

# Complex and Social Networks: Lab session 7

Simulation of SIS model over networks

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## 1 Introduction

In this session we will have to simulate the spreading of a disease in the SIS model and check that the epidemic threshold for arbitrary networks is indeed  $\frac{1}{\lambda}$  as forecast by [Chakrabarti et al., 2008]. In particular, we consider the spreading of the disease following these rules at each time step:

- An infected node recovers with probability  $\gamma$
- An infected node attempts to infect each neighbor with probability  $\beta$

Initially, only a random fraction  $p_0$  of nodes are infected.

## 2 Methods

### 2.1 Models

#### 2.1.1 Base

The model that we use to simulate is the following:

- Let  $x_i(t)$  be the probability that node  $i$  is infected at time  $t$
- Let  $\zeta_i(t)$  be the probability that a node  $i$  will not receive infections from its neighbors in the next time step.

$$\begin{aligned}\zeta_i(t) &= \prod_{j:i-j} \overbrace{x_j(t-1)(1-\beta)}^{j \text{ fails to pass infection}} + \overbrace{(1-x_j(t-1))}^{j \text{ is not infected}} \\ &= \prod_{j:i-j} 1 - x_j(t-1)\beta\end{aligned}$$

$$x_i(t) = 1 - (1 - (1 - \gamma)x_i(t-1))\zeta_i(t)$$

Finally, the fraction of infecteds is computed as:

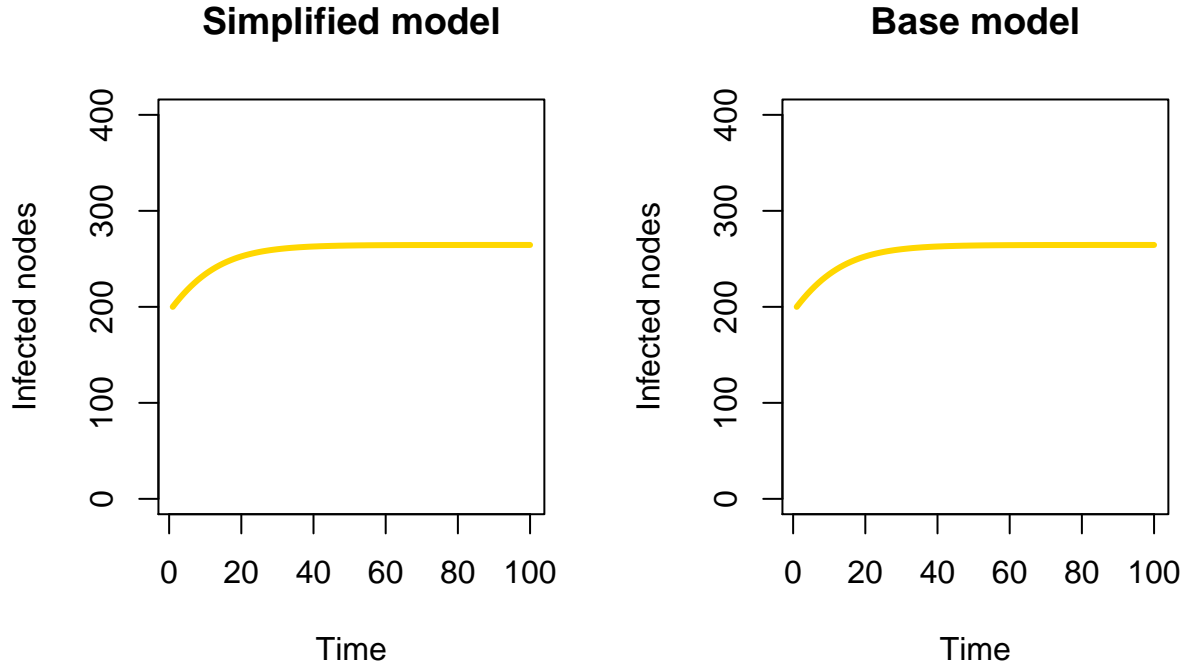
$$x(t) = \sum_i x_i(t)$$

### 2.1.2 Simplified

In some cases, we can use a simplified version of the model, since if the graph is **regular** is easy to see that  $x_i$  is the same  $\forall i$ , and the same is true for  $\zeta_i$ .

So we can speed up the calculation without losing information.

For example, using a regular undirected lattice with 1000 nodes and 1 neighbor, we can take a glance to result obtained with the same set of parameters, both with the base and the simplified model.



## 2.2 Ensemble of graphs

All the networks have 1000 nodes, and are connected.

We calculate here the max eigenvalue and the threshold  $(\frac{1}{\lambda_1})$  that we'll need in the tasks.

Table 1: Data

	Number of edges	Leading eigenvalue	Trashold	Mean degree
Lattice with 1 neighbor	1000	2.00000	0.5000000	2.000
Lattice with 2 neighbor	2000	4.00000	0.2500000	4.000
Erdos renyi with p=0.015	7446	15.94737	0.0627063	14.892
Erdos renyi with p=0.1	50315	101.55027	0.0098473	100.630
Barabasi albert	50500	191.24417	0.0052289	101.000
Complete graph	499500	999.00000	0.0010010	999.000

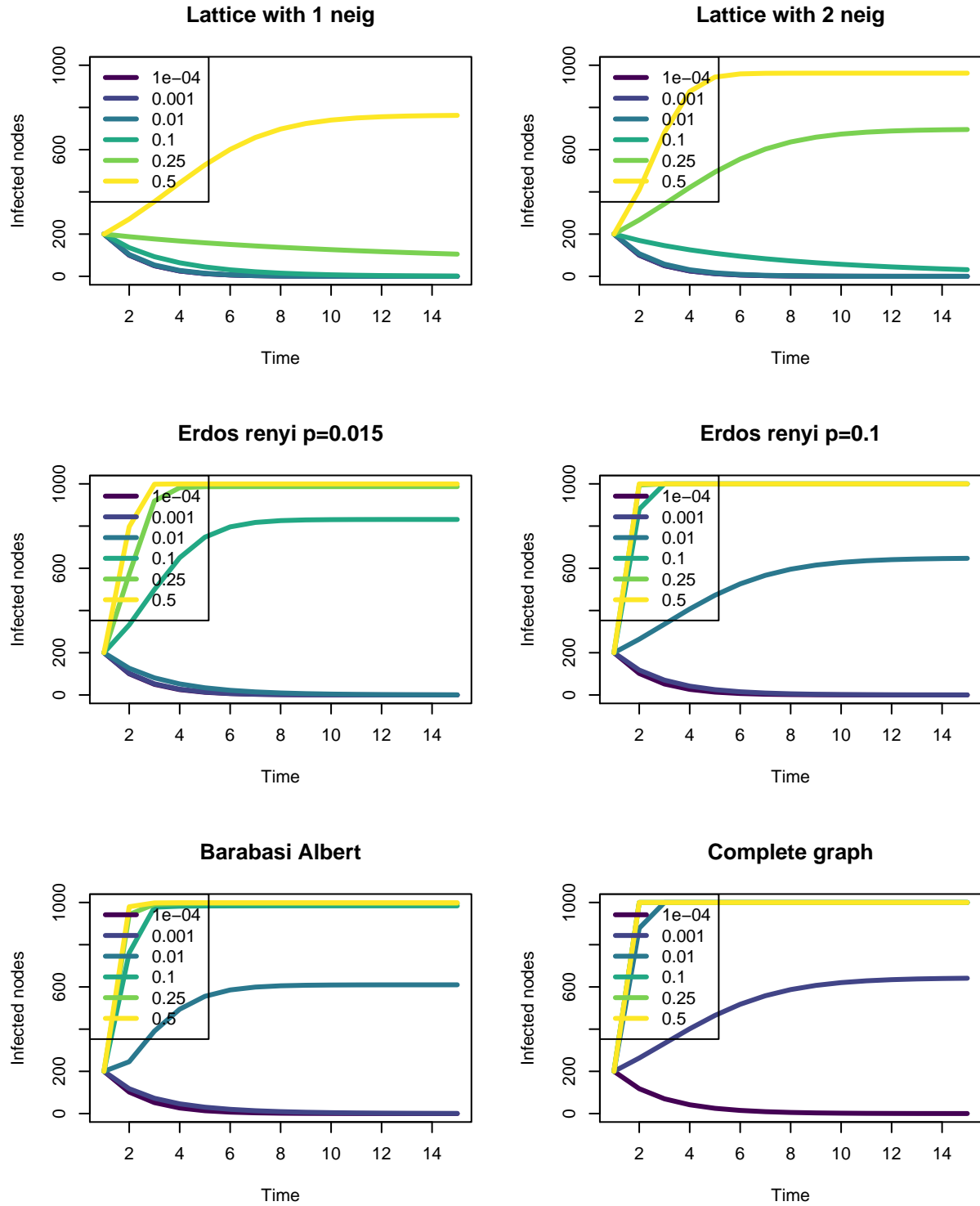
Note: everything in the construction of the graphs is standard. For Barabasi albert we used as a starting point a lattice of 100 nodes, and we added 56 edges each time to have a number of edges similar to the second erdos renyi graph, for comparison. We also specified a power of 2 for the preferential attachment to get a strong effect that could help us enfasyze results.

### **3 Results**

#### **3.1 Task 1: what network is more prone to epidemic?**

We decided to leave  $p_0$  fixed, and inspect the behaviour at first by changing  $\beta$  with  $\gamma$  fixed, and than doing the opposite.

### 3.1.1 Modeling with different betas



As we expect, more dense networks are more epidemic-prone.

An interesting thing to notice is that the degree distribution does not seem to affect the behaviour of the spread, since, an Erdos renyi graph and an Albert Barabasi graph (with strong preferential attachment) seem

to have almost the same resistance to the virus, *ceteris paribus*.

### 3.1.2 Modeling with different gammas

—TODO WILMER

here you only have to do the same that i did for betas, but trying different gammas

## 3.2 Task 2: are simulation results consistent with theory thresholds?

—TODO WILMER

I already calculated the theoretical threshold, here you have to produce plots similar to the task 1 by fixing  $p_0$  and gamma but modeling the different betas around the beta that guarantees the threshold

for example in the first graph the threshold is 0.5 so if we fix as gamma 0.5, we have the “threshold beta” =0.25, so we can maybe plot three curves, one with beta 0.25, and one with beta 0.2 and 0.3

i took only a first glance but seems that the threshold is not a “heavy” cut, a little bit under the threshold we still have epidemic behaviour but only a few nodes stay infected.

## 4 Discussion

—TODO Wilmer

comment results