Using Monte-Carlo method to simulate the spread of viruses in networks

The interview challenge report

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1 Summary of the challenge

The interview challenge was about a scenario in which a virus spreads in a network. In the initial stage, only one node is infected with the virus. Other nodes get infected with a probability of $\frac{|I_r|}{|\Gamma_r|}$ where I_r is the set of infected nodes in node r's neighborhood and Γ_r is the set of all nodes in r's neighborhood.

Each infected node stays infected for k days (assuming $k = 5$) and becomes immune afterward. We say that a pandemic has occurred when a constant percentage of nodes are infected simultaneously (taking $c = 10\%$).

The challenge is to find out the probability of occurrence of a pandemic and the amount of time it takes for the pandemic to end (in cyclic, complete, and Erdos-Renyi networks).

Considering that the network's size was not given in the challenge, I took $n = 500$, and the p in Erdos-Renyi equal to 0.4. Plus, I assumed that once a node is recovered from the infection, it becomes immune and can no longer get infected again (although different assumptions can be tested too).

2 The methodology

The first point about the challenge is that it involves a complicated process. Both, the infection and spread of the virus can change according to the structure of the underlying network and the previous stages of the process. Therefore, I decided to use the Monte-Carlo simulation, which is known to be a practical solution to answer similarly complicated problems, such as a self-avoiding random walker.

Monte-Carlo simulations rely on random sampling to answer complex procedures. As the number of samples grows, the average value tends to get closer to the expected value (the law of large numbers).

3 The implementation

To implement a Monte-Carlo simulation, I used Python programming language. The Command Line Interface (CLI) application receives a few input arguments, including the type of network, the number of nodes, the number of initially infected nodes, the condition to stop the procedure, etc. After reading the inputs, it starts to repeat the simulation.

4 The findings

To simulate the procedure, I used Monte-Carlo simulation for all three types of networks with 500 nodes, 1 initially infected node, 5 days of rehabilitation gap, and I used the condition of full immunity to stop the process (which means that the process has to stop if either the number of infected nodes is zero or the whole nodes in the network have become immune). I ran the simulation for 1000 times. The results of the simulations are as follows:

4.1 Cyclic networks

In a cyclic network, a node has only two neighbors. This directly influences the probability of infection of neighbor nodes $\frac{|I_r|}{|\Gamma_r|}$. Considering that in the first stage only one node is infected (initially infected node), this means that the spread of the virus will happen in a sequential/linear manner; therefore, the probability of infection will be a maximum of 0.5. And in case a spread doesn't take place in 5 consecutive days ($k = 5$), the spread of the virus will stop in one of the two directions.

The result of the simulations showed that **in non of the cases did a pandemic take place (probability of occurrence of a pandemic = 0%), and, on average, it took 40 days for each simulation to end**.

4.2 Complete networks

In a complete network, all nodes are connected; therefore, even the infection of one node creates the probability of infection for all other nodes. Consequently, a pandemic is more expected in these networks.

The result of simulations showed that only **in 2% of the simulations does the process end without a pandemic. On average, it took 19.6 days for each simulation to end.**

4.3 Erdos-Renyi networks

In an Erdos-Renyi network, each of n nodes in the network is connected to another node with a probability of p. In simulations, I chose $p = 0.4$.

The result of simulations showed that **in 99% of the simulations, the process ended in a pandemic. On average, it took 19.7 days for each simulation to finish**.

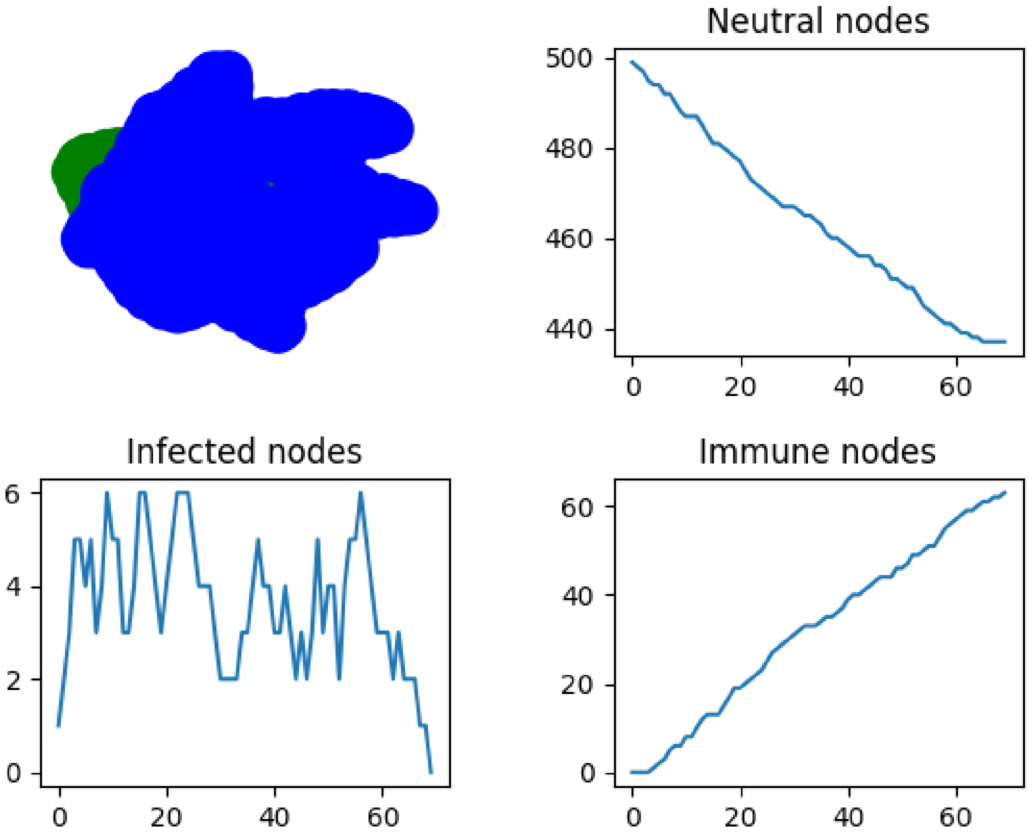

Figure 1: The Figure shows the results of a simulation on a cyclic network. The top left corner shows the network (the representation is not clear because of the limited space). The top right corner shows the number of neutral nodes in the network. The bottom left and right figures show the number of infected and immune nodes over time.

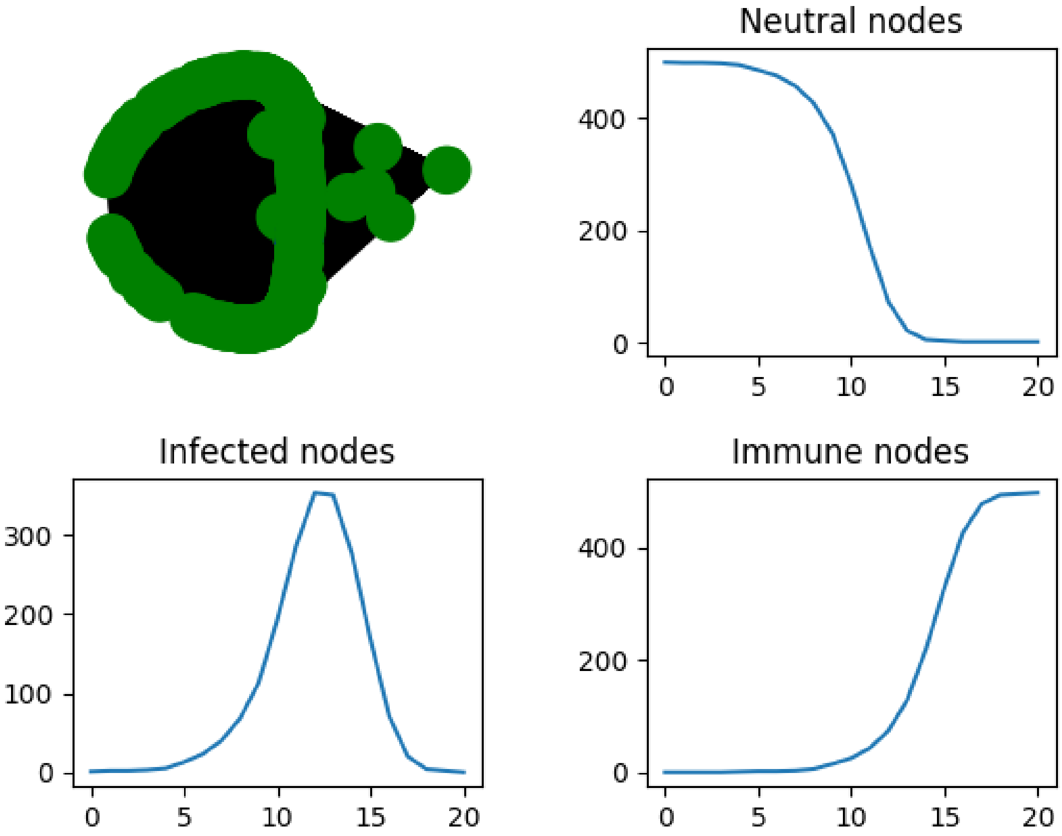

Figure 2: The Figure shows the results of a simulation on a complete network. The top left corner shows the network (the representation is not clear because of the limited space). The top right corner shows the number of neutral nodes in the network. The bottom left and right figures show the number of infected and immune nodes over time.

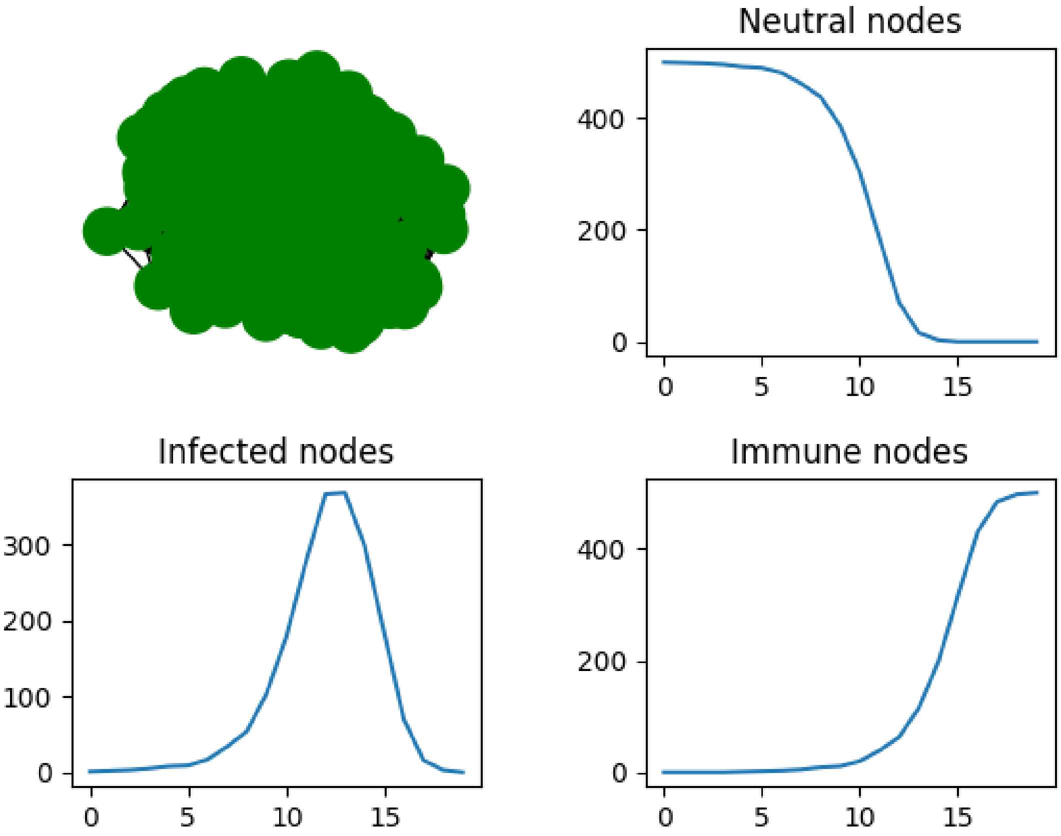

Figure 3: The Figure shows the results of a simulation on an Erdos-Renyi network. The top left corner shows the network (the representation is not clear because of the limited space). The top right corner shows the number of neutral nodes in the network. The bottom left and right figures show the number of infected and immune nodes over time.