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Global stability of an epidemic model with nonlinear incidence rate and differential infectivity

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Abstract

This paper considers an SI_1I_2R epidemic model that incorporates two classes of infectious individuals with differential infectivity, and the incidence rate is nonlinear. The basic reproduction number R_0 is found. If $R_0 \leqslant 1$, the disease-free equilibrium is globally asymptotically stable and the disease always dies out eventually. If $R_0 > 1$, a unique endemic equilibrium is locally asymptotically stable for general assumption. For a special case the global stability of the endemic equilibrium is proved.

Keywords: Epidemic model; Basic reproduction number; Disease-free equilibrium; Endemic equilibrium; Stability

1. Introduction

Many diseases are transmitted by viruses. Viral levels often determine the ability of transmission for some diseases such as malaria and dengue fever, where the infectivity depends on parasite or viral loads in infected hosts or

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vectors [1,2]. For HIV transmission a differential infectivity model was proposed in [3,4].

Bilinear incidence rate βSI and standard incidence rate $\frac{\lambda SI}{N}$ (where S, I, and N denote the number of susceptible individuals, infectious individuals, and total population, respectively) have been frequently used in classical epidemic model [5–8]. A saturation incidence rate $\frac{\beta SI}{H+S}$, where H is a positive constant, was proposed in [9], and it was used in many epidemic models afterwards [10,11].

In this paper, we introduce an incidence rate of the form $\beta I\phi(S)$ into a differential infectivity epidemic model. This incidence rate generalizes the saturation incidence rate. In Section 2, an epidemic model with differential infectivity is established. In Section 3, global stability of the disease-free equilibrium is discussed. In Section 4, the existence and local stability of the endemic equilibrium are investigated, and global stability of the endemic equilibrium is shown for a special case. The conclusion obtained are summarized in Section 5.

2. Model

The model considered in this paper is of SI_1I_2R type, which means that susceptible individuals become the infected individuals with differential infectivity, and become the removed individuals with permanent immunity. Corresponding to the differential infectivity, the infectious individuals are divided into two classes, I_1 and I_2.

Let $S(t)$ be the number of susceptible individuals, $I_i(t)$ $(i = 1, 2)$ be the number of individuals in the class I_i, $R(t)$ be the number of removed individuals at time t, respectively. The epidemic model considered here is as follows:

$$\begin{cases} \frac{dS}{dt} = A - \mu S - [\beta_1 I_1 \phi_1(S) + \beta_2 I_2 \phi_2(S)], \\ \frac{dI_1}{dt} = p_1[\beta_1 I_1 \phi_1(S) + \beta_2 I_2 \phi_2(S)] - (\mu + \alpha_1 + \gamma_1) I_1, \\ \frac{dI_2}{dt} = p_2[\beta_1 I_1 \phi_1(S) + \beta_2 I_2 \phi_2(S)] - (\mu + \alpha_2 + \gamma_2) I_2, \\ \frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 - \mu R. \end{cases} \tag{2.1}$$

In model (2.1), A is the recruitment rate of population, μ is the natural death rate, α_i is the disease-related death rate in the class I_i, γ_i is the recovery rate in the class I_i, p_i is the probability entering the class I_i, $p_1 + p_2 = 1$. $\beta_i I_i \phi_i(S)$ is the incidence rate of class I_i. For function $\phi_i(S)$ we assume the following:

$$\phi_i(0) = 0, \quad \phi_i'(S) > 0 \quad \text{for } S > 0.$$