Optimal epidemic spreading on complex networks with heterogeneous waiting time distribution

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HIGHLIGHTS

- A susceptible–infected–susceptible model with heterogeneous waiting time distribution is proposed.
- A mean-field theory is generalized to analyze the model.
- The epidemic threshold is dependent on both the network topology and the waiting time distribution.
- There is an optimal waiting time distribution at which the epidemic threshold reaches its maximum value.

ABSTRACT

In this paper, the effects of heterogeneous waiting time on spreading dynamics is studied based on network-dependent information. A new non-Markovian susceptible–infected–susceptible (SIS) model is first proposed, in which node's waiting time is dependent on its degree and may be different from each other. Every node tries to transmit the epidemic to its neighbors after the waiting time. Moreover, by using the mean-field theory and numerical simulations, it is discovered that the epidemic threshold is correlated to the network topology and the distribution of the waiting time. Furthermore, our results reveal that an optimal distribution of the heterogeneous waiting time can suppress the epidemic spreading.

1. Introduction

Dynamical behaviors of epidemic spreading have attracted a great deal of attention in the last decades due to their wide applications in controlling epidemic [1]. Up to date, much efforts have been focused on the effects of network topology on the epidemic threshold [2–5], the spreading velocity [6–9], and epidemic size [10–13], and some fascinating results have been obtained. For instance, Pastor-Satorras and his colleagues found that strong heterogeneity of degree distribution can reduce or even vanish the epidemic threshold [4,14], Wang et al. found that heterogeneous weight distribution hinders the epidemic spreading [10].

In the literature, there are many results on the effects of heterogeneous waiting time on the spreading of epidemics in a network and several susceptible–infected (SI) model have been proposed. It is well known that heterogeneous waiting time (i.e., the time interval between two consecutive activities initiated by the same user) can alter the spreading behavior of the epidemic and is unavoidable in networks due to the wide existence in physical contacts [15,16], communications [17,18], text messages [19,20] and human activity [21,22]. It is reported in Ref. [23] that epidemic spreading dynamics

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with heterogeneous waiting time exhibits non-Markovian character and the nodes' waiting time satisfies the power-law distribution. They found that the prevalence decay time is significantly larger than the model's waiting time with Poisson distribution. In addition, the average number of new-infected nodes decades in a power-law way in a long-time limit [24]. With the help of percolation theory, Min et al. found that the strong heterogeneous waiting time distribution suppresses the epidemic spreading [25]. However, Takaguchi et al. noted that strong heterogeneous waiting time distribution promotes spreading dynamics [26], while Jo et al. found that the heterogeneous waiting time promotes the SI spreading dynamics at middle spreading time, and suppresses the spreading dynamics at late time in the well-mixed population [27]. To analysis the non-Markovian character in spreading dynamics, some other theories are also proposed, such as renewal process [28,29], edge-based compartmental theory [30], and pairwise approximation [31]. Note that the references mentioned above considered the effects of nodes' waiting time on the epidemic spreading under the assumption of stochastic waiting time, i.e., in a stochastic setting, the waiting time of all agents follows a same distribution.

However, each agent in a realistic network may have a different waiting time because node's waiting time is tightly related to its inherent characteristics such as, age, gender, and hobbies [32–34]. Therefore, each agent's waiting time may not be identical, which is specific manifestation of heterogeneous epidemic spreading [35–37]. In this paper a novel non-Markovian SIS model with heterogeneous waiting time is proposed. In this model, every node transmits the epidemic to its neighbors after a waiting time which is assigned according to its degree. A mean-field analytical technique is established to study the effects of heterogeneous waiting time distribution on the epidemic threshold. Our results show that the epidemic threshold is heavily dependent on the topology of network and the distribution of the waiting time. Moreover, it is discovered that, for a given network, there exists an optimal waiting time distribution by which the epidemic threshold reaches the maximum value. For a network with fixed epidemic spreading probability, the fraction of infected nodes in the steady state can also reach a minimum value by adjusting the distribution of individual's waiting time. An optimal phenomenon is discovered which enriches the abnormal phenomenon [38,39] in epidemic spreading dynamics.

2. Epidemic spreading model

This section will introduce an epidemic spreading model on complex networks. The network is coupled by N nodes. A node represents an agent and edge stands for relationship between connected nodes. We first assume that each node can be in susceptible or infected state at any time step. Considering the fact that individual's waiting time is always dependent on his career, education background, hobbies, etc. [32–34]we also assume that waiting time of every node is completely dependent on its degree. This assumption is reasonable in reality. For instance, usually a star has large degree, which makes it easy to transmit the epidemic to others since he/she always attends some activities. Nevertheless, a housewife often exhibits small degrees and it is difficult to transmit her epidemic to others. For simplicity, let τ_{k_i} be the static waiting time of node i, where k_i is the degree of node i. Moreover, we assume that if node i is infected at time t, then it can infect each neighbor with probability β at time $t + m\tau_{k_i}$ before its recovery, where $m \geq 1$ is a positive integer. It is followed from the above assumptions that each infected node can remember the time-step when it is infected and transmits the epidemic to its neighbors. Thus, the proposed model has the non-Markovian character. At every time step, the infected nodes become susceptible with the same recovery probability γ but the infection time differs per node. The discrete synchronous updating method [40] is applied to renewal the states of nodes.

Recently, under the assumption that node's response time (i.e., the time interval between receiving a message and forwarding it) is positively dependent on its degree, Cui et al. [41] studied the effects of heterogeneous response time on SI model by simulations. Inspired by Ref. [41], we assume that the waiting time of node i is dependent on the degree k_i in this case. More specifically, the waiting time of node i is

$$\tau(k_i, \alpha) = \varpi(\alpha)\left(\frac{k_i}{k_{\max}}\right)^{\alpha}, \tag{1}$$

where $\varpi(\alpha)$ and $k_{\max}$ are the normalization, and α is a tunable parameter. Without special statements, denote $\tau(k_i, \alpha)$ as τ_{k_i} for simplicity. It can be seen from Eq. (1) that, in the case of $\alpha > 0$, node with larger degree has longer waiting time; for $\alpha < 0$, the opposite situation happens; when $\alpha = 0$, all nodes have the same waiting time.

For the sake of investigating the effects of α on the epidemic dynamics directly, the sum of the waiting time for all edges is set to be a constant. In other words, for any values α_1 and α_2 the following relationship fulfills

$$\sum_{i}^{N} k_i \tau(k_i, \alpha_1) = \sum_{i}^{N} k_i \tau(k_i, \alpha_2). \tag{2}$$

For $\alpha = 0$, one can get $\varpi(0) = \langle\tau\rangle\langle k\rangle N$, where $\langle\tau\rangle$ and $\langle k\rangle$ represent the average waiting time and mean degree, respectively. Eq. (2) can be further written as

$$2L\varpi(0) = \sum_{i}^{N} k_i \tau(k_i, \alpha_1) = \sum_{i}^{N} k_i \tau(k_i, \alpha_2), \tag{3}$$