CSN LAB 7

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1 Introduction

In this session we will simulate the spreading of a disease in the SIS model and check that the epidemic threshold for arbitrary networks is indeed $\frac{1}{\lambda_1}$.

The SIS model has the following parameters:

- p_0 : The initial number of infected nodes.
- γ : The probability of recovery of an infected node.
- β : The probability of infection. (An infected node attempts to infect each neighbor with probability β)

2 Methods

We have used the Python programming language for this assignment. It is a powerful yet simple language, and it has the networkx library which has helped us generating graph models, simulating the SIS epidemic model and calculating eigenvalues.

We have considered four different models:

- Erdös-Renyi graph
- Complete graph
- Star graph
- 2D lattice graph

For all the graphs considered, we have aimed for a number of vertices n=1000. For the 2D lattice, we have a 32x32 grid, yielding 1024 vertices in total.

3 Results

3.1 Task 1

In this task we want to simulate the spread of a disease over time. We also want to compare between the different networks which ones are more prone to epidemic and comparing the empirical results to the theoretical ones.

We have chosen: $p_0=0.01,\,\gamma=0.1$ and $\beta=0.01$

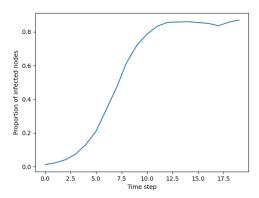


Figure 1: Proportion of infected nodes at each time step in an Erdös-Renyi model $\,$

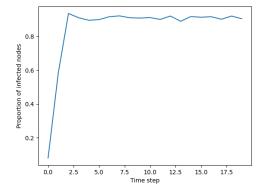


Figure 2: Proportion of infected nodes at each time step in an complete graph

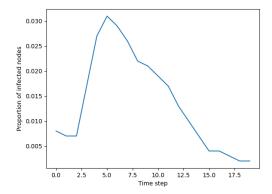


Figure 3: Proportion of infected nodes at each time step in an star graph

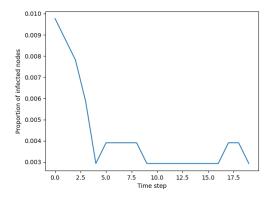


Figure 4: Proportion of infected nodes at each time step in an 2D lattice

With the values chose, we see that for the Erdös-Renyi (1), we have a smooth transition from p_0 nodes infected to around an 80% - 90% of nodes infected.

For the complete graph (2) there is an abrupt transition and in 2 iterations of the process, the number of infected nodes goes to almost all of them, for the rest of iterations, the value oscillates but remains around 90% - 100% of the nodes (this is because the 10% of recovery in each iteration).

For the star graph (3) and 2D lattice (4) we see the proportion of infected nodes going to 0. In the latter one occurs faster than in the other one, but in both cases the infection disappears.

3.2 Task 2

In task two, we first determined the threshold for each of the four selected network types. We then selected two sets of parameter values for β and γ , one set slightly above and one set slightly below the threshold, and simulated the spread of the disease using these values. Finally, we evaluated whether the results of the epidemic simulation were consistent with the Threshold phenomenon by comparing the chosen parameter values to the calculated threshold value.

The threshold theorem is a theoretical result in the study of epidemic spreading in networks. It states that for a given network and set of disease transmission and recovery rates, there exists a critical threshold value below which the disease will die out and above which it will spread indefinitely. More formally, consider a network described by a graph G=(V,E), where V is the set of nodes and E is the set of edges. Each node in the network can be in one of two states: infected or susceptible. The transmission rate of the disease is represented by a parameter β , and the recovery rate is represented by a parameter γ .

The threshold theorem states that there exists a critical threshold value $\frac{1}{\lambda_1}$, such that if $\frac{\beta}{\gamma} > \frac{1}{\lambda_1}$, the disease will spread indefinitely, while if $\frac{\beta}{\gamma} < \frac{1}{\lambda_1}$, the disease will die out. Here, λ_1 is the largest eigenvalue of the adjacency matrix of the underlying network. This threshold value $\frac{1}{\lambda_1}$ is often referred to as the "epidemic threshold" or "threshold parameter".

The following table presents our results:

Network type	Threshold	β	γ	$\frac{\beta}{\gamma}$	Result
Erdos Renyi	24.405	0.024649	0.0099	24.895	Epidemic occurs
Erdos Renyi	24.405	0.023917	0.0102	23.438	No epidemic occurs
Complete network	31.623	0.03194	0.0099	32.258	Epidemic occurs
Complete network	31.623	0.03099	0.0102	30.371	No epidemic occurs
Star network	1.414	0.01428	0.0099	1.443	Epidemic occurs
Star network	1.414	0.01386	0.0102	1.358	No epidemic occurs
Regular lattices	16.053	0.016213	0.0099	16.375	Epidemic occurs
Regular lattices	16.053	0.015732	0.0102	15.417	No epidemic occurs

Table 1: Influence of β and γ on the spread of a disease in different types of networks

Based on the results of our simulations, the threshold theorem seems to hold for all four types of networks. This means that the likelihood of a disease spreading on a network depends on the values of the parameters β and γ and whether they are close to a certain value called the threshold. The threshold value and the likelihood of a disease spreading varied for different types of networks, indicating that the structure of the network can play a significant role in the spread of a disease.

Overall, these results suggest that understanding the threshold theorem can be useful for predicting the spread of a disease on a network and identifying strategies for preventing or mitigating epidemics.

4 Conclusions

To conclude, in this report we have simulated the spread of a disease in four different network models: Erdös-Renyi, complete, star, and 2D lattice. We have studied the behavior of the disease over time and evaluated the influence of different parameter values on the spread of the disease. In addition, we have verified the threshold theorem, which states that there exists a critical threshold value below which the disease will die out and above which it will spread indefinitely.

Our simulations showed that the threshold value for each network type was consistent with the theoretical result of $\frac{1}{\lambda_1}$, where λ_1 is the largest eigenvalue of the adjacency matrix of the underlying network.

Our results suggest that the SIS model can be a useful tool for understanding the spread of diseases in different types of networks, and can help inform strategies for controlling the spread of epidemics.