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Stability analysis in a class of discrete SIRS epidemic models☆

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ABSTRACT

In this paper, the dynamical behaviors of a class of discrete-time SIRS epidemic models are discussed. The conditions for the existence and local stability of the disease-free equilibrium and endemic equilibrium are obtained. The numerical simulations not only illustrate the validity of our results, but also exhibit more complex dynamical behaviors, such as flip bifurcation, Hopf bifurcation and chaos phenomenon. These results reveal far richer dynamical behaviors of the discrete epidemic model compared with the continuous epidemic models.

1. Introduction

In the theory of epidemics, there are two kinds of mathematical models: the continuous-time models described by differential equations and the discrete-time models described by difference equations. The continuous-time epidemic models have been widely investigated in many articles (for example, [1–10] and the references cited therein). In recent years, we have seen more attention being given to the discrete-time epidemic models (see, [11–32] and the references cited therein). The reasons are as follows: first, because statistical data on epidemics is collected in discrete time, it is more convenient and accurate to describe epidemics using discrete-time models than the continuous-time models. Second, we can get more accurate numerical simulation results using discrete-time models. Moreover, the numerical simulations of continuous-time models are obtained by discretizing the models. At last, the discrete-time models have more wealthy dynamical behaviors, for example, the single-species discrete-time models have bifurcations, chaos and more complex dynamical behaviors.

Usually, there are two ways to construct discrete-time epidemic models: (i) by directly making use of the property of the epidemic disease (see [11,12]) and (ii) by discretizing a continuous-time epidemic model using techniques such as, the forward Euler scheme and Mickens' nonstandard discretization (see [13]).

Until now, some studies have been done on discrete-time epidemic models (for example, [14–32] and the references cited therein). These studies focused on: the computation of the basic reproduction number; the local stability and global stability of the disease-free equilibrium; the existence, local stability and global stability of the endemic equilibrium; the extinction, permanence and persistence of the disease. The authors in [14–17] discussed the local and global stability of the disease-free equilibrium and endemic equilibrium for some SI, SIS and SIR type discrete-time epidemic models. The oscillation and stability have been discussed in [18–22] for some SIR type discrete-time epidemic models. Allen and Driessche [23]

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derived a new technique to compute the basic reproduction number for some discrete-time models. Li and Wang [24] and Li et al. [25] discussed the dynamical behaviors of some discrete epidemic models with stage structure and nonlinear incidence rate, respectively, including the transcritical bifurcation, flip bifurcation, Hopf bifurcation and chaos phenomena. The permanence, extinction and global stability for some discrete-time epidemic models have been investigated in [28,30–32].

Generally, for the continuous-time epidemic models (for example, see [5–10] and the references cited therein), there is a threshold $\mathcal{R}_0$ which is called basic reproduction number. In general, when $\mathcal{R}_0 < 1$, the disease dies out and when $\mathcal{R}_0 > 1$, the disease persist in the population. However, for the corresponding discrete-time epidemic models, whether $\mathcal{R}_0 > 1$ or $\mathcal{R}_0 < 1$, there may be very complex dynamical behaviors, such as, bifurcation and chaos phenomenon.

In this paper, we consider the following continuous-time SIRS type epidemic model described by differential equations.

$$\begin{aligned} \dot{S}(t) &= \Lambda - d_1 S - g(S, I, R) + \sigma R, \\ \dot{I}(t) &= g(S, I, R) - (d_2 + \gamma) I, \\ \dot{R}(t) &= \gamma I - (d_3 + \sigma) R, \end{aligned} \tag{1}$$

where $S(t)$, $I(t)$ and $R(t)$ denote the numbers of susceptible, infective and recovered individuals at time t, respectively, Λ is the recruitment rate of the population, d_i $(i = 1, 2, 3)$ is the death rate of $S(t)$, $I(t)$ and $R(t)$, respectively, γ is the recovery rate of the infective individuals, function $g(S, I, R)$ is the disease incidence rate, σ is the rate which the recovered individuals become susceptible again. When $g(S, I, R) = \beta SI$, it is said to be bilinear incidence rate, when $g(S, I, R) = \frac{\beta SI}{S+I+R}$, it is said to be standard incidence rate and when $g(S, I, R) = \frac{\beta SI}{1+\alpha S}$ or $g(S, I, R) = \frac{\beta SI}{1+\alpha I}$, it is said to be saturated incidence rate, where β is the contact coefficient and α is the saturated coefficient. In [5], the authors obtained the basic reproduction number $\mathcal{R}_0$ of model (1) for the bilinear incidence rate and the standard incidence rate, respectively, and proved that if $\mathcal{R}_0 \leq 1$, then the disease-free equilibrium is globally asymptotically stable and if $\mathcal{R}_0 > 1$, then the endemic equilibrium is locally asymptotically stable.

Now, by using the forward Euler scheme, we can discretize model (1). In model (1), we choose a time step size $h > 0$. For any $t \geq 0$, let $S_t = S(t)$, $I_t = I(t)$, $R_t = R(t)$, $S_{t+1} = S(t + h)$, $I_{t+1} = I(t + h)$ and $R_{t+1} = R(t + h)$. Since

$$\dot{S}(t) = \lim_{h\to 0} \frac{S_{t+1} - S_t}{h}, \qquad \dot{I}(t) = \lim_{t\to H} \frac{I_{t+1} - I_t}{h}, \qquad \dot{R}(t) = \lim_{h\to 0} \frac{R_{t+1} - R_t}{h},$$

we can assume that for small enough $h > 0$

$$\dot{S}(t) = \frac{S_{t+1} - S_t}{h}, \qquad \dot{I}(t) = \frac{I_{t+1} - I_t}{h}, \qquad \dot{R}(t) = \frac{R_{t+1} - R_t}{h}.$$

Thus, from model (1) we can directly obtain the following discrete-time SIRS type epidemic model

$$\begin{aligned} S_{t+1} &= S_t + h[\Lambda - d_1 S_t - g(S_t, I_t, R_t) + \sigma R_t], \\ I_{t+1} &= I_t + h[g(S_t, I_t, R_t) - (d_2 + \gamma) I_t], \\ R_{t+1} &= R_t + h[\gamma I_t - (d_3 + \sigma) R_t]. \end{aligned} \tag{2}$$

In this paper, for model (2) we will firstly introduce basic reproduction number $\mathcal{R}_0$ and further obtain the existence of the disease-free equilibrium and endemic equilibrium. Next, we will establish the criteria on the local stability of the disease-free equilibrium and endemic equilibrium by using the linearization method and the expression of roots of cubic polynomial equation. Further, as applications of main results, aim at four special cases of model (2), we will establish much detailed criteria on the local asymptotical stability of the endemic equilibrium. At last, we will use the numerical simulations illustrating our results obtained in this paper and further discussing the Hopf bifurcation and complex dynamical behaviors of model (2) with different $g(S, I, R)$ by means of the Matlab software.

The organization of this paper is as follows. In the second section, the basic assumptions are introduced, and the theorem on the existence of the disease-free equilibrium and endemic equilibrium for model (2) is stated and proved. In the third section, the results on the local stability of the disease-free equilibrium and endemic equilibrium for model (2) are stated and proved. In the fourth section, the four special cases of model (2) are discussed and the local asymptotical stability of the endemic equilibrium is obtained. In the fifth section, we present the numerical simulations, which not only illustrate the validity of the theoretical analysis, but also exhibit the complex dynamical behaviors, such as flip bifurcation, Hopf bifurcation and chaos phenomenon. At last, a discussion is given in the sixth section.

2. Existence of equilibria

For model (2) we always introduce the following assumptions.

- (H_1) All parameters Λ, d_i $(i = 1, 2, 3)$, σ and γ are positive constants.
- (H_2) Function $g(S, I, R)$ is continuously differentiable for all $S \geq 0, I \geq 0$ and $R \geq 0$, $g(0, I, R) \equiv 0, g(S, 0, R) \equiv 0$, $g(S, I, R) > 0$ for all $S > 0$, $I > 0$ and $R \geq 0$.