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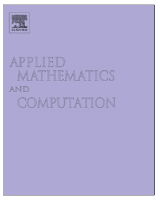

Global stability of a multi-group SEI model

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ABSTRACT

In this paper, a multi-group SEI model with the bilinear incidence and variable susceptibility and infectivity is analyzed. The susceptible individuals are divided into n groups according to their susceptibility, and infected individuals are divided into m groups according to infectivities. Each group of infected individuals has an exposed period. The basic reproduction number R_0 is obtained, and globally asymptotic stability of disease-free equilibrium is proved if $R_0 \leqslant 1$. If $R_0 > 1$, the disease-free equilibrium is unstable and the endemic equilibrium exists and is unique, which is globally asymptotically stable. Finally, some numerical examples are given to illustrate the above analysis.

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1. Introduction

Multiple groups models have been introduced in the literature to describe the transmission dynamics of infectious diseases. This work can be traced back to Lajmanovich and Yorke [1], which proposed and analyzed multiple groups models about sexually transmitted diseases (STDs). Since then, much work has been done about STDs models by Castillo-Chaves et al. [2–5], which promoted the methods of K-monotone systems.

Besides that, variable infectivity (VI) model and staged-progression (SP) model were proposed by Hyman, Li and Stanley in [6] when they studied the epidemic dynamics of HIV model. Then the expressions of the basic reproduction number for the spread disease in heterogeneous were formulated in [7], which not only included the VI model and SP model, but also included the variable susceptibility (VS) model, and the combined variable susceptibility and variable infectivity (VSVI) model. The dynamical behavior of VS model had been studied in [8,9]. Ma, Liu and Li had studied the dynamic behavior of VI model in [10]. Furthermore, Okuonghae and Korobeinikov also recognized the importance of variable susceptibility and variable infectivity models when they studied tuberculosis in Nigeria, and proposed the multiple parallel infectious stages models [11,12].

A VSVI model was studied in paper [13] by Hyman and Li, in which the basic reproduction number R_0 was obtained, and global stability of disease-free equilibrium was proved, then the existence of endemic equilibrium was discussed with bilinear incidence and standard incidence. However the dynamical behavior of endemic equilibrium was not discussed. Moreover many diseases (such as Rabies, Hepatitis B, Influenza and so on) have an exposed period, which does not have infectivities. For those diseases, it is also important to divide susceptible individuals and infected individuals into different groups according to variable susceptibilities and infectivities [14]. On the basis of previous work, we propose a multi-group SEI model with the bilinear incidence and variable susceptibility and infectivity. Variable susceptibility means differences between susceptible people. Variable infectivity means differences between infected people. In the multi-group model, the removing of infected class may be due to death or recovery. We use Lyapunov functions to prove the global asymptotic stability of

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disease-free equilibrium and endemic equilibrium. In addition, globally asymptotic stability of endemic equilibrium in paper [13] is proved with bilinear incidence as a remark in this paper.

The organization of this paper is as follows. In Section 2, the model will be described. The following Section mainly discusses the existence of equilibria and basic reproduction number. In Section 4, the analysis about dynamical behavior of the model is presented. Numerical examples are given in Section 5. In Section 6, we give a brief summary and some discussions.

2. The model description

The susceptible individuals are divided into n groups according to their susceptibilities, infected individuals are divided into m groups according to infectivities, and each group of infected individuals has an exposed period. Then the corresponding transfer diagram is given in Fig. 1, and the corresponding equations of SEI model can be formulated as:

$$\begin{cases} \frac{dS_i}{dt} = r_i B - \mu_i S_i - \lambda_i S_i, \quad i = 1,2,\ldots,n, \\ \frac{dE_j}{dt} = \sum_{i=1}^{n} q_{ij}\lambda_i S_i - d_j E_j - \gamma_j E_j, \quad j = 1,2,\ldots,m, \\ \frac{dI_j}{dt} = \gamma_j E_j - \kappa_j I_j, \end{cases} \tag{1}$$

where $\sum_{i=1}^{n} r_i = 1$ and $\sum_{j=1}^{m} q_{ij} = 1$. B is the recruitment rate into the susceptible class, and r_i is the recruitment proportion of the i-th susceptible group. The per capita mortality rate of the i-th susceptible group is μ_i, d_j and κ_j denote the per capita removing rate of the j-th exposed group and j-th infected group, and γ_j is the transfer rate from the j-th exposed class to the j-th infected class. q_{ij} is the possibility that the susceptible individual in the i-th susceptible group enter the j-th infected group through infection. λ_i is the rate of infection for the i-th group. Since it is assumed that all individuals are well mixed in the population, the bilinear incidence [7,13] is chosen, and

$$\lambda_i = c_0 \alpha_i \sum_{k=1}^{m} \beta_k I_k, \tag{2}$$

where α_i is the susceptibility of the i-th susceptible group, c_0 is the average number of contacts in the population, and β_k is the infectiousness of infected individuals in the k-th infected group. In this paper, it is assumed that $B, r_i, \mu_i, d_j, \gamma_j, \kappa_j, \beta_k, c_0, \sum_{i=1}^{n} q_{ij}\alpha_i$ are positive, and q_{ij} and α_i are nonnegative, where $i = 1,2,\ldots,n, j = 1,2,\ldots,m, k = 1,2,\ldots,m$.

3. Equilibria and basic reproduction number

It is easy to see the system (1) has a disease-free equilibrium E^0,

$$S_i^0 = \frac{r_i B}{\mu_i}, \quad i = 1,2,\ldots,n,$$

and

$$E_1^0 = E_2^0 = \cdots = E_m^0 = I_1^0 = I_2^0 = \cdots = I_m^0 = 0.$$

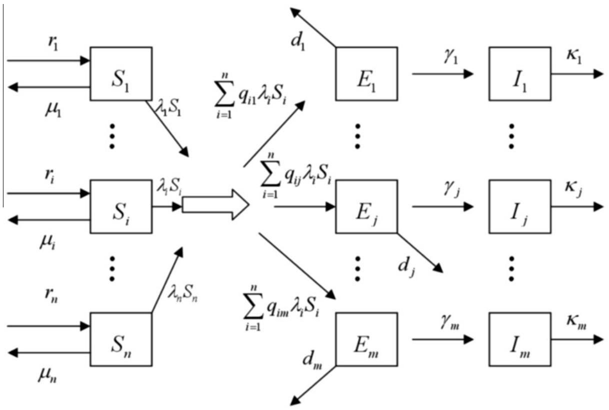

Fig. 1. The corresponding transfer diagram.