Modeling an Epidemic in a Population with Complex Contact Network

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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. A standard model in epidemiology is the SIR model, in which individuals are classified in three components (**S**usceptible, **I**nfected, **R**ecovered). Commonly, the contact among individuals and the disease transmission rate is considered the same during the epidemic. Contact network and disease transmission play an important role to model the system in order to estimate the time of disease outbreak, basic reproductive ratio of the disease virus, etc. These two concepts are important for applying preventive care such as vaccination, and closing schools. What preventive methods do is changing the connectivity or transmission rates over time.

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Susceptible  ───────▶  Infected  ───────▶  Recovered
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Fig1: SIR Model

To model and study the dynamics of this system, I have combined the SIR model, which can be represented as a set of ordinary differential equations, with a Markov chain-based model, which represents the contact network as a large transition matrix among individuals.

SIR Model:

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

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

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

S: Number of individuals who not yet infected or are susceptible to disease.
I: Number of individuals who have been infected with the disease and can spread the disease.
R: Number of individuals who have been infected and recovered from the disease and are not able to be infected again.
N: Population size.
N=S+I+R.

Markov chain:

$$Pr(j|i) = P_{i,j}$$

P_{ij} is the probability of movement (transition) from state i to state j.

If X_{n+1} and X_n are two consecutive state vectors of a Markov chain with transition matrix P, then

$$X_{n+1} = P X_n.$$

Therefore the continuous time markov process and the transition between different states can be described by the Kolmogorov equation:

$$\dot{X} = P X$$

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$$\frac{d(XI)}{dt} = P * XS - XR$$

XI(t): V_{nx1} Probability each person is Infected at time t.

$$\frac{d(XS)}{dt} = -P * XS$$

XS(t): V_{nx1} Probability each person is Susceptible at time t.

$$\frac{d(XR)}{dt} = L * XI$$

XR(t): V_{nx1} Probability each person is Recovered at time t.
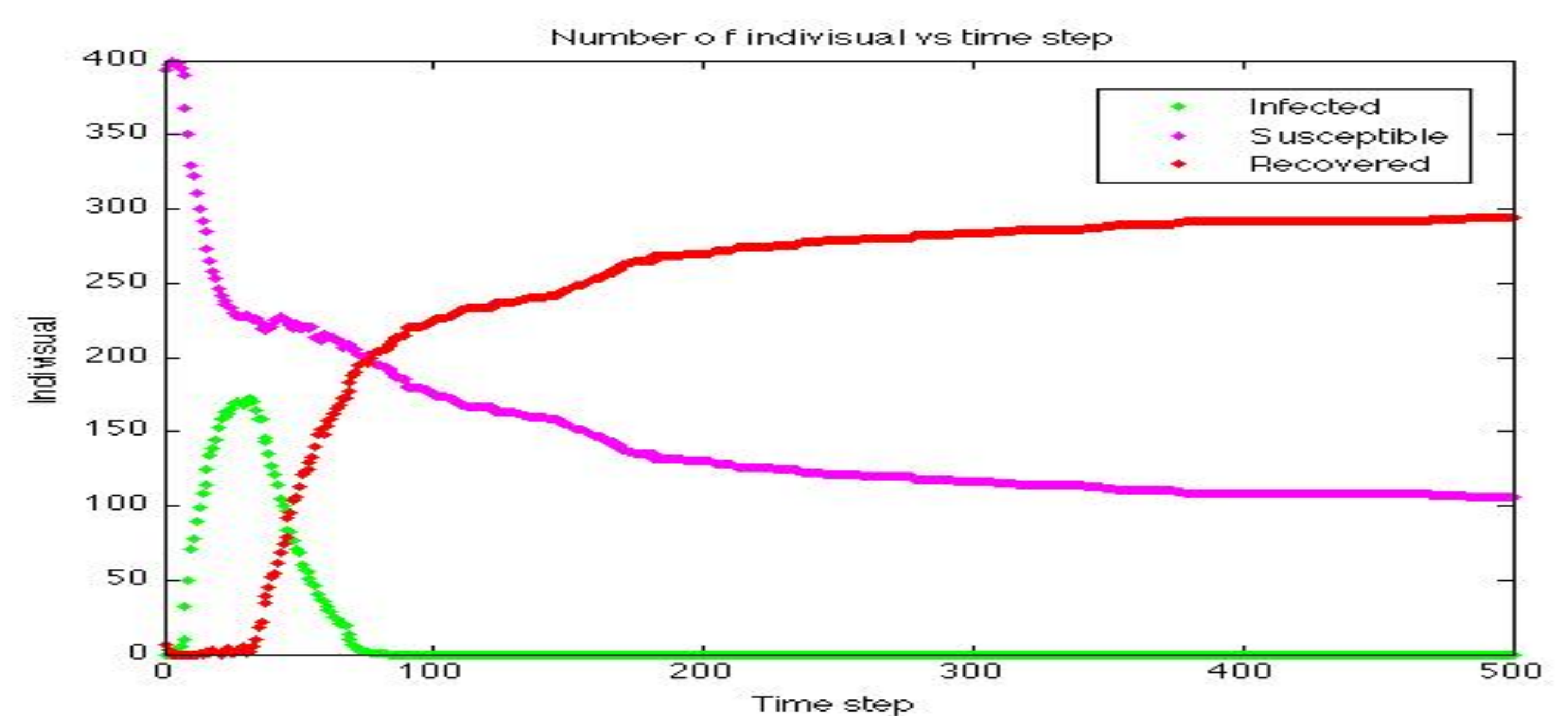

Fig2: Number of People in each state over time

The code is been run for different simulated network models: (a) Erdos-Renyi random graph (ER) , (b) Watts-Strogatz graph (WS) and (c) Barbasai-Albert graph (BA).
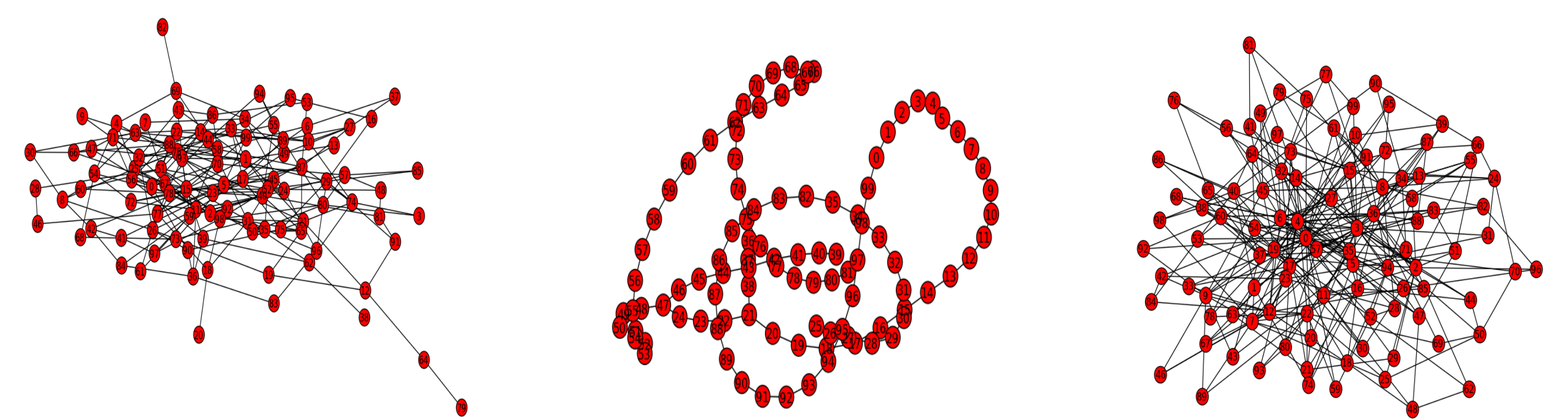

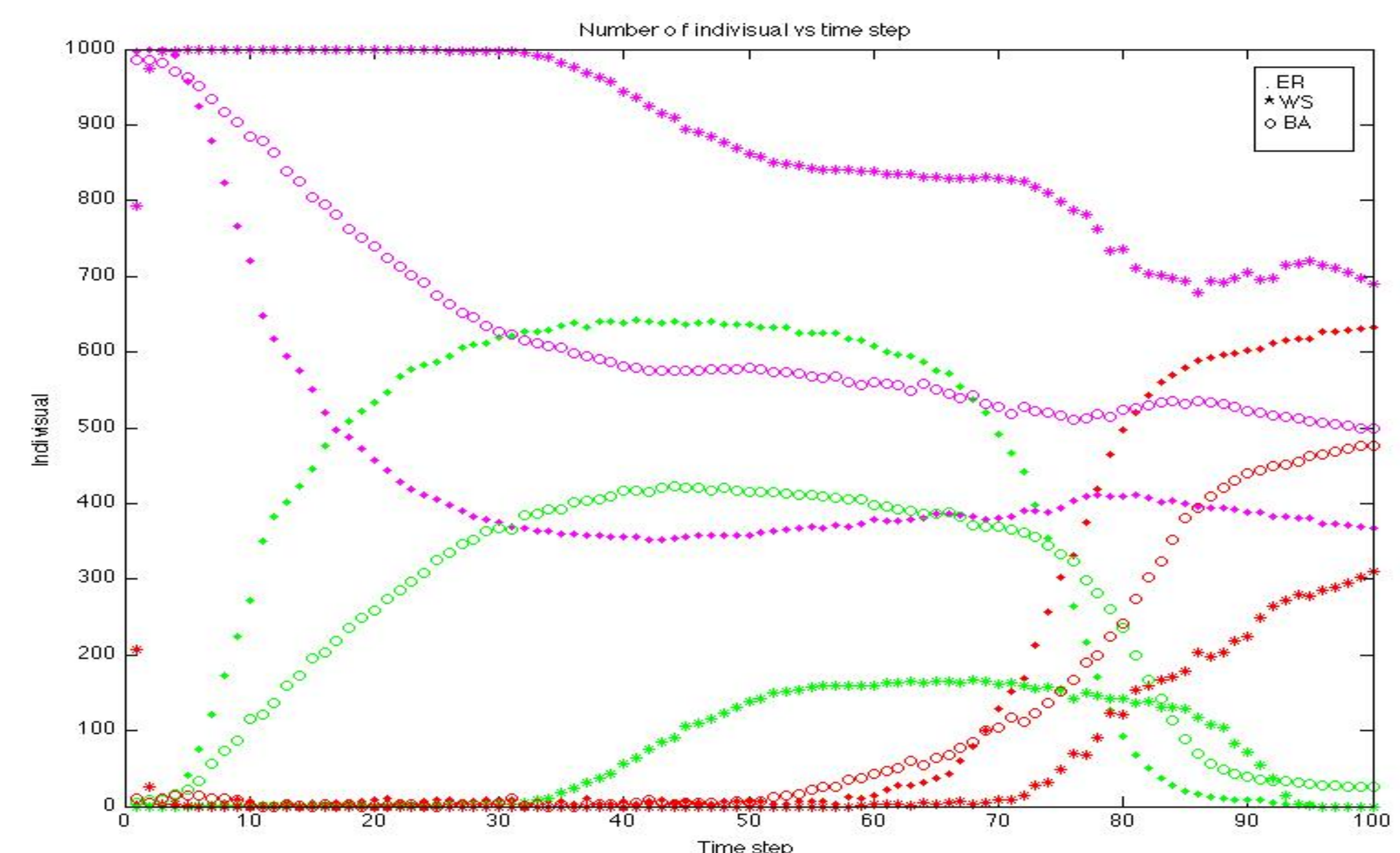*Fig3: left: Erdos , middle: Watts, Right: Barbaras network*

Fig4: Number of People in each state over time for three networks

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