

# 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

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## 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, measles, 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  $k = 1, 2, \dots, n$  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:

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

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

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

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,  $\varphi(k) = ak^\alpha/(1+bk^\alpha)$  ( $0 \leq \alpha < 1, a > 0, b \geq 0$ ) [18],  $\lim_{k \rightarrow +\infty} \varphi(k) = a/b$  when  $b \neq 0$ , 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

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

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