# CS166 - Final Project

Minerva University

CS166 - Modeling and Analysis of Complex Systems

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# CS166 Final Project - Modeling of Epidemic

## Simulation

  The following is a model of epidemiology or disease dispersion in a population in a network in which nodes are individuals, and edges between nodes are the contact between individuals, allowing disease transmission. Each node can be susceptible or infected with corresponding probability. It was proposed that the time difference between infected and infecting nodes (generation interval) would be used and generated from a Normal Distribution, however, that would indicate that we would need an event-based simulation and the simulation time would not be discrete anymore, since it would depend on the generation internally. Here we are interested in the application of lockdown or quarantine in the population infected by a contagious disease. Since we are studying the impact of lockdown/quarantine, we will adopt the susceptible-infected-susceptible (SIS) model, so that the only way someone cannot be infected again is when an infected person will adopt self-quarantine. The quarantine is adopted as a certain probability (severance) in those infected nodes and it is done by breaking up an edge between an infected node with a susceptible node with the same probability. We will run the model with instantaneous updates so that the simulation is more accurate to reality.

## Variables:

We are measuring the following values:
- **Average degree:** The average degree of the network will be measured for each iteration
- **Percentage of infected:** the percentage of infected nodes in the network for each iteration

## Parameters:

- **Number of nodes:** the number of nodes that the network initialized with.
- **Average degree:** the average number of neighbors of each node.
- **Infection probability:** the probability in which an infected node will pass the disease to a susceptible node.
- **Recovery probability:** the probability that an infected node will be cured and become susceptible again
- **Severance probability:** the probability that an infected node will break its edge with a susceptible node
- **Type of Network:** either random (Erdos-Renyi or Watts-Strogatz) or scale-free (Barabasi-Albert)

## Assumptions:

- **No acquired immunity:** We are assuming the only way a person can not be infected again is when the edge connected between an infected and susceptible person is broken, and the disease cannot spread anymore. This edge break will be related to the impact of lockdown or quarantine. We still assume a probability and evaluate it with a number from a uniform distribution because even though the quarantine is highly recommended (and in some cases mandatory by law), some infected people still do not quarantine themselves. Therefore, the severance probability compasses the chances of infected people breaking a connection with susceptible individuals in their proximal neighborhood.
- **Discrete-time:** the time in this model is discrete, indicating that at each step size we evaluate the status of the nodes and run random numbers to compute the probability as a threshold for a node to become infected, recovered, or an edge to break. The time unit is defined as a discrete interaction between each node with its neighbors.
- **Reproduction number is a parameter:** most of the simulations in real life are interested in calculating the average instantaneous reproduction number (R), which is the rate in which each infected node infects susceptible nodes. This number is crucial to evaluate the impact of real-world epidemics since the epidemic will only cess when R < 1. However, it is really hard to predict this value in the course of a pandemic, because we would need future information. Some predictions say that

## Rules:

- Create a network either as an Erdos-Renyi, Watts-Strogatz, or Barabasi-Albert
- Start the simulation by randomly infecting a node with a probability of 10% while changing its state to 1, otherwise state 0.
- At each step, evaluate each node by checking it is infected or (state=1) or susceptible (state=0).
- If it is susceptible, evaluate its neighbors, and if at least one neighbor is infected, infect the node with a probability of infection.
- With severance probability break the edge between the nodes
- If the node is infected, change the state back to zero with the probability of recovery.
- Run the steps for a certain time

# Test cases

## Test Case 1

Starting the simulation with the following parameters:

```
nodes = 1000
avr_degree = 10
inf_prob = 0.01
rec_prob = 0.05
sever_prob = 0.01
```

Table 1: Parameters Test case 1

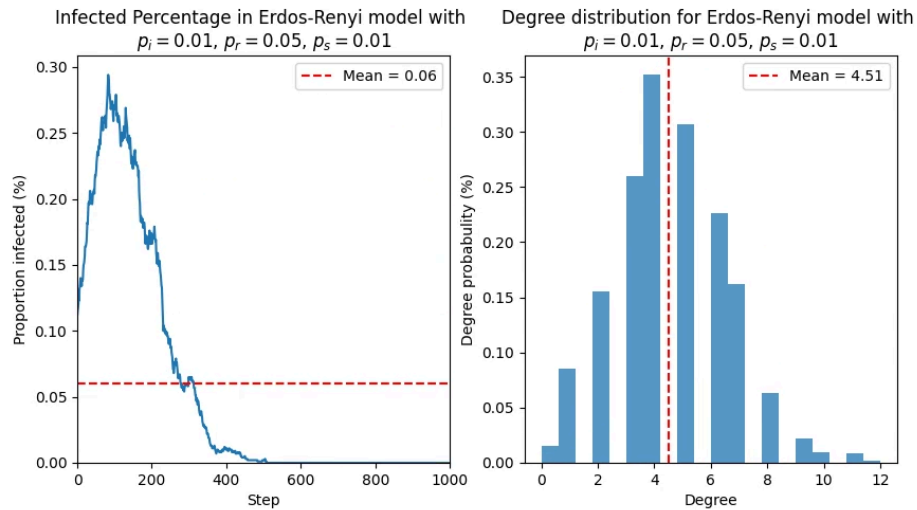We have the following scenarios after 1000 steps:



Figure 1: Proportion Infected and degree distribution for an Erdos-Renyi network

We see in Figure 1, that for the parameters of Table 1, we see the disease leaves the Erdos-Renyi (ER) network after 500 steps with a degree average of 4.5, around half of which it started with.

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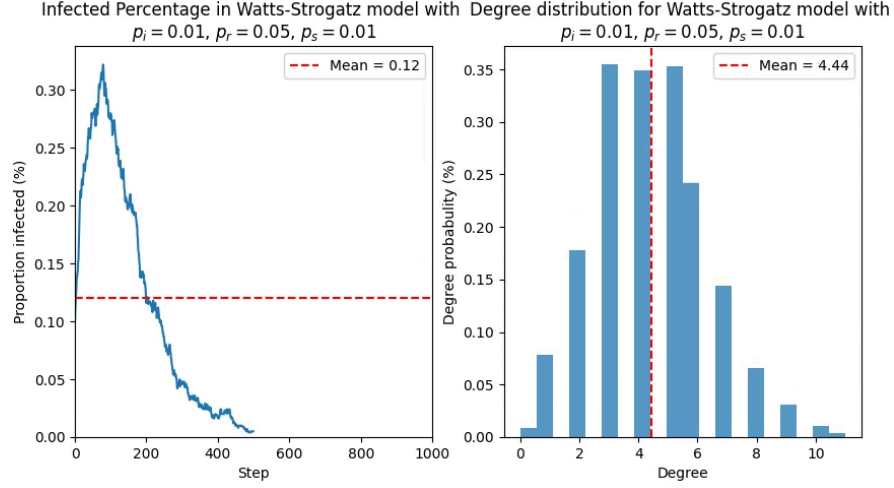


Figure 2: Proportion Infected and degree distribution for a Watts-Strogatz network

In Figure 2, we see a similar behavior as in Figure 1. For the Watts-Strogatz (WS) model there is a mean degree of 4.44 and the diseases leave the network around 500 steps.
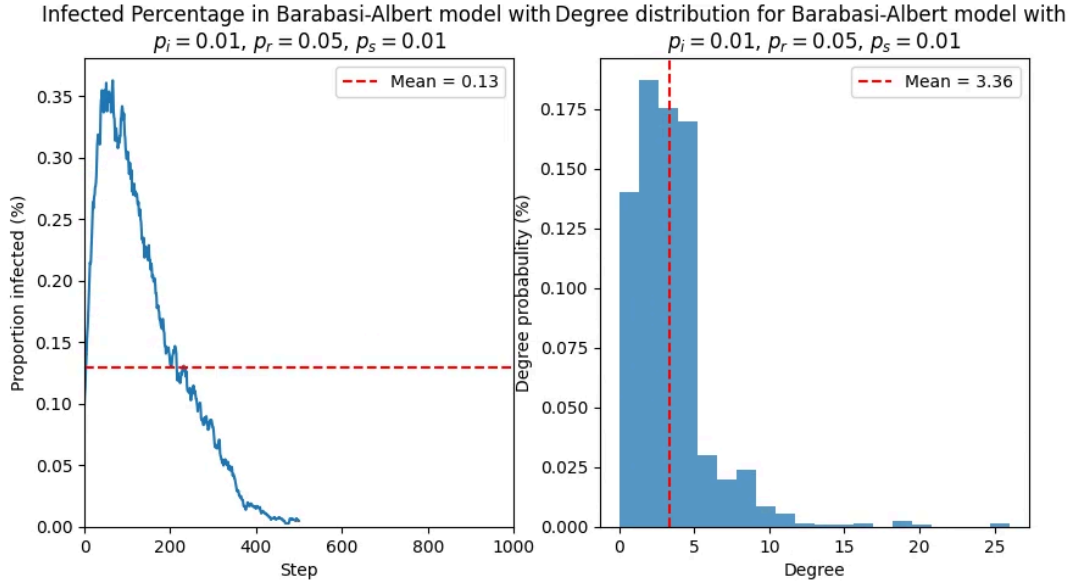


Figure 3: Proportion Infected and degree distribution for a Barabasi-Albert network

In Figure 3, we see that for the Barabasi-Albert (BA) model, the average degree at the end of the simulation is 3.36 and the disease leaves the network also after around 500 steps.

## Test Case 2

Now we use the following parameters

```
nodes = 1000
avr_degree = 10
inf_prob = 0.01
rec_prob = 0.05
sever_prob = 0.005
```

<div align="center">Table 2: Parameters for Test Case 2</div>

Now the parameters are the same value but the severance probability is half as in Table 1 (0.5%).
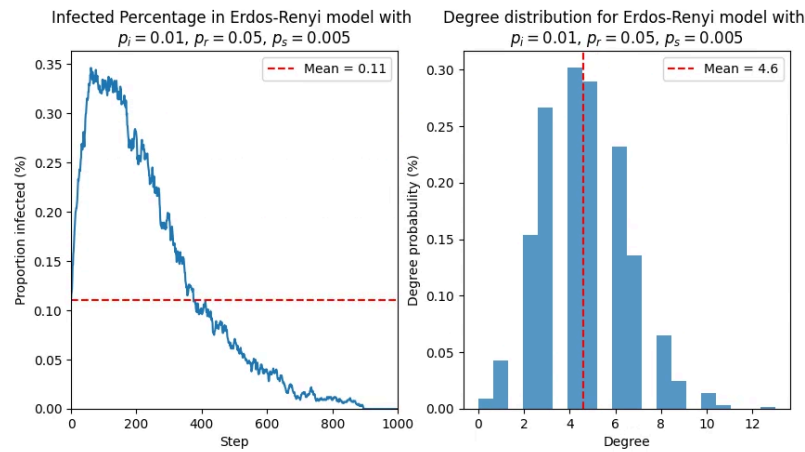
We got the following results:



Figure 4: Proportion Infected and degree distribution for Erdos-Renyi network parameters from Table 2
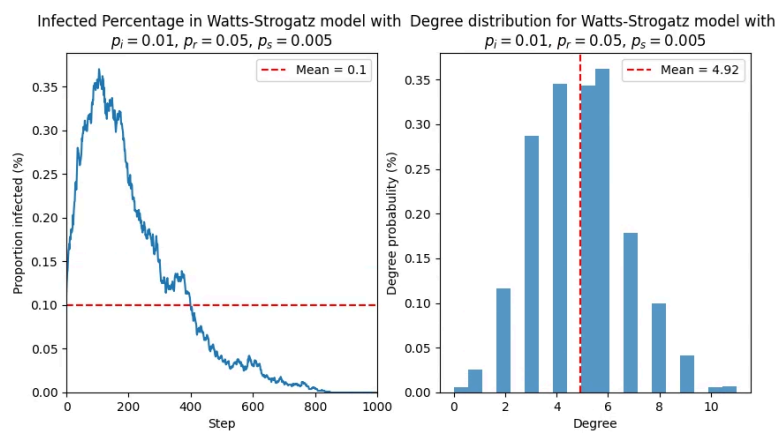


Figure 5: Proportion Infected and degree distribution for Watts-Strogatz network parameters from Table 2
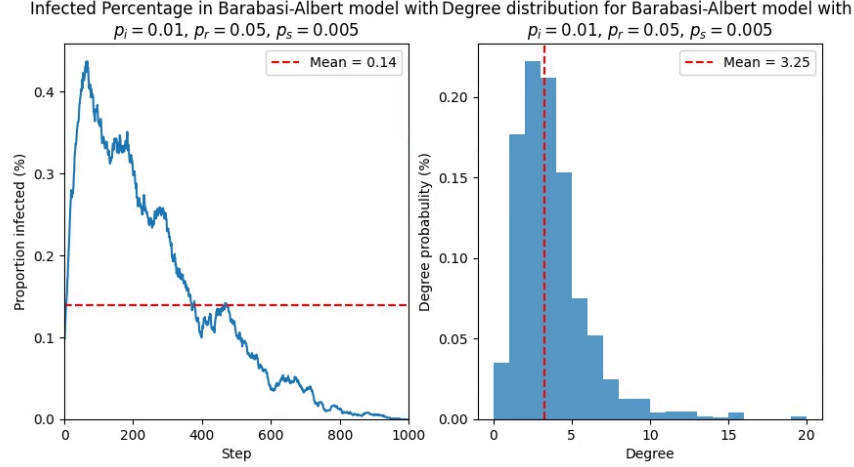
Figure 6: Proportion Infected and degree distribution for Barabasi-Albert network parameters from Table 2

In these results, we can see that decreasing the severance probability, makes the epidemics die out at a slower rate. The mean degree seems to be around the same but slightly lower than before. In the ER model the disease leaves the network after 900 steps, in the WS, around 850 steps, and in BA around 1000 steps.

## Test Case 3

For the following parameters:

```
nodes = 1000
avr_degree = 10
inf_prob = 0.01
rec_prob = 0.05
sever_prob = 0.02
```

Table 3: Parameters for test case 3

Using the parameters in Table 3, where we double the severance probability from test case 1 and kept the same values for the other parameters, we have the following results:
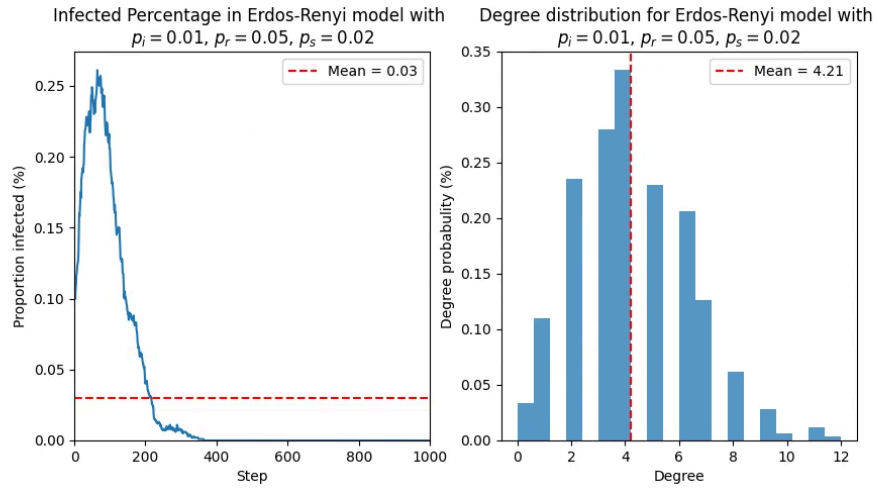
Figure 7: Proportion Infected and degree distribution for Erdos-Renyi network parameters from Table 2
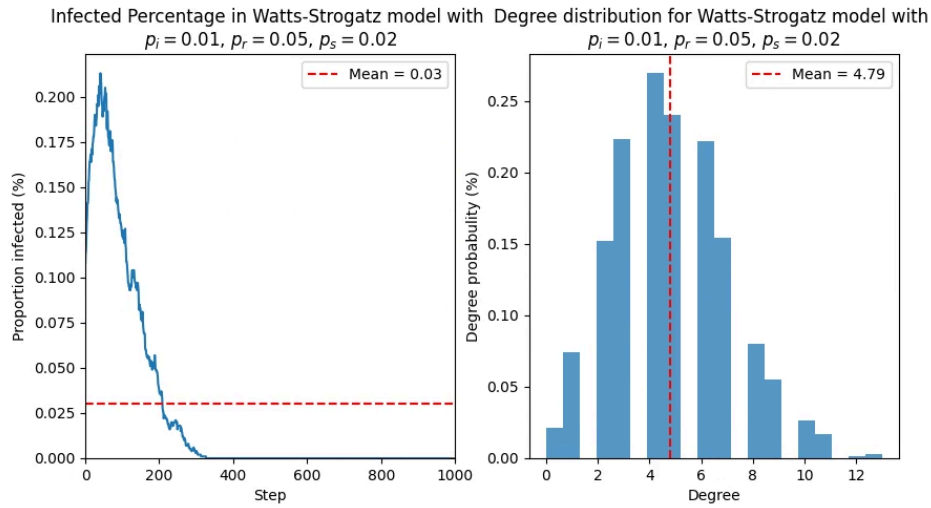


Figure 8: Proportion Infected and degree distribution for Watts-Strogatz network parameters from Table 2
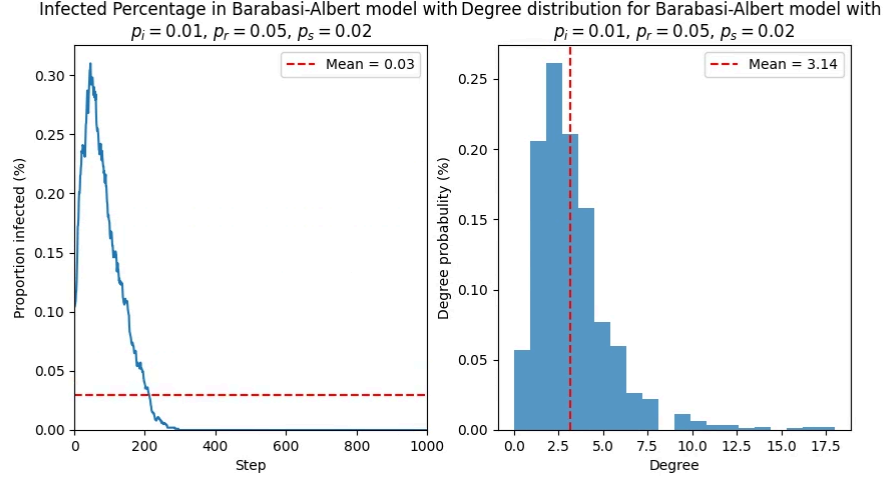
Figure 9: Proportion Infected and degree distribution for Barabasi-Albert network parameters from Table 2

We see an expected pattern, that the severance probability can slow up or down the rate at which each simulation reaches the equilibrium of no infection. In all network types (Figure 7-9) we see that the disease leaves the population around 300-400 steps with degree mean a bit smaller than before. Now we should compare the Empirical and Theoretical results.

# Theoretical Analysis

We calculate the Mean-Field Approximation on Random Networks as the main theoretical value to predict the equilibrium or the pandemic threshold. Hiroki Sayama in his book "Introduction to the Modeling and Analysis of Complex Systems" derives the following formula:

$$p_i > \frac{p_r}{<k>}$$

In which $p_i$ is the probability of infection, $p_r$ is the probability of recovery, and $< k >$, from now on only $k$, is the average degree of the network. This model was designed for a random network, but here we will extrapolate it for the three networks we are using, small-world and scale-free for means of comparison. The formula tells us the epidemic threshold or the conditions in which a disease will persist in a society, indicating that the disease will persist as long as the probability of infection is higher than the rate between the probability of recovery and the average degree. Since $p_i$ and $p_r$ are unchanging parameters in our model, we are interested to know what is the optimal value of $k$ in order to end an epidemic. In our model, we are indirectly changing the value $k$ according to the value of the severance probability. So we are interested in the optimal value of the severance probability for a given $p_i$ and $p_r$.

From the formula we have, that the disease will persist if:

$$k > \frac{p_r}{p_i}$$

And the disease will die when

$$k < \frac{p_r}{p_i}$$

So in order for a pandemic to stop, we need the average degree to be equal or less to the ratio between the probability of recovery and the probability of infection.

# Empirical Analysis

For the empirical analysis we are running the simulation for the same parameters as in Table 1, but we are varying the severance probability ($s_p$). For each value of the $s_p$ We are calculating the average degree. We have the following results:
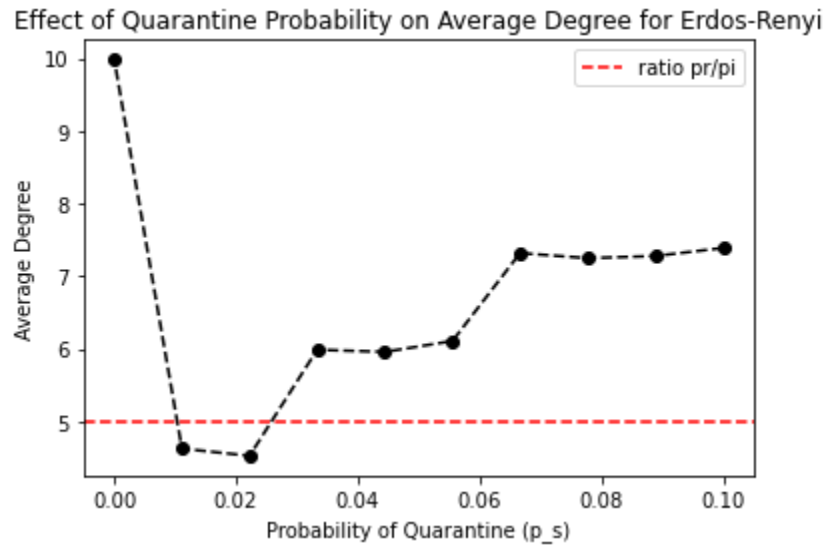


Figure 10: Average Degree for increasing Probability of Severance for ER model
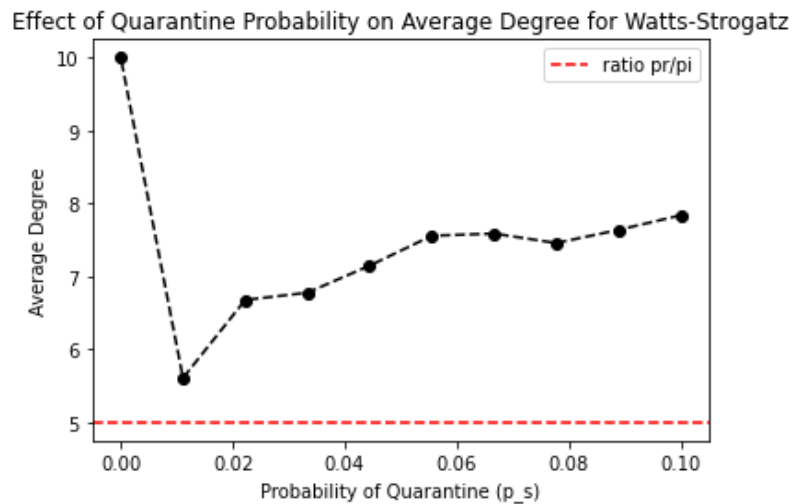


Figure 11: Average Degree for increasing Probability of Severance for the WS model
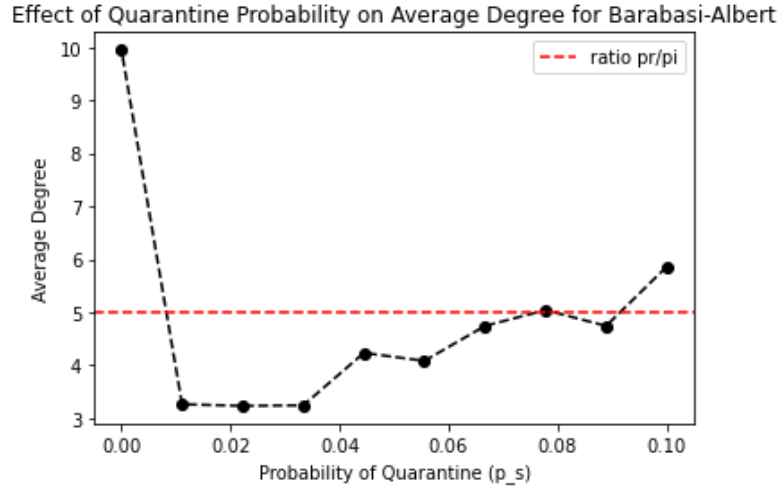
Figure 12: Average Degree for increasing Probability of Severance for BA model

For the ER model, the optimal value $p_s$ is around 0.02, while there is no optimal value for WS, indicating the pandemic will never die in those initial conditions. We have a set of values for the BA model, $p_s$ ranging from 0.02 to 0.08 in order for the pandemic to stop. All of these conditions are supported by the theoretical analysis but the WS does not seem to be a good model in which the formula can be used. It is surprising the BA (the most accurate model) has a bigger range of probabilities, indicating that in a scale-free network, the probability of quarantine does not need to necessarily be strict in order to stop a disease from spreading. This is explained by its scale-free property in which few nodes are very high connected and the majority are low connected.

# Appendix A

Code used  ∞ Copy of [original] CS166/Parav.ipynb

AI was used to fix minor issues in the code.