# A4: Epidemic spreading

Santiago del Rey Juárez        Yazmina Zurita Martel

April 2022

## 1   Introduction

In this work, we will consider SIS-type epidemic spreading on several networks. We will obtain phase diagrams using Monte Carlo simulations with different parameters of the networks and the infection process. The phase diagrams will include the theoretical curves according to the Microscopic Markov Chain Approach (MMCA) model.

## 2   Software and decisions

Since the Monte Carlo simulations may be time-expensive, we decided to use a compiled language. Particularly, we chose Java because we were already familiarised with the language. We also generated the networks in Java, using a popular library called `JGraphT`[1]. However, `JGraphT` can not read or save networks in Pajek format, so we resorted to the library `igraph`[2] in R when we needed these functionalities. Finally, the plots of the phase diagrams and the computation of the theoretical curves according to the MMCA model [1] were generated in Python. The reason is that these tasks do not require much computation time and we found it easier to implement them in this language.

The parameters used in the Monte Carlo simulations correspond to the ones recommended in the document containing the details of this exercise:

$$N_{rep} = 100; \quad \rho_0 = 0.2; \quad T_{max} = 1000; \quad T_{trans} = 900; \tag{1}$$

We made sure that the infection density had reached the stationary state after $T_{trans}$ time steps by plotting it against the time steps for each of the simulations.

We consider that infected nodes infect each of their neighbours with probability $\beta$ and recover at a rate $\mu$. Susceptible nodes have a probability $(1-\beta)^{n_I}$ of remaining susceptible and $1-((1-\beta)^{n_I})$ of being infected, where $n_I$ is the number of infected neighbours the node has.

---

[1] https://jgrapht.org/
[2] https://igraph.org/r/

1

# 3    Results

In this section we show the different results obtained from the simulation of the SIS-type epidemic spreading model in different networks.

The synthetic networks have been created using the `ScaleFreeGraphGenerator`, the `BarabasiAlbertGraphGenerator` and the `GnpRandomGraphGenerator` classes of the JGraphT library.
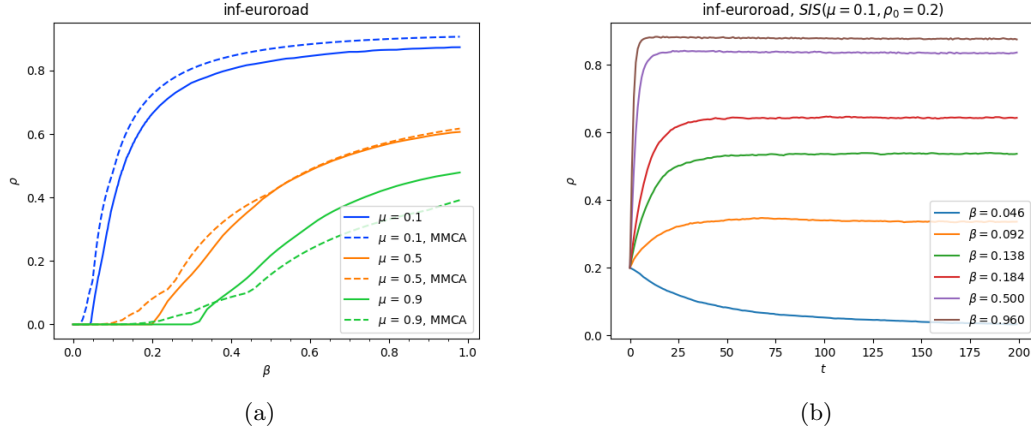
## 3.1    Real networks



Figure 1: SIS epidemic model simulation in the network inf-euroroad [2]. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.1$.

## 3.2    Scale-free networks
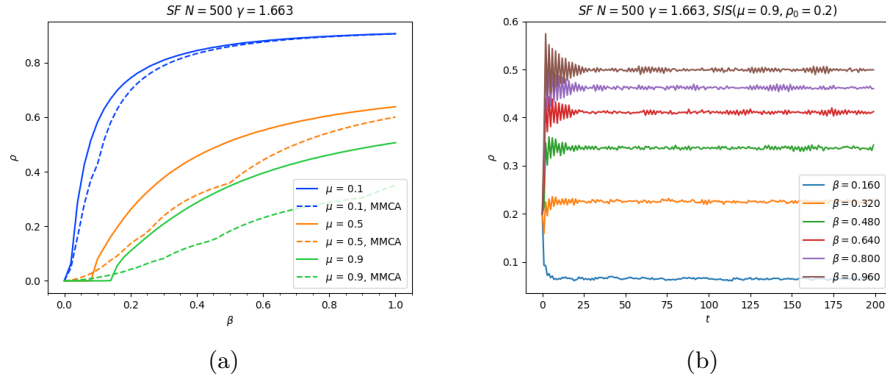


Figure 2: SIS epidemic model in a SF network with $N = 500$, $\gamma = 1.663$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
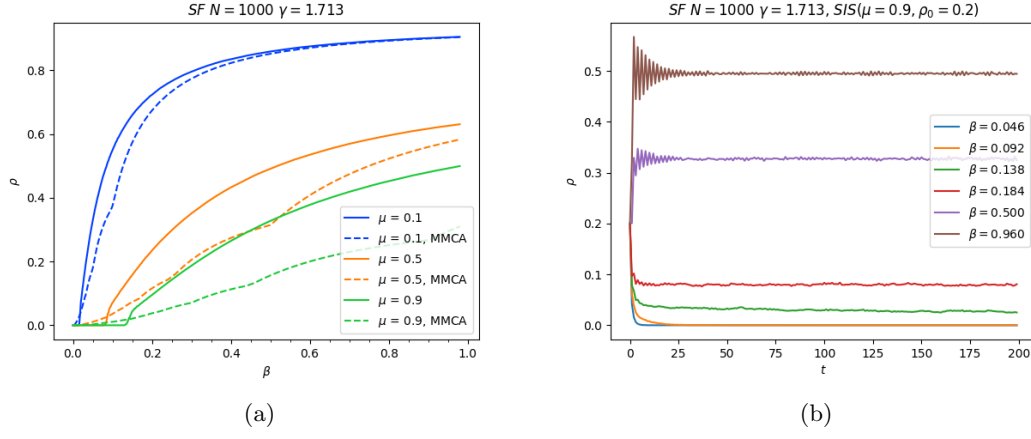
Figure 3: SIS epidemic model in a SF network with $N = 1000$, $\gamma = 1.713$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
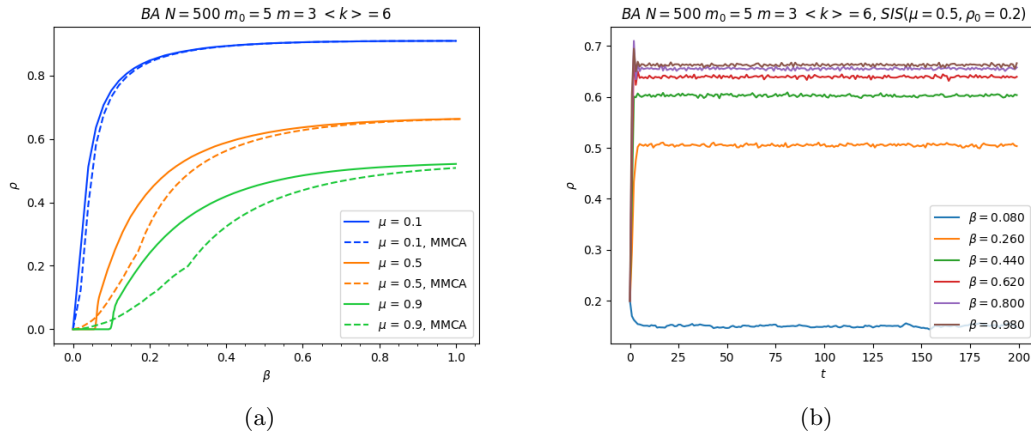
### 3.2.1 Barabási & Albert networks



Figure 4: SIS epidemic model in a BA network with $N = 500$, $m_0 = 5$ and $m = 3$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.5$.
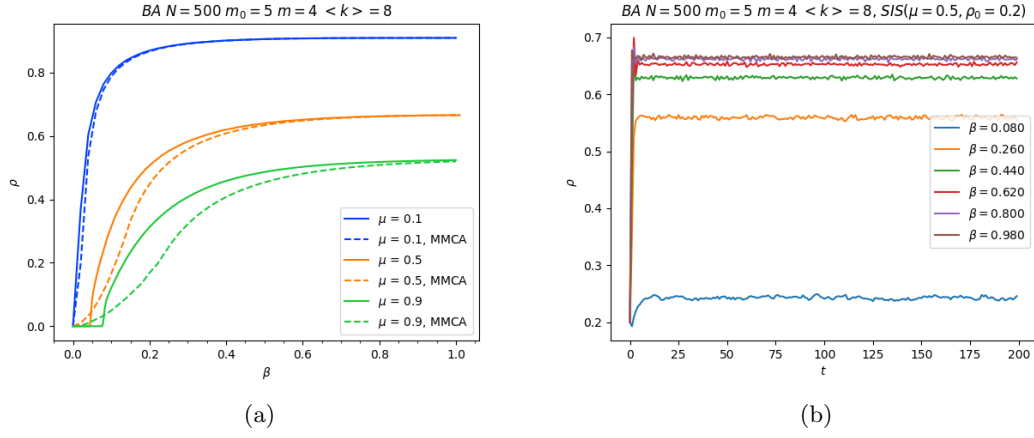
Figure 5: SIS epidemic model in a BA network with $N = 500$, $m_0 = 5$ and $m = 4$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.5$.
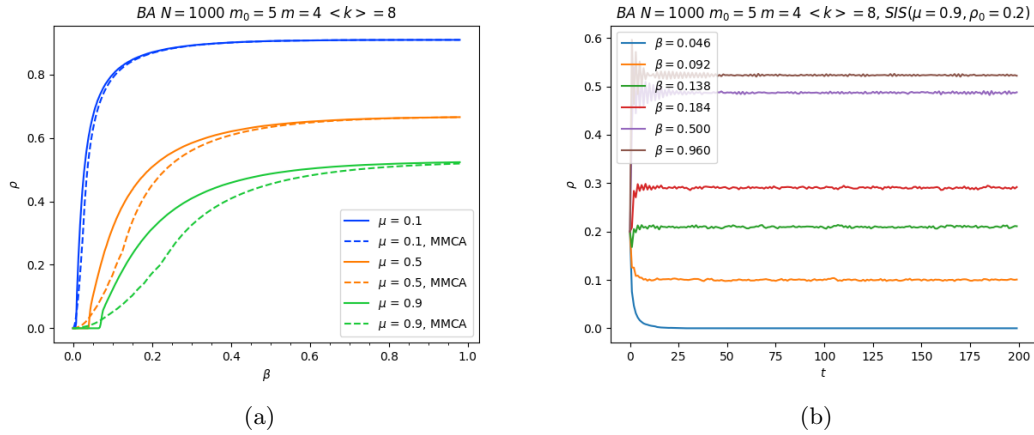




Figure 6: SIS epidemic model in a BA network with $N = 1000$, $m_0 = 5$ and $m = 4$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
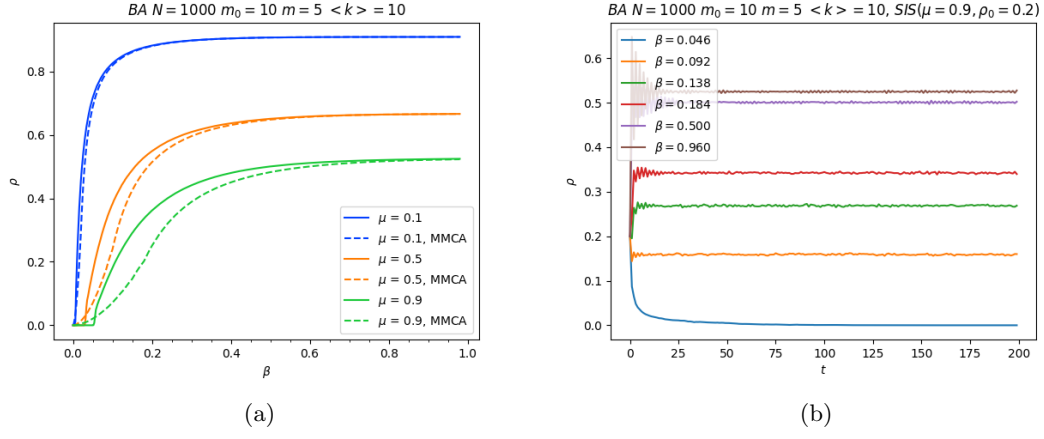
4

Figure 7: SIS epidemic model in a BA network with $N = 1000$, $m_0 = 10$ and $m = 5$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
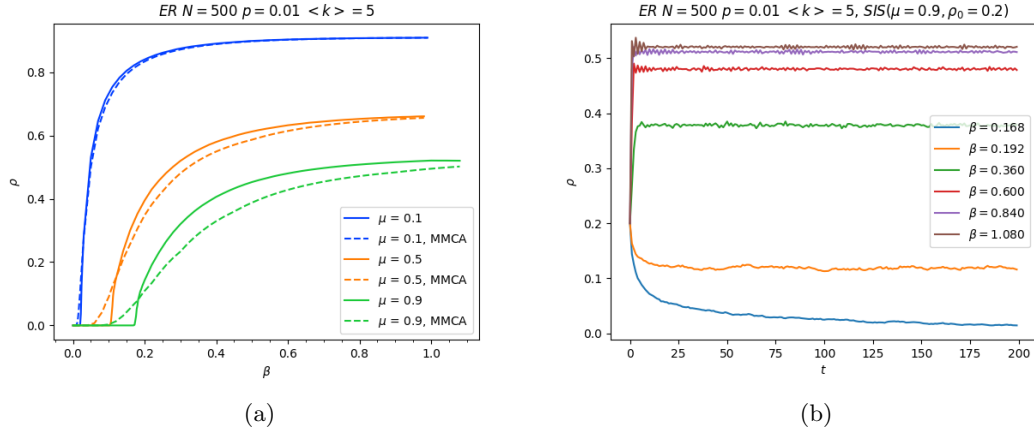
## 3.3 Erdös-Rényi networks



Figure 8: SIS epidemic model in a ER network with $N = 500$, $p = 0.01$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
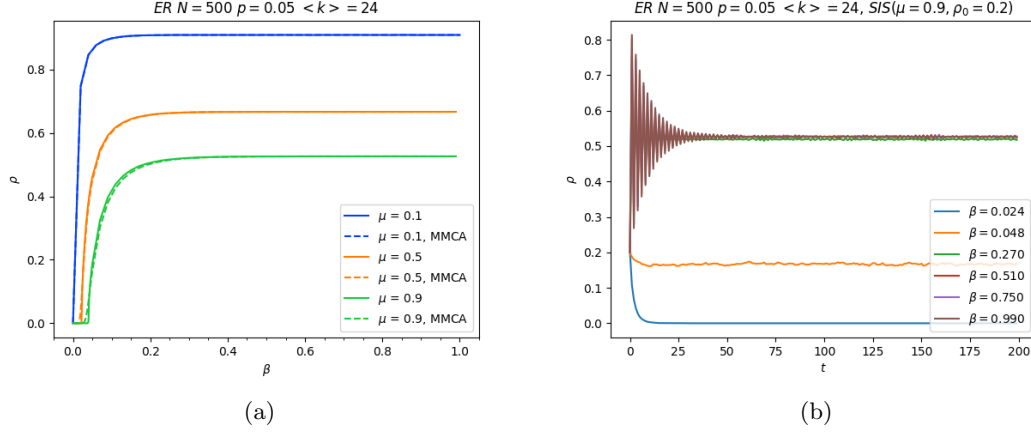
Figure 9: SIS epidemic model in a ER network with $N = 500$, $p = 0.05$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.9$.
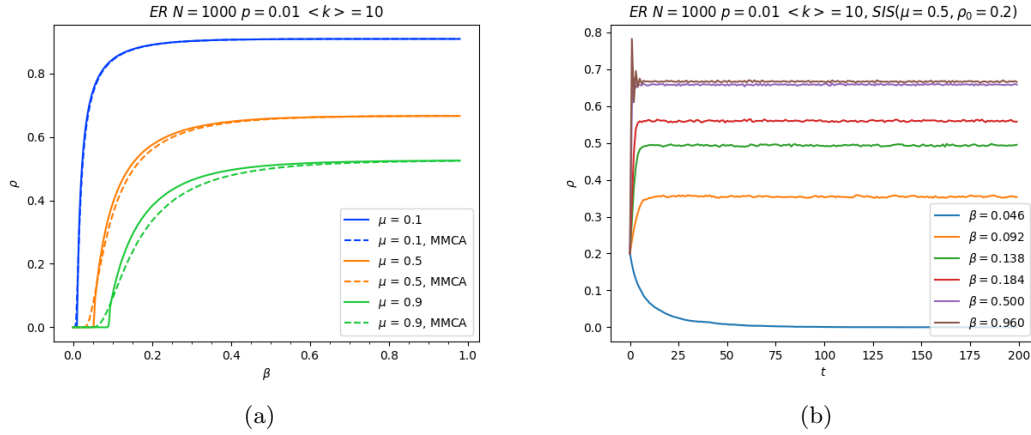


Figure 10: SIS epidemic model in a ER network with $N = 1000$, $p = 0.01$. (a) Phase diagram for the SIS model. (b) Evolution of average $\rho$ in 100 Monte Carlo simulations using $\mu = 0.5$.

# References

[1] Sergio Gómez et al. "Discrete-time Markov chain approach to contact-based disease spreading in complex networks". In: *EPL (Europhysics Letters)* 89.3 (2010), p. 38009.

[2] Ryan A. Rossi and Nesreen K. Ahmed. "The Network Data Repository with Interactive Graph Analytics and Visualization". In: *AAAI*. 2015. URL: `https://networkrepository.com`.