The spread of disease with birth and death on networks

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Abstract

In this paper, we introduce a modified epidemic model on regular and scale-free networks respectively. We consider the birth rate $\delta$, cure rate $\gamma$, infection rate $\lambda$, $\alpha$ from the infectious disease, and death rate $\beta$ from other factors. Through mean-field analysis, we find that on regular network there is an epidemic threshold $\lambda_c$ dependent on the parameters $\delta, \gamma, \alpha, \text{ and } \beta$; while for power law degree distribution network epidemic threshold is absent in the thermodynamic limit. The result is the same as that of the standard SIS model. This reminds us the structure of the networks plays a very important role in the spreading property of the infectious disease.

Key words: Epidemic model; Complex networks
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1 Introduction

During the past few years, the spread of disease has been one of the focuses in the field of statistical physics. A great deal of epidemiological research work has been done on various networks. Two epidemic models SIS and SIR have been widely studied[1-9]. In these models, each node of networks represents an individual and each link is the connection along which the individuals interact and the disease can spread. For SIS epidemic model, each individual can exist in two possible states: susceptible (or healthy) and infected. At each time step, each healthy individual can be infected at rate $\lambda$ if there is one or more infected individuals in its nearest neighbors. Meanwhile, an infected

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individual may recover and become susceptible at rate $\gamma$. The SIR model assumes that individuals can exist in three possible states: susceptible (or healthy), infected and removed. The main difference from the SIS model is that once an individual gets infected, it is removed and can not be infected any more. It is easy to understand that both the properties of disease and network topology determine the dynamical behaviors of the disease spreading. Studies of SIS model and SIR model show that, on regular networks there is an epidemic threshold $\lambda_c$. If the effective spreading rate $\lambda > \lambda_c$, the infection spreads and becomes endemic. Otherwise, the infection will disappear. While the epidemic threshold is absent on scale-free networks in the thermodynamic limit[10-12].

From the definitions of SIS and SIR models, we know that both SIS and SIR models assume the number of individuals to be a constant. However, some disease may cause enough deaths to influence the population size. So it is necessary to take the birth and death rates into account. In this paper, we introduce a modified model, considering the birth rate $\delta$, treatment rate $\gamma$, infection rate $\lambda$, and two death rates: $\beta$ due to this infectious disease and $\alpha$ due to other factors, which will be described later. Our work is to study the influence of above parameters to the epidemic thresholds on different complex networks.

2 Model

We think of our individuals as being spatially distributed on the network $Z$. Each site of $Z$ is empty or occupied by at most one individual. We give each site a number: 0, 1 or 2. They describe empty state, a healthy individual occupation and an infected individual occupation respectively. The state of the system at time $t$ can be described by a set of numbers, 0, 1, 2. That means if the system is in state $A$ and the site $x \in Z$, then $A_t(x) \in \{0, 1, 2\}$. Each site can change its state with a certain rate. An empty site can give birth to a healthy individual at rate $\delta$. A healthy individual can be infected by contact at rate $\lambda$ if there are infected individuals in its nearest neighbors, or die at rate $\alpha$ due to other factors. An infected individual can be cured at rate $\gamma$ or die at rate $\beta$ due to this infectious disease. If an individual dies, there is an empty site left. Of course, each site can also maintain its state. We define $n_i(x, t)$ as
the number of the nearest neighbors of site $x$ in state $i$ at time $t$.

$$
0 \to 1 \text{ at rate } \delta \\
1 \to 0 \text{ at rate } \alpha \\
1 \to 2 \text{ at rate } n_2 \lambda \\
2 \to 1 \text{ at rate } \gamma \\
2 \to 0 \text{ at rate } \beta
$$

In above expressions, $\delta$, $\alpha$, $\beta$, $\gamma$ and $\lambda$ are all non-negative. We assume $\alpha$ is relatively very small. The expression $n_2 \lambda$ means that a healthy individual with $n_2$ infected nearest neighbors gets infected at rate $n_2 \lambda$. Not difficult to see, if $\delta$, $\alpha$ and $\beta$ equal 0, this model turns to SIS model; if $\delta$, $\alpha$, and $\gamma$ equal 0, this model turns to SIR model. If $\alpha$ and $\gamma$ equal 0, this model turns to “forest fire”, which has been widely studied[13].

2.1 Mean-field Method on regular networks

First, we solve the model by mean-field method on regular network without the consideration of spatial fluctuation. We use the density $x$ and $y$ ($x, y \in [0, 1]$) to replace the numbers of the healthy individuals and the infected individuals respectively. ”$n_2 \lambda$” can be replaced as ”$\lambda \langle k \rangle y$”, where $\langle k \rangle$ is the average number of the nearest neighbors of one node. The evolution equations of $x$ and $y$ are governed by:

$$
\frac{\partial x}{\partial t} = (1 - x - y) \delta - \alpha x - \lambda \langle k \rangle xy + \gamma y \\
\frac{\partial y}{\partial t} = \lambda \langle k \rangle xy - \gamma y - \beta y
$$

In Eq.(1), the expression $(1 - x - y)$ is the density of empty site. $\langle k \rangle y$ is the probability that the nearest neighbors of one healthy individual are infectious.

Let $\frac{\partial x}{\partial t} = 0$ and $\frac{\partial y}{\partial t} = 0$, we get the steady-state solutions:

(I) $$x = \frac{\delta}{\alpha + \delta}, \ y = 0; \quad (3)$$

and

(II) $$x = \frac{\gamma + \beta}{\lambda \langle k \rangle}, \ y = \frac{\delta \lambda \langle k \rangle - (\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} \quad (4)$$
Now, I will do stability analysis. For solution (I), the Jacobean is:

\[
J = \begin{pmatrix}
-\alpha - \delta & \gamma - \delta - \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} \\
0 & \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta)
\end{pmatrix}
\]  

(5)

The determinant and the trace of \(J\):

\[
|J| = -(\alpha + \delta) \left[ \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta) \right]
\]  

(6)

\[
Tr(J) = -\alpha - \delta + \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta)
\]  

(7)

Clearly, if \(|J| > 0\), then \(Tr(J) < 0\), and the solution is stable. So we can get the critical value \(\lambda_c\) of \(\lambda\). For simplicity, we let \(\delta = 1\). Then

\[
\lambda_c = \frac{(\alpha + 1)(\gamma + \beta)}{\langle k \rangle}
\]  

(8)

If \(\lambda < \lambda_c\), the solution (I) is stable, and the disease will die out. Otherwise solution (I) is not stable.

For solution (II), the Jacobean is:

\[
J = \begin{pmatrix}
-(\alpha + \delta) - \frac{\delta \lambda \langle k \rangle -(\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} & -(\beta + \delta) \\
0 & \frac{\delta \lambda \langle k \rangle -(\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)}
\end{pmatrix}
\]  

(9)

Considering \(y = \frac{\delta \lambda \langle k \rangle -(\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} \geq 0\), we also can get \(\lambda_c\)(let \(\delta = 1\)):

\[
\lambda_c = \frac{(\alpha + 1)(\gamma + \beta)}{\langle k \rangle}
\]  

(10)

When \(\lambda > \lambda_c\), the solution (II) is stable, which means that the disease will pervade the network; otherwise the disease will disappear. Noticing the expressions (8) and (10), we find that \(\lambda_c\) is a critical parameter. If \(\lambda < \lambda_c\), the solution (I) is stable, and the disease will disappear from the network; if \(\lambda > \lambda_c\), the solution (II) is stable, and the disease will spread in the system. From (8) and (10), it is obvious that \(\lambda_c\) is governed by the parameters \(\alpha\), \(\beta\), \(\gamma\), and \(\langle k \rangle\). We can increase the treatment rate or decrease \(\langle k \rangle\) to raise the threshold to prevent disease from spreading.
2.2 The spread of disease with treatment on scale-free network

In the above section, we have studied the epidemic model on regular network. But the investigations have shown that a large number of systems, such as internet, world-wide-web, physical, biological, and social network, exhibit complex topological properties[14-16], particularly scale-free network feature[14]. Recent works have examined the spread of computer viruses on the scale free networks[7,8,10]. The results show that the intrinsic epidemic threshold is absent in both SIS model and SIR model on scale-free(SF) networks. In this section, we analyze our modified model on the scale free networks, of which the degree distribution is

\[ p(k) = C f(k) k^{-\nu}, \]

where \( f(k) \) is the function of \( k \). Suppose \( x_k(t) \) and \( y_k(t) \) are the density of the healthy and infected nodes with given degree \( k \), and the mean-field equations are[9,10]:

\[
\frac{\partial x_k(t)}{\partial t} = \delta (1 - x_k - y_k) - \alpha x_k - \lambda k x_k \Theta_k(y(t)) + \gamma y_k \tag{11}
\]

\[
\frac{\partial y_k(t)}{\partial t} = \lambda k x_k \Theta_k(y(t)) - (\gamma + \beta) y_k \tag{12}
\]

where \( \Theta_k(y(t)) \) stands for the probability that an edge emanating from a node of degree \( k \) points to an infected site, \( \Theta_k(y(t)) = \sum_{k'} p(k'/k) y_{k'}(t) \), where \( p(k'/k) \) is the probability that a node with \( k \) degree points to a node with \( k' \) degree. For uncorrelated networks[17], \( p(k'/k) = k' p(k') / \langle k \rangle \), which means that the probability that a node points to a node with \( k' \) degree is proportional to its degree and the degree distribution \( p(k') \), and \( \langle k \rangle \) is the normalization factor. From the definition of \( \Theta_k(y(t)) \), we find that it is independent of \( k \) for uncorrelated networks[17]:

\[
\Theta_k(y(t)) = \Theta(y(t)) = \langle k \rangle^{-1} \sum_{k'} k' p(k') y_{k'}(t) \tag{13}
\]

Let \( \frac{\partial x_k(t)}{\partial t} = 0 \) and \( \frac{\partial y_k(t)}{\partial t} = 0 \), we can get stationary solution:

\[
x_k = \frac{\gamma + \beta}{(1 + \alpha)(\gamma + \beta) + (1 + \beta) \lambda k \Theta} \tag{14}
\]

\[
y_k = \frac{\lambda k \Theta}{(1 + \alpha)(\gamma + \beta) + (1 + \beta) \lambda k \Theta} \tag{15}
\]

In the above expression, we have let \( \delta = 1 \).

Substituting the expression (15) into (13), we get self-consistent equation of \( \Theta \):

\[
\Theta = \frac{1}{(1 + \beta) \langle k \rangle} \sum_k p(k) \lambda' k^2 \Theta = \frac{1}{(1 + \beta) \langle k \rangle} \left\langle \frac{\lambda' k^2 \Theta}{1 + \lambda' k \Theta} \right\rangle \tag{16}
\]
where $\lambda' = \frac{1+\beta}{(1+\alpha)(\gamma+\beta)} \lambda$.

We can see that $\Theta = 0$ is a solution of Eq.(16). To allow a nonzero solution $\Theta(\Theta \in (0, 1])$ of Eq.(16), the following inequality must be assumed:

$$
\left( \frac{1}{(1 + \beta) \langle k \rangle} \langle \lambda' k^2 \Theta \rangle \right) \geq 1 \tag{17}
$$

From Eq. (17), we get the threshold value of $\lambda'$:

$$
\lambda' = (1 + \beta) \frac{\langle k \rangle}{\langle k^2 \rangle} \tag{18}
$$

where $\langle k^2 \rangle = \sum k^2 p(k)$, then:

$$
\lambda_c = (1 + \beta)(\gamma + \alpha) \frac{\langle k \rangle}{\langle k^2 \rangle} \tag{19}
$$

From (19), we can see that $\lambda_c$ is dependent on $\gamma$, $\alpha$, $\beta$, and $\langle k \rangle / \langle k^2 \rangle$. If $\lambda > \lambda_c$, the disease will spread on the networks, otherwise the disease will die out. We now discuss $\lambda_c$ for different $f(k)$.

(I) For $f(k) = \delta_{k,k_c}$, then $p(k) = C k^{-\nu} \delta_{k,k_c} (k_c \geq 2)$. The network is homogeneous, $\langle k \rangle = k_c$, $\langle k^2 \rangle = k_c^2$, so

$$
\lambda_c = \frac{(1 + \alpha)(\gamma + \beta)}{k_c} \tag{20}
$$

Clearly, there is a nonzero threshold $\lambda_c$, in agreement with the result on the regular network (see Eq. (10)). When $\lambda > \lambda_c$, there is a nonzero $\Theta = \frac{\lambda(k) - (\delta + \alpha)(\gamma + \beta)}{\lambda(k)(1+\beta)}$ of Eq.(16). $\lambda_c$ is an increasing function of $\gamma$, $\alpha$ and $\beta$. We can increase the threshold $\lambda_c$ by increasing the rate of treatment $\gamma$ and decreasing $k_c$.

(II) For $f(k) = 1$, the network is scale free with a power law degree distribution $p(k) = C k^{-\nu} (\nu \in (2, 3])$, then

$$
\langle k \rangle = \sum_{k=m}^{+\infty} kp(k) \simeq C \frac{1}{\nu} m^{2-\nu} \tag{21}
$$

$$
\langle k^2 \rangle = \sum_{k=m}^{+\infty} k^2 p(k) \simeq \int_{m}^{\infty} k^{2-\nu} dk \tag{22}
$$
As \((2 - \nu)\) is bigger than \(-1\), so \(\langle k^2 \rangle\) is divergent, and \(\langle k \rangle / \langle k^2 \rangle \to 0\), then \(\lambda_c \to 0\) for \(k \to \infty\). Therefore the threshold is absent. Thus the treatment is of no effect to the disease.

(III) For \(f(k) = e^{-k/k_c}\), \(f(k)\) decreases rapidly for \(k > k_c\), the network is a finite size scale free network[18]. Then

\[
\lambda_c = (1 + \alpha)(\gamma + \beta)\frac{\langle k \rangle}{\langle k^2 \rangle}
= (1 + \alpha)(\gamma + \beta)\frac{\sum_k k^{1-\nu}e^{-k/k_c}}{\sum_k k^{2-\nu}e^{-k/k_c}}
= (1 + \alpha)(\gamma + \beta)k_c^{-1}\frac{\Gamma(-\nu, m/k_c)}{\Gamma(1 - \nu, m/k_c)}
\]

(23)

Where \(\Gamma(x, y)\) is the incomplete gamma function. The threshold \(\lambda_c\) is nonzero for finite \(k_c\). Without surprise, the threshold is an increasing function of \(\gamma, \alpha, \beta\). Comparing (23) with (20), one can see, for network with degree distributions \(p(k) = Ck^{-\nu}e^{-k/k_c}\), \(\lambda_c\) is also very small. From (I)-(III), we find that the network degree distribution, in some sense, determines the spread of infectious disease.

3 Conclusion

To summary, we have suggested an epidemic model with birth rate and death rate. Through mean-field analysis, we find that on regular network the epidemic threshold is an increasing function of treatment rate \(\gamma\), death rates \(\alpha, \beta\); while for power law degree distribution network epidemic threshold is absent in the thermodynamic limit, so that the treatment thus is of no effect to the disease, which is the same as the result of standard SIS model. So to prevent the infectious disease spreading in the "networks", apart from increasing the cure rate, we should pay more attention to the structure of "networks". We should point out that we do not analyze specific disease in our model. For a specific disease, there is a great need to analyze the disease through modelling and comparing the epidemic model with real data.

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