

The spread of disease with treatment on networks

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Abstract

In this paper, we introduce a modified epidemic model on regular networks and on scale-free networks respectively. We consider the birth rate δ , treatment rate γ , infection rate λ , and death rates α , β from the infectious disease and other factors respectively in this model. Through mean-field analysis, we find that on regular network there is an epidemic threshold λ_c of λ dependent on δ , γ , α , and β ; while for power law degree distribution network $p(k) = ck^{-\nu}$ ($\nu \in (2, 3]$), there is no epidemic threshold in the thermodynamic limit and the treatment thus is of no effect to the disease, which is the same as the result from standard SIS model. That means the structure of the networks plays a very important role in the spreading property of the infectious disease.

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I. INTRODUCTION

In the past few years, the spread of disease has been one of the focuses in the field of statistical physics. A number of epidemiological research works have been done on various networks, and two main epidemic models SIS and SIR have been widely studied[1][2][3][4][5][6]. In these models, each node of the network represents an individual and each link is the connection along which the individuals interact and the disease can spread. For SIS epidemic, 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 λ if there is one or more infected individuals in its nearest neighbors. At the same time, an infected individual can recover and becomes susceptible at rate γ . 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 again. It is easy to understand, both the properties of disease and network topology may determine the dynamics behavior of the spread of disease. Studies of SIS model and SIR model show that, on regular networks there is an epidemic threshold λ_c . If the effective spreading rate $\lambda > \lambda_c$, the infection spreads and becomes endemic. Otherwise, the infection will die out. While, on scale-free networks the threshold disappears in the thermodynamic limit[2][7][8]. Both SIS model and SIR model assume that the number of individuals in the system is invariable. In this paper, we will introduce a modified model, considering the birth rate δ , treatment rate γ , infection rate λ , and two death rates β due to this infectious disease and α due to other factors, which will be described later. Our main attention will be put to the study of the influence of above parameters($\delta, \gamma, \beta, \alpha$) to the epidemic threshold on different complex networks. The current paper contains five sections: 1) introduction; 2) description of the model; 3) mean-field method on regular networks; 4) the model on complex networks; 5) conclusions.

II. MODEL

Now we introduce our 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. 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 certain rate. An empty site can give birth to a healthy individual at rate δ . A healthy individual can be infected by contact at rate λ if there are infected individuals in its nearest neighbors, or die at rate α due to other factors. An infected individual can be cured at rate γ or die at rate β 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 .

$0 \rightarrow 1$ at rate δ

$1 \rightarrow 0$ at rate α

$1 \rightarrow 2$ at rate $n_2\lambda$

$2 \rightarrow 1$ at rate γ

$2 \rightarrow 0$ at rate β

In above expressions, δ , α , β , γ and λ are all non-negative. We assume α is relatively very small. $n_2\lambda$ means that a healthy individual with n_2 infected nearest neighbors gets infected at rate $n_2\lambda$. Not difficult to see that if δ , α and β equal 0, this model turns to SIS model; if δ and α equal 0, this model turns to SIR model. If α and γ equal 0, this model turns to “forest fire”, which has been widely studied[9].

III. MEAN-FIELD METHOD ON REGULAR NETWORKS

First, we will 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 is governed by:

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

$$\frac{\partial y}{\partial t} = \lambda \langle k \rangle xy - \gamma y - \beta y \quad (2)$$

In Eq.(1), $(1 - x - y)$ 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 will get the steady-state solutions:

(I)

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

and

(II)

$$x = \frac{\gamma + \beta}{\lambda \langle k \rangle}, \quad y = \frac{\delta \lambda \langle k \rangle - (\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} \quad (4)$$

Now, I will do stability analysis. For solution (I), the Jacobean is:

$$\mathbf{J} = \begin{pmatrix} -\alpha - \delta & \gamma - \delta - \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} \\ 0 & \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta) \end{pmatrix} \quad (5)$$

The determinant and the trace of \mathbf{J} :

$$|\mathbf{J}| = -(\alpha + \delta) \left[\frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta) \right] \quad (6)$$

$$Tr(\mathbf{J}) = -\alpha - \delta + \frac{\delta \lambda \langle k \rangle}{\delta + \alpha} - (\gamma + \beta) \quad (7)$$

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

$$\lambda_c = \frac{(\alpha + 1)(\gamma + \beta)}{\langle k \rangle} \quad (8)$$

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:

$$\mathbf{J} = \begin{pmatrix} -(\alpha + \delta) - \frac{\delta \lambda \langle k \rangle - (\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} & -(\beta + \delta) \\ \frac{\delta \lambda \langle k \rangle - (\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle (\delta + \beta)} & 0 \end{pmatrix} \quad (9)$$

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

$$\lambda_c = \frac{(\alpha + 1)(\gamma + \beta)}{\langle k \rangle} \quad (10)$$

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 λ_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 on the network. From (8) and (10), it is obvious that we can increase the treatment rate to raise the threshold to prevent disease from spreading.

IV. THE SPREAD OF DISEASE WITH TREATMENT ON SCALE-FREE NETWORK

In the above section, we have done 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[10][11][12][13], particularly scale-free network feature[14]. Recent works have examined the spread of computer viruses on the scale free networks[2][3][4][7] which give a good description of the connectivity structure showed in the Internet and WWW[14]. The results show that the intrinsic epidemic threshold is absent in both SIS model and SIR model in scale-free(SF) networks. In this section, we will work on our model on the scale free networks, of which the degree distribution is $p(k) = Cf(k)k^{-\nu}$ [11][14], which expresses the probability that a node has k nearest neighbors. $f(k)$ 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 as below[3][4][7]:

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

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

$\Theta_k(y(t))$ stands for the probability that an edge emanating from a node of degree k points to an infected site, and $\Theta_k(y(t)) = \sum_{k'} p(k'/k) y_{k'}(t)$, where $p(k'/k)$ is the probability that a node with k degree points to a node with k' degree. For uncorrelated networks[15], $p(k'/k) = k' p(k') / \langle k \rangle$, 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, and the expression is[7]:

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

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

$$x_k = \frac{\gamma + \beta}{(1 + \alpha)(\gamma + \beta) + (1 + \beta)\lambda k \Theta} \quad (14)$$

$$y_k = \frac{\lambda k \Theta}{(1 + \alpha)(\gamma + \beta) + (1 + \beta)\lambda k \Theta} \quad (15)$$

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

By substituting the expression (15) into (13), the self-consistent equation of Θ is below:

$$\Theta = \frac{1}{(1 + \beta) \langle k \rangle} \sum_k p(k) \frac{\lambda' k^2 \Theta}{1 + \lambda' k \Theta} = \frac{1}{(1 + \beta) \langle k \rangle} \langle \frac{\lambda' k^2 \Theta}{1 + \lambda' k \Theta} \rangle \quad (16)$$

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 Θ ($\Theta \in (0, 1]$) of Eq.(16), the following inequality must be assumed:

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

We can get the threshold value of λ' from Eq. (17):

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

So we get:

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

From (19), we can see that λ_c is dependent on γ , α , β , and $\frac{\langle k \rangle}{\langle k^2 \rangle}$. If $\lambda > \lambda_c$, the disease will spread on the networks, otherwise the disease will die out. We now discuss λ_c for different $f(k)$.

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

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

Clearly, there is a nonzero threshold λ_c , in agreement with the result on the regular network(see Eq. (10)). When $\lambda > \lambda_c$, there is a nonzero $\Theta = \frac{\lambda \langle k \rangle - (\delta + \alpha)(\gamma + \beta)}{\lambda \langle k \rangle + (1 + \beta)}$ of Eq.(16). λ_c

is an increasing function of β , γ , and α . We can increase the threshold λ_c by increasing the rate of treatment γ .

(II). $f(k) = 1$. The network is scale free with a power law degree distribution $p(k) = Ck^{-v}$ ($v \in (2, 3]$), and

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

$$\langle k^2 \rangle = \sum_{k=m}^{+\infty} k^2 p(k) \simeq \int_m^{\infty} k^{2-v} dk \quad (22)$$

As $(2 - v)$ is bigger than -1 , so $\langle k^2 \rangle$ is divergent, and $\frac{\langle k \rangle}{\langle k^2 \rangle} \rightarrow 0$, then $\lambda_c \rightarrow 0$ for $k \rightarrow \infty$. Therefore the threshold is absent. Thus the treatment is of no effect to the disease.

(III). $f(k) = e^{-k/k_c}$, $f(k)$ decreases rapidly for $k > k_c$, and $p(k) = Ck^{-v}e^{-k/k_c}$. In this case, the network is a finite size scale free network[3]. We have:

$$\begin{aligned} \lambda_c &= (1 + \alpha)(\gamma + \beta) \frac{\langle k \rangle}{\langle k^2 \rangle} \\ &= (1 + \alpha)(\gamma + \beta) \frac{\sum_k k^{1-v} e^{-k/k_c}}{\sum_k k^{2-v} e^{-k/k_c}} \\ &= (1 + \alpha)(\gamma + \beta) k_c^{-1} \frac{\Gamma(-v, m/k_c)}{\Gamma(1 - v, m/k_c)} \end{aligned} \quad (23)$$

Where $\Gamma(x, y)$ is the incomplete gamma function. The threshold λ_c is nonzero for finite k_c . Without surprise, the threshold is an increasing function of treatment rate α , γ , β . Comparing (23) with (20), we can see, for network with degree distribution $p(k) = Ck^{-v}e^{-k/k_c}$ λ_c is also very small. From (I)-(III), we find that the network degree distribution, in some sense, determines the spreading characteristic of infectious disease.

V. CONCLUSION

In this paper, we have suggested an epidemic model on both regular and scale free networks. Though mean-field analysis, we find that the epidemic threshold λ_c is much bigger on regular network than on scale-free networks. Therefore disease can spread on scale-free networks more easily. The reason is that on regular network the clustering coefficient is very small, and the average path length is relatively long; while in complex (scale-free) networks the clustering coefficient is relatively big and the average length is short[12][13], which lead to small threshold. We also find that treatment has different effect on diseases spreading on

regular network and scale free networks. In particular, that the treatment has no effect on power law degree distribution network. Therefore to prevent the infectious disease spreading in the "networks", apart from increasing the treatment rate, we can change the structure of the "networks".

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- [1] M. Kuperman and G. Abramson, Phys. Rev. Lett. **86**, 2909(2001).
 - [2] R. M. May and A. L. Lloyd, Infection dynamics on scale-free networks, Phys. Rev. E **64**, 066112 (2001).
 - [3] R. Pastor-Satorras and A. Vespignani, Epidemic dynamics in finite size scale-free networks, Phys. Rev. E **65**, 035108(R) (2002).
 - [4] M. E. J. Newman, The spread of epidemic disease on networks, Phys. Rev. E **66**, 016128 (2002).
 - [5] Víctor M. Eguíluz and Konstantin Klemm, Phys. Rev. Lett. **89**, 108701 (2002).
 - [6] A. Vázquez and Y. Moreno, Phy. Rev. E **67**, 015101(R) (2003).
 - [7] R. Pastor-Satorras and A. Vespignani, Phys. Rev. Lett. **86**, 3200 (2001); Phys. Rev. E **63**, 066117 (2001).
 - [8] Y. Moreno and A. Vazquez, Disease Spreading in Structured Scale-Free Networks, European Physical Journal B **31**, 265 (2003).
 - [9] Kuulasmaa, The spatial general epidemic and locally dependent random graphs, J. Appl. Prob. **19**, 745-758 (1982), Durrett and Neuhauser (1995).
 - [10] L. A. N. Amaral, A. Scala, M. Barthy, and H. E. Stanley, Proc. Natl. Acad. Sci. U. S. A. **97**, 11 149 (2000).
 - [11] S. H. Strogatz, Nature (London) **410**, 268 (2001).
 - [12] S.N. Dorogovtsev and J.F.F. Mendes, Adv. Phys. **51**, 1079(2002).

- [13] R. Albert and A.-L. Barabási, Rev. Mod. Phys. **74**, 47 (2002).
- [14] R. Albert, H. Jeong, and A. -L. Barabási, Nature (London) **401**, 130(1999).
- [15] M. Boguñá, R. Pastor-Satorras and A. Vespignani, e-print cond-mat/0301149 (2003).