STOCHASTIC DYNAMICS IN EPIDEMIC NETWORKS

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INTRODUCTION

Human life and diseases are inseparable. Diseases can be caused by our own bodies as they age and degenerate or by infectious pathogens. Our study is about infectious diseases, such as flu or sexually transmitted diseases. The simple model of progress of an epidemic in a large population divides the population into three different compartments: Susceptible, Infected, and Recovered (SIR). There are several important factors on modeling epidemic diseases such as the structure of the population representing the possible contact among individuals and the virus transmission, the time to recover from the disease, and life history of the virus affecting incubation time and infectiousness. The contacts can be modeled as a weighted, static or dynamic network; the virus transmission can be modeled as transition rates of becoming infected when in direct contact with an infectious person; the recovery can be expressed as rate at which the individual heals and becomes resistant to the disease.

Method

We have used weighted dynamic networks as a representation of population structure and we represent these as weighted adjacency matrices. The transition and recovery rate are considered as independent random variables. The incubation times are also arbitrary variables based on the virus and disease behavior.

We have used the continues time Markov process concept as well as forward Kolmogorov equation to formulate our model. The result is as a system of differential equations that describe the time-evolution of the probabilities of interest. Each individual in the network is represented by 3 probabilities or state vectors:
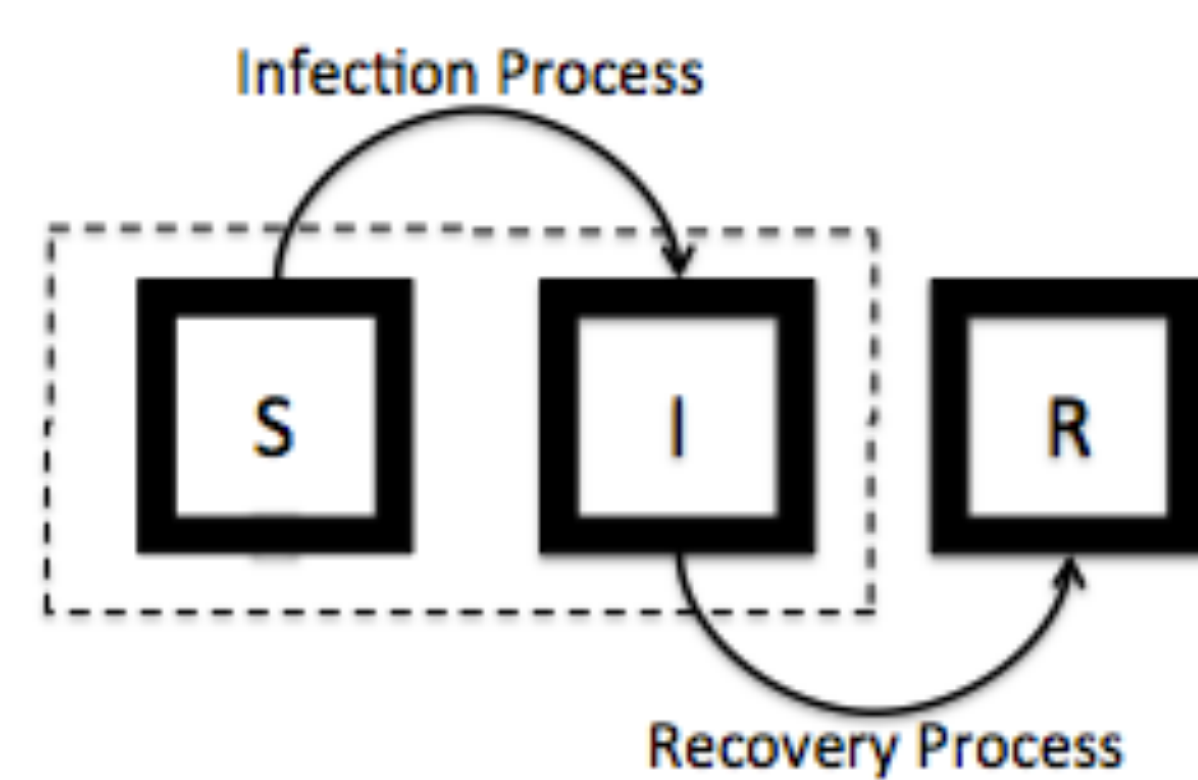
$$P_i = [P_{I,i}, P_{S,i}, P_{R,i}]$$

We rearrange the individual's probability into 3 state vectors:

$$P_I = [P_{I,1}, P_{I,2}, ..., P_{I,N}]$$
$$P_S = [P_{S,1}, P_{S,2}, ..., P_{S,N}]$$
$$P_R = [P_{R,1}, P_{R,2}, ..., P_{R,N}]$$
$$P_{R,i} = 1 - (P_{I,i} + P_{S,i}).$$

Infection Process

Recovery Process

Each individual is in one of the processes at each time step, so we only need to calculate one probability per person per time.

$$\frac{d(P_I)}{dt} = (\sum_i \sum_j \beta_i C_{ij} (P_I)_j),$$

$$\frac{d(P_R)}{dt} = -\gamma_i P_I.$$

β is the transition rate. γ is the recovery rate.

By combining, we get:

$$\frac{d(P_I)}{dt} = \delta(\sum_i \sum_j \beta_i C_{ij} (P_I)_j) + (\delta - 1)(\gamma_i P_I)$$

$$\delta = \begin{cases} 1 & \text{if } \frac{P_I}{\tau_{SI}} \leqslant 1, \\ 0 & \text{otherwise.} \end{cases}$$

τ_{SI} is the incubation period of the infection process.

R0 Formulation

The growth of a disease is usually expressed by the basic reproduction ratio R0 which is the average number of additional infections caused by a newly infected individual. The epidemic threshold is the separation point where a disease dies out or where it grows exponentially, it is at R0=1.

The mean degree $<\kappa>$, and mean-square degree $<\kappa^2>$ of a network and the transition and recovery rate have been used to formulated R0, but $<\kappa>$ and $<\kappa^2>$ can be the same for two networks even though they have different epidemic behavior, thus the standard R0 is sometimes inaccurate as a predictor of the epidemic threshold. We formulate a more accurate R0 by using another property of connectivity network in addition to what other methods have used. By using Singular Value Decomposition methods, the matrix A can be written as:

$$A = U \Sigma V^T$$

Matrix A can also be viewed as writing A as the sum of rank one matrices

$$A = \vec{u_1}\sigma_1 \vec{v_1}^T + \vec{u_2}\sigma_2 \vec{v_2}^T + ... + \vec{u_r}\sigma_r \vec{v_r}^T = \sum_{i=1}^{r} \vec{u_i}\sigma_i \vec{v_i}^T$$

By truncating this series after p terms, meaning that using the first p largest eigenvalues, we have an approximation to **A**, that captures the most significant features of the data. The rate of change is been calculated using the derivative definition. The slope m of the line through the first p eigenvalues is been used a metric of the rate changes. Therefor the R0 is been formulated as

$$R0 = \frac{\beta}{\beta + \gamma} \frac{\langle k^2 \rangle - \langle k \rangle}{\langle k \rangle} \frac{1}{m}.$$
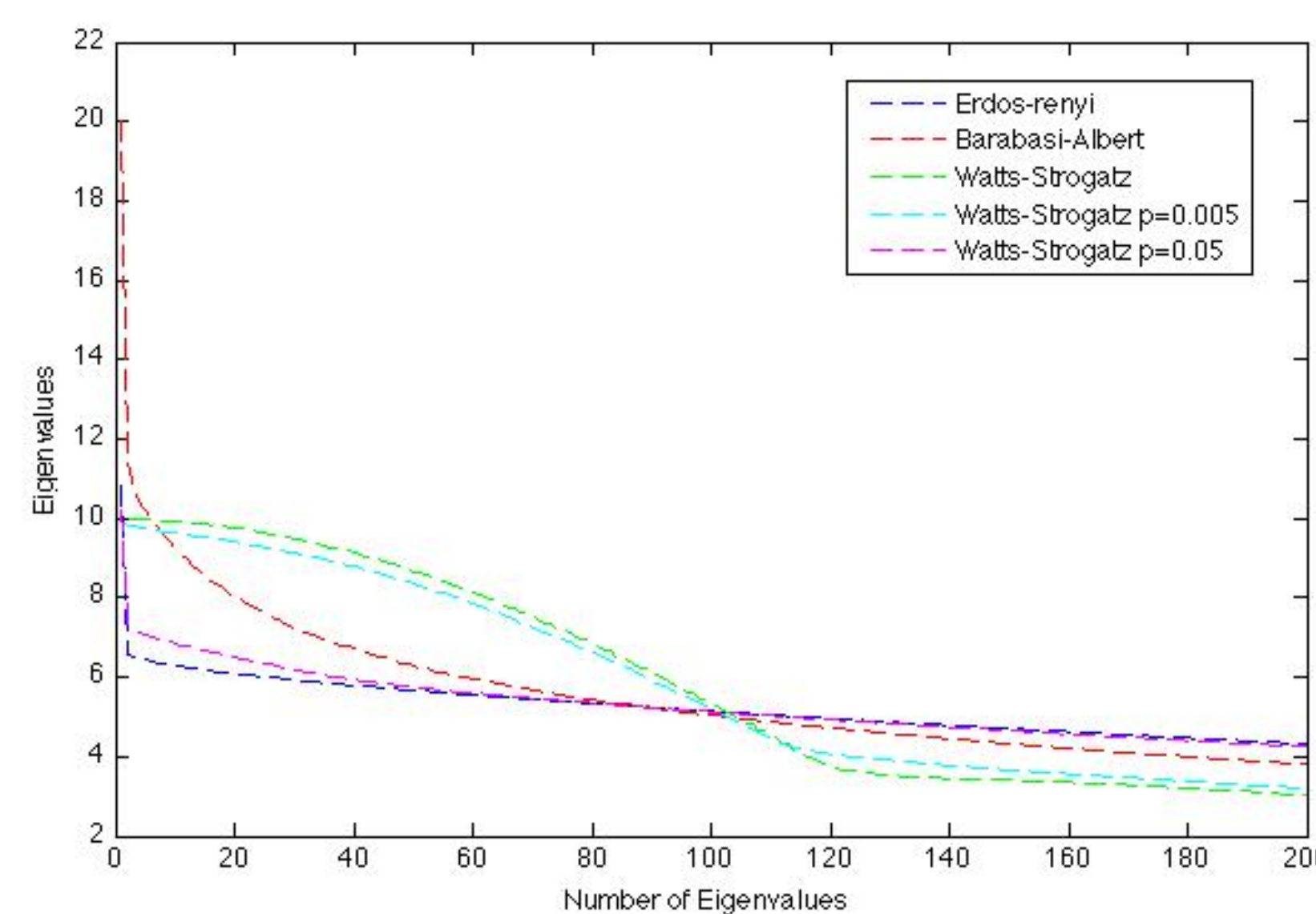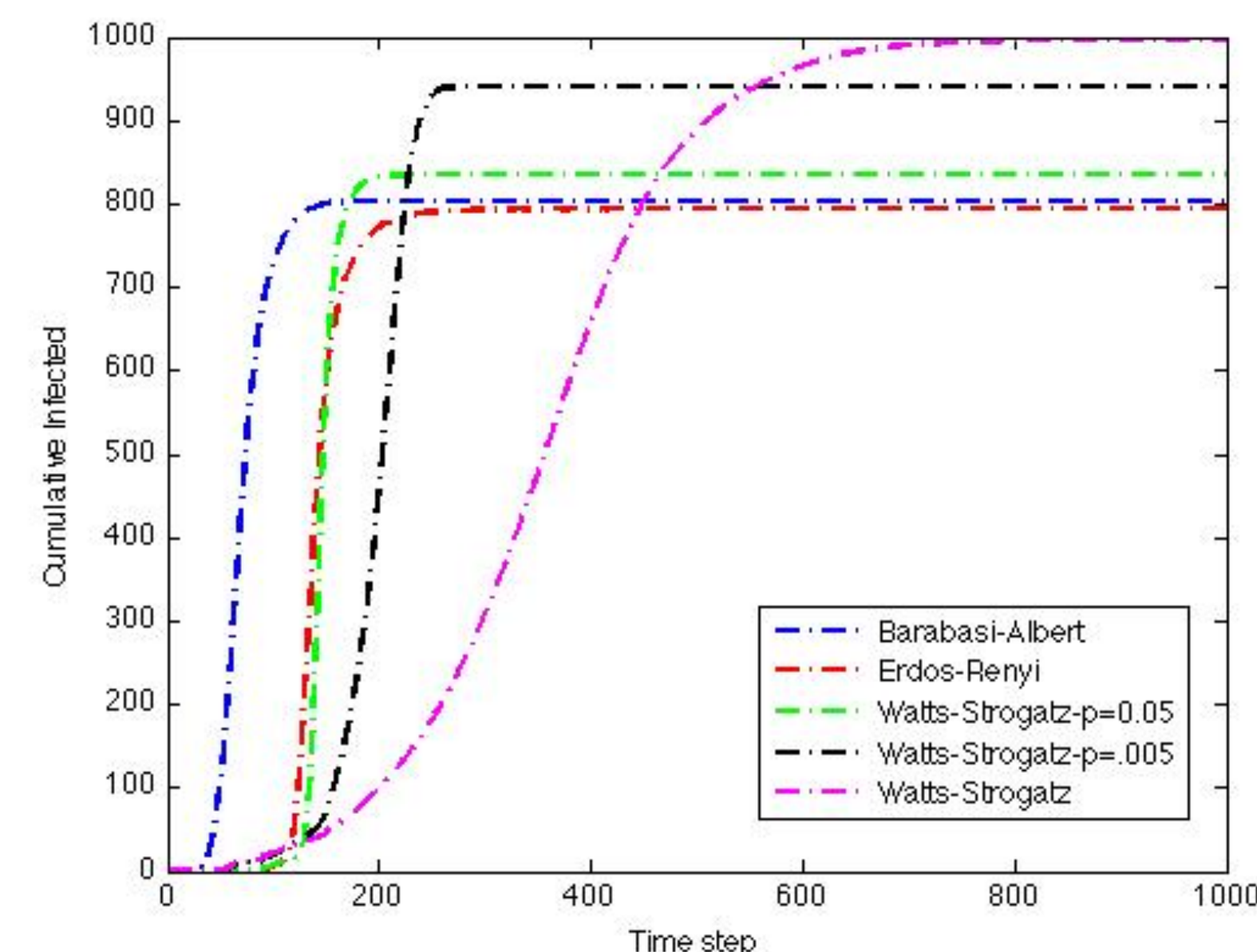

Fig1: Eigenvalues of all Random Networks   Fig2: Course of an epidemic

Table 1: Slope of the line of first (C-value) eigenvalues and comparison of our R0*

Networks	Cutoff values	Slope of the line	R0	R0*
Barabasi-Alber	31	-0.4336	1.67	3.87
Erdos-Renyi	11	-0.4806	0.809	1.63
Watts-strogatz P=0.05	22	-0.18880	0.7545	3.9961
Watts-strogatz P=0.005	46	-0.0343	0.7272	21.20
Watts-strogatz	7	-0.0109	0.7272	66.71

REFERENCES

1. Karrer, B. and Newman, M. E. J., 2011 Competing epidemics on complex networks. Physical Review E 84.
2. Erdős, P., Renyi, A., 1959 On the evolution of random graph. Publicationes Mathematicae 6: 290-297.
3. Barabasi, A. and Albert, R., 1999 Emergence of scaling in random networks. Science 286: 509-512.
4. Watts D., Strogatz S., 1998 Collective dynamics of `small-world' networks. Nature 393.