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A4. Epidemic spreading on complex networks

Complex Networks (MAI)



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Abstract

The main objective of this work is to understand and implement the SIS model for the modeling of epidemics in different types of networks, with different parameters, as well as to observe which ones affect or disturb the system the most. As is well known, these types of models are very useful for understanding real problems such as pandemics and viruses that are constantly evolving, which facilitates the understanding and eventually the control of these types of diseases. In this approach, infections are called the disease that is lodged in an individual or in this case in a node and which is transmitted by contact.

For this project, said epidemic model is implemented and simulated by means of the Monte Carlo (MC) method and it was tested for four different models for generating random graphs, as well as for different parameters. We explore the effects of these variations on the obtained results of the network, and we do so by computing the average of the fraction of infected individuals, ρ , over the stationary state for each case.

The complete code can be found in our repository below:

https://github.com/EjbejaranosAI/Complex_Networks

Keywords: Complex networks, community detection, optimization of modularity, network analysis, Networks representation.

1 Methodology description

For this project, the process was structured in the following parts:

- **Problem Statement:**

In this project, a typically used model within the discipline of epidemiology is implemented to illustrate the application of complex network dynamics: the Susceptible-Infected-Susceptible (SIS) epidemic spreading model.

The details of the SIS model are described further down in section 2. Nevertheless and as a quick overview, the problem here presented focuses on analysing how the infection probability of a disease affects the proportion of the infected population once the stationary state has been reached, that is, β versus ρ . In parallel, several cases of the model are developed, varying the different parameters of the problem each time in order to study their effects on the results. Thus analogous plots of $\rho(\beta)$ are generated for the different cases, which are then discussed in sections 3 and 4 below.

- **Decisions:** The moment when we approached this problem, we found several contradictions while making certain decisions. Some of them addressed aspects such as the following:

- Parameters: One of the crucial decisions for this lab was the parameter μ , and it was calculated for values of 0.1, 0.5 and 0.9, and at the same time, for each combination a beta list from 0 to 1.02 with a spacing of 0.02, and all these combinations were tested for 5 different random graphs with different parameters.
- The execution time for each network together with all the possible combinations was a big problem and that is why it was tried to take into account using parameters with less complexity and it was tried to implement a parametrization in the code to optimize the performance of the code and reduce its time.

- **Software:** As software used for this project, it is mentioned that Python was chosen as the main language, because it is the most comfortable for us, which allows us to develop our ideas and knowledge more quickly and without much complexity, also adding that the time of development and deployment is less compared to others. On the other hand, as is well known, the execution time and performance is lower than others but it compensates due to its great simplicity and resources. As principal libraries used, it was implemented Igraph to manage and create random networks, and also we used numpy for the vectorization, indexing and manage the array computing. Also it is used another libraries as random, matplotlib and glob.

- **Analysis:** The main analysis of the project consisted of taking the β (infection probability) of a susceptible individual (S) when contacted by an infected one (I) and comparing it with the average fraction of infected nodes in the network.
- **Coordination:** The coordination of this project was done in the following manner:
 - Initial Investigation.
 - Identification and distribution of tasks.
 - Initial tests.
 - For each network, perform the corresponding partition and evaluation.
 - Merge the results.

2 SIS epidemic Model

In the context of epidemiology, the spread of an infectious disease can be modelled through robust analytical and numerical frameworks. The three most frequently used models for that purpose are the so-called Susceptible-Infected (SI), Susceptible-Infected-Susceptible (SIS) and Susceptible-Infected-Recovered (SIR) models. The three of them are based on the same compartmentalization, meaning that each individual can belong to one of the following *compartments* or *states* at a given time, t :

- **Susceptible, S :** the individuals that are healthy and thus, prone to becoming infected when they get in contact with an infected individual. Given a population of N individuals, the fraction of the susceptible population can be written as $s(t) = S(t)/N$.
- **Infected, I :** the individuals that are infected and thus, can pass the disease on to the susceptible ones when they get in contact with them. Considering the same population as before, the fraction of the infected population is referred to as $\rho(t) = I(t)/N$.
- **Recovered, R :** the recovered individuals are those who have developed immunity after being infected and therefore can not be infected again.

For the model of our interest, the SIS model, only the two first states, S and I , are used to describe the evolution of the disease through the population. Starting with a certain initial fraction of the population being infected, $\rho(0) = \rho_0$, it is assumed that each one of them has a probability of β of infecting a single healthy or susceptible individual at the moment they come into contact. Meanwhile, the infected individuals are able to spontaneously recover at a fixed rate of μ (meaning that at time step t , the individual recovers with probability μ). This model is a good approximation to many real pathogens, where in spite of patients being able to recover thanks to either treatment or their own immune system, they are not free of becoming infected again.

Simple analytical expressions can be developed to describe the three models mentioned above (SI, SIS and SIR) by making a series of assumptions. In this way, these models are able to predict different long-term outcomes, which give us a general idea of what to expect in each model: in the SI model the totality of the population becomes infected eventually, $\rho(\infty) = 1$; in the SIS model the fraction of infected individuals can either converge to a finite number, $\rho(\infty) < 1$, or die out, $\rho(\infty) = 0$ (depending on the β to μ ratio); in the SIR model every individual in the population recovers given sufficient time, thus $\rho(\infty) = 0$. Said assumptions that enable the most elemental form of the implementation for these models, can be formulated as the *homogeneous mixing hypothesis*, according to which any individual can come into contact with any other individual that exists in the same network and every individual has the same constant number of contacts. However, these approximations can be very far from truth when considering a pathogen spreading through a much more complex contact network, where not all individuals are connected among each other, and individuals with more links are more likely to be in contact with an infected individual. These characteristics can be incorporated into the study my means of using complex networks with underlying community structures. To be able to implement this model in such a manner, each individual is represented by a node that exists inside a complex network where the different communities are represented [5].

3 Results

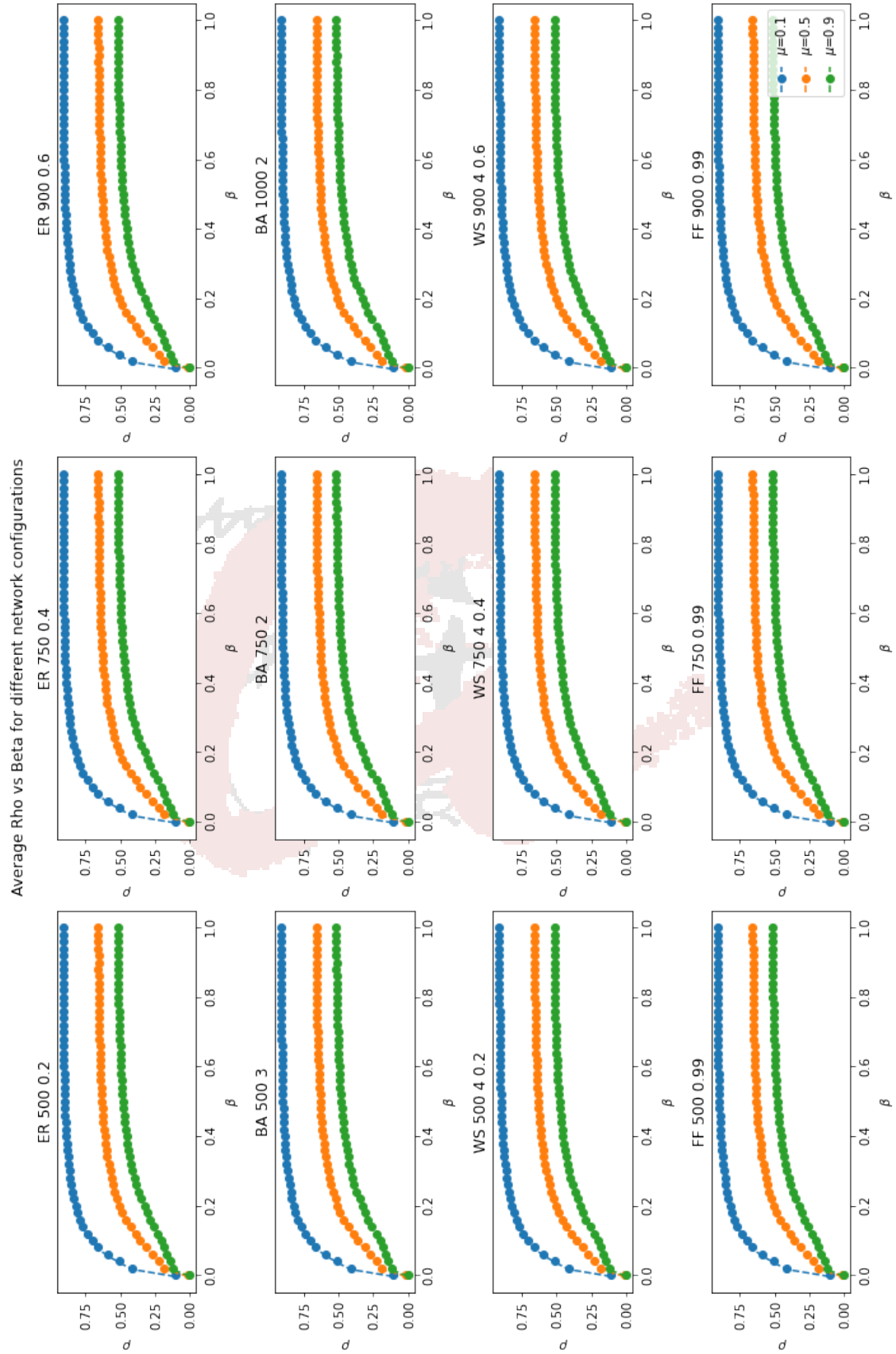


Figure 1 – Average Rho vs Beta for different network configurations

4 Discussion

As it is observed in figure 1, the average rho was obtained, again the Beta for the Erdos, Barabasi, wats and forest fire models generators in the graphs. On other hand, all of these networks was computed for 0.1, 0.5 and 0.9 μ , and finally it was computed all of these parameters for many β values to obtain the desire graphic.

With the previous results, we can observe the difference between all the models and the behavior that are different between them, taking into account that have the same parameters, and only change the graph the are given for the generator.

References

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Appendix A. Implementation details

