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The analysis of an epidemic model with time delay on scale-free networks

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HIGHLIGHTS

- Established a new *SIS* epidemic model with time delay on scale-free networks.
- Obtain the basic reproductive number for the epidemic spreading with or without immunization schemes.
- Obtain global stability criteria of the disease-free equilibrium and uniform persistence criteria of the disease. Q2
- Discuss the influence of structure of the networks and time delay on the results.

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ABSTRACT

A new epidemic *SIS* model with time delay on scale-free networks is presented. We give the formula of the basic reproductive number for the model and prove that the disease dies out when the basic reproductive number is less than unity and the disease is uniformly persistent when the basic reproductive number is more than unity. The effects of various immunization schemes are studied. Numerical simulations are given to demonstrate the main results.

1. Introduction

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Since the scale-free network by Barabási and Albert [1], in which the probability of $p(k)$ for any node with k links to other nodes is distributed according to the power law $p(k) = Ck^{-\gamma}$ $(2 < \gamma \leq 3)$, the study of epidemic spreading behavior has attracted more and more interest.

The *SIS* model and *SIR* model are two important and fundamental epidemic models. It has been pointed out that the spreading process on networks is primarily dominated by two factors [2]: the macroscopic topology of the underlying network and the microscopic infection scheme which includes properties of disease, infection pattern, individual differences, infectivity of individuals, etc. The traditional epidemiology [3] is based on homogeneous networks such as the random networks or the small-world networks [4], which have degree distributions that are approximately Poisson, and the infectivity rate is equally likely over all links. However, it is well-acknowledged that the real disease transmission networks exhibit scale-free properties (for example Refs. [5,6]) and the traditional epidemiology becomes unrealistic. Recently, the epidemic spreading on scale-free networks, i.e., heterogeneous networks, has been studied by many researchers [7–21].

On a scale-free network, nodes represent individuals, and edges describe potential contacts between pairs of individuals. For epidemic spreading of *SIS* process, the nodes may be susceptible or infected. Let $I_k(t)$ represent the relative density of

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infected nodes with a given degree k at time t, thus the mean-field approximation [15,16] yields

$$\frac{dI_k(t)}{dt} = \lambda k(1 - I_k(t))\Theta(t) - I_k(t), \tag{1}$$

where the factor $\Theta(t)$ represents the probability that any given link points to an infected site. Under the assumption that the connectivities of nodes in whole network are uncorrelated [8], we have

$$\Theta(t) = \frac{\sum_k \varphi(k)p(k)I_k(t)}{\langle k\rangle}, \tag{2}$$

where $\langle k\rangle = \sum_k p(k)k$ stands for the average node degree and we also define $\langle f(k)\rangle = \sum_k f(k)p(k)k$ in which $f(k)$ is a function.

Many models are special cases of model (1) with $\varphi(k)$ taking different forms, such as $\varphi(k) = k$ in Refs. [7,8], $\varphi(k) = A$ in Ref. [10], $\varphi(k) = k^\alpha, 0 < \alpha < 1$ in Ref. [11], and $\varphi(k) = ak^\alpha/(1 + bk^\alpha), 0 < \alpha < 1$ in Ref. [12]. Note that $\varphi(k)$ in Refs. [10–12] is suitable than $\varphi(k) = k$ in Refs. [7,8] since an infected cannot contact all acquaintances in one time step.

Continuous time deterministic epidemic models are traditionally formulated as systems of ordinary differential equations. More realistic models should include some past states of these systems, and ideally, a real system including some past states can usually be better modeled with functional differential equations. The method has drawn enough attention on the epidemic model on homogeneous networks and time delays are introduced to the model to represent the incubation periods of infectious diseases, the infection periods of infective members, the periods of recovered individuals with immunity and so on [3]. Unfortunately, little attention has been given to the model on heterogeneous networks. Xu et al. [19] introduced the effect of infection delay to the standard *SIS* model in 2006, but they failed to give a concrete mathematical model. In 2009, Xu et al. gave a *SIS* model reflecting the effect of infection delay, however, by a set of ordinary differential equations in Ref. [20]. Similarly, Xia et al. [21] also discussed the effect of delaying the time of recovery for *SIS* model in 2013. In this paper, we will present a suitable *SIS* model with time delay on heterogeneous networks by functional differential equations to investigate the epidemic spreading.

The rest of this paper is organized as follows: in Section 2, the *SIS* model on scale-free networks with time delay and nonlinear infectivity is presented. The thresholds are given and the attractiveness of disease-free equilibrium and the persistence of the disease are analyzed in Section 3. Several models of immunization are considered in Section 4. In Section 5, numerical simulations are given to demonstrate the main results and related issues are discussed. Conclusions are finally drawn in Section 6.

2. The SIS model with time delays in complex networks

In 1973, Cooke presented an epidemic *SIS* model with time delay on homogeneous networks [3,22]:

$$\frac{dI(t)}{dt} = \beta S(t)I(t) - \beta S(t-\tau)I(t-\tau), \quad I(t) + S(t) = 1, \tag{3}$$

where τ is the average infectious period of the disease. The basic reproductive number for the system (3) is $\bar{R}_0 = \beta\tau$, and this result is consistent with that on small-world networks in Ref. [19].

Now we extend the model to one on scale-free networks. Suppose the size of the network is a constant N during the period of epidemic spreading, n is the maximum number of contact of each node, and suppose that the degree of each node is time invariant. Let $S_k(t)$ and $I_k(t)$ be the relative densities of susceptible node and infected node of connectivity k at time t, respectively, where $k = 1, 2, \ldots, n$. The densities $I_k(t)$ and $S_k(t)$, at the mean-field level, satisfy the following set of coupled functional differential equations when $t > \tau$.

$$\frac{dI_k(t)}{dt} = \lambda kS_k(t)\Theta(t) - \lambda kS_k(t-\tau)\Theta(t-\tau) \tag{4}$$

with the normalization condition

$$I_k(t) + S_k(t) = 1, \tag{5}$$

due to the fact that the number of total nodes with degree k is a constant $p(k)N$ during the period of epidemic spreading, where τ is the average infectious period of the disease (the time it takes for the node to seek out and receive treatment), i.e., each infected node becomes susceptible after τ. In reality, if a person is infected by some disease such as the common cold, gonorrhea, and encephalitis, there is always a period of time before the person recovers [20,22], and the person may be infected again. In addition, τ also may mean the latent period of a computer network virus, network virus will be found and killed after τ due to its destruction of the user.

We obtain from (5) the following equivalent functional differential equation system of model (4).

$$\begin{aligned} &\frac{dI_k(t)}{dt} = \lambda k(1 - I_k(t))\Theta(t) - \lambda k(1 - I_k(t-\tau))\Theta(t-\tau), \\ &I_k(t) + S_k(t) = 1, \quad t > \tau. \end{aligned} \tag{6}$$

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