

Numerical Studies on the Epidemic Spreading on Correlated Networks

Jian Huang¹, Jiazeng Wang¹, Zengrong Liu² *

¹Mathematics Department, Shanghai University, Shanghai. 200444, China

² Institute of systems biology, Shanghai University, Shanghai. 200444, China

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Abstract: Start from the network with given degree distribution and inter-connection probability matrix, we rewire the edges of network and get different correlated networks. And do the epidemic spreading on these networks numerically through Monte-carlo methods. The results show that the spreading threshold is not necessarily correlate to the type of connections of the network.

Key words: network; assortative and disassortative; epidemic spreading

1 Introduction

Many social, biological and communication systems can be properly described by complex networks, with individuals or agents represented by nodes and the interactions among them mimicked by links. Lots of these complex networks are not connected together as regular lattices or random graphs. They show abundant structure properties. In particular, small-world property[1] and scale-free degree distributions[2] appear as common features of many real-world networks. The studies of complex networks have attracted a lot of interests within the physics community[3, 4]. One of the ultimate goals in statistic physics is to understand and explain how these structure affect the dynamical processes built upon them, phase transitions and critical phenomena[5, 6, 10].

As one of the typical cases of interacting particle systems on networks, epidemic spreading has been studied intensively. Many recent works on epidemic spreading, mainly focus on how the combination of the properties of the disease and the topology structure of network to determine the dynamics of spreading, have present us many new knowledge in understanding of computer virus spreading and epidemiology[5–7, 11]. Using susceptible-infected-susceptible(SIS)[7] and susceptible-infected-removed(SIR) models[8, 14], it was shown that epidemic processes on scale-free networks with infinite size do not exhibit the threshold phenomenon typically seen in epidemiology: computer viruses can spread and persist even when the probability of transmission is vanishingly small[7, 8, 12, 13]. One way to reinduce the epidemic threshold is considering the finite size effects[9, 14].

Recently, it has been recognized that many of real-world networks possess, along with scale-free properties, nontrivial degree correlations[15, 16]. For instance, many social networks show the property of "assortative mixing", which means nodes are more preferably connect to nodes with similar degree. On the opposite side, many technological and biological networks show "disassortative mixing"; i.e., highly connected nodes are preferably connected to nodes with low degree[17, 18]. Several recent works are focused on the effects of degree correlations in epidemic spreading. Whereas the results are far from coincident.

Recently, we have find theoretically that connection correlations have no uniform effect on the epidemic spreading. In this paper, starting with an artificial network with degree distribution $P(k)$, we construct several kinds of networks through edge reconnection. And the epidemic spreading is done numerically.

* Corresponding author. E-mail address: zrongliu@online.sh.cn.

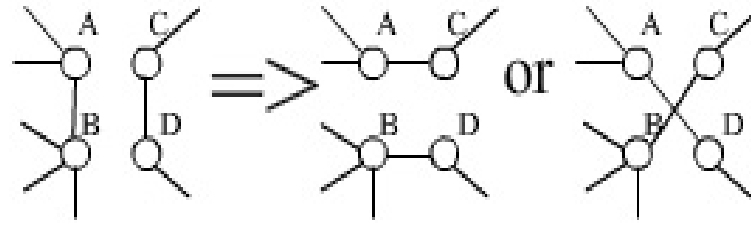


Figure 1: The rewiring of two edges.

2 Numerical simulation algorithm

Suppose there is a connected network of N nodes. $P(k)$ is the degree distribution of this network. We fix $P(k)$ as follows and it will never change.

k	1	2	3	4	5	6
P(k)	0.3679	0.3679	0.1840	0.0613	0.0153	0.0036

Thus we can calculate $\langle k^2 \rangle = \sum_k k^2 P(k) = 4.9882$, $\langle k \rangle = \sum_k k P(k) = 1.9990$, and $\frac{\langle k^2 \rangle}{\langle k \rangle} = 2.4954$. It is the comparing benchmark.

$P(k'|k)$ is the connection probability of the node of degree k and the node of degree k' . And the neighbor connection matrix A is defined as follows:

$$A = \begin{pmatrix} 1P(1|1) & 2P(2|1) & \dots & kP(k|1) & \dots & k_c P(k_c|1) \\ 1P(1|2) & 2P(2|2) & \dots & kP(k|2) & \dots & k_c P(k_c|2) \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1P(1|k') & 2P(2|k') & \dots & kP(k|k') & \dots & k_c P(k_c|k') \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ 1P(1|k_c) & 2P(2|k_c) & \dots & kP(k|k_c) & \dots & k_c P(k_c|k_c) \end{pmatrix}$$

According to matrix A , we can find that the average degree of the nearest neighbors of nodes with degree k is $k_{nn}(k) = \sum_{k'} k' P(k'|k)$.

The maximum of the absolute values of eigenvalue of A is denoted by Λ_m . Just as mentioned before, $\Lambda_m = \frac{\langle k^2 \rangle}{\langle k \rangle}$ if and only if the network is uncorrelated. If we rewire the edges of the network appropriately, the network will become correlated, and Λ_m will change accordingly. By comparison of Λ_m and $\frac{\langle k^2 \rangle}{\langle k \rangle}$, we can know the effects of the correlation of connection on the epidemic spreading.

We start with a network having positive relationship with a given neighbor connection matrix A . The rewiring process is as follows.

Step 1: Generate linking matrix which has the known degree distribution $P(k)$.

Step 2: Fix the degree distribution and modify the network construction through edge rewiring to make the network dis-assortative (or assortative). This step can be separated as follows.

(1) Find two nodes having relatively big degree (denoted by A, B) and two nodes having relatively small degree (denoted by C, D). Nodes A, B are connected together directly, also is nodes C, D . But there is no edge between nodes A, B and nodes C, D .

(2) Delete the edge between A, B and the edge between C, D . Then inter-change the nodes of two sides of these two edges. So we have two possible connections of the new network, see the construction shown in the Fig.1.

Since the original network is connected, there must exist at least one path between nodes A, B and nodes C, D . After the edges are rewired, there is at least one of the two constructions in Fig.1 that is connected. So we can assure that the originally connected network will be still connected.

(3) Compute the correlation coefficient C of $k_{nn}(k)$ and k of the network.

(4) Modify the network until no more nodes can be modified or we get the objective Λ_m .

Step 3: Then make numerical simulation of infection spreading on this network by Monte-Carl method.

Make one node infected randomly at time T_0 . At time T_{n+1} , the node infected at time T_n will infect other nodes linking with them in possibility λ , and at the end of time T_{n+1} , the nodes infected at time T_n will be removed. The process will end until no more nodes are infected. With the different possibility λ from 0 to 1, we get the different infective prevalence.

Use this process, we produce three kinds of networks, and do the spreading process on them.

3 Results

Here we set the network has $N = 1937$ nodes. Denotes three networks as G_1 , G_2 , and G_3 respectively, we have the following neighbor connection matrices.

$$A_{G_1} = \begin{pmatrix} 0 & 1.95 & 0 & 0 & 0 & 0.16 \\ 0.49 & 0 & 1.5 & 0 & 0.05 & 0.03 \\ 0 & 1.33 & 0 & 1.33 & 0 & 0 \\ 0 & 0 & 2.25 & 0 & 1.25 & 0 \\ 0 & 0.17 & 0 & 3.2 & 0 & 0.68 \\ 0.45 & 0.29 & 0 & 0 & 2.02 & 0 \end{pmatrix}$$

$$A_{G_2} = \begin{pmatrix} 0 & 1.58 & 0 & 0.01 & 0.79 & 0.29 \\ 0.40 & 0 & 1.5 & 0.31 & 0.11 & 0.03 \\ 0 & 1.33 & 0 & 1.33 & 0 & 0 \\ 0.00 & 0.47 & 2.25 & 0 & 0.05 & 0 \\ 0.76 & 0.41 & 0 & 0.13 & 0 & 0 \\ 0.83 & 0.33 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$A_{G_3} = \begin{pmatrix} 0 & 0.68 & 0.01 & 1.77 & 0.83 & 0.29 \\ 0.17 & 0 & 2.16 & 0.34 & 0.11 & 0.03 \\ 0.00 & 1.92 & 0.01 & 0.15 & 0 & 0 \\ 0.66 & 0.50 & 0.25 & 0 & 0 & 0 \\ 0.79 & 0.41 & 0 & 0 & 0 & 0 \\ 0.83 & 0.33 & 0 & 0 & 0 & 0 \end{pmatrix}$$

And three kinds of nearest neighbors $k_{nn}^{G_i}(k)$, $i = 1, 2, 3$. Thus we can identify correlation coefficient of $k_{nn}(k)$ and k of these three network: $C_{G_1} = 0.6898$, $C_{G_2} = -0.3$, and $C_{G_3} = -0.5$. So the first network G_1 is assortative, the second network G_2 and the third network G_3 are dis-assortative.

In another aspect, we calculate the maximum eigenvalue of A_{G_i} , that is $\Lambda_m^{G_1} = 3.0067$, $\Lambda_m^{G_2} = 2.5390$, and $\Lambda_m^{G_3} = 2.3182$. Compared with $\frac{\langle k^2 \rangle}{\langle k \rangle} = 2.4954$, we find that $\Lambda_m^{G_1} > \frac{\langle k^2 \rangle}{\langle k \rangle}$, $\Lambda_m^{G_2} > \frac{\langle k^2 \rangle}{\langle k \rangle}$, and $\Lambda_m^{G_3} < \frac{\langle k^2 \rangle}{\langle k \rangle}$.

Compared with the situation of pure randomly connected networks that the spreading threshold is just $\frac{\langle k \rangle}{\langle k^2 \rangle}$, we know that G_1 has positive effect on spreading and G_2 and G_3 have negative effect on spreading.

As the spreading rate λ increase from 0 to 1, we calculate the prevalence ρ and the derivative $\rho'(\lambda)$. The results are shown in Fig.2.

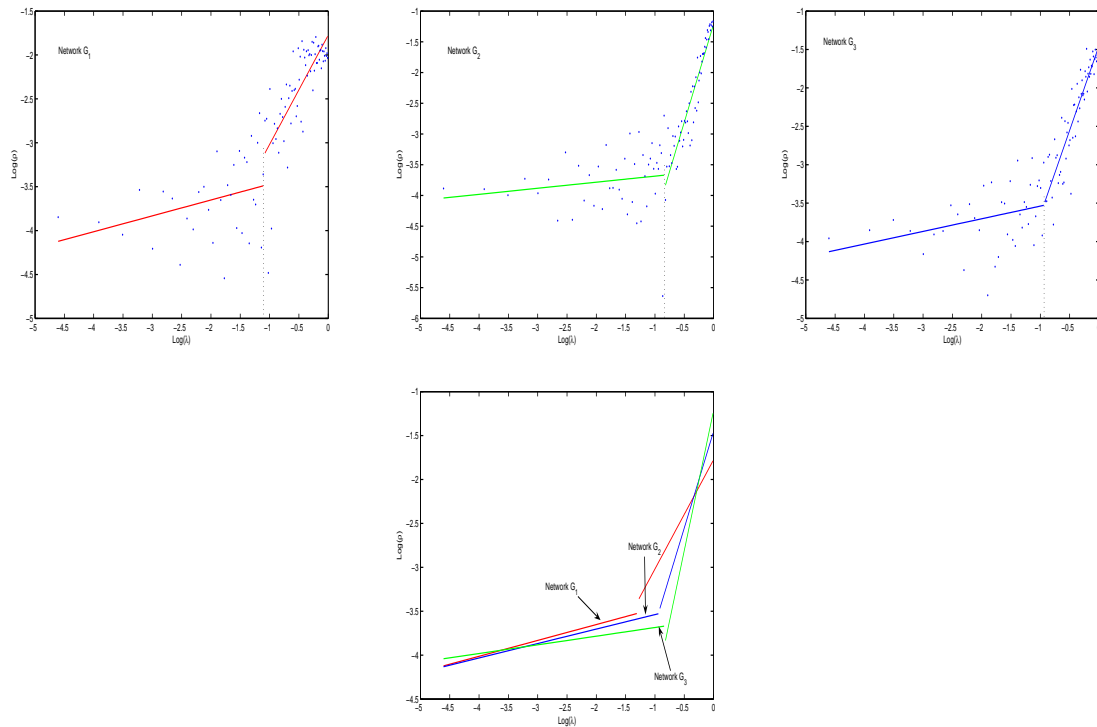


Figure 2: The results of spreading in three networks.

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