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Dynamics of epidemic spreading model with drug-resistant variation on scale-free networks

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HIGHLIGHTS

- A novel *SIVRS* epidemic model with the drug-resistant variation on scale-free networks.
- Determination of the basic reproductive number and the equilibriums.
- The variant parameter can affect the epidemic spreading and the endemic level.
- The global attractivity of endemic equilibrium is proved in detail.

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ABSTRACT

Considering the influence of the virus' drug-resistant variation, a novel *SIVRS* (susceptible–infected–variant–recovered–susceptible) epidemic spreading model with variation characteristic on scale-free networks is proposed in this paper. By using the mean-field theory, the spreading dynamics of the model is analyzed in detail. Then, the basic reproductive number R_0 and equilibriums are derived. Studies show that the existence of disease-free equilibrium is determined by the basic reproductive number R_0. The relationships between the basic reproductive number R_0, the variation characteristic and the topology of the underlying networks are studied in detail. Furthermore, our studies prove the global stability of the disease-free equilibrium, the permanence of epidemic and the global attractivity of endemic equilibrium. Numerical simulations are performed to confirm the analytical results.

1. Introduction

It is well known that epidemic diseases always bring great harm to human beings. Therefore, the disquisition of epidemic models is of great important, which plays a significant role in controlling and predicting the epidemic outbreak [1–3]. According to the situation of individual diseases, most of traditional epidemic models are based on a compartmentalization of individuals, which generates two important and fundamental epidemic models: the *SIS* model [4] and the *SIR* model [5]. Obviously, these simple models cannot completely reflect the realistic feature of the epidemic transmission, which are subsequently extended in ways towards making them more realistic in recent years.

Early classical representations of epidemic disease dynamics are all based on the assumption of homogeneous mixing, which means that all individuals mix uniformly and all hosts have identical contact rate. Virtually, the epidemic disease

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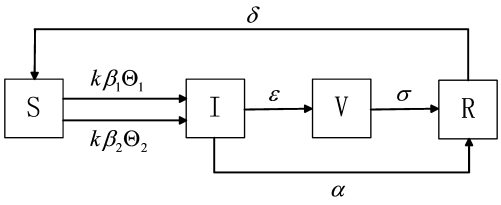

Fig. 1. The transmission sketch of the *SIVRS* model.

transmission exhibits heterogeneity [6,7]. A novel heterogeneous network is the *BA* scale-free network, which is characterized by degree distribution that follows the power-law distribution [8]. In networks, the nodes denote individuals and the edges represent the relationships between individuals. Recently, the scale-free property of networks has been taken into account by many epidemic models [9–17]. One of the famous representative works in this area was done by Pastor-Satorras and Vespingani [9,10]. They first presented a detailed analytical and numerical study about *SIS* epidemic model on scale-free networks. So far, a large number of research results confirmed that the heterogeneity of underlying networks topology plays a key role in epidemic spreading [18–27].

Some epidemic disease, such as tuberculosis, influenza and HBV etc., the drug-resistant variation will emerge by the individual physiological differences in the course of treatment [28–32]. That is to say, the infected individual may be resistant to the drug during the course of treatment and become the variant individual. Apparently, the drug-resistant variation of virus makes patient worse. In addition to the infected individual with infectious, the variant individual is also contagious. The susceptible individual who contacts with the infected or variant individual might be infected, and then become infected individual [30–32]. This may cause the virus with different infectivity at different stages. Therefore, it is of great significance to study the infection mechanism and dynamical behaviors of the drug-resistant variation in the epidemic spreading.

Very recently, for investigating the epidemic disease with drug-resistant characteristic, Xu et al. [33] proposed a *SIVRS* (susceptible–infected–variant–recovered–susceptible) epidemic model and analyzed it in detail. However, the *SIVRS* model which they studied was based on homogeneous network rather than heterogeneous network. Liu et al. [34] proposed a *SIVRS* model on the scale-free network. However, they neglected to prove the global attractivity of endemic equilibrium and analyze the influence of drug-resistant variation in epidemic spreading, which are worthy of further exploration. In this paper, considering the virus' drug-resistant variation, we establish a novel *SIVRS* epidemic spreading model with variant group on scale-free networks and comprehensively prove the stability of the model in detail.

The rest of this paper is organized as follows. In Section 2, we present a novel *SIVRS* spreading model with the drug-resistant variation on scale-free networks in detail. In Section 3, the basic reproduction number and the equilibriums of the proposed model are obtained at first. Then, we analyze the globally asymptotic stability of disease-free equilibrium, the permanence of the disease and the global attractivity of endemic equilibrium in detail. Section 4 presents the results of our numerical simulation. Finally, we conclude the paper in Section 5.

2. Model formulation

As mentioned earlier, we consider the influence of the drug-resistant variation to build a susceptible–infected–variant–recovered–susceptible (*SIVRS*) epidemic spreading model. In this paper, the whole population is divided into four groups: susceptible (S), infected (I), variant (V), recovered (R). And we suppose that $S_k(t)$, $I_k(t)$, $V_k(t)$ and $R_k(t)$ be the densities of the above-mentioned nodes with the connectivity degree$k$ at time t. The transmission sketch is described in Fig. 1. During the epidemic spreading, if a susceptible individual is connected to an infected individual or a variant individual, it will be infected with probability β_1 or β_2 respectively. An infected individual turns into a variant individual with probability ε when he or she occur the drug-resistant variation. Infective individuals or variant individuals are recovered from disease with probability α or σ respectively. Some recovered individuals turn into susceptible individuals with probability δ due to immunization-lost.

Then, the dynamic mean-field reaction rate equations can be described as follows:

$$\begin{cases} \dfrac{dS_k(t)}{dt} = \delta R_k(t) - k\beta_1\Theta_1(t)S_k(t) - k\beta_2\Theta_2(t)S_k(t) \\ \dfrac{dI_k(t)}{dt} = k\beta_1\Theta_1(t)S_k(t) + k\beta_2\Theta_2(t)S_k(t) - \varepsilon I_k(t) - \alpha I_k(t) \\ \dfrac{dV_k(t)}{dt} = \varepsilon I_k(t) - \sigma V_k(t) \\ \dfrac{dR_k(t)}{dt} = \alpha I_k(t) + \sigma V_k(t) - \delta R_k(t) \end{cases} . \tag{1}$$