Universitat Rovira i Virgili

Complex Networks

Practical Report

Report of the Exercise 3: Monte Carlo simulation of SIS epidemic spreading process

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Motivation

Epidemic spreading simulation is a very hot topic within the complex networks applications, since it has become critical for governments to be able to anticipate to possible pandemics, in order to avoid facing dramatically expensive outcomes on public health systems.

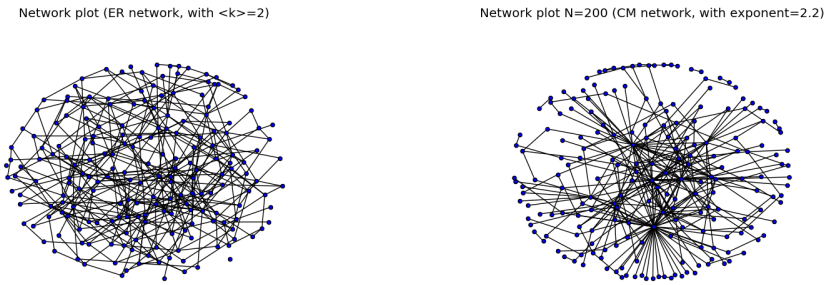
The critical importance of fast response of the epidemic spreading simulation systems in case of epidemics detection has increased in the last decades. This fact was due to the world globalisation and the increase in air transport usage.

This exercise is motivated by the thirst of knowledge and understanding on the epidemic spreading process. Together with the effects of using different parameters for the simulations on networks of different topologies.

The requirements of this exercise demanded:

- Implementing a the code for the "Monte Carlo" SIS simulation.
- Performing experiments of epidemic spreading simulation, with the code implemented.
- Showing and discussing the results obtained during the experiments.

Here we show a plot of the different types of networks that have been used for the experiments:



(a) Erdös-Rényi random network. (b) Scale free network (CM).

Figure 1: Sample of the different types of networks used (for making the plots more understandable, the size has been reduces to 200 nodes instead of 500, as in the experiments).

In figure 1 we can observe a sample of the different types of networks used for this exercise. Which as can be observed are the Erdös-Rényi random networks and the Scale free networks produces from the Configuration Model. This both models have been deeper reviewed in the report for the first practical work of *Complex Networks*.

In the following part of this report we will show directly the experiments with the obtained results and discuss them.

Experiments

This is the main section of this report. Here we will focus on presenting some of the most interesting configurations proved during the experiments performed for this practical work.

The aim of this section is to provide for enough information to permit us to extract robust conclusions on the studied methodologies, giving a complete and deep insight view about SIS epidemic spreading simulation in complex networks.

Configurations

In this section we will show the configurations used for the experiments, which are discussed together with the results obtained on the section.

Network parameters			SIS parameters			
Network Type	Size	Exp/k	p_0	μ values		
ER	500	2	0.2	0.1	0.5	0.9
ER	500	4	0.2	0.1	0.5	0.9
ER	500	6	0.2	0.1	0.5	0.9
ER	500	8	0.2	0.1	0.5	0.9
SF	500	2.2	0.2	0.1	0.5	0.9
SF	500	2.5	0.2	0.1	0.5	0.9
SF	500	2.7	0.2	0.1	0.5	0.9
SF	500	3	0.2	0.1	0.5	0.9

Table 1: Different networks and SIS parameters configurations for the experiments.

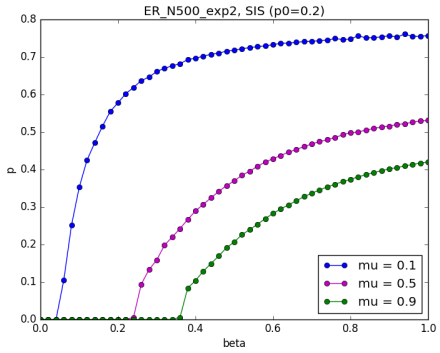
In table 1 the different configurations for the experiments of this report are exposed. I decided to use two sets of networks, ER random networks and SF networks, in order to be able to extract significant conclusions depending on the type of network (i.e. ER or SF), for each type four networks with different settings were tested.

Results

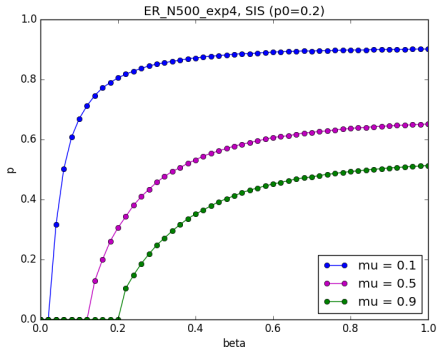
In this section the results from each configuration shown in 1 are shown and discussed.

The results are shown as graphical plots, were we can appreciate the interesting value of $< p >$ (percentage of infected individuals) as a function of β (spread probability), for a fixed value of μ (each one in one different color).

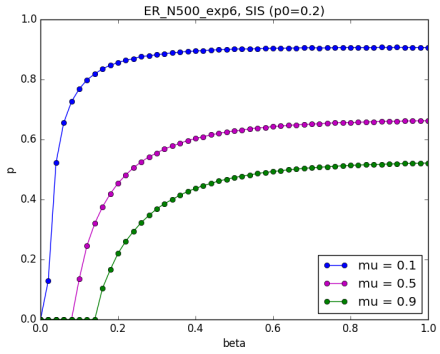
Here we show some plots of the results obtained for this practical exercise:



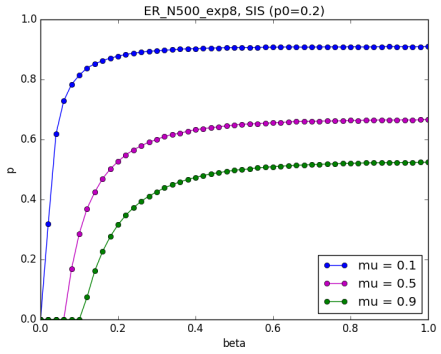
(a) ER random network with $k = 2$.



(b) ER random network with $k = 4$.



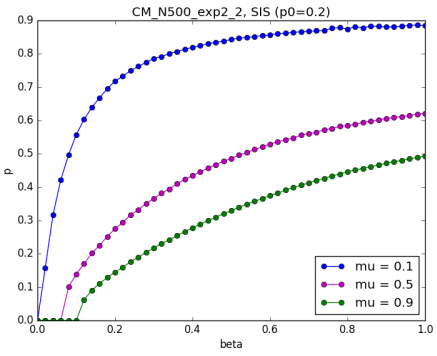
(c) ER random network with $k = 6$.



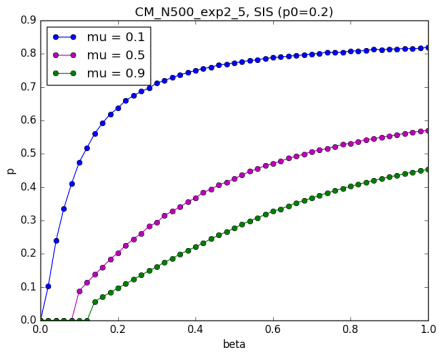
(d) ER random network with $k = 8$.

Figure 2: Results obtained with ER networks of size of 500 nodes.

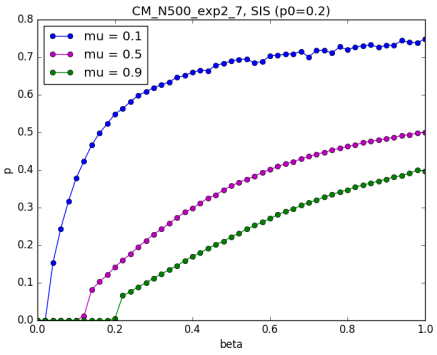
In figure 2 it can be observed the values that takes $< p >$ shown as a function of β, with different ER networks average degree configurations (k values, which correspond to the number next to the *exp* notation on the graphic titles), with the same number of nodes. On each plot there are also shown the $< p >$ values according to different configurations of the μ parameter.



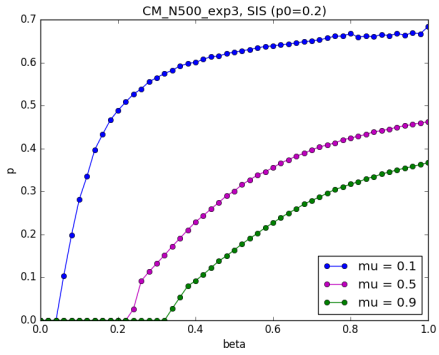
(a) SF random network with $exp = 2.2$.



(b) SF random network with $exp = 2.5$.



(c) SF random network with $exp = 2.7$.



(d) SF random network with $exp = 3$.

Figure 3: Results obtained with SF networks of size of 500 nodes.

In figure 3 it can be observed the values that takes $< p >$ shown as a function of β, with different SF networks (produced with the Configuration Model) exponent degree configurations (exp values, which correspond to the number next to the *exp* notation on the graphic titles), with the same number of nodes. On each plot there are also shown the $< p >$ values according to different configurations of the μ parameter.

Discussion on the Results

In this section the results shown on the previous section are being discussed.

Results from the ER networks

In the ER networks generated with the configuration model, when observing the results comparing the results from networks with lower average degree, with the obtained from networks with higher average degree. Since, the average degree determines the average number of neighbours, that nodes might have in the network. Since, the SIS Monte Carlo simulation, implies that at each round, every infected node will contact all its susceptible neighbours. It is straight forward to deduce that as more neighbours, more easily will the infection become epidemic. Therefore, the epidemic critical points will decrease as the is determining the negative slope degree of the log-log histogram of the network nodes degrees. Therefore, as higher is the average degree increases. It can be observed in figure 2 that in graphic 2a all three epidemic thresholds (each one corresponding to a different μ value), are higher than the epidemic thresholds appearing in graphic 3d.

Results from the SF networks

In the SF networks generated with the configuration model, when observing the results comparing the results from networks with lower exponent, with the obtained from networks with higher exponent. Since, the exponent is determining the negative slope degree of the log-log histogram of the network nodes degrees. Therefore, as higher is the degree, more steep is the slope, which implies that more nodes will have low degrees and less high ones. This might also imply that the network average degree may also decrease when increasing the exponent. Therefore, as we already deduced in the discussion of the results obtained for the ER random networks, lowering the average degree connectivity of a network will usually imply having higher epidemic thresholds (the β infection rate needed for having an epidemic effect, will have to be higher). It can be observed in figure 3 that in graphic 3a all three epidemic thresholds (each one corresponding to a different μ value), are smaller than the epidemic thresholds appearing in graphic 3d.

Strengths and Weaknesses

In this section I will comment some issues that were not planned and altered the planification of performing the exercise.

Strengths

- The literature provided by the teacher was very complete, although difficult to understand at some point the methods on the literature, we were able to choose among many different alternatives. Though, finding an easier algorithm, if the one being reviewed showed to be unfeasible (in complexity terms, due to the weak background on the area).
- So the only kind of research needed was for clarification and support to the already available, to double check concepts and algorithms meanings.
- The amount of time provided was widely more than needed, which permitted to get a deeper understanding on the target topics.
- The previous work and knowledge acquired in practical works 1 and 2, has shown to be really useful, and permitted understand completely the practical exercise much faster than the previous times.

Weaknesses

- Even there was an explicit advice on the time high time consuming requirements for performing this practical exercise, the estimation done was too short. As a consequence, many of the desired configurations for the results had to be omitted for the feasible scope of the exercise.
- Due to hardware memory constraints, experiments with larger networks have not been possible, although many other reductions on the complexity of the network were tried.
- Finally, it was not possible perform any experiment with networks larger than 500 nodes, the experiments had to be aborted after being running for days.

Conclusions and Future Work

Conclusions

- From this exercise we learnt how to perform epidemic spreading simulation over complex networks topologies. To interpret the characteristics of the simulations. Moreover, we are able to "intuitively" predict (approximate) outcomes of SIS epidemic spreading simulations just by observing the parameters of the network and the μ and β.
- It was also an interesting experience realising how long could become experiments depending on the parameters used, since using different μ values for the experiments, implied the difference of few hours to more than one day, maintaining all the other parameters fixed.

Future work

- As future work, it wold be interesting to obtain a deeper insight on how the time evolution counter measures (e.g. avoiding contacting with other individuals, which in fact are temporal modifications on the network) taken by individuals, as counter measures taken by the government (e.g. closing the borders, which are also temporal modifications of the network, but in macro-scale compared to the previous) could be modelled in an epidemic spreading simulation.
- It would have also been interesting to deeper analyse how to predict the outcome of given configurations by means of the Microscopic Markov-Chain Approach (MMCA). Which states that an approximation of the epidemic threshold may be obtained from:

$$\beta_c = \frac{\mu}{\Lambda_{max}(R)} \tag{1}$$

where $\Lambda_max(R)$ is the largest eigenvalue of the contact matrix R. For the contact process $\beta_c = \mu$, and for the reactive process $\beta_c = \mu/\Lambda_{max}(A)$, where A is the adjacency matrix of the network (see Gmez et al., 2010).

References

S. Gmez, A. Arenas, J. Borge-Holthoefer, S. Meloni, and Y. Moreno. Discrete-time markov chain approach to contact-based disease spreading in complex networks. *EPL (Europhysics Letters)*, 89(3):38009, 2010. URL `http://stacks.iop.org/0295-5075/89/i=3/a=38009`.