

CSN 06 - Simulation of SIS model over networks

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1 Introduction

In this delivery we are asked to study the SIS model infection. To do so, we are asked to create a function that simulates an SIS infection on a given network.

After having our function implemented, then we have to check what the epidemic threshold is.

Theoretically speaking, it should be

$$\frac{1}{\lambda_1}$$

So we are going to check that among other things.

The graph models we are going to use in this study are five and always with size $n = 1000$:

1. Erdos-Renyi (ER) graph. 1.1. Probability of generating an edge between two nodes of 0.5.
2. A fully connected graph.
3. Barabasi-Albert (BA) graph. Power of preferential attachment = 1.
4. A star.
5. Watts-Strogatz (WS) Small world. 5.1. Dimension 1, neighborhood 4, rewiring probability of 0.4.

Let's see their basic metrics:

Table 1: Summary table of all 5 graphs

Graph	N	E	$\langle k \rangle$	δ	Diameter
Erdo-Renyi	1000	249308	498.62	0.50	2
Full graph	1000	499500	999.00	1.00	1
Barabasi-Albert	1000	999	2.00	0.00	20
Star	1000	999	2.00	0.00	2
Watts-Strogatz	1000	4000	8.00	0.01	6

We can see... TODO

2 Spread of the disease

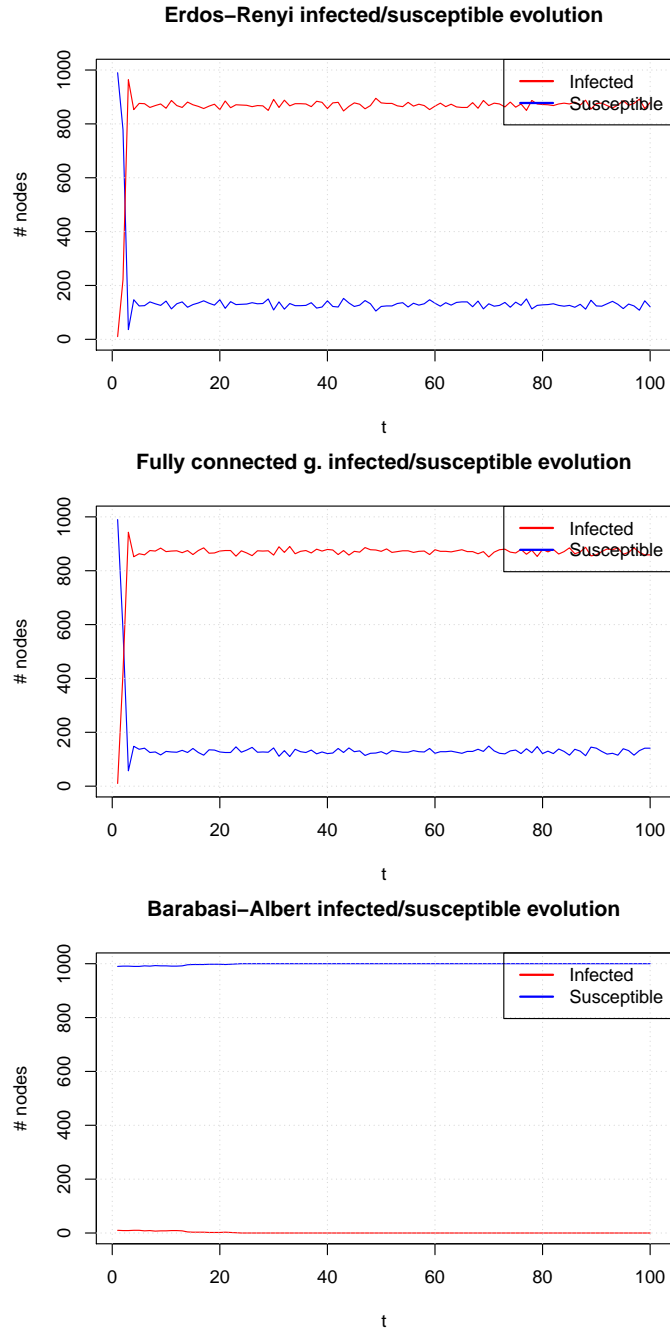
Let's first address Task 01. Having implemented the function that simulates the spread of an infection in a SIS model for a given graph, we are going to check the evolution of the infected nodes and susceptible ones.

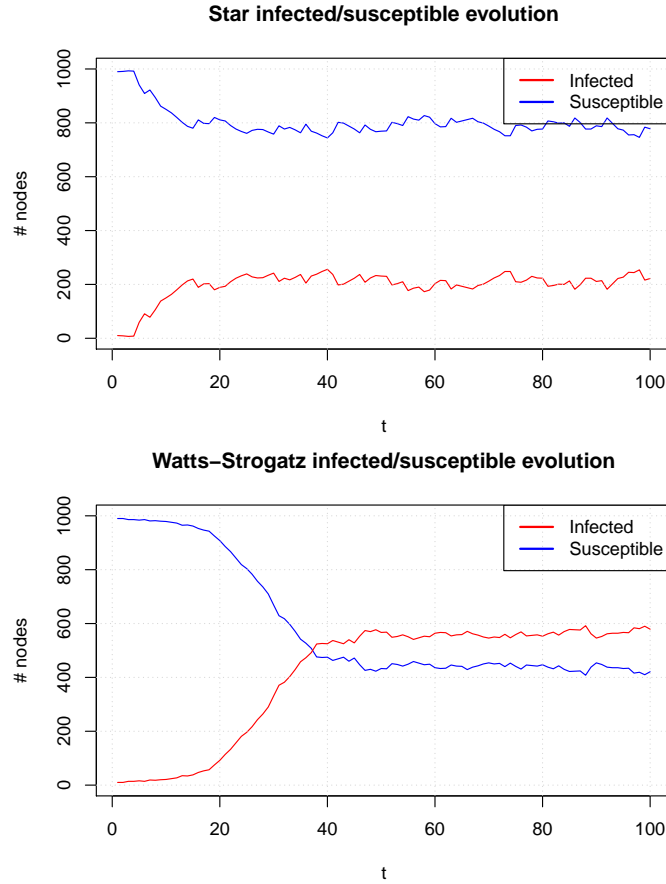
For fixed parameters such that:

- $\beta = 0.05$
- $\gamma = 0.15$
- $p = 10$. 1% of the total nodes start on t_0 as infected.

below are the evolutions of the number of infectes nodes vs. the number of susceptible nodes.

We have fixed the parameters such that $\beta \ll \gamma$, meaning that there should be more recoveries than infected nodes.





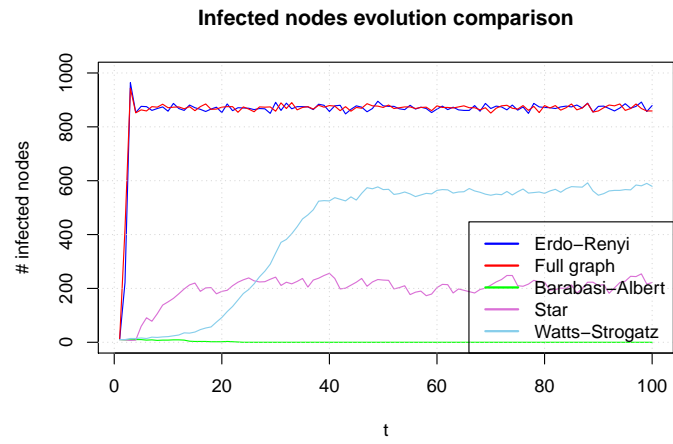
We can see how the ER and Full graph are very prone on infection, since they are pretty well-connected. The infection spreads really fast and the number of infected nodes steadies on a very large number, meaning that many nodes are going to be infected onwards.

In the BA model the contrary happens. The disease does not really spread and it actually dies a little bit before the 20 iteration.

On the star model, the disease does not spread much and does it slower than on ER and the full graph. We can see how this network is pretty resistant and the number of susceptible (thus, not infected) is really higher than dose infected.

Finally, on the last model, the WS, we can see how the disease spreads even slower than on the star network, but it actually reaches a higher number of infected nodes than it. It then steadies around $t = 50$.

For a better comparison, we can plot the evolution of infected together:



TODO: Justify it a little bit more using the metrics from the previous metrics tabl