

Monte Carlo simulation of SIS epidemic spreading

A Susceptible-Infected-Susceptible (SIS) epidemic spreading model is characterized by two parameters:

- μ : spontaneous recovery probability.
- β : infection probability of a susceptible (S) individual when it is contacted by an infected (I) one.

A typical set-up for an SIS dynamics in a complex network consists in supposing that every node is an individual which can be in either state S or state I, the time is discrete, and at each time step each node contacts (synchronously) with all of its neighbors.

We are interested in the calculation of $\langle p \rangle$, the average fraction of infected node in the network. This requires two kinds of averages:

- For one simulation, average of $p(t)$ over many time steps, when the systems has reached the stationary state.
- Repeat the simulation many times to average over initial conditions and temporal evolutions.

Therefore, the final value of $\langle p \rangle$ is an average (over repetitions) of averages (over time steps).

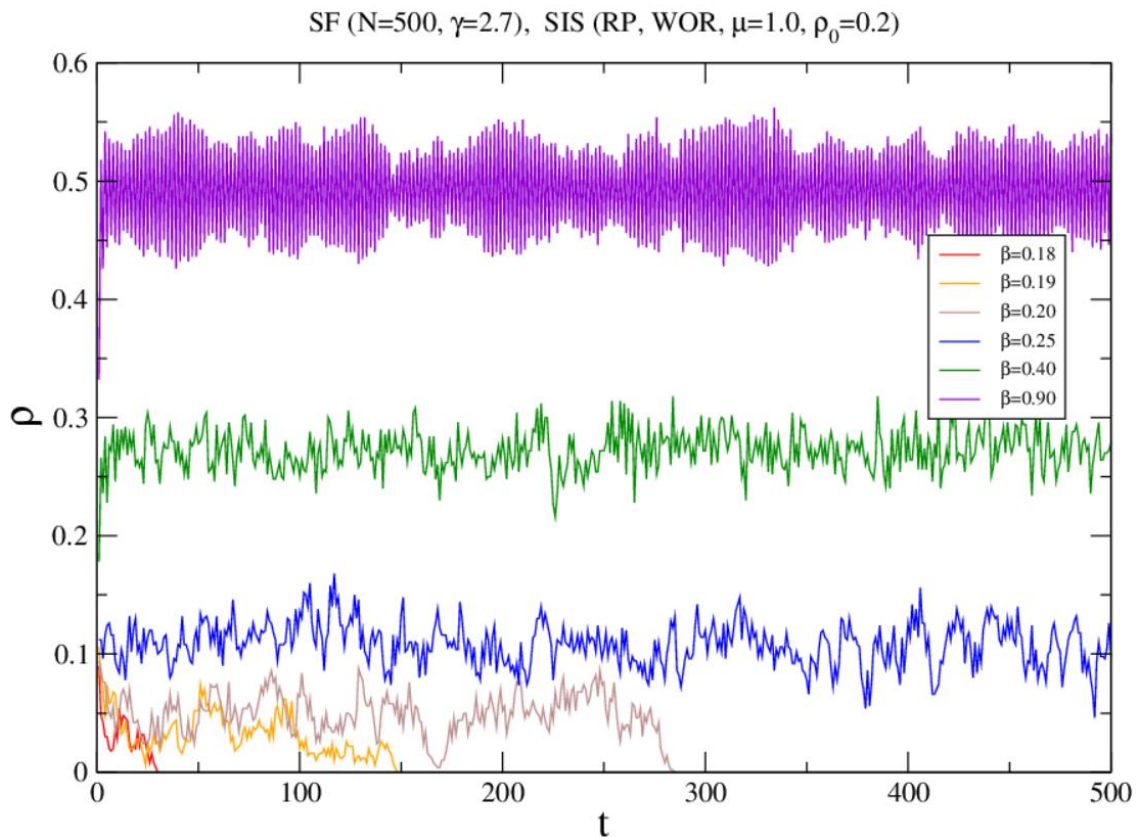
The Monte Carlo simulation requires some extra parameters:

- N_{rep} : number of repetitions of the simulation.
- $p(0)$: initial fraction of infected nodes.
- T_{max} : maximum number of time steps of each simulation.
- T_{trans} : number of steps of the transitory.

As a general guide, we could select values for these parameters as follows:

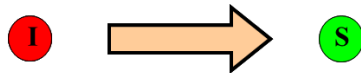
- $N_{rep} = 100$ (could be reduced to 50 if the simulation takes too much time).
- $p(0) = 0.2$: this means a 20% probability of each node being initially infected.
- $T_{max} = 1000$: simulations of 1000 time steps.
- $T_{trans} = 900$: the first 900 time steps are considered as transitory, and the stationary is formed by just the last $T_{max} - T_{trans} = 100$ steps (the ones used for the calculation of $\langle p \rangle$).

For the last two parameters it would be better to adjust them using a simulation: plot $p(t)$ to be sure that, after T_{trans} time steps, the value of p has not a clear tendency to increase or decrease, despite the oscillations due to the stochastic nature of the simulation process.

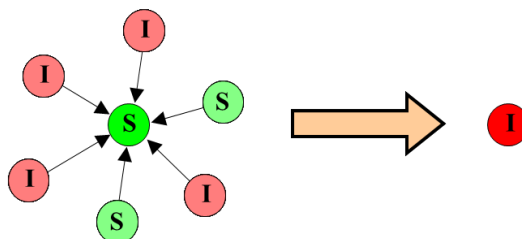


We need now to explain how it works a single time step of the SIS simulation:

1. For each infected node at time step t , we recover it with probability μ : we generate a uniform random number between 0.0 and 1.0, and if the value is lower than μ the state of that node in the next time step $t+1$ will be susceptible, otherwise it will remain being infected.



2. For each susceptible node at time step t , we traverse all of its neighbors. For each infected neighbor (at time step t), the reference node becomes infected with probability β . For example, if node A has 6 neighbors, 4 of them being infected, we repeat 4 times the generation of a random number and its comparison with β . If at the third attempt the random number is lower than β , node A will be infected in the next time step $t+1$, and we may stop the generation of the remaining random number; otherwise, node A will continue to be susceptible at time step $t+1$. Of course, the larger the number of infected neighbors, the larger the probability of becoming infected.



We are interested in the value of $\langle \rho \rangle$ as a function of β (keeping μ fixed), to obtain plots like the following one:

