EPIDEMIC DYNAMICS ON COMPLEX NETWORKS WITH GENERAL INFECTION RATE AND IMMUNE STRATEGIES

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ABSTRACT. This paper mainly aims to study the influence of individuals’ different heterogeneous contact patterns on the spread of the disease. For this purpose, an SIS epidemic model with a general form of heterogeneous infection rate is investigated on complex heterogeneous networks. A qualitative analysis of this model reveals that, depending on the epidemic threshold $R_0$, either the disease-free equilibrium or the endemic equilibrium is globally asymptotically stable. Interestingly, no matter what functional form the heterogeneous infection rate is, whether the disease will disappear or not is completely determined by the value of $R_0$, but the heterogeneous infection rate has close relation with the epidemic threshold $R_0$. Especially, the heterogeneous infection rate can directly affect the final number of infected nodes when the disease is endemic. The obtained results improve and generalize some known results. Finally, based on the heterogeneity of contact patterns, the effects of different immunization schemes are discussed and compared. Meanwhile, we explore the relation between the immunization rate and the recovery rate, which are the two important parameters that can be improved. To illustrate our theoretical results, the corresponding numerical simulations are also included.

1. Introduction. The outbreaks of infectious diseases, such as SARS, Ebola virus and MERS, always bring great threats to public security and individual health. Fortunately, more and more scholars have analyzed the spread and control of infectious diseases. In many epidemic systems, disease transmission can be represented as complex networks where nodes stand for individuals and an edge connecting two nodes denotes the interaction between individuals. What’s more, many real world
networks show the edge between two nodes is usually not uniform but heterogeneous [27]. That is to say, the number of contacts with other individuals for each individual is not always the same in the real world. Therefore, the node with more edges has a higher possibility of being infected. Recently, starting with the seminal works by Pastor-Satorras and Vespignani [20, 21], there has been a burst of activity on investigating the effects of the network topology on the behavior of epidemic spreading (see [1], [3]–[8], [11], [13]–[16], [18], [19], [23], [25]–[29], [31], [32]).

To deal with the heterogeneity of contact patterns, the difference of node degree should be considered. The degree of a node is the number of its neighbors. For epidemic spreading of SIS process, each node in the network can be either susceptible (S) or infected (I) at any time. In considering the heterogeneous contact (i.e., every node can contact more than one node located in its neighboring nodes), one can assume that at each time step, each infected node spreads the disease to its susceptible neighbors with probability \( \lambda \), and it returns to the susceptible node with recovery rate \( \gamma \) at the end of the infection. Thus, each susceptible node is infected (per unit time) by a probability of \( 1 - (1 - \lambda)^{k_{i,n,t}} \) (referred as nonlinear contagion scheme in [17]). Here \( k_{i,n,t} \) is the total number of infected neighbors.

In reality, different individual may have different infection rate, which is related to the number of infected neighbors. This means the infection rate will increase with the increasing density of infected nodes around. Consequently, the probability to be infected is varying according to the environment. Under this consideration, Qin and Zhong et al. [23] proposed the environment aware SIS model (abbr. EA-SIS) as follows:

\[
\frac{d\rho_k(t)}{dt} = -\rho_k(t) + [1 - (1 - \lambda)^{k_{i,n,t}}](1 - \rho_k(t)), \quad k = 1, 2, \ldots, \tag{1}
\]

where \( \rho_k(t) \) represents the relatively density of infected nodes with degree \( k \) at time \( t \). Here, the recovery rate \( \gamma \) is assumed to be time invariant, that is, it is denoted as unity. \( \Theta(t) \) is the probability that any given link pointing to an infected node. Considering uncorrelated networks, \( \Theta(t) = \frac{1}{N} \sum_k k P(k) \rho_k(t) \) [20, 21], where \( P(k) \) is the probability that a randomly chosen node has degree \( k \) (i.e., the degree distribution) and \( \langle k \rangle = \sum_k k P(k) \) is the average degree. For convenience, the usual notation \( \langle f(k) \rangle := \sum_k f(k) P(k) \) is used. The heterogeneous infection rate of model (1) is \( 1 - (1 - \lambda)^{k_{i,n,t}} \). It is showed that the expected number of infected neighbors of a susceptible node with degree \( k \) is approximated by \( k \Theta(t) \). Based on the theoretical analysis and simulation results, the authors found that the transmission threshold \( \lambda_c \) of model (1) is smaller than that of the well-known SIS model in [20, 21], which means the disease is easier to spread out in the EA-SIS model (1). However, the stability analysis of the disease-free equilibrium and endemic equilibrium of (1) has not been further studied. Moreover, some diseases, such as tuberculosis, can last for an individual’s lifetime. In this case, the influence of birth and death cannot be ignored in modelling of infectious disease dynamics.

Consequently, we establish the following network-based SIS epidemic model with a general form of heterogeneous infection rate, as well as the birth and death rates:

\[
\begin{align*}
\frac{dS_k(t)}{dt} & = bN_k(t) - \mu S_k(t) - g(k, \lambda, \Theta(t)) S_k(t) + \gamma I_k(t), \\
\frac{dI_k(t)}{dt} & = g(k, \lambda, \Theta(t)) S_k(t) - (\mu + \gamma) I_k(t),
\end{align*} \tag{2}
\]

where \( S_k(t) \) and \( I_k(t) \) represent the relative densities of susceptible and infected nodes with degree \( k \) at time \( t \), respectively. \( N_k(t) \) represents the number of nodes with degree \( k \) at time \( t \), that is, \( N_k(t) = S_k(t) + I_k(t), \quad k = 1, 2, \ldots \). The natural
births and deaths are proportional to the densities of nodes with birth rate $b$ and death rate $\mu$, respectively. According to [7, 29, 32],

$$\Theta(t) = \frac{1}{\langle k \rangle} \sum_k \varphi(k) P(k) I_k(t),$$

(3)

which has the same meaning as in (1). $\varphi(k)$ represents the infectivity of a node with degree $k$, i.e., $\varphi(k)$ denotes the average number of occupied edges from which a node with degree $k$ can transmit the disease [11, 19]. This means that $\varphi(k) \leq k$. Recently, various types of the infectivity $\varphi(k)$ were studied, such as $\varphi(k) = k$ [20, 21, 23, 25]; $\varphi(k) = A$ [28]; $\varphi(k) = \min\{A, \alpha k\}, 0 < \alpha \leq 1$ [5]; $\varphi(k) = k^n$ [3] and $\varphi(k) = \rho k^{\alpha}/(1 + \nu k^\alpha), \rho > 0, \nu \geq 0$ [6, 7, 29, 32]. That is, the function $\varphi(k)$ in (3) can take any of the above forms according to the degree of real networks. Other parameters have the same meanings as in model (1) and all the parameters are positive.

The general form of heterogeneous infection rate in model (2) is defined by $g(k, \lambda, \Theta(t))$. For convenience, we let $f_k(\Theta) := g(k, \lambda, \Theta(t))$, where $\lambda$ is the per edge transmission rate between a susceptible node and an infected node, and $\lambda \in (0, 1]$ ($\lambda = 0$ is meaningless for the theoretic analysis). In order to comply with the real experience, we assume that $f_k(\Theta)$ is a monotone function with $(H_1)$: $f_k(\Theta) \geq 0$ and $f_k(\Theta) = 0$ only if $\Theta = 0$; $(H_2)$: $f_\nu(\Theta) > 0$ and $(H_3)$: $f_\nu(\Theta) \leq 0$, where $f_\nu(\Theta) := \frac{d}{d\nu} f_k(\Theta)$ and $f_\nu(\Theta) := \frac{d^2}{d\nu^2} f_k(\Theta)$. Under the assumptions $(H_1) - (H_3)$, the function $f_k(\Theta)$ covers some examples appearing in the literature. For instance, $f_k(\Theta) = \lambda k \Theta$ [5, 20, 25, 29]; $f_k(\Theta) = \lambda k \Theta$ [6, 7, 19, 32]; $f_k(\Theta) = 1 - (1 - \lambda \Theta)^k$ [14, 27] and $f_k(\Theta) = 1 - (1 - \lambda)^{k\Theta}$ [23].

In this paper, we assume that the birth rate equals the dead rate, i.e., $b = \mu$. It follows from (2) that $dN_k(t)/dt = 0$. It implies that the total number of nodes $N(t) = \sum_k N_k(t)$ remains time invariant. Although the adding and removal nodes and edges may change the structure of the network, they only take a small proportion in the huge network and will change slightly the network topology [13, 32]. Hence, we focus on the case that the network size is time invariant. Since the number of individuals is finite in a real system, we shall study the dynamic behavior on finite-size network in the following. Note $n$ is the maximum node degree of the finite-size network, implying that $P(k) = 0$ for all $k > n$. From a practical perspective, only the case of $P(k) > 0$, for $k = 1, 2, \cdots, n$, is considered, and the initial conditions for system (2) satisfy:

$$I_0(0) \geq 0, \quad S_0(0) = 1 - I_0(0) > 0, \quad k = 1, 2, \cdots, n, \text{ and } \Theta(0) > 0.$$

Therefore, we have $N_k(t) \equiv 1$, for all $k = 1, 2, \cdots, n$, this yields the following model:

$$\begin{cases}
\frac{dS_k(t)}{dt} &= \mu - \mu S_k(t) - f_k(\Theta(t))S_k(t) + \gamma I_k(t), \\
\frac{dI_k(t)}{dt} &= f_k(\Theta(t))S_k(t) - (\mu + \gamma) I_k(t).
\end{cases}$$

(5)

Some special cases of model (5) were studied, such as $\mu = 0, \gamma = 1, \varphi(k) = k$ and $f_k(\Theta(t)) = \lambda k \Theta(t)$ in [20, 21, 25]; $\mu = 0, \gamma = 1, \varphi(k) = \min\{A, \alpha k\}$ and $f_k(\Theta(t)) = \lambda k \Theta(t)$ in [5]; $\mu = 0, \gamma = 1$ and $f_k(\Theta(t)) = \lambda k \Theta(t)$ in [29]; $f(\Theta(t)) = \lambda k \Theta(t)$ in [32]; $\mu = 0, \gamma = 1, \varphi(k) = k$ $f_k(\Theta(t)) = 1 - (1 - \lambda \Theta(t))^k$ [14]; and $\mu = 0, \gamma = 1, \varphi(k) = k$ and $f_k(\Theta(t)) = 1 - (1 - \lambda)^{k\Theta(t)}$ in [23].
When fighting an epidemic in a heterogeneous population, it is natural to look for specifically devised immunization strategies. As a result, many effective immunization through vaccination on heterogeneous networks have been proposed and investigated, including uniform immunization [6, 22], targeted immunization [5, 16, 22], acquaintance immunization [5, 16] and so on. As was pointed out by Madar et al. [16], in the immunization process, choosing which kind of individuals to be immunized is a very important step. It may increase the efficiency of the immunization strategy, and then can prevent loss of time and funds due to the disease. That is to say, successful immunization strategies can be developed well by taking good advantage of the inhomogeneous connectivity properties of contact patterns. Thus, in this paper, the effects of different vaccination strategies based on the heterogeneity of the infection rate are studied and compared. Meanwhile, we also investigate the relation between the immunization rate and the recovery rate, which are the two important parameters that can be improved.

In mathematical epidemiology, as we have seen in the literatures [6, 8, 7, 11, 12, 13, 25, 27, 31, 32], one of the most important problem is to study the global behavior of epidemic spreading. For the spreading of infections on heterogeneous networks, Pastor-Satorras and Vespignani [20, 21] proposed and studied a well-known SIS epidemic model, which has inspired a great number of related works. A strict mathematical proof of the conclusions about the global dynamics of this model was given by Wang and Dai [25]. Later, Zhu and Fu et al. [32] extended this model by considering the effects of birth and death, as well as nonlinear infectivity, on the spread of diseases. Both [25] and [32] show that the endemic equilibrium is globally attractive by using a monotone iterative technique. Recently, Huang and Jiang [8] proved the global asymptotical stability of the endemic equilibria of the model in [25] and the model with the constraint condition $\lambda(k) = \lambda k$ in [32]. It is noticed that the problem about the global asymptotical stability of the endemic equilibrium of the model without the condition $\lambda(k) = \lambda k$ in [25] is worth studying further.

To date, there has still been relatively little research studied on the global dynamics of the network-based epidemic models, especially the generalized models. Liu and Ruan [15] proposed an SIS epidemic model with a generalized nonlinear incidence rate on scale-free networks. They derived the basic reproduction number and investigated the stability of the disease-free equilibrium, but they neglected to explore the stability problem of the endemic equilibrium. Zhang and Sun [31] presented an SIS epidemic model with a generalized feedback mechanism on weighted networks and obtained the global asymptotical stability of the disease-free equilibrium and the local asymptotical stability of the endemic equilibrium. Huang and Jiang [8] developed and analyzed a new SIS epidemic model with a general nonlinear incidence rate on complex heterogeneous networks. They proved the permanence of the disease and the global asymptotical stability of disease-free equilibrium in detail. Meanwhile, they obtained that the unique endemic equilibrium is globally asymptotically stable under some sufficient conditions. Furthermore, the authors in [8, 31] numerically found that the endemic equilibrium is globally asymptotically stable only when the epidemic threshold is greater than one (i.e., without requiring any extra conditions). However, to the best of our knowledge, the rigorous mathematical proof of this conclusion is not yet available, which is a very challenging issue.
Motivated by the above analysis, in this paper, we investigate the global dynamics of model (5) with a general form of heterogeneous infection rate. The rest of this paper is organized as follows. In Sect. 2, the positivity of solutions and the epidemic threshold are obtained. In Sect. 3, a global analysis of the model is presented. In Sect. 4, different immunization strategies are studied and compared. In Sect. 5, some related issues are discussed and the theoretical results are supported by numerical simulations. Finally, we conclude the paper in Sect. 6.

2. Positivity of solutions and the epidemic threshold. Before going into details, let us simply system (5). Substituting $S_k(t) = 1 - I_k(t)$ into system (5), it is natural to obtain the equivalent system:

$$\frac{dI_k(t)}{dt} = f_k(\Theta(t))(1 - I_k(t)) - (\mu + \gamma)I_k(t), \quad k = 1, 2, \cdots, n. \quad (6)$$

In order to investigate the global stability of system (5), we only need to study the global stability of system (6). Now, we establish the positivity of solutions in the following lemma.

Lemma 2.1. Suppose that $(S_1(t), I_1(t), \cdots, S_n(t), I_n(t))$ is a solution of system (5) with initial conditions (4), then $0 < S_k(t), I_k(t), \Theta(t) < 1$ for all $t > 0$, $k = 1, 2, \cdots, n$.

Proof. First, for all $k \in \{1, 2, \cdots, n\}$, we will prove that $I_k(t) < 1$ for all $t > 0$. It follows from (4) that $I_k(0) = 1 - S_k(0) < 1$. Due to the continuity of $I_k(t)$, we can find a small $\varepsilon > 0$ such that $I_k(t) < 1$ for $t \in (0, \varepsilon)$. Now we want to show that $I_k(t) < 1$ for all $t > 0$ and $k = 1, 2, \cdots, n$. Suppose not, then there exists $j \in \{1, 2, \cdots, n\}$ and the first time $t_1 \geq \varepsilon > 0$ such that $I_k(t_1) = 1$ and $I_k(t) < 1$ for $t \in (0, t_1)$. It follows from system (6) that $\frac{dI_k(t)}{dt} \bigg|_{t=t_1} = -(\mu + \gamma) < 0$, which implies that there exists $t_2 \in (0, t_1)$ such that $I_j(t_2) > I_j(t_1) = 1$. This is apparently a contradiction.

Note that $\Theta(0) = \sum_{k=1}^{n} \varphi(k)P(k)I_k(0) > 0$, then we have $I_k(0) > 0$ for some $k$. Therefore, we can claim that $I_k(t) > 0$ for all $t > 0$ and $k = 1, 2, \cdots, n$. If not, there exists an integer $i \in \{1, 2, \cdots, n\}$ and the first time $t_0 > 0$ such that $I_i(t_0) = 0$ and $I_i(t) > 0$ for all $t \in (0, t_0)$. Then, from (3), it holds that $\Theta(t) > 0$ for $t \in (0, t_0)$. By integrating (6) from 0 to $t$, it follows that

$$I_k(t) = I_k(0)e^{-(\mu + \gamma)t} + \int_0^t f_k(\Theta(s))(1 - I_k(s))e^{-(\mu + \gamma)(t-s)}ds.$$  

So we have

$$I_i(t_0) = I_i(0)e^{-(\mu + \gamma)t_0} + \int_0^{t_0} f_i(\Theta(s))(1 - I_i(s))e^{-(\mu + \gamma)(t_0-s)}ds > 0.$$  

This leads to a contradiction.

Hence, we reach that $0 < I_k(t) < 1$ for all $k \in \{1, 2, \cdots, n\}$ and all $t > 0$, and it follows from (3) that $0 < \Theta(t) < 1$ for all $t > 0$. Since $S_k(t) + I_k(t) = 1$, then we have $0 < S_k(t) < 1$ for all $k \in \{1, 2, \cdots, n\}$ and all $t > 0$. The proof is completed. $\square$

Next we will compute all biologically feasible equilibria admitted by system (6). It can easily be seen that there exists a zero equilibrium $I_k = 0$ ($k = 1, 2, \cdots, n$), which is corresponding to the disease-free equilibrium $E^0 = \{1, 0, 1, 0, \cdots, 1, 0\}$. Let

$$\frac{dI_k(t)}{dt} = 0,$$

then it follows from system (6) that

$$I_k = \frac{f_k(\Theta)}{\mu + \gamma + f_k(\Theta)}, \quad (7)$$
where $\Theta = \frac{1}{(k)} \sum_{k=1}^{n} \varphi(k) P(k) I_k$. Substituting (7) into $\Theta$ leads to the following equation:

$$\Theta = \frac{1}{(k)} \sum_{k=1}^{n} \varphi(k) P(k) \frac{f_k(\Theta)}{\mu + \gamma + f_k(\Theta)} =: h(\Theta).$$  (8)

Since $h(1) < 1$, $h'(\Theta) = \frac{1}{(k)} \sum_{k=1}^{n} \varphi(k) P(k) \frac{(\mu + \gamma) f_k(\Theta)}{[\mu + \gamma + f_k(\Theta)]^2} > 0$ and $h''(\Theta) = \frac{1}{(k)} \sum_{k=1}^{n} \varphi(k) P(k) \frac{(\mu + \gamma) f_k(\Theta) [(\mu + \gamma) + f_k(\Theta)]^2 - 2[(\mu + \gamma) + f_k(\Theta)]^2}{[\mu + \gamma + f_k(\Theta)]^3} < 0$, there exists a unique nontrivial solution $\Theta^* (\Theta^* \in (0, 1))$ if and only if $h'(0) > 1$, which yields a threshold value

$$R_0 = \frac{\langle \varphi(k) f_k(0) \rangle}{(\mu + \gamma)} > 1.$$  (9)

From the above discussion, we have the following result.

**Lemma 2.2.** System (5) has a unique positive equilibrium $E^* = (S^*_1, I^*_1, S^*_2, I^*_2, \ldots, S^*_n, I^*_n)$ if and only if $R_0 > 1$, where

$$0 < I^*_k = \frac{f_k(\Theta^*)}{\mu + \gamma + f_k(\Theta^*)} < 1, \quad 0 < S^*_k = \frac{\mu + \gamma}{\mu + \gamma + f_k(\Theta^*)} < 1$$  (10)

and

$$0 < \Theta^* = \frac{1}{(k)} \sum_{k=1}^{n} \varphi(k) P(k) I_k^* < 1.$$

**Remark 1.** (1) The expression of $R_0$ shows that the recovery rate $\gamma$ and the natural death (birth) rate $\mu$ have the same effect. That is, their increase will lead to the decrease of the threshold value $R_0$. Therefore, it will be easier to control the spread of the disease.

(2) In system (5), if $f_k(\Theta(t)) = \lambda_k(\Theta(t))$, then $R_0 > 1$ simplifies to $\lambda > \lambda_1$, where $\lambda_1 = \langle k \rangle / \langle k^2 \rangle$, which consists with Ref. [32].

(3) In system (5), let $\mu = 0$, $\gamma = 1$, $\varphi(k) = k$. If $f_k(\Theta(t)) = \lambda_k(\Theta(t))$, then $R_0 > 1$ is simplified to $\lambda > \lambda_1$, where $\lambda_1 = \langle k \rangle / \langle k^2 \rangle$, which consists with Ref. [20, 25]; and if $f_k(\Theta(t)) = 1 - (1 - \lambda)^{k(t)}$, then $R_0 > 1$ becomes $\lambda > \lambda_2$, where $\lambda_2 = 1 - 1/e(\langle k \rangle / \langle k^2 \rangle)^k$, in accord with Ref. [23]. Clearly, $\lambda_1 > \lambda_2$. Therefore, the EA-SIS model has a smaller transmission threshold than that in [20, 25]. This implies that it can be easier for the disease to spread in the network, which agrees with Ref. [23]. However, if $f_k(\Theta(t)) = 1 - (1 - \lambda^t \Theta(t))^k$, then $R_0 > 1$ is simplified to $\lambda > \lambda_1$, which is consistent with Ref. [14], which meant that it has the same transmission threshold as that in [20, 25]. Consequently, the epidemic threshold $R_0$ is completely dependent on the functional form of the infection rate (i.e., the different heterogeneous contact patterns).

3. **Global dynamics of the model.** In this section, we first consider the stability of the disease-free equilibrium and then the permanence of the disease. Finally, the global behavior of the endemic will be analyzed.

Now, we consider system (6) (equivalently, system (5)). The Jacobin matrix evaluated at the zero equilibrium $I_k = 0 (k = 1, 2, \ldots, n)$ is given by the $n \times n$ matrix:

$$J = \begin{pmatrix}
-(\mu + \gamma) + l_1 q_1 & l_1 q_2 & \cdots & l_1 q_n \\
l_2 q_1 & -(\mu + \gamma) + l_2 q_2 & \cdots & l_2 q_n \\
\vdots & \vdots & \ddots & \vdots \\
l_n q_1 & l_n q_2 & \cdots & -(\mu + \gamma) + l_n q_n
\end{pmatrix},$$

where $q_k = \frac{1}{(k)} \varphi(k) P(k)$ and $l_k = f_k'(0)$. Using induction on $n$, the corresponding characteristic polynomial can be expressed as:
Theorem 3.3. If \((s)\), the result of Thieme in Theorem 4.6 \([24]\).

and important question to explore is the permanence besides stability \([6, 7, 12, 24]\).

Remark 2. According to (11), we have (1)

The disease-free equilibrium \(E\)

Theorem 3.1. The disease-free equilibrium \(E\) of system (5) is locally asymptotically stable if \(R_0 < 1\), and it is unstable if \(R_0 > 1\).

Remark 2. According to (11), we have (1) \(s(J) > 0 \Leftrightarrow R_0 > 1\), (2) \(s(J) = 0 \Leftrightarrow R_0 = 1\), and (3) \(s(J) < 0 \Leftrightarrow R_0 < 1\), where \(s(J) = \max_{i \leq n} \Re \lambda_i\) and \(\lambda_1, \lambda_2, \cdots, \lambda_n\) are the eigenvalues of matrix \(J\).

Furthermore, we can obtain the global stability of the disease-free equilibrium \(E\).

Theorem 3.2. If \(R_0 < 1\), then the disease-free equilibrium \(E\) of system (5) is globally asymptotically stable.

Proof. According to the equivalent system (6), we have the Lyapunov function by

\[
V(t) = \sum_{k=1}^{n} w_k I_k(t),
\]

where \(w_k = \frac{\varphi(k) P(k)}{\mu + \gamma(k)} > 0\), for \(k = 1, 2, \cdots, n\). Since \(R_0 < 1\), the time derivative of \(V(t)\) along the trajectories of system (6) satisfies:

\[
\frac{dV}{dt} |_{(6)} = \sum_{k=1}^{n} w_k [f_k(\Theta)((1 - I_k(t)) - (\mu + \gamma)I_k(t)]
\]

\[
\leq -\Theta(t) + \frac{\Theta(t)}{\mu + \gamma(k)} \sum_{k=1}^{n} f_k(0) \varphi(k) P(k) = \Theta(t)(R_0 - 1) \leq 0,
\]

where \(0 < \xi < \Theta\). And \(\frac{dV}{dt} = 0\) holds only if \(\Theta(t) = 0\), i.e., \(I_k(t) = 0\) for \(k = 1, 2, \cdots, n\). By the LaSalle Invariant Principle, the zero equilibrium of system (6) (i.e., the disease-free equilibrium \(E\) of system (5)) is globally asymptotically stable. The proof is completed.

It is well-known that, in the theory of mathematical epidemiology, another basic and important question to explore is the permanence besides stability \([6, 7, 12, 24]\).

So we will study the permanence of the disease by using the permanence theory (specifically, the result of Thieme in Theorem 4.6 \([24]\)).

Theorem 3.3. If \(R_0 > 1\), the disease is permanent on the network, i.e., there exists \(\delta > 0\) (independent of initial conditions \((4)\)), such that \(\liminf_{t \to +\infty} I(t) = \liminf_{t \to +\infty} \sum_{k=1}^{n} P(k) I_k(t) \geq \delta\), for any solution of system (5) with \((4)\).

Proof. We will use the result of Theorem 4.6 in \([24]\) to finish the proof. For this purpose, we choose

\[
X = \{(S_1, I_1, S_2, I_2, \cdots, S_n, I_n) : S_k, I_k \geq 0 \text{ and } S_k + I_k = 1, \ k = 1, 2, \cdots, n\},
\]

\[
X_1 = \{(S_1, I_1, S_2, I_2, \cdots, S_n, I_n) \in X : \sum_{k=1}^{n} P(k) I_k > 0\}, \quad X_2 = X \setminus X_1.
\]
It follows from Lemma (2.1) that $X$ is positively invariant with respect to system (5). Note that $\Theta(0) = \frac{1}{(kh)} \sum_{k=1}^{n} \varphi(k)P(k)I_k(0) > 0$, then we have $I_k(0) > 0$ for some $k$. Thus, $I(0) = \sum_{k=1}^{n} P(k)I_k(0) > 0$. Since $I'(t) \geq -(\mu + \gamma) \sum_{k=1}^{n} P(k)I_k(t) = -(\mu + \gamma)I(t)$, it holds that $I(t) \geq I(0)e^{-(\mu + \gamma)t} > 0$. Hence, $X_1$ is also positive invariant. So there exists a compact set $B$, in which all solutions of system (5) initiated in $X$ ultimately enter and remain forever after. The compactness condition $(C_{4.2})$ in [24] is easily verified for this set $B$.

Let $\omega(\tilde{x}_0)$ be the omega limit set of the solution $x(t, \tilde{x}_0)$ of system (5) starting in $\tilde{x}_0 \in X$. Now, we need to determine the following set:

$$\Omega_1 = \bigcup_{y \in Y} \{\omega(y)\}, \quad Y = \{\tilde{x}_0 \in X \cup [x(t, \tilde{x}_0) \in X, \forall t > 0\}.$$  

It is clear that $E^0$ is the unique equilibrium of system (5) in

$$M_0 = \{\tilde{x}_0 \in X_2 : x(t, \tilde{x}_0) \in X_2, \forall t \geq 0\},$$

at the same time, $E^0$ is globally asymptotically stable. Therefore, we observe that $\Omega_1 = \{E^0\}$. And $E^0$ is a covering of $\Omega_1$, which is isolated and acyclic (since there is no nontrivial solution in $M_0$ which links $E^0$ to itself). Note that if it is shown that $E^0$ is a weak repeller for $X_1$, the proof of Theorem is complete.

By definition, $E^0$ is a weak repeller for $X_1$ if for every solution starting in $\tilde{x}_0 \in X_1$,

$$\limsup_{t \to +\infty} d(x(t, \tilde{x}_0), E^0) > 0. \quad (12)$$

According to the proof of Lemma 3.5 in [12], to show that (12) holds, we need only to prove $W^s(E^0) \cap X_1 = \phi$, where $W^s(E^0)$ is the stable manifold of $E^0$. Suppose it is not true, then there exists a solution $\tilde{x}_1 \in X_1$, such that

$$S_k(t) \to 1, \quad I_k(t) \to 0, \quad \text{as} \quad t \to +\infty \quad (k = 1, 2, \cdots, n). \quad (13)$$

Let $F(\Theta) = \frac{1}{(kh)} \sum_{k=1}^{n} \varphi(k)P(k)f_k(\Theta)$. Obviously, we know that

$$F'(\Theta) = \frac{1}{(kh)} \sum_{k=1}^{n} \varphi(k)P(k)f_k'(\Theta) > 0 \quad \text{and} \quad F''(\Theta) = \frac{1}{(kh)} \sum_{k=1}^{n} \varphi(k)P(k)f_k''(\Theta) \leq 0.$$

Since $R_0 = \frac{\langle \varphi(k)f_k(0) \rangle}{(\mu + \gamma)(k)} > 1$, we have

$$F'(0) - (\mu + \gamma) = \frac{1}{(kh)} \sum_{k=1}^{n} \varphi(k)P(k)f_k'(0) - (\mu + \gamma) > 0.$$

By the continuity of function $F'(x)$, $0 \leq x \leq 1$, we can choose positive constant $\varepsilon_0$ $(0 < \varepsilon_0 < 1)$ such that $\Gamma := (1 - \varepsilon_0)F'(\varepsilon_0) - (\mu + \gamma) > 0$. For given $\varepsilon_0 > 0$, from (13), there exists a $T > 0$ such that for all $t > T$, one has $1 - \varepsilon_0 < S_k(t) < 1 + \varepsilon_0$, $0 \leq I_k(t) < \varepsilon_0$, $k = 1, 2, \cdots, n$.

If $\Theta(t) \geq \varepsilon_0 > 0$, then the disease is obviously permanent. If $\Theta(t) < \varepsilon_0$, then we consider a function $L(t) = \sum_{k=1}^{n} \varphi(k)P(k)I_k(t)$. It is seen that

$$L'(t) = \sum_{k=1}^{n} \varphi(k)P(k)[f_k(\Theta)(1 - I_k(t)) - (\mu + \gamma)I_k(t)]$$

$$= \sum_{k=1}^{n} \varphi(k)P(k)[\Theta f_k'(\xi)(1 - I_k(t)) - (\mu + \gamma)I_k(t)]$$

$$\geq \Theta(1 - \varepsilon_0) \sum_{k=1}^{n} \varphi(k)P(k)f_k'(\xi) - (\mu + \gamma) \sum_{k=1}^{n} \varphi(k)P(k)I_k(t)$$

$$= (1 - \varepsilon_0)(\frac{1}{kh}) \sum_{k=1}^{n} \varphi(k)P(k)I_k(t) \sum_{k=1}^{n} \varphi(k)P(k)f_k'(\xi) - (\mu + \gamma)L(t)$$
\[ \frac{dx}{dt} = G_i(x_1, \ldots, x_n) = G_i(x), \quad i = 1, 2, \ldots, n, \]  
\tag{14}

is called cooperative in an open set \( D \subset R^n \), if \( \frac{\partial G_i}{\partial x_j}(x) \geq 0 \) for \( i \neq j \) and for all \( x \in D \).

**Lemma 3.5.** [9] Suppose that \( D = R^n \), or \( \text{Int} R^n_+ \), or \([p, q]\). Then the cooperative system (14) has a globally asymptotically stable equilibrium if and only if the following conditions hold in \( D \):

(a) every forward semi-obit has compact closure; and 
(b) there is not more than one equilibrium.

Denote \( \Omega_2 := \{ I = (I_1, I_2, \ldots, I_n) \in R^n_+ | 0 \leq I_k \leq 1, k = 1, 2, \ldots, n \} \). Let \( G : \Omega_2 \rightarrow R^n \) be the right-hand side of system (6), where \( G = (G_1, G_2, \ldots, G_n) \). That is,

\[ G_k(I) = f_k(\Theta(t))(1 - I_k(t)) - (\mu + \gamma)I_k(t), \quad k = 1, 2, \ldots, n. \]

Note that

\[ \frac{\partial G_k}{\partial I_j}(I) = f'_k(\Theta) \frac{1}{(k)} \varphi(j)P(j)(1 - I_k(t)) \geq 0, \]  
\tag{15}

where \( k, j = 1, 2, \ldots, n \) and \( k \neq j \), then \( G \) is cooperative in the region \( \Omega_2 \). It follows from Lemma 2.1 and Lemma 2.2 that the conditions (a) and (b) of Lemma 3.5 hold in the region \( \Omega_2 \setminus \{0\} \), respectively. So we obtain the following theorem.

**Theorem 3.6.** If \( R_0 > 1 \), then the endemic equilibrium \( I^*_k \) \((k = 1, 2, \ldots, n)\) of system (6) \(\text{i.e., the endemic equilibrium } E^* \text{ of system (5)} \) is globally asymptotically stable in \( \Omega_2 \setminus \{0\} \).

There is an interesting study should not be ignored in [20, 23, 25, 32], that is, for the special case \( R_0 = 1 \), the dynamics of the corresponding system in [20, 23, 25, 32] can be further explored with the help of Corollary 3.2 of Zhao and Jing [30]. For this purpose, we verify that system (3.5) satisfies the assumptions in Corollary 3.2 [30] as follows.

(1) From (15), we know that \( G \) is cooperative in \( R^n_+ \), and the matrix \( DG(I) = (\partial G_k/\partial I_j)_{1 \leq k, j \leq n} \) is irreducible.

(2) \( G(0) = 0 \) and for all \( I = (I_1, I_2, \ldots, I_n) \in R^n_+ \), when \( I_k = 0 \), we have \( G_k(I) = f_k(\Theta) \geq 0 \), where \( k = 1, 2, \ldots, n \) and \( \Theta = \frac{1}{(k)} \sum_{j=1}^{n} \varphi(j)P(j)I_j \geq 0 \).
(3) For any $\alpha \in (0, 1)$, it follows from $(H_1) - (H_3)$, i.e., $f_k(0) = 0$, $f''_k(\Theta) > 0$ and $f''_k(\Theta) \leq 0$, that $f_k(\alpha \Theta) < f_k(\Theta)$ and $f''_k(\alpha \Theta) \geq f_k(\Theta)$. Let $Q_k(\Theta) = f_k(\Theta) - \alpha f_k(\Theta)$, then $Q_k(\Theta) = \alpha f''_k(\Theta) - \alpha f_k(\Theta) \geq 0$. Therefore, $Q_k(\Theta) \geq Q_k(0) = 0$, that is, $f_k(\Theta) \geq \alpha f_k(\Theta)$. Furthermore, for all $I \geq 0$ and $k = 1, 2, \cdots, n$, we have

$$G_k(\alpha I) - \alpha G_k(I) = [f_k(\alpha \Theta)(1 - \alpha I_k) - \alpha(\mu + \gamma)I_k] - [\alpha f_k(\Theta)(1 - I_k) - \alpha(\mu + \gamma)I_k] = [f_k(\alpha \Theta) - \alpha f_k(\Theta)] + \alpha I_k(f_k(\Theta) - f_k(\Theta)) > 0.$$  

This implies that $G$ is strictly sublinear on $\Omega_2$. So, according to Corollary 3.2 [30], if $R_0 = 1$, i.e., $s(DG(0)) = 0$ (see Remark 2), then the zero equilibrium $I_k = 0$ ($k = 1, 2, \cdots, n$) of system (6) (i.e., the disease-free equilibrium $E^0$ of system (5)) is globally asymptotically stable in the region $\Omega_2 \setminus \{0\}$. It should be noted that, by applying Corollary 3.2 of Zhao and Jing [30], the results of Theorem 3.2 and Theorem 3.6 are also derived. In summary, we have the following conclusion.

**Theorem 3.7.** If $R_0 \leq 1$, then the disease-free equilibrium $E^0$ of system (5) is globally asymptotically stable in $\Omega$, i.e., the disease will disappear; while if $R_0 > 1$, then the unique endemic equilibrium $E^*$ of system (5) is globally asymptotically stable in $\Omega \setminus \{0\}$, i.e., the disease will persist and converge to a positive stationary state.

**Remark 3.** As mentioned before, if $\mu = 0$, $\gamma = 1$ and $f_k(\Theta(t)) = \lambda k \Theta(t)$, then system (6) is simplified to system (2) in [29]; If $f_k(\Theta(t)) = \lambda(\Theta(t))$, then system (5) (equivalently, system (6)) becomes system (2) in [32]; If $\mu = 0$, $\varphi(k) = k$, $f_k(\Theta) = 1 - (1 - \Theta)^k$, then system (6) is simplified to system (4) in [14]; And if $\mu = 0$, $\gamma = 1$, $\varphi(k) = k$ and $f_k(\Theta(t)) = 1 - (1 - \lambda)^{\Theta(t)}$, then system (6) becomes system (2) in [23]. Then, from Theorem 3.7, the globally asymptotical stability of the endemic equilibria in [14, 23, 29, 32] is naturally obtained. Consequently, the outstanding problems about the global asymptotical stability of the endemic equilibria of the models in [14, 23, 29, 32] are solved.

4. **Immunization strategies.** Immunization through vaccination is a very effective controlling strategy to the prevalence of the disease [1, 4, 5, 6, 18, 22, 23, 26]. In this section, we will discuss system (5) with different immunization schemes.

4.1. **Uniform immunization.** In uniform immunization [6, 22], a fraction of the whole nodes is randomly selected to be vaccinated in advance. This means that each node in the whole network has the same probability to be selected. Let $\sigma \in [0, 1)$ be the proportion of immune nodes in the network. Since the vaccinated fraction only works for the susceptible nodes, then for $k = 1, 2, \cdots, n$, system (6) becomes

$$\begin{cases}
\frac{dS_k(t)}{dt} = \mu - \mu S_k(t) - f_k(\Theta(t))(1 - \sigma)S_k(t) + \gamma I_k(t), \\
\frac{dI_k(t)}{dt} = f_k(\Theta(t))(1 - \sigma)S_k(t) - (\mu + \gamma)I_k(t).
\end{cases} \quad (16)$$

By similar arguments to those in Sect. 2, the corresponding epidemic threshold for system (16) is determined as follows.

$$R_0^U = \frac{(1 - \sigma)(\mu + \gamma)\theta}{(\varphi(k)f'_k(0))} = (1 - \sigma)R_0. \quad (17)$$

From (17), we can obtain the following result.

**Theorem 4.1.** Suppose $R_0 > 1$. Define $\sigma_c = 1 - \frac{(\mu + \gamma)\theta}{(\varphi(k)f'_k(0))}$. 


(1) When $\sigma > \sigma_c$ (i.e. $R_0^U < 1 < R_0$), then the disease will disappear regardless of the initial number of infected nodes. And as $\sigma \to 1$, $R_0^U \to 0$. This means in the case of a full immunization, it would be impossible for the disease to spread in the network.

(2) Otherwise,
(a) When $\sigma = 0$, that is, no immunization were done, then $R_0^U = R_0 > 1$;
(b) When $0 < \sigma < \sigma_c$ (i.e. $1 < R_0^U < R_0$), that is the immunization scheme is effective, but not so effective to control the spread of the disease.

4.2. Targeted immunization. It is well-known that the heterogeneous nature of scale-free networks makes them have a great resistance to random attack, but they are fragile to selective attack. That is to say, when the most highly connected nodes are firstly targeted, removal of just a small proportion of the nodes will lead to the network’s collapse. Therefore, we can devise a targeted immunization scheme [5, 16, 22]. Suppose all nodes with degree $k > k_c$ are immunized, here $k_c$ is an upper threshold. Then the immunization rate $\sigma_k$ can be defined by

$$\sigma_k = \begin{cases} 1, & k > k_c, \\ c, & k = k_c, \\ 0, & k < k_c, \end{cases}$$

where $0 < c \leq 1$. So for $k = 1, 2, \cdots, n$, the epidemic dynamic model is

$$\begin{cases} \frac{dS_k(t)}{dt} = \mu - \mu S_k(t) - f_k(\Theta(t))(1 - \sigma_k)S_k(t) + \gamma I_k(t), \\ \frac{dI_k(t)}{dt} = f_k(\Theta(t))(1 - \sigma_k)S_k(t) - (\mu + \gamma)I_k(t), \end{cases} \quad (18)$$

We can obtain the self-consistency equality

$$\Theta = \frac{1}{\langle k \rangle} \sum_{k=1}^{n} \varphi(k)P(k) \frac{\hat{f}_k(\Theta)(1 - \sigma_k)}{\mu + \gamma + f_k(\Theta)(1 - \sigma_k)} := \hat{g}(\Theta).$$

The epidemic threshold is determined by the following inequality:

$$\left. \frac{d\hat{g}(\Theta)}{d\Theta} \right|_{\Theta = 0} = \sum_{k=1}^{n} \varphi(k)P(k)f'_k(0)(1 - \sigma_k) = \frac{\langle \varphi(k)f'_k(0) \rangle - \langle \sigma_k \varphi(k)f'_k(0) \rangle}{(\mu + \gamma)\langle k \rangle} > 1.$$

Let $\sigma$ be the average immunization rate, that is, $\sigma = \sum_{k=1}^{n} \sigma_k P(k)$. Note that

$$\langle \sigma_k \varphi(k)f'_k(0) \rangle = \langle \sigma_k \rangle \langle \varphi(k)f'_k(0) \rangle + \hat{\sigma} = \sigma \langle \varphi(k)f'_k(0) \rangle + \hat{\sigma},$$

where

$$\hat{\sigma} = \text{cov}(\sigma_k, \varphi(k)f'_k(0)) = \left( \langle \sigma_k - \sigma \rangle \right) \left( \varphi(k)f'_k(0) - \langle \varphi(k)f'_k(0) \rangle \right).$$

According to the analysis of targeted immunization scheme in [5], for appropriate $k_c$, $\sigma_k - \sigma$ and $\varphi(k)f'_k(0) - \langle \varphi(k)f'_k(0) \rangle$ have the same signs, except for some $k'$s where $\sigma_k = \sigma$ and/or $\varphi(k)f'_k(0) = \langle \varphi(k)f'_k(0) \rangle$. Thus, there exists $\hat{\sigma} > 0$ for appropriate $k_c$. Then we have the following result.

**Theorem 4.2.** Define

$$R_0^T = \frac{\langle \varphi(k)f'_k(0) \rangle - \langle \sigma_k \varphi(k)f'_k(0) \rangle}{(\mu + \gamma)\langle k \rangle}, \quad (19)$$

then the following statements hold.

(1) When $R_0^T \leq 1$, the disease can be controlled by the targeted immunization. Otherwise, the disease still exists, and it will persist on a unique endemic level.
(2) \( R_0^T < R_0 \), which means that the targeted immunization scheme is effective;

(3) \( R_0^T < \frac{1}{\sigma} R_0^T \). If \( 0 < \sigma = \sigma < 1 \), then \( R_0^T < R_0^T \), which means that the targeted immunization scheme is more efficient than the uniform scheme for the same average immunization rate.

4.3. Acquaintance immunization. Although the targeted immunization scheme is really more efficient than the uniform immunization, it requires some global information about the degree of each node on the network [5]. Its practical application may be limited by this shortcoming. So this subsection will discuss another immunization scheme, i.e., acquaintance immunization [1, 4, 5], which is applied for this immunization of random acquaintances of random nodes. That is, we choose randomly a fraction \( q_0 \) of the \( N \) nodes, and then immunize randomly a neighbor node from each chosen node. Since the probability that a particular node with degree \( k \) is \( kP(k)/(N(k)) \) [4], then we take \( \sigma_k = q_0 N \cdot \frac{kP(k)}{N(k)} = \frac{q_0}{\sigma} kP(k) \) in (19). In this case, the epidemic threshold for this immunization strategy is

\[
R_0^T = \frac{\langle \varphi(k) f_k'(0) \rangle - \frac{q_0}{\sigma} \langle k\varphi(k)P(k)f_k'(0) \rangle}{\langle \varphi(k) f_k'(0) \rangle} = \frac{\langle \varphi(k) f_k'(0) \rangle - \frac{q_0}{\sigma} \langle k\varphi(k)P(k)f_k'(0) \rangle}{\langle \varphi(k) f_k'(0) \rangle - \sigma} \cdot R_0^T.
\]

Note that

\[
(1 - \sigma) \langle \varphi(k) f_k'(0) \rangle - \sigma = (1 - \sigma) \langle \varphi(k) f_k'(0) \rangle - \langle (\sigma_k - \sigma) (\varphi(k)f_k'(0) - \langle \varphi(k)f_k'(0) \rangle) \rangle > (1 - \sigma) \langle \varphi(k) f_k'(0) \rangle - (1 - \sigma) \langle \varphi(k) f_k'(0) \rangle = 0.
\]

As for the BA scale-free network [2], \( P(k) = 2m^2k^{-3} \). If \( q_0 < \frac{(k)}{2m^2} \), then

\[
\langle \varphi(k) f_k'(0) \rangle - \frac{q_0}{\sigma} \langle k\varphi(k)P(k)f_k'(0) \rangle = \langle \varphi(k) f_k'(0) \rangle - \frac{2m^2 q_0}{(k)} \langle k^{-2}\varphi(k)f_k'(0) \rangle > 0
\]

Therefore, \( R_0^T = hR_0^T \), where \( h \) is a positive constant. This means that the acquaintance immunization scheme is also effective. Furthermore, compared with the targeted immunization scheme, it doesn’t require any other global knowledge of the node degrees.

The above analysis can be written as the following result.

**Theorem 4.3.** Define

\[
R_0^A = \frac{\langle \varphi(k) f_k'(0) \rangle - \frac{q_0}{\sigma} \langle k\varphi(k)P(k)f_k'(0) \rangle}{\langle \varphi(k) f_k'(0) \rangle}.
\]

(1) When \( R_0^A \leq 1 \), the disease can be controlled by the acquaintance immunization scheme. Otherwise, the disease will persist on the network;

(2) When \( q_0 < \frac{(k)}{2m^2} \), then \( R_0^A = hR_0^T \), where \( h \) is a positive constant and the degree distribution \( P(k) = 2m^2k^{-3} \). This means that, in effectiveness, the acquaintance immunization scheme is comparable to the targeted immunization scheme.

4.4. High-risk immunization. This section introduces a high-risk immunization scheme [18]: only vaccinate the susceptible nodes which have infectious neighbour nodes. Thus, for \( k = 1, 2, \ldots, n \), the epidemic model becomes

\[
\begin{align*}
\frac{dS_k(t)}{dt} &= \mu - \mu S_k(t) - f_k(\Theta(t))(1 - v_0\Phi)S_k(t) + \gamma I_k(t), \\
\frac{dI_k(t)}{dt} &= f_k(\Theta(t))(1 - v_0\Phi)S_k(t) - (\mu + \gamma)I_k(t),
\end{align*}
\]

(20)
where \( v_0 \) is the probability that one node requires immunity by vaccinating per unit time, and \( \Phi = kP(k)/(N\langle k \rangle) \) is the probability that any given node is a neighbour of some specific node [18]. Then, we obtain the epidemic threshold

\[
R_0^H = \frac{\langle \phi(k) f_k^r(0) \rangle - v_0 \Phi \phi(k) f_k^r(0)}{(\mu + \gamma)\langle k \rangle} = R_0 - \frac{v_0 (kP(k) \phi(k) f_k^r(0))}{N(\mu + \gamma)\langle k \rangle^2} < R_0,
\]

which implies that the immunization we discuss here is indeed effective, and the greater the term \( v_0 (kP(k) \phi(k) f_k^r(0)) \) is, the more effective this scheme is.

On the basis of drug therapy in treating the disease, as we all know, the recovery rate \( \gamma \) can be improved by strengthening dietotherapy and psychological therapy. Thus, different from [5, 6, 18, 22, 23], we further explore how much value the recovery rate need to reach in attempts to curb the transmission of the disease for a given immunization rate (i.e., \( \sigma, k, q_0 \) or \( v_0 \) is given). The corresponding results are obtained as follows.

**Theorem 4.4. Define**

\[
\delta_1 := \langle \phi(k) f_k^r(0) \rangle / \langle k \rangle, \quad \delta_2 := \langle kP(k) \phi(k) f_k^r(0) \rangle / \langle (k) \rangle^2, \quad \gamma_0 := \delta_1 - \mu, \quad \gamma_1 := \gamma_0 - \sigma \delta_1, \quad \gamma_2 := \gamma_0 - (\sigma k \phi(k) f_k^r(0)) / \langle k \rangle, \quad \gamma_3 := \gamma_0 - q_0 \delta_2, \quad \gamma_4 := \gamma_0 - v_0 \delta_2 / N.
\]

(1) When \( \gamma > \gamma_0 \), the disease can be controlled on the network without immunization.

(2) When \( \gamma > \gamma_1 \) (here \( \gamma_1 < \gamma_0 \)), the disease can be controlled on the network under uniform immunization with the immunization rate \( \sigma \).

(3) When \( \gamma > \gamma_2 \) (here \( \gamma_2 < \gamma_0 \)), the disease can be controlled on the network under targeted immunization with the immunization rate \( \sigma_k \).

(4) When \( \gamma > \gamma_3 \) (here \( \gamma_3 < \gamma_0 \)), the disease can be controlled on the network under acquaintance immunization with the proportion rate \( q_0 \).

(5) When \( \gamma > \gamma_4 \) (here \( \gamma_4 < \gamma_0 \)), the disease can be controlled on the network under high-risk immunization with the immunization rate \( v_0 \).

In the next section, we will discuss what is the suitable immunization rate to control the spread of infectious diseases on the networks if the recovery rate of nodes is given.

5. Discussions and simulations. From above theoretical analysis, \( R_0 = \frac{\langle \phi(k) f_k^r(0) \rangle}{(\mu + \gamma)\langle k \rangle} \) is also called the basic reproduction number, which is an important threshold value in disease control. That is, when \( R_0 \leq 1 \), the disease will die out; otherwise, when \( R_0 > 1 \), the disease will persist on a unique endemic level. Undeniably, the value of \( R_0 \) is dependent on the topology of the underlying networks, the heterogeneous infection rate and some other model parameters.

A principal complex heterogeneous network is the BA scale-free network [2]. Let us consider a generalized scale-free network with a normalized degree distribution [21], which is given by \( P(k) = (1 + \tau) m^{1 + \tau} k^{-2 - \tau} \), the exponent \( 0 < \tau \leq 1 \).

By regarding the degree \( k \) as a continuous variable and the exponent \( \tau = 1 \), we obtain that the average degree \( \langle k \rangle \approx 2m(n - m)/n \) and \( \langle k^2 \rangle \approx 2m^2 \ln(n/m) \), where \( n(m) \) is the maximum(minimum) degree of any node. Suppose the heterogeneous infection rate \( f_k(\theta) = 1 - (1 - \lambda)^k \), then \( f_k^r(0) = -\ln(1 - \lambda)k \). This means that the initial infection rate of network node increases with the increase of degree value. Further, there exit some special cases of the relation between the network structure and the threshold value \( R_0 \).

(a) If every node has the same number of contacts per unit time, i.e., the infectivity function \( \phi(k) = A \) (here \( A \) is constant), then \( R_0 = \frac{-\ln(1 - \lambda)}{\mu + \gamma} \), which is a
threshold value for the regular networks. That is to say, the epidemic threshold $R_0$ bears no relation to the network structure.

(b) If each infected node will contact every neighbor per unit time, i.e., the infectivity function $\varphi(k) = k$, then $R_0 = -\ln(1-\lambda)/(\mu+\gamma/k) \approx -\ln(1-\lambda) mn \ln(n/m) / (\mu+\gamma)(n-m)$. For an infinite-size heterogeneous network, the threshold value $R_0$ becomes sufficiently large. In this case, the disease will persist on the network.

(c) If the infectivity of a node partially depend on the node degree, i.e., the infectivity function $\varphi(k)$ is a nonlinear function of the node degree, then $R_0 = -\ln(1-\lambda)/\langle k\varphi(k) \rangle / \langle k \rangle$. It is clear that the value of $R_0$ is in direct proportion to the value of the heterogeneous factor $\langle k\varphi(k) \rangle / \langle k \rangle$, then network heterogeneity may make the disease easy to spread. This will be discussed in the following by simulations.

Now we show several numerical simulations to verify and visualize the theoretical results. The simulations are based on a scale-free network, where the degree distribution $P(k) = Ck^{-\zeta}$, $2 < \zeta \leq 3$ and the parameter $C$ is chosen to satisfy $\sum_{k=1}^{n} P(k) = 1$. Since $S_k(t) + I_k(t) \equiv 1$, the variables $I_k (k = 1, 2, \cdots, n)$ are only considered. Then we study the dynamical behaviors of system (6) with $\zeta = 2.6$, $n = 100$ and $\varphi(k) = \rho k^\alpha / (1+\nu k)^\beta$, in which $\rho = 0.3$, $\alpha = 0.75$, $\nu = 0.02$.

First of all, we examine the effect of heterogeneous infection rate on epidemic spreading. Fig. 1 displays the time series $I(t)$ with different forms of infection rate. Here $I(t) = \sum_{k=1}^{n} P(k) I_k(t)$ is the global average densities of the infected nodes. For this example, we let $g(k, \lambda, \Theta) = \lambda k \Theta$ [20, 25]; $g(k, \lambda, \Theta) = 1 - (1 - \lambda)^k$ [14, 27] and $g(k, \lambda, \Theta) = 1 - (1 - \lambda)^{k\Theta}$ [23]. In Fig. 1(a), we choose $\lambda = 0.05$, $\mu = 0.01$, $\gamma = 0.05$, and the initial value is $I(0) = 0.8$. In Fig. 1(b), the parameters $\lambda = 0.15$, $\mu = 0.02$, $\gamma = 0.06$, and the initial value is $I(0) = 0.01$. It can be seen from Fig. 1 that, no matter what form the infection rate is, when $R_0 < 1$, the disease will disappear; when $R_0 > 1$, the disease will persist on the network. Furthermore, by the comparison of the threshold value $R_0$, it is shown that the epidemic model, which considers the changing number of the infected nodes around a susceptible node, such as $g(k, \lambda, \Theta) = 1 - (1 - \lambda)^{k\Theta}$ [23], has a higher threshold value $R_0$ than the classical PV-SIS model with $g(k, \lambda, \Theta) = \lambda k \Theta$ in [19, 20]. This means that the critical point $R_0 = 1$ of the disease outbreak can be easier to be reached, which agrees with that given in [23]. However, the network-based epidemic
model with \( g(k, \lambda, \Theta) = 1 - (1 - \lambda \Theta)^k \) in [14] has the same value of \( R_0 \) as the model with \( g(k, \lambda, \Theta) = \lambda k \Theta \) in [20, 21]. The remarkable findings are highlighted here: regardless of the functional form of the heterogeneous rate (i.e., no matter what form the heterogeneous contact pattern is), whether the disease will disappear or not is completely determined by the epidemic threshold \( R_0 \), but the heterogeneous infection rate is in fact closely related with the epidemic threshold \( R_0 \), especially it can directly affect on the final number of infected nodes when the disease is endemic.

To further study the detailed outcome of system (6), we should examine the time series of those nodes with different degree. Without loss of generality, in the following Figs. 2-4, we let \( g(k, \lambda, \Theta) = 1 - (1 - \lambda \Theta)^k \Theta \). In Fig. 2(a) and Fig. 2(b), the initial value and the parameters are the same as those of Fig. 1(a) and Fig. 1(b), respectively. From Fig. 2(a) it is seen that the lower the degree number, the faster the disease died out when \( R_0 < 1 \). From Fig. 2(b) it is seen that the larger the degree number, the larger value of the endemic level when \( R_0 > 1 \). The two figures also illustrate that when \( R_0 < 1 \), the disease-free equilibrium is globally asymptotically stable; when \( R_0 > 1 \), the epidemic equilibrium is globally asymptotically stable.

\[
\begin{align*}
\text{Figure 2.} & \quad \text{The densities of infected nodes with different degrees. The lines from bottom to top are } I_1(t), I_{10}(t), I_{20}(t), \ldots, I_{90}(t), I_n(t). \\
(a) & \quad R_0 = 0.7242 < 1. \\
(b) & \quad R_0 = 1.7208 > 1.
\end{align*}
\]

Next, we examine the influence of initial conditions on the density of infected nodes. Here we choose \( k = 30 \) on behalf of other degrees. It should be noted that the time evolution of the infected nodes with other degrees are analogous. From Fig. 3, we can see that the initial conditions have no impact on the steady state.

\[
\begin{align*}
\text{Figure 3.} & \quad \text{The influence of initial conditions on the density of } I_{30}(t). \\
(a) & \quad R_0 = 0.7242 < 1. \\
(b) & \quad R_0 = 1.7208 > 1.
\end{align*}
\]
of average density of infected nodes. Specifically, if there exist infected nodes at the beginning, no matter how few or how many, the density function $I_k(t)$ ($k = 1, 2, \cdots, n$) tends to 0 and approaches to a positive stationary level according to above two cases, respectively. The numerical results mentioned above are in accord with our theoretical analysis.

Finally, we introduce the results of numerical simulations to investigate the effectiveness of the immunization schemes. In Fig. 4, the initial value is $I(0) = 0.8$, and the parameters are the same as those of Fig. 1(b), except for $\gamma = 0.05$. Under the parameters above, $R_0 = 1.9667 > 1$, which implies that the disease will be permanent without immunization. It follows from Theorem 4.1 that $\sigma_c = 0.4915$. This means that, under uniform immunization, the immunization rate $\sigma$ should be as high as 0.4915 to control disease. On the other hand, let $\sigma = 0.2$, 0.4 and 0.5, then, according to Theorem 4.4, the corresponding $R_0 = 0.9901$, 0.0625 and 0.0488, respectively. Thus, when the recovery rate $\gamma = 0.05 > \gamma_1 = 0.0488$, the disease can be controlled on the network under uniform immunization with immunization rate $\sigma = 0.5$, which can be shown in Fig. 4(a).

For the targeted immunization scheme, we choose $c = 1$. Fig. 4(b) shows that the higher the upper threshold $k_c$, the faster the epidemic threshold $R_0^T$ increase. Suppose $k_c = 9, 10$ and 11, according to Theorem 4.2 and Theorem 4.4, the corresponding $R_0^T = 0.9445, 0.9892, 1.0298$ and $\gamma_2 = 0.0461, 0.0492, 0.0521$. Hence, when the recovery rate $\gamma = 0.05 > \gamma_2 = 0.0492$ (i.e., $R_0^T = 0.9892 < 1$), the disease can be controlled on the network under targeted immunization with the upper threshold $k_c \leq 10$. Fig. 4(b) also illustrates that immunizing these nodes that degrees are greater than 10 can get very good result. But if the degrees of nodes that are immunized are greater than 65 (i.e., $k_c \geq 65$), the final outcomes seem to be no different. Similarly, we can repeat the simulations about Fig. 4 when the immunization schemes, acquaintance and high-risk, are implemented.

A good immunization strategy can reduce the final density of infected nodes at the cost of a relatively low vaccinated density [1]. What is the suitable immunization scheme if the fund to vaccinate people is limit? To answer this question, we suppose the average immunization rates for uniform immunization and targeted immunization are the same. So in Fig. 4, we choose $\sigma = \bar{\sigma} = 0.0127$, which is corresponding to $k_c = 10$. Then we have $R_0^T = 0.9892 < 1 < R_0^U = 1.9417$. Likewise, Fig. 5 also illustrates that targeted immunization has the absolute advantage to control the disease, compared with uniform immunization. However, it requires global information about the degrees of nodes on the network, i.e, the upper threshold $k_c$. 

![Figure 4](image-url)
Figure 5. Comparison of the effectiveness of different immunization schemes: uniform immunization with $\sigma = 0.0026$, targeted immunization with $\bar{\sigma} = 0.0026$ (i.e., $k_c = 25$) and acquaintance immunization with $q_0 = 0.35$. Here the parameters and initial value are the same as those of Fig. 1(b).

Figure 6. The time evolutions of $I(t)$ for different recovery rate $\gamma$ under the given acquaintance immunization rate $q_0$ and high-risk immunization rate $v_0$. Here, the other parameters and initial value are the same as those of Fig. 4.

Figure 7. Effectiveness of high-risk immunization schemes with different value of $v_0$. Here the parameters and initial value are the same as those of Fig. 1(b), except for $n = 30$.

For the acquaintance immunization scheme, if we choose $q_0 = 0.35 < (k_c)/C = 2.1809$, then it is comparable to the targeted immunization scheme in effectiveness (see Fig. 5). It can also easily be seen from Fig. 5 that acquaintance immunization shows a higher average density of infected nodes than targeted immunization, but its
endemic level is still lower than uniform immunization. Further, Fig. 6(a) illustrates that if the recovery rate $\gamma > \gamma_3 = 0.1129$, the disease can be controlled in the network under the acquaintance immunization with the proportion rate $q_0 = 0.35$. Note that acquaintance immunization only requires local information about randomly selected nodes and their neighbours. Consequently, it is a suitable replacement for targeted immunization sometimes.

As for the high-risk immunization scheme, it just need to vaccinate some neighbors of infected nodes. Obviously, the vaccinated nodes are a small fraction of all susceptible nodes, which means that the cost is relative small. Fig. 6(b) shows that if the recovery rate $\gamma > \gamma_4 = 0.0886$, the disease can be controlled in the network under the high-risk immunization with the immunization rate $v_0 = 0.3$. Furthermore, Fig. 7 shows that the larger the value of $v_0$ is, the lower the endemic level will be. Therefore, the high-risk immunization is also effective and feasible in practice.

6. Conclusions. In this paper, to better understand the influences of individuals’ different heterogeneous contact patterns on epidemic dynamics, we construct and investigate a network-based SIS model with a general form of heterogeneous infection rate, as well as the birth and death rates. Some special cases of this model were studied in [5, 14, 20, 23, 25, 29, 32]. We derive the epidemic threshold $R_0$, which depends on the topology of the underlying networks and some model parameters. It is indicated by the analysis that the threshold $R_0$ determines not only the existence of endemic equilibrium but also the global dynamics of the model. That is, by constructing Lyapunov function, we show that when $R_0 < 1$, the disease-free equilibrium $E^0$ is globally asymptotically stable, i.e., the disease will disappear. By using the permanence theory [24], we obtain that when $R_0 > 1$, the epidemic disease is permanent on the network. By applying the theory of cooperative system, we prove that when $R_0 > 1$, the endemic equilibrium $E^*$ is globally asymptotically stable, which solves the outstanding problem about the global asymptotical stability of the positive (endemic) equilibria in [14, 23, 29, 32]. Furthermore, with the help of Corollary 3.2 of Zhao and Jing [30], an interesting finding is that when $R_0 = 1$, the disease-free equilibrium $E^0$ is also globally asymptotically stable. The results obtained here are more general and richer.

Together with numerical illustrations, theoretical analysis of this paper shows significantly different impacts of various forms of heterogeneous infection rate on epidemic spreading. For instance, the network-based epidemic model, which considers the changing number of the infected nodes around a susceptible node, such as $g(k, \lambda, \Theta) = 1 - (1 - \lambda)^k \Theta$ [23], has a higher value of $R_0$ than the well-known SIS epidemic model with $g(k, \lambda, \Theta) = \lambda k \Theta$ [20, 21]. This means that the critical point $R_0 = 1$ of the disease outbreak can be easier to be reached, which agrees with the result in [23]. However, the network-based epidemic model with $g(k, \lambda, \Theta) = 1 - (1 - \lambda \Theta)^k$ in [14] has the same value of $R_0$ as that in [20, 21]. Consequently, the epidemic threshold $R_0$ is closely related with the functional forms of the heterogeneous infection rate (i.e., the different heterogeneous contact patterns). Especially, when the disease is endemic, the heterogeneous infection rate can directly affect the final number of infected nodes (see Fig. 1).

On the other hand, based on the heterogeneity of contact patterns, the effects of different immunization schemes are discussed and compared. Different from [5, 6, 18, 22, 23], we further explore the relation between the immunization rate and the recovery rate, which are the two important parameters that can be improved. For a
given recovery rate, we get the suitable immunization rate to control the spread of the disease on the networks. Meanwhile, for a given immunization rate, we discuss how much value the recovery rate need to reach in attempts to curb the spread of the disease (see Fig. 4 and Fig. 6). The study can help in adopting pragmatic strategies against infectious diseases in structured populations.

We should point out that our study only focuses on the network-based SIS epidemic model with a general infection rate. So it is worthy to study other generalized network-based epidemic models, like SIR, SIRS and so on, which may have complex dynamic behavior. Besides, we also should recognize the limitations of our present epidemic model based on the static networks (i.e., the network size is time invariant). Especially for a long-standing disease, demographic changes should not just be reflected by balancing births and deaths. In this case, it is necessary for us to consider the spread of infectious diseases on the dynamic networks [10]. Furthermore, there is a long way to go, especially when getting global information about the population and matching our model to the real data. These and other questions deserve further exploration in our future work.

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REFERENCES

[1] E. Alfinito, M. Beccaria, A. Fachechi and G. Macorini, Reactive immunization on complex networks, EPL (Europhysics Letters), 117 (2017), 18002.
[2] A. L. Barabási and R. Albert, Emergence of scaling in random networks, Science, 286 (1999), 509–512.
[3] X. Chu, Z. Zhang J. Guan and S. Zhou, Epidemic spreading with nonlinear infectivity in weighted scale-free networks, Physica A, 390 (2011), 471–481.
[4] R. Cohen, S. Havlin and D. Ben-Avraham, Efficient immunization strategies for computer networks and populations, Phys. Rev. Lett., 91 (2003), 247901.
[5] X. Fu, M. Small, D. M. Walker and H. Zhang, Epidemic dynamics on scale-free networks with piecewise linear infectivity and immunization, Phys. Rev. E, 77 (2008), 036113, 8pp.
[6] S. Huang, Dynamic analysis of an SEIRS model with nonlinear infectivity on complex networks, Int. J. Biomath., 9 (2016), 1650009, 25pp.
[7] S. Huang, F. Chen and L. Chen, Global dynamics of a network-based SIQRS epidemic model with demographics and vaccination, Commun. Nonlinear Sci. Numer. Simul., 43 (2017), 296–310.
[8] S. Huang and J. Jiang, Global stability of a network-based SIS epidemic model with a general nonlinear incidence rate, Math. Biosci. Eng., 13 (2016), 723–739.
[9] J. Jiang, On the global stability of cooperative systems, B. Lond. Math. Soc., 26 (1994), 455–458.
[10] Z. Jin, G. Sun and H. Zhu, Epidemic models for complex networks with demographics, Math. Biosci. Eng., 11 (2014), 1295–1317.
[11] H. Kang and X. Fu, Epidemic spreading and global stability of an SIS model with an infective vector on complex networks, Commun. Nonlinear Sci. Numer. Simul., 27 (2015), 30–39.
[12] P. D. Leenheer and H. Smith, Virus dynamics: A global analysis, SIAM J. Appl. Math., 63 (2003), 1313–1327.
[13] C. Li, C. Tsai and S. Yang, Analysis of epidemic spreading of an SIRS model in complex heterogeneous networks, Commun. Nonlinear Sci. Numer. Simul., 19 (2014), 1042–1054.
[14] X. Li and L. Cao, Diffusion processes of fragmentary information on scale-free networks, Physica A, 450 (2016), 624–634.
[15] M. Liu and J. Ruan, Modelling of epidemics with a generalized nonlinear incidence on complex networks, Complex Sciences, Springer Berlin Heidelberg, (2009), 2118–2126.
[16] N. Madar, T. Kalisky, R. Cohen, D. ben-Avraham and S. Havlin, Immunization and epidemic dynamics in complex networks, The European Physical Journal B, 38 (2004), 269–276.
[17] V. Nagy, Mean-field theory of a recurrent epidemiological model, *Phys. Rev. E*, **79** (2009), 066105.

[18] F. Nian and X. Wang, Efficient immunization strategies on complex networks, *J. Theor. Biol.*, **264** (2010), 77–83.

[19] R. Olinky and L. Stone, Unexpected epidemic thresholds in heterogeneous networks: The role of disease transmission, *Phys. Rev. E*, **70** (2004), 030902.

[20] R. Pastor-Satorras and A. Vespignani, Epidemic spreading in scale-free networks, *Phys. Rev. Lett.*, **86** (2001), 3200.

[21] R. Pastor-Satorras and A. Vespignani, Epidemic dynamics and endemic states in complex networks, *Phys. Rev. E*, **63** (2001), 066117.

[22] R. Pastor-Satorras and A. Vespignani, Epidemics and immunization in scale-free networks, *Handbook of Graphs and Networks: From the Genome to the Internet*, (2003), 111–130.

[23] Y. Qin, X. Zhong, H. Jiang and Y. Ye, An environment aware epidemic spreading model and immune strategy in complex networks, *Appl. Math. Comput.*, **261** (2015), 206–215.

[24] H. R. Thieme, Persistence under relaxed point-dissipativity (with application to an endemic model), *SIAM J. Math. Anal.*, **24** (1993), 407–435.

[25] L. Wang and G.-Z. Dai, Global stability of virus spreading in complex heterogeneous networks, *SIAM J. Appl. Math.*, **68** (2008), 1495–1502.

[26] Q. Wu and X. Fu, Immunization and epidemic threshold of an SIS model in complex networks, *Physica A*, **444** (2016), 576–581.

[27] Q. Wu, X. Fu and G. Zhu, Global attractiveness of discrete-time epidemic outbreak in networks, *Int. J. Biomath.*, **5** (2012), 1250004, 12pp.

[28] R. Yang, B. Wang, J. Ren, W. Bai, Z. Shi, W. Wang and T. Zhou, Epidemic spreading on heterogeneous networks with identical infectivity, *Phys. Lett. A*, **364** (2007), 189–193.

[29] H. Zhang and X. Fu, Spreading of epidemics on scale-free networks with nonlinear infectivity, *Nonlinear Anal. Theory Methods Appl.*, **70** (2009), 3273–3278.

[30] X. Zhao and Z. Jing, Global asymptotic behavior in some cooperative systems of functional differential equations, *Canad. Appl. Math. Quart.*, **4** (1996), 421–444.

[31] J. Zhang and J. Sun, Analysis of epidemic spreading with feedback mechanism in weighted networks, *Int. J. Biomath.*, **8** (2015), 1550007, 11pp.

[32] G. Zhu, X. Fu and G. Chen, Global attractivity of a network-based epidemic SIS model with nonlinear infectivity, *Commun. Nonlinear Sci. Numer. Simul.*, **17** (2012), 2588–2594.

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