STOCHASTIC DYNAMICS IN EPIDEMIC NETWORKS

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INTRODUCTION

Being healthy is one of the big concerns of each individual, but that has been influenced not only by individual health and life style but also by population health. The spreading and dynamics of a disease within a population is the subject of many studies. To model the progress of an epidemic in a large population, individuals have been classified in two or more groups based on the behavior of disease. A very simple model groups the population into three different compartments: Susceptible, Infected, and Recovered. The contact network, disease transmission and recovery rate play an important role to model the system in order to estimate the time of disease outbreak and the basic reproductive ratio of the disease virus. These two concepts are important for applying preventive care such as vaccination or closing public places. These preventive methods change the connectivity or transition rates over time.

The following ordinary differential equations describe the SIR model. This model implies fully conected network whose transition and recovery rates are constant.

$$\frac{dS}{dt} = -\beta S I$$

$$\frac{dI}{dt} = \beta S I - \gamma I$$

$$\frac{dR}{dt} = \gamma I$$

S: Number of uninfected individuals who are susceptible to disease.
I: Number of infected individuals who can spread the disease.
R: Number of recovered individuals who are not able to be infected again.
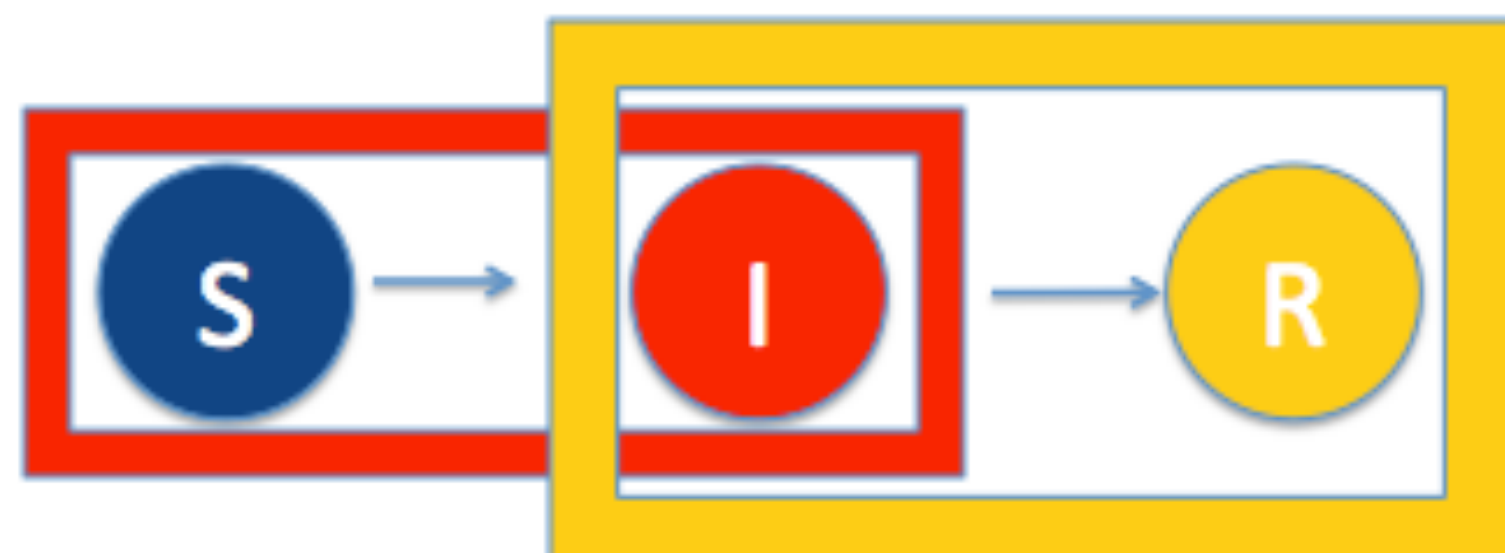*N: Population size.*
N=S+I+R.

Fig1: SIR Model

In Figure 1 there are two processes that describe the model states (S, I, R). Switching between infection process and recovery process is been dictated by an arbitrary infection threshold.

Infection process:
   States and probabilities:
     S: P(S) & I:P(I)   P(S)+ P(I)=1

Recovery process:
   States and probabilities:
     I: P(I)   &   R:P(R)   P(I)+ P(R)=1

To model and study the dynamics of this system, I have taken the population contact network into account. The transition and recovery rates are an unique random variables.

I have formulated the model as a Kolmogorov forward equation and calculated the probability of being in each state for each individual at any time step.

$$P_{n+1}(I) = \delta\left(P_n + \sum_j \beta_i C_{ij} P_n(I)_j\right) + (1-\delta)(P_n(I) - \gamma_i P_n(I))$$

$$\delta = \begin{cases} 1, & \text{if } a \geqslant \text{infected threshold,} \\ 0, & \text{otherwise.} \end{cases}$$

β_i:Transition rate, C_{ij}:Connection, γ_i:Recovery rate

Result

Figure 2 shows the course of an epidemic in a population of size N=200. Shortly after the begin of the epidemic the number of infected individuals increases while the number of susceptible decreases until the number of infected individuals reaches a peak, which is called the outbreak size. After that peak the number of infected individuals declines because they recover and also because the number of susceptible individuals is diminishing.

Figure 3 shows propagation of the disease in the population contact network.

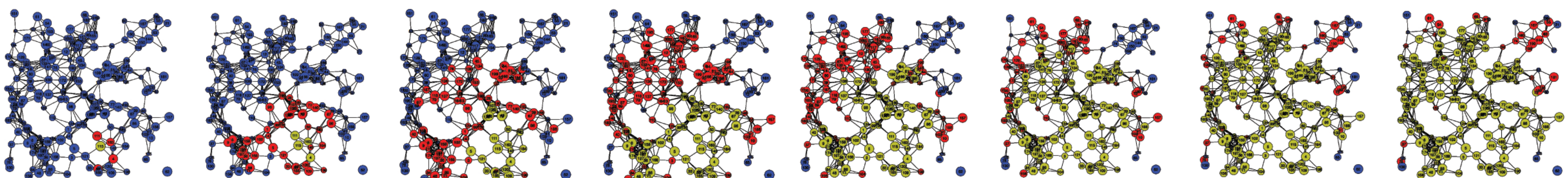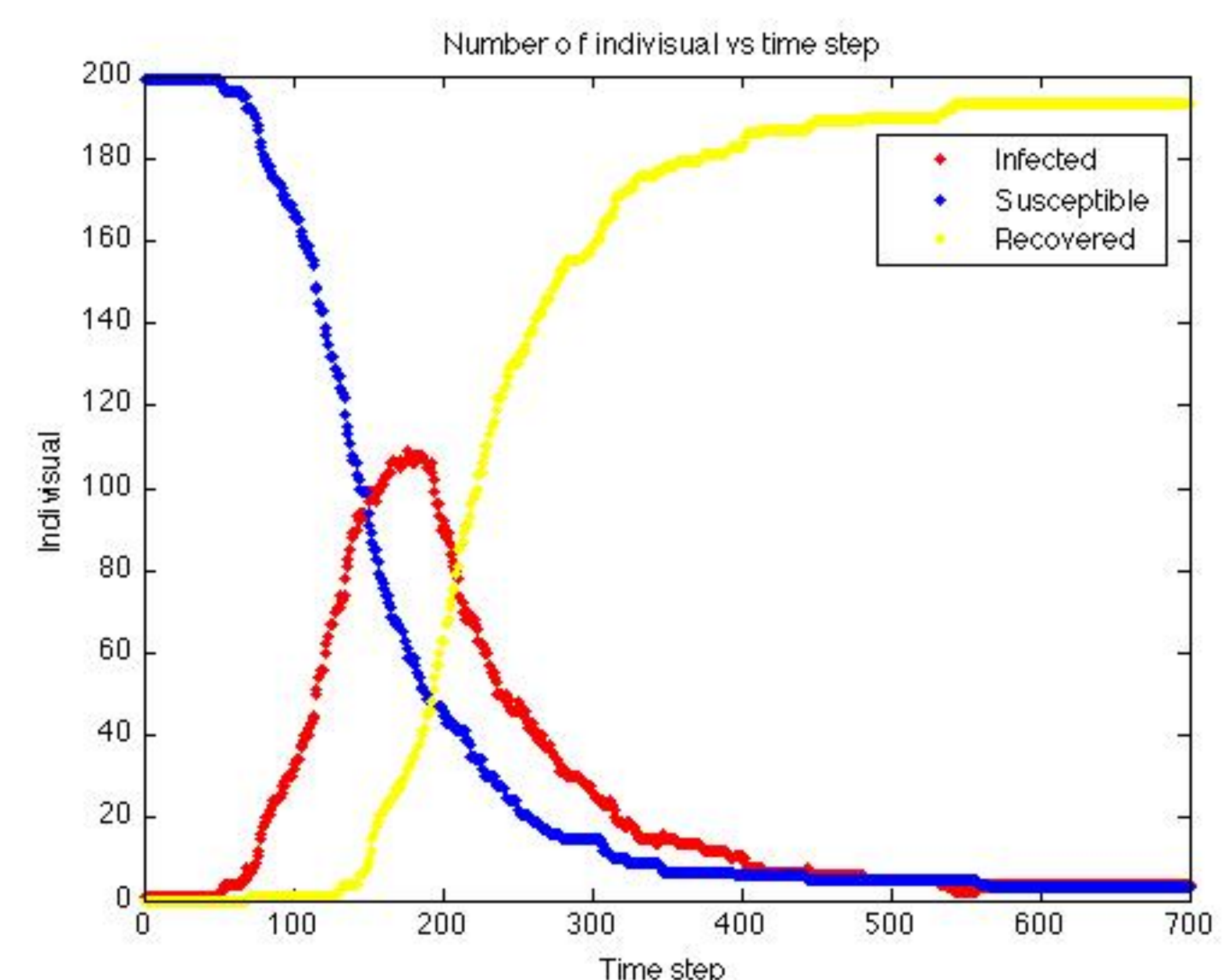*Fig2: course of an epidemic*

Fig3: Propagation of disease in population
Blue: Susceptible   Red: Infected   Yellow: Recovered
Edges: Population Connectivity
Node's size : Disease transition rate
The figures were taken at times: 50, 100, 150, 200, 250, 300, 350, 400.

REFERENCES

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