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Extinction and Persistent of a Stochastic Multi-group SIR Epidemic Model

Xiaojing Zhong and Feiqi Deng

Systems Engineering Institute, South China University of Technology, Guangzhou 510640, P.R. China

Abstract: We establish a stochastic differential equation epidemic model of multi-group SIR type based on the deterministic multi-group SIR mode. Then, we define the basic reproduction number R_0^S and show that it is a sharp threshold for the dynamic of the stochastic multi-group SIR model. More specially, if $R_0^S < 1$, then the disease-free equilibrium will be asymptotically stable which means the disease will die out, if $R_0^S > 1$, the disease-free equilibrium will unstable, and our model will positively recurrence to a positive domain which implies the persistence of our model. Numerical simulation examples are carried out to substantiate the analytical results.

Key words: Stochastic, multi-group SIR model, threshold dynamics, positive recurrence, stochastic persistence.

1. Introduction

For the past decades, many epidemic models have been proposed for modeling the spread process of infectious diseases, and in the meantime considerable attention has been paid to study the dynamical properties of these various models. Most models descend from the classical SIR model of Kermack and McKendrick [1], and then different type of epidemic models have been researched by many scholars [2-10]. In particular, multi-group models have been proposed to describe the transmission dynamics of infectious diseases in heterogeneous host populations, such as meals, mumps, gonorrhea, HIV/AIDS, WNV (West-Nile virus) and vector borne diseases such as malaria. One of the earliest works on multi-group models is the seminal paper by Laj-manovich and Yorke [11] on a class of SIS (suspectible, infected, suspectable) multi-group models for the transmission dynamics of Gonorrhea, which established a complete analysis of the global dynamics. The global stability of the unique equilibrium is proved by using a complete analysis of the global Lyapunov function. Subsequently, much research has been done on multi-group models [12-18]. Recently, a group-theoretic approach to the method of global Lyapunov function was proposed by Michael et al. [19].In the paper, the authors studied the following SIR model:

$$\begin{cases} S_k' = A_k - d_k^s S_k - \sum_{j=1}^n \beta_{kj} S_k I_j, \\ I_k' = \sum_{j=1}^n \beta_{kj} S_k I_j - (d_k^I + \varepsilon_k + \gamma_k) I_k, \\ R_k' = \gamma_k I_k - d_k^R R_k, \end{cases} \quad (1)$$

The model describes the spread of an infectious disease in a heterogeneous population, which is partitioned into n homogeneous group. Each group k is further compartmentalized into S_k, I_k and R_k, here S_k, I_k and R_k denote the susceptible, infective and recovered population at time t, respectively. All parameters in the above model are nonnegative constants and summarized in the following list:

β_{ij}: transmission coefficient between compartments S_i and I_j;

Corresponding author: Feiqi Deng, Professor, research fields: stability, stabilization and robust and variable structure control theory of complex systems, including time-delay systems, nonlinear systems and stochastic systems, and machine learning.E-mail:aufqdeng@scut.edu.cn.

d_k^S, d_k^I, d_k^R :nature death rates of S, I, R compartments in the *k*-th group, respectively;

A_k: influx of individuals into the *k*-th group;

γ_i: recovery rate of infectious individuals in the *i*-th group;

ε_k: disease-caused death rate in the *k*-th group.

All parameter values are assumed to be nonnegative and $d_k^S, d_k^I, d_k^R, A_k > 0$ for all *k*. According to Michael et al. [19], there is a disease-free equilibrium: $P_0 = (S_1^0, 0, 0, \cdots, S_n^0, 0, 0)$ on the boundary of Γ, where $S_i^0 = A_i / d_i^S$ and

$$\Gamma = \{(S_1, I_1, \cdots, S_n, I_n) \in R_+^{2n} \Big| S_k \le \frac{A_k}{d_k^S}, S_k + I_k \le \frac{A_k}{min\{d_k^S, d_k^I + \varepsilon_k, d_k^R\}}\} \quad (2)$$

A threshold R_0 is defined which decide the epidemic will prevalent or not, where

$$R_0 = \rho(M_0) \quad (3)$$

denote the spectral radius of the matrix

$$M_0 = M(S_1^0, S_2^0, \ldots, S_n^0) = (\frac{\beta_{ij} S_i^0}{d_i^I + \gamma_i + \varepsilon_i}), 1 \le i, j \le n \quad (4)$$

Here we give more details. If $R_0 \le 1$, then, P_0 is the unique equilibrium and it is globally asymptotically stable in Γ; If $R_0 > 1$, then P_0 is unstable and it is uniformly persistent. Furthermore, there exists an endemic equilibrium P^* and it is globally asymptotically stable in Γ. In the whole proof, a very important graph theorem was used.

Given a nonnegative matrix $A = (\beta_{ij})$ the directed graph *G*(A) associated with $A = (\beta_{ij})$ has vertices 1, 2, ···, *n* with a directed arc (*i*, *j*) from *i* to *j* if $\beta_{ij} \ne 0$. It is strongly connected if any two distinct vertices are joined by an oriented path. The matrix *A* is irreducible if and only if *G*(A) is strongly connected. A tree is a connected graph with no cycles. A sub tree *T* of a graph *G* is said to be spanning if *T* contains all the vertices of *G*. A directed tree is a tree in which each edge has been replaced by an arc directed one way or the other. A directed tree is said to be rooted at a vertex, called the root, if every arc is oriented in the direction towards the root. An oriented cycle in a directed graph is a simple closed oriented path. A unicyclic graph is a directed graph consisting of a collection of disjoint rooted directed trees whose root are on an oriented cycle. For a given nonnegative matrix *A*=(a_{ij}), let:

$$L = \begin{bmatrix} \sum_{l \ne 1} \beta_{1l} & -\beta_{21} & \cdots & -\beta_{n1} \\ -\beta_{12} & \sum_{l \ne 2} \beta_{2l} & \cdots & \beta_{n2} \\ \vdots & \vdots & \cdots & \vdots \\ -\beta_{1n} & -\beta_{2n} & \cdots & \sum_{l \ne n} \beta_{nl} \end{bmatrix} \quad (5)$$

be the Laplacian matrix of the directed graph *G*(A) and C_{ij} denote the cofactor of the (*i*, *j*) entry of *L*. In light of these results, complete determination of the global dynamic of these models is essential for their application and further development.

Whereas the statement above, the large-scale biological system's parameters are assumed as constants, but in the real situation, parameters involved with the model always fluctuate around some average value due to the continuous fluctuation in the environment. In order to study the dynamics of interacting population under realistic situation, we need to analyse the associated stochastic model. In fact, the stochastic epidemic models have been studied by many authors [20-36], they established related stochastic epidemic model based on the deterministic model. By using the Lyanupov method, Tornatore et al.[30],Yu et al. [31], Ji et al. [32], Liu et al. [33] and Ji et al. [34] found out sufficient conditions of the stability of the steady-state based on the deterministic threshold R_0. Gray et al. [35] established a stochastic SIS model and found out the sufficient and necessary condition of the disease-free equilibrium and the condition of the persistence of the disease. Liu et al.[37] gave many stochastic persistence definitions about epidemic model.

In this paper, we perturb the death rate and transmission coefficient of the deterministic multi-group SIR model Eq. (1) by replacing d_k^I, d_k^I and β_{kk}, by $d_k^I + \sigma_I \dot{B}(t), d_k^R + \sigma_R \dot{B}(t)$ and $\beta_{kk} + \sigma_k \dot{B}(t)$

where, $B_I(t), B_R(t), B_\beta(t)$ are independent standard Brownian motions with $B_I(0) = 0, B_R(0) = 0$, $B_\beta(0) = 0$. Then we formulate a stochastic multi-group SIR model as follows:

$$\begin{cases} \mathrm{d}S_k = (A_k - d_k^S S_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j)\,\mathrm{d}t - \sigma_k S_k I_k\,\mathrm{d}B_\beta, \\ \mathrm{d}I_k = [\sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^I + \varepsilon_k + \gamma_k) I_k]\,\mathrm{d}t \\ \qquad + \beta_{kk} S_k I_k dB_\beta - \sigma_I I_k\,\mathrm{d}B_I, \\ \mathrm{d}R_k = (\gamma_k I_k - d_k^R R_k)\,\mathrm{d}t - \sigma_R R_K\,\mathrm{d}B_R. \end{cases} \tag{6}$$

We prove the global existence of the positive solution in Section 2. The stability of the disease-free equilibrium is derived in Section 3, we will find out a new threshold R_0^S different from the deterministic R_0 which determine the extinction and persistence of the disease. In Section 4, we give the proof of our model's stochastic persistence. Examples and the simulation results are considered to illustrate our main results.

Throughout the article, unless otherwise specified, we will employ the following notions. Let $(\Omega, F, \{F_t\}_{t\geq 0}, P)$ be a complete probability space with a filtration $\{F_t\}_{t\geq 0}$ satisfying the usual conditions, i.e., it is right continuous and F_0 contains all P-null sets. We use $a \vee b$ to denote max(a, b), $a \wedge b$ to denote min(a, b) and a.s. to mean almost surely.

2. Existence and Uniqueness of the Positive Global Solution

In this section, we prove the global existence of the positive solution of our stochastic system Eq. (6). As a stochastic differential equation, the functions involved with stochastic system are generally required to satisfy the Lipschitz condition and linear growth condition. Obviously, the functions in Eq. (6) do not satisfy the linear growth condition, so the solutions may explode at finite times. To solve this problem, we first show that the local positive solutions exist before the explode times, then we use the lyapunov function method to prove that the solutions exist globally.

Theorem 2.1 If $B=(\beta_{ij})_{n\times n}$ is irreducible, then for any initial value $(S_1(0), I_1(0), R_1(0), \cdots, S_n(0), I_n(0), R_n(0)) \in R_+^{3n}$, there exists a unique solution $(S_1(t), I_1(t), R_1(t), \cdots, S_n(t), I_n(t), R_n(t)) \in R_+^{3n}$ to system Eq. (6) and it satisfies $P((S_1(t), I_1(t), R_1(t), \cdots, S_n(t), I_n(t), R_n(t) \mid (S_1(t), I_1(t), R_1(t), \cdots, S_n(t), I_n(t), R_n(t) \in R_+^{3n}) = 1$, Which mean $(S_1(t), I_1(t), R_1(t), \cdots, S_n(t), I_n(t), R_n(t) \in R_+^{3n}$.

Proof. Since the coefficients of the equation are locally Lipschitz continuous, there is unique local solution on $t \in [0, \tau_e)$, where τ_e is the explosion time [38].Using the Itô formula, the solution can be expresses as:

$$S_k(t) = e^{-d_k^S t - \int_0^t (\sum_{j=1}^n \beta_{kj} I_j(u) + \frac{\sigma_k^2}{2} I_k^2(u))\mathrm{d}u - \sigma_k \int_0^t I_k(u)\mathrm{d}B_\beta(u)}$$

$$\times [S_k(0) + A_k \int_0^t e^{d_k^S u + \int_0^u (\sum_{j=1}^n \beta_{kj} I_j(v) + \frac{\sigma_k^2}{2} I_k^2(v))\mathrm{d}v + \sigma_k \int_0^u I_k(v)\mathrm{d}B_\beta(v)} \mathrm{d}u] \tag{7}$$

then $S_k(t) > 0, t \in [0, \tau_e)$, By the same way we get

$$\mathrm{I_k(t)} = \mathrm{e}^{-(d_k^I + \varepsilon_k + \gamma_k + \frac{\sigma_I^2}{2})\mathrm{t} + \int_0^t (\beta_{kk} S_k(u) - \frac{\sigma_k^2}{2} S_k^2(u))\mathrm{d}u}$$
$$\times e^{\sigma_k \int_0^t S_k(\mathrm{u})\mathrm{d}B_\beta(\upsilon) + \sigma_I B_I(t)} \times \{I_k(0)$$
$$+ \int_0^t \sum_{k\neq j} \beta_{kj} S_k I_j(v) [e^{(d_k^I + \varepsilon_k + \gamma_k + \frac{\sigma_I^2}{2})u}$$
$$\times e^{-\int_0^u ((\beta_{kk} S_k(v) - \frac{\sigma_k^2}{2} S_k^2(v))\mathrm{d}v - \sigma_k \int_0^u S_k(v)\mathrm{d}B_\beta(v) + \sigma_I B_I(u)}] du\} \tag{8}$$

$$R_k(t) = e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}$$
$$\times [R_k(0) + \int_0^t \gamma_k I_k(u) e^{(d_k^R + \frac{\sigma_R^2}{2})u - \sigma_R B_R(u)} \mathrm{d}u] \tag{9}$$

then we can conclude that $S_k(t)$, $I_k(t)$, $R_k(t)$ are positive on $t \in [0, \tau_e)$. Then we want to show that this solution is a global solution. To prove this, we need to show that $\tau_e = \infty$ almost surely. We choose a sufficiently large number 0 such that $S(0)$, $I(0)$, $R(0)$ all lie with the interval $(0, m_0)$, For each integer $m > m_0$, we define the stopping time:

$$T_m = \inf\{t \in [0, \tau_e) : \max\{S_k(t) + I_k(t) + R_k(t), \\ k = 1,2,\cdots,n > m\} \quad (10)$$

where, $\inf\varnothing=\infty$. Set $\tau_\infty = \lim_{k\to\infty}$ whence $\tau_\infty < \tau_e$. If we can show that $\tau_\infty = \infty$ a.s. it is sufficient to prove that $\tau_e = \infty$ a.s. for all $t \geq 0$. If this statement were false, then there is a pair of constants $T > 0$ and $\varepsilon \in (0, 1)$ such that $P\{\tau_\infty \leq T\} > \varepsilon$, hence there is an integer $m_1 \geq m_0$ such that $P\{\tau_m \leq T\} \geq \varepsilon$ for all $m \geq m_1$.

Define a function $V(S_1,I_1,R_1,\cdots, S_n, I_n, R_n) = \sum_{k=1}^{n} (S_k+I_k+R_k)$,using the Itô formula, for any $t\in (0, T]$ and $m \geq m_1$,

$$EV(S_1(t\wedge\tau_m), I_1(t\wedge\tau_m), R_1(t\wedge\tau_m),\cdots, S_n(t\wedge\tau_m), \\ I_n(t\wedge\tau_m), R_n(t\wedge\tau_m)) = V(S_1(0), I_1(0), R_1(0),\cdots, \\ S_n(0), I_n(0), R_n(0)) + E\int_0^{t\wedge\tau_m} LV(S_1(s), I_1(s), R_1(s),\cdots, \\ S_n(s), I_n(s), R_n(s))ds, \quad (11)$$

where, LV is

$$LV = \sum_{k=1}^{n}[A_k - d_k^S S_k - (d_k^I + \varepsilon_k)I_k - d_k^R R_k] \\ \leq \sum_{k=1}^{n} A_k = A \quad (12)$$

Therefore, if $t \leq T$, we have

$$EV(S_1(t\wedge\tau_m), I_1(t\wedge\tau_m), R_1(t\wedge\tau_m),\ldots, S_n(t\wedge\tau_m), \\ I_n(t\wedge\tau_m), R_n(t\wedge\tau_m)) = V(S_1(0), I_1(0), R_1(0),\cdots, \\ S_n(0), I_n(0), R_n(0)) + AT \quad (13)$$

Set $\Omega_m = \{\tau_m \leq T\}$, for $m \geq m_1$, then we know $P(\Omega_m)$. For every $\omega \in \Omega_m$, $\max\{S_k(t) + I_k(t) + R_k(t), k = 1, 2,\cdots, n\} \geq m$, hence

$$V(S_1(0), I_1(0), R_1(0),\ldots, S_n(0), I_n(0), R_n(0)) + AT \\ \geq E[I_{\Omega_m}(\omega)V(S_1(t\wedge\tau_m), I_1(t\wedge\tau_m), R_1(t\wedge\tau_m),\cdots, \\ S_n(t\wedge\tau_m), I_n(t\wedge\tau_m), R_n(t\wedge\tau_m))] \\ \geq \varepsilon max\{S_k(t) + I_k(t) + R_k(t), k = 1,2,\cdots,n\} \\ \geq \varepsilon m \quad (14)$$

Letting $m\to\infty$ leads to the contradiction $\infty > V(S(0), I(0), R(0)) + AT > \infty$, so we have $\tau_\infty=\infty$ a.s. whence the proof is complete.

3. Extinction of the Epidemic

In the study of population systems, extinction and persistence are two of the most important issues. In this section, we will discuss the extinction of Eq. (6). Since the coexisting disease-free equilibrium P_0 of the deterministic SIR model Eq. (1), we make the variable changes $u_i(t) = S_k(t) - S_k^0$, $v_i(t) = I_k(t)$ and $w(t) = R_k(t)$, so that the origin will represent the disease-free equilibrium, by this we consider the linearized system:

$$\begin{cases} \mathrm{d}\,u_k = (-d_K^S u_k - \sum_{j=1}^{n}\beta_{kj}S_k^0 v_j)dt - \sigma_k S_k^0 v_k\,\mathrm{d}\,B_\beta(t), \\ \mathrm{d}\,v_k = [\sum_{j=1}^{n}\beta_{kj}S_k^0 v_j - (d_k^I + \varepsilon_k + \gamma_k)v_k]\,\mathrm{d}\,t \\ \qquad - \sigma_I v_k\,\mathrm{d}\,B_I + \sigma_k S_k^0 v_k\,\mathrm{d}\,B_\beta(t), \\ \mathrm{d}\,w_k = [\gamma_k v_k - d_k^R w_i]\,\mathrm{d}\,t - \sigma_R w_k\,\mathrm{d}\,B_R(t). \end{cases} \quad (15)$$

Considering the second Eq. (15), let $x(t) = (v_1(t), v_2(t), \cdots, v_n(t))$, we rewrite the second equation as

$$\mathrm{d}\,x(t) = Fx(t)\,\mathrm{d}\,t + G_1 x(t)\,\mathrm{d}\,B_\beta(t) - G_2 x(t)\,\mathrm{d}\,B_I(t) \quad (16)$$

Where,

$$F = \begin{bmatrix} \beta_{11}S_1^0 - d_1^I - \varepsilon_1 - \gamma_1 & \cdots & \beta_{1n}S_1^0 \\ \vdots & \ddots & \vdots \\ \beta_{nn}S_n^0 & \cdots & \beta_{n1}S_n^0 - d_n^1 - \varepsilon_n - \gamma_n \end{bmatrix} \quad (17)$$

$$G_1 = \begin{bmatrix} \sigma_1 S_1^0 & & & \\ & \sigma_2 S_2^0 & & \\ & & \ddots & \\ & & & \sigma_n S_n^0 \end{bmatrix} \quad (18)$$

$$G_1 = \begin{bmatrix} \sigma_I & & & \\ & \sigma_I & & \\ & & \ddots & \\ & & & \sigma_I \end{bmatrix} \quad (19)$$

We assume that $\sigma_k S_k^0 = \sigma_\beta$, then the matrices F, G_1, G_2 commute, the explicit solution of the linearized system in Eq.(16) can be solved as

$$x(t) = x(0)\exp[(F - \frac{1}{2}G_1^2 - \frac{1}{2}G_2^2)t + G_1 B_\beta(t) - G_2 B_I(t) \quad (20)$$

where,

$$F - \frac{1}{2}G_1^2 - \frac{1}{2}G_2^2 =$$

$$\begin{bmatrix} \beta_{11}S_1^0 - d_1^I - \varepsilon_1 - \gamma_1 - \frac{\sigma_I^2}{2} - \frac{(S_1^0\sigma_1)^2}{2} & \cdots & \beta_{1n}S_1^0 \\ \vdots & \ddots & \vdots \\ \beta_{n1}S_n^0 & \cdots & \beta_{n1}S_n^0 - d_n^I - \varepsilon_n - \gamma_n - \frac{\sigma_I^2}{2} - \frac{(S_n^0\sigma_n)^2}{2} \end{bmatrix} \tag{21}$$

Let $R_0^S = \rho(M_0^S)$ denote the spectral radius of the matrix

$$M_0^S = \left(\frac{\beta_{kj}S_k^0}{d_i^I + \varepsilon_k + \gamma_k + \frac{\sigma_k^2}{2} + \frac{(S_i^0\sigma_i)^2}{2}} \right)_{1 \le k, j \le n} \tag{22}$$

In this case, there is a pair of positive constants C and λ, so that

$$\left\| \exp[(F - \frac{1}{2}G_1^2 - \frac{1}{2}G_2^2)t] \right\| \le Ce^{-\lambda t} \tag{23}$$

It then follows from Eq.(23) that

$$|x(t)| \le C|x(0)|\exp[-\lambda t + \|G_I\|\|B_\beta(t)| + \|G_2\|\|B_I(t)|] \tag{24}$$

Using the strong law of large numbers, we get that $\lim_{t\to m} \frac{B_\beta(t)}{t} = 0$ a.s. and $\lim_{t\to m} \frac{B_I(t)}{t} = 0$ a.s., thus we obtain

$$\limsup_{t\to 0} \frac{1}{t}\log|x(t)| \le \lambda \quad \text{a.s.}$$

In other words, the solution of Eq.(15) is almost surely exponentially stable. Next, we give estimate for $u_k(t)$, $w_k(t)$. Using the Itˆo formula, we derive that

$$w_k(t) = e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}[R_k(0) + \int_0^t \gamma_k \nu_k e^{-(d_k^R + \frac{\sigma_R^2}{2})u - \sigma_R B_R(u)} \mathrm{d}u] \tag{25}$$

Substituting Eq. (24) into Eq. (25) we get

$$w_k(t) \le e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}[R_k(0) + \int_0^t \gamma_k \nu_k e^{-(d_k^R + \frac{\sigma_R^2}{2} - \lambda)u + \sigma_\beta|B_\beta(u)| + \sigma_I|B_I(u)| + \sigma_R B_R(u)} \mathrm{d}u] \tag{26}$$

By the law of the iterated logarithm,

$$\limsup_{t\to 0} \frac{B(s)}{\sqrt{2s\log\log s}} = 1 \quad \text{a.s.}$$

thus there is a $T > 0$ such that, if $t > T$, then we have $B(s) \le \sqrt{2s\log\log s}$. Using this for the estimation of $w_k(t)$, we obtain that

$$\begin{aligned} w_k(t) &\le e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}[R_k(0) + \int_0^t \gamma_k \nu_k e^{(d_k^R + \frac{\sigma_R^2}{2} - \lambda)u + (\sigma_\beta\sigma_I + \sigma_R)\sqrt{2u\log\log u}} du] \\ &\le e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}[R_k(0) + \int_0^T \gamma_k \nu_k e^{(d_k^R + \frac{\sigma_R^2}{2} - \lambda)u + (\sigma_\beta\sigma_I + \sigma_R)\sqrt{2u\log\log u}} du + \\ &\quad + \gamma_k e^{(\sigma_\beta\sigma_I + \sigma_R)\sqrt{2t\log\log t}} \int_T^t \nu_k e^{(d_k^R + \frac{\sigma_R^2}{2} - \lambda)u} du] \\ &= e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}[R_k(0) + \int_0^T \gamma_k \nu_k e^{(d_k^R + \frac{\sigma_R^2}{2} - \lambda)u + (\sigma_\beta\sigma_I + \sigma_R)\sqrt{2u\log\log u}} du] \\ &\quad + \frac{\gamma_k}{d_k^R - \frac{\sigma_R^2}{2} - \lambda} e^{-\lambda t + (\sigma_\beta + \sigma_I + \sigma_R)\sqrt{2t\log\log t} - \sigma_R B_R(t)} \\ &\quad - \frac{\gamma_k}{d_k^R - \frac{\sigma_R^2}{2} - \lambda}[e^{-(d_k^R - \frac{\sigma_R^2}{2} - \lambda)T(\sigma_\beta + \sigma_I + \sigma_R)\sqrt{2T\log\log T}} \\ &\quad \times e^{-(d_k^R + \frac{\sigma_R^2}{2})t - \sigma_R B_R(t)}] \end{aligned} \tag{27}$$

therefore,

$$\limsup_{t\to\infty} \frac{1}{t}\log|w_k(t)| = -(d_k^R + \frac{\sigma_R^2}{2}) \vee -\lambda < 0 \tag{28}$$

Similarly, we can get the assertion for $u_k(t)$ as

$$\limsup_{t\to\infty} \frac{1}{t}\log|u_k(t)| = -\lambda \vee -(d_k^R + \frac{\sigma_R^2}{2}) \vee -d_k^S < 0 \tag{29}$$

In this way we proved that Eq. (15) is exponentially stable. According to the Oseledec multiplicative ergodic theorem [39], the necessary and sufficient condition for the almost sure asymptotic stability, of the trivial solution of the system is that the largest lyapunov exponent of the linearized system is negative. Therefore, we have the following results:

Theorem 3.1 Assume that $B = (\beta_{ij})_{n\times n}$ is irreducible.

(1) If $R_0^S < 1$, then the disease-free equilibrium P_0 is almost sure asymptotically stable, which means the disease will die out almost surely.

(2) If $R_0^S > 1$, then the disease-free equilibrium P_0 is unstable.

Remark 3.2 It is useful to observe that in either the classical deterministic model or the stochastic model, there is a threshold which reflect the

prevalent or extinction of the epidemic, but the thresholds are different between them, the stochastic threshold R_0^S is smaller than the deterministic one. In other words, the conditions for I(t) to become extinct in the SDE epidemic model are weaker than in the classical deterministic epidemic model. We give the following example illustrates this result more explicitly.

Example 3.3 For simplicity, let k = 2 and we choose the following system parameters

$$A_1=100; A_2=300; d_1^S=2; d_2^S=3; d_1^I=3; d_2^I=5; d_1^R=3;$$

$$d_2^R=5; \beta_{11}=0.1; \beta_{12}=0.2; \beta_{21}=0.3; \beta_{22}=0.4; \varepsilon_1=1;$$

$$\varepsilon_2=1; \gamma_1=1; \gamma_2=1;$$

so the stochastic multi-group SIR model in Eq. (6) becomes

$$\begin{cases} \mathrm{d}S_1=(100-2S_1-0.1S_1I_1-0.2S_1I_2)\,\mathrm{d}t-\sigma_1S_1I_1\,\mathrm{d}B(t), \\ \mathrm{d}I_1=(0.1S_1I_1+0.2S_1I_2-5E_1)\,\mathrm{d}t+\sigma_1S_1I_1\,\mathrm{d}B(t)-\sigma_1I_1\,\mathrm{d}B(t), \\ \mathrm{d}R_1=(I_1-3R_1)\,\mathrm{d}t-\sigma_RR_1\,\mathrm{d}B(t), \\ \mathrm{d}S_2=(300-3S_1-0.3S_2I_1-0.4S_2I_2)\,\mathrm{d}t-\sigma_2S_2I_2\,\mathrm{d}B(t), \\ \mathrm{d}I_2=(0.3S_2I_1+0.4S_2I_2-7I_2)\,\mathrm{d}t+\sigma_2S_2I_2\,\mathrm{d}B(t)-\sigma_1I_2\,\mathrm{d}B(t), \\ \mathrm{d}R_1=(I_2-5R_2)\,\mathrm{d}t-\sigma_RR_2\,\mathrm{d}B(t). \end{cases} \tag{30}$$

Clearly, if $\sigma_1=\sigma_2=\sigma_I=\sigma_R=0$, Eq. (30) becomes to be the related deterministic multi-group SIR model and $R_0>1$ so $I_1(t)$, $I_2(t)$ will tend to their endemic equilibrium. In Fig. 1, we start our numerical simulation with $\sigma_1=0.2$, $\sigma_2=0.1$, $\sigma_I=\sigma_R=0$, and the initial value are $I_1(0)=10$, $I_2(0)=20$. Noting that $R_0^S<1$, by Theorem 3.1, $I_1(t)$, $I_2(t)$ will tend to zero exponentially. Computer simulation in Fig.1 illustrates the extinction of disease.

Next we keep the parameter value and start our computer simulation at the initial value $I_1(0)=I_2(0)=1$,we gain the same results in Fig. 2.

If we decrease the environment intensity to $\sigma_1=0.02$, $\sigma_2=0.01$, $\sigma_I=\sigma_R=0$ and starting from $I_1(0)=I_2(0)=1$, which means $R_0^S>1$. From Theorem 3.1, the disease-free equilibrium will be unstable, result of one simulation run in Fig. (3) proves our results.

4. Stochastic Persistence

For a deterministic model, persistence is implied by showing the endemic equilibrium is a global attractor. But for our stochastic model Eq. (6), there is no endemic equilibrium.

In fact, the solution of our model is a process, if we can prove the process is positive recurrence relative to a positive domain, and then this conclusion implies the persistence of our stochastic model in stochastic version. Before proving the main result of this section, we give the concept of recurrence [40].

Definition 4.1 Let U be some bounded or unbounded domain, and we denote its complement U^c by U_1. A process $X(t)$ is said to be recurrence relative to the domain U (or U−recurrence) if it is regular and foe every $s, x \in U_1$.

$$p^{s,x}\{\tau_{U_1}<\infty\}=1 \tag{31}$$

where, τ_{U_1} is the first exit time from U_1. A recurrent process with finite mean recurrence time is said to be positive recurrent.

The proof of positive recurrence result for the stochastic Eq. (6) is based upon the following lemma (see Theorem 3.12 in [41]).

Lemma 4.2 A necessary and sufficient condition for positive recurrence with respect to a domain $U = D \times l \subset R^r \times M$ is that for each $I \in$ M, there exists a nonnegative function $V(x, i)$:$\mathrm{D}^c \to R$ such that $V(x, i)$ is twice continuously differentiable and that

$$\mathrm{LV}(x,i)=-1, (x,i)\in D^c\times M. \tag{32}$$

Following theorem is the positive recurrence result for the stochastic system in Eq. (6).

Theorem 4.3 Assume that $B=(\beta_{ij})_{n\times n}$ is irreducible and $R_0^S>1$. If the random perturbation coefficient satisfies,

$$2(d_k^I+\varepsilon_k+\gamma_k)>\frac{(d_k^S+d_k^1+\varepsilon_k+\gamma_k)^2}{d_k^S}+\sigma_I^2, \qquad d_k^R>\sigma_R^2,$$

then our model Eq. (6) is positive recurrence relative to a positive domain, where $P^*=(S_1^*, I_1^*, R_1^*, \ldots, S_n^*, I_n^*, R_n^*)$ is the endemic equilibrium of the related deterministic system of Eq.(1).

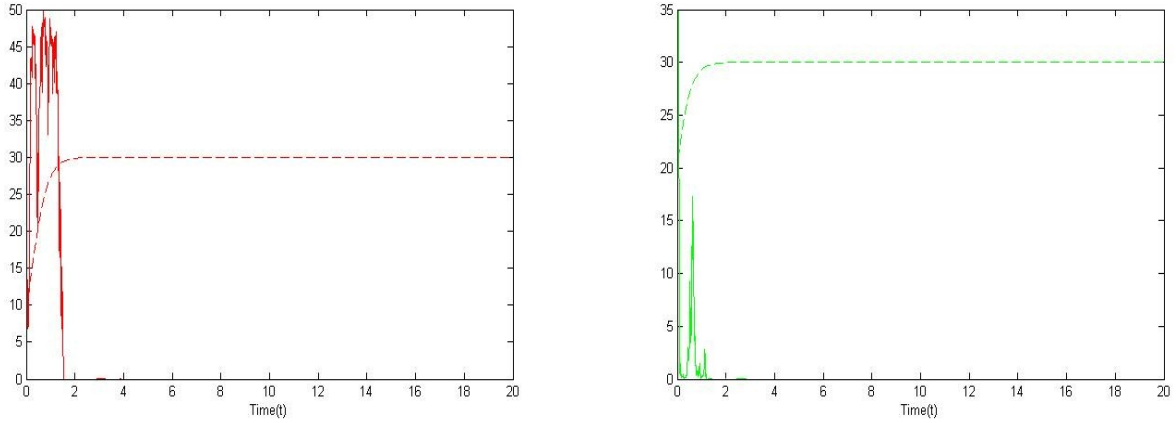

Fig. 1 Computer simulation of path $I_1(t)$, $I_2(t)$ for Eq. (30) and its corresponding deterministic model, using the EM method with step size 0.001, with initial value$I_1(0)$ = 10, $I_2(0)$ = 20. The full line express stochastic model's simulation, and the dotted line express the related deterministic model.

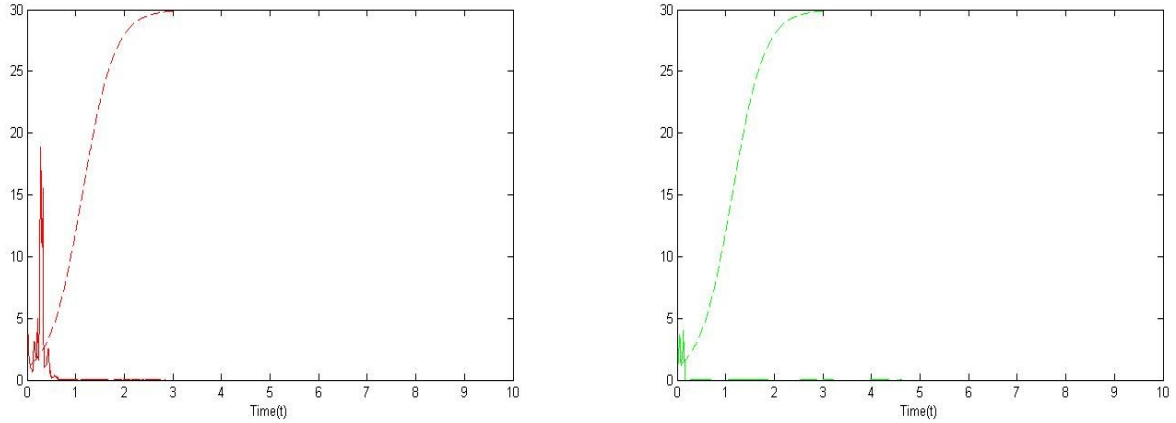

Fig. 2 Computer simulation of path $I_1(t)$, $I_2(t)$ for Eq. (30) and its corresponding deterministic model, using the EM method with step size 0.001, with initial value $I_1(0)$ = 1 = $I_2(0)$ = 1. The full line express stochastic model's simulation, and the dotted line express the related deterministic model.

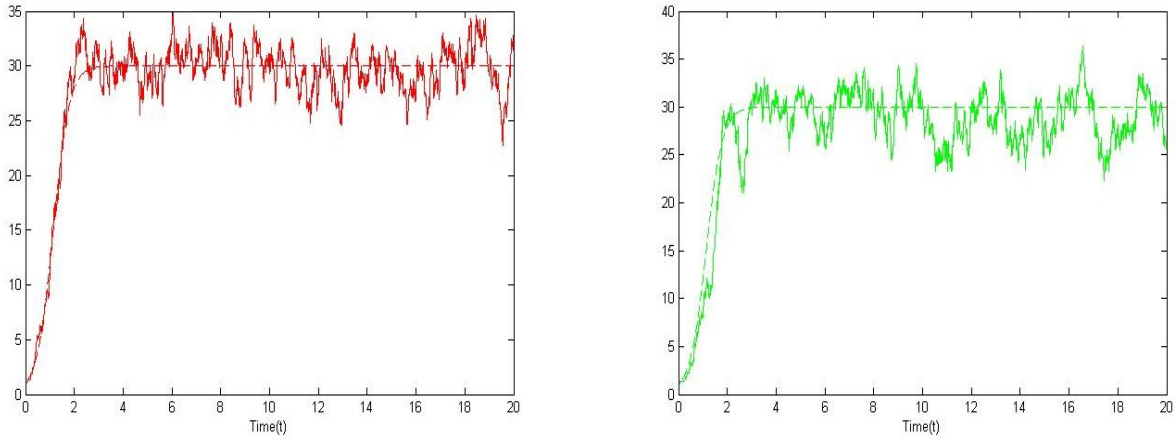

Fig. 3 Computer simulation of path $I_1(t)$, $I_2(t)$ for Eq. (30) and its corresponding deterministic model, using the EM method with step size 0.001, with initial value $I_1(0)$ =1, $I_2(0)$ = 1. The full line express stochastic model's simulation and the dotted line express the related deterministic model.

Proof. Since $1 < R_0^S < R_0$, there is an endemic equilibrium $P^* = (S_1^*, I_1^* R_1^*, \cdots, S_n^*, E_n^*, I_n^*)$ for the deterministic system of Eq. (15). We obtain the following equation

$$A_k = d_k^S S_k^* + \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^*; \sum_{j=1}^{n} \beta_{kj} S_k^* I_j^* = (d_k^I + \varepsilon_k + \gamma_k) I_i; \gamma_k I_k = d_k^R R_k, \tag{33}$$

Set

$$\begin{aligned} V &= \sum_{k=1}^{n} v_k (S_k - S_k^* \ln S_k + I_i - I_i^* \ln I_i) + a_k (S_k - S_k^* \\ &\quad + I_k - I_k^*)^2 + b_k (R_k - R_k^*)^2 \\ &= V_1 + V_2 + V_3. \end{aligned} \tag{34}$$

Using the same method as that for the proof of Theorem 3.3 [7], we choose $\overline{\beta}_{kj} = \beta_{kj} S_k^* I_j^*, 1 \le k, j \le n$, $\overline{B} = (\overline{\beta}_{kj}), \{v_1, \ldots, v_n\}, v_k > 0$ such that $\overline{B} v = 0$. Applying Itô formula, we can calculate that

$$\begin{aligned} LV_1 &= \sum_{k=1}^{n} v_k [A_k - d_k^S S_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j - A_k \frac{S_k^*}{S_k} + d_k^S S_k^* + \sum_{j=1}^{n} \beta_{kj} S_k^* I_j \\ &\quad + \frac{S_k^* \sigma_k^2 I_k^2}{2} + \sum_{j=1}^{n} \beta_{kj} S_k I_j - (d_k^I + \varepsilon_k + \gamma_k) I_k - \sum_{j=1}^{n} \beta_{kj} S_k I_j \frac{I_k^*}{I_k} + \\ &\quad + (d_k^I + \varepsilon_i + \gamma_k) I_k^* + \frac{I_k^* (\sigma_k^2 S_k^2 + \sigma_I^2)}{2}] \\ &= \sum_{k=1}^{n} v_k [d_k^S S_k^* (2 - \frac{S_k^*}{S_k} - \frac{S_k}{S_k^*}) + (\sum_{j=1}^{n} \beta_{kj} S_k^* I_j - (d_k^I + \gamma_k + \varepsilon_k) I_k \\ &\quad + (2 \sum_{j=1}^{n} \beta_{kj} S_k^* I_k^* - \sum_{j=1}^{n} \beta_{kj} I_j^* \frac{(S_k^*)^2}{S_k} - \sum_{j=1}^{n} \beta_{kj} S_k I_j \frac{I_k^*}{I_k}) + \\ &\quad + \frac{S_k^* \sigma_k^2}{2} I_k^2 + \frac{I_k^* \sigma_k^2}{2} S_k^2 + \frac{I_k^* \sigma_I^2}{2}] \\ &\le \sum_{k=1}^{n} v_k [(2 \sum_{j=1}^{n} \beta_{kj} S_k^* I_k^* - \sum_{j=1}^{n} \beta_{kj} I_j^* \frac{(S_k^*)^2}{S_k} - \sum_{j=1}^{n} \beta_{kj} S_k I_j \frac{I_k^*}{I_k}) \\ &\quad + \frac{S_k^* \sigma_k^2}{2} I_k^2 + \frac{I_k^* \sigma_k^2}{2} S_k^2 + \frac{I_k^* \sigma_I^2}{2}] \\ &\le \sum_{k=1}^{n} v_k [\overline{\beta}_{kj} (2 - \frac{S_k^2}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*}) + \frac{S_k^* \sigma_k^2}{2} I_k^2 + \frac{I_k^* \sigma_k^2}{2} S_k^2 \\ &\quad + \frac{I_k^* \sigma_I^2}{2}] \end{aligned} \tag{35}$$

Calculating LV_2 we obtain

$$\begin{aligned} LV_2 = \sum_{k=1}^{n} a_k [2(S_k - S_k^* + I_k - I_k^*)(A_k - d_k^S S_k - \\ (d_k^I - \varepsilon_k + \gamma_k) I_k) + \sigma_I^2 I_k^2] \end{aligned} \tag{36}$$

Substituting Eq. (33) into (36) yields

$$\begin{aligned} LV_2 &= \sum_{k=1}^{n} a_k [2(S_k - S_k^* + I_k - I_k^*)(-d_k^S (S_k - \\ &\quad S_k^*) - (d_k^I + \varepsilon_k + \gamma_k)(I_k - I_k^*)) + \sigma_I^2 I_k^2] \\ &= \sum_{k=1}^{n} a_k [-2 d_k^S (S_k - S_k^*)^2 - 2(d_k^I + \varepsilon_k + \\ &\quad \gamma_k)(I_k - I_k^*)^2 + \sigma_I^2 I_k^2 - 2(d_k^S + d_k^I + \varepsilon_k + \\ &\quad \gamma_k)(S_k - S_k^*)(I_k - I_k^*)] \\ &\le \sum_{k=1}^{n} a_k [-d_k^S (S_k - S_k^*)^2 - [2(d_k^I + \varepsilon_k + \gamma_k) \\ &\quad - \frac{(d_k^S + d_k^I + \varepsilon_k + \gamma_k)^2}{d_k^S}] (I_k - I_k^*)^2 + \sigma_I^2 I_k^2]. \end{aligned} \tag{37}$$

Similarly, we can calculate LV_3

$$\begin{aligned} LV_3 &= \sum_{k=1}^{n} b_k [2(R_k - R_k^*)(\gamma_k (I_k - I_k^*) - d_k^R (R_k - R_k^*)) + \sigma_R^2 R_k^2] \\ &= \sum_{k=1}^{n} b_k [2\gamma_k (I_k - I_k^*)(R_k - R_k^*) - 2 d_k^R (R_k - R_k^*)^2 + \sigma_R^2 R_k^2] \\ &\le \sum_{k=1}^{n} b_k [\frac{\gamma_k^2}{d_k^R} (I_k - I_k^*)^2 - d_k^R (R_k - R_k^*)^2 + \sigma_R^2 R_k^2]. \end{aligned} \tag{38}$$

Choose

$$\begin{aligned} m_k &= 2(d_k^I + \varepsilon_k + \gamma_k) - \frac{(d_k^S + d_k^I + \varepsilon_k + \gamma_k)^2}{d_k^S}, b_k = \varepsilon, a_k \\ &= (\frac{v_k I_k^* \sigma_k^2}{2 d_k^S} + \varepsilon) \vee (\frac{\varepsilon \gamma_k^2}{(m_k - \sigma_I^2) d_k^R} + \varepsilon) \end{aligned}$$

then

$$\begin{aligned} LV &\le \sum_{k=1}^{n} v_k \overline{\beta}_{kj} (2 - \frac{S_k^*}{S_k} - \frac{I_j S_k I_k^*}{I_k S_k^* I_j^*} + \frac{I_k^* \sigma_I^2}{2}) \\ &\quad + \sum_{k=1}^{n} [\frac{v_k I_k^* \sigma_k^2}{2} S_k^2 - (\frac{v_k I_k^* \sigma_k^2}{2} + \varepsilon)(S_k - S_k^*)^2] \\ &\quad + \sum_{k=1}^{n} [\frac{\varepsilon \gamma_k^2}{d_k^R} I_k^2 - (\frac{\varepsilon \gamma_k^2}{d_k^R} + \varepsilon)(I_k - I_k^*)^2] \\ &\quad + \sum_{k=1}^{n} [\varepsilon \sigma_R^2 R_k^2 - \varepsilon d_k^R (R_k - R_k^*)^2] \\ &= H(S_1, I_1, R_1, \ldots, S_n, I_n, R_n). \end{aligned} \tag{39}$$

Note that

$$2(d_k^I + \varepsilon_k + \gamma_k) > \frac{d_k^S + d_k^I + \varepsilon_k + \gamma_k)}{d_k^S} + \sigma_I^2, d_k^R > \sigma_R^2.$$

It is clearly that

$$\begin{aligned} \lim_{S_k, I_k, R_k \to 0} H(S_1, I_1, R_1, \ldots, S_n, I_n, R_n) = -\infty \\ \lim_{S_k, I_k, R_k \to \infty} H(S_1, I_1, R_1, \ldots, S_n, I_n, R_n) = -\infty \end{aligned} \tag{40}$$

So there exists a domain U lies entirely in R_+^{3n}. For $(S_1, I_1, R_1, \ldots, S_n, I_n, R_n) \in U_+^{3n}$, $LV <$ -M, where M is a positive constant. According to Lemma 4.2, the

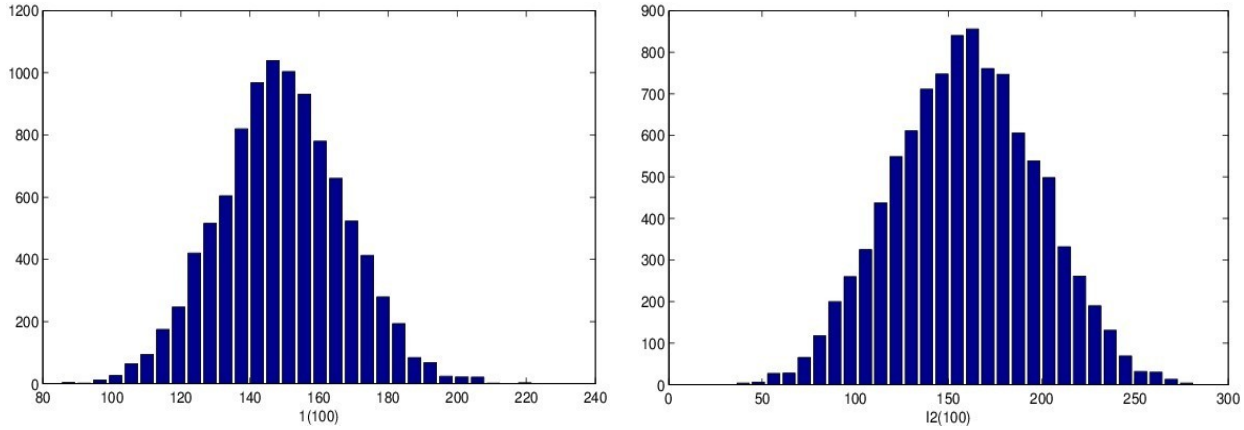

Fig. 4 Frequency histograms of path $I_1(t)$, $I_2(t)$ for Eq. (30) based on 10000 stochastic simulations for each population at time t = 100, using the EM method with step size 0.001,with initial value $I_1(0)$ = 1, $I_2(0)$ = 1.

solution of our model is positive recurrence related to the positive domain U. The proof is complete.

Example 5.4 To substantiate the analytic findings above, we provide numerical simulation results for the stochastic model Eq. (30). We also use the same parameters in Example 3.3, and let σ_1 = 0.02, σ_2 = 0.01, $\sigma_I = \sigma_R = 0$. We have shown in Fig. 3 that $I_1(t)$, $I_2(t)$ will not tend to 0, Theorem 4.3 tell us that the solution will recurrence relative to a positive domain. Fig. 4 shows histograms of the approximate distribution of the infective classes.

5. Conclusions

In this paper, we have considered the general multi-group SIR epidemic model which in presence of multiplicative noise terms to understand the dynamics in presence of environmental driving forces. First we guarantee the existence and uniqueness of positive global solution of our stochastic epidemic model. Then we find out a sharp threshold which determines the extinction or persistence of disease. Specifically, If $R_0^S < 1$, then the disease-free equilibrium will be asymptotically stable which means the disease will die out, if $R_0^S > 1$, our model will positively recurrence to a positive domain which implies the persistence of our model. We need to point out that the sharp threshold we found is different from the related deterministic model's threshold, it smaller then the deterministic one. It makes sense in biological systems, because it means the environment perturbation increase the parameter values of the extinction of disease. After the theoretic proof, we give some numerical examples to illustrate our results.

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