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Stationary distribution of a stochastic SIS epidemic model with vaccination☆

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HIGHLIGHTS

- It is the first time that stationary distribution for stochastic SISV model and its asymptotic stability are obtained.
- We get the support of the invariant density.
- The solution of stochastic SISV model is ergodic.

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ABSTRACT

In this paper, we consider a stochastic SIS epidemic model with vaccination. We prove that the densities of the distributions of the solution can converge in L^1 to an invariant density under appropriate conditions. Also we find the support of the invariant density.

1. Introduction

In recent years epidemiological modeling of infectious disease transmission has had an increasing influence on the theory and practice of disease management and control. In order to eliminate infectious disease vaccination has been an important strategy. Many authors considered epidemic models with vaccination, see (e.g., Refs. [1–6]). The following model is one of classic SIS models with vaccination:

$$\begin{cases} \dfrac{dS_t}{dt} = A(1-q) - \beta S_t I_t - (\mu + p)S_t + \gamma I_t + \varepsilon V_t, \\ \dfrac{dI_t}{dt} = \beta S_t I_t - (\mu + \gamma + \alpha)I_t, \\ \dfrac{dV_t}{dt} = \mu q + pS_t - (\mu + \varepsilon)V_t. \end{cases} \tag{1.1}$$

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All parameter values in the model are assumed to be nonnegative ($\mu, A > 0$) and summarized in the following list:

A: a constant input of new members into the population per unit time;
q: a fraction of vaccinated for newborns;
β: transmission coefficient between compartments S and I;
p: the proportional coefficient of vaccinated for the susceptible;
μ: the natural death rate of S, I, V compartments;
γ: recovery rate of infectious individuals;
ε: the rate of losing their immunity for vaccinated individuals;
α: disease-caused death rate of infectious individuals.

Due to the existence of environmental noise, the parameters involved in (1.1) are not absolute constants, and they always fluctuate around some average values due to continuous fluctuations in the environment. As a result, the parameters in the model exhibit continuous oscillation around some average values but do not attain fixed values with the advancement of time. In model (1.1) the disease transmission coefficient β is the key parameter to disease transmission. It is of special interest to evaluate the effect of perturbed parameter β on our model. Here we assume that β is subject to the environmental white noise, that is

$$\beta \to \beta + \sigma \dot{B}_t.$$

Consequently, $\beta \mathrm{d}t \to \beta \mathrm{d}t + \sigma \mathrm{d}B_t$, where B_t is a standard Brownian motion, $\sigma^2 > 0$ is the intensity of environmental white noise. Then model (1.1) becomes

$$\begin{cases} \mathrm{d}S_t = [A(1-q) - \beta S_t I_t - (\mu + p)S_t + \gamma I_t + \varepsilon V_t]\mathrm{d}t - \sigma S_t I_t \mathrm{d}B_t, \\ \mathrm{d}I_t = [\beta S_t I_t - (\mu + \gamma + \alpha)I_t]\mathrm{d}t + \sigma S_t I_t \mathrm{d}B_t, \\ \mathrm{d}V_t = (\mu q + pS_t - (\mu + \varepsilon)V_t)\mathrm{d}t. \end{cases} \tag{1.2}$$

The system (1.2) has been considered by Zhao et al. [7]. They obtained that, when the noise is large, the infective decays exponentially to zero regardless of the magnitude of R_0; When the noise is small, sufficient conditions for extinction exponentially and persistence in the mean are established. But in the case of persistence they cannot obtain the existence of stationary distribution of system (1.2). The aim of this paper is to fill the gap. Hence our work can be considered as the further work of Zhao et al. [7].

We assume that $\alpha = 0$ and $A = \mu$. So the total size of the whole population of (1.2) is constant. That is, $S_t + I_t + V_t = 1$. Noting that V_t does not arise explicitly in the first two equations of (1.2), we just need to consider the following two-dimensional system:

$$\begin{cases} \mathrm{d}S_t = [\mu(1-q) - \beta S_t I_t - (\mu + p)S_t + \gamma I_t + \varepsilon(1 - S_t - I_t)]\mathrm{d}t - \sigma S_t I_t \mathrm{d}B_t, \\ \mathrm{d}I_t = [\beta S_t I_t - (\mu + \gamma)I_t]\mathrm{d}t + \sigma S_t I_t \mathrm{d}B_t. \end{cases} \tag{1.3}$$

The deterministic part of system (1.3) has been considered in Ref. [3].

In this paper we are devoted to studying the existence of a stationary distribution of system (1.3) and its asymptotic stability. We will prove that the densities can converge in L^1 to an invariant density under appropriate conditions. Also we find the support of the invariant density.

The difficulty in obtaining stationary distribution derives form the fact that the Fokker–Planck equation corresponding to system (1.3) is of degenerate type, which leads to the invalidity of the approach used in Refs. [8,9]. Here we will employ the Markov semigroup approach [10–12] to obtain the existence of stationary distribution.

Throughout this paper, let $(\Omega, \mathscr{F}, \{\mathscr{F}_t\}_{t\geq 0}, \mathrm{Prob})$ be a complete probability space with a filtration $\{\mathscr{F}_t\}_{t\geq 0}$ satisfying the usual conditions (i.e. it is right continuous and $\mathscr{F}_0$ contains all Prob-null sets). Denote

$$\mathbb{R}^2_+ := \{(x, y) \in \mathbb{R}^2 : x > 0, y > 0\}.$$

Since the existence of positive solution of model (1.3) has been obtained by Zhao et al. [7], we take $\mathbb{R}^2_+$ as the whole space. Moreover, it is easy to check that the region $\Gamma^* = \{(x, y) \in \mathbb{R}^2_+ : 0 < x + y < 1\}$ is a positively invariant set of system (1.3). Hence, we always assume that $(S_0, I_0) \in \Gamma^*$.

The rest of this paper is organized as follows. In Section 2, we present our main results and make numerical simulation to support our results. In Section 3, the proof of our results are given. In Section 4, we give a brief conclusion. For the convenience of the reader, in the Appendix we present some auxiliary results concerning Markov semigroups, which contain the main tools used in this paper.

2. Main results and numerical simulation

In this section, we present our result as follows.