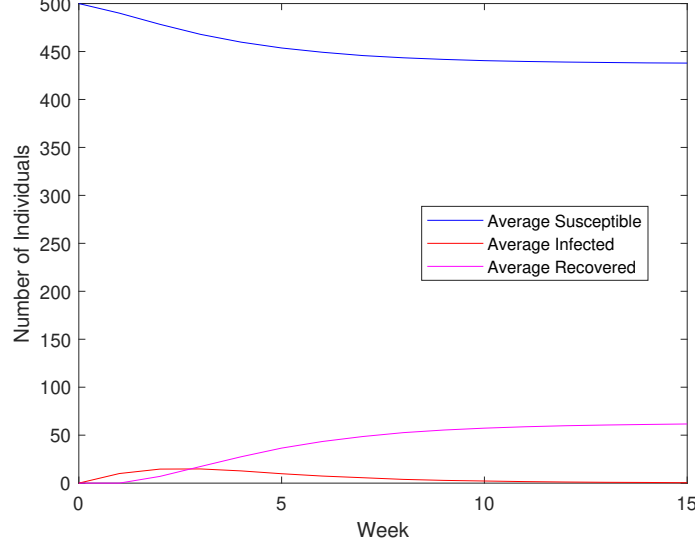


Figure 3: The average total number of susceptible, infected, and recovered individuals

The figure (3) looks logical since the total number of infected individuals peaked around week 2 and declined rapidly thereafter. It means that the total number of recovered individuals increases quickly after week 2.

1.2 Generate a random graph

In this task, we will generate a random graph according to the preferential attachment model with an average degree close to k .

Using the preferential attachment rule, at every time-step $t \geq 2$, every new node added at time t will have a degree $w_t(t) = c = k/2$. When k is an even number, the average degree k can be evenly divided among the existing nodes, resulting in a balanced distribution of connections. However, when k is an odd number, it is not possible to evenly distribute the degree k among the existing nodes. To handle this, we use $c = \text{floor}(k/2)$ when t is an even number, and $c = \text{ceil}(k/2)$ when t is an odd number. By doing this we ensure that when a large number of nodes are added to the graph, the average degree will converge to k .

If we denote the new node n_t , the probability that there will be a link between node n_t and node $i \in \mathcal{V}_{t-1}$ is

$$\mathbb{P}(W_{n_t, i}(t) = W_{i, n_t}(t) = 1 | \mathcal{G}_{t-1} = (\mathcal{V}_{t-1}, \mathcal{E}_{t-1})) = \frac{w_i(t-1)}{\sum_{j \in \mathcal{V}_{t-1}} w_j(t-1)}$$

where $W(t)$ is the adjacency matrix and $w_i(t-1)$ is the degree of node i before adding the new node.



Figure 4: Random graph generated according to the preferential attachment model

2 Simulate a pandemic without vaccination

In this task, we will simulate an epidemic using the random graph from task 1.2. We use the same setup from task 1.1, except for $k = 6$.

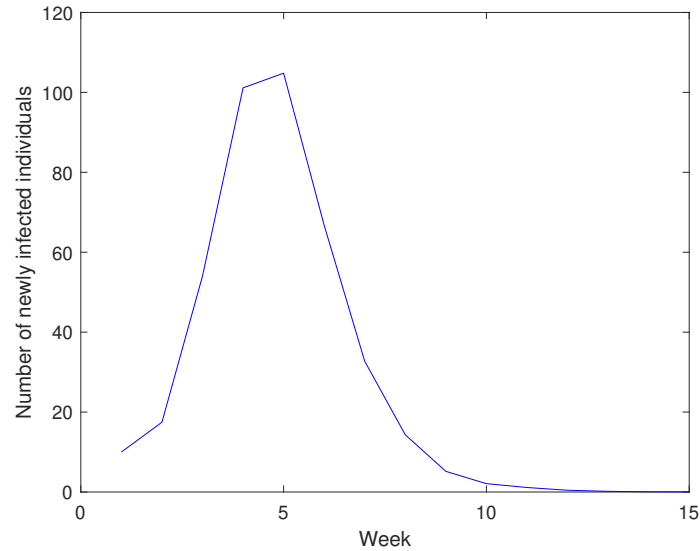


Figure 5: Newly infected individuals

Since each infected node is connected to $k = 6$ nodes, the total number of neighbors for the 10 infected nodes would be $10 * 6 = 60$. Therefore, with 10 infected nodes, each having 60 neighbors, and with $\beta = 0.3$, the expected number of newly infected individuals in the second week would be approximately $60 * 0.3 = 18$. This value is similar to what we get from the simulation.

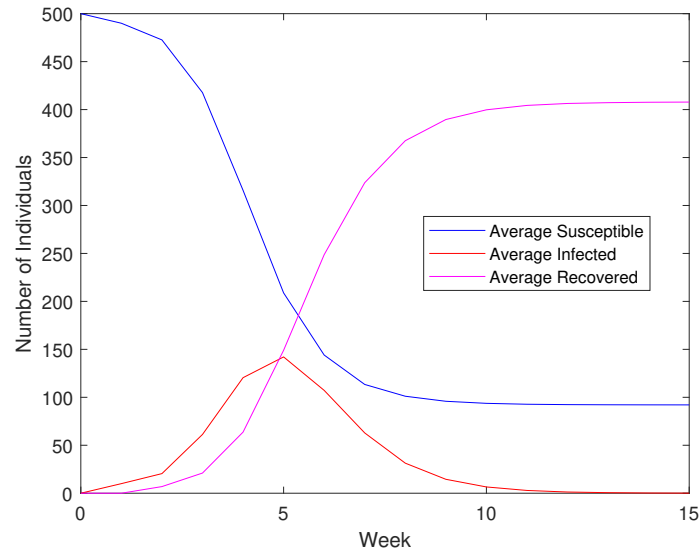


Figure 6: The average total number of susceptible, infected, and recovered individuals

After the total number of infected individuals peaked around week 5, which causes the total number of susceptible individuals to decline rapidly, the total number of recovered individuals increases quickly.

3 Simulate a pandemic with vaccination

In this task, we use the same setup as task 2. In addition, we add vaccinations to the simulation. The vaccine distribution is given as

$$Vacc(t) = [0, 5, 15, 25, 35, 45, 55, 60, 60, 60, 60, 60, 60, 60, 60].$$

One example for $Vacc(t)$ is that 15% of the population has received vaccination by week 3, and 10% received vaccination during week 3.

Individuals to vaccinate should be selected uniformly at random from the population that has not been vaccinated. After that, they will not be infected or infect any other individuals.

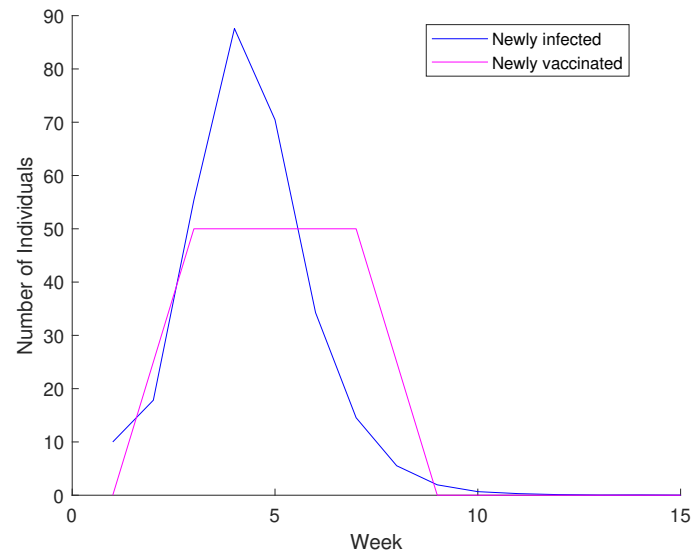


Figure 7: Newly infected and vaccinated individuals

Compared to the figure (5), the peak of newly infected individuals is significantly reduced because of vaccination.

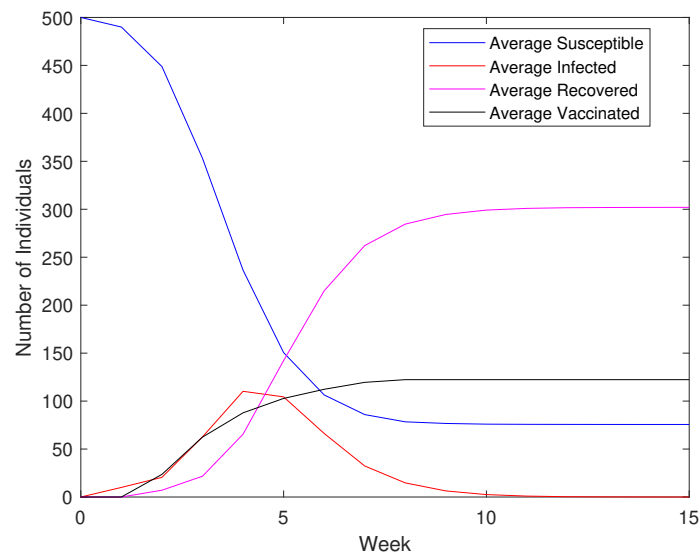


Figure 8: The average total number of susceptible, infected, vaccinated and recovered individuals

The total number of infected individuals peaked around week 4, which is earlier than what we observed from task 2. Because of vaccination, the total number of recovered individuals is reduced to nearly 300. In the last task, it was nearly 400.

4 The H1N1 pandemic in Sweden 2009

In this task, we will simulate the pandemic in Sweden during the fall of 2009. The vaccine distribution is given as

$$Vacc(t) = [5, 9, 16, 24, 32, 40, 47, 54, 59, 60, 60, 60, 60, 60, 60, 60].$$

We use the graph with $n = 934$ nodes. The number of newly infected individuals each week is given as

$$I_0(t) = [1, 1, 3, 5, 9, 17, 32, 32, 17, 5, 2, 1, 0, 0, 0, 0].$$

The root-mean-square error (RMSE) is used to find the best set of k_0, β_0, ρ_0 from the parameter-space $k \in \{k_0 - \Delta_k, k_0, k_0 + \Delta_k\}$, $\beta \in \{\beta_0 - \Delta_\beta, \beta_0, \beta_0 + \Delta_\beta\}$, and $\rho \in \{\rho_0 - \Delta_\rho, \rho_0, \rho_0 + \Delta_\rho\}$

$$RMSE = \sqrt{\frac{1}{15} \sum_{t=1}^1 5(I(t) - I_0(t))^2}$$

where $I(t)$ is the average number of newly infected individuals each week.

The number of newly infected individuals of the first 2 weeks is 1 so I choose an initial configuration with 1 infected node selected at random from the node set \mathcal{V} . We update k_0, β_0, ρ_0 to find the lowest RMSE and keep training until we get the same set. I add one more condition to stop when $k_0 = 3$ to prevent the software from crashing.

The best set of parameter that I can find is:

k	β	ρ
7	0.15	0.5

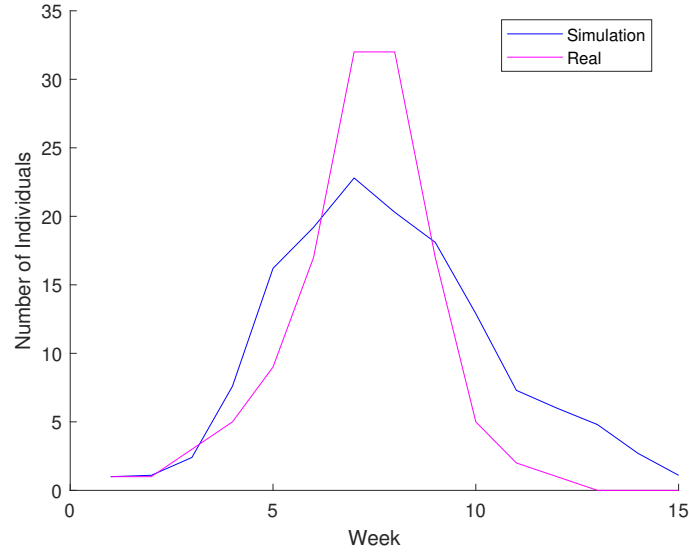


Figure 9: Simulation and Real number of newly infected individuals

The simulation simulates the real data quite well. I have tried multiple times and it is difficult to find the set of parameters to simulate exactly the real data.

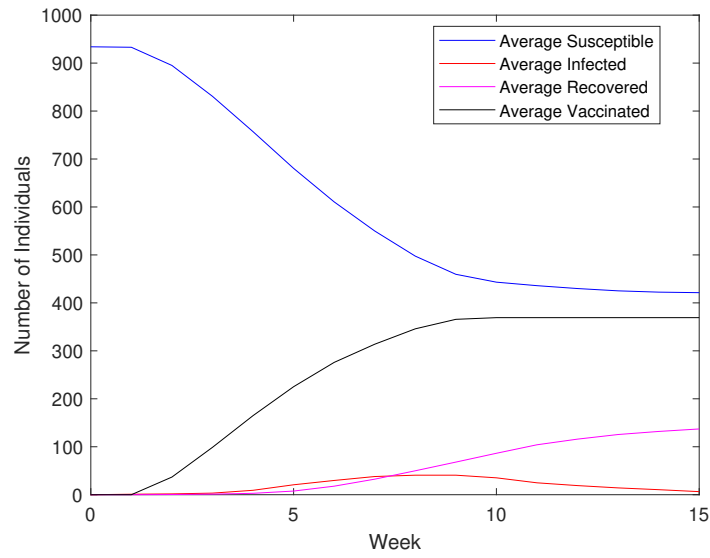


Figure 10: The average total number of susceptible, infected, vaccinated and recovered individuals

The simulation does not fit the real peak of newly infected individuals so the average total number of infected will be less than the real data. Nevertheless, the simulation looks good as the average total number of infected and susceptible go down while the average total number of vaccinated and recovered go up rapidly.