

STAGED PROGRESSION MODEL FOR EPIDEMIC SPREAD ON HOMOGENEOUS AND HETEROGENEOUS NETWORKS*

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Abstract In this paper, epidemic spread with the staged progression model on homogeneous and heterogeneous networks is studied. First, the epidemic threshold of the simple staged progression model is given. Then the staged progression model with birth and death is also considered. The case where infectivity is a nonlinear function of the nodes' degree is discussed, too. Finally, the analytical results are verified by numerical simulations.

Key words Complex network, epidemic, heterogenous, homogeneous, the staged progression model.

1 Introduction

In the past few years, complex networks have attracted increasing attention, because many real-life technological, social and biological systems have complex network-like structures, some important examples include the Internet, the World Wide Web (WWW), and scientific collaboration networks, etc. As a result, many researchers studied the dynamical behaviors of complex networks from different aspects, an important dynamical process on complex networks is the spread of epidemics. The dynamical behavior of the SIS (susceptible-infected-susceptible) model and the SIR (susceptible-infected-recovered/removed) model, which are considered as the conventional way to describe the fundamental mechanism of diseases, have been widely studied on regular networks and complex networks^[1–16].

For some kind of networks, whose most nodes have similar degrees, that is, the degree distributions have small fluctuations, e.g., random networks, regular networks, small-world networks^[17], we call these kind of networks as homogeneous networks. In contrary to homogeneous networks, those networks with large fluctuations in degree distributions are called

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heterogeneous networks, such as scale-free networks^[18]. Of course, the mechanism of the spreading of epidemics on different kind of networks are different, so the values of the thresholds for the outbreak of epidemics on them are also different. When epidemics spread on homogeneous networks, the results both for SIS and SIR models are that the transmission of an infectious agent can be characterized by the epidemic threshold λ_c . The disease will break out when the infection rate $\lambda > \lambda_c$; Otherwise, the contagion is self-limiting. However, when epidemics spread on heterogenous networks, the most striking result is that for SIS and SIR models the epidemic threshold λ_c is null if the size of a heterogenous network is sufficiently large^[1–3].

Because of the different mechanisms of different diseases, the SIS and SIR models can only faithfully be applied to model a limited range of actual diseases (albeit, highly effectively). Often, for real diseases, the infected individuals may experience several distinct stages^[4], e.g., individuals who are infected by HIV-AIDS may pass through several stages: Being highly infectious in the first few weeks after becoming infected, then having low infectivity for many years, and becoming gradually more infectious as their immune system break down, eventually, they progress to AIDS. Moreover, such staged progression models may be applied to situations where the behavior of infected individuals changes with time, and so does their infectivity. In view of all the above facts, an alternative staged progression model is introduced in this paper, and the epidemic spread for the staged progression model both on homogeneous and heterogeneous networks is discussed.

The rest of this paper is organized as follows. In Section 2, the simple staged progression model on networks is discussed. In Section 3, the staged progression model with birth and death on networks is studied. Then, infectivity described as a nonlinear function of nodes' degree is considered in Section 4. In order to verify our theoretical results, we give numerical simulations in Section 5. Finally, conclusions are presented in Section 6.

2 The Simple Staged Progression Model

We now consider the basic staged progression model. In Section 2.1 we treat the homogeneous case, and in Section 2.2 we consider the heterogeneous case. In the following section we introduce birth and death to this basic model.

2.1 Staged Progression Model on Homogeneous Networks

We assume that the individuals can exist in two states: Susceptible (S) and infected (I), where the infected individuals are subdivided into subgroups I_1, I_2, \dots, I_n with different infection stages such that infected susceptible individuals enter the first subgroup I_1 and then gradually progress from this subgroup to subgroup I_n . Let λ_i be the infection rate when susceptible individuals acquire infection from an infected neighbor belonging to subgroup i , for $i = 1, 2, \dots, n$, and β_i be the average percentage of infected individuals transiting from subgroup i to subgroup $i + 1$, for $i = 1, 2, \dots, n - 1$, and let β_n be the rate at which infected become susceptible individuals again^[4].

On homogeneous network, we suppose that every node has same degree $\langle k \rangle$, where $\langle k \rangle = \sum_k kP(k)$ is the average number of the nearest neighbors of one node. Denote by $S(t)$ and $I_i(t)$ the densities of the susceptible population and the infected population in subgroup i at time step t , respectively. So

$$S(t) + \sum_{i=1}^n I_i(t) = 1 \quad (1)$$

with the population unchanged.

At first, a susceptible individual may become infected through contact with its infected neighbors, then all the infected individuals will enter the first stage and pass through different stages with different rates. Finally, some of the infected individuals may become recovered and then become susceptible again. So the evolution equations of densities can be expressed as follows:

$$\begin{aligned} \frac{dS(t)}{dt} &= -S\langle k \rangle \sum_{i=1}^n \lambda_i I_i + \beta_n I_n, \\ \frac{dI_1(t)}{dt} &= S\langle k \rangle \sum_{i=1}^n \lambda_i I_i - \beta_1 I_1(t), \\ \frac{dI_i(t)}{dt} &= \beta_{i-1} I_{i-1}(t) - \beta_i I_i, \quad i = 2, 3, \dots, n. \end{aligned} \tag{2}$$

We are interested in the equilibrium (steady-state) of the system and therefore we let the left-hand side of the Equation (2) be zero. Then, we get

$$I_i = \frac{\beta_1}{\beta_i} I_1, \quad i = 2, 3, \dots, n. \tag{3}$$

From Equation (3), we can find that $I_i \neq 0$ when $I_1 \neq 0$, so it is enough to consider the first two equations of the Equation (2). Because

$$S\langle k \rangle \sum_{i=1}^n \lambda_i I_i - \beta_1 I_1(t) = 0, \tag{4}$$

when Equations(1) and (3) are substituted to above equation, we can get two steady solutions for I_1 :

$$I_1 = 0$$

or

$$I_1 = \frac{\langle k \rangle A - 1}{\beta_1 \langle k \rangle A \sum_{i=1}^n \frac{1}{\beta_i}},$$

where $A = \sum_{i=1}^n \frac{\lambda_i}{\beta_i}$. By using the stability analysis we have the following conclusion:

The steady state $I_1 = 0$ is unstable if

$$A > \frac{1}{\langle k \rangle}, \text{ i.e., } \sum_{i=1}^n \frac{\lambda_i}{\beta_i} > \frac{1}{\langle k \rangle}, \tag{5}$$

however, the other steady solution

$$I_1 = \frac{\langle k \rangle A - 1}{\beta_1 \langle k \rangle A \sum_{i=1}^n \frac{1}{\beta_i}}$$

is stable, that is, the disease will exist on the network.

2.2 Staged Progression Model on Heterogenous Networks

In the previous subsection we have discussed the epidemic threshold of the staged progression models on homogeneous networks. However, many real-world networks show heterogeneous

properties. For instance, scientific-collaboration networks, Internet networks, World Wide Web networks, are all observed to be heterogeneous networks. So we will study the staged progression models on this type of networks. Here, $S_k(t)$ denotes the density of the susceptible individuals with degree k at step t , and $I_{i,k}(t)$ denotes the density of the infected individuals with degree k and belongs to subgroup i at step t . We also have

$$S_k(t) + \sum_{i=1}^n I_{i,k}(t) = 1. \quad (6)$$

Similar to the homogeneous case, the mean-field equations for heterogeneous networks are

$$\begin{aligned} \frac{dS_k(t)}{dt} &= -S_k \sum_{i=1}^n k\lambda_i \Theta_i + \beta_n I_{n,k}, \\ \frac{dI_{1,k}(t)}{dt} &= S_k \sum_{i=1}^n k\lambda_i \Theta_i - \beta_1 I_{1,k}(t), \\ \frac{dI_{i,k}(t)}{dt} &= \beta_{i-1} I_{i-1,k}(t) - \beta_i I_{i,k} \quad i = 2, 3, \dots, n, \end{aligned} \quad (7)$$

where Θ_i , $i = 1, 2, \dots, n$, denote the probability that a link emanate from a susceptible node with degree k to an infected individual in subgroup i . So $\Theta_i(t) = \sum_{k'} P(k'|k) I_{i,k'}(t)$, where $P(k'|k)$ is the probability that a node with degree k points to a node with degree k' . For uncorrelated networks, $P(k'|k) = \frac{k'P(k')}{\langle k \rangle}$, then we have

$$\Theta_i(t) = \sum_{k'} P(k'|k) I_{i,k'}(t) = \frac{\sum_{k'} k' P(k') I_{i,k'}}{\langle k \rangle}, \quad i = 1, 2, \dots, n. \quad (8)$$

By letting the left-hand side of Equation (7) be zero, we have

$$I_{i,k} = \frac{\beta_1}{\beta_i} I_{1,k}, \quad \Theta_i = \frac{\beta_1}{\beta_i} \Theta_1, \quad i = 2, 3, \dots, n. \quad (9)$$

So the ubiquity of disease on the network is equivalent to the existence of $I_{1,k}$. From Equations (6), (7), and (9), we obtain the following equation

$$\frac{dI_{1,k}(t)}{dt} = \left(1 - I_{1,k} \sum_{i=1}^n \frac{\beta_1}{\beta_i} \right) k\beta_1 \Theta_1 A - \beta_1 I_{1,k}(t), \quad (10)$$

here $A = \sum_{i=1}^n \frac{\lambda_i}{\beta_i}$. By setting the left-hand side of Equation (10) be zero, then,

$$I_{1,k} = \frac{k\Theta_1 A}{1 + k\beta_1 \Theta_1 A \sum_{i=1}^n \frac{1}{\beta_i}}. \quad (11)$$

Since $I_{1,k}$ is in turn a function of $\Theta_1 = \frac{1}{\langle k \rangle} \sum_k kP(k) I_{1,k}(t)$, we obtain a self-consistency equation

$$\Theta_1 = \frac{\Theta_1 A}{\langle k \rangle} \sum_k \frac{k^2 P(k)}{1 + k\beta_1 \Theta_1 A \sum_{i=1}^n \frac{1}{\beta_i}}, \quad (12)$$

where $\theta_1 = 0$ always satisfies the Equation (12), a nontrivial solution exists only if^[1-2]

$$\frac{d}{d\theta_1} \left(\frac{\theta_1 A}{\langle k \rangle} \sum_k \frac{k^2 P(k)}{1 + k\beta_1 \theta_1 A \sum_{i=1}^n \frac{1}{\beta_i}} \right) \Big|_{\theta_1=0} > 1, \tag{13}$$

that is,

$$A > \frac{\langle k \rangle}{\langle k^2 \rangle}, \text{ i.e., } \sum_{i=1}^n \frac{\lambda_i}{\beta_i} > \frac{\langle k \rangle}{\langle k^2 \rangle}, \tag{14}$$

where $\langle k^2 \rangle = \sum_k k^2 P(k)$. Because the degree distribution of scale-free network is $P(k) \sim k^{-\gamma}$, with $2 < \gamma \leq 3$ in most cases, for which $\langle k^2 \rangle \rightarrow +\infty$ when the size of network is sufficiently large, then the inequality (2.14) is always satisfied. In other words, the staged progression models will prevail on sufficiently large heterogenous networks and the infection becomes endemic, even if only a small density of population was infected.

3 The Staged Progression Model with Birth and Death

In [5], Liu and coworkers analyzed the spread of diseases with birth and death. In their paper, they supposed that individuals are distributed on a network, and each node of the network is empty or occupied by at most one individual. They used the numbers 0, 1, 2 to denote that the node has no individual, a healthy (susceptible) individual and an infected individual, respectively. Each node can change its state with certain rate. An empty node can give birth to a healthy (susceptible) individual at the rate δ . The susceptible individual can be infected at a rate proportional to the number of infected individuals in the neighborhood or die at certain rate α . The infected individual can be cured at certain rate γ or die at certain rate β . If an individual dies, that node will become an empty node again.

In this section we will discuss the staged progression model with birth and death. In order to be consistent with the above section, the symbols which have been used in above section will have the same meaning in this section. In addition, we use δ and α to denote the birth rate and death rate of susceptible individual respectively, and $\gamma_i, i = 1, 2, 3, \dots, n$, stand for the death rate of individuals who are infected and belong to subgroup i . Now, we consider the epidemic thresholds for this model on homogeneous and heterogenous networks respectively.

3.1 Staged Progression Model with Birth and Death on Homogeneous Networks

On homogeneous networks, the dynamical equations of staged progression model with birth and death are:

$$\begin{aligned} \frac{dS(t)}{dt} &= \delta \left(1 - S - \sum_{i=1}^n I_i \right) - \alpha S - S \langle k \rangle \sum_{i=1}^n \lambda_i I_i + \beta_n I_n, \\ \frac{dI_1(t)}{dt} &= S \langle k \rangle \sum_{i=1}^n \lambda_i I_i - \beta_1 I_1(t) - \gamma_1 I_1, \\ \frac{dI_i(t)}{dt} &= \beta_{i-1} I_{i-1}(t) - \beta_i I_i - \gamma_i I_i, \quad i = 2, 3, \dots, n. \end{aligned} \tag{15}$$

By using the same method as in Section 2.1, the two steady-state solutions for I_1 are

$$I_1 = 0$$

or

$$I_1 = \frac{\langle k \rangle \delta \sum_{i=1}^n \lambda_i A_i - (\delta + \alpha)(\beta_1 + \gamma_1)}{\langle k \rangle \sum_{i=1}^n \lambda_i A_i \left\{ (\beta_1 + \gamma_1) + \delta \sum_{i=1}^n A_i - \beta_n A_n \right\}}, \quad (16)$$

where

$$A_i = \frac{\prod_{j=1}^{i-1} \beta_j}{\prod_{j=2}^i (\beta_j + \gamma_j)}, \quad i = 2, 3, \dots, n,$$

and set $A_1 = 1$. The disease will pervade on the network when

$$\sum_{i=1}^n \lambda_i A_i > \frac{(\delta + \alpha)(\beta_1 + \gamma_1)}{\delta \langle k \rangle}. \quad (17)$$

3.2 Staged Progression Model with Birth and Death on Heterogenous Networks

For the staged progression model with birth and death on heterogenous networks, we have the following dynamical equations:

$$\begin{aligned} \frac{dS_k(t)}{dt} &= \delta \left(1 - S_k - \sum_{i=1}^n I_{i,k} \right) - \alpha S_k - S_k \sum_{i=1}^n k \lambda_i \Theta_i + \beta_n I_{n,k}, \\ \frac{dI_{1,k}(t)}{dt} &= S_k \sum_{i=1}^n k \lambda_i \Theta_i - \beta_1 I_{1,k}(t) - \gamma_1 I_{1,k}, \\ \frac{dI_{i,k}(t)}{dt} &= \beta_{i-1} I_{i-1,k}(t) - \beta_i I_{i,k} - \gamma_i I_{i,k}, \quad i = 2, 3, \dots, n. \end{aligned} \quad (18)$$

By letting the left-hand side of Equation (18) be zero, we obtain

$$I_{i,k} = A_i I_{1,k}, \quad \Theta_i = A_i \Theta_1, \quad i = 2, 3, \dots, n. \quad (19)$$

Substituting $I_{i,k}$ and Θ_i in Equation (19) into the first two equations of Equation (18), we have

$$\begin{aligned} \frac{dS_k(t)}{dt} &= \delta \left(1 - S_k - I_{1,k} \sum_{i=1}^n A_i \right) - \alpha S_k - S_k k \Theta_1 \sum_{i=1}^n \lambda_i A_i + \beta_n A_n I_{1,k}, \\ \frac{dI_{1,k}(t)}{dt} &= S_k k \Theta_1 \sum_{i=1}^n \lambda_i A_i - \beta_1 I_{1,k}(t) - \gamma_1 I_{1,k}, \end{aligned}$$

then we have equilibrium for S_k and $I_{1,k}$:

$$S_k = \frac{\beta_1 + \gamma_1}{k \Theta_1 \sum_{i=1}^n \lambda_i A_i} I_{1,k}, \quad I_{1,k} = \frac{\delta - (\delta + \alpha) S_k}{\delta \sum_{i=1}^n A_i + (\beta_1 + \gamma_1) - \beta_n A_n},$$

i.e.,

$$I_{1,k} = \frac{k \delta \Theta_1 \sum_{i=1}^n \lambda_i A_i}{\left(\delta \sum_{i=1}^n A_i + (\beta_1 + \gamma_1) - \beta_n A_n \right) k \Theta_1 \sum_{i=1}^n \lambda_i A_i + (\beta_1 + \gamma_1)(\alpha + \delta)}.$$

Then, by using the method as in Section 2.2, we obtain the epidemic threshold:

$$\sum_{i=1}^n \lambda_i A_i > \frac{(\delta + \alpha)(\beta_1 + \gamma_1)\langle k \rangle}{\delta \langle k^2 \rangle}. \tag{20}$$

From (17) and (20), we can find the effects of birth and death rates on the epidemic thresholds λ_i , $i = 1, 2, \dots, n$.

4 Nonlinear Infectivity

The obtained results on heterogenous networks are based on the hypothesis that the larger the degree of an infected individual, the greater the capability for infection it has, i.e., hub=super-spreader^[13]. However, in [6–8], Zhou, et al. argued that this hypothesis is not always true. For example, for human sexual network, although a few individuals have many sexual partners, their sexual activities are not far beyond a normal level due to physiological limitations. So they assumed that the infectivity is identical, that is, C , for every node regardless their different degrees. Therefore,

$$\theta = \sum_{k'} \frac{CP(k'|k)I_{k'}}{k'}, \tag{21}$$

where the factor $\frac{1}{k'}$ accounts for the probability that one of the infected neighbors of a node, with degree k' , will contact this node at the present time step. Then they obtained the positive epidemic threshold $\lambda_c = 1/C$ for SIS, SI and SIR model on networks, which does not depend on the degree distribution^[6–8].

Because the equation $\theta = \sum_{k'} P(k'|k)I_{k'}$ can be rewritten as

$$\theta = \sum_{k'} P(k'|k)I_{k'} = \sum_{k'} \frac{k'P(k'|k)I_{k'}}{k'}, \tag{22}$$

the above two equations can be read in a coherent form as:

$$\theta = \sum_{k'} \frac{\varphi(k')P(k'|k)I_{k'}}{k'}, \tag{23}$$

here $\varphi(k)$ denotes the infectivity of a node with degree k . Equation (23) will become Equation (21) if $\varphi(k) = C$, and Equation (23) will become Equation (22) if $\varphi(k) = k$, respectively.

If the identical infectivity is assumed for the staged progression model on heterogenous networks, the epidemic threshold is also nonzero, take the case in Section 3.2 as an example, we have the following conclusion:

$$\sum_{i=1}^n \lambda_i A_i > \frac{(\delta + \alpha)(\beta_1 + \gamma_1)}{C\delta}. \tag{24}$$

The result does not depend on the degree distribution of the network.

Because the following two reasons: Firstly, the infectivity may partially depend on the nodes' degree, for example, the individual who has more acquaintances may contact more individuals but not all of his/her acquaintances; secondly, the infectivity may be approximately proportional to nodes' degree k when k is relative small, and then is saturated when degree

k increases, at last, it is a constant when degree k is sufficiently large. Based on the above reasons, we follow and let $\varphi(k)$ is as^[15]

$$\varphi(k) = \frac{ak^\nu}{1+bk^\nu},$$

here $0 \leq \nu \leq 1$ is a variable, and $a > 0, b \geq 0$ are two constants. So $\varphi(k) = ak$ when $\nu = 1, b = 0$; $\varphi(k) = a/(b+1)$ when $\nu = 0$; and $\varphi(k)$ is a nonlinear function if $0 < \nu < 1$ and $b \neq 0$, which becomes greater when a node's degree k increased, when k is relatively small, then it saturates when degree k is big, and eventually, it is a constant $\varphi(k) \approx \frac{a}{b}$ when degree k is sufficiently large. Now, we have

$$\Theta = \sum_{k'} \frac{\varphi(k')P(k'|k)I_{k'}}{k'} = \sum_{k'} \frac{\frac{ak'^\nu}{1+bk'^\nu}P(k'|k)I_{k'}}{k'}.$$

For uncorrelated networks, $P(k'|k) = \frac{k'P(k')}{\langle k \rangle}$, the above equation can be written as:

$$\Theta = \frac{\sum_{k'} \frac{ak'^\nu}{1+bk'^\nu}P(k')I_{k'}}{\langle k \rangle}. \quad (25)$$

We substitute

$$\Theta_i = \frac{\sum_{k'} \frac{ak'^\alpha}{1+bk'^\alpha}P(k')I_{i,k'}}{\langle k \rangle} \quad (26)$$

for Θ_i in Section 3.2, then the epidemic threshold of the staged progression on scale-free networks is:

$$\sum_{i=1}^n \lambda_i A_i > \frac{(\delta + \nu)(\beta_1 + \gamma_1)\langle k \rangle}{\delta \langle \frac{ak^{\nu+1}}{1+bk^\nu} \rangle}, \quad (27)$$

where $\langle \frac{ak^{\nu+1}}{1+bk^\nu} \rangle = \sum_k P(k) \frac{ak^{\nu+1}}{1+bk^\nu}$. From (27), we can see:

Case A

$$(27) \Rightarrow \begin{cases} (20), & a = 1, b = 0, \nu = 1, \\ (24), & \frac{a}{b+1} = C, \nu = 0. \end{cases}$$

For the case of $0 < \nu < 1$ and scale-free networks with degree distribution $P(k) = k^{-\gamma}, 2 < \gamma \leq 3$, then

$$\left\langle \frac{ak^{\nu+1}}{1+bk^\nu} \right\rangle = \sum_k k^{-\gamma} \frac{ak^{\nu+1}}{1+bk^\nu} \approx \int_m^\infty \frac{ak^{\nu+1-\gamma}}{1+bk^\nu} dk, \quad (28)$$

here m is the least degree of the network.

Case B

If $\varphi(k) = \frac{ak^\nu}{1+bk^\alpha} = ak^\nu$ with $b = 0$, then

$$\left\langle \frac{ak^{\nu+1}}{1+bk^\nu} \right\rangle = \int_m^\infty \frac{a}{k^{\gamma-(\nu+1)}} dk \approx \frac{a}{(\gamma - (\nu + 2))m^{\nu+2-\gamma}}. \quad (29)$$

The integral of the above equation is bounded when $\gamma > 2 + \nu$.

Case C

If $\varphi(k) = \frac{ak^\nu}{1+bk^\nu}$ with $b \neq 0$,

$$\left\langle \frac{ak^{\nu+1}}{1+bk^\nu} \right\rangle = \int_m^\infty \frac{a}{k^{\gamma-(1+\nu)} + bk^{\gamma-1}} dk, \tag{30}$$

when $0 < \nu < 1$ and $2 < \gamma \leq 3$, the left-hand side of Equation (30) is bounded.

From the above analysis, we know that the epidemic thresholds $\lambda_i, i = 1, 2, \dots, n$, are bounded values when the nonlinear infectivity is considered, even though the sufficiently large heterogenous network is considered. In contrast to (24), this result depends on the degree distribution of networks.

5 Numerical Examples

In this section, we present numerical simulations to support our results, which are based on the BA networks with $P(k) = k^{-\gamma}, \gamma = 3$, and $\langle k \rangle \approx 6$, if we set $N = 200$, then $\langle k^2 \rangle \approx 61$; and if we set $N = 2000$, then $\langle k^2 \rangle \approx 98$. We only consider that the infected individuals have two stages, that is, $n = 2$.

In Figure 1, we simulate the results in Section 2. For simplicity, we give a fixed value for λ_2 each time, just to find out the threshold for λ_1 . This method is also used in other simulations. With $N = 200, \beta_1 = 0.2, \beta_2 = 0.2$ unchanged, from (5) and (14), we have

$$\begin{aligned} \lambda_2 = 0.02, \text{ heterogenous} &\Rightarrow \lambda_1 = 0, \\ \lambda_2 = 0.01, \text{ heterogenous} &\Rightarrow \lambda_1 = 0.0096, \\ \lambda_2 = 0.02, \text{ homogenous} &\Rightarrow \lambda_1 = 0.0233. \end{aligned} \tag{31}$$

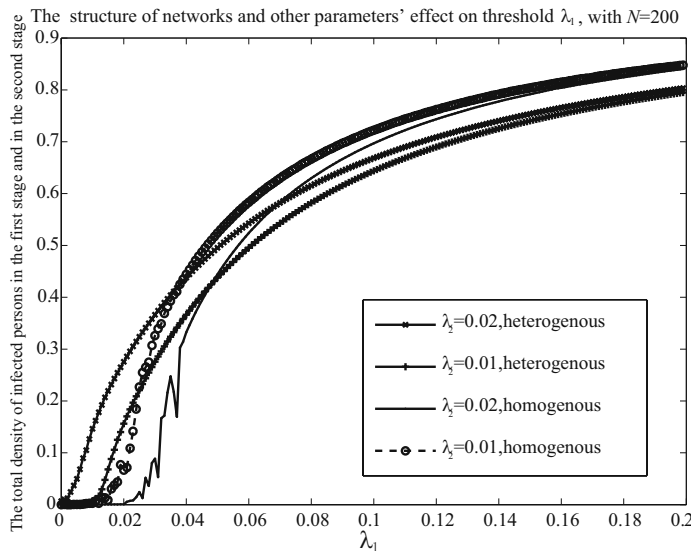


Figure 1 Simulations are conducted to verify the threshold λ_1 given in (5) and (14), by changing the structure of networks and some parameters as in Equation (31). We can see the threshold λ_1 is in accordance with Equation (31)

In Figure 2, we simulate the results in Section 3, with $N = 200, \alpha = 0.1, \gamma_1 = \gamma_2 = 0.2, \beta_1 = 0.3, \beta_2 = 0.4, \delta = 0.1$ unchanged. According to (17) and (20), we have

$$\begin{aligned}
 \lambda_2 = 0.1, \text{ homogeneous} &\Rightarrow \lambda_1 = 0.1167, \\
 \lambda_2 = 0.35, \text{ homogeneous} &\Rightarrow \lambda_1 = 0, \\
 \lambda_2 = 0.1, \text{ heterogenous} &\Rightarrow \lambda_1 = 0.0484, \\
 \lambda_2 = 0.35, \text{ heterogenous} &\Rightarrow \lambda_1 = 0.
 \end{aligned}
 \tag{32}$$

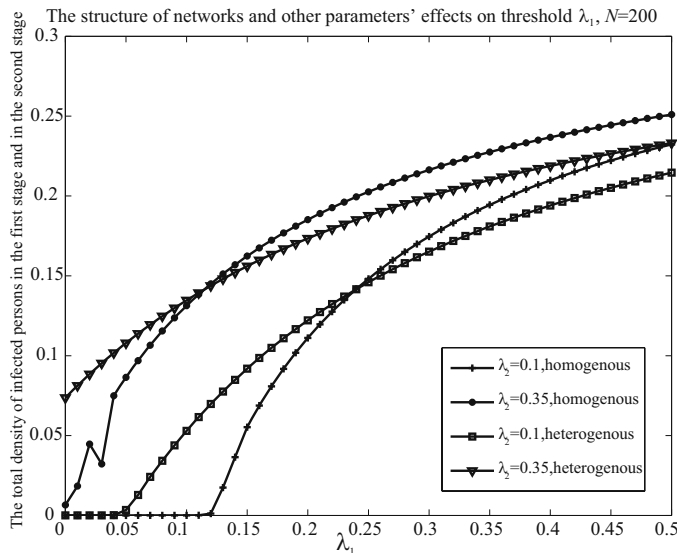


Figure 2 Simulations are conducted to verify (17) and (20), by changing the structure of networks and some parameters as in Equation (32). The threshold λ_1 is in accordance with Equation (32)

In Figure 3, we also simulate the results in Section 3, however, we just compare the effects of the size of heterogenous networks on the threshold λ_1 , with $\delta = 0.1, \alpha = 0.3, \gamma_1 = \gamma_2 = 0.2, \delta = 0.1$ unchanged. According to (17) and (20), we have

$$\begin{aligned}
 N = 2000, \langle k^2 \rangle \approx 98 &\Rightarrow \lambda_1 = 0.0724, \\
 N = 200, \langle k^2 \rangle \approx 61 &\Rightarrow \lambda_1 = 0.1467, \\
 N = 200 \text{ or } 2000, \text{ homogenous} &\Rightarrow \lambda_1 = 0.2833.
 \end{aligned}
 \tag{33}$$

From Figure 3 we can see that for heterogenous networks the larger the network is, the smaller the threshold λ_1 is, which coincides with the Equation (33). This case is also true for other cases, so we do not compare the effects of the size of heterogenous networks on the threshold again.

In Figure 4, we verify the results obtained in Section 4, we compare the effects of different kinds of infectivity on the threshold λ_1 , with $N = 2000, \alpha = 0.3, \gamma_1 = \gamma_2 = 0.2, \lambda_2 = 0.1, \beta_1 = 0.3, \beta_2 = 0.4, \delta = 0.1$ unchanged. According to (20), (24), and (27).

$$\begin{aligned}
 f(k) = k &\Rightarrow \lambda_1 = 0, \\
 f(k) = 2k^{\frac{1}{2}} &\Rightarrow \lambda_1 = 0.094, \\
 f(k) = \frac{2k^{\frac{1}{2}}}{1 + \frac{1}{2}k^{\frac{1}{2}}} &\Rightarrow \lambda_1 = 0.375, \\
 f(k) = 4 &\Rightarrow \lambda_1 = 0.2.
 \end{aligned}
 \tag{34}$$

From Figure 4, we can see that the threshold λ_1 is positive for nonlinear infectivity, although the threshold $\lambda_1 = 0$ for linear infectivity.

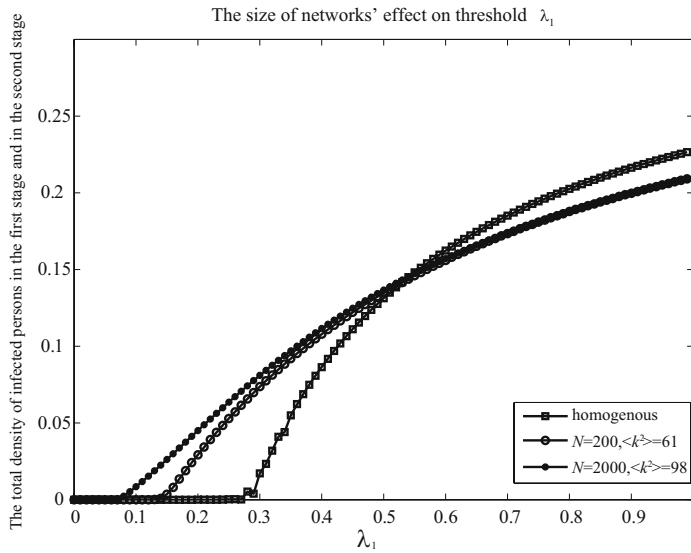


Figure 3 Simulations are also conducted to verify (17) and (20), but just simulate the effects of the size of heterogenous networks on the threshold λ_1 . The threshold λ_1 is in accordance with Equation (33)

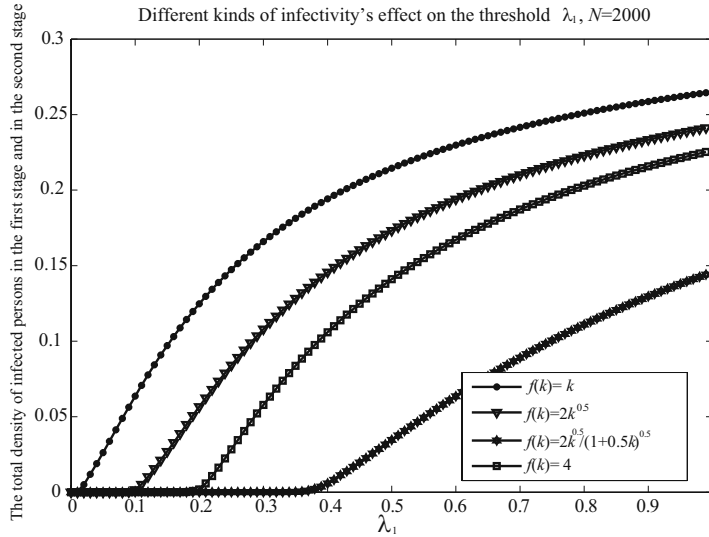


Figure 4 Simulations are conducted to verify the effects of different kinds of infectivity on the threshold λ_1 . The threshold λ_1 is in accordance with Equation (34)

6 Conclusions

In this paper we have discussed the epidemic threshold of the staged progression model on homogeneous and heterogenous networks, including a simple model and the model with both

birth and death. We also have analyzed infectivity as a nonlinear function of node degree, and compared this case to cases with constant or linear infectivity. Our results show that the absence of an epidemic threshold observed for SIS epidemics on scale-free networks also holds for staged epidemic models. Similarly, if one introduces a nonlinear (sub-linear) scaling of infectivity with connectivity, one observed a nonzero threshold. These results are consistent with, and extend, those that have been previously reported for simple disease models. However, our results are more widely applicable to realistic disease situations when the infection (or the hosts response to an infection) undergoes several distinct stages. This is applicable to common infections (colds and influenza viruses) in which the infected individuals will change their behavior over time, and immune deficiency disorders (such as HIV-AIDS) in which the level of infectivity changes with time. Our results also address the previous idealization of an infinite tail in the power law distribution and we find that it is only in the idealized case that one observes a zero threshold. All of these conclusions are verified by numerical simulations.

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