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Permanence and extinction in a nonautonomous discrete SIRVS epidemic model with vaccination

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ABSTRACT

In this paper, by applying a nonstandard finite difference scheme, we formulate a discretized SIRVS epidemic model which takes into account vaccination. Under quite weak assumptions, the threshold value conditions on permanence and extinction of disease are established. Some new threshold values in product forms $\mathcal{R}_0^*$ and $\mathcal{R}_1^*$ are obtained. We show that the disease is permanent if $\mathcal{R}_0^* > 1$, and if $\mathcal{R}_1^* < 1$, then the disease is extinct. When the model degenerates into a periodic model, a sharp threshold value $\mathcal{R}_0$ is obtained for permanence versus extinction of disease. In order to illustrate our analytic analysis, some numerical simulations are also included in the end.

1. Introduction

Mathematical epidemic models has been widely used to describe transmission dynamics of infections diseases. The most important one is the classical Kermack–Mckendrick SIR epidemic model from which most infectious disease models descend [12]. There are two types of epidemic models: continuous-time models and discrete-time models. Traditionally, continuous-time epidemic models have enjoyed a preference over discrete-time epidemic models because of the mathematical tractability of continuous systems [5,20].

As an important part of epidemiology, the studies on discrete epidemic models have never been stopped up to now. Over the last century, some discrete-time epidemic models have been formulated to analyze the spread and control of infectious diseases [1,2,4,9–11,13–15,19,21,24,30,31]. In [4], a deterministic discrete-time epidemic model is constructed, under certain assumptions, the stabilities of equilibria for the model are studied and the threshold conditions are obtained. In [24], a discrete-time epidemic model is developed to predict the prevalence of the influenza in England and Welsh. Allen [2] formulated three types of discrete-time model: SIS model with constant population size, SIS model with variable population size, and SIR model with constant population size. The extinction and persistence of the disease are obtained. These discrete-time models may be considered as approximations to the continuous-time models. There is an increasing interest in the study and application of discrete epidemic models [3,8,17,18,34]. Zhou, Ma and Brauer formulated a discrete mathematical model to investigate the transmission of SARS, and gave the basic reproductive number [34]. Li, Ma and Brauer studied some new discrete-time SI and SIS epidemic models with vital dynamics [16]. These new models do not exhibit period doubling and chaotic behavior and are thus better approximations to the continuous models. Liu et al. presented four discrete epidemic models with nonlinear incidence rate and discussed the effect of two discretizations on the stability of the endemic equilibria [18].

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Recently, some discrete-time models from nonstandard finite difference techniques have received much attention (see [6,22,23,25,26,32], and the references cited therein). Sekiguchi and Ishiwata derived a discretized SIRS epidemic model with time delay by applying a nonstandard finite difference scheme and analyzed its global dynamics [26]. Strictly speaking, everything in the real world has a relevance with time. So non-autonomous phenomenon should widely exist in all aspects of populations. Non-autonomous epidemic models have been considered by many researchers [7,27–29] and the references cited therein. In [28,29], Thieme studied the persistence and extinction of a non-autonomous SIRS epidemic dynamical system. Applying the theory of persistence and permanence for non-autonomous semi-flows in the population biology, the author obtained sufficient conditions for the persistence and extinction of the disease. In [7], Herzog and Redheffer studied the positivity of solutions and the extinction of the disease. Furthermore, vaccination is considered to be the most effective strategy against the spread of epidemics, especially for the childhood diseases. One may become immune to bacteria, viruses, and other germs after being vaccinated. Vaccination does not necessarily imply life-long immunity. Vaccine-induced immunity usually wanes with time. That is to say, a vaccinated individual will lose his/her acquired vaccination and becomes a susceptible one again.

For continuous epidemic models, the models assuming that the recovery class has permanent immunity but the vaccinated class has only temporary immunity are so called "SIRVS epidemic models". Many infectious diseases have this character such as viral Hepatitis A, chicken pox, measles, rubella, pertussis, etc. Zhang, Teng and Gao investigate the following continuous SIRVS epidemic model with time-dependent coefficients [33]

$$\begin{cases} S'(t) = \Lambda(t) - \beta(t)SI - (\mu(t) + p(t))S + \eta(t)V, \\ I'(t) = (\beta(t)S + \sigma(t)V)I - (\mu(t) + \gamma(t) + \alpha(t))I, \\ R'(t) = \gamma(t)I - \mu(t)R, \\ V'(t) = p(t)S - (\mu(t) + \eta(t))V - \sigma(t)VI. \end{cases} \tag{1.1}$$

Since the infection data of infectious diseases were reported by daily, monthly or yearly etc. Under this circumstance, discrete epidemic models represent a more realistic situation than continuous ones. Motivated by the above-mentioned works, applying Mickens' nonstandard finite difference methods to the continuous model (1.1), we give a discrete non-autonomous SIRVS epidemic model

$$\begin{cases} S_{n+1} - S_n = \Lambda(n) - \beta(n)S_{n+1}I_n - (\mu(n) + p(n))S_{n+1} + \eta(n)V_{n+1}, \\ I_{n+1} - I_n = (\beta(n)S_{n+1} + \sigma(n)V_{n+1})I_n - (\mu(n) + \gamma(n) + \alpha(n))I_{n+1}, \\ R_{n+1} - R_n = \gamma(n)I_{n+1} - \mu(n)R_{n+1}, \\ V_{n+1} - V_n = p(n)S_{n+1} - (\mu(n) + \eta(n))V_{n+1} - \sigma(n)V_{n+1}I_n. \quad n = 0, 1, 2, \ldots \end{cases} \tag{1.2}$$

where S_n is the susceptible class, I_n is the infective class , R_n is the recovery class and V_n is the vaccinated class at time n. $\Lambda(n)$ is the growth rate of population at time n, $\mu(n)$ is the instantaneous per capita natural death rate at time n, $p(n)$ is the vaccination rate of the susceptible class at time n, $\beta(n)$ and $\sigma(n)$ are the average contact rate of which an infective individual contacts a susceptible and a vaccinated individual at time n, respectively, $\alpha(n)$ is the disease induced death rate at time n, $\gamma(n)$ and $\eta(n)$ are the instantaneous per capita rates of leaving the infective stage and vaccinated stage at time n, respectively.

The rest of this paper is organized as follows. In Section 2, we introduce some notations, assumptions and lemmas which will be needed in our main results. Sections 3 and 4 deal with the permanence and extinction of the disease for the model (1.2). In Section 5, some examples and simulations are given to illustrate the analytic results.

2. Preliminaries

We give the following notations:

$$f^l = \inf_{n\in\mathbb{N}} f(n), \quad f^u = \sup_{n\in\mathbb{N}} f(n).$$

For system (1.2), our basic assumptions are stated as follows.

($\mathbf{H}_1$) Functions $\Lambda(n)$, $\beta(n)$, $\sigma(n)$, $\mu(n)$, $p(n)$, $\alpha(n)$, $\gamma(n)$ and $\eta(n)$ are bounded and positive on the natural number set $\mathbb{N}$.

($\mathbf{H}_2$) There exists a positive integer ω_1 such that

$$\limsup_{n\to\infty} \prod_{k=n}^{n+\omega_1} \left(\frac{1}{1+\mu(k)}\right) < 1.$$

($\mathbf{H}_3$) There exist two positive integers ω_2 and ω_3 such that

$$\liminf_{n\to\infty} \sum_{k=n+1}^{n+\omega_2} \Lambda(k) > 0 \text{ and } \liminf_{n\to\infty} \sum_{k=n+1}^{n+\omega_3} p(k) > 0.$$

Particularly, when system (1.2) degenerates into an ω−periodic system, that is, $\Lambda(n)$, $\beta(n)$, $\sigma(n)$, $\mu(n)$, $p(n)$, $\alpha(n)$, $\gamma(n)$ and $\eta(n)$ are all positive periodic functions with common period $\omega > 0$, then the assumptions (H_2) and (H_3) are equivalent to the following conditions

($\mathbf{H}_4$)

$$\prod_{k=0}^{\omega-1} \left(\frac{1}{1+\mu(k)}\right) < 1, \quad \sum_{k=0}^{\omega-1} \Lambda(k) > 0 \text{ and } \sum_{k=0}^{\omega-1} p(k) > 0.$$