Network Dynamics and Learning

Homework III

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1 Epidemic on a known graph

1.1 Simulation on a symmetric k-regular graph

We simulated a discrete-time simplified version of the SIR epidemic model on a symmetric k-regular undirected graph. The graph $\mathcal{G} = (\mathcal{V}, \mathcal{E})$ has $n = 500$ nodes and every node is directly connected to the $k = 4$ nodes whose index is closest to their own modulo n. The disease propagation parameters were set to $\beta = 0.3$ and $\rho = 0.7$. The simulation ran for 15 weeks with an initial configuration of 10 infected nodes selected at random.

We performed $N = 100$ simulations to compute the average behavior.

1.2 Results

We plotted the following:

- **Average number of newly infected individuals:** The number of new infections decrease.

- **Average total number of individuals:** The evolution of susceptible, infected, and recovered individuals at each week.
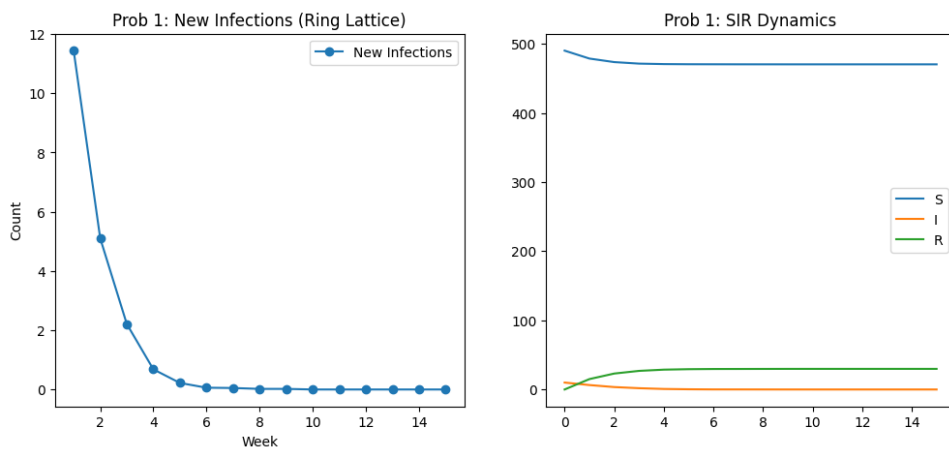

Figure 1: Average number of newly infected individuals (left) and total S, I, R individuals (right) on the symmetric k-regular graph.

2   Simulate a pandemic without vaccination

2.1   Generate a random graph

We generated a random graph using the preferential attachment model. We started with a complete graph of $k + 1$ nodes. New nodes were added sequentially and connected to existing nodes with a probability proportional to the current degree of the node they are connecting to. This ensures the average degree is close to k.

2.2   Simulation Results

Using the generated preferential attachment random graph with $n = 500$ and average degree $k = 6$, we simulated the epidemic for 15 weeks ($\beta = 0.3$, $\rho = 0.7$). Comparing the results to the symmetric k-regular graph, the epidemic spreads differently due to the network structure.
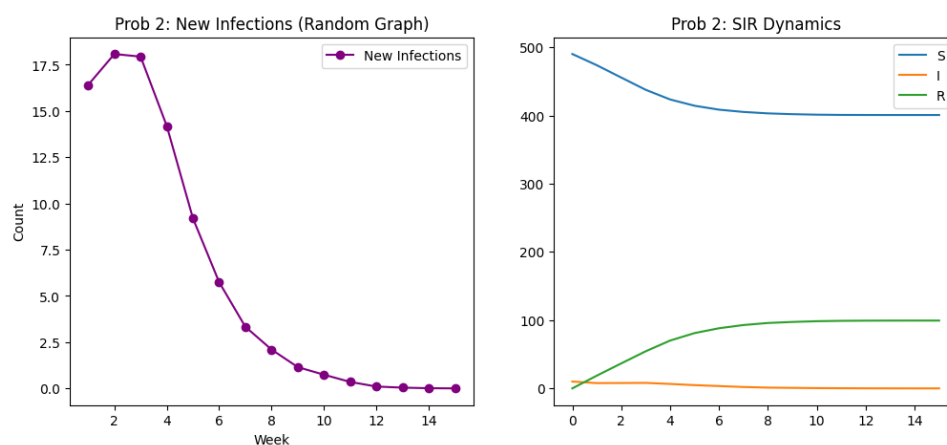

Figure 2: Average number of newly infected individuals and total S, I, R individuals on the preferential attachment random graph.

3   Simulate a pandemic with vaccination

3.1   Vaccination Scheme

We simulated the disease propagation on the same random graph ($k = 6$) but included a vaccination program to slow down the epidemic. The vaccination followed the scheme Vacc(t), where a specific fraction of the population received vaccination each week. Individuals were selected uniformly at random from the population that had not yet received vaccination. Once vaccinated, an individual cannot be infected nor infect others.

3.2   Results

We plotted the average number of newly infected and newly vaccinated individuals each week, as well as the total number of susceptible, infected, recovered, and vaccinated individuals. The results show that the vaccination program reduces the spread of the infection.
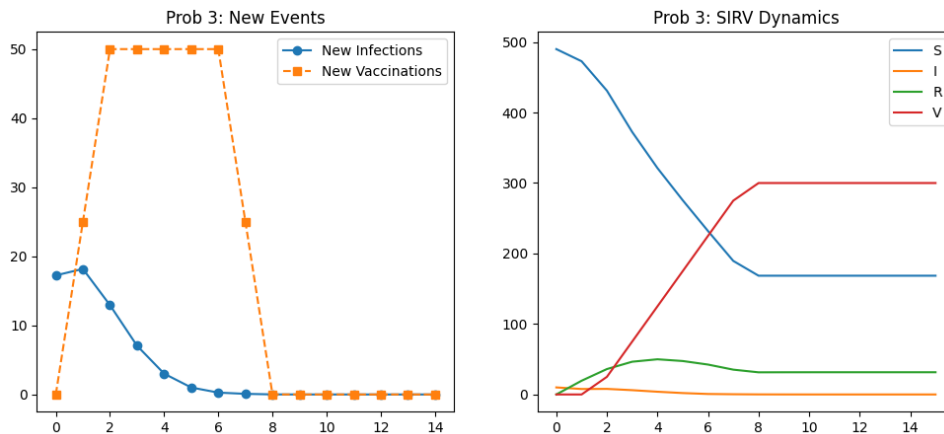
Figure 3: Epidemic dynamics with vaccination. The plot shows the effect of the vaccination scheme Vacc(t).

4   The H1N1 pandemic in Sweden 2009

4.1   Parameter Estimation

We used the previous methods to estimate the social structure and disease-spread parameters for the H1N1 pandemic in Sweden. The simulation was scaled down to $n = 934$ nodes. We used the real vaccination data Vacc(t) and the real number of newly infected individuals $I_0(t)$.

We implemented a gradient-based search over the parameter space of k, β, and ρ to minimize the root-mean-square error (RMSE) between the simulation and the real pandemic data.

4.2   Estimation Results

The algorithm found the set of parameters that best matches the real pandemic:

- Estimated average degree k: 10

- Estimated β: 0.23

- Estimated ρ: 0.40

The plots below show the average number of newly infected individuals according to the model with these parameters compared to the true value.
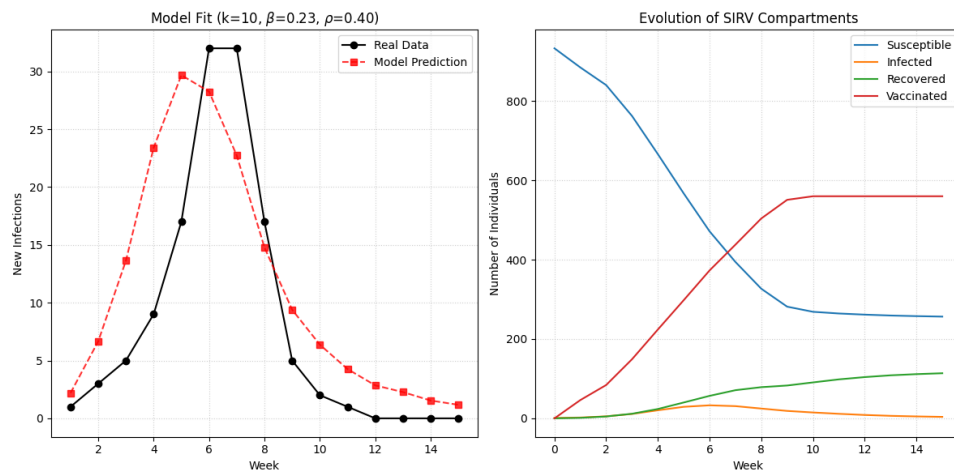
Figure 4: Comparison of the model estimation (dashed line) with the real H1N1 pandemic data (solid line).