

# Topic 21: Expected Epidemic Threshold in Random Graphs and SF Networks

Project Report - Complex Networks Science

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## 1 Introduction

Our goal for this project is to analyse disease spreading and figure out the expected epidemic threshold in random graphs and scale-free networks. This can be applied to the real world since the network of people and how they interact with each other often follows the composition of random graphs and scale-free networks.

By reading paper [1], we realized that the Internet has a very complex connectivity that can be modelled by the class of Scale-free networks. Despite this characteristic favouring the connectivity of a large computer network, it also favours the spread of computer viruses. The same thing can be said for the real-life world, in which the network of human beings resembles a scale-free network. This means that analyses on the spreading of computer viruses can be used to study real life epidemics, and that is why studying either environment has direct applications in the other.

The standard model used in the study of epidemic spreading is the SIS (Susceptible Infected Susceptible) epidemiological model. In this model, each node of the network represents an individual and a link between two nodes is a connection along which the infection can spread to other individuals. Every node can have two distinct states: "healthy" (susceptible) and "infected". A susceptible node can become infected with an infection rate  $\beta$  if it has at least one infected neighbour. At the same time, at every time step, an infected node can become susceptible with a recovery rate  $\delta$ . Both these definitions create an effective spreading rate:

$$\lambda = \frac{\beta}{\delta} \tag{1}$$

In Random Graphs and Scale-Free Networks, the most significant result in general is the prediction of a nonzero epidemic threshold  $\lambda_c$ . If the value of  $\lambda$  is above the threshold,  $\lambda \geq \lambda_c$ , the infection spreads and becomes more persistent, but if  $\lambda \leq \lambda_c$ , then the infection dies out exponentially fast.

To gather results we generated two graph structures: one Random Graph, with a number  $N$  of nodes, where each node has 6 edges (to mimic the average connectivity of the Scale-Free Network that will be introduced later), therefore making the total amount of edges  $E = 6 * \frac{N}{2}$ ; and a Scale-Free Network, generated by using the algorithm devised in [2], where we start from a small number of  $m_0$  disconnected nodes and every time step a new node is added, with  $m$  links that are connected to an old node  $i$  with  $k_i$  links according to the probability  $\frac{k_i}{\sum_j k_j}$ . After a certain number of time steps  $t$ , we obtained a network composed by  $N$  nodes with connectivity distribution  $P(k) \sim k^{-3}$ , a total number of edges  $tm$  and average connectivity  $\langle k \rangle = 2m$ . In our work we take  $m = 3$ , just like in the work [1].

## 2 Gathered Results

We first followed the simulation of vanishing epidemic threshold in SF networks for the SIS model found in <sup>1</sup>. We start with an initial number of infected nodes *in.inf* and at each time step, for every node in the graph, if it is susceptible and has at least one infected neighbour, then it has a probability  $\beta$  of becoming infected, and if it is infected it has a probability of becoming susceptible again with probability  $\delta$ . Figure 1 shows what we found.

We repeated this process for  $t = 100$  time steps, where  $N = 1000$  is the number of nodes. We chose a  $\lambda$  between 0 and 1, which means that the infection rate  $\beta$  is smaller than the recovery rate  $\delta$ . Then we ran the exact same tests but over a Random Graph, where we used the function `random_regular_graph`<sup>2</sup> function to generate the graph and the degree  $d = 6$  of each node. In our experiment, we tried to follow the experiment of [1], where different values of nodes initially infected are used (more specifically 10 nodes, 250 nodes, 500 nodes, 750 nodes and 1000 nodes) as in figure 1, because we wanted to see if the obtained results were similar between them, while maintaining the other parameters unchanged, more specifically, the number of nodes, infection rate and recovery rate. Results are found in Figure 2.

After these experiments we came to realize that the number of time steps needed for the networks to stabilize was probably a much lower than 100. With this in mind, we set out to discover the amount of time steps necessary. After

<sup>1</sup>[https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19\\_NetSci\\_class10-Epidemics-PartI.pdf](https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19_NetSci_class10-Epidemics-PartI.pdf)

<sup>2</sup>[https://networkx.github.io/documentation/networkx-1.10/reference/generated/networkx.generators.random\\_graphs.random\\_regular\\_graph.html#networkx.generators.random\\_graphs.random\\_regular\\_graph](https://networkx.github.io/documentation/networkx-1.10/reference/generated/networkx.generators.random_graphs.random_regular_graph.html#networkx.generators.random_graphs.random_regular_graph)

some experiments we concluded that with  $N = 1000$  the time steps needed for the network to stabilize was between 1 and 20. We then used  $N = 10000$  to calculate the minimum time steps needed and the results varied between 5 and 10. With this, it is expected that when  $N$  gets bigger, the time steps,  $t$ , needed will probably be around 7. For the reasons just mentioned, we set the time step value equal to 20 time steps.

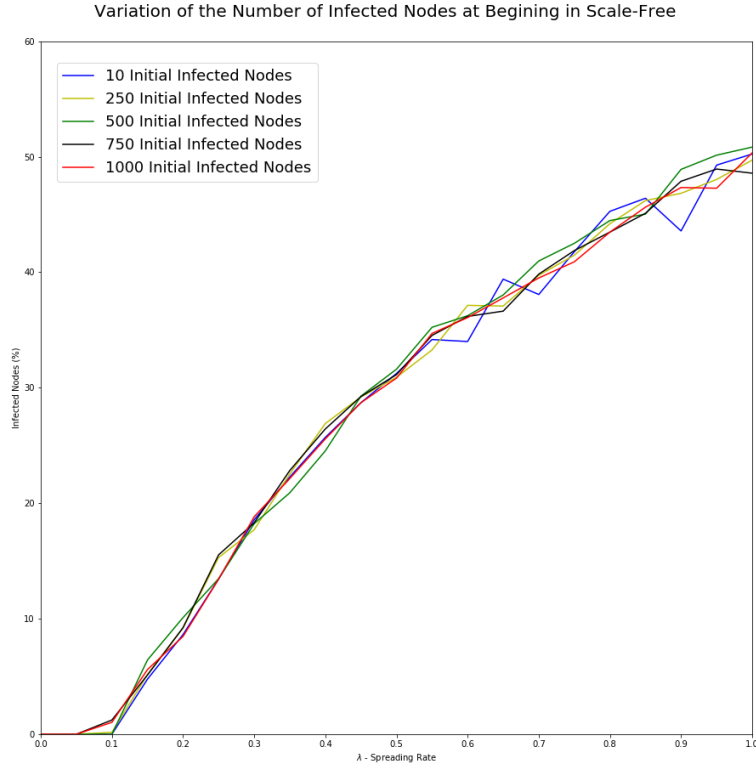


Figure 1: In this part of our experiment we maintain the total nodes of the network, 1000 nodes, and only vary the amount of the nodes that are initially infected.

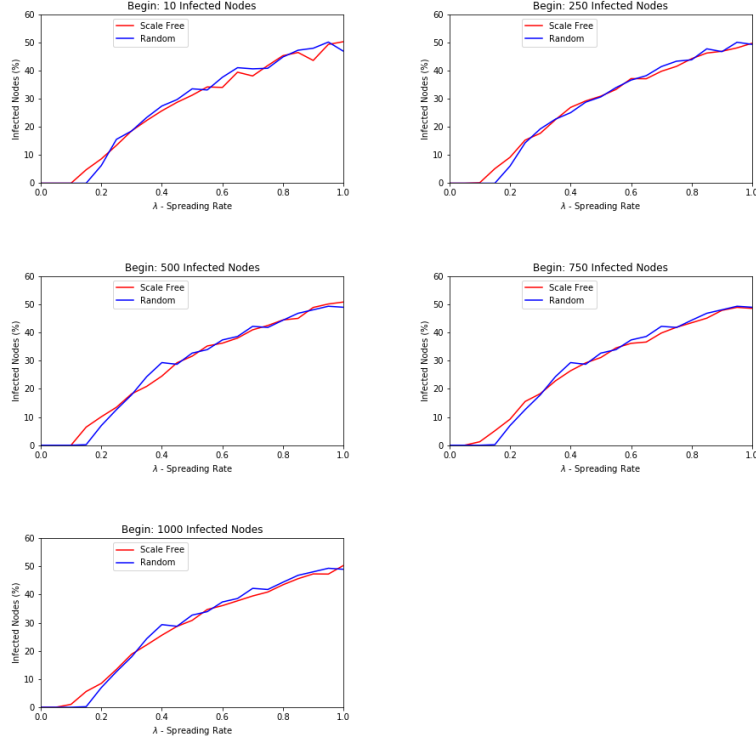


Figure 2: The total number of nodes of the network is 1000 nodes, and we vary the number of infected nodes at the beginning. In this figure, we present the comparison between Scale-Free Graphs and Random Graphs under the same conditions.

### 3 Discussion of the Results

We understood that if we chose a certain  $\lambda$  value, calculated by equation 1, independently of the initial number of infected nodes, the network stabilizes with the same correlation of infected nodes and healthy nodes.

After looking at the graphs, we realized that the SF networks had an epidemic threshold  $\lambda_c$  that tends to 0, which means that even if the infection rate  $\beta$  is much smaller than the recovery rate  $\delta$ , if it is different than 0, the infection persists and a finite fraction of the population is infected at any given

time. In the case of Random Graphs, the epidemic threshold is closer to 0.17. However, we used the SIS epidemiological model with different smaller values of  $\{25, 50, 75, 100\}$ , and we concluded that with few nodes the threshold is greater than 0.20, as can be seen in Figure 3.

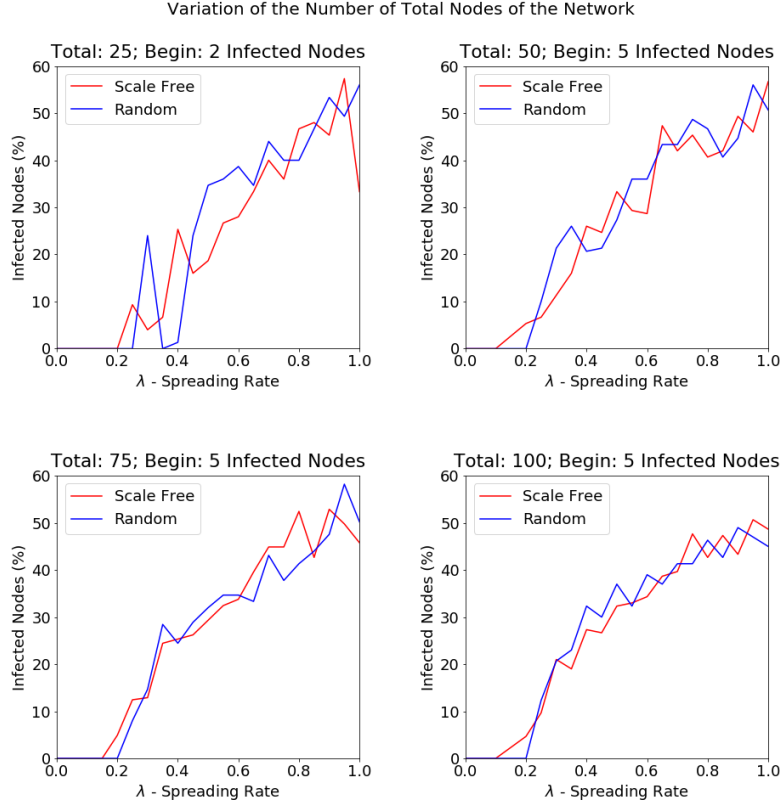


Figure 3: We repeat the same experience, but for smaller number of total nodes. Here we only vary the total number of nodes.

Next, we tested with  $N = 10000$  and the results of the threshold  $\lambda_c$  were the same as when  $N = 1000$ . Overall, our results are similar to the ones presented in Figure 4, which we took from the theoretical class <sup>3</sup>.

We also timed our experiments, which can be observed in Table 1.

<sup>3</sup>[https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19\\_NetSci\\_class10-Epidemics-PartI.pdf](https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19_NetSci_class10-Epidemics-PartI.pdf)

## Vanishing epidemic threshold in SF nets (SIS)

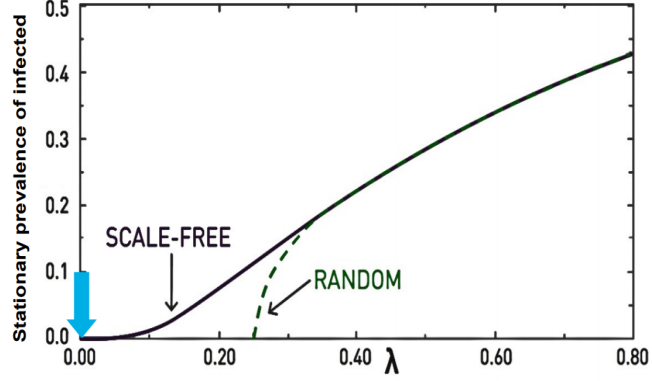


Figure 4: Epidemic Threshold as it appears in the theoretical slides

## 4 Conclusion

With these results we tried to make a parallelism with a real-life disease spreading to better understand how it works. We took as example the disease mentioned on theoretical class <sup>4</sup>, gonorrhea. This disease has the same behaviour of our simulation results. In another words, the spreading rate tends to 0, but unfortunately it never quite reaches this goal.

# Total Nodes; # Infected Nodes	Random	Scale-Free
25 nodes; 2 infected	4.64 sec	6.30 sec
50 nodes; 5 infected	10.50 sec	13.60 sec
75 nodes; 5 infected	19.46 sec	21.92 sec
100 nodes; 5 infected	30.07 sec	33.58 sec
1000 nodes; 10 infected	55 min 3.50 sec	32 min 35.58 sec
1000 nodes; 250 infected	44 min 13.09 sec	42 min 19.66 sec
1000 nodes; 500 infected	43 min 2.38 sec	29 min 22.13 sec
1000 nodes; 750 infected	34 min 6.21 sec	42 min 42.04 sec
1000 nodes; 1000 infected	33 min 37.88 sec	28 min 31.23 sec

Table 1: Run Times taken when running the code, by type of the network and for each experiment made, i.e. total amount of nodes on the network and number of nodes infected at the beginning.

<sup>4</sup>[https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19\\_NetSci\\_class10-Epidemics-PartI.pdf](https://fenix.tecnico.ulisboa.pt/downloadFile/1407993358876273/2018-19_NetSci_class10-Epidemics-PartI.pdf)

## 5 Code

Given that the obtained results weren't mathematical inferences, they change a little in every simulation. For that reason, we run 3 iterations for each experiment, and the shown values on the figures are the mean values of the 3 iterations.

We submitted the developed code to the *fénix* platform. Although we used the Python (3.6) library *Networkx* (version 2.2) we had to implement additional code to create the network structure of the Scale-Free networks according to the description of the experiments made in paper [2], and the manipulation of the resulting data.

The instructions of how to run the developed code are in more detail on the file README.md. We also implemented a script that eases our understanding of the data.

## References

- [1] R. Pastor-Satorras and A. Vespignani, “Epidemic spreading in scale-free networks,” *Physical Review Letters*, vol. 86, no. 14, 2001.
- [2] A.-L. Barabasi and R. Albert, “Emergence of scaling in random networks,” *Science*, vol. 286, no. 5439, pp. 509–512, 1999.