Complex and Social Networks
Lab Session Report 7
Simulation of SIS model over networks
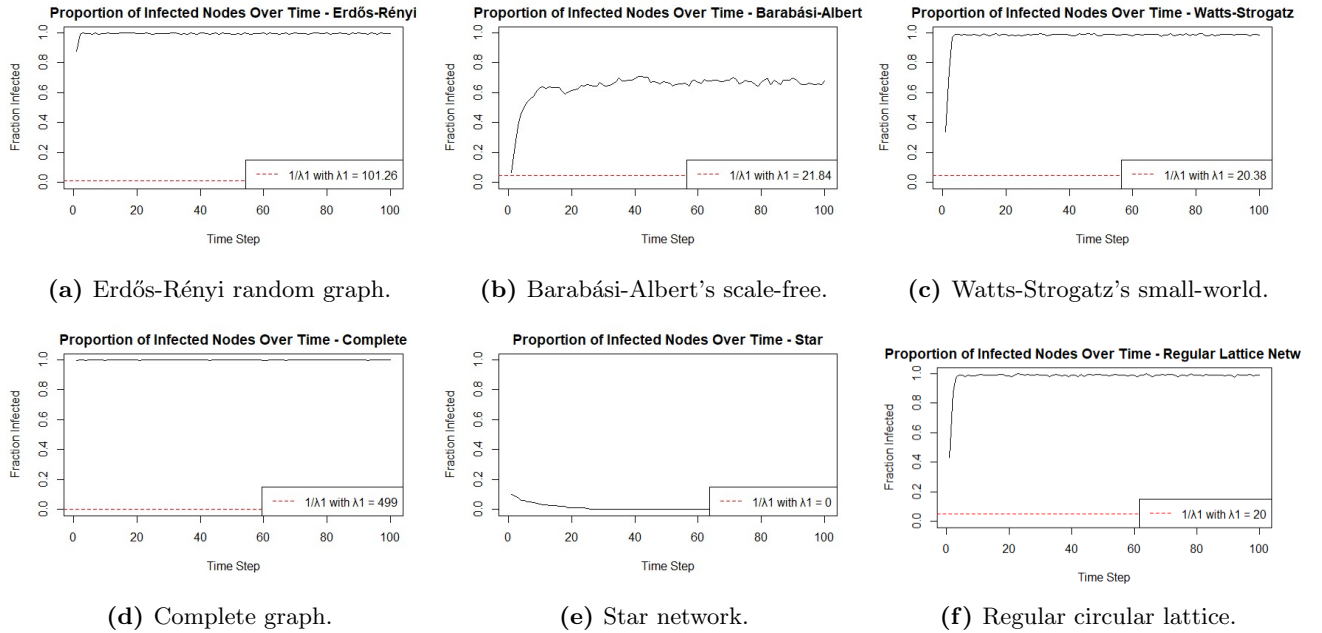
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1 Introduction

In the final laboratory assignment of the subject Complex and Social Networks we are asked to simulate the spreading of a disease in the SIS model, where individuals can be in either a *susceptible* or an *infective* state. We then have to check that the epidemic threshold for arbitrary networks holds and is $\frac{1}{\lambda_1}$, where λ_1 is the largest eigenvalue of the adjacency matrix of the network (Chakrabarti et al. [1]). For our analysis we chose the following networks:

- Erdős-Rényi random graph
- Scale-free network of Barabási-Albert
- Small-world network of Watts-Strogatz
- Complete graph
- Star network
- Regular (circular) lattice

2 Results

2.1 Task 1

For the first task we chose the following fixed values for the parameters: $\beta = 0.2$, $\gamma = 0.1$, and $p_0 = 0.1$. They represent the infection probability, the recovery probability, and the initial fraction of infected nodes respectively. We first present the resulting plot for each one of the networks, followed by a summary table of the leading eigenvalues λ_1 and their inverse value $\tau = 1/\lambda_1$.

(a) Erdős-Rényi random graph.   (b) Barabási-Albert's scale-free.   (c) Watts-Strogatz's small-world.

(d) Complete graph.   (e) Star network.   (f) Regular circular lattice.

Figure 1: Proportion of infected nodes over time for the different networks.

Network	Leading eigenvalue	$1/\lambda_1$
Erdős-Rényi	101.26	0.009
Barabási-Albert	21.84	0.045
Watts-Strogatz	20.38	0.049
Complete graph	499	0.002
Star network	0	-
Regular lattice	20	0.050

Table 1: Summary of the leading eigenvalues λ_1 and their inverse for each network.

2.2 Task 2

The Table below shows a summary of the different values of β and γ considered for each network.

β	γ	β/γ
0.007	0.9	0.0078
0.008	0.9	0.0089
0.9	1.2	0.75
1.1	1.2	0.917
1.1	0.8	1.375
0.9	0.8	1.125

Table 2: Summary of ratios for different values for β and γ.

The resulting figures show the proportion of infected nodes over time for different values of β and γ in the types of networks under analysis. For each network type, we show the effects of four ratios of the parameters. In consideration of space constraints, the aforementioned figures can be found in the Appendix (see Section 5).

3 Methods

We simulated all of the networks using the library *igraph* in R. Even though the size of the networks is supposed to be $n = 1000$, due to computational limitations we reduced it to $n = 500$. In favor of replication and comparison of results, we set a seed of 3013 for the generation of random networks. The results for bigger networks could have been slightly different and more accurate, nevertheless, some patterns and conclusions can still be drawn from our smaller-scale analysis.

For the regular lattice network we chose to simulate a circular network instead of a linear one, in order to see how it may affect the spread of the disease.

To analyze the consistency of simulation results with theory, we select parameter values for β and γ such that their ratio is above and below the calculated threshold λ_i for each network type i. This allows to compare the simulation outcomes with the theoretical expectations based on the epidemic threshold. Since the thresholds of the networks under analysis typically lie between 0 and 0.05 (with the exception of the Star graph, where $\lambda = 0$), we choose β and γ in order to have $\beta/\gamma = \{0.0078, 0.0089, 0.75, 0.917, 1.125, 1.375\}$. as shown in Table 2.

4 Discussion

The plots showing the spread of a disease for fixed β, γ, and p_0 have yielded some interesting results. The Barabási-Albert network seems to have more than half of its nodes infected at all times with the percentage ranging from around 50% to 70% except the beginning of the simulation where the percentage of the nodes is not yet that infected. The leading eigenvalue of the adjacency matrix of the network is $\lambda_1 = 21.84$ which, as we will see below compared to the other networks, lies somewhere in the middle regarding the spread of the disease and the strength of the nodes' connectivity. Also, the network exhibits medium recovery capabilities among the other networks.

Figure 2 illustrates the influence of varying β and γ parameters on the BA network. When the β/γ ratio is below the epidemic threshold of $1/\lambda_1$, the infection fails to propagate. Upon surpassing the threshold and achieving a ratio greater than $1/\lambda_1$, the system, following an initial transient pattern, stabilizes in a state where the proportion

of infected nodes remains relatively stable. With an escalating β/γ ratio, the fraction of infected nodes attains a higher plateau, resulting in a more extensive infection throughout the network.

The Erdős-Rényi and Watts-Strogatz networks along with the complete graph and the circular lattice show similarities in the proportion of infected nodes over time. They all get a quite high proportion infected (over 80%) from an early stage (less than 10 time steps) and have difficulties recovering the nodes as the time progresses. The leading eigenvalues of the Watts-Strogatz and the circular lattice networks are very similar to the Barabási-Albert network's λ_1 as we can see in Table 1, while the Erdős-Rényi has $\lambda_1 = 101.26$ and the Fully Connected network $\lambda_1 = 499$. The worst case among them is the Fully Connected network shown in Figure 1d, with over 95% of its nodes infected during the first 5 time steps and an eigenvalue more than five times higher than the other networks. This is reasonable given that every node is directly connected to every other node.

Taking this into account, we see that having an eigenvalue of $\lambda_1 = 499$ has a higher influence within its network compared to the much smaller one, resulting in a better and quicker propagation of information (in our case, the spread of the disease). The results were expected regarding the last network, but what surprised us was the behaviour of the Regular Circular Lattice. We were expecting a better recovery of the nodes, a smaller percentage of infection and better recovery capabilities. Now, let's explore the influence of β/γ on these randomly generated networks. In the case of complete graphs (Fig. 5), variations in these parameters have a limited impact. The β/γ ratio consistently surpasses the epidemic threshold, which is very close to 0 (given $\lambda = 499$). Consequently, an epidemic always occurs, although to a lower extent for ratios closer to the theoretical threshold. An additional contributing factor could be the high level of connectivity inherent in complete graphs, where every node is directly linked to every other node. This extensive connectivity enhances the efficiency of disease spread within the network.

ER (Fig. 3), Regular Lattice, and WS graphs (Figures 6 and 4) illustrate that when the ratio falls below the epidemic threshold, the infection does not propagate. As the ratio surpasses the theoretical threshold, the epidemic begins to spread. Additionally, in the case of a higher β/γ ratio, the epidemic reaches a slightly elevated plateau, but the underlying pattern remains consistent.

Finally, the Star network shows incredibly good node recovery capabilities, with the percentage of infected nodes consistently lying below 10%. These results were expected if we take into account the layout of such a network and the value of the leading eigenvalue of the network's adjacency matrix that is equal to zero. The majority of nodes are not directly connected to each other, so the infection cannot propagate widely. Also, when the leading eigenvalue is zero, it indicates that the network is not connected in a way that allows information to propagate effectively. This results in a quick recovery and a low proportion of infected nodes over time. We may assume that the plot 1e would look completely different had the central node be infected, but actually the central node has no influence over the peripheral nodes in the network due to the null eigenvalue. This means that even if the central node was initially infected, it cannot easily transmit the infection to the peripheral nodes because there is no direct connection between them. The result would be the infection remaining confined to the central node. For different values of β and γ, the Star network has roughly the same behaviour for all the combinations. The plots in Fig. 7 suggest that the infection is not able to spread within the network, even though there is an initial fraction of infected nodes. A possible explanation of this phenomenon is that the epidemic threshold is infinite (the largest eigenvalue of the underlying contact network is 0), then no epidemic occurs. Another possible explanation for this scenario is that the central hub, which is highly connected to all the other nodes, may not have been initially infected. Since the central hub is critical for transmitting the infection to other nodes, if it remains uninfected, the disease won't spread to the peripheral nodes.
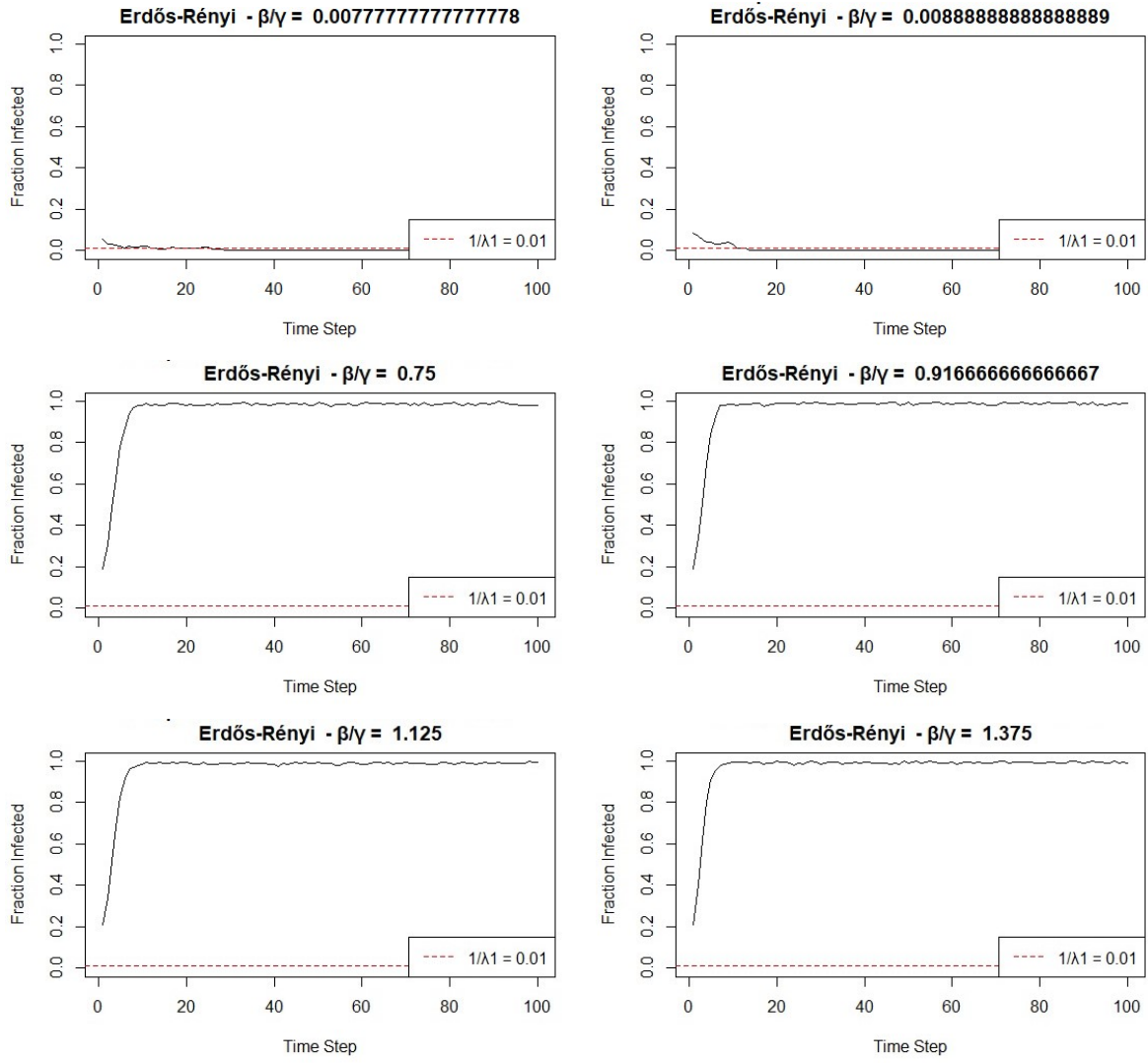
References

[1] Deepayan Chakrabarti et al. "Epidemic thresholds in real networks". In: *ACM Trans. Inf. Syst. Secur.* 10 (2008), 1:1–1:26. URL: https://api.semanticscholar.org/CorpusID:6478129.
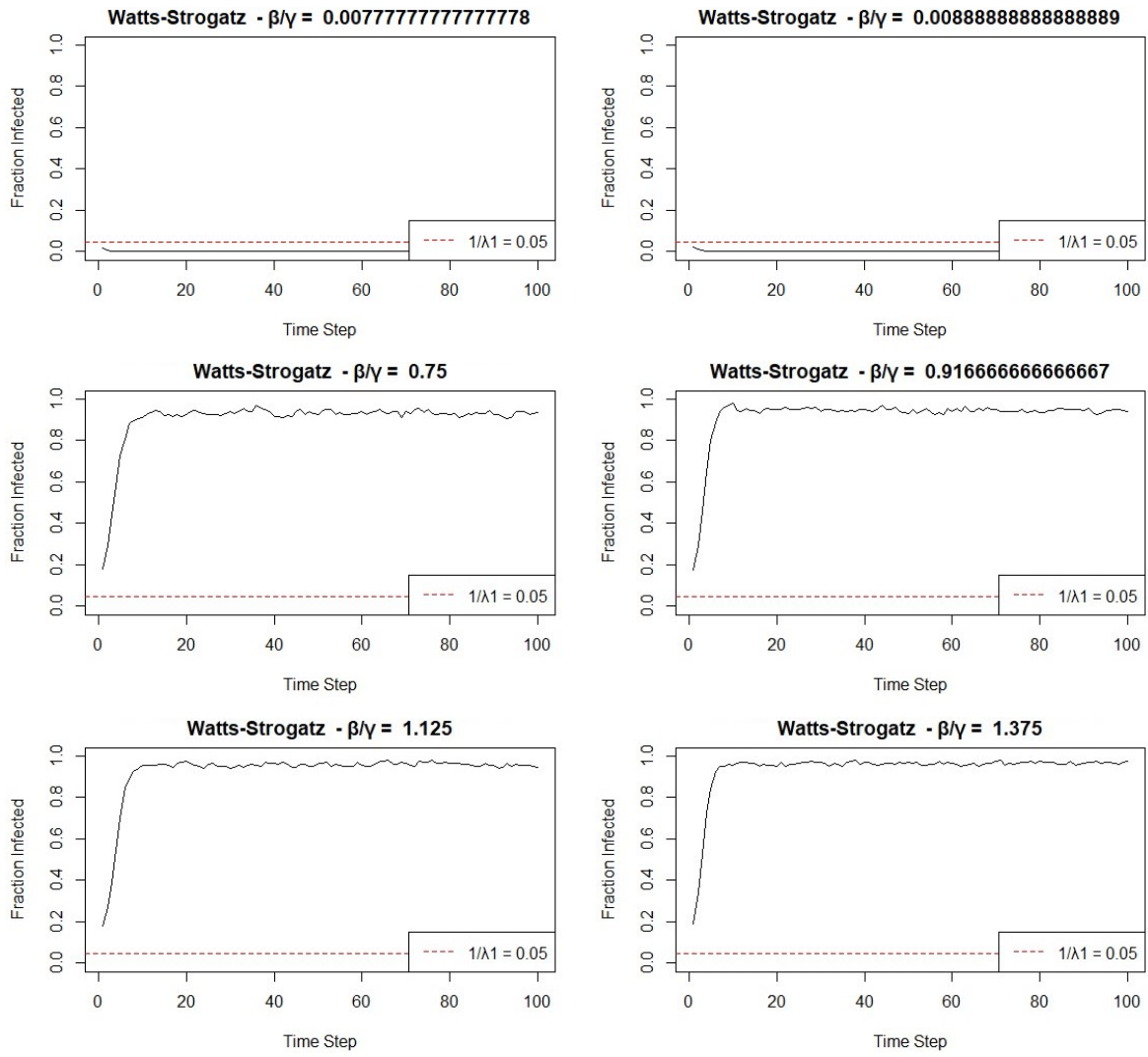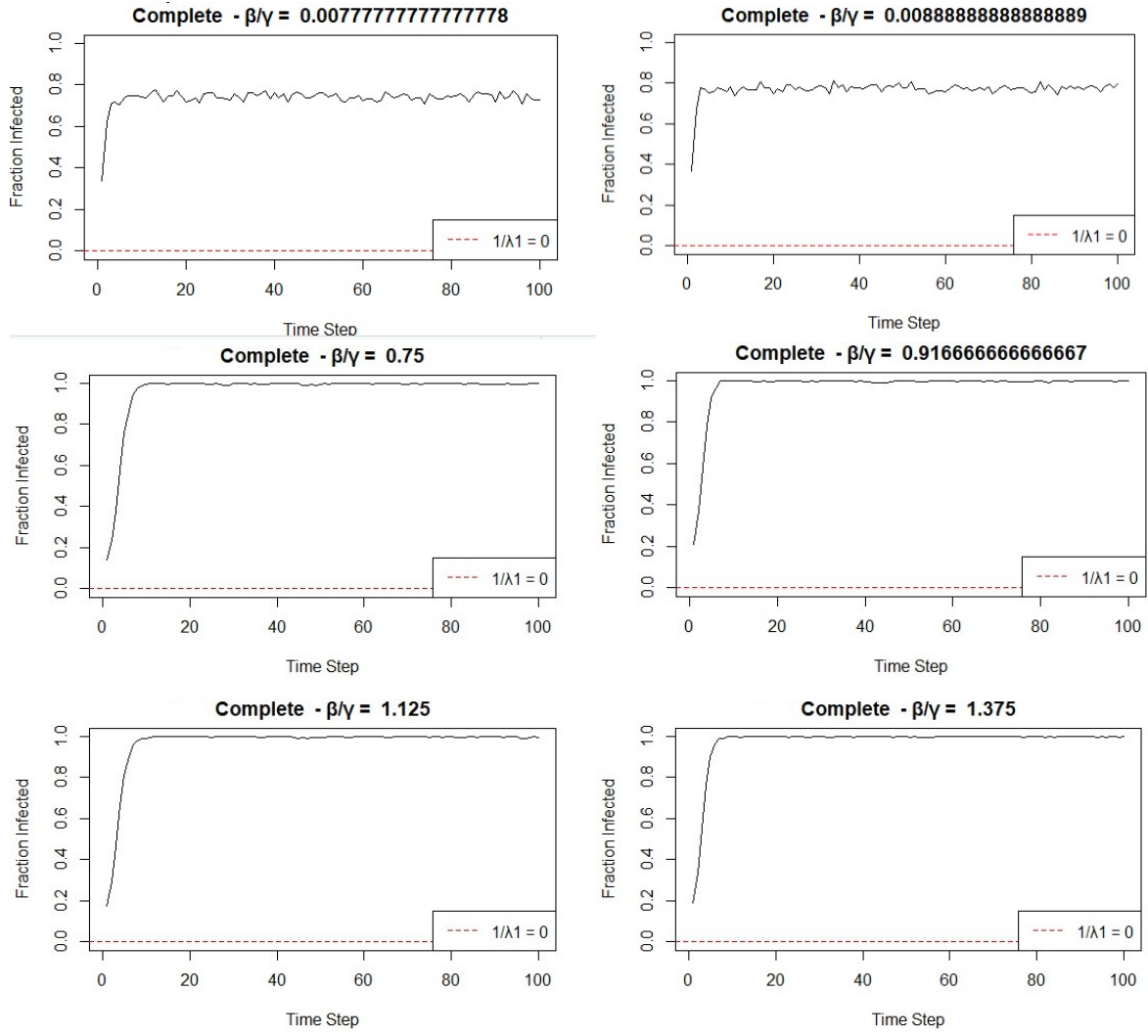
5 Appendix
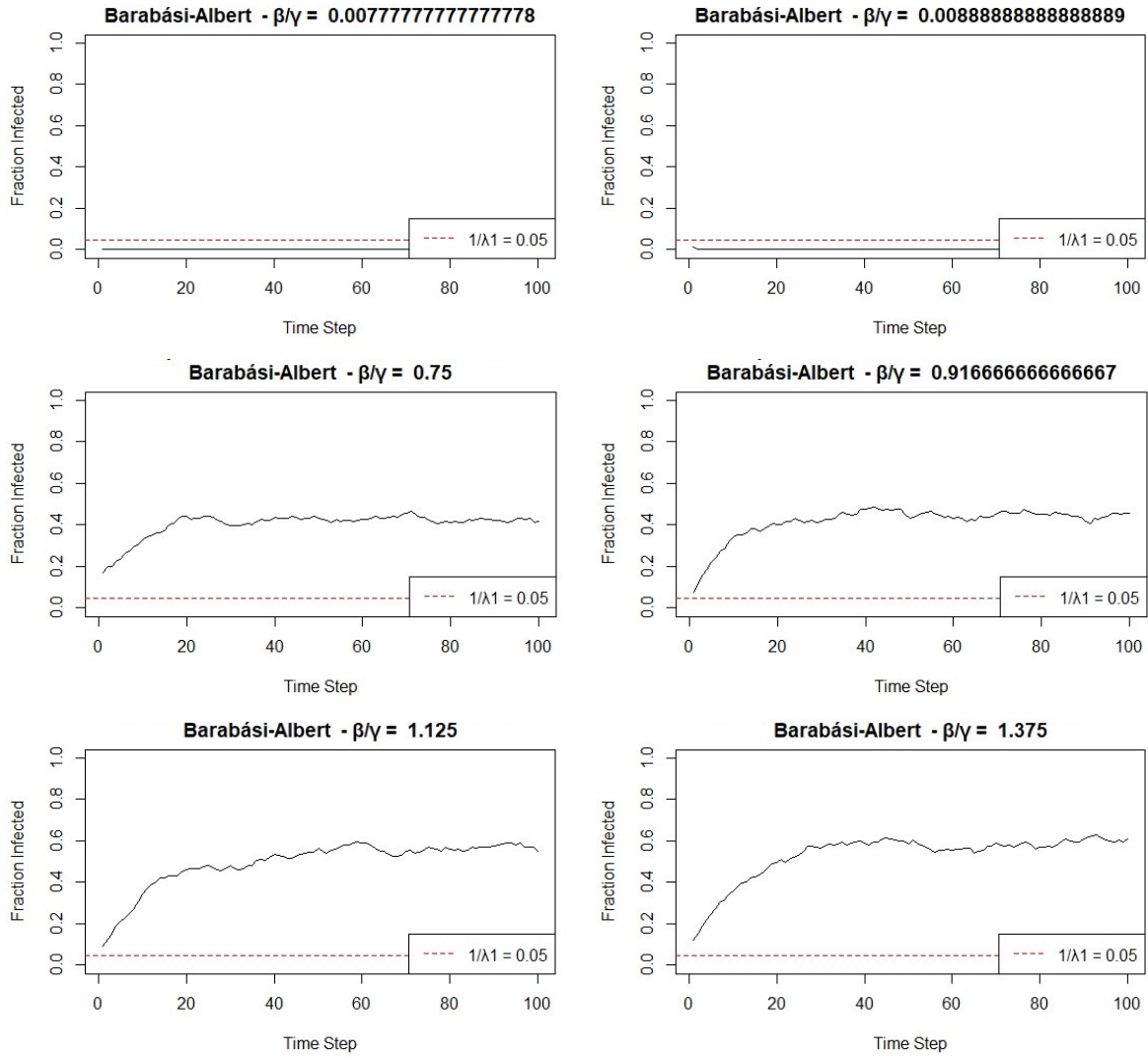
Figure 2: Proportion of Infected Nodes over time for different values of β and γ in a BA network.

Figure 3: Proportion of Infected Nodes over time for different values of β and γ in an ER network.
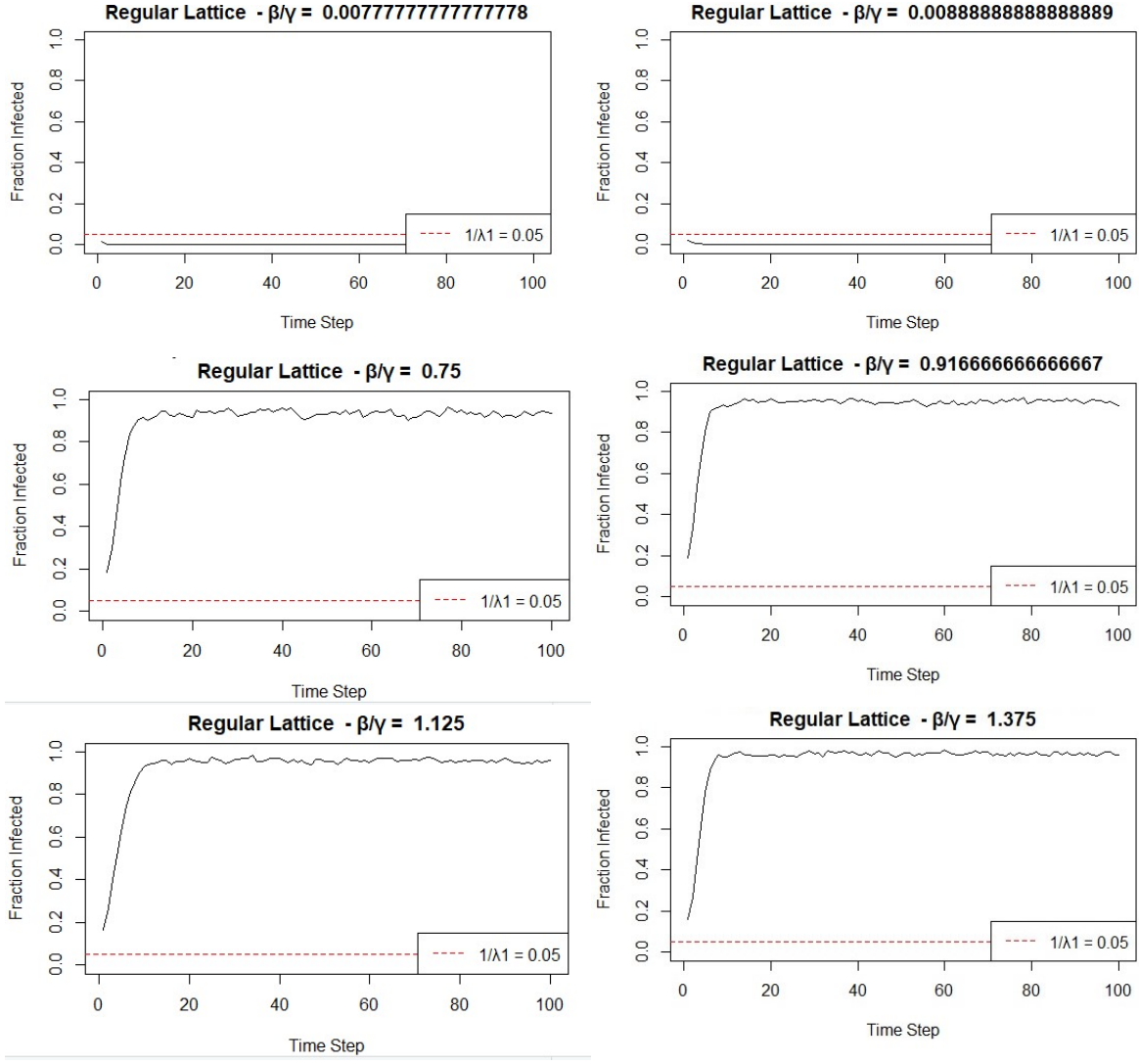
Figure 4: Proportion of Infected Nodes over time for different values of β and γ in a WS network.
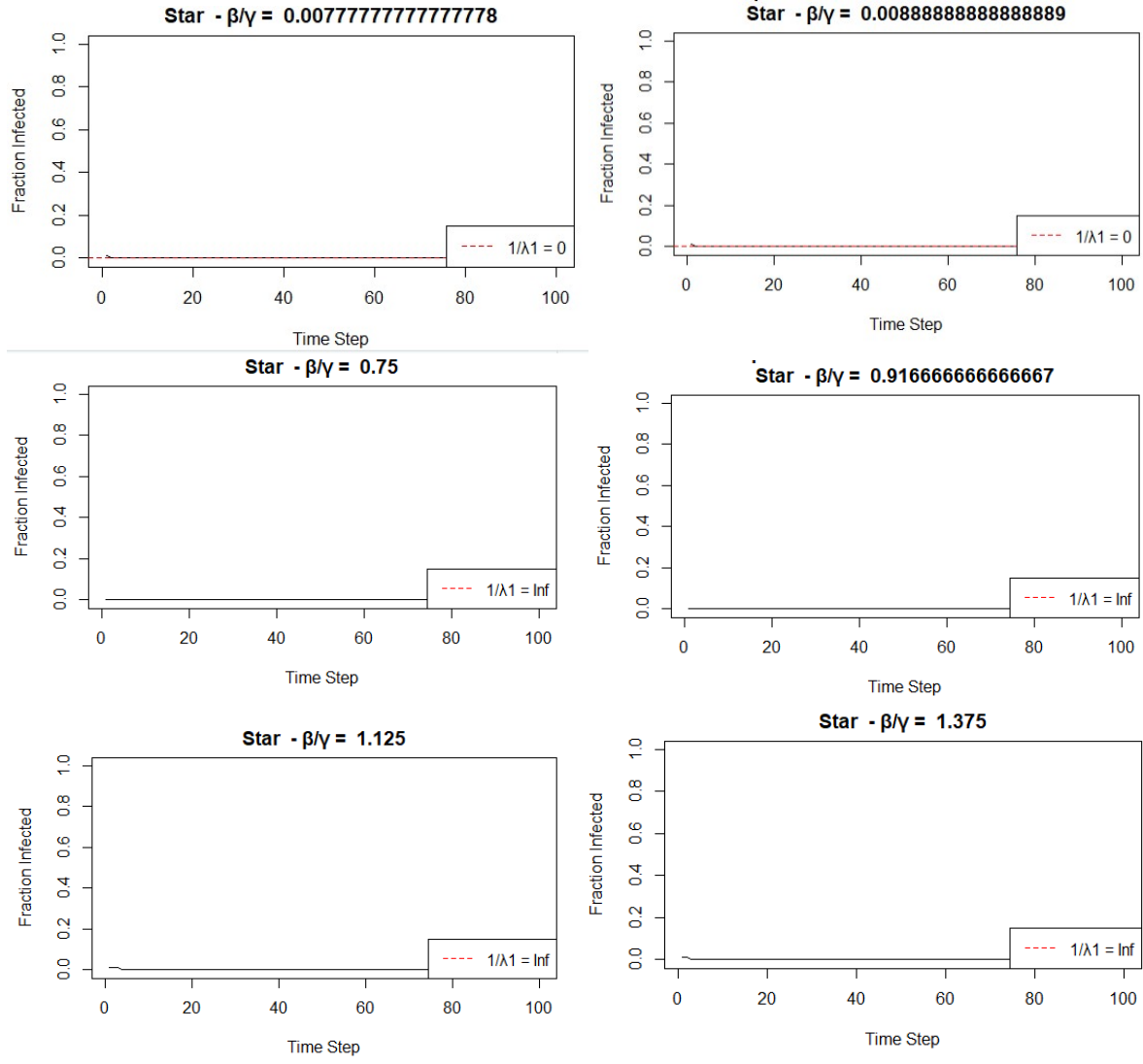
Figure 5: Proportion of Infected Nodes over time for different values of β and γ in a Fully Connected network.

Figure 6: Proportion of Infected Nodes over time for different values of β and γ in a Regular Lattice network.

Figure 7: Proportion of Infected Nodes over time for different values of β and γ in a Star network.