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 , the average fraction of infected node in the network. This requires two kinds of averages:

- For one simulation, average of $\rho(t)$ 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 $\langle \rho \rangle$ is an average (over repetitions) of averages (over time steps).

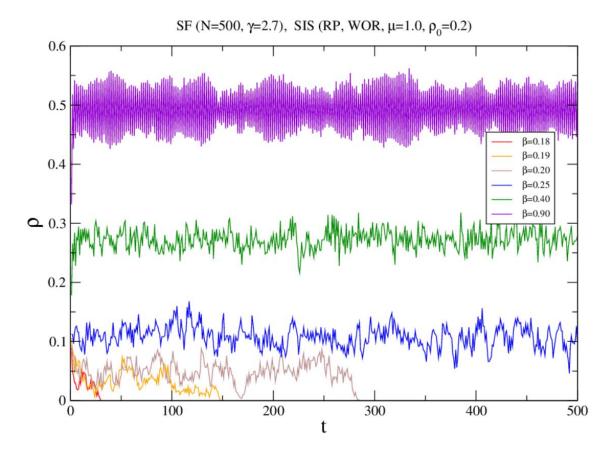
The Monte Carlo simulation requires some extra parameters:

- N_{rep} : number of repetitions of the simulation.
- ρ(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:

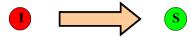
- $N_{rep} = 100$ (could be reduced to 50 if the simulation takes too much time).
- $\rho(0) = 0.2$: this means a 20% probability of each node being initially infected.
- T_{max} = 1000: simulations of 1000 time steps.
- T_{trans} = 900: the first 900 time steps are considered as transitory, and the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

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

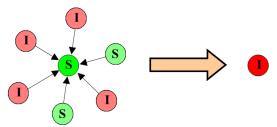


We need now to explain how it works a single time step of the SIS simulation:

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 as a function of β (keeping μ fixed), to obtain plots like the following one:

