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Hopf bifurcation of an epidemic model with a nonlinear birth in population and vertical transmission ☆

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ABSTRACT

In this paper, an epidemic model involving a nonlinear birth in population and vertical transmission was studied. When $\mathscr{R}_0 < 1$, the disease-free equilibrium was stable, while if $\mathscr{R}_0 > 1$, the disease-free equilibrium was unstable. We researched the existence of Hopf bifurcation and obtained the stability and direction of the Hopf bifurcation by using the normal theory and the center manifold theorem. Numerical simulations were carried out to illustrate the main theoretical results and a brief discussion was given to conclude this work.

1. Introduction

Mathematical epidemiology, i.e. the construction and analysis of mathematical models are one of the major areas of biology to describe the spread and control of infectious diseases. Since Kermack and Mckendrick constructed a system of ODE [1] to study epidemiology in 1927, the concept of "Compartment model" have been used until now. Most of the research literatures described the spread of a non-lethal disease in a large population by dividing the total population into three classes: the susceptible (S), the infectious (I), and the recovered (i.e. with a permanent or temporary acquired immunity) (R). We usually call these compartmental models SIR models or SIRS models, and each letter in SIR or SIRS denotes a compartment. And there must be an individual belong to one compartment.

In real life, some diseases may be passed from one individual to another via vertical transmission. That is to say, vertical transmission of diseases refer to diseases are infected to the offspring by their infected parentage. In recent years, a few studies of vertical transmission have been conducted to describe the effects of various and demographical factors [2–5]. For example, Busenberg and Cooke [5] discussed a variety of diseases which contained both of horizontally and vertically transmitting, a comprehensive and formulation survey. They also provided the mathematical analysis of compartmental models including vertical transmission. Some examples of such diseases are AIDS, Rubella, Hepatitis, etc.

2. The model

Classical epidemic models assume that the total population size is constant, and that concentrate on describing the spread of disease based on the population. In recent years more and more models pay attention to a variable population size, and then disease causing death for a longer time scale should be taken into account to reduce reproduction. For example, according to the paper [6], a nonlinear birth term $B(N)$ is considered and we can also find that the form $B(N)N$ is important

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in determining the qualitative dynamics. In the absence of disease, the paper [7] assumes that the total population size N changes according to a population growth equation

$$\frac{dN(t)}{dt} = B(N)N - dN.$$

Here $d > 0$ is the death rate constant, and $B(N)N$ is a birth rate function with $B(N)$ satisfying with following basic assumptions for $N \in (0, \infty)$:

(A1) $B(N) > 0$;
(A2) $B(N)$ is continuously differentiable with $B'(N) < 0$;
(A3) $B(0^+) > d > B(\infty)$.

Based on the above description, we choose a $B(N) = \frac{A}{N} + B$. It is clear that $B(N)$ meets (A1) and (A2). Because of (A3), we can choose $B, \mu = \min\{\mu_1, \mu_2, \mu_3\}$ satisfying $B < \mu$. Under these assumptions, the following epidemic model is considered as one model with nonlinear birth in population and nonlinear incidence.

$$\begin{cases} \frac{dS(t)}{dt} = A - (\mu_1 - B)S(t) + BqI(t) + BR(t) - \frac{\beta S(t)I(t)}{1+\alpha I(t)} + \gamma e^{-\mu_3 \tau} I(t-\tau), \\ \frac{dI(t)}{dt} = \frac{\beta S(t)I(t)}{1+\alpha I(t)} + BpI(t) - (\gamma + \mu_2)I(t), \\ \frac{dR(t)}{dt} = \gamma I(t) - \mu_3 R(t) - \gamma e^{-\mu_3 \tau} I(t-\tau), \end{cases} \tag{2.1}$$

where $A, B, \mu_i (i = 1, 2, 3), q, p, \beta, \alpha, \gamma$ are nonnegative. $S(t), I(t), R(t)$ denote the number of susceptible, infected and recover population stage at time t, respectively. A is constant immigrants, B is the birth rate and $\mu_i (i = 1, 2, 3)$ are natural death rate. q is the probability that a child who is born from infectious mother is susceptible; p is the probability that a child who is born from infectious mother is infected, then $p + q = 1$. β is contact rate between the susceptible and the infection. γ is the recovery rate. τ is the time delay.

The initial conditions for system (2.1) are

$$(\psi_1(\theta), \psi_2(\theta), \psi_2(\theta)) \in C_+ = C([-\tau, 0], \mathbb{R}^3_+), \quad \psi_i(0) > 0, \ i = 1, 2, 3, \tag{2.2}$$

where

$$\mathbb{R}^3_+ = \{(x_1, x_2, x_3) \in \mathbb{R}^3 : x_i \geqslant 0, i = 1, 2, 3\}.$$

Theorem 2.1. *For any solution $S(t), I(t), R(t)$ of system (2.1) with initial conditions (2.2), $S(t) < M$, $I(t) < M, R(t) < M$ for all large t, where $M = \frac{A}{\mu - B}$.* □

This paper is organized as following: in the next section, we obtain the basic reproduction number by the next generation method and the existence of equilibriums. We verify when $\mathscr{R}_0 < 1$, the disease-free equilibrium was stable, while if $\mathscr{R}_0 > 1$, the disease-free equilibrium was unstable. Then we focus on the local stability of the endemic equilibrium and the existence of the Hopf bifurcation. In Section 4, we obtain the stability and direction of the Hopf bifurcation by using the normal theory and the center manifold theorem. Numerical simulations are carried out in Section 5 to illustrate the main theoretical results and a brief discussion is given in last part to conclude this work.

3. The existence and stability of equilibria

3.1. The existence of equilibria and the stability of the disease-free equilibrium

It is easy to obtain the disease-free equilibrium $E_0 = (S_0, 0, 0) = \left(\frac{A}{\mu_1 - B}, 0, 0\right)$. Then, we define the basic reproduction number $\mathscr{R}_0$ of our model by directly using the next generation method presented in Diekmann et al. [8] and van den Driessche and Watmough [9].

Then

$$\mathscr{R}_0 = \frac{\beta A}{(\mu_1 - B)(\mu_2 + \gamma - Bp)}.$$

Theorem 3.1. *When $\mathscr{R}_0 < 1$, there exists the unique disease-free equilibrium E_0. When $\mathscr{R}_0 > 1$, there also exist a endemic equilibrium $E^* = (S^*(\tau), I^*(\tau), R^*(\tau))$, where $S^*(\tau) = \frac{(\mu_2 + \gamma - Bp)(1+\alpha I^*)}{\beta}$, $R^*(\tau) = \frac{\gamma I^*}{b_3}(1 - e^{-\mu_3 \tau})$ and $I^*(\tau) = \frac{[\beta A - (\mu_1 - B)(\mu_2 + \gamma - Bp)]\mu_3}{\alpha\mu_3(\mu_1 - B)(\mu_2 + \gamma - Bp) + \beta\gamma B(1 + e^{-\mu_3 \tau}) + \beta\mu_3(\mu_2 - B) + \beta\gamma\mu_3(1 - e^{-\mu_3 \tau})}$.*