# LONG-TIME BEHAVIOR OF STOCHASTIC STAGED PROGRESSION EPIDEMIC MODEL WITH HYBRID SWITCHING FOR THE TRANSMISSION OF HIV

Songnan Liu<sup>1</sup>, Xiaojie Xu<sup>2,†</sup> and Zhangyi Dong<sup>3</sup>

**Abstract** In this paper, one stochastic hybrid switching SP (staged progression) model for the transmission of HIV is proposed and investigated. The system disturbed by both white and telegraph noises, sufficient conditions for positive recurrence and the existence of an ergodic stationary distribution to the solutions are established. The existence of stationary distribution implies stochastic weak stability to some extent. Furthermore, sufficient conditions for extinction of disease are established. At last, some examples and simulations are provided to illustrate our results.

**Keywords** Stochastic staged progression infectious disease models, Lyapunov function, Extinction, stationary distribution and ergodicity, hybrid switching.

MSC(2010) 60H10, 34F05.

## 1. Introduction

In 1981, human immunodeficiency virus (HIV) spreads at a very rapid speed to every corner of the world since the discovery of acquired immune deficiency syndrome (AIDS), and it causes a serious threat to people's health. Mathematical models based on the underlying transmission mechanisms of the disease can evaluate the potential effectiveness of different approaches for bringing an epidemic under control and help the medical/scientific community anticipate and understand the spread of an epidemic. The behavior of the epidemic is a highly non-linear function of the parameter values and levels of intervention strategies, because the transmission dynamics form a complex non-linear dynamical system. This at times may even lead to changes in infection spread that are counter to both intuition and simple extrapolated predictions. We can use the knowledge gained from studying models to help set priorities in research, saving time, resources, and lives, see [9, 12, 15, 25, 31].

All these mentioned HIV models are ordinary differential equations and do not take into account the random variations on the model parameters. Previously, through experimental data, Singh et al. have showed that HIV transcription is

<sup>&</sup>lt;sup>†</sup>The corresponding author. Email: xuxiaojie77@sohu.com(X. Xu)

 $<sup>^1 \</sup>rm School of Statistics and Data Science, LPMC & KLMDASR Nankai University, Tianjin 300071, China$ 

 $<sup>^2\</sup>mathrm{College}$  of Science, China University of Petroleum (East China), Qingdao 266580, China

 $<sup>^3</sup>$ Jiaonan Sub-district Office, Huangdao District, Qingdao City, Shandong Province, China

an inherently random process [27] and Liu et al. investigated stochastic differential susceptibility (DS) susceptible-infective-AIDS (SIA) models in [16, 17]. They discussed the sufficient conditions for positive recurrence and the existence of an ergodic stationary distribution to the solutions. The existence of stationary distribution implies stochastic weak stability to some extent. Furthermore, sufficient conditions for extinction of disease are established.

In this paper we studied a simple version of a staged-progression (SP) model, in which every infected individual goes through the same series of stages. The parameters we use for the SP model give a short, early, highly infectious, stage equivalent to the acute phase of infection; a middle period of low infectiousness; and a late chronic stage with higher infectiousness. Thus the SP model captures differences in time within the same individual. [10,11] simulated the transient dynamics. Hyman et al. also developed a robust method for initializing multigroup epidemic models. For the SP model, these studies provided further insight into the observations in [13,14] that, when partner acquisition rates are high, the bulk of the infections early in the epidemic are caused by those in the acute infectious stage.

The SP model accounts for the temporal changes in the infectiousness of an individual by a staged Markov process of n infected stages, progressing from the initial infection to AIDS. The equations for the SP model illustrated in Fig. 1 are



Figure 1. In the SP model every infected individual goes through the same series of stages. This model can account for a short early highly infectious stage equivalent to the acute phase of infection, a middle period of low infectiousness, and a late chronic stage with higher infectiousness, where  $\lambda = r \sum_{i=1}^{n} \beta_i I_i(t) S(t)$ .

$$\begin{cases} dS(t) = [\mu(S^0 - S(t)) - r \sum_{i=1}^n \beta_i I_i(t) S(t)] dt, \\ dI_1(t) = [r \sum_{i=1}^n \beta_i I_i(t) S(t) - (\mu + \gamma_1) I_1(t)] dt, \\ dI_i(t) = [\gamma_{i-1} I_{i-1} - (\gamma_i + \mu) I_i] dt, \quad 2 \le i \le n, \\ dA(t) = (\gamma_n I_n - \delta A) dt. \end{cases}$$
(1.1)

Here, r is the average number of partners per individual per unit of time,  $\beta_1, \ldots, \beta_n$ are the transmission probability per partner with an infected individual in subgroup  $I_1, \ldots, I_n$ . Individuals enter the susceptible class at a constant rate  $\mu S^0 > 0$ . The natural death rate is assumed to be constant d > 0 and Sexually active removal rate is  $\alpha > 0$ . Thus the total removal rate is assumed to be proportional to the population number in each class, with rate constant  $\mu = d + \alpha > 0$ . In addition, there is an AIDS-related death in the AIDS class which is assumed to be proportional to the population number in that class, with rate constant  $\delta > 0$  which is the sum of natural mortality rate and mortality due to illness. System (1.1) has only two kinds of equilibrium: the disease-free equilibrium and the endemic equilibrium. Hyman and Li showed that the reproductive number can be defined by [10]

$$R_0 = \sum_{i=1}^n \frac{r\beta_i q_i S^0}{\gamma_i + \mu},$$

where  $q_i = \prod_{j=1}^{i-1} \frac{\gamma_j}{\gamma_j + \mu}$ , i = 2, ..., n and  $q_1 = 1$ . When  $R_0 > 1$ , the infection-free equilibrium is unstable, and thus the number of infected individuals will grow when a small number of individuals are infected. The epidemic will die out in the neighborhood of the infection-free equilibrium when  $R_0 < 1$ .

Since the dynamics of group A has no effect on the disease transmission dynamics, thus we only consider subgroup  $S, I_1, \dots, I_n$ .

However, as we know, real life is full of randomness. Hence it is necessary to consider stochasticity into epidemic models (see e.g. [3, 5, 18, 19]. For these models, the nature of epidemic growth and spread is random due to the unpredictability in person-to-person contacts [26]. Therefore the variability and randomness of the environment is fed through the state of the epidemic [1]. And in epidemic dynamics, stochastic systems may be a more appropriate way of modeling epidemics in many circumstances (see e.g. [20-22, 35]). Motivated by the above discussion, in this paper, we tend to do some work in this field. By taking into account the effect of randomly fluctuating environment, we adopt the approach used in Liu et al. [18] and assume that the environmental noise is proportional to the variables of system (1.1). Then the stochastic version corresponding to system (1.1) takes the following form:

$$\begin{cases} dS(t) = [\mu(S^0 - S(t)) - r \sum_{i=1}^n \beta_i I_i(t) S(t)] dt + \sigma_1 S(t) dB_1(t), \\ dI_1(t) = [r \sum_{i=1}^n \beta_i I_i(t) S(t) - (\mu + \gamma_1) I_1(t)] dt + \sigma_2 I_1(t) dB_2(t), \\ dI_i(t) = [\gamma_{i-1} I_{i-1} - (\gamma_i + \mu) I_i] dt + \sigma_{i+1} I_i(t) dB_{i+1}(t), \quad 2 \le i \le n, \end{cases}$$
(1.2)

where  $B_1(t), \dots, B_n(t)$ , and  $B_{n+1}(t)$  are independent Brownian motions, and  $\sigma_1^2 > 0, \sigma_2^2 > 0, \dots, \sigma_{n+1}^2 > 0$  represent the intensities of white noise. Other parameters are the same as in system (1.1).

Besides white noise, epidemic models may be disturbed by telegraph noise which makes population systems switch from one regime to another. Let us now take a further step by considering another type of environmental noise, namely, telegraph noise (see Refs [23, 30]) and Liu et al. investigated stochastic differential susceptibility (DS) susceptible-infective-AIDS (SIA) models disturbed by both white and telegraph noises (see Refs [16, 17]). The telegraph noise can be illustrated as a switching between two or more regimes of environment, which differs by factors such as nutrition or as rain falls [4, 28, 32, 33]. For example, the growth rate for some fish in dry season will be much different from that in rainy season. Therefore the regime switching can be modeled by a continuous time finite-state Markov chain  $(\xi(t))_{t\geq 0}$  with values in a finite state space  $\mathcal{M} = \{1, 2, \ldots, L\}$ . In this paper, we consider the HIV disease spread between environmental regimes. Because the HIV epidemic model may be influenced by different social cultures, we also introduce the telegraph noise to consider HIV disease spread between different social cultures that is the large disturbance in environment. That is following stochastic SP model disturbed by white and telephone noises.

$$\begin{cases} dS(t) = [\mu(l)(S^0 - S(t)) - r(l)\sum_{i=1}^n \beta_i(l)I_i(t)S(t)]dt + \sigma_1(l)S(t)dB_1(t), \\ dI_1(t) = [r(l)\sum_{i=1}^n \beta_i(l)I_i(t)S(t) - (\mu(l) + \gamma_1(l))I_1(t)]dt + \sigma_2(l)I_1(t)dB_2(t), \\ dI_i(t) = [\gamma_{i-1}(l)I_{i-1} - (\gamma_i(l) + \mu(l))I_i]dt + \sigma_{i+1}(l)I_i(t)dB_{i+1}(t), \quad 2 \le i \le n. \end{cases}$$

$$(1.3)$$

The switching between these L regimes is governed by a Markov chain on the state space  $\mathcal{M} = \{1, 2, \ldots, L\}$ . The SP systems under regime switching can therefore be described by the following stochastic model (SDE):

$$\begin{cases} dS(t) = [\mu(\xi(t))(S^0 - S(t)) - r(\xi(t))\sum_{i=1}^n \beta_i(\xi(t))I_i(t)S(t)]dt + \sigma_1(\xi(t))S(t)dB_1(t), \\ dI_1(t) = [r(\xi(t))\sum_{i=1}^n \beta_i(\xi(t))I_i(t)S(t) - (\mu(\xi(t)) + \gamma_1(\xi(t)))I_1(t)]dt \\ + \sigma_2(\xi(t))I_1(t)dB_2(t), \\ dI_i(t) = [\gamma_{i-1}(\xi(t))I_{i-1} - (\gamma_i(\xi(t)) + \mu(\xi(t)))I_i]dt + \sigma_{i+1}(\xi(t))I_i(t)dB_{i+1}(t), \\ 2 \le i \le n, \end{cases}$$

$$(1.4)$$

where  $\xi(t)$  is a continuous time Markov chain with values in finite state space  $\mathcal{M} = \{1, 2, \ldots, L\}$ , the parameters  $\mu(l), r(l), \beta_1(l), \beta_2(l), \gamma_1(l), \gamma_2(l), \sigma_k(l), k = 1, 2, \cdots n + 1$ , are all positive constants for each  $l \in \mathcal{M}$ . This system is operated as follows: If  $\xi(1) = l_1$ , the system obeys systems (1.3) with  $l = l_1$  till time  $\tau_1$  when the Markov chain jumps to  $l_2$  from  $l_1$ ; the systems will then obey (1.3) with  $l = l_2$  from  $\tau_1$  till  $\tau_2$  when the Markov chain jumps to  $l_3$  from  $l_2$ . The system will continue to switch as long as the Markov chain jumps. We aim to investigate the positive recurrence and extinction. Since system (1.4) is perturbed by both white and telegraph noises, the existence of positive recurrence of the solutions is an important issue. However, to the best of our knowledge, there has been no result related this. In this paper, we attempt to do some work in this field to fill the gap. The theory we used is developed by Zhu and Yin [34]. The key difficulty is how to construct a suitable Lyapunov function and a bounded domain. So one of the main aim of this paper is to establish sufficient conditions for the existence of an ergodic stationary distribution of the solutions to system (1.4).

This paper is organized as follows. In the next section, we present some preliminaries that will be used in our following analysis. In section 3, we obtain the existence of a unique ergodic stationary distribution according to the theory of Has<sub>i</sub><sup>-</sup>minskii [7]. We establish the sufficient conditions for the extinction of HIV infection, by constructing suitable Lyapunov functions in Section 4. In Section 6, we perform numerical simulations to discuss how the white noises and telegraph noises affect the dynamic behavior based on the referenced parameter values obtained from the previous literatures. Finally, we summary our main results and identify future work.

#### 2. Preliminaries

Throughout this paper, unless otherwise specified, let  $(\Omega, \mathcal{F}, \{\mathcal{F}_t\}_{t\geq 0}, P)$  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 P-null sets). Denote

$$\mathbb{R}^n_+ = \{ x \in \mathbb{R}^d : x_i > 0 \text{ for all } 1 \le i \le n \}$$

We consider the general d-dimensional stochastic differential equation

$$dx(t) = f(x(t), t)dt + g(x(t), t)dB(t), \text{ for } t \ge t_0$$
(2.1)

with initial value  $x(t_0) = x_0 \in \mathbb{R}^d$ , where B(t) denotes *d*-dimensional standard Brownian motions defined on the above probability space.

Define the differential operator  $\mathcal{L}$  associated with Eq.(2.1) by

$$\mathcal{L} = \frac{\partial}{\partial t} + \Sigma f_i(x, t) \frac{\partial}{\partial x_i} + \frac{1}{2} \Sigma [g^T(x, t)g(x, t)]_{ij} \frac{\partial^2}{\partial x_i \partial x_j}.$$

If  $\mathcal{L}$  acts on a function  $V \in C^{2,1}(\mathbb{R}^d \times \overline{\mathbb{R}}_+; \overline{\mathbb{R}}_+)$ , then

$$\mathcal{L}V(x,t) = V_t(x,t) + V_x(x,t)f(x,t) + \frac{1}{2}trac[g^T(x,t)V_{xx}(x,t)g(x,t)]$$

where  $V_t = \frac{\partial V}{\partial t}, V_x = (\frac{\partial V}{\partial x_1}, \cdots, \frac{\partial V}{\partial x_d})$  and  $V_{xx} = (\frac{\partial^2 V}{\partial x_i \partial x_j})_{d \times d}$ . By Itô's formula, if x(t) is a solution of Eq.(2.1), then

$$dV(x(t),t) = \mathcal{L}V(x(t),t)dt + V_x(x(t),t)g(x(t),t)dB(t).$$

In Eq.(2.1), we assume that f(0,t) = 0 and g(0,t) = 0 for all  $t \ge t_0$ . So  $x(t) \equiv 0$  is a solution of Eq.(2.1), called the trivial solution or equilibrium position.

By the definition of stochastic differential, the equation (2.1) is equivalent to the following stochastic integral equation

$$x(t) = x_0 + \int_{t_0}^t f(x(s), s) ds + \sum_{r=1}^d \int_{t_0}^t g_r(x(s), s) dB_r(s), \text{ for } t \ge t_0$$
(2.2)

For any vector  $g = (g(1), \ldots, g(L))$ , set  $\hat{g} = \min_{k \in \mathcal{M}} \{g(k)\}$  and  $\check{g} = \max_{k \in \mathcal{M}} \{g(k)\}$ . Suppose the generator  $\Gamma = (\gamma_{ij})_{L \times L}$  of the Markov chain is given by

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

where  $\delta > 0, \gamma_{ij} \ge 0$  for any  $i \ne j$  is the transition rate from *i* to *j* if  $i \ne j$ while  $\sum_{j=1}^{N} \gamma_{ij} = 0$ . In this paper, we assume  $\gamma_{ij} > 0$ , for any  $i \ne j$ . Assume further that Markov chain  $\xi(t)$  is irreducible and has a unique stationary distribution  $\pi = \{\pi_1, \pi_2, \ldots, \pi_N\}$  which can be determined by equation

$$\pi\Gamma = 0, \tag{2.3}$$

subject to

$$\sum_{h=1}^{L} \pi_h = 1, \text{and } \pi_h > 0, \forall h \in \mathcal{M}.$$

We assume that Brownian motion and Markov chain are independent. Let  $(X(t), \xi(t))$  be the diffusion process described by the following equation:

$$dX(t) = b(X(t),\xi(t))dt + \sigma(X(t),\xi(t))dB(t), \quad X(0) = x_0,\xi(0) = \xi,$$
(2.4)

where  $b(\cdot, \cdot) : \mathbb{R}^n \times \mathcal{M} \to \mathbb{R}^n, \sigma(\cdot, \cdot) : \mathbb{R}^n \times \mathcal{M} \to \mathbb{R}^{n \times n}$ , and  $D(x, l) = \sigma(x, l)\sigma^T(x, l) = (d_{ij}(x, l))$ . For each  $l \in \mathcal{M}$ , let  $V(\cdot, l)$  be any twice continuously differentiable function, the operator  $\mathcal{L}$  can be defined by

$$\mathcal{L}V(x,l) = \sum_{i=1}^{n} b_i(x,l) \frac{\partial V(x,l)}{\partial x_i} + \frac{1}{2} \sum_{i,j=1}^{n} d_{ij}(x,l) \frac{\partial^2 V(x,l)}{\partial x_i \partial x_j} + \sum_{m=1}^{L} \gamma_{lm} V(x,m).$$

Lemma 2.1 ([34]). If the following conditions are satisfied:

- (a)  $\gamma_{ij} > 0$  for any  $i \neq j$ ;
- (b) for each  $k \in \mathcal{M}$ ,  $D(x,k) = (d_{ij}(x,k))$  is symmetric and satisfies

$$\lambda |\xi|^2 \le \langle D(x,k)\xi,\xi \rangle \le \lambda^{-1} |\xi|^2$$
for, all  $\xi \in \mathbb{R}^n$ ,

with some constant  $\lambda \in (0, 1]$  for all  $x \in \mathbb{R}^n$ ;

(c) there exists a nonempty open set  $\mathcal{D}$  with compact closure, satisfying that, for each  $k \in \mathcal{M}$ , there is a nonnegative function  $V(\cdot, k) : \mathcal{D}^c \to \mathbb{R}$  such that  $V(\cdot, k)$  is twice continuously differential and that for some  $\alpha > 0$ ,

$$\mathcal{L}V(x,k) \leq -\alpha, \quad (x,k) \in \mathcal{D}^c \times \mathcal{M},$$

then  $(X(t),\xi(t))$  of system (2.4) is positive recurrent and ergodic. That is to say, there exists a unique stationary distribution  $\mu(\cdot, \cdot)$  such that for any Borel measurable function  $f(\cdot, \cdot) : \mathbb{R}^n \times \mathcal{M} \to \mathbb{R}$  satisfying

$$\sum_{k=1}^N \int_{\mathbb{R}^n} |f(x,k)| \mu(dx,k) < \infty,$$

we have

$$\mathcal{P}(\lim_{t\to\infty}\frac{1}{t}\int_0^t f(X(t),\xi(t))ds) = \sum_{k=1}^L \int_{\mathbb{R}^n} f(x,k)\mu(dx,k) = 1.$$

## 3. Existence and uniqueness of positive solution

#### 3.1. Theorem and Lemma

To study the dynamical behavior of an epidemic model, the first concern is whether the solution is global and positive. The following result is concerned with the existence and uniqueness of the global positive solution which is prerequisite for investigating the long-term behavior of model (1.4). **Theorem 3.1.** There is a unique positive solution  $X(t) = (S(t), I_1(t), \ldots, I_n(t))$  of system (1.4) on  $t \ge 0$  for any initial value  $(S(0), I_1(0), \ldots, I_n(0)) \in \mathbb{R}^{n+1}_+$ , and the solution will remain in  $\mathbb{R}^{n+1}_+$  with probability 1, namely,  $(S(t), I_1(t), \ldots, I_n(t)) \in \mathbb{R}^{n+1}_+$  for all  $t \ge 0$ .

**Proof.** Since the coefficients of the equation are locally Lipschitz continuous for given initial value  $(S(0), I_1(0), \ldots, I_n(0)) \in \mathbb{R}^{n+1}_+$ . By using the same approach as that in Liu et al. [16], we can easily obtain the above results. Define a  $C^2$ -function  $V: R^{n+1}_+ \to \bar{R}_+$  by

$$V(S, I_1, \dots, I_n) = (S - 1 - \ln S) + \sum_{i=1}^n (I_i - 1 - \ln I_i) + \frac{p}{\check{\mu}}(S + \sum_{i=1}^n I_i),$$

where  $p = \max{\{\check{r}\check{\beta}_i, i = 1, ..., n\}}$ . The non-negativity of this function can be see from  $u - 1 - \log u \ge 0$ ,  $\forall u > 0$ . Let  $m \ge m_0$  and T > 0 be arbitrary then by Itô's formula one obtains

$$dV(S, I_1, \dots, I_n) = \mathcal{L}V(S, I_1, \dots, I_n)dt + \sigma_1(\xi(t))(S-1)dB_1(t) + \sum_{i=1}^n \sigma_{i+1}(\xi(t))(I_i - 1)dB_{i+1}(t) + \frac{p}{\tilde{\mu}}[\sigma_1(\xi(t))SdB_1(t) + \sum_{i=1}^n \sigma_{i+1}(\xi(t))I_idB_{i+1}(t)],$$

where

$$\begin{aligned} \mathcal{L}V &= (1 - \frac{1}{S})[\mu(l)(S^0 - S) - r(l)\sum_{i=1}^n \beta_i(l)I_iS] + (1 - \frac{1}{I_1})[r(l)\sum_{i=1}^n \beta_i(l)I_iS - (\mu(l) \\ &+ \gamma_1(l))I_1] + \sum_{i=2}^n (1 - \frac{1}{I_i})[\gamma_{i-1}(l)I_{i-1} - (\mu(l) + \gamma_i(l))I_i] + \sum_{i=1}^{n+1} \frac{\sigma_i^2(l)}{2} + \frac{p\mu(l)}{\check{\mu}}S^0 \\ &- \frac{p\mu(l)}{\check{\mu}}(S + \sum_{i=1}^n I_i) - \frac{p\gamma_n(l)}{\check{\mu}}I_n \\ &< (\check{\mu} + p)S^0 + \check{\mu} + \sum_{i=1}^n (\check{\mu} + \check{\gamma}_1) + \sum_{k=1}^{n+1} \frac{\check{\sigma}_k^2}{2} - p\sum_{i=1}^n I_i + \sum_{i=1}^n \check{\tau}\check{\beta}_iI_i \\ &< (\check{\mu} + p)S^0 + \check{\mu} + \sum_{i=1}^n (\check{\mu} + \check{\gamma}_1) + \sum_{k=1}^{n+1} \frac{\check{\sigma}_k^2}{2} := C \end{aligned}$$

$$(3.1)$$

where C is a positive constant which is independent of  $S, I_1, \ldots, I_n$  and t. The remainder of the proof follows that in ref. [16].

### 4. Recurrence and ergodicity

Our study about epidemic models lies in the fact that when the disease will prevail in the population. In the deterministic models, the problem can be solved by verifying that the endemic equilibrium of the corresponding model is local asymptotically stable. However for system (1.4), there is no endemic equilibrium. In this section, based on the theory of Has'minskii [7], we prove that there is an ergodic stationary distribution, which reveals that the disease will persist. The classic infectious disease model is mainly concerned with the existence and global stability of the equilibrium point of the model. In recent years, due to the more general infection rate in the infectious disease model, this makes the infectious disease model have more complex dynamics. So it is difficult to obtain complete qualitative analysis results by traditional analytical methods. However, in the epidemiological sense, studying the persistence of disease is as important as studying the ultimate behavior of the disease, some scholars have studied the persistence of epidemics. We define a parameter

$$\begin{split} R_0^s &:= \frac{\left(\sum_{l=1}^L \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})} \\ &+ \sum_{i=2}^n \frac{\left(\sum_{l=1}^L \pi_l (\mu(l) + \frac{\sigma_1^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l)\beta_i(l)\mu(l)S^0 \prod_{j=2}^i \gamma_{j-1}(l))^{i+1}}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2}) \prod_{j=2}^i \sum_{l=1}^L \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})}. \end{split}$$

$$(4.1)$$

**Theorem 4.1.** Assume that  $R_0^s > 1$ , then system (1.4) has a unique stationary distribution  $\pi(\cdot)$  and it has the ergodic property.

**Proof.** By Theorem (3.1), we have obtained that for any initial value  $(S(0), I_1(0), \ldots, I_n(0)) \in \mathbb{R}^{n+1}_+$ , there is a unique global solution  $(S(t), I_1(t), \ldots, I_n(t)) \in \mathbb{R}^{n+1}_+$ . For brevity we denote  $I_1(t), \ldots, I_n(t)$  and S(t) as  $I_1, \ldots, I_n$  and S, respectively. In order to show Theorem (4.1), we only need to verify that conditions (a), (b), (c) of Lemma (2.1) are satisfied. By using the same method as those in [29], we consider the following bounded open subset:

$$\mathcal{D} = (\frac{1}{\beta}, \beta) \times \ldots \times (\frac{1}{\beta}, \beta) \subset \mathbb{R}^{n+1}_+,$$

where  $\beta$  is a sufficiently large number. Then  $\overline{\mathcal{D}} \subset \mathbb{R}^{n+1}_+$ . We have  $D(S, I, k) = R(S, I, k)R^T(S, I, k)$ , in which  $R(S, I, l) = diag(S\sigma_1(l), I_1\sigma_2(l), \ldots, I_n\sigma_{n+1}(l)), l \in \mathcal{M}$ . Then D(S, I, k) is positive semi-definite and since R(S, I, l) is a nonsingular matrix, we deduce that D(S, I, k) is positive definite. Hence

$$\lambda_{max}(D(S,I,k)) \ge \lambda_{min}(D(S,I,k)) > 0.$$

$$(4.2)$$

On the other hand, we have for all  $\xi \in \mathcal{D}$ 

$$\lambda_{\min}(D(S, I, k))|\xi|^2 \le \xi^T D(S, I, k)\xi \le \lambda_{\max}(D(S, I, k))|\xi|^2.$$
(4.3)

It is easy to see that  $\lambda_{min}(D(S, I, k))$  and  $\lambda_{max}(D(S, I, k))$  are two continuous functions of S, I. Therefore we show that  $\hat{\lambda} = \min_{(S,I,k)\in\bar{\mathcal{D}}\times\mathcal{M}}\lambda_{min}(D(S, I, k)) > 0$ and  $\check{\lambda} = \max_{(S,I,k)\in\bar{\mathcal{D}}\times\mathcal{M}}\lambda_{max}(D(S, I, k)) > 0$  from (4.2). Moreover, (4.3) implies that

$$\lambda |\xi|^2 \le \xi^T D(S, I, k) \xi \le \lambda^{-1} |\xi|^2,$$

where  $\lambda = \min{\{\hat{\lambda}, \check{\lambda}^{-1}\}}$ . We have therefore verified condition (b) in Lemma (2.1).

Earlier we have proved that the first two conditions of the lemma are established, now we mainly prove whether the condition (c) is established. Now our focus is on the proof of innovation in condition (c). By the Itô's formula and system (1.2), we have

$$\mathcal{L}(-\ln S) = -\frac{\mu(l)S^0}{S} + r \sum_{i=1}^n \beta_i(l) I_i + \mu(l) + \frac{\sigma_1^2(l)}{2},$$

$$\mathcal{L}(-\ln I_1) = -r(l) \frac{\sum_{i=1}^n \beta_i(l) I_i}{I_1} S + \mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}$$
$$= -r(l)\beta_1(l)S - r(l)S \frac{i=2}{I_1} + \mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2},$$
$$\mathcal{L}(-\ln I_i) = -\frac{\gamma_{i-1}(l)I_{i-1}}{I_i} + \mu(l) + \gamma_i(l) + \frac{\sigma_{i+1}^2(l)}{2}. \quad 2 \le i \le n.$$

Then we define:

$$\begin{aligned} \widehat{V}(S_1, S_2, \dots, S_n, I, l) &= M[-\ln I_1 - \sum_{i=1}^n a_i \ln S - \sum_{i=2}^n \sum_{j=2}^i c_{ji} \ln I_j + \omega(l) \\ &+ \frac{\widetilde{r}}{\widetilde{\mu}} \sum_{i=1}^n \sum_{j=2}^n a_i \check{\beta}_j (\sum_{k=2}^n I_k)] - \sum_{i=1}^n \ln I_i - \ln S \\ &+ (\sum_{i=1}^n I_i + S)^{1+\theta} \\ &=: M[V_1 + \omega(l) + V_2] + V_3 + V_4, \end{aligned}$$

with

$$c_{ji} = \frac{(\sum_{l=1}^{L} \pi_l {}^{i+1} \sqrt{r\beta_i \mu S^0 \prod_{j=2}^{i} \gamma_{j-1}(l)})^{i+1}}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_{1}^2(l)}{2}) \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \prod_{j=2}^{i} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})},$$

where i = 2, 3, ..., n, j = 2, 3, ..., i;

$$a_{1} = \frac{\left(\sum_{l=1}^{L} \pi_{l} \sqrt{r(l)\beta_{1}(l)\mu(l)S^{0}}\right)^{2}}{\sum_{l=1}^{L} \pi_{l}(\mu(l) + \frac{\sigma_{1}^{2}(l)}{2})^{2}},$$
  
$$a_{i} = \frac{\left(\sum_{l=1}^{L} \pi_{l} \sqrt{r(l)\beta_{i}(l)\mu(l)S^{0} \prod_{j=2}^{i} \gamma_{j-1}(l)}\right)^{i+1}}{\sum_{l=1}^{L} \pi_{l}(\mu(l) + \frac{\sigma_{1}^{2}(l)}{2})^{2} \prod_{j=2}^{i} \sum_{l=1}^{L} \pi_{l}(\mu(l) + \gamma_{j}(l) + \frac{\sigma_{j+1}^{2}(l)}{2})},$$

where i = 2, 3, ..., n, and M and theta are positive constants satisfying the following inequalities, respectively

$$C_1 + f^u + \sum_{i=2}^n g_i^u - M(\mu + \gamma_1 + \frac{\sigma_2^2}{2})(R_0^s - 1) < -2,$$
(4.4)

$$\rho := \hat{\mu} - \frac{\theta}{2} (\check{\sigma}_1^2 \bigvee \cdots \bigvee \check{\sigma}_{n+1}^2) > 0, \qquad (4.5)$$

and  $\omega(t)$  determined by the following proof. Thus we have:

$$\begin{aligned} \mathcal{L}V_{1} &\leq -r(l)\beta_{1}(l)S - r(l)S\frac{\sum_{i=2}^{n}\beta_{i}(l)I_{i}}{I_{1}} + \mu(l) + \gamma_{1}(l) + \frac{\sigma_{2}^{2}(l)}{2} + \sum_{i=1}^{n}a_{i}(-\frac{\mu(l)S^{0}}{S} \\ &+ r(l)\sum_{j=1}^{n}\beta_{j}(l)I_{j} + \mu(l) + \frac{\sigma_{1}^{2}(l)}{2}) + \sum_{i=2}^{n}\sum_{j=2}^{i}c_{ji}(-\frac{\gamma_{j-1}(l)I_{j-1}}{I_{j}} + \mu(l) \\ &+ \gamma_{j}(l) + \frac{\sigma_{j+1}^{2}(l)}{2}) \end{aligned}$$

$$\begin{split} &= -r(l)\beta_1(l)S - a_1\frac{\mu(l)S^0}{S} + a_1(\mu(l) + \frac{\sigma_1^2(l)}{2}) - \sum_{i=2}^n (r(l)S\frac{\beta_i(l)I_i}{I_1} \\ &+ \sum_{j=2}^i c_{ji}\frac{\gamma_{j-1}(l)I_{j-1}}{I_j} + a_i\frac{\mu(l)S^0}{S}) + \sum_{i=2}^n a_i(\mu(l) + \frac{\sigma_1^2(l)}{2}) \\ &+ \sum_{i=2}^n \sum_{j=2}^i c_{ji}(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \\ &+ (\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) + \sum_{i=1}^n a_i r(l) \sum_{j=1}^n \beta_j(l)I_j \\ &\leq -2(r(l)\beta_1(l)\mu(l)S^0a_1)^{\frac{1}{2}} + a_1(\mu(l) + \frac{\sigma_1^2(l)}{2}) - \sum_{i=2}^n [(i+1)(r(l)\beta_i(l)\mu(l)S^0a_i) \\ &\times \prod_{j=2}^i \gamma_{j-1}(l)c_{ji})^{\frac{1}{i+1}} - a_i(\mu(l) + \frac{\sigma_1^2(l)}{2}) - \sum_{j=2}^i c_{ji}(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})] \\ &+ (\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) + \sum_{i=1}^n a_i r(l) \sum_{j=1}^n \beta_j(l)I_j \\ &:= \bar{R}_0(l) + \sum_{i=1}^n a_i r(l) \sum_{j=1}^n \beta_j(l)I_j. \end{split}$$

 $\operatorname{Let}(w(1), w(2), \dots, w(L))^T$  be the solution of the following Poisson system

$$\Gamma w = \sum_{h=1}^{L} \pi_h \bar{R}_0(h) \begin{pmatrix} 1\\1\\\vdots\\1 \end{pmatrix} - \bar{R}_0, \qquad (4.6)$$

where  $\bar{R}_0 = (\bar{R}_0(1), \bar{R}_0(2), \dots, \bar{R}_0(L))^T$  then

$$\sum_{h=1}^{L} \gamma_{lh} w(h) + \bar{R}_0(l) = \sum_{h=1}^{L} \pi_h \bar{R}_0(h), l = 1, 2, \dots, L.$$

By  $c_{ji}, a_1, a_i, i = 2, ..., n, \ j = 2, 3, ..., i$  we obtain:

$$\begin{aligned} a_1 \sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2}) &= \frac{\left(\sum_{l=1}^{L} \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(l)(l)}{2})}, \\ c_{ji} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \\ &= a_i \sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2}) \\ &= \frac{\left(\sum_{l=1}^{L} \pi_l \frac{i+\sqrt{r(l)\beta_i(l)\mu(l)S^0\prod_{j=2}^i \gamma_{j-1}(l)}\right)^{i+1}}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2})\prod_{j=2}^i \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})}. \end{aligned}$$

Then we get

$$\begin{split} \mathcal{L} V_1 &\leq -2 \frac{\left(\sum_{l=1}^{L} \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(0)}{12})} + \frac{\left(\sum_{l=1}^{L} \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(0)}{12})} \\ &- \sum_{i=2}^n \left[ (i+1) \frac{\left(\sum_{l=1}^{L} \pi_l + i^{+1}\sqrt{r(l)\beta_i(l)\mu(l)S^0} \prod_{j=2}^{l} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})} \right] \\ &+ i \frac{\left(\sum_{l=1}^{L} \pi_l + i^{+1}\sqrt{r(l)\beta_i(l)\mu(l)S^0} \prod_{j=2}^{l} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})} \right] \\ &+ i \frac{\left(\sum_{l=1}^{L} \pi_l (\mu(l) + \frac{\sigma_1^2(l)}{2}\right) \prod_{j=2}^{l} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2})} \right] \\ &+ \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) + \sum_{i=1}^{n} a_i \tilde{r} \sum_{j=1}^{n} \tilde{\beta}_j I_j \\ &= - \left[ \frac{\left(\sum_{l=1}^{L} \pi_l \sqrt{r(l)\beta_i(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^{L} \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2})} \prod_{j=2}^{l} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \right] \\ &+ \sum_{i=2}^n \frac{\left(\sum_{l=1}^{L} \pi_l \sqrt{r(l)\beta_i(l)\mu(l)S^0}\right)^2}{\sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})} \prod_{j=2}^{l} \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \right] \\ &+ \sum_{l=1}^n \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) \prod_{j=2}^n \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \right] \\ &+ \sum_{l=1}^n \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) (R_0^s - 1) + \sum_{i=1}^n a_i \tilde{r} \sum_{j=1}^n \tilde{\beta}_j I_j \\ &= \sum_{l=1}^n \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) (R_0^s - 1) + \sum_{i=1}^n a_i \tilde{r} \sum_{j=1}^n \tilde{\beta}_j I_j \\ &= \sum_{l=1}^n \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2}) (R_0^s - 1) + \sum_{i=1}^n a_i \tilde{r} \sum_{j=1}^n \tilde{\beta}_j I_j \\ &\leq \frac{\tilde{\mu}}{\tilde{\mu}} \sum_{i=1}^n \sum_{j=2}^n a_i \tilde{\beta}_j \tilde{\gamma}_1 I_1 - \tilde{\mu} \sum_{k=2}^n I_k \right) \\ &\leq \frac{\tilde{\mu}}{\tilde{\mu}} \sum_{i=1}^n \sum_{j=2}^n \tilde{\mu}_i \tilde{\beta}_i I_i + \tilde{\mu} + \frac{\tilde{\sigma}_1^2}{2} - \sum_{i=2}^n \frac{\tilde{\gamma}_{i-1} I_{i-1}}{I_i} + \sum_{i=2}^n (\tilde{\mu} + \tilde{\gamma}_i + \frac{\tilde{\sigma}_{i+1}^2}{2}) \right) \\ &\leq \mathcal{L} \leq (\theta + 1) (S + \sum_{i=1}^n I_i)^\theta [\tilde{\mu} S^0 - \tilde{\mu}(S + \sum_{i=1}^n I_i) - \tilde{\gamma}_n I_n] + \frac{\theta}{2} (\theta + 1) (S + \sum_{i=1}^n I_i)^{\theta - 1} \\ &\times (\tilde{\sigma}_1^2 S^2 + \sum_{i=1}^n \tilde{\sigma}_i^2 I_i)^{\theta + 1} \\ &\leq A - \frac{\theta + 1}{2} \rho(S^{\theta + 1} + \sum_{i=1}^n I_i)^{\theta + 1} \\ &\leq A - \frac{\theta + 1}{2} \rho(S^{\theta + 1} + \sum_{i=1}^n I_i)^{\theta + 1} \\ &\leq A - \frac{\theta + 1}{2} \rho(S^{\theta + 1}$$

where  $A = \sup_{(S,I_1,...,I_n) \in \mathbb{R}^{n+1}_+} \left\{ -\frac{\theta+1}{2} \rho(S + \sum_{i=1}^n I_i)^{\theta+1} + \check{\mu} S^0(\theta+1)(S + \sum_{i=1}^n I_i)^{\theta} \right\}.$ Therefore

$$\begin{aligned} \mathcal{L}V &\leq -M \sum_{l=1}^{L} \pi_{l}(\mu(l) + \gamma_{1}(l) + \frac{\sigma_{2}^{2}(l)}{2})(R_{0}^{s} - 1) + M \sum_{i=1}^{n} a_{i}\check{r}(\check{\beta}_{1} + \sum_{j=2}^{n} \frac{\check{\beta}_{j}\check{\gamma}_{1}}{\hat{\mu}})I_{1} \\ &- \frac{\hat{\mu}S^{0}}{S} - \sum_{i=2}^{n} \frac{\hat{\gamma}_{i-1}I_{i-1}}{I_{i}} - \frac{\theta + 1}{2}\rho(S^{\theta + 1} + \sum_{i=1}^{n}I_{i}^{\theta + 1}) + \check{r}\sum_{i=1}^{n}\check{\beta}_{i}I_{i} + \check{\mu} + \frac{\check{\sigma}_{1}^{2}}{2} \\ &+ \sum_{i=2}^{n}(\check{\mu} + \check{\gamma}_{i} + \frac{\check{\sigma}_{i+1}^{2}}{2}) + A \\ &:= f(S) + \sum_{i=2}^{n}g_{i}(I_{i}) + h(I_{1}) - \sum_{i=2}^{n} \frac{\gamma_{i-1}I_{i-1}}{I_{i}} + C_{1}, \end{aligned}$$

in which

$$C_{1} = \check{\mu} + \frac{\check{\sigma}_{1}^{2}}{2} + \sum_{i=2}^{n} (\check{\mu} + \check{\gamma}_{i} + \frac{\check{\sigma}_{i+1}^{2}}{2}) + A,$$
  
$$f(S) = -\frac{\hat{\mu}S^{0}}{S} - \frac{\theta + 1}{2}\rho S^{\theta + 1},$$
  
$$g_{i}(I_{i}) = -\frac{\theta + 1}{2}\rho I_{i}^{\theta + 1} + \check{r}\check{\beta}_{i}I_{i}, \quad i = 2, \dots, n,$$

and

$$\begin{split} h(I_1) &= -M \sum_{l=1}^{L} \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})(R_0^s - 1) \\ &+ M \sum_{i=1}^{n} a_i \check{r}(\check{\beta}_1 + \sum_{j=2}^{n} \frac{\check{\beta}_j \check{\gamma}_1}{\hat{\mu}})I_1 - \frac{\theta + 1}{2}\rho I_1^{\theta + 1} + \check{r}\check{\beta}_1 I_1. \end{split}$$

Next, our main task is to construct a compact subset D such that (b) in Lemma 2.1 holds. Consider the following bounded subset

$$D = \Big\{ \varepsilon_1 \le S \le \frac{1}{\varepsilon_1}, \varepsilon_i \le I_i \le \frac{1}{\varepsilon_i}, i = 2, \dots, n \Big\},\$$

where  $\varepsilon_i, i = 1, \dots, n+1$  are sufficiently small positive constants satisfying the following inequalities

$$C_1 + \sum_{i=2}^n g_i^u + h^u - \frac{\hat{\mu}S^0}{\varepsilon_1} < -1,$$
(4.7)

$$C_{1} + f^{u} + \sum_{i=2}^{n} g_{i}^{u} - M[\sum_{l=1}^{L} \pi_{l}(\mu(l) + \gamma_{1}(l) + \frac{\sigma_{2}^{2}(l)}{2})(R_{0}^{s} - 1)$$

$$(4.8)$$

$$+\sum_{i=1}^{n} a_i \check{r}(\check{\beta}_1 + \sum_{j=2}^{n} \frac{\beta_j \check{\gamma}_1}{\hat{\mu}})\varepsilon_2] + \check{r}\check{\beta}_1\varepsilon_2 < -1,$$

$$C_1 + f^u + \sum_{i=2}^n g_i^u + h^u - \sum_{i=2}^n \frac{\hat{\gamma}_{i-1}}{\varepsilon} < -1, \quad i = 2, \dots, n,$$
(4.9)

$$C_1 - \frac{\theta + 1}{2}\rho\varepsilon_1^{\theta + 1} < -1, \tag{4.10}$$

$$C_2 + f^u + \sum_{i=2}^n g_i^u - \frac{\theta + 1}{4} \rho \varepsilon_2^{\theta + 1} < -1$$
(4.11)

$$C_i + f^u + h^u - \frac{\theta + 1}{4}\rho\varepsilon_i^{\theta + 1} < -1, i = 3, \dots, n + 1,$$
(4.12)

and  $\varepsilon_i = \varepsilon^i, i = 1, ..., n + 1$ , where inequality (4.8) can be derived from (4.4), and the constants  $C_i, i = 2, ..., n + 1$  will be determined later. Then

$$\mathbb{R}^{n+1}/D = D_1^c \bigcup D_1^c \bigcup \cdots \bigcup D_{2n+2}^c,$$

with

$$\begin{split} D_1^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | 0 < S < \varepsilon_1 \right\}, \\ D_2^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | 0 < I_1 < \varepsilon_2 \right\} \\ D_{i+1}^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | I_{i-1} > \varepsilon_{i-1}, 0 < I_i < \varepsilon_i \right\}, \quad i = 2, \dots, n, \\ D_{n+2}^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | S > \frac{1}{\varepsilon_1} \right\}, \\ D_{n+3}^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | I_1 > \frac{1}{\varepsilon_2} \right\} \\ D_{n+2+i}^c &= \left\{ (S, I_1, \dots, I_n) \in \mathbb{R}_+^{n+1} | I_i > \frac{1}{\varepsilon_i} \right\}, \quad i = 2, \dots, n. \end{split}$$

Next, we will prove condition (b) in Lemma 2.1.

**Case 1:** If  $(S, I_1, \ldots, I_n) \in D_1^c$ , (4.7) implies that

$$\mathcal{L}V \le C_1 + \sum_{i=2}^n g_i^u + h^u - \frac{\hat{\mu}S^0}{\varepsilon_1} < -1.$$

**Case 2:** If  $(S, I_1, ..., I_n) \in D_2^c$ , (4.8) we obtain that

$$\begin{aligned} \mathcal{L}V \leq & C_1 + f^u + \sum_{i=2}^n g_i^u - M[\sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})(R_0^s - 1) \\ & + \sum_{i=1}^n a_i \check{r}(\check{\beta}_1 + \sum_{j=2}^n \frac{\check{\beta}_j \check{\gamma}_1}{\hat{\mu}})\varepsilon_2] + \check{r}\check{\beta}_1\varepsilon_2 \\ < & - 1. \end{aligned}$$

**Case 3:** If  $(S, I_1, \ldots, I_n) \in D_{i+1}^c$ ,  $i = 2, \ldots, n$ , it follows that

$$\mathcal{L}V \le C_1 + f^u + \sum_{i=2}^n g_i^u + h^u - \sum_{i=2}^n \frac{\hat{\gamma}_{i-1}\varepsilon_i}{\varepsilon_{i+1}}, \quad i = 2, \dots, n,$$

Choosing  $\varepsilon_i = \varepsilon^i, i = 2, \dots, n+1$ , combining (4.9), yields

$$\mathcal{L}V \le C_1 + f^u + \sum_{i=2}^n g_i^u + h^u - \sum_{i=2}^n \frac{\hat{\gamma}_{i-1}}{\varepsilon} < -1, \quad i = 2, \dots, n.$$

**Case 4:** If  $(S, I_1, ..., I_n) \in D_{n+2}^c$ , (4.10) implies that

$$\mathcal{L}V \le C_1 - \frac{\theta + 1}{2}\rho \frac{1}{\varepsilon_1^{\theta + 1}} < -1.$$

**Case 5:** If  $(S, I_1, \ldots, I_n) \in D_{n+3}^c$ , we have

$$\mathcal{L}V \le C_2 + f^u + \sum_{i=2}^n g_i^u - \frac{\theta+1}{4}\rho \frac{1}{\varepsilon_2^{\theta+1}} < -1,$$

which follows from (4.11), where

$$C_{2} = \sup_{I_{1} \in (0,+\infty)} \left\{ -\frac{\theta+1}{4} \rho I_{1}^{\theta+1} - M \left[ \sum_{l=1}^{L} \pi_{l} (\mu(l) + \gamma_{1}(l) + \frac{\sigma_{2}^{2}(l)}{2}) (R_{0}^{s} - 1) + \sum_{i=1}^{n} a_{i} \check{r} (\check{\beta}_{1} + \sum_{j=2}^{n} \frac{\check{\beta}_{j} \check{\gamma}_{1}}{\hat{\mu}}) I_{1} \right] + r\beta_{1} I_{1} \right\} < \infty.$$

**Case 6:** If  $(S, I_1, \ldots, I_n) \in D_{n+2+i}^c$ , it follows that

$$\mathcal{L}V \le C_i + f^u + h^u - \frac{\theta + 1}{4}\rho \frac{1}{\varepsilon_i^{\theta + 1}} < -1, i = 3, \dots, n + 1,$$

where

$$C_{i} = \sup_{I_{1} \in (0, +\infty)} \left\{ -\frac{\theta + 1}{4} \rho I_{i}^{\theta + 1} + r\beta_{i} I_{i} \right\} < \infty, \quad i = 3, \dots, n+1,$$

which together with (4.12) implies that

$$\mathcal{L}V \leq -1.$$

Synthesize the above proof results, we get the following conclusion

$$\mathcal{L}V \leq -1, \quad (S, I_1, \dots, I_n) \in \mathbb{R}^{n+1}/D,$$

which implies that (b) in Lemma 2.1 is verified.

#### 5. Extinction

Infectious diseases are an important factor threatening human survival, therefore, the elimination of infectious diseases as soon as possible is of great significance to the survival and development of human beings. Next, our main task is how to adjust the dynamics of infectious diseases so that infectious diseases can be eliminated as soon as possible. In this section, we shall give sufficient conditions for the extinction of HIV infection in the stochastic model (1.4). Firstly, we will give a lemma as follows.

Consider the following first-order linear stochastic differential equation under regime switching

$$dZ(t) = \mu(r(t))(S^0 - Z(t))dt + \sigma_1(r(t))Z(t)dB(t),$$
(5.1)

with initial value Z(0) = S(0). Then equation (5.1) has a unique stationary distribution  $v(\cdot, \cdot)$  which is ergodic. Let  $\rho(t) = \log Z(t)$  and the  $C^2$ -function  $V(\rho, l)$  takes the following form:

$$V(\rho, l) = e^{\rho} - 1 - \rho.$$

Using Itô's formula to Eq.(5.1) results in

$$\begin{aligned} \mathcal{L}V(\rho,l) &= \ \mu(l)(S^0 - e^{\rho}) - \frac{\mu(l)}{e^{\rho}}(S^0 - e^{\rho}) + \frac{1}{2}\sigma_1^2(l) \\ &= \ \mu(l)S^0 - \mu(l)e^{\rho} - \frac{\mu(l)S^0}{e^{\rho}} + \mu(l) + \frac{1}{2}\sigma_1^2(l) \\ &\leq \ -\hat{\mu}e^{\rho} - \frac{\hat{\mu}S^0}{e^{\rho}} + (S^0 + 1)\check{\mu} + \frac{1}{2}\check{\sigma_1}^2 \\ &=: \Phi(\rho). \end{aligned}$$

Obviously,  $\Phi(\rho) \to -\infty$ , as  $\rho \to -\infty$ ;  $\Phi(\rho) \to -\infty$ , as  $\rho \to +\infty$ . Take  $\varepsilon > 0$ small enough and let  $U = [\log \varepsilon, \log \frac{1}{\varepsilon}]$ , and we have  $LV(\rho, l) < -1$ ,  $\rho \in \mathbb{R}_+ \setminus U$ . In addition, the intensity of the white noise on nutrient  $\sigma_1^2(l) > 0$ . Thus the conditions in Lemma 2.2 are satisfied, (5.1) has a unique stationary distribution  $v(\cdot, \cdot)$  which is ergodic.

Integrating the both sides of Eq. (5.1) from 0 to t, we have

$$Z(t) - Z(0) = \int_0^t \mu(r(s))(S^0 - Z(s))ds + \int_0^t \sigma_1(r(s))Z(s)dB(s).$$
(5.2)

Taking the expectation on the both sides of (5.2), one can observe that

$$\mathbb{E}[Z(t)] - \mathbb{E}[Z(0)] = \int_0^t \mathbb{E}[\mu(r(s))(S^0 - Z(s))]ds$$
  
=  $S^0 \int_0^t \mu(r(s))ds - \int_0^t \mathbb{E}[\mu(r(s))Z(s)]ds.$  (5.3)

Then

$$\frac{\mathbb{E}[Z(t)]}{dt} = S^0 \mathbb{E}[\mu(r(s))] - \mathbb{E}[\mu(r(s))Z(s)] \le S^0 \check{\mu} - \hat{\mu}\mathbb{E}[Z(s)].$$

Therefore  $\limsup_{t\to\infty} \mathbb{E}[Z(t)] \leq \frac{S^0\check{\mu}}{\hat{\mu}}$ , which means  $\mathbb{E}[Z(t)]$  is bounded. Using the dominated convergence theorem, it follows from (5.3) that

$$0 = \lim_{t \to \infty} \frac{\mathbb{E}[Z(t)] - \mathbb{E}[Z(0)]}{t}$$
$$= S^0 \lim_{t \to \infty} \frac{1}{t} \int_0^t \mu(r(s)) ds - \lim_{t \to \infty} \frac{1}{t} \int_0^t \mathbb{E}[\mu(r(s))Z(s)] ds$$
$$= S^0 \sum_{l=1}^L \pi_l \mu(l) - \sum_{l=1}^L \pi_l \mu(l) \int_{\mathbb{R}_+} Z\nu(dZ, k).$$

According to the comparison theorem we get

$$S(t) \le Z(t), \quad t > t_0.$$

**Theorem 5.1.** Let  $(S(t), I_1(t), \ldots, I_n(t))$  be the positive solution of system (1.4). Then for almost  $\omega \in \Omega$ , we obtain

$$\limsup_{t \to \infty} \frac{1}{t} \ln\{\sum_{i=1}^{n-1} [\frac{\check{\beta}_i}{\hat{\mu} + \hat{\gamma}_i} + \sum_{j=i+1}^n \frac{\check{\beta}_j q_j}{(\hat{\mu} + \hat{\gamma}_j) q_i}]I_i + \frac{\check{\beta}_n}{\hat{\mu} + \hat{\gamma}_n}I_n \le m \ a.s., \tag{5.4}$$

where  $q_1 = 1$ ,  $q_i = \prod_{j=1}^{i-1} \frac{\check{\gamma}_j}{\hat{\gamma}_j + \hat{\mu}}$ ,  $i = 2, \dots, n$  and

$$\begin{split} \tilde{R}_0 &= \sum_{i=1}^n \frac{\check{r}\check{\beta}_i q_i S^0}{\hat{\gamma}_i + \hat{\mu}}, \\ m &= (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} \\ &+ \frac{\tilde{R}_0}{S^0} (\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) \sum_{l=1}^L \pi_l \int_{\mathbb{R}_+} Z\nu(dZ, k) \\ &- \tilde{R}_0 (\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1} \end{split}$$

and  $a_i = \frac{\check{\beta}_i}{\hat{\mu} + \hat{\gamma}_i} + \sum_{j=i+1}^n \frac{\check{\beta}_j q_j}{(\hat{\mu} + \hat{\gamma}_j)q_i}$ ,  $i = 1, \ldots, n-1, a_n = \frac{\check{\beta}_n}{\hat{\mu} + \hat{\gamma}_n}$ . Particularly, if m < 0, then the disease  $I_i$ ,  $i = 1, \ldots, n$  will go to extinction exponentially with probability one, i.e.,

$$\limsup_{t \to \infty} \frac{\ln I_i}{t} < 0, \quad i = 1, \dots, n \ a.s.$$

Furthermore, S(t) admits a unique ergodic stationary distribution  $\nu(\cdot, \cdot)$ . **Proof.** Define a  $C^2$ -function  $V : \mathbb{R}^n_+ \to \mathbb{R}_+$  as follows:

$$V(I_1,\ldots,I_n) = \sum_{i=1}^n a_i I_i,$$

where  $a_i = \frac{\check{\beta}_i}{\hat{\mu} + \hat{\gamma}_i} + \sum_{j=i+1}^n \frac{\check{\beta}_j q_j}{\hat{\mu} + \hat{\gamma}_j}, \ i = 1, \dots, n-1, a_n = \frac{\check{\beta}_n}{\hat{\mu} + \hat{\gamma}_n}$ . Thus we can obtain

$$\beta_i + a_{i+1}\check{\gamma}_i = a_i(\hat{\mu} + \hat{\gamma}_i) \ i = 1, \dots, n.$$
 (5.5)

Applying the Itô's formula to  $\ln V$  gives

$$d(\ln V) = \mathcal{L}(\ln V)dt + \frac{1}{V} [\sum_{i=1}^{n} a_i \sigma_{i+1}(l) I_i dB_{i+1}(t)].$$

Here,

$$\mathcal{L}(\ln V) \leq \frac{a_1}{V} [\check{r} \sum_{i=1}^n \check{\beta}_i I_i S - (\hat{\mu} + \hat{\gamma}_1) I_1] + \frac{1}{V} \sum_{i=2}^n a_i [\check{\gamma}_{i-1} I_{i-1} - (\hat{\mu} + \hat{\gamma}_i) I_i] - \frac{\sum_{i=1}^n a_i^2 \hat{\sigma}_{i+1}^2 I_i^2}{2V^2}.$$

On the other hand, we obtain

$$V^{2} = \left(\sum_{i=1}^{n} a_{i} \hat{\sigma}_{i+1} I_{i} \frac{1}{\hat{\sigma}_{i+1}}\right)^{2} \le \left(\sum_{i=1}^{n} a_{i}^{2} \hat{\sigma}_{i+1}^{2} I_{i}^{2}\right) \left(\sum_{i=1}^{n} \frac{1}{\hat{\sigma}_{i+1}^{2}}\right),$$
(5.6)

and by (5.5), we can obtain

$$\frac{a_1}{V} [\check{r} \sum_{i=1}^n \check{\beta}_i I_i S - (\hat{\mu} + \hat{\gamma}_1) I_1] + \frac{1}{V} \sum_{i=2}^n a_i [\check{\gamma}_{i-1} I_{i-1} - (\hat{\mu} + \hat{\gamma}_i) I_i]$$

$$\begin{split} &= \frac{1}{V} \left[ \check{r}a_{1} \sum_{i=1}^{n} \check{\beta}_{i} I_{i} S - a_{1} (\hat{\mu} + \hat{\gamma}_{1}) I_{1} + \sum_{i=2}^{n-1} a_{i+1} \check{\gamma}_{i} I_{i} - \sum_{i=2}^{n} a_{i} (\hat{\mu} + \hat{\gamma}_{i}) I_{i} \right] \\ &= \frac{1}{V} \left[ \check{r}a_{1} \sum_{i=1}^{n} \check{\beta}_{i} I_{i} S - a_{1} (\hat{\mu} + \hat{\gamma}_{1}) I_{1} + a_{2} \hat{\gamma}_{1} I_{1} + \sum_{i=2}^{n-1} a_{i+1} \check{\gamma}_{i} I_{i} - \sum_{i=2}^{n-1} a_{i} (\hat{\mu} + \hat{\gamma}_{i}) I_{i} \right] \\ &- a_{n} (\hat{\mu} + \hat{\gamma}_{n}) I_{n} \right] \\ &\leq \frac{1}{V} \left[ \check{r}a_{1} \sum_{i=1}^{n} \check{\beta}_{i} I_{i} (Z - S^{0}) + \check{r}a_{1} \sum_{i=1}^{n} \check{\beta}_{i} I_{i} S^{0} - \sum_{i=1}^{n} \check{\beta}_{i} I_{i} \right] \\ &= \frac{1}{V} (\tilde{R}_{0} - 1) \sum_{i=1}^{n} \check{\beta}_{i} I_{i} + \frac{1}{V} \check{r}a_{1} \sum_{i=1}^{n} \check{\beta}_{i} I_{i} (Z - S^{0}) \\ &= \frac{1}{V} (\tilde{R}_{0} - 1) \sum_{i=1}^{n} \check{\beta}_{i} I_{i} + \frac{\tilde{R}_{0}}{S^{0}} \sum_{i=1}^{n} \frac{a_{i} I_{i} (Z - S^{0})}{V} \frac{\check{\beta}_{i}}{a_{i}} \\ &\leq \frac{1}{V} (\tilde{R}_{0} - 1) \sum_{i=1}^{n} a_{i} I_{i} (\frac{\check{\beta}_{1}}{a_{1}} \bigwedge \cdots \bigwedge \frac{\check{\beta}_{n}}{a_{n}}) E_{\tilde{R}_{0} \leq 1} \\ &+ \frac{1}{V} (\tilde{R}_{0} - 1) \sum_{i=1}^{n} a_{i} I_{i} (\frac{\check{\beta}_{1}}{a_{1}} \bigvee \cdots \bigvee \frac{\check{\beta}_{n}}{a_{n}}) - \tilde{R}_{0} (\frac{\check{\beta}_{1}}{a_{1}} \bigwedge \cdots \bigwedge \frac{\check{\beta}_{n}}{a_{n}}) E_{\tilde{R}_{0} > 1} \\ &+ \frac{Z}{S^{0}} \tilde{R}_{0} (\frac{\check{\beta}_{1}}{a_{1}} \bigwedge \cdots \bigwedge \frac{\check{\beta}_{n}}{a_{n}}) - \tilde{R}_{0} (\frac{\check{\beta}_{1}}{a_{1}} \bigwedge \cdots \bigwedge \frac{\check{\beta}_{n}}{a_{n}}) - \tilde{R}_{0} (\frac{\check{\beta}_{1}}{a_{1}} \bigwedge \cdots \bigwedge \frac{\check{\beta}_{n}}{a_{n}}). \end{split}$$
(5.7)

In view of (5.6) and (5.7), one can see that

$$\mathcal{L}(\ln V) \leq (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} + \frac{Z}{S^0} \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) - \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1}.$$

Consequently, we get

$$d(\ln V) \leq [(\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} + \frac{Z}{S^0} \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) - \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1}]dt + \frac{1}{V} [\sum_{i=1}^n a_i \sigma_{i+1}(l) I_i dB_{i+1}(l)].$$

$$(5.8)$$

Integrating (5.8) from 0 to t and then dividing by t on the both sides lead to

$$\frac{\ln V(t)}{t} \leq \frac{\ln V(0)}{t} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} \\
+ (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} \\
+ \frac{\int_0^t Z dt}{t S^0} \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) - \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1} \\
+ \frac{1}{t} \int_0^t \frac{\sum_{i=1}^n a_i \sigma_{i+1}(t) I_i dB_{i+1}(t)}{V} \\
\leq \frac{\ln V(0)}{t} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} \\
+ (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} \\
+ \frac{\int_0^t Z(r(s)) ds}{t S^0} \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n}) - \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n}) \\
- (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1} + \frac{M(t)}{t},$$
(5.9)

where  $M(t) = \int_0^t \frac{\sum_{i=1}^n a_i \sigma_{i+1}(l) I_i dB_{i+1}(t)}{V}$  which is a local martingale whose quadratic variation is  $\langle M(t), M(t) \rangle_t = \int_0^t (\frac{\sum_{i=1}^n a_i \sigma_{i+1}(l) I_i}{V})^2 ds \leq (\sum_{i=1}^n \check{\sigma}_{i+1}^2) t$ . By using the strong law of large numbers [24] yields

$$\lim_{t \to \infty} \frac{M(t)}{t} = 0 \ a.s. \tag{5.10}$$

Taking the superior limit on the both sides of (5.9) and combining with (5.10) yield

$$\begin{split} &\limsup_{t \to \infty} \frac{\ln V(t)}{t} \\ \leq & (\tilde{R}_0 - 1) (\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} + (\tilde{R}_0 - 1) (\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} \\ &+ \frac{\tilde{R}_0}{S^0} (\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) \sum_{l=1}^L \pi_l \int_{\mathbb{R}_+} Z\nu(dZ, k) - \tilde{R}_0 (\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1} \end{split}$$

:=m a.s.,

which is the required assertion (7.1). Moreover, if m < 0, one can easily conclude that

$$\limsup_{t \to \infty} \frac{\ln I_i}{t} < 0, \quad i = 1, \dots, n \ a.s.,$$

which indicates that  $\lim_{t\to\infty} I_i = 0$ ,  $i = 1, \ldots, n$ . In other words, the disease  $I_i$ ,  $i = 1, \ldots, n$  will tend to zero exponentially with probability one. Through system (1.4) and (1.1)'s equations expression, we can easily analyze that when  $\lim_{t\to\infty} I(t) = 0$  a.s., in that way  $\lim_{t\to\infty} A(t) = 0$  a.s. This completes the proof.

#### 6. Simulation

In this section, we will test our theory conclusion by the Milstein's Higher Order Method in [8] to obtain the following discretization transformation of system (1.2).

$$\begin{cases} S_{j+1} = S_j + [\mu(S^0 - S_j) - r \sum_{i=1}^n \beta_i I_{i,j} S_j] \triangle t + \sigma_1 S_j \sqrt{\triangle t} + \frac{\sigma_1^2 S_j}{2} (\varepsilon_{1,j} \triangle t - \triangle t), \\ I_{1,j+1} = I_{1,j} + [r \sum_{i=1}^n \beta_i I_{i,j} S_j - (\mu + \gamma_1) I_{1,j}] \triangle t + \sigma_2 I_{1,j} \sqrt{\triangle t} + \frac{\sigma_2^2 I_{1,j}}{2} (\varepsilon_{2,j} \triangle t - \triangle t), \\ I_{i,j+1} = I_{i,j} + [\gamma_{i-1} I_{i-1,j} - (\gamma_i + \mu) I_{i,j}] \triangle t + \sigma_{i+1} I_{i,j} \sqrt{\triangle t} + \frac{\sigma_{i+1}^2 I_{i,j}}{2} (\varepsilon_{i+1,j} \triangle t - \triangle t), \\ 2 \le i \le n, \end{cases}$$

where the time increment  $\Delta t > 0$ ,  $\sigma_i^2 > 0 (i = 1, 2, ..., n + 1)$  are the intensities of the white noise,  $\varepsilon_{i,j}(i = 1, 2, ..., n + 1)$  are independent Gaussian random variables which follow the distribution N(0, 1). First we consider the situation of system (1.2) with constant coefficients when n = 4. Its corresponding deterministic model (1.1) for parametric values are given by [10]:

 Table 1. The parameter values.

Parameter	Interpretation	Value
$\gamma_i$	Progression rates by group	(13.0, 0.177, 0.177, 0.333)
$\beta_i$	Relative infection rate	(1.9,  0.019,  0.019,  0.19)
r	Partner acquisition rate	5 partners/year
$\mu$	Total removal rate	$0.07 \ yr^{1}$
$S^0$	Normalized infection-free equilibrium	1
$R^0$	Reproductive number	3.9

Here we choose  $\sigma_1 = 0.3$ ,  $\sigma_2 = 0.2$ ,  $\sigma_3 = 0.1$ ,  $\sigma_4 = 0.2$  and  $\sigma_5 = 0.2$  respectively. Thus we obtain:

Case1

$$\begin{cases} dS(t) = [0.07(1.5 - S(t)) - 5(1.9I_1(t) + 0.019I_2(t) + 0.019I_3(t) + 0.19I_4(t))S(t)]dt \\ + 0.3S(t)dB_1(t), \\ dI_1(t) = [5(1.9I_1(t) + 0.019I_2(t) + 0.019I_3(t) + 0.19I_4(t))S(t) - (0.07 + 13)I_1(t)]dt \\ + 0.2I_1(t)dB_2(t), \\ dI_2(t) = [13I_1(t) - (0.0.07 + 0.177)I_2(t)]dt + 0.2I_2(t)dB_3(t), \\ dI_3(t) = [0.177I_1(t) - (0.0.07 + 0.177)I_3(t)]dt + 0.1I_2(t)dB_4(t), \\ dI_4(t) = [0.177I_1(t) - (0.0.07 + 0.333)I_4(t)]dt + 0.2I_2(t)dB_3(t). \end{cases}$$

According to the condition of deterministic model, we can obtain that system (1.2) has a unique stationary distribution  $\pi(\cdot)$  and it has the ergodic property when the solution  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  of system (1.1) with any initial value  $(S(0), I_1(0), I_2(0), I_3(0), I_4(0)) = (0.7, 0.3, 0.3, 0.3, 0.3) \in \mathbb{R}^5_+$ . That is to say, the disease will prevail. Using the Milstein's Higher Order Method, we give the simulations shown in Fig.2 to support our results.



**Figure 2.**  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  has ergodic property. The pictures on the right are the density functions of system (1.1) for  $\sigma_1 = 0.3$ ,  $\sigma_2 = 0.2$ ,  $\sigma_3 = 0.1$ ,  $\sigma_4 = 0.2$  and  $\sigma_5 = 0.2$ . We employ the Milstein's Higher Order Method with initial value  $(S(0), I_1(0), I_2(0), I_3(0), I_4(0)) = (0.3, 0.7, 0.3)$ .

Table 2. The parameter values.			
Parameter	Interpretation	Value	
$\gamma_i$	Progression rates by group	(13.0, 0.23553, 0.23553, 0.47)	
$\beta_i$	Relative infection rate	(0.87, 0.0196, 0.0196, 0.1802)	
r	Partner acquisition rate	5 partners/year	
$\mu$	Total removal rate	$0.07 \ yr^{1}$	
$S^0$	Normalized infection-free equilibrium	1	
$R^0$	Reproductive number	1.88	

If the corresponding deterministic model (1.1) for parametric values are given by [6]:

Here we choose  $\sigma_1 = 0.8$ ,  $\sigma_2 = 0.9$ ,  $\sigma_3 = 0.9$ ,  $\sigma_4 = 0.9$  and  $\sigma_5 = 0.9$  respectively. Thus we obtain:

Case2

$$\begin{cases} dS(t) = [0.07(1 - S(t)) - 5(0.87I_1(t) + 0.0196I_2(t) + 0.0196I_3(t) + 0.1802I_4(t))S(t)]dt \\ + 0.8S(t)dB_1(t), \\ dI_1(t) = [5(0.87I_1(t) + 0.0196I_2(t) + 0.0196I_3(t) + 0.1802I_4(t))S(t) \\ - (0.07 + 13)I_1(t)]dt + 0.9I_1(t)dB_2(t), \\ dI_2(t) = [13I_1(t) - (0.007 + 0.25553)I_2(t)]dt + 0.9I_2(t)dB_3(t), \\ dI_3(t) = [0.25553I_1(t) - (0.007 + 0.47)I_4(t)]dt + 0.9I_2(t)dB_3(t). \end{cases}$$

According to the condition of deterministic model, we can obtain that  $I_1(t)$ ,  $I_2(t)$ ,

 $I_3(t)$  and  $I_4(t)$  will tends to zero exponentially with probability one. That is to say, the disease will die out. Using the Milstein's Higher Order Method, we give the simulations shown in Fig.3 to support our results.



**Figure 3.**  $I_1(t)$   $I_2(t)$ ,  $I_3(t)$  and  $I_4(t)$  will tends to zero exponentially with probability one. The pictures on the right are the density functions of system (1.1) for  $\sigma_1 = 0.8$ ,  $\sigma_2 = 0.9$ ,  $\sigma_3 = 0.9$ ,  $\sigma_4 = 0.9$  and  $\sigma_5 = 0.9$ . We use the Milstein's Higher Order Method with initial value  $(S(0), I_1(0), I_2(0), I_3(0), I_4(0)) = (0.7, 0.3, 0.3, 0.3, 0.3)$ .

Then we consider persistence and stationary distribution of system(1.4), when n = 4. Let the generator of the Markov chain  $\gamma_{ij}$  be

$$\Gamma = \begin{pmatrix} -0.1 & 0.1 \\ 0.3 & -0.3 \end{pmatrix},$$

in which  $\gamma_{ij}$  is a right-continuous Markov chain taking value in  $\mathcal{M} = \{1, 2\}$ . By solving the linear equation (2.3) we obtain the unique stationary (probability) distribution

$$\pi = (\pi_1, \pi_2) = (0.75, 0.25).$$

We can get the SDE (1.4) as the result of the following forms switching from Case1 to Case2 according to the movement of the Markovian chain. Compute

$$\begin{split} R_0^s &:= \frac{(\sum_{l=1}^L \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0})^2}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})} \\ &+ \sum_{i=2}^n \frac{(\sum_{l=1}^L \pi_l (\mu(l) + \frac{\sigma_1^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l)\beta_i(l)\mu(l)S^0 \prod_{j=2}^i \gamma_{j-1}(l))^{i+1}}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2}) \prod_{j=2}^i \sum_{l=1}^L \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})} \\ &\approx 2.626 > 1. \end{split}$$

Therefore by condition of Theorems (4.1), as the result of Markovian switching, the solution  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  of system (1.4) with initial value  $(S(0), I_1(0), I_2(t), I_3(0), I_4(0)) = (0.7, 0.3, 0.3, 0.3, 0.3, 0.3) \in \mathbb{R}^5_+$ . System (1.4) switching from Case1 to Case2, and the disease will prevail. Using the Milstein's Higher Order Method, we give the simulations shown in Fig.4 Fig.5 Fig.6 and Fig.7 to support our results.



Figure 4.  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  is positive recurrence. The pictures on the left are Markovian chain. The pictures on the right are the density functions of system (1.4) for  $l \in \mathcal{M} = \{1, 2\}$ . We employ the Milstein's Higher Order Method with initial value  $(S(0), I_1(0), I_2(0), I_3(0), I_4(0)) = (0.7, 0.3, 0.3, 0.3, 0.3)$ .

Finally we consider extinction of system(1.4), when n = 4. Let the white noise exchange to  $\sigma_1 = (13.5, 14)$ ,  $\sigma_2 = (14, 14.5)$ ,  $\sigma_3 = (14, 14.5)$ ,  $\sigma_4 = (14, 14.5)$  and  $\sigma_5 = (14, 14.5)$  respectively.

We can get the SDE (1.4) as the result of the following forms switching from Case1 to Case2 according to the movement of the Markovian chain.

As  $\limsup_{t\to\infty} \mathbb{E}[Z(t)] \leq \frac{S^0\check{\mu}}{\hat{\mu}}$  we can compute

$$m \leq (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \leq 1} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1} + \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) - \tilde{R}_0(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) - (2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2})^{-1} \approx -2.782 < 0$$

Therefore by condition of Theorems (5.1), we can obtain that  $I_1(t)$ ,  $I_2(t)$ ,  $I_3(t)$ and  $I_4(t)$  will tends to zero exponentially with probability one. That is to say, the disease will die out. Using the Milstein's Higher Order Method, we give the simulations shown in Fig.8 to support our results.



Figure 5. Computer simulation of a single path of  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  for the SDE model (1.4) with initial condition (0.7, 0.3, 0.3, 0.3, 0.3).



Figure 6. Computer simulation of 1000 pathes of  $(S(t), I_1(t), I_2(t), I_3(t), I_4(t))$  for the SDE model (1.4).

# 7. Conclusion

In previous articles, we have studied a simple three-dimensional stochastic SP infectious disease model, but the infectious disease model in real life is very complicated, and there are many situations. Therefore in this paper, we further extended from studying 3D SP models to studying multidimensional SP models. In this multi-



Figure 7. This picture is the 95% confidence intervals from 1000 stochastic simulations.



**Figure 8.**  $I_1(t)$ ,  $I_2(t)$ ,  $I_3(t)$  and  $I_4(t)$  will tends to zero exponentially with probability one. The pictures on the left are Markovian chain. The pictures on the right are the density functions of system (1.4) for  $l \in \mathcal{M} = \{1, 2\}$ . We employ the Milstein's Higher Order Method with initial value  $(S(0), I_1(0), I_2(0), I_3(0), I_4(0)) = (0.7, 0.3, 0.3, 0.3, 0.3).$ 

dimensional SP epidemic model, improved the problems of the classic SP model,

we further consider the interference of white noise and telegraph noise on the SP stochastic epidemic model. Discussing the nature of the solution to the randomized SP infectious disease model is an important part of studying the dynamics of infectious diseases. Therefore, in the first part of the article, we have proved and calculated that the solution of the HIV SP random infectious disease model we studied has existence and uniqueness meanwhile it is global. Next we have studied the long-term behavior of our randomized SP epidemic model. We established conditions for extinction and persistence of disease which both are sufficient but not necessary. We also have proved that the SP model (1.4) has an ergodic stationary distribution. About the persistence of the model, in the fourth part of the article, we talked about the conditions under which the disease persists and whether the disease continues to develop. In other words, we explored the long-term behavior of this disease. The results of the discussion in the fourth section indicate the disease is bounded, that is, the disease will be endemic and cannot spread to the entire susceptible population or to extinction. The most concerned is the conditions for the extinction of infectious diseases, we discuss the sufficient conditions for the extinction of infectious diseases in the fifth part of the article, this means that the disease cannot spread or become endemic disease.

In this article we also found some very interesting conclusions, that is the behavior of a stochastic system has a certain relationship with the behavior of each equations in the system. About the persistence of the system, we have found that if all the conditions in Theorem 4.1 are satisfied, then all the equations in (1.4) is stochastically permanent, respectively. Hence according to theorem 4.1 we can get the conclusion that if every individual equations are stochastically permanent, then as the result of Markovian switching, the overall behavior, i.e. SDE (1.4), remains stochastically permanent. The same reason, if Theorem 5.1's conditions are both satisfied, for some  $l \in \mathcal{M}$ , then every individual equations in (1.4) are extinctive. Hence Theorem 5.1 shows that if every individual equations are extinctive, then as the result of Markovian switching, the overall behavior of SDE (1.4) remains extinctive.

However, Theorems 4.1 and 5.1 provide more interesting results that if some individual equations in (1.4) are random permanent while some are extinctive, again as the result of Markovian switching, the overall behavior of SDE (1.4) may be stochastically permanent or extinctive, depending on the sign of the stationary distribution  $(\pi_1, \ldots, \pi_L)$  of the Markov chain  $\xi(t)$ .

Above mentioned conclusion shows that the stationary distribution  $(\pi_1, \ldots, \pi_L)$  of the Markov chain  $\xi(t)$  plays an important role in determining extinction or persistence of the infectious disease in the population. We have come to the clear conditions for the extinction or persistence of this infectious disease:

(1) Let  $(S(t), I_1(t), \ldots, I_n(t))$  be the positive solution of system (1.4). Then for almost  $\omega \in \Omega$ , we obtain

$$\limsup_{t \to \infty} \frac{1}{t} \ln\{\sum_{i=1}^{n-1} [\frac{\check{\beta}_i}{\hat{\mu} + \hat{\gamma}_i} + \sum_{j=i+1}^n \frac{\check{\beta}_j q_j}{(\hat{\mu} + \hat{\gamma}_j) q_i}] I_i + \frac{\check{\beta}_n}{\hat{\mu} + \hat{\gamma}_n} I_n \le m \ a.s.,$$
(7.1)

where  $q_i = \prod_{j=1}^{i-1} \frac{\check{\gamma}_j}{\hat{\gamma}_j + \hat{\mu}}$ ,  $i = 2, \dots, n$  and  $\tilde{R}_0 = \sum_{i=1}^n \frac{\check{r}\check{\beta}_i q_i S^0}{\hat{\gamma}_i + \hat{\mu}}$ ,  $m = (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigwedge \dots \bigwedge \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 \le 1} + (\tilde{R}_0 - 1)(\frac{\check{\beta}_1}{a_1} \bigvee \dots \bigvee \frac{\check{\beta}_n}{a_n}) E_{\tilde{R}_0 > 1}$ 

$$+ \frac{\tilde{R}_0}{S^0} \left( \frac{\check{\beta}_1}{a_1} \bigvee \cdots \bigvee \frac{\check{\beta}_n}{a_n} \right) \sum_{l=1}^L \pi_l \int_{\mathbb{R}_+} Z\nu(dZ,k)$$
$$- \tilde{R}_0 \left( \frac{\check{\beta}_1}{a_1} \bigwedge \cdots \bigwedge \frac{\check{\beta}_n}{a_n} \right) - \left( 2\sum_{i=1}^n \frac{1}{\hat{\sigma}_{i+1}^2} \right)^{-1}$$

and  $a_i = \frac{\check{\beta}_i}{\hat{\mu}+\hat{\gamma}_i} + \sum_{j=i+1}^n \frac{\check{\beta}_j q_j}{(\hat{\mu}+\hat{\gamma}_j)q_i}$ ,  $i = 1, \ldots, n-1, a_n = \frac{\check{\beta}_n}{\hat{\mu}+\hat{\gamma}_n}$ . Particularly, if m < 0, then the disease  $I_i$ ,  $i = 1, \ldots, n$  will go to extinction exponentially with probability one, *i.e.*,

$$\limsup_{t \to \infty} \frac{\ln I_i}{t} < 0, \quad i = 1, \dots, n \ a.s.,$$

Furthermore, S(t) admits a unique ergodic stationary distribution  $\nu(\cdot, \cdot)$ .

(2) Assume that  $R_0^s > 1$ , then system (1.4) has a unique stationary distribution  $\pi(\cdot)$  and it has the ergodic property.

Let  $(S(t), I_1(t), \ldots, I_n(t), \xi(t))$  be the solution of system (1.4) with initial value  $(S(0), I_1(0), \ldots, I_n(0), \xi(0)) \in \mathbb{R}^{n+1}_+ \times \mathcal{M}$ . Assume that  $R_0^s > 1$ , where

$$\begin{split} R_0^s &:= \frac{(\sum_{l=1}^L \pi_l \sqrt{r(l)\beta_1(l)\mu(l)S^0})^2}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})} \\ &+ \sum_{i=2}^n \frac{(\sum_{l=1}^L \pi_l (\mu(l) + \frac{\sigma_1^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l)\beta_i(l)\mu(l)S^0 \prod_{j=2}^i \gamma_{j-1}(l))^{i+1}}{\sum_{l=1}^L \pi_l(\mu(l) + \frac{\sigma_1^2(l)}{2}) \prod_{j=2}^i \sum_{l=1}^L \pi_l(\mu(l) + \gamma_j(l) + \frac{\sigma_{j+1}^2(l)}{2}) \sum_{l=1}^L \pi_l(\mu(l) + \gamma_1(l) + \frac{\sigma_2^2(l)}{2})}, \end{split}$$

then  $(S(t), I_1(t), \ldots, I_n(t), \xi(t))$  is persistence and has an ergodic stationary distribution.

Finally, this paper is only a first step in introducing switching regime into an SP epidemic model. In the course of our future study and research we will introduce white and color noises into more realistic SP epidemic models, and use the conclusions of these random infectious disease mathematical models to solve practical problems.

#### Acknowledgements

The authors thank the referees and associate editor for their constructive comments on an earlier version of this paper. My special thanks also go to Professor Daqing Jiang. He helped and encouraged me to undertake the writing of this thesis. My sincere appreciation also goes to Jiaqi Li for her continuous support and encouragement. She helped me a lot with my daily study and life.

**Data Availability.** Data sharing is not applicable to this article as no new data were created or analyzed in this study.

#### References

 T. Caraballo, M. E. Fatini and M. E. Khalifi, Analysis of a stochastic distributed delay epidemic model with relapse and gamma distribution kernel, Chaos Solitons Fractals, 2020, 133, 109–643.

- [2] Y. Cao, L. Qin, L. Zhang, J. Safrit and D. D. Ho, Virologic and immunologic characterization of long-term survivors of HIV type 1 infection, N. Engl. J. Med., 1995, 332, 201.
- [3] R. Durrett, Stochastic spatial models, SIAM Rev., 1999, 41, 677–718.
- [4] N. Du, R. Kon, K. Sato and Y. Takeuchi, Dynamical behavior of Lotka-Volterra competition systems: Non-autonomous bistable case and the effect of telegraph noise, J. Comput. Appl. Math., 2004, 170, 399–422.
- [5] A. Gray, D. Greenhalgh, L. Hu, X. Mao and J. Pan, A stochastic differential equation SIS epidemic model, SIAM J. Appl. Math., 2011, 71, 876–902.
- [6] J. Hyman, J. Li and E. Stanley, Modeling the impact of random screening and contact tracing in reducing the spread of HIV, Mathematical Biosciences, 2003, 181, 17–54.
- [7] R. Z. Has'minskii, Stochastic Stability of Differential Equations, Sijthoff and Noordhoff, Alphen aan den Rijn, The Netherlands, 1980.
- [8] D. J. Higham, An algorithmic introduction to numerical simulation of stochastic differential equations, SIAM Rev., 2001, 43, 525–546.
- [9] J. Hyman and J. Li, An intuitive formulation for the reproductive number for the spread of diseases in heterogeneous populations, Math. Biosci., 2000, 167, 65–86.
- [10] J. M. Hyman, J. Li and E. A. Stanley, The differential infectivity and staged progression models for the transmission of HIV, Math. Biosci., 1999, 155, 77.
- [11] J. M. Hyman, J. Li and E. A. Stanley, The initialization and sensitivity of multigroup models for the transmission of HIV, J. Theor. Biol., 2001, 208, 227.
- [12] A. Ida, S. Oharu and Y. Oharu, A mathematical approach to HIV infection dynamics, J. Comput. Appl. Math., 2007, 204, 172–186.
- [13] J. A. Jacquez, J. S. Koopman, C. P. Simon and I. M. Longini, Role of the primary infection in epidemics of HIV infection in gay cohorts, J. AIDS., 1994, 7, 1169.
- [14] J. A. Jacquez, C. P. Simon and J. Koopman, Core groups and the R0s for subgroups in heterogeneous SIS and SI models, in: Mollison (Ed.), Epidemic Models: Their Structure and Relation to Data, Cambridge University, Cambridge, 1995, 279.
- [15] J. Y. Kim, J. H. Ko, Y. Kim, Y. J. Kim and B. S. Chin, Viral load kinetics of SARS-CoV-2 infection in first two patients in Korea, J. Korean Med. Sci., 2020, 35, e86.
- [16] S. Liu, X. Xu, D. Jiang, T. Hayatb and B. Ahmadb, Stationary distribution and extinction of the DS-I-A model disease with periodic parameter function and Markovian switching, Appl. Math. Comput., 2017, 311, 66–84.
- [17] S. Liu, D. Jiang, X. Xu, T. Hayatb and B. Ahmadb, Dynamics of hybrid switching DS-I-A epidemic model, Scientific Reports, 2017, 7(1).
- [18] Q. Liu, D. Jiang, N. Shi, T. Hayat and A. Alsaedi, Nontrivial periodic solution of a stochastic non-autonomous SISV epidemic model, Physica A, 2016, 462, 837–845.

- [19] Q. Liu and D. Jiang, Stationary distribution of a stochastic staged progression HIV model with imperfect vaccination, Phys. A, 2019, 527, 121–271.
- [20] A. Lahrouz and L. Omari, Extinction and stationary distribution of a stochastic SIRS epidemic model with non-linear incidence, Stat. Prob. Lett., 2013, 83, 960–968.
- [21] F. Li, S. Zhang and X. Meng, Dynamics analysis and numerical simulations of a delayed stochastic epidemic model subject to a general response function, Comput. Appl. Math., 2019, 38, 95.
- [22] Z. Liu, Dynamics of positive solutions to SIR and SEIR epidemic models with saturated incidence rates, Nonlinear Anal. Real World Appl., 2013, 14, 1286– 1299.
- [23] Q. Luo and X. Mao, Stochastic population dynamics under regime switching, J. Math. Anal. Appl., 2007, 334, 69–84.
- [24] X. Mao, Stochastic Differential Equations and Their Applications, Horwood, Chichester, 1997.
- [25] S. E. Park, Epidemiology, virology, and clinical features of severe acute respiratory syndrome -coronavirus-2 (SARS-CoV-2; Coronavirus Disease-19), Clin. Exp. Pediatr., 2020, 63, 119–124.
- [26] S. Spencer, Stochastic epidemic models for emerging diseases, PhD. thesis, University of Nottingham, 2008.
- [27] A. Singh, B. Razooky, C. D. Cox, et al., Transcriptional bursting from the HIV-1 promoter is a significant source of stochastic noise in HIV-1 gene expression, Biophys, 2010, 98(8), L32–L34.
- [28] M. Slatkin, The dynamics of a population in a Markovian environment, Ecology, 1978, 59, 249–256.
- [29] A. Settati and A. Lahrouz, Stationary distribution of stochastic population systems under regime switching, Appl. Math. Comput., 2014, 244, 235–243.
- [30] Y. Takeuchi, N. Du, N. T. Hieu and K. Sato, Evolution of predator-prey systems described by a Lotka-Volterra equation under random environment, J. Math. Anal. Appl., 2006, 323, 938–957.
- [31] G. Zeluf-Andersson and L. Eriksson, Beyond viral suppression: The quality of life of people living with HIV in Sweden, AIDS Care, 2019, 31(4), 403–412.
- [32] L. Zu, D. Jiang and D. ORegan, Conditions for persistence and ergodicity of a stochastic lotkacvolterra predatorcprey model with regime switching, Commun. Nonlin. Sci. Numer. Simul., 2015, 29, 1–11.
- [33] X. Zhang, D. Jiang, A. Alsaedi and T. Hayat, Stationary distribution of stochastic SIS epidemic model with vaccination under regime switching, Appl. Math. Lett., 2016, 59, 87–93.
- [34] C. Zhu and G. Yin, Asymptotic properties of hybrid diffusion systems, SIAM J. Control Optim., 2007, 46, 1155–1179.
- [35] B. Zhou, X. Zhang and D. Jiang, Dynamics and density function analysis of a stochastic SVI epidemic model with half saturated incidence rate. Chaos Solitons Fractals, 2020, 137, 109–865.