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The threshold of a stochastic Susceptible–Infective epidemic model under regime switching



Hybrid Systems

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HIGHLIGHTS

- A stochastic SI epidemic model under regime switching is proposed and investigated.
- We establish sufficient conditions for the existence of a unique ergodic stationary distribution.
- We obtain the threshold which ensures the extinction and the existence of the stationary distribution of the epidemic.

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ABSTRACT

In this paper, we consider a stochastic Susceptible–Infective (SI) epidemic model under regime switching. Firstly, by constructing suitable Lyapunov functions, we establish sufficient criteria for the existence and uniqueness of an ergodic stationary distribution. Then we obtain the threshold which guarantees the extinction and the existence of the stationary distribution of the epidemic. Finally, some numerical simulations are introduced to illustrate our main results.

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1. Introduction

Recently, mathematical models describing the population dynamics of infectious diseases have played an important role in understanding epidemiological patterns [1]. When analyzing an epidemic model, it is an issue to find the threshold which guarantees whether the disease occurs or dies out. Kermack and McKendrick [2] discovered a threshold condition for the spread of a disease. From then on, their threshold theory has been extended to some more realistic models.

In the literatures deterministic epidemic models have received much attention (see e.g. [3-6]) and for these deterministic epidemic models there exists a threshold which is defined as the average number of secondary infectious produced [7]. But we note that in latest literatures concerning the threshold of stochastic epidemic models (see e.g. [1,8-11]), the threshold was not investigated analytically for the stochastic SI epidemic model under regime switching. This inspires us to do some work about the threshold of a stochastic SI epidemic model under regime switching.

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The deterministic nonautonomous SI epidemic model with bilinear incidence is of the following form

$$\begin{cases} \frac{dS(t)}{dt} = \Lambda(t) - \beta(t)S(t)I(t) - \mu(t)S(t),\\ \frac{dI(t)}{dt} = \beta(t)S(t)I(t) - \mu(t)I(t), \end{cases}$$
(1.1)

where S(t) and I(t) denote the susceptible and infective density at time t, respectively. $\Lambda(t)$ denotes the recruitment rate, $\mu(t)$ stands for the natural death rate of the susceptible and the infective, $\beta(t)$ is the effective transmission rate of the disease. $\Lambda(t)$, $\beta(t)$ and $\mu(t)$ are all positive continuous bounded functions on $[0, \infty)$.

On the other hand, as we know, population systems are always affected by the environmental noise, which is an important component in an ecosystem (see e.g. [12–14]). Therefore, for better understanding the dynamics of the epidemic models, many authors have introduced stochastic perturbations into the population systems to reveal richer and more complex dynamics (see e.g. [15–17]). Motivated by the above works, in this paper, we assume that fluctuations in the environment mainly affect the natural death rate $\mu(t)$. In practice, we can estimate it by an average value plus an error term. In general, in view of the central limit theorem, the error term follows a normal distribution. That is to say, we can replace the rate $-\mu(t)$ by an average value plus a random fluctuation term $-\mu(t) + \sigma(t)\dot{B}(t)$, where $\dot{B}(t)$ is a Gaussian white noise, i.e., B(t) is a standard Brownian motion, $\sigma^2(t) > 0$ denotes the intensity of the white noise. Then corresponding to system (1.1), the stochastic SI epidemic model takes the following form

$$dS(t) = (\Lambda(t) - \beta(t)S(t)I(t) - \mu(t)S(t))dt + \sigma(t)S(t)dB(t), dI(t) = (\beta(t)S(t)I(t) - \mu(t)I(t))dt + \sigma(t)I(t)dB(t).$$
(1.2)

However, in the real world, epidemic models can be perturbed by the colored noise which can cause the population system to switch from one environmental regime to another (see e.g. [18,19]). Usually, the switching between environmental regimes is often memoryless and the waiting time for the next switching follows the exponential distribution [20]. Thus, we can model the regime switching by a continuous-time Markov chain $\{r(t)\}_{t\geq 0}$ taking values in a finite state space $S = \{1, ..., N\}$, then system (1.2) with Markov chain becomes the following form

$$dS(t) = (\Lambda(r(t)) - \beta(r(t))S(t)I(t) - \mu(r(t))S(t))dt + \sigma(r(t))S(t)dB(t), dI(t) = (\beta(r(t))S(t)I(t) - \mu(r(t))I(t))dt + \sigma(r(t))I(t)dB(t).$$
(1.3)

Stochastic differential equations with regime switching have been widely studied (see e.g. [21–27]). Zhu and Yin [23] investigated the asymptotic properties such as recurrence and ergodicity of regime-switching diffusions and established sufficient and necessary conditions for positive recurrence. Zu et al. [27] obtained sufficient conditions for the ergodic stationary distribution of the solution to a stochastic Lotka–Volterra predator–prey model. In this paper, by constructing suitable Lyapunov functions, we mainly study the positive recurrence and the existence of the stationary distribution for system (1.3). Then we present sufficient conditions for the extinction of the disease. At the same time, the threshold of the extinction and stationary distribution of the epidemic is also obtained.

The organization of this paper is as follows. In Section 2, we present some notations and lemmas concerning the nonsingular *M*-matrix and the existence of the ergodic stationary distribution. In Section 3, we establish sufficient conditions for the existence of a unique stationary distribution. Section 4 is devoted to studying the conditions for the extinction of the disease. In Section 5, some numerical simulations are provided to demonstrate the analytical findings. Finally, some conclusions and future directions are given.

2. Preliminaries

Throughout this paper, unless otherwise specified, let $(\Omega, \mathcal{F}, \mathbb{P})$ be a complete probability space with a filtration $\{\mathcal{F}_t\}_{t\geq 0}$ satisfying the usual conditions (i.e., it is right continuous and \mathcal{F}_0 contains all \mathbb{P} -null sets). Moreover, for the sake of convenience, we define the following symbols. Let $\mathbb{R}_+ = [0, \infty)$, $\mathbb{R}_+^n = \{x = (x_1, \ldots, x_n) \in \mathbb{R}^n : x_i > 0, i = 1, \ldots, n\}$ and $Z^{n \times n} = \{A = (a_{ij})_{n \times n} : a_{ij} \le 0, i \ne j\}$. Let $\{r(t), t \ge 0\}$ be a right-continuous Markov chain on this probability space $(\Omega, \mathcal{F}, \mathbb{P})$ taking values in a finite state space $\mathbb{S} = \{1, 2, \ldots, N\}$. For any vector $g = (g(1), \ldots, g(N))$, set $\hat{g} = \min_{k \in \mathbb{S}} \{g(k)\}$ and $\check{g} = \max_{k \in \mathbb{S}} \{g(k)\}$. If f is a bounded function on \mathbb{R}_+ , define $f^u = \sup_{t \in \mathbb{R}_+} f(t)$. Assume the generator $\Gamma = (\gamma_{ij})_{N \times N}$ of the Markov chain is given by

$$\mathbb{P}\{r(t+\Delta) = j | r(t) = i\} = \begin{cases} \gamma_{ij}\Delta + o(\Delta), & \text{if } i \neq j, \\ 1 + \gamma_{ii}\Delta + o(\Delta), & \text{if } i = j, \end{cases}$$

where $\Delta > 0$, $\gamma_{ij} \ge 0$ is the transition rate from *i* to *j* if $i \ne j$ while $\sum_{i=1}^{N} \gamma_{ij} = 0$. We suppose that the Markov chain is independent of the Brownian motion. Suppose further that the Markov chain r(t) is irreducible and has a unique stationary

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