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The spread of infectious disease on complex networks with household-structure

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Abstract

In this paper, we study the household-structure SIS epidemic spreading on general complex networks. The household structure gives us the way to distinguish the inner and the outer infection rates. Unlike household-structure models on homogenous networks, such as regular and random networks, we consider heterogeneous networks with arbitrary degree distribution $p(k)$. Through mean field analysis and computer simulations, we find some unique phenomena only existing in divergent network with household structure. In our model, disease can spread on the scale-free network even when local recovery rate is greater than inner infection rate in every household. This implies that no disease is spreading in every single household, but for the whole network disease is spreading. Since our society network seems like this structure, maybe this conclusion remind us that during disease spreading we should pay more attention to network structure than local cure condition.

1. Introduction

The spread of disease has been one of the focuses in the field of statistical physics for many years. The dynamical behaviors of so-called susceptible-infected-susceptible (SIS) model and susceptible-infected-removed (SIR) model have been widely investigated on regular network and complex networks [1–12]. Within the studying, individuals

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are modelled as sites and possible contacts between individuals are linked by edges between the sites. It is easy to understand that both the properties of disease and topological characters of network determine the dynamics of the spread of disease. Studies have showed that there is an epidemic threshold λ_c on regular networks. If the effective spreading rate $\lambda > \lambda_c$, the infection spreads and becomes endemic; otherwise the infection will die out. While the threshold disappears on scale-free networks [4].

Usually, infectious diseases, such as HIV and computer virus, have the similar spreading property. They not only can spread in one household, but also can spread from one household to another. To study this spreading character, there have been of considerable interests to epidemic models spreading among a community of households [12–17]. These studies were mainly concerned with SIR model, which cannot yield endemic behavior. In 1999, Ball introduced the SIS household-structure model [18], in which the population is partitioned into m households with N members in each household. A threshold parameter R_* was defined. It was shown that for the household with 2 members, if $R_* < 1$ then the epidemic die out; if $R_* > 1$ the epidemic will exist at an endemic equilibrium. This model has also been studied on homogeneous network by the mean of self-consistent field approximations [19,20]. The similar results have been obtained. These previous studies about household-structure epidemic model were mainly on regular networks. However, studies have showed that a large number of systems, such as Internet, world-wide-web, physical, biological, and social networks, exhibit complex topological properties [21–23]. In particular, small-world properties [24] and scale-free degree distributions [25] appear in many real network systems. In this paper, we analyze the SIS household-structure epidemic model on complex networks. The outline is as follows: (1) introduction; (2) description of the model; (3) mean-field quations; (4) steady-state solutions; (5) simulation; (6) summary.

2. Model

In complex networks with degree distribution $p(k)$, which is the probability that a given site has k connections (links) connecting it with other k sites (we say that the degree of the given site is k), there are N individuals that are grouped as a household on every site. We assume that these N individuals contact each other fully and one individual can only exist in one of the two states: healthy (susceptible) and infected. A healthy individual may get infected from within the household and from outside its household. The parameters λ and β are the infection rates from outside and from within the household, respectively. We give each site x a number $i (i \in [0, N])$, which means that there are i infected individuals in the household at site x. The number of infected individuals at a given site x changes according to the following transition rates:

$$0 \to 1 \text{ at rate } \lambda \sum_{\langle x,y \rangle} i_y \,,$$

$$i \to i + 1 \text{ at rate } i\beta \text{ for } 1 \leqslant i \leqslant N - 1 \,,$$

$$i + 1 \to i \text{ at rate } \gamma \text{ for } 0 \leqslant i \leqslant N - 1 \,.$$

In the above expressions $\langle x, y \rangle$ means that site x and site y are nearest neighbors, and we suppose there is a connection (link) between them. Infected individuals may infect healthy individuals in their household with rate β, and also can infect healthy individuals in their nearest neighbors with rate λ. We assume that once a site is infected, infections within the site are much more likely than infections from outside, so we can neglect the latter. And also, an infected individual in a site can recover with rate γ. We suppose that all the individuals in a household have the same external connectivity and do not take the birth and death into account.

3. Mean-field equations

We now solve the above model with mean-field method. Let $u_{k,i}$ be the density of individuals whose household has i infected individuals and the corresponding site's degree is k, which means this site has k nearest neighbors. It is worth noticing that $\sum_{i=0}^{N} u_{k,i} = 1$. According to the transitions rate described in the above section, the evolution equations of $u_{k,i}$ are written as follows [4,6]:

$$\frac{\partial u_{k,0}(t)}{\partial t} = \gamma u_{k,1} - \lambda k \Theta_k(t) u_{k,0} , \tag{1}$$

$$\frac{\partial u_{k,1}(t)}{\partial t} = \lambda k \Theta_k(t) u_{k,0} - \beta u_{k,1} + \gamma u_{k,2} - \gamma u_{k,1} , \tag{2}$$

$$\frac{\partial u_{k,i}(t)}{\partial t} = (i-1)\beta u_{k,i-1} - i\beta u_{k,i} + \gamma u_{k,i+1} - \gamma u_{k,i} \quad (i \in [2, N-1]) , \tag{3}$$

$$\frac{\partial u_{k,N}(t)}{\partial t} = (N-1)\beta u_{k,N-1} - \gamma u_{k,N} . \tag{4}$$

In Eqs. (1)–(4), $\Theta_k(t)$ is the probability that a link from a site points to another site with at least one infected individual. And the expression of $\Theta_k(t)$ is

$$\Theta_k(t) = \sum_{k'} p(k'/k) \sum_{j=1}^{N} j u_{k',j}(t) , \tag{5}$$

where $p(k'/k)$ is the probability that a site with k degrees points to another site with k' degrees. For uncorrelated networks the expression of $p(k'/k)$ is [7]

$$p(k'/k) = \frac{k' p(k')}{\sum_{k'} k' p(k')} = \frac{1}{\langle k \rangle} k' p(k') . \tag{6}$$

Substituting (6) to (5), we get $\Theta_k(t) = \Theta(t)$ independent of k:

$$\Theta_k(t) = \Theta(t) = \frac{1}{\langle k \rangle} \sum_{k'} k' p(k') \sum_{j=1}^{N} j u_{k',j}(t) . \tag{7}$$

Now we are going to get steady solutions of Eqs. (1)–(4).

4. Steady-state solutions

Let $\partial u_{k,i}/\partial t = 0$ $(i = 1, 2, \ldots, N)$. Suppose $\mathbf{U}_k = (u_{k,1}, u_{k,2}, \ldots, u_{k,N})^{\mathbf{T}}$ and $\mathbf{V} = (1, 0, \ldots, 0)^{\mathbf{T}}$. Considering $\sum_{j=0}^{N} u_{k,j} = 1$, then Eqs. (1)–(4) can be written as

$$\mathbf{S}\mathbf{U}_k = -\lambda k\Theta\mathbf{V} . \tag{8}$$

The matrix $\mathbf{S}$ is

$$\mathbf{S} = \begin{pmatrix} -\gamma - \beta - \lambda k\Theta & \gamma - \lambda k\Theta & -\lambda k\Theta & \cdots & -\lambda k\Theta & -\lambda k\Theta \\ \beta & -2\beta - \gamma & \gamma & \cdots & 0 & 0 \\ 0 & 2\beta & -3\beta - \gamma & \cdots & 0 & 0 \\ \vdots & \vdots & \vdots & \cdots & \vdots & \vdots \\ 0 & 0 & 0 & \cdots & -(N-1)\beta - \gamma & \gamma \\ 0 & 0 & 0 & \cdots & (N-1)\beta & -\gamma \end{pmatrix} . \tag{9}$$

Since $\det(\mathbf{S}) = (-\gamma)^N - \lambda k\Theta \sum_{j=1}^{N} (j-1)!(-\gamma)^{N-j}(-\beta)^{j-1} \neq 0$, so $\mathbf{S}^{-1}$ exists. Thus

$$\mathbf{U}_k = -\lambda k\Theta\mathbf{S}^{-1}\mathbf{V} , \tag{10}$$

$$\sum_{j=1}^{N} j u_{k,j} = \mathbf{n} \cdot \mathbf{U}_k = (-\lambda k\Theta)\mathbf{n}\mathbf{S}^{-1}\mathbf{V} = -\lambda k\Theta\mathbf{n}(\mathbf{S}^{-1}\mathbf{V}) = -\lambda k\Theta\sum_{j=1}^{N} \mathbf{n}_j\mathbf{S}_{j1}^{-1} , \tag{11}$$

where $\mathbf{n} = (1, 2, \ldots, N)$ and $\mathbf{n}_j = j$.

From (9), we get $\mathbf{S}_{j1}^{-1}$:

$$\mathbf{S}_{j1}^{-1} = \frac{(-\gamma)^{N-j}(-\beta)^{j-1}(j-1)!}{(-\gamma)^N - \lambda k\Theta \sum_{j=1}^{N}(j-1)!(-\gamma)^{N-j}(-\beta)^{j-1}} . \tag{12}$$

Substituting (12) and (11) to (7), we get the self-consistent equation of Θ:

$$\Theta = -\frac{1}{\langle k \rangle}\sum_{k}\sum_{j}\frac{\lambda k^2\Theta\, p(k)(-\gamma)^{N-j}(-\beta)^{j-1}j!}{(-\gamma)^N - \lambda k\Theta \sum_{j=1}^{N}(j-1)!(-\gamma)^{N-j}(-\beta)^{j-1}} . \tag{13}$$

That is,

$$\Theta = -\frac{1}{\langle k \rangle}\left\langle \sum_{j}\frac{\lambda k^2\Theta(-\gamma)^{N-j}(-\beta)^{j-1}j!}{(-\gamma)^N - \lambda k\Theta \sum_{j=1}^{N}(j-1)!(-\gamma)^{N-j}(-\beta)^{j-1}}\right\rangle . \tag{14}$$

Obviously, $\Theta = 0$ is a solution of Eq. (14). In addition, a non-zero solution with $\Theta \neq 0$ and $u_{k,i} \neq 0$ $(i = 1, 2, \ldots, N)$ is allowed if the following inequality holds:

$$\left(-\frac{1}{\langle k \rangle}\left\langle \sum_{j}\frac{\lambda k^2(-\gamma)^{N-j}(-\beta)^{j-1}j!}{(-\gamma)^N}\right\rangle\right) \geqslant 1 . \tag{15}$$

That is,

$$\lambda \frac{\langle k^2 \rangle}{\langle k \rangle} \sum_{j=1}^{N} \frac{1}{\gamma} \left(\frac{\beta}{\gamma} \right)^{j-1} j! \geqslant 1 \;, \tag{16}$$

where $\langle k \rangle = \sum_k k p(k), \langle k^2 \rangle = \sum_k k^2 p(k)$. From (16), we get the epidemic threshold:

$$\lambda_c = \frac{1}{f(N,\beta,\gamma)} \frac{\langle k \rangle}{\langle k^2 \rangle} \;, \tag{17}$$

where $f(N,\beta,\gamma) = \sum_{j=1}^{N} 1/\gamma (\beta/\gamma)^{j-1} j!$, and $f(N,\beta,\gamma)$ can be written as follows [26]:

$$\begin{aligned}
f(N,\beta,\gamma) &= \sum_{j=1}^{N} \frac{1}{\gamma} \left(\frac{\beta}{\gamma} \right)^{j-1} j! \\
&= \frac{1}{\beta} \left[-1 - \frac{\gamma}{\beta} e^{-\gamma/\beta} \left(\Gamma \left(0, -\frac{\gamma}{\beta} \right) + (-1)^N (N+1)! \Gamma \right. \right. \\
&\qquad \left. \left. \times \left(-1 - N, -\frac{\gamma}{\beta} \right) \right) \right] \\
&= \frac{1}{\beta} [-1 - \alpha e^{-\alpha} (\Gamma(0,-\alpha) + (-1)^N (N+1)! \Gamma(-1-N,-\alpha))] \;, \tag{18}
\end{aligned}$$

where $a = \gamma/\beta$ and $\Gamma(z,x)$ is the incomplete gamma function. Expression (18) gives the complete dependence of $f(N,\beta,\gamma)$ on the household size N. For large N, $(-1)^N(N+1)!\Gamma(-1-N,-\alpha)$ increases rapidly, then the epidemic threshold λ_c decays greatly. From the definition of function $f(N,\beta,\gamma)$, one also can found that $f(N,\beta,\gamma)$ is an increasing function of β, but a decreasing function of the recovery rate γ. So the epidemic threshold is determined by three parameters (N,β,γ) and the networks degree distribution $p(k)$. We notice that the expression (17) involves multiplication of the well-known term $\langle k \rangle / \langle k^2 \rangle$ [2,4,6,9], which is closely related to the "average" number of secondary infections [7,8]. Not surprising, this result is the same as that of the standard SIS model [4].

For $p(k) = \delta_{k,k_c}$, the network is homogeneous. Then $\lambda_c = [1/f(N,\beta,\gamma)]1/k_c$, we can increase the recovery rate γ or decrease the site degree k_c and the size of the household N to prevent the infectious disease from spreading. For large N, the threshold λ_c is very small.

For $p(k) = Ck^{-\upsilon}$ ($\upsilon \in (2,3]$), the network is scale-free [21]. When $k \to \infty, \langle k \rangle / \langle k^2 \rangle \to 0$, then $\lambda_c = [1/f(N,\beta,\gamma)]\langle k \rangle / \langle k^2 \rangle \to 0$. So the threshold is absent for scale-free network even if γ is much larger than β. This implies that for any positive value of λ, the infection can pervade the system even with high recovery rate.

5. Simulation result

In above section, we have given the analytical result of the SIS model with household structure. We find that for regular network there is an epidemic threshold λ_c; while for
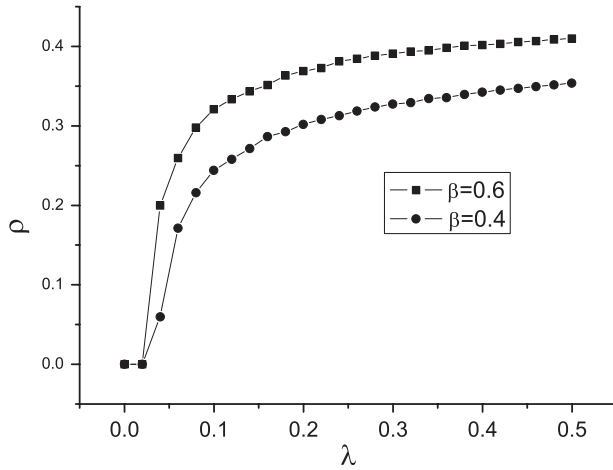
Fig. 1. The fraction of the infected individuals, ρ, as a function of the outside infection rate λ for household structure SIS model on regular networks with $k_c = 4, N = 4$. The simulations have been averaged over 200 different realizations.
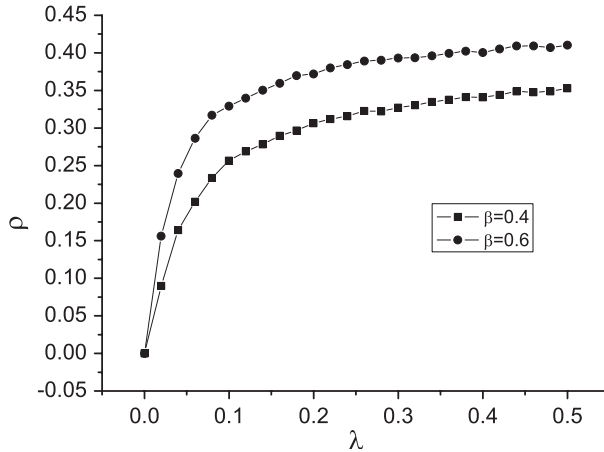

Fig. 2. The fraction of the infected individuals, ρ, as a function of the outside infection rate λ for household structure SIS model on scale-free networks with $\langle k \rangle = 6, N = 4$. The simulations have been run in networks with 10^5 nodes.

scale-free network the threshold disappears. For comparison, we simulate the model on regular network (see Fig. 1) and on scale free network (see Fig. 2), respectively. For simplicity (without lack of generality), we set $\gamma = 1, N = 4$. In Fig. 1, we plot the fraction of infected individuals in the stationary state, ρ, for different values of β on regular network with $k_c = 4$. Obviously, there is a threshold λ_c for each β. For $\beta = 0.6, \lambda_c$ is 0.026, in agreement with the corresponding analytical result, $\lambda_c = 0.026$,

which can be obtained from (17). Only when λ is increased above λ_c is a significant prevalence observed. In Fig. 2, we plot the fraction of infected individuals in the stationary state, ρ, for different values of β on scale-free network with $\langle k \rangle = 6$. We observe that λ_c is absent. In contract with the standard SIS model [27], of which the prevalence ρ increases slowly when increasing λ, our current epidemic model exhibits that ρ increases rapidly with λ. In the end, we should mention that for other parameters, the pictures are found to be qualitatively the same.

6. Summary

In this work, we analyze the SIS model that incorporates social household. We have focused on the effect of geometrical property of complex networks and the role of several parameters in the spreading thresholds. We find that the large household size N and the high within household infection rate β are more likely to cause the spread of disease. It is worth noticing that, even when local recovery rate is greater than effective infection rate, disease can spread in divergent networks such as scale-free network! This means that even the local recovery condition is good enough to give local protection, there is still some probability for a wide range disease spreading. It seems that this phenomenon can only exist in divergent networks with household structure. So we should care about the network structure much more than recovery condition during disease spreading.

Of course, the model we have studied seems more ideal. For example, we have supposed that the existence of the N-member households do not affect the property of the complex networks, and also we do not take the movement of the individuals into account. However, the result reveals that the properties of the complex networks play the most important role in the epidemic spreading.

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