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# Spreading Analysis of an SEIR Epidemic Model with Distributed Delay on Scale-Free Network*

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**Abstract** A novel epidemic SEIR model with distributed delay on scale-free network is proposed in this paper. The formula of the basic reproduction number $R_0$ for the model is given, and globally dynamic behaviours of the model are discussed. Numerical simulations are carried out to demonstrate the main results.

**Keywords** Epidemic model, network, distributed delay, basic reproduction number, stability

**MSC(2010)** 34K20, 92C42.

## 1. Introduction

The epidemic dynamics models have been widely investigated for a long time, which can effectively explained the process of disease transmission. Since the modelling of the seminal works on the scale-free network, in which the probability of $p(k)$ for any node with $k$ links to other nodes is distributed according to the power law $p(k) = Ck^{-\gamma}$ $(2 < \gamma \leq 3)$, suggested by Barabási and Albert [1], the studies of complex network have attracted more and more interests. In recent years, the compartmental spreading models of epidemic diseases on scale-free network has been established and discussed by many scholars [2, 4, 5, 7–21].

In order to describe the effects of disease incubation or immunity, the delay is often incorporated in the epidemic model. Unfortunately, compared with the ordinary differential equation models on scale-free network, a relatively small number of scholars has studied the epidemic model with time delays. Let the delay represent the incubation period during which the infectious agents develop in the vector, Guan and Guo [5] discussed an epidemic model with time delay and saturated incidence, Wang etc [14] discussed the delayed SIR model. Noting that in the process of the epidemic propagation, when a susceptible node is infected by the infected nodes, it first becomes an exposed node, then becomes an infected node after a certain latent period, Liu and Li [10] and Kang etc [8] discussed $SEIR$ model with discrete delay in which time delay represents latent period of disease, respectively.

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Considering the time taken from the moment of a new infected but non-infectious case arising to the moment of the individual becoming infectious may differ from individual to individual (Almost all infectious disease such as varicella, measle, diphtheria, Ebola hemorrhagic fever, etc. have this characteristic.), Huang etc [7] discussed one $SIR$ model with distributed delay. In this paper, we propose a novel epidemic $SEIR$ model with distributed delay on scale-free network to investigate the epidemic spreading.

Consider the while population as a scale-free network, and suppose that the number of total nodes is time invariant constant $N$. The total nodes are divided into four classes: susceptible nodes, infected nodes, exposed nodes and recovered nodes. let $S_k(t), E_k(t), I_k(t)$ and $R_k(t)$ be the relative density of susceptible nodes, exposed nodes, infected nodes and recovered nodes of connectivity $k$ at time $t$, respectively, where $k = 1, 2, \cdots, n$ and $n$ is the maximum degree number in the network. Based on the mean-field approximation, one can formulate the following compartmental model on the scale-free network:

$$\begin{cases} \dot{S}_k(t) = \mu - \lambda(k)S_k(t)\Theta(t) - \mu S_k(t), \\ \dot{E}_k(t) = \lambda(k)S_k(t)\Theta(t) - \lambda(k)\displaystyle\int_0^{+\infty} S_k(t-\tau)\Theta(t-\tau)f(\tau)\mathrm{e}^{-\mu\tau}d\tau - \mu E_k(t), \\ \dot{I}_k(t) = \lambda(k)\displaystyle\int_0^{+\infty} S_k(t-\tau)\Theta(t-\tau)f(\tau)\mathrm{e}^{-\mu\tau}d\tau - \beta I_k(t) - \mu I_k(t), \\ \dot{R}_k(t) = \beta I_k(t) - \mu R_k(t) \end{cases} \tag{1}$$

with the normalization conditions

$$S_k(t) + E_k(t) + I_k(t) + R_k(t) = 1,$$

where $\lambda(k)$ be the $k$-dependent infection rate such as $\lambda k$, $\lambda c(k)$ [14, 16], $\beta$ is the recovery rate of the infected nodes, and the recruitment rate and the removal rate are identical, this is denoted by $\mu$. Assuming that the network has no degree correlations [10, 16], and

$$\Theta(t) = \frac{1}{\langle k\rangle}\sum_{k=m}^{n}\varphi(k)p(k)I_k(t), \tag{2}$$

where $\langle k\rangle = \sum_k p(k)k$ stands for the average node degree and $\varphi(k)$ denotes an infected node with degree $k$ occupied edges which can transmit the disease, so $\Theta(t)$ represents the probability that any given link points to an infected node, $\varphi(k) = ak^\alpha/(1+bk^\alpha)(0 \le \alpha < 1, a > 0, b \ge 0)$ [18], $\lim_{k\to+\infty}\varphi(k) = a/b$ when $b \ne 0$, i.e., $\varphi(k)$ gradually become saturated with the increase of degree $k$. Infectiousness varies over time, which is described by a kernel function $f(\tau)$, which denotes the probability that the exposed nodes becomes an infected person over time $\tau$, $f(\tau)$ is continuous on $[0, +\infty)$ and satisfies

$$f(\tau) \ge 0, \int_0^{+\infty} f(\tau)d\tau = 1, \int_0^{+\infty} f(\tau)\mathrm{e}^{r\tau}d\tau < +\infty, \tag{3}$$

where $r > 0$ is a positive real number.There are many kinds of kernel functions such as Gamma distribution, Delta-distribution and so on. Standard theory of functional

differential equation implies that system (1) has a unique solution satisfying the initial conditions

$$S_k(\theta) = \phi_{1k}(s),\ I_k(\theta) = \phi_{2k}(s),\ R_k(\theta) = \phi_{3k}(s),$$

$$\phi_{ik}(s) \geq 0, s \in (-\infty, 0], \phi_{ik}(0) > 0.\ i = 1, 2, 3,\ k = 1, 2, \cdots, n.$$

where $(\phi_{11}(s), \phi_{21}(s), \phi_{31}(s) \cdots, \phi_{1n}(s), \phi_{2n}(s), \phi_{3n}(s)) \in X$. It can be verified that solutions of system (1) with initial conditions above remain positive for all $t \geq 0$.

The rest of this paper is organized as follows. In Section 2, the dynamical behaviors of the $SIR$ model (1) with distributed delay are discussed. In Section 3, numerical simulations are performed to demonstrate the main results. Finally, the conclusion is provided in Section 4.

## 2. Spreading analysis for the model

In this section, we aim to fully analyze the dynamic properties of the system (1), including the equilibriums and their global stability.

Denote

$$R_0 = \frac{\langle \lambda(k)\varphi(k) \rangle}{(\mu + \beta)\langle k \rangle} \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} d\tau, \tag{4}$$

where $\langle \lambda(k)\varphi(k) \rangle = \sum_k \lambda(k)\varphi(k)p(k)$.

We will conclude that $R_0$ is the basic reproduction number for the model (1). The $R_0$ represents the average number of secondary infectious infected by an infected node during whose whole course of disease in the case that all the members of the population are susceptible nodes.

Since $E_k$ and $R_k$ do not appear in the first equation and the third equation of system (1), it suffices to study the following two-dimensional system (5).

$$\begin{cases} \dot{S}_k(t) = \mu - \lambda(k)S_k(t)\Theta(t) - \mu S_k(t), \\ \dot{I}_k(t) = \lambda(k) \displaystyle\int_0^{+\infty} S_k(t-\tau)\Theta(t-\tau) f(\tau)\mathrm{e}^{-\mu\tau} d\tau - \beta I_k(t) - \mu I_k(t). \end{cases} \tag{5}$$

**Theorem 2.1.** *System* (5) *has always a disease-free equilibrium* $E_0$*, and if* $R_0 < 1$*, the disease-free equilibrium* $E_0$ *of system* (5) *is globally asymptotically stable. Where* $E_0 = (S_1^0, S_2^0, \cdots, S_n^0, I_1^0, I_2^0, \cdots, I_n^0)$ *in which* $S_k^0 = 1, I_k^0 = 0, k = 1, 2, \cdots, n$.

**Proof.** Obviously, system (5) has always a disease-free equilibrium $E_0$.

Consider the following Lyapunov function

$$V(t) = \frac{1}{2}\Theta^2(t) + \eta \int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau} \int_{t-\tau}^{t} \Theta^2(s) ds d\tau,$$

where $\eta = \frac{1}{2}\frac{\langle\lambda(k)\varphi(k)\rangle}{\langle k\rangle} = \frac{1}{2}\frac{1}{\langle k\rangle}\sum_k \lambda(k)\phi(k)p(k)$. We have

$$\begin{aligned}
\dot{V}(t)\Big|_{(5)} &= \Theta(t)\left[\frac{1}{\langle k\rangle}\sum_k \lambda(k)\phi(k)p(k)\int_0^{+\infty} S_k(t-\tau)\Theta(t-\tau)f(\tau)\mathrm{e}^{-\mu\tau}d\tau\right] \\
&\quad -(\mu+\beta)\Theta^2(t) + \eta\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}(\Theta^2(t)-\Theta^2(t-\tau))d\tau \\
&\le \Theta(t)\left[\frac{1}{\langle k\rangle}\sum_k \lambda(k)\phi(k)p(k)\int_0^{+\infty} \Theta(t-\tau)f(\tau)\mathrm{e}^{-\mu\tau}d\tau\right] \\
&\quad -(\mu+\beta)\Theta^2(t) + \eta\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}(\Theta^2(t)-\Theta^2(t-\tau))d\tau \\
&\le \left[\frac{1}{\langle k\rangle}\sum_k \lambda(k)\phi(k)p(k)\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}d\tau\frac{1}{2}(\Theta^2(t)+\Theta^2(t-\tau))\right] \\
&\quad -(\mu+\beta)\Theta^2(t) + \eta\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}(\Theta^2(t)-\Theta^2(t-\tau))d\tau \\
&= \Theta^2(t)(\mu+\beta)(R_0-1).
\end{aligned}$$

Thus $\dot{V}(t)\Big|_{(5)} \le 0$ when $R_0 < 1$, and the largest invariant set of $\dot{V}(t)\Big|_{(5)} = 0$ is a singleton $E_0$. Hence the disease-free equilibrium $E_0$ of system (5) is globally asymptotically stable when $R_0 < 1$ according to LaSalle Invariance Principle [9]. □

**Theorem 2.2.** *If $R_0 > 1$, System (5) has a unique endemic equilibrium $E_*$, and it is globally asymptotically stable.*

**Proof.** First, suppose that $E_* = (S_1^*, S_2^*, \cdots, S_n^*, I_1^*, I_2^*, \cdots, I_n^*)$, it satisfies the following equation according to system (5).

$$\begin{cases} \lambda(k)S_k^*\Theta^* + \mu S_k^* = \mu, \\ \lambda(k)S_k^*\Theta^*\displaystyle\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}d\tau = (\mu+\beta)I_k^*, \end{cases} \tag{6}$$

where

$$\Theta^* = \frac{1}{\langle k\rangle}\sum_k \varphi(k)p(k)I_k^*. \tag{7}$$

By similar method in [10], one can conclude that the endemic equilibrium $E_*$ exists.

Second, we will prove that $E_*$ is globally asymptotically stable when $R_0 > 1$.

System (5) can be rewritten as the following system according to (6).

$$\begin{cases} \dot{S}_k(t) = -\sum\limits_{l=1}^{n} \beta_{kl} S_k(t) I_l(t) + \sum\limits_{l=m}^{n} \beta_{kl} S_k^* I_l^* \\ \qquad\qquad -\mu(S_k(t) - S_k^*), \\ \dot{I}_k(t) = \sum\limits_{l=1}^{n} \beta_{kl} \int_0^{+\infty} S_k(t-\tau) I_l(t-\tau) f(\tau) \mathrm{e}^{-\mu\tau} d\tau \\ \qquad\qquad -\dfrac{1}{I_k^*} \left( \sum\limits_{l=1}^{n} \beta_{kl} S_k^* I_l^* \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} d\tau \right) I_k(t), \end{cases} \tag{8}$$

where $\beta_{kl} = \dfrac{1}{\langle k \rangle} \lambda(k) \varphi(l) p(l), k, l = 1, 2, \cdots, n.$

Since the solutions of system (5) with initial conditions remain positive for all $t \geq 0$, let us consider

$$\begin{aligned} V_k(t) = & \left( S_k(t) - S_k^* - S_k^* \ln \frac{S_k(t)}{S_k^*} \right) \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} d\tau + \left( I_k(t) - I_k^* - I_k^* \ln \frac{I_k(t)}{I_k^*} \right) \\ & + \sum_{l=1}^{n} \beta_{kl} \int_0^{+\infty} \int_{t-\tau}^{t} f(\tau) \mathrm{e}^{-\mu\tau} (S_k(s) I_l(s) - S_k^* I_l^* - S_k^* I_l^* \ln \frac{S_k(s) I_l(s)}{S_k^* I_l^*}) ds d\tau \end{aligned} \tag{9}$$

Calculating the derivative of $V_k(t)$ along solution of system (8), we get

$$\begin{aligned} \dot{V}_k(t)\Big|_{(8)} = & -\mu \frac{(S_k - S_k^*)^2}{S_k^*} \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} d\tau \\ & + \sum_{l=1}^{n} \beta_{kl} S_k^* I_l^* \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} \left[ 2 - \frac{S_k^*}{S_k} + \frac{I_l}{I_l^*} - \frac{I_k}{I_k^*} - \frac{S_k(t-\tau) I_l(t-\tau) I_k^*}{S_k^* I_k I_l^*} \right. \\ & \left. - \ln \frac{S_k(t) I_l(t)}{S_k^* I_l^*} + \ln \frac{S_k(t-\tau) I_l(t-\tau)}{S_k^* I_l^*} \right] d\tau. \end{aligned} \tag{10}$$

Noting that

$$\begin{aligned} & 2 - \frac{S_k^*}{S_k(t)} + \frac{I_l(t)}{I_l^*} - \frac{I_k(t)}{I_k^*} - \frac{S_k(t-\tau) I_l(t-\tau) I_k^*}{S_k^* I_k I_l^*} \\ & - \ln \frac{S_k(t) I_l(t)}{S_k^* I_l^*} + \ln \frac{S_k(t-\tau) I_l(t-\tau)}{S_k^* I_l^*} \\ & = H(\frac{I_k(t)}{I_k^*}) - H(\frac{I_l(t)}{I_l^*}) - G(\frac{S_k^*}{S_k(t)}) - G(\frac{S_k(t-\tau) I_l(t-\tau) I_k^*}{S_k^* I_k I_l^*} \\ & \leq H(\frac{I_k(t)}{I_k^*}) - H(\frac{I_l(t)}{I_l^*}), \end{aligned}$$

where $H(x) = -x + \ln x$ and $G(x) = x - 1 - \ln x \geq 0$, it follows that

$$\dot{V}_k(t)\Big|_{(9)} \leq \sum_{l=1}^{n} \beta_{kl} S_k^* I_l^* \int_0^{+\infty} f(\tau) \mathrm{e}^{-\mu\tau} \left( H(\frac{I_k(t)}{I_k^*}) - H(\frac{I_l(t)}{I_l^*}) \right). \tag{11}$$

In addition, the following matrix

$$(\beta_{kl}S_k^*I_l^*)_{n\times n} = \left(\frac{\lambda(k)\varphi(l)p(l)}{\langle k\rangle}S_k^*I_l^*\right)_{n\times n}$$

is a irreducible, and the following matrix $B$ is also irreducible.

$$B = \begin{pmatrix} \sum_{l\neq 1}\beta_{1l}S_m^*I_l^* & -\beta_{21}S_2^*I_1^* & \cdots & -\beta_{n1}S_n^*I_1^* \\ -\beta_{12}S_1^*I_2^* & \sum_{l\neq 2}\beta_{2l}S_2^*I_l^* & \cdots & -\beta_{n2}S_n^*I_2^* \\ \cdots & \cdots & \cdots & \cdots \\ -\beta_{1n}S_1^*I_n^* & -\beta_{2n}S_2^*I_n^* & \cdots & \sum_{l\neq n}\beta_{nl}S_n^*I_l^* \end{pmatrix}$$

Hence there exists a positive vector $C = (c_1, c_2, \cdots, c_n)$ such that $BC = 0$ in which $c_k$ is the cofactor of the $k$th diagonal of $B$, $1 \leq k \leq n$ [6], which means that

$$\sum_{l=1}^{n} c_l\beta_{lk}S_l^*I_k^* = c_k\sum_{l=1}^{n}\beta_{kl}S_k^*I_l^*, k = 1, 2, \cdots, n,$$

and hence

$$\sum_{k=1}^{n} c_k\sum_{l=1}^{n}\beta_{kl}S_k^*I_l^*\int_0^{+\infty} f(\tau)\mathrm{e}^{-\mu\tau}(H(\frac{I_k}{I_k^*}) - H(\frac{I_l}{I_l^*}))d\tau = 0. \tag{12}$$

Define a Lyapunov function

$$V(t) = \sum_{k=1}^{n} c_kV_k(t)$$

in which $V_k(t)$ is defined by (9).

We have from (9), (11) and (12) that

$$\dot{V}(t)\Big|_{(8)} \leq 0.$$

Note that the fact the largest invariant set of $\dot{V}(t)\Big|_{(8)} = 0$ is a singleton $E^*$. Therefore, LaSalle Invariance Principle implies that the endemic equilibrium $E^*$ of system (5) is globally asymptotically stable when $R_0 > 1$. □

The basic reproduction number for system (5) (i.e., system (1)) is $R_0$ (shown in (4)) according to Theorem 2.1 and 2.2. $R_0$ not only depends on the epidemic properties and topology structure of the network, but also depends on distributed delay.

**Remark 2.1.** Model (1) in this paper reduce to model (6) in [8] when $\lambda(k) = \lambda k$ and kernel functions is Delta-distribution function i.e.,

$$f(\tau) = \delta(\tau) = \begin{cases} +\infty, \tau = h, \\ 0, \quad \tau \neq h, \end{cases}$$

$$\int_0^{+\infty} \delta(\tau)d\tau = 1.$$

Based on screening nature of $\delta$ function, the basic reproduction number also reduce to $R_0 = \frac{\lambda\langle k\varphi(k)\rangle}{(\mu+\beta)\langle k\rangle}e^{-\mu h}$, which is consistent with one in [8]. Therefore, more general results are obtained in this paper.

## 3. Numerical simulations

For further understanding of the proposed model, numerical simulations will be performed on a scale-free network in which the degree distribution is $p(k) = Ck^{-\gamma}$, and $C$ satisfies $\sum_{k=m}^{n} p(k) = 1$. $n = 100$ and $m = 1$ is a suitable assumption. Meanwhile, we set $\phi(k) = ak^p/(1 + bk^p)$ in which $a = 0.5, p = 0.75, b = 0.02$ and $\lambda(k) = \lambda k$. Let $f(\tau)$ follows the simpler Gamma distribution $f(\tau) = 1/be^{-\tau/b}, b > 0$. The initial functions are $I_k(s) = 0.45, k = 2, 3, 4, 5$ and $I_k = 0, k \neq 2, 3, 4, 5$ for $s \in (-\infty, 0]$.

Denote

$$I(t) = \sum_k p(k)I_k(t).$$

Obviously, $I(t)$ is the relative average density of the infected nodes.

Case 1: Letting $\gamma = 2.5$, $\lambda = 0.05, \beta = 0.1, \mu = 0.03$, $f(\tau) = 1/be^{-\tau/b}$ $(b = 5)$, we can obtain from (4) that $R_0 = 0.5360 < 1$. Fig. 1 (a) shows the dynamical behaviors of system (5). The numerical simulation shows $\lim_{t\to+\infty} I(t) = 0$, it follows that $\lim_{t\to+\infty} I_k(t) = 0$, the infection eventually disappear. The numerical result is consistent with Theorem 2.1.

Case 2: Letting $\gamma = 2.5, \lambda = 0.15, \beta = 0.1, \mu = 0.03, f(\tau) = 1/be^{-\tau/b}$ $(b = 5)$. We can obtain from (4) that $R_0 = 1.6079 > 1$. Fig. 1 (b) shows the dynamic behaviors of system (5). The endemic equilibrium is globally stable, and the relative density $I_k(t)$ and the relative average density $I(t)$ converge to positive constant as $t \to +\infty$ respectively. The numerical result is consistent with Theorem 2.2.

Case 3: Letting $\gamma = 2.5, \lambda = 0.15, \beta = 0.1, \mu = 0.03, f(\tau) = 1/be^{-\tau/b}$. When $b = 5$, the endemic equilibrium $E_*$ is globally stable, but the equilibrium $E_*$ may lose its stability as $b$ increases because $R_0 < 1$ according to $\int_0^{+\infty} f(\tau)e^{-\mu\tau}d\tau = \frac{1}{1+b\mu}$ and the disease-free equilibrium becomes globally asymptotically stable. Fig. 2 shows the dynamic behaviors of system (5). This means kernel function $f(\tau)$ has a great influence on the dynamic behaviours of system (5), and this also implies that it is interesting to discuss the epidemic model with distributed delay on heterogeneous network.

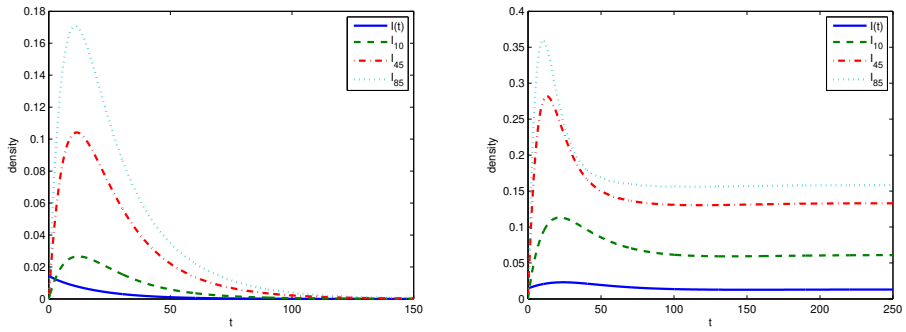


**Figure 1.** (a) Dynamical behaviors of system (5) with $R_0 = 0.5630$. (b) Dynamical behaviors of system (5) with $R_0 = 1.6079$.

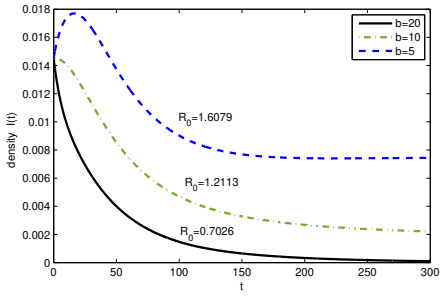


**Figure 2.** Behaviors of system (5) with $f(\tau) = 1/be^{-\tau/b}$ in which $b = 5, 10, 20$.

# 4. Conclusion

An novel $SEIR$ epidemic dynamical model with distributed delay describing the incubation period of disease has been proposed on scale-free network in this paper. The formula of the basic reproduction number $R_0$ for the model is given. By constructing suitable Lyapunov function, we proved that the disease-free equilibrium is globally asymptotically stable and the disease dies out when $R_0 < 1$, the endemic equilibrium is globally asymptotically stable and the disease will always exist when $R_0 > 1$. Of course, for specific epidemic, the reasonable selection of parameters and kernel function, as well as the verification of actual data, are important tasks, we leave this for our future work.

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