

SIR dynamics with Vaccination in a large Configuration Model

Emanuel Javier Ferreyra, Matthieu Jonckheere, Juan Pablo Pinasco
Universidad de Buenos Aires

The main objective is to analyze how the vaccination process interferes with the spread of a disease, starting from the studies carried out in models of this type but without vaccinations. For this, we will work with a population whose interactions are given by a Configuration Model graph.

At any moment of a continuous time period, individuals can be in any of the four states: Susceptible, Infected, Recovered or Vaccinated. Following a Poisson process, the agents interact with their neighbors in the graph and transmit the disease from the Infected ones to the Susceptibles. In addition, there will be a vaccination strategy consisting on the rate at which an agent in Susceptible status transitions to Vaccinated and that will depend on the connectivity of the node.

We focus on four measures of the connectivity network and we prove the convergence of empirical measures to a fluid limit determined by a system of countable differential equations showing the dependency of the degree distribution in the spread of the disease.