Dynamical Analysis of a Delayed SIQS Epidemic Model on Scale-free Networks*

Rundong Zhao[1] and Qiming Liu[1,†]

Abstract In this paper, we establish a novel delayed SIQS epidemic model on scale-free networks, where time delay represents the average quarantine period. Through mathematical analysis, we present the basic reproduction number R_0. Then, we provide the global asymptotical stability of the disease-free equilibrium and the local asymptotical stability of the endemic equilibrium. Finally, we perform numerical simulations to verify the correctness of the main results and analyze the sensitivity of parameters. Our research shows that when $R_0 > 1$, lengthening the quarantine period can slow the spread of the disease and reduce the number of infected individuals.

Keywords Epidemic model, Network, Quarantine period, Stability.

MSC(2010) 92B05, 34K20, 65L03.

1. Introduction

Infectious diseases have always been the great enemy of human health. Through out the history, the epidemics of infectious diseases have brought great disasters to human survival and national economy. To study the propagation dynamics and curb strategies of infectious diseases, the mathematical compartmental model is an important method [1].

In recent years, with the development of global transportation network [4], human behavior and social interpersonal communication are heterogeneous. Thus, it is necessary and reasonable to construct epidemic models on complex networks. In the field of complex networks, a research [2] showed that many networks, such as contact networks, have the property of being scale-free. For example, the distribution of connectivity degrees follows the power-law $p(k) = Ck^{-\gamma}$ ($2 < \gamma \leq 3$). In 2001, Pastor-Satorras et al. first denied an SIS model on scale-free networks, and concluded the absence of an epidemic threshold on a wide range of scale-free networks [22]. Moreno et al. studied an SIR epidemic model on two complex networks [20]. These results have attracted more researchers to study this field [3, 8–10, 12, 13, 15–18, 25, 27, 28].

After the disease breaks out, how to control the spread of disease effectively is an important issue. One effective method is quarantine, which has long been widely used to control the spread of disease. By cutting off contact between individuals,

---

[†]the corresponding author.
Email address: zrdmath@outlook.com (R. Zhao), lqmmath@163.com (Q. Liu)
[1]Department of Science and Culture, Shijiazhuang Branch, Army Engineering University of People's Liberation Army, Shijiazhuang, Hebei 050003, China

epidemics are often brought under control. In 2014, Li et al. proposed an SIQRS epidemic model on scale-free networks and proved the stability of disease-free equilibrium and the permanence of the disease [13]. Then, Huang et al. investigated a novel SIQRS epidemic model with demographics and analyzed the global epidemic behavior [8]. In 2019, Li et al. introduced an SIQS model on complex networks with birth and death mechanism, and introduced its optimal control [12]. Chen et al. established two epidemic models including variable population size, degree-related imperfect vaccination and quarantine on scale-free networks and proved the global stability of disease-free and endemic equilibrium [3].

To reflect the propagation process of the epidemic more realistically, many researchers analyzed delayed compartment models on complex networks. Time delays in the models represent average infectious period of the disease [15, 16, 28], average incubation period [9, 25] and the immunity period of recovery [17]. However, few researchers studied the effects of quarantine period on the spread of diseases. In this paper, we focus on the effectiveness of quarantine period on epidemics and construct a novel delayed SIQS epidemic model on scale-free networks.

In the delayed SIQS model, infected individuals may be quarantined and treated for a period of time, and become full susceptibility to the infection again. The primary purpose of this paper is to investigate the dynamical behavior of this model. In Section 2, we present the delayed SIQS model on scale-free networks. In Section 3, we define the basic reproduction number and analyze the dynamical behavior. In Section 4, we give numerical simulations to demonstrate the main results. In Section 5, we summarize this work.

2. Model

Let us make following assumptions:

(H1) Each node on the network represents an individual. All nodes on the networks can be classified into one of three categories: susceptible(S), infected(I) and quarantined(Q).

(H2) A susceptible node can be infected by contact with every infected node.

(H3) Every infected node will become susceptible to infection again after a period of quarantine.

(H4) Similar to [11, 12], we suppose the total nodes on the network is a constant. For example, the number of birth nodes is equal to the number of natural death nodes.

(H5) Every new birth node is susceptible.

Based on above assumptions, we consider a delayed SIQS epidemic model on scale-free networks. Let $S_k(t)$, $I_k(t)$ and $Q_k(t)$ represent the relative density of susceptible nodes, infected nodes and quarantined nodes respectively with degree k $(k = 1, 2, ..., n)$ at time t. The SIQS epidemic model is as follows:

$$
\begin{cases}
\dfrac{\mathrm{d}S_k(t)}{\mathrm{d}t} = \mu - \lambda(k)S_k(t)\Theta(t) + \gamma I_k(t - \tau)e^{-\mu\tau} - \mu S_k(t), \\
\dfrac{\mathrm{d}I_k(t)}{\mathrm{d}t} = \lambda(k)S_k(t)\Theta(t) - (\mu + \gamma)I_k(t), \\
\dfrac{\mathrm{d}Q_k(t)}{\mathrm{d}t} = \gamma I_k(t) - \gamma I_k(t - \tau)e^{-\mu\tau} - \mu Q_k(t),
\end{cases}
\tag{2.1}
$$