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Epidemic spreading on uniform networks with two interacting diseases☆

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HIGHLIGHTS

- Established a model considering two interacting diseases spreading on uniform networks.
- Verified the sufficient condition when diseases will break out through simulation.
- Obtained the condition when the two interacting diseases can exist in the networks.

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ABSTRACT

In this paper, we consider a pair of homogeneous diseases spreading concurrently on uniform networks based on the SIS model. A new model describing the transmission process of the interacting diseases is established. The influence of the transmission parameters, the interacting parameter and the initial density value of infected nodes on the epidemic spreading is presented by simulating the transmission process of the proposed model. The mathematical expressions of the conditions among the transmission parameters, the interacting parameter and the network parameter when diseases can exist in the network based on the simplified model are presented. Comparing the transmission process of this interacting model under different intervals of the interacting parameter, it is found that the interacting of the two diseases leads to larger scale prevalence with a relatively larger interacting parameter when the infection breaks out.

1. Introduction

Epidemic spreading has attracted an increasing amount of attention from researchers for decades. One of the well-studied problems is to examine the transmission behavior of the disease over networks.

In the past several years, tremendously significant models have been proposed to investigate the epidemic spreading behavior such as the susceptible–infected (SI) model [1–3], susceptible–infected–susceptible (SIS) model [4–7] and the susceptible–infected–removed (SIR) model [8–14]. In the SIS model, all the individuals in the network are divided into two sections according to their current states: susceptible and infected. The cured one can be infected by the same disease again. One of the important conclusions among the studies of the SIS model is the threshold of transmissibility, below which the disease extinguishes while breaking out beyond. It has been known that the threshold of the uniform networks is determined by the averaged degree of the network, such as the ER networks [15] and the small-world networks [16]. However, when it comes to the nonuniform networks, such as the BA scale-free network [17], the threshold is always zero [18].

All the above studies are focused on the epidemic spreading behavior of one disease. Recently, two kinds of diseases competing for the same hosts and spreading in one network have been studied [19–21]. For example, in Ref. [19], the

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behavior of two competing diseases with complete cross immunity spreading concurrently over a static network is studied, and the coexistence phase, a region of the parameter space in which both diseases spread to infect a fraction of the network has been found. In Ref. [22], the impacts of clustering on interacting epidemics have been studied and it provides a significant insight into the relationship between the network structure and the potential epidemic prevalence. However, the limitation of these works is that each individual in the network can be infected by only one of the two diseases each time. In fact, it is more natural that each individual could get infected with more than one disease at the same time. Furthermore, the one who has been infected will be more vulnerable to be infected by another disease.

Motivated by the above considerations, we consider two interacting diseases spreading in uniform networks based on SIS model in this paper. When one individual has been infected by one of the two diseases, it has the possibility of being infected by the other. Specially, to simplify the analysis, we consider a pair of homogeneous diseases spreading concurrently. Here the so called homogeneous diseases are defined by two interacting diseases sharing the same infectivity exponent and recovery exponent, when one individual has been infected by one of the diseases, it has the same possibility of being infected by the other.

The contributions of this paper are given as follows. Firstly, a dynamical model considering two interacting diseases spreading concurrently in uniform networks is established. Secondly, a sufficient condition consists of the transmission parameters, the interacting parameter and the initial density value of infected individuals when diseases will break out is found by simulating the transmission process of the interacting model. Thirdly, the mathematical expressions of the conditions among the transmission parameters, the interacting parameter and the network parameter when diseases can exist in the network based on the simplified model are presented. Lastly, it is observed that the interaction of the two diseases causes more nodes to be infected in comparison with independent diseases spreading in the same network.

The paper is organized as follows. In Section 2, a new model considering two interacting diseases spreading concurrently in the uniform networks based on the SIS model is established and some numerical results of the threshold conditions are given, the properties of the transmission dynamical process are investigated. In Section 3 the theoretical analysis of the threshold conditions and their numerical simulation results are presented based on a simplified model. Finally, we conclude this paper in Section 4.

2. Modeling and analysis of the interacting diseases spreading model

2.1. The interacting diseases spreading model

We consider two diseases spreading in uniform networks concurrently, denoted by disease A and disease B here. The infected node can be recovered with the possibility γ, while the susceptible node can be infected with the probability β. Considering the effects of the interactions on the infection probability β, the probability of cross infections is denoted by $p\beta$ here. The value of p indicates the relationship and the interacting strength between the two diseases. The relationship of the two diseases is divided into four aspects according to different value of p, then p is defined as the interacting parameter of the two diseases. When $p = 0$, the interactions between the diseases constrain the other's spreading completely, we define that the two diseases are competing with each other for hosts. When the value of p is on the interval of $(0, 1)$, the two diseases are constraining each other on spreading to a certain degree. Besides, when $p = 1$, the two diseases have no effects on the other's spreading, we define that they are independent diseases. However, once the value of p is on the interval of $(1, +\infty)$, the diseases promote each other's spreading. On the diffusion of the diseases, it is assumed that the infections can only happen when the individual that can be infected has at least one neighbor carrying the disease. Therefore, there are four kinds of individuals in the network according to their current states. We define that a node has state S_0 if it is susceptible and state S_1 and state S_2 stand for the node which has been infected by disease A or B respectively. State S_3 describes the node that has been infected by both diseases.

Denote $\rho_i(t)$ $(i = 0, 1, 2, 3)$ as the density of individuals belonging to each state at instant t. The following equations are presented to describe the transmission dynamical process of the proposed model.

$$\begin{cases} \dfrac{\mathrm{d}\rho_i(t)}{\mathrm{d}t} = -\sum\limits_{j=0, j\neq i}^{3} P_{S_i\to S_j} + \sum\limits_{j=0, j\neq i}^{3} P_{S_j\to S_i}, \\ \sum\limits_{i=0}^{3} \rho_i(t) = 1 \quad (i = 0, 1, 2, 3), \end{cases} \tag{2.1}$$

where

$$\begin{aligned} &P_{S_0\to S_1} = \beta\langle k\rangle(\rho_1(t) + \rho_3(t))\rho_0(t)[1 - \beta\langle k\rangle(\rho_2(t) + \rho_3(t))], \\ &P_{S_0\to S_2} = \beta\langle k\rangle(\rho_2(t) + \rho_3(t))\rho_0(t)[1 - \beta\langle k\rangle(\rho_1(t) + \rho_3(t))], \\ &P_{S_0\to S_3} = (\beta\langle k\rangle)^2\rho_0(t)(\rho_1(t) + \rho_3(t))(\rho_2(t) + \rho_3(t)), \\ &P_{S_1\to S_0} = \gamma\rho_1(t)[1 - p\beta\langle k\rangle(\rho_2(t) + \rho_3(t))], \qquad P_{S_1\to S_2} = \gamma p\beta\langle k\rangle\rho_1(t)(\rho_2(t) + \rho_3(t)), \\ &P_{S_1\to S_3} = p\beta\langle k\rangle\rho_1(t)(\rho_2(t) + \rho_3(t))(1 - \gamma), \end{aligned}$$