

# Homework 3

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## Exercise 1

### 1.1 Epidemic on a known graph

In this first part of the homework, an epidemic is simulated on a symmetric  $k$ -regular undirected graph with node set  $v = \{1, \dots, n\}$  where every node is directly connected to the  $k = 4$  nodes whose index is closest to their modulo  $n$ . The disease propagation model used is the discrete-time simplified version of the SIR epidemic model: there are three possible states of the nodes (susceptible(S), infected(I), recover (R)).

The parameters taken into consideration are:

- $\beta$ : the probability of infection between an infected and a susceptible individual
- $\rho$ : the probability that an infected individual will recover during one time step
- $m$ : the number of infected neighbors of node  $i$

The epidemic is driven by this following transition probabilities:

$$\mathbb{P}(X_i(t+1) = I | X_i(t) = S, \sum_{j \in v} W_{ij} \delta_{x_j(t)}^I = m) = 1 - (1 - \beta)^m \quad (0.1)$$

$$\mathbb{P}(X_i(t+1) = R | X_i(t) = I) = \rho \quad (0.2)$$

The epidemic in this section is simulated on a symmetric  $k$ -regular graph with 500 nodes and  $k = 4$ . The week is taken as one time unit and the epidemic is simulated for 15 weeks; the initial configuration is with 10 infected nodes selected at random from the node set. The parameters used are  $\beta = 0.3$  and  $\rho = 0.7$ . This is simulated  $N=100$  times and through the simulation I achieved the result in Fig. 1 and 2.

### 1.2 Epidemic on a random graph with preferential attachment model

In this section the simulation is done on a random graph generated according to the *preferential attachment model*. Starting from a complete graph, at every time step a new node is added according to the rule that its degree must be  $\omega(t) = k/2 = c$ . At each step the link is added proportionally to the current grade of each node with probability:

$$\mathbb{P}(W_{n_t, i}(t) = 1) = \frac{\omega_i(t-1)}{\sum_{j \in \mathcal{V}_{t-1}} \omega_j(t-1)} \quad (0.3)$$

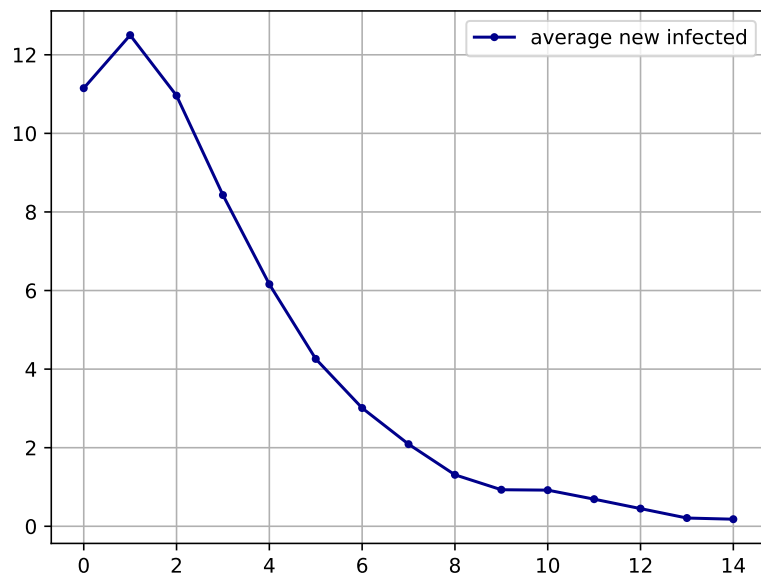


Figure 1: The average number of new infected individuals each week

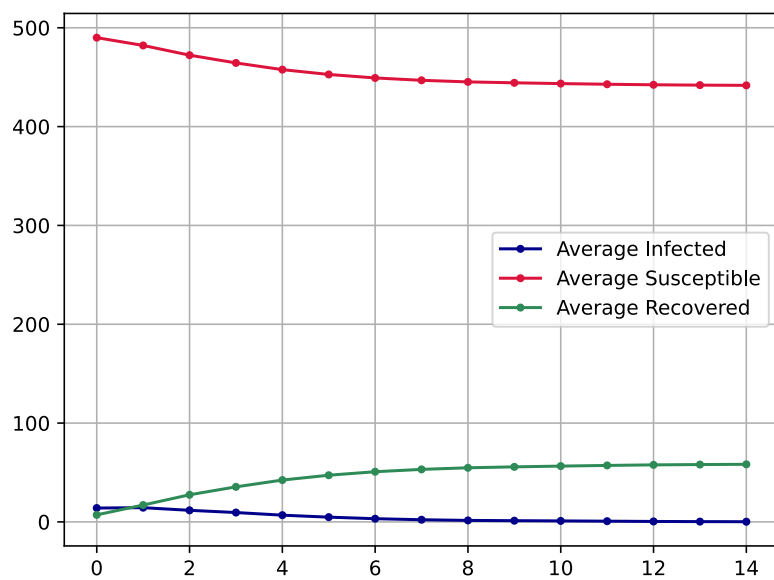


Figure 2: The average number of total infected, susceptible and recovered individuals each week

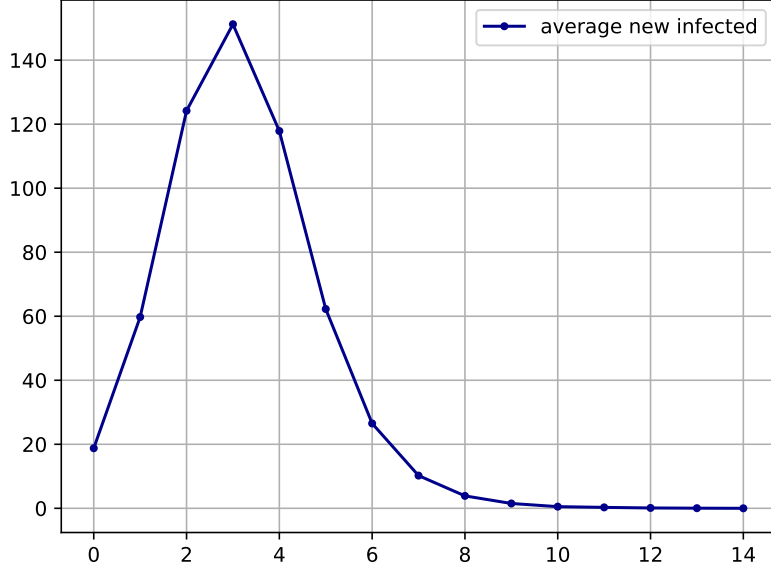


Figure 3: The average number of new infected individuals each week

where  $W(t)$  is the adjacency matrix for the next time step  $t$  and  $\omega_i(t-1)$  is the degree of node  $i$  prior to adding the new node.

Using this generated preferential attachment random graph with  $|\mathcal{V}| = 500$  nodes, average degree  $k = 6$ ,  $\beta = 0.3$ ,  $\rho = 0.7$ . The simulation is set as the exercise 1.1. The result obtained are showed in Fig. 3 and 4.

### 1.3 Simulate a pandemic with vaccination

In order to slow the epidemic, vaccination is introduced. The total fraction of population that has received vaccination by each week is provided by the vector:

$$Vacc(t) = [0, 5, 15, 25, 35, 45, 55, 60, 60, 60, 60, 60, 60, 60, 60] \quad (0.4)$$

The individuals to vaccinate are selected randomly from the population that has not yet received vaccination (an infected individual might receive vaccination as well and if it becomes vaccinated he will not be able to infect another individual). The epidemic is simulated on a random graph, generated according to the previous section, with 500 nodes and average degree  $k=6$ , for 100 times with the same parameters as previous points. The first step of the simulation is vaccinate the individuals since the immediate effect of the vaccine is presumed and then simulate the epidemic as before. The result obtained are shown in Fig 5,6 and 7.

### 1.4 The H1N1 pandemic in Sweden 2009

In this section the goal consist in estimate the social structure of the Swedish population and the disease-spread parameters during the H1N1 pandemic. During the weeks of simulation the fraction of population that has received vaccination is:

$$Vacc(t) = [5, 9, 16, 24, 32, 40, 47, 54, 59, 60, 60, 60, 60, 60, 60] \quad (0.5)$$

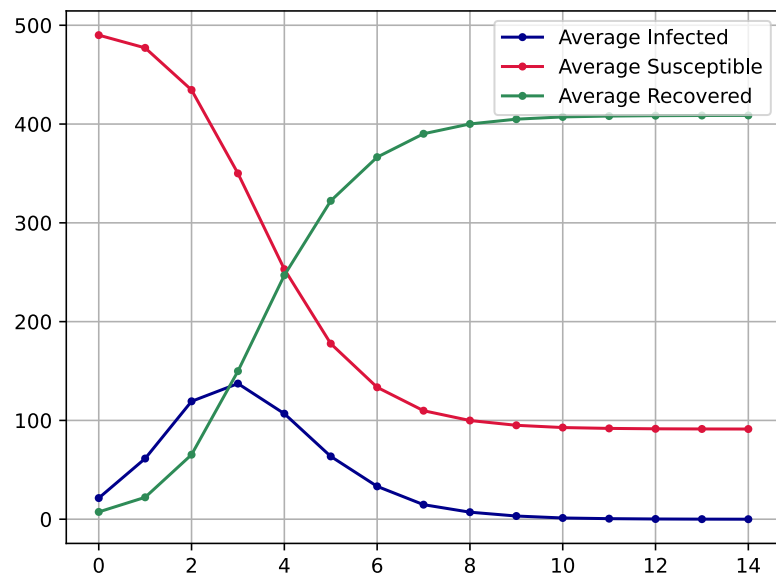


Figure 4: The average number of total infected, susceptible and recovered individuals each week

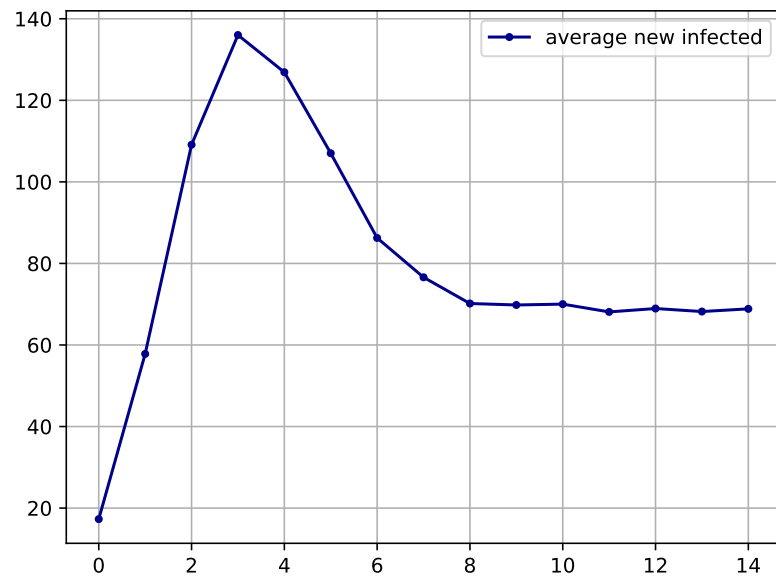


Figure 5: The average number of new infected individuals each week

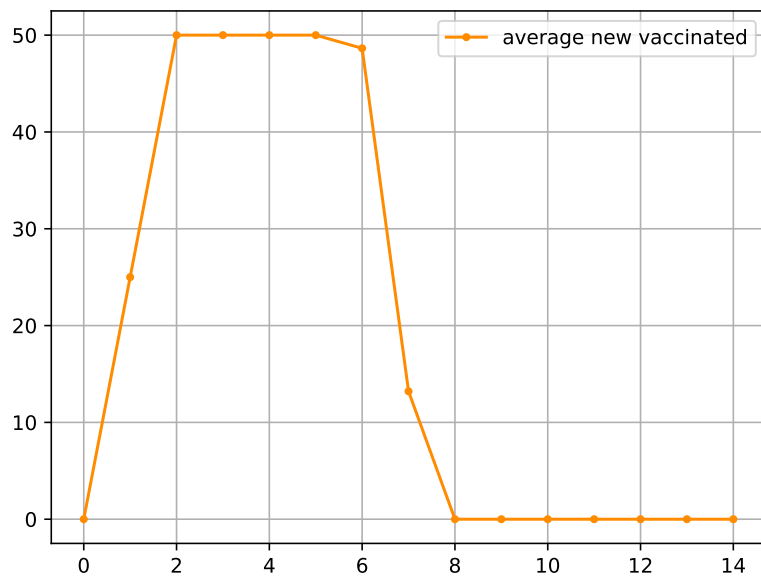


Figure 6: The average number of new vaccinated individuals each week

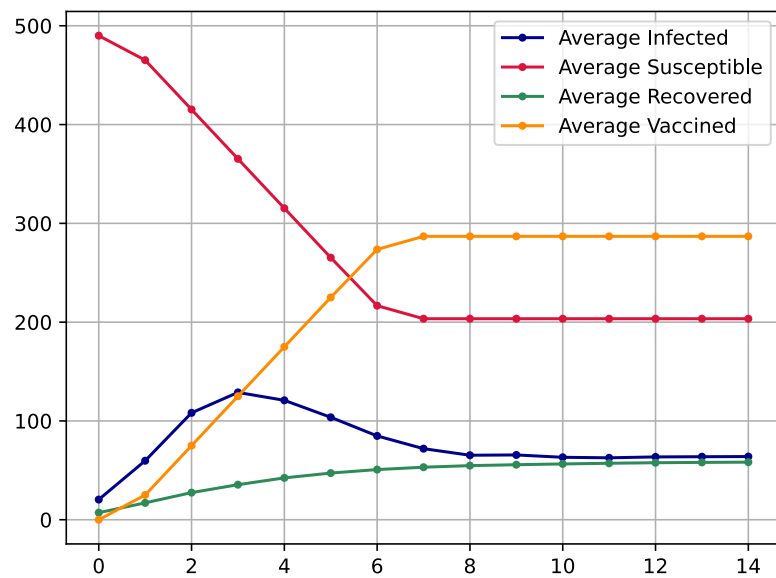


Figure 7: The average number of total infected, susceptible, recovered and vaccinated individuals each week

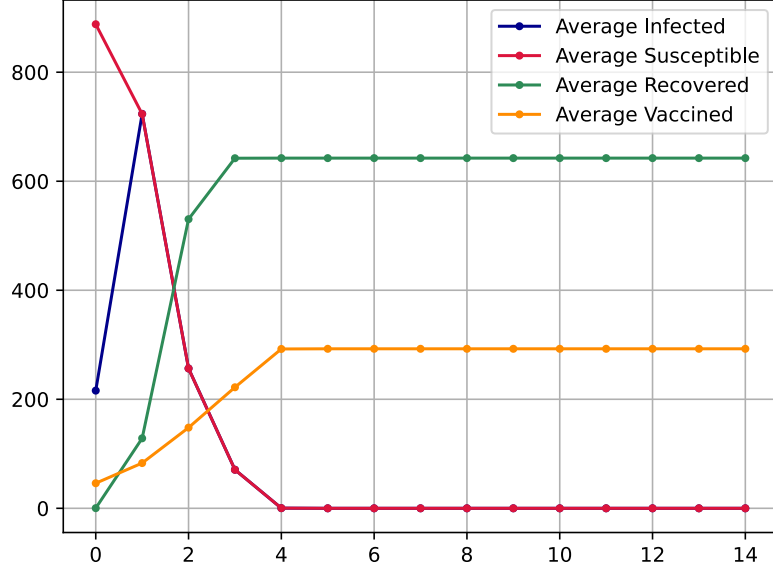


Figure 8: The average number of total infected, susceptible, recovered and vaccinated individuals each week

The (scaled) population is  $n = |\mathcal{V}| = 934$ . The number of newly infected population each week was:

$$I_0(t) = [1, 1, 3, 5, 9, 17, 32, 32, 17, 5, 2, 1, 0, 0, 0, 0] \quad (0.6)$$

In order to predict the new infected people during the pandemic, the optimization algorithm should minimize the root-mean-square error:

$$RMSE = \sqrt{\frac{1}{15} \sum_{t=1}^{15} (I(t) - I_0(t))^2} \quad (0.7)$$

where  $I(t)$  is the average number of newly infected individuals each week in the simulation and  $I_0(t)$  is the true value of newly infected individuals each week. We start with an initial guess of the parameters  $k_0 = 10, \beta_0 = 0.3, \rho_0 = 0.6$  along with  $\Delta k = 1, \Delta \beta = 0.1, \Delta \rho = 0.1$ .

For each set in the parameter space:

$$k \in \{k_0 - \Delta k, k_0, k_0 + \Delta k\}, \beta \in \{\beta_0 - \Delta \beta, \beta_0, \beta_0 + \Delta \beta\}, \rho \in \{\rho_0 - \Delta \rho, \rho_0, \rho_0 + \Delta \rho\} \quad (0.8)$$

a random graph is generated using the preferential attachment model and the epidemic is simulated for 15 weeks  $N=10$  times. The result obtained are shown in Fig.8

## Exercise 2 - Coloring

In this exercise we will study coloring as an application of distributed learning in potential games. The aim of coloring is to assign a color to each node in a given undirected graph, such that none of the neighbors of a node have the same color as that node.

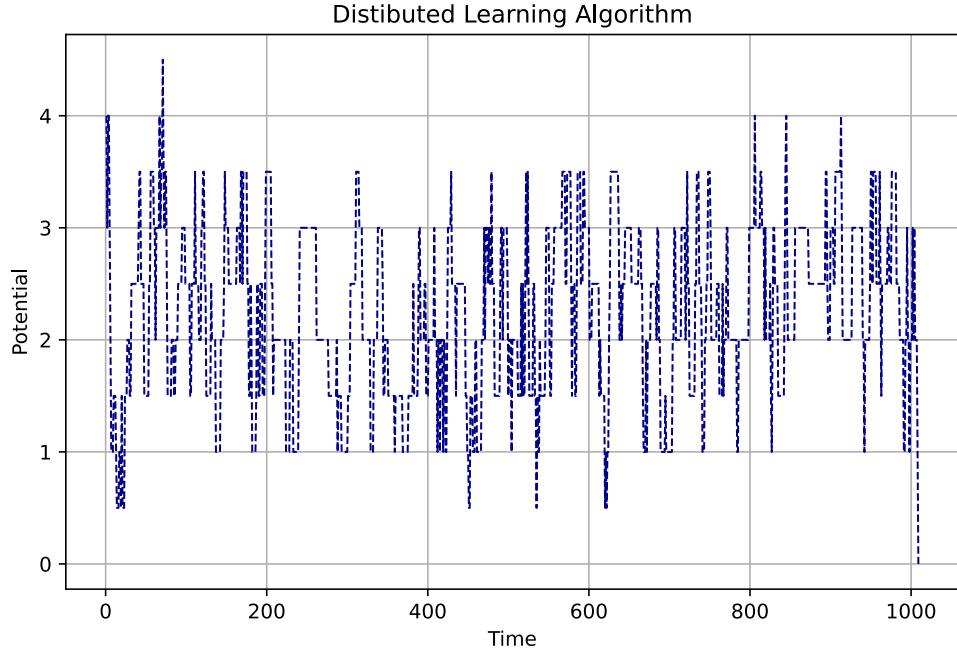


Figure 9: Learning dynamics

### Question a

In this section we will study a line graph with 10 nodes. The possible state of the nodes are only two: red and green. At initialization each node is red; every discrete time instance  $t$ , one node  $I(t)$ , chosen uniformly at random, wakes up and updates its color, chosen from a probability distribution given by:

$$P(X_i(t+1) = a | X(t), I(t) = i) = \frac{e^{-\eta(t) \sum_j W_{ij} c(a, X_j(t))}}{\sum_{s \in C} e^{-\eta(t) \sum_j W_{ij} c(s, X_j(t))}}$$

where the cost is given by:

$$c(s, X_j(t)) = \begin{cases} 1 & \text{if } X_j(t) = s \\ 0 & \text{otherwise} \end{cases}$$

In these expression  $\eta(t)$  is the inverse of the noise, in this case  $\eta(t) = \frac{t}{100}$ . In order to study how close to a solution the learning algorithm is, a potential function is considered, given by:

$$U(t) = \frac{1}{2} \sum_{i,j \in \mathcal{V}} W_{ij} c(X_i(t), X_j(t))$$

The algorithm stops when all nodes have neighbors of different color, that correspond to the potential function begin zero. The learning dynamics is shown in Fig. 9

### Question b

In this section the same process is applied to the network represented in Fig. 10.

In this case the set of possible colors/state is  $C = 1 : \text{red}, 2 : \text{green}, 3 : \text{blue}, 4 : \text{yellow}, 5 : \text{magenta}, 6 : \text{cyan}$ ,

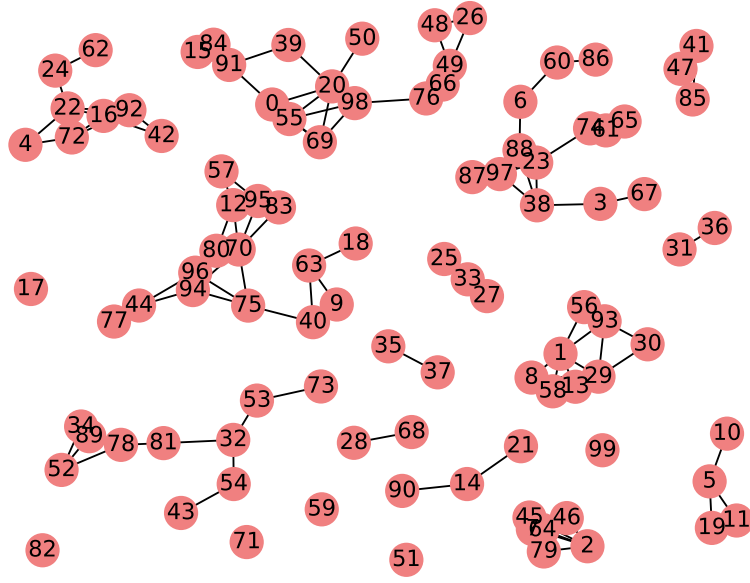


Figure 10: WI-FI network

where each color represents a frequency band and the cost function is:

$$c(s, X_j(t)) = \begin{cases} 2 & \text{if } X_j(t) = s \\ 1 & \text{if } |X_j(t) - s| = 1 \\ 0 & \text{otherwise} \end{cases}$$

The final configuration is represented in Fig. 11



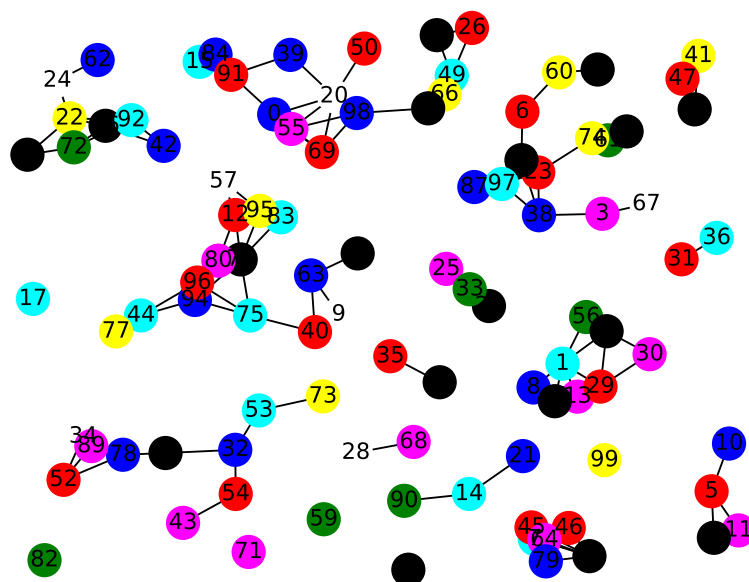


Figure 11: WI-FI network final configuration