Simulation of SIS Model over Networks

Complex and Social Networks (Fall 2024-2025)

Adrià Casanova, Emma Meneghini

December 29th, 2024

1 Introduction

The SIS (Susceptible-Infected-Susceptible) epidemic model simulates the spread of a disease over a network. The model is regulated by two parameters, β and γ, where the former is the probability of an infected node to infect other nodes, and the latter is the probability of an infected node to recover at time step t. However, the spread of the disease is also regulated by the topology of the network, and in particular by the first eigenvalue of its adjacency matrix, which determines the *epidemic threshold*. In this report, we will discuss the results obtained by experimenting with 7 types of graphs with 1,000 nodes (Erdös-Renyi, Barabási-Albert, Watts-Strogaz, fully connected, (binary) tree, star and lattice), and different sets of values for β and γ, to explore their effect on the spread of the disease over t_{max} time steps. Furthermore, the experiments involve varying also p_0, the proportion of individuals initially infected.

2 Results

Task 1 requires us to experiment with different graphs and compare how the disease spreads over the network for a fixed set of triplets (p_0, β, γ). We choose a list of pairs of values for β and γ such that $\frac{\beta}{\gamma}$ is increasing. We simulated the SIS model on every proposed network for all the triplets that can be constructed with $p_0 \in \{0.01, 0.05, 0.1, 0.2\}$ and $(\beta, \gamma) \in \{(0.0004, 0.4), (0.0025, 0.05), (0.16, 0.8), (0.45, 0.9), (0.9, 0.45)\}$, and computed the proportion of infected nodes at every time step from 0 to $t_{max} = 50$. Figure 1 shows the plots we obtained.

Task 2 requires us to investigate the spread of the disease for different values of $\frac{\beta}{\gamma}$ for every graph, such that they are slightly above or below their epidemic threshold. We proceeded similarly as before, computing the proportion of infected nodes at each time step t, for each graph and each triplet (p_0, β, γ), where β and γ are now adjusted depending on the individual epidemic thresholds of the networks. To do so, we selected a fixed set of values for β and then chose $\gamma = \frac{1.5}{\lambda_1 \beta}$ for the set "below" the threshold and $\gamma = \frac{0.5}{\lambda_1 \beta}$ for the set "above" it. When γ was larger than 1, we set it to 0.5 in the "above" case, but we did not simulate the epidemic in the "below" case, so that $\frac{\beta}{\gamma}$ was always 1.5 times larger or 0.5 times smaller than $\frac{1}{\lambda_1}$, respectively. We chose three different subsets of values for β because the epidemic thresholds in the networks vary a lot. Values are selected deterministically, such that they are equally spaced, from three logarithmic sequences with ranges $[10^{-4}, 5 \times 10^{-4}]$, $[0.01, 0.1]$ and $[0.14, 0.3]$, with lengths 3, 3 and 5, respectively. This ensures that we can perform the study on the fully connected network and the binary tree using parameters that are not exceedingly small.

The results are shown in Figures 2, 3, 4, 5, 6 and 7.

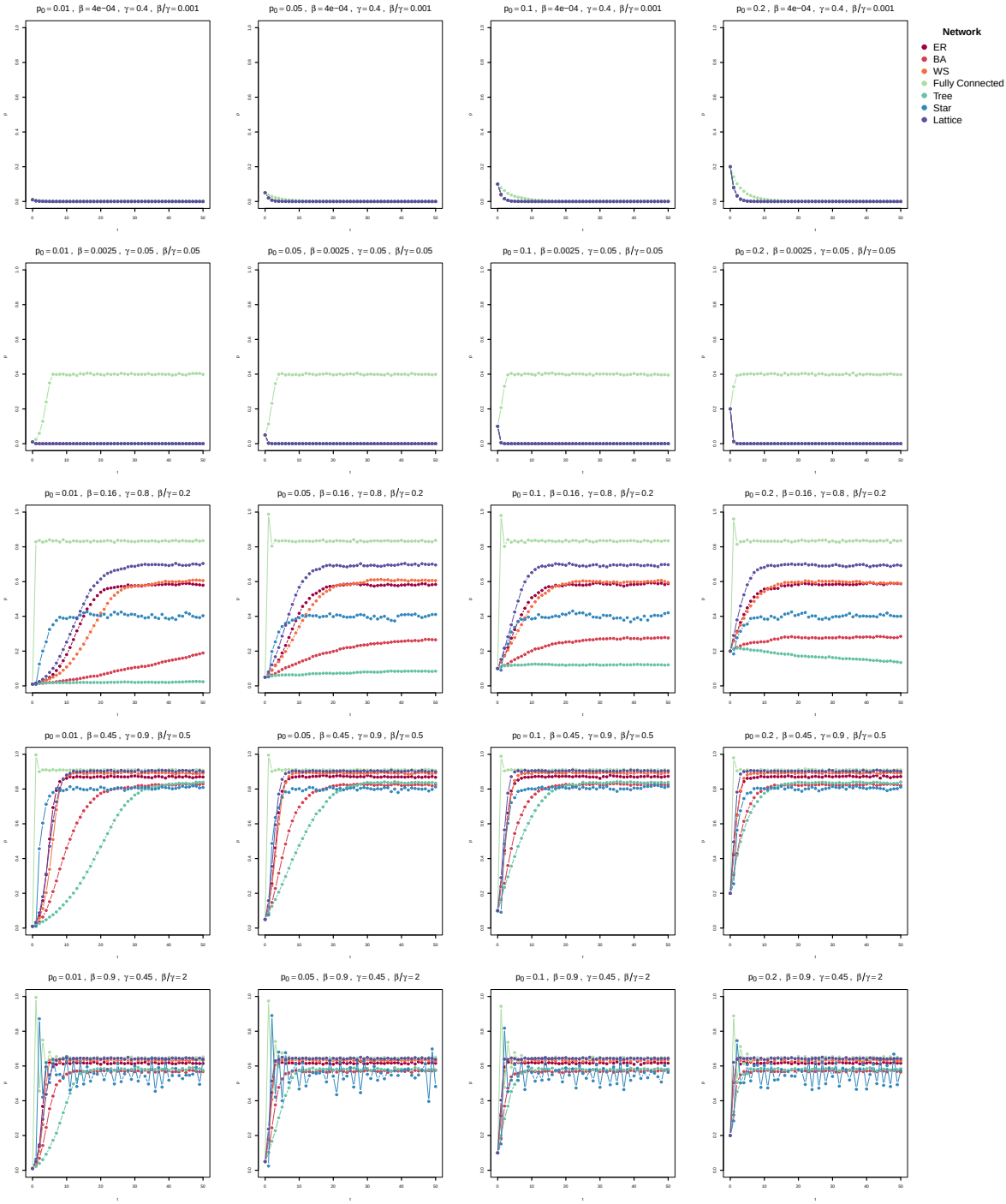

Figure 1: The evolution of the proportion of infected nodes on different networks with **Task 1** (p_0, β, γ) configurations. $\frac{\beta}{\gamma}$ increases with rows, while p_0 increases with columns. Results have been averaged over 15 simulations.

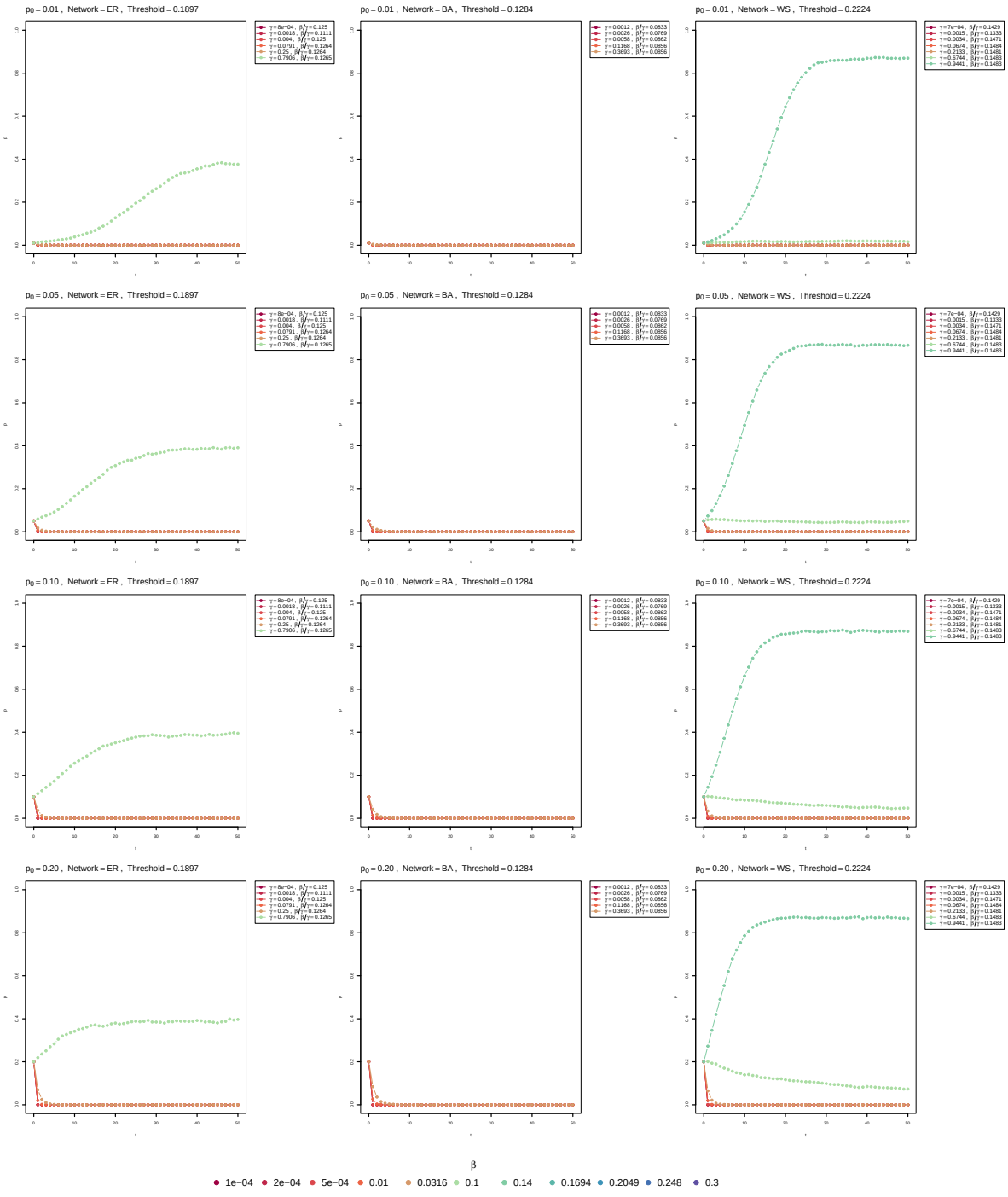

Figure 2: The evolution of the proportion of infected nodes on ER, BA and WS networks with **Task 2** below-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

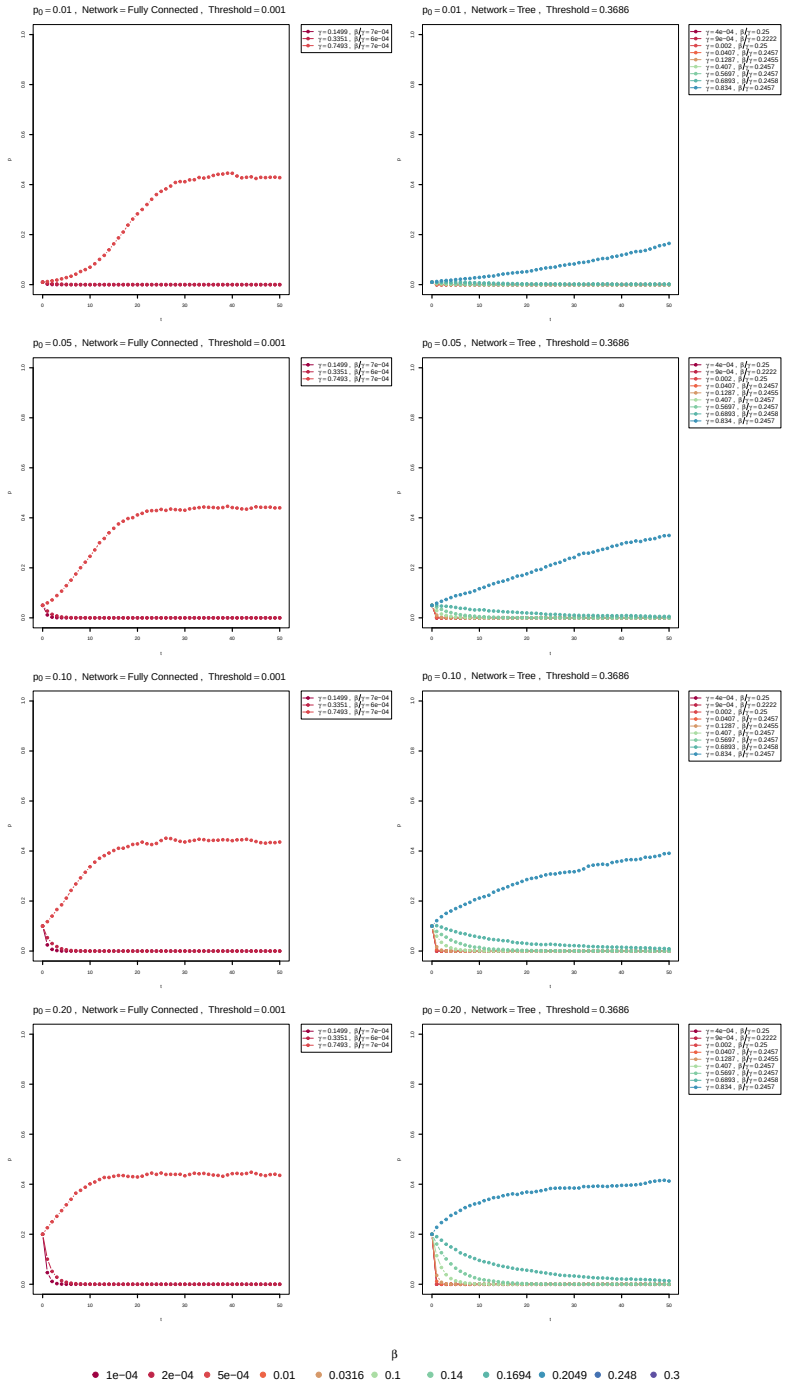

Figure 3: The evolution of the proportion of infected nodes on fully connected and binary tree networks with **Task 2** below-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

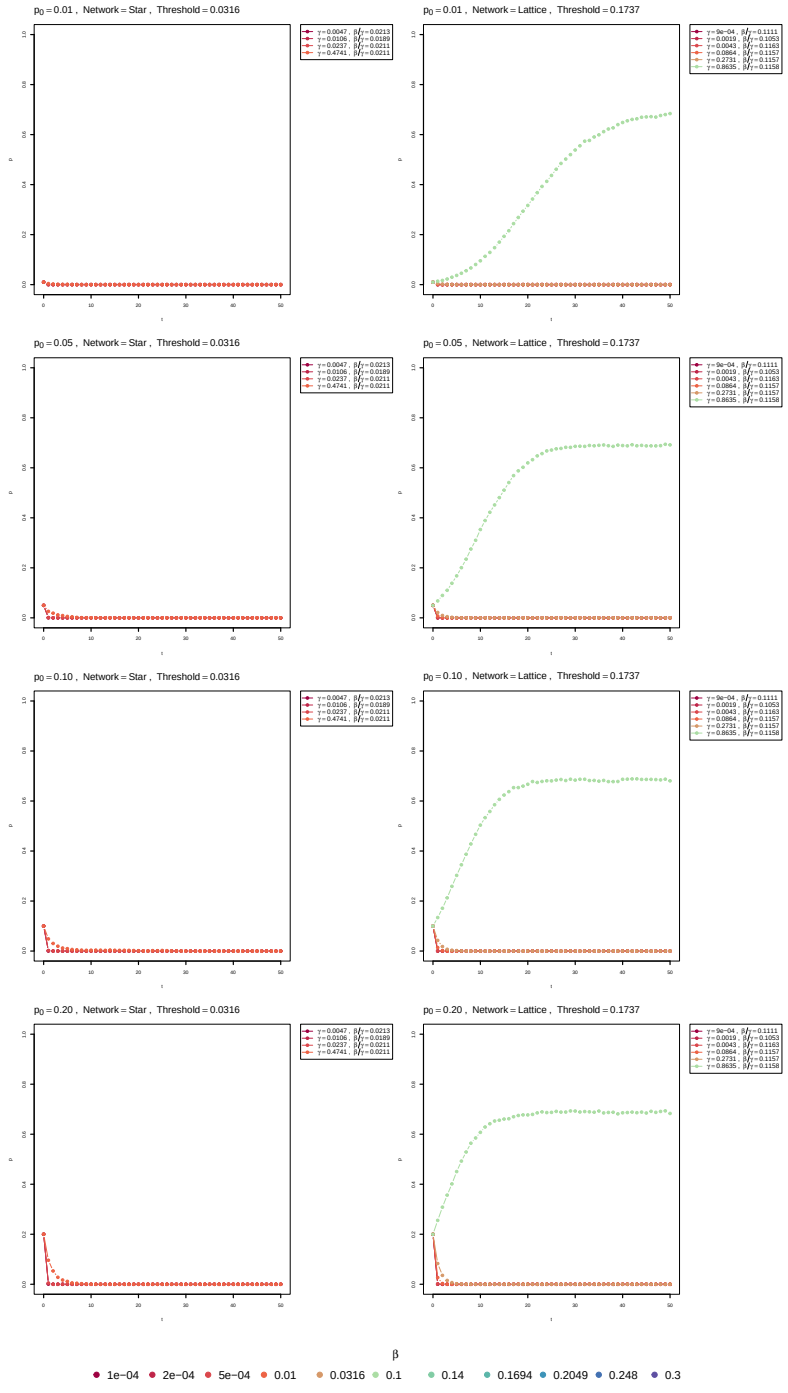

Figure 4: The evolution of the proportion of infected nodes on star and lattice networks with **Task 2** below-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

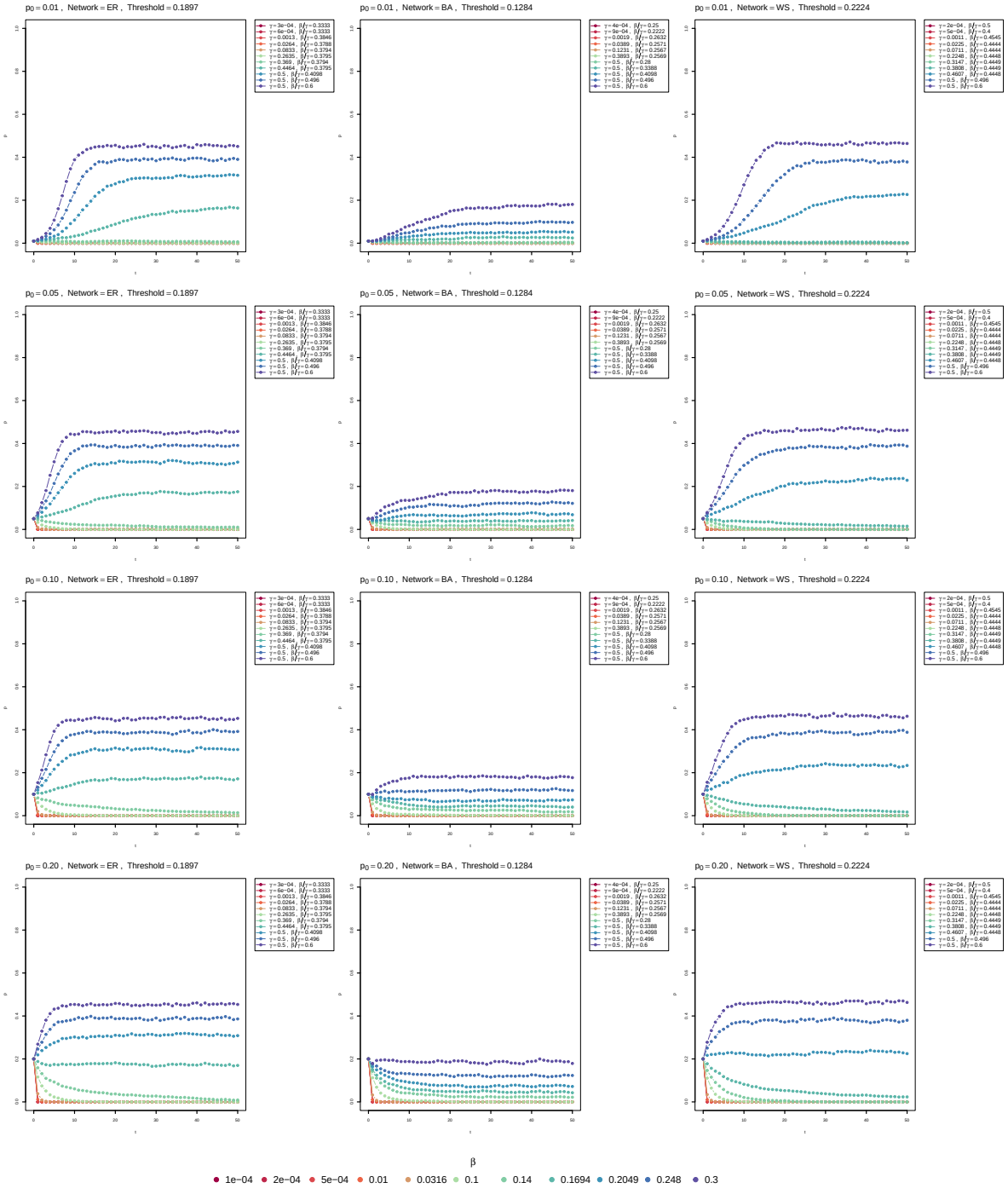

Figure 5: The evolution of the proportion of infected nodes on ER, BA and WS networks with **Task 2**, above-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

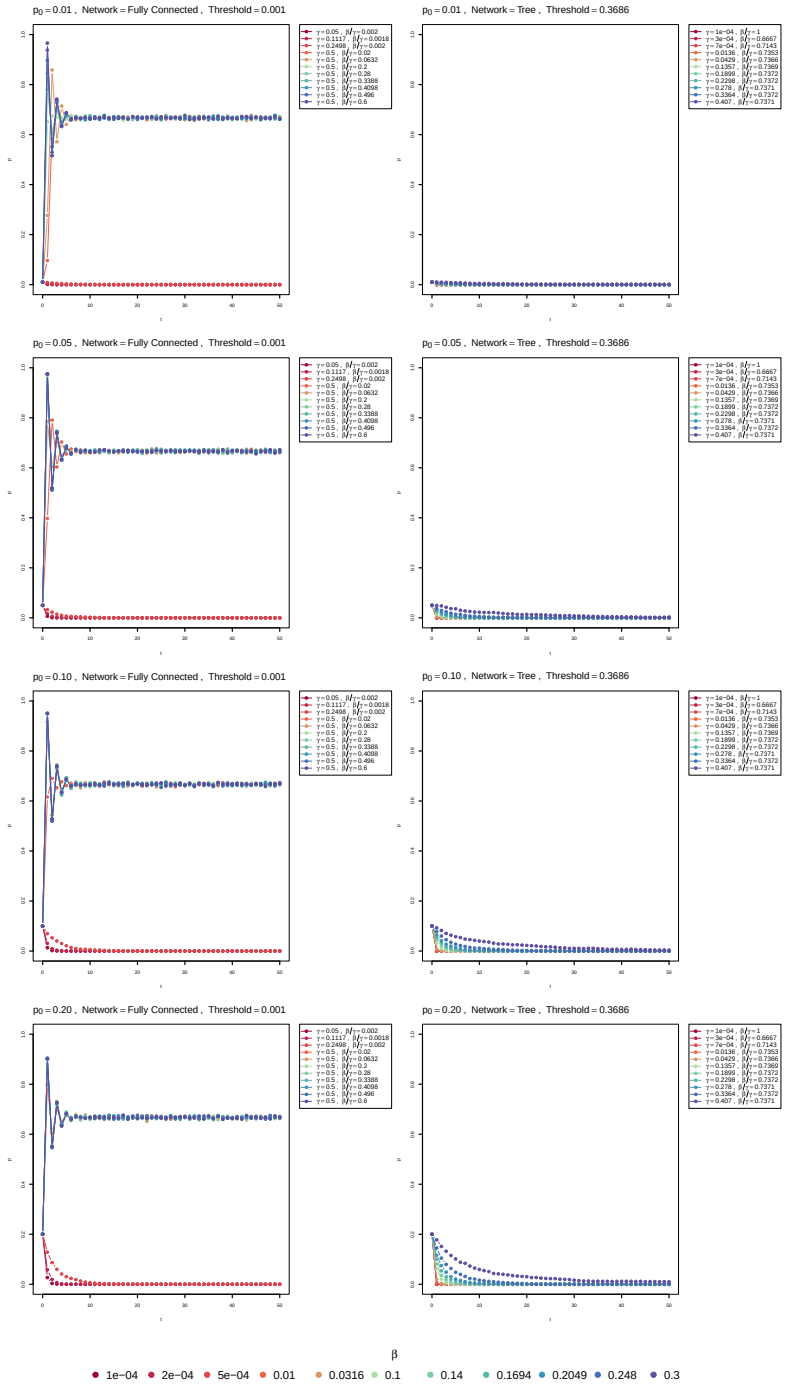

Figure 6: The evolution of the proportion of infected nodes on fully connected and binary tree networks with **Task 2**, above-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

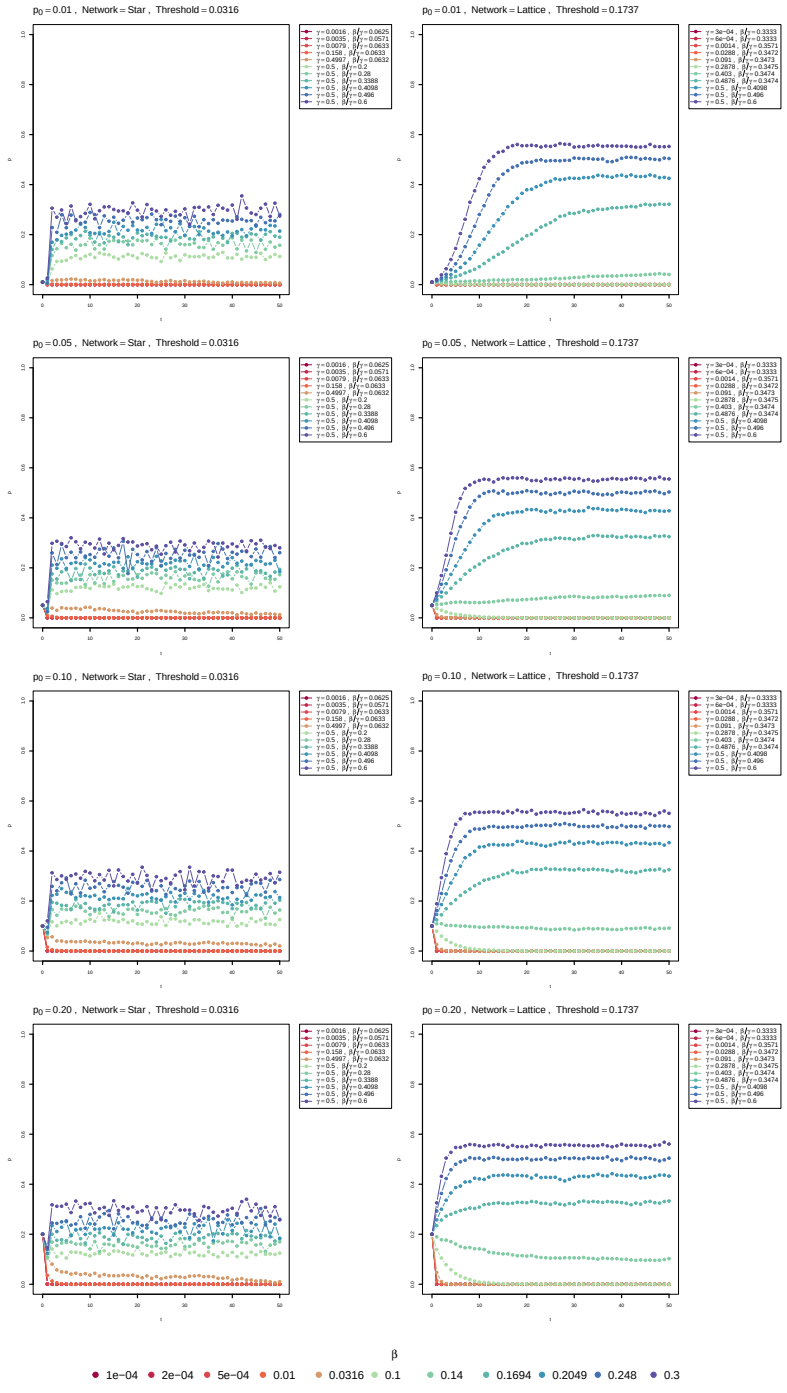

Figure 7: The evolution of the proportion of infected nodes on star and lattice networks with **Task 2**, above-threshold (p_0, β, γ) configurations. Rows correspond to increasing values of p_0, while columns refer to networks. Results have been averaged over 15 simulations.

3 Discussion

3.1 Task 1

Figure 1 shows that p_0 does not affect the epidemic threshold of the network, consistently with the theoretical results by [Chakrabarti et al., 2008]. However, high values of p_0 speed up the expansion of the epidemic, making it reach a state of equilibrium faster. In fact, using a large value of p_0 can be thought of as starting the simulation some time after the infection appeared, hence accelerating the whole process.

The figure shows that the proportion of infected nodes approaches quickly an asymptotic value. When the epidemic bursts out, the proportion of infected grows (as a logistic curve) to a value that depends solely on β, γ and the topology of the network, but not on p_0 (more details about this in Section 4). On the other hand, when it dies out the proportion of infected decays exponentially to 0 or at most p_0. The former state of the system can be interpreted as the stationary distribution of the Markov Chain that describes the SIS model [Chakrabarti et al., 2008], while the latter is its absorbing state. Finally, an interesting phenomenon can be observed for the binary tree: the proportion of infected nodes tends to p_0 instead of 0 if $\frac{\beta}{\gamma} \geq 0.2$, despite it being below the epidemic threshold. This result is not fully consistent with theory, but we hypothesise this is due to random fluctuations in the process.

As for β and γ, we are interested in comparing our results with the expected theoretical behavior. Specifically, we expect an infection to become an epidemic *if and only if* $\frac{\beta}{\gamma} \geq \frac{1}{\lambda_1}$. Tables 1 and 2 contain the values of the epidemic threshold $\frac{1}{\lambda_1}$ in the simulated networks and indicate whether an epidemic is expected to occur for the set of (β, γ) values used for this task.

Network	ER	BA	WS	Fully Connected	Tree	Star	Lattice
$\frac{1}{\lambda_1}$	0.1936	0.1783	0.2204	0.0010	0.3686	0.0316	0.1737

Table 1: Theoretical epidemic thresholds ($\frac{1}{\lambda_1}$) of each considered network.

	Network						
β/γ	ER	BA	WS	Fully Connected	Tree	Star	Lattice
0.001	F	F	F	F	F	F	F
0.05	F	F	F	T	F	T	F
0.2	T	T	F	T	F	T	T
0.5	T	T	T	T	T	T	T
2	T	T	T	T	T	T	T

Table 2: Wether the epidemic is expected to outburst. That is, whether $\frac{\beta}{\gamma}\lambda_1 \geq 1$. T = Epidemic should burst out, F = Epidemic should die out.

Note that networks such as the fully connected or the star graph have remarkably low epidemic thresholds, making them more prone to epidemics: for $\frac{\beta}{\gamma} \geq 0.01$ and $\frac{\beta}{\gamma} \geq 0.2$ the epidemic spreads out in the former and in the latter, respectively. However, in theory, in the star network an epidemic should also occur for $\frac{\beta}{\gamma} = 0.05$. Another discrepancy can be found for the Watts-Strogatz model, for which the epidemic should die out when $\frac{\beta}{\gamma} = 0.2$, but it does not. We believe these small variations between results and theory are acceptable because $\frac{1}{\lambda_1}$ is an approximation of the real threshold and simulations are affected by a random component. On the other hand, the binary tree has the largest

epidemic threshold (0.3686) and an epidemic only appears for $\frac{\beta}{\gamma} \geq 0.5$, hence coinciding with the theoretical results. The rest of the networks show the expected behaviour as well.

Furhtermore, the fully connected and the star networks stand out because their proportion of infected oscillates, even after averaging the results. The complete graph shows a large spike at $t = 1$ when $\frac{\beta}{\gamma} \geq 0.5$, and then stabilises. On the opposite, the proportion of infected of the star network keeps oscillating. This phenomenon is more evident when $\frac{\beta}{\gamma}$ is large, but we have not been able to give it an explanation.

3.2 Task 2

In this second task, we focus on the epidemic thresholds and look at how the epidemic evolves when $\frac{\beta}{\gamma}$ is slightly above or below $\frac{1}{\lambda_1}$.

Regarding the impact of p_0 on the spread of the disease, we observe similar results as in Task 1: it does not affect neither the epidemic threshold nor the proportion of infected nodes at equilibrium.

Moreover, the conditions under which the epidemic spreads are generally consistent with theory, but do not coincide exactly. As explained before, this is probably caused by the randomness in the simulations. On the one hand, the epidemic is expected to die out in the simulations with $\frac{\beta}{\gamma} \leq 0.5\frac{1}{\lambda_1}$ (see figures 2, 3 and 4). The results are consistent with the theory, except when β and γ are large, e.g. $\gamma > 0.7$. On the other hand, we should see the epidemic grow in the simulations with $\frac{\beta}{\gamma} \geq 1.5\frac{1}{\lambda_1}$ (see figures 5, 6 and 7). Nonetheless, it fails when β and γ are low and in all the binary tree simulations. Networks with small thresholds (fully connected and star) need that $\frac{\beta}{\gamma}$ be way larger than the threshold to start an epidemic. In our observations, $\frac{\beta}{\gamma}$ had to be about 10 times larger than $\frac{1}{\lambda_1}$ in the star network and 20 times larger in the fully connected graph. The unexpected extinction of the epidemic in the binary tree suggests that $\frac{\beta}{\gamma}$ should be raised further for an epidemic to burst out on it, as it happens with the aforementioned networks.

3.3 Conclusions

To sum up, our results largely coincide with the expected theoretical behavior of epidemics, although some discrepancies are present. In **Task 1**, we observed that $\frac{1}{\lambda 1}$ is not always a precise estimate of the epidemic threshold in practice, as simulations are affected by a random component. Meanwhile, in the extended experiments of **Task 2**, we have realized that for low values of β and γ, the epidemic is prone to die out even if $\frac{\beta}{\gamma} \geq \frac{1.5}{\lambda_1}$. Symmetrically, an epidemic is likely to appear if both β and γ are large even though $\frac{\beta}{\gamma} \leq \frac{0.5}{\lambda_1}$. Moreover, in practice the network's topology also appeared to play a role beyond the value of λ_1 in the growth of epidemics, since they started appearing for values of $\frac{\beta}{\gamma} \geq \frac{c}{\lambda_1}$, where c depends on the type of network. A conclusive observation is that the proportion of infected nodes may oscillate over time in graphs with low epidemic thresholds, such as the fully connected and star networks.

4 Methods

4.1 The Topology of the Graphs

The evolution of the epidemic over a network was studied on the following undirected graphs with $n = 1,000$ nodes:

- Erdös-Renyi with edge density $\delta = 0.004$.
- Barabási-Albert build using preferential attachment and adding one new node of degree 1 at each time step, and $\delta = 0.002$.
- Watts-Strogaz initialized with 2 neighbours per node and a rewiring probability $p = 0.2$, where multiple edges are removed at the end of the process yielding $\delta = 0.004$.

- Fully connected network with $\delta = 1$.
- Binary tree graph with $\delta = 0.002$.
- Star network with $\delta = 0.002$.
- Lattice with 3 dimensions and 10 nodes for each of them, with $\delta = 0.005$.

Notice that, apart from the fully connected network, all the graphs have a relatively low edge density, and they differ mainly in the configuration of edges rather than their number.

4.2 The SIS Model

4.2.1 The Algorithm

Algorithm 1 Implements the SIS model, returning also the proportion of infected nodes at each time step.

Require: $G = (V, E)$, p_0, β, γ, n, t_{max}.
Ensure: A list $l[p_t]$ with the proportion of infected nodes at each time step t.

```
Calculate the adjacency matrix A from G.
Initialize a vector of binary node labels deciding which nodes are infected (label: 1) by sampling them uniformly at random with probability p_0.
Initialize the list l[p_0].
for t = 1, ..., t_max do
    for all infected nodes at t − 1 do
        Recover them (label: 0) with probability γ i.e. runif(0, 1) ≤ γ.
    end for
    for all susceptible nodes at t − 1 do
        Compute the number of infected neighbours i using A and the node labels vector.
        Compute the aggregate probability of getting infected as p_i = 1 − (1 − β)^i.
        Infect the node (label: 1) with probability p_i i.e. runif(0, 1) ≤ p_i.
    end for
    Update the node labels vector for iteration t + 1 with the new labels.
    Compute the proportion of infected nodes at t and add it to l.
end for
return The list l.
```

We implemented the SIS model and computed the proportion of infected nodes at each time step using Algorithm 1. Then, we averaged the results across 15 repetitions. The algorithm follows the prescription that, at each time step t, an infected node attempts to infect each of its neighbours with probability β, and can be simultaneously cured with probability γ. An infection attempt on an already infected node has no effect, and the probability of a node to get infected is independent of that of the other nodes (*independence assumption*) [Chakrabarti et al., 2008].

4.2.2 The Epidemic Threshold and Score

We now summarise a few theoretical notions about this model which have proven useful for interpreting the results in Section 3. The main reference for them is [Chakrabarti et al., 2008]. They proved that the epidemic threshold for real networks depends solely on their topology, being determined by the largest eigenvalue of their adjacency matrix:

Theorem 1. *In a non-linear dynamical system, the epidemic threshold τ for an undirected graph is*

$$\tau = \frac{1}{\lambda_{1,A}},$$

where $\lambda_{1,A}$ is the largest eigenvalue of the adjacency matrix A of the network.

It follows that, given two values of β and γ, the epidemic spreads *if an only if* the ratio $\frac{\beta}{\gamma}$ is greater or equal to τ:

Theorem 2 (Necessity of the epidemic threshold)**.** *In order to ensure that, over time, the infection probability of each node in the graph goes to zero (that is, the epidemic dies out), we must have $\frac{\beta}{\gamma} < \tau = \frac{1}{\lambda_{1,A}}$.*

Theorem 3 (Sufficiency of the epidemic threshold)**.** *If $\frac{\beta}{\gamma} < \tau = \frac{1}{\lambda_{1,A}}$, then the epidemic will die out over time, irrespective of the size of the initial outbreak of infection.*

Furthermore, the epidemic can be modeled as a random walk over the network: the virus spreads across one hop (i.e. connection, edge) according to βA, and thus it spreads across h hops according to $(\beta A)^h$, which grows as $\beta\lambda_{1,A}$ at every hop. On the other hand, the virus dies off at rate γ. Thus, the effective rate of spread is $\frac{\beta\lambda_{1,A}}{\gamma}$. This is the score s of the epidemic, which spreads *if an only if* $s \geq 1$.

Finally, Chakrabarti et al. proved that below the epidemic threshold infections die out at an exponential rate.

4.2.3 The Markovian Properties of the SIS Model

As just mentioned, the spread of an epidemic regulated by the SIS model can be described as a Markov Chain with 2^n states, where each of them corresponds to a particular system configuration of n nodes that can be either susceptible or infected. The conditional independence property of the Markov Chain is reflected in the configuration at time step t depending only on the configuration at time step $t-1$, as implemented in our algorithm.

This Markov Chain has an absorbing state, that is the stage when all nodes are susceptible. This state can be reached from any starting point, and in the infinite time limit it is reached with probability 1. However, it is reached exponentially fast when the rate of spread of the epidemic is below the threshold, and never reached in practice when it is above.

When an epidemic occurs in the network, the number of infected reaches an asymptote, i.e. a steady state of the Markov Chain. Given a topology and specific values of β and γ, this may be calculated as $\eta_{t_{max}} = \sum_{i=1}^{n} p_{i_t}$, where p_{i_t} is the probability that node i is infected at time step t.

References

[Chakrabarti et al., 2008] Chakrabarti, D., Wang, Y., Wang, C., Leskovec, J., and Faloutsos, C. (2008). Epidemic thresholds in real networks. *ACM Trans. Inf. Syst. Secur.*, 10(4).