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Research Article

Extinction analysis of infected compartment in stochastic SI system with beddington-deangelis incidence rate

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Abstract: *It presents a deterministic susceptible-infected (SI) model and the corresponding stochastic model with a Beddington-DeAngelis type incidence rate in the present work. Disease extinction thresholds offer crucial information for managing, controlling, or eliminating diseases. Ito's formula is used for extinction analysis in disease-free states. Additionally, we attempt to demonstrate that the SDE model has disease extinction with probability one, but the deterministic model has an endemic. Lastly, our analytical results are validated using numerical simulations.*

Keywords: *SI model; Endemic state; Stochastic time series; Extinction analysis*

1. Introduction and model formulation

The most straightforward method for mathematically simulating epidemics is the traditional SI Model of epidemic spreading (1; 2). Over the past few decades, numerous researchers have proposed SI models to study a variety of infectious diseases worldwide (3; 4; 5; 6; 7; 8; 9). Some researchers have recently taken into account different kinds of nonlinear incidence rates in their research (10; 11; 12; 13; 14). To account for the crowding effect of sick people or the inhibitory effect of the healthy population's shifting behaviour, a saturated type incidence rate is also preferable (15). Beddington-DeAngelis type incidence rate is considered for incidence rate (16). There is a fixed total number of people. Based on the above assumption, the following deterministic model is given below:

$$\frac{dS}{dt} = \lambda - \frac{\beta SI}{1 + b_1 S + b_2 I} - \mu S + \gamma I$$

$$\frac{dI}{dt} = \frac{\beta SI}{1+b_1 S+b_2 I} - (\gamma + \mu + \alpha) I \qquad (1)$$

with nonnegative initial conditions $S(0) \geq 0, I(0) \geq 0$ and $S + I = \lambda$, which is a constant. Here, the densities of the susceptible and infected population at any given time t are denoted by $S(t)$ and $I(t)$. The duration of recovery for infected individuals is γ, the rate of illness-induced mortality for infected individuals is α, the rate of natural mortality for the overall population is μ, and the total recruitment at any given time t is λ. Also, β is the transmission rate, the inhibition effect is

measured by b_1, which includes preventive measures taken by susceptible ones, and the prevention effect is measured by b_2, which includes therapy with regard to infectious agents.

The state of the epidemics is influenced by the environment's unpredictability and fluctuation (17; 18). In many situations, stochastic differential equation (SDE) models may be a better method of simulating epidemic dynamics. Based on their deterministic formulations, numerous realistic stochastic epidemic models can be obtained (19; 7; 20). In order to investigate the stochastic dynamics of a SIS model and reflect the impact of environmental fluctuations on the dynamics of the disease, we take into consideration the stochastic version of system (1) that follows:

$$dS = \left[\lambda - \frac{\beta SI}{1 + b_1 S + b_2 I} - \mu S + \gamma I\right] dt - \sigma_1 \frac{SI}{1 + b_1 S + b_2 I} dB_1(t)$$
$$dI = \left[\frac{\beta SI}{1 + b_1 S + b_2 I} - (\gamma + \mu + \alpha) I\right] dt + \sigma_2 \frac{SI}{1 + b_1 S + b_2 I} dB_2(t) \qquad (2)$$

In this context, $B_1(t)$ and $B_2(t)$ represent two independent standard Brownian motions established within a complete probability space denoted as $(\Omega, F, \{F_t\}_{\{t \geq 0\}}, P)$, accompanied by a filtration $\{F_t\}_{\{t \geq 0\}}$ that adheres to the standard conditions. Also, $\sigma_i^2, i = 1,2$ are the intensities of the white noises.

The paper is organised as follows: preliminaries for extinction analysis is covered in Section 2. Sections 3 deftly examine the extinction analysis of infected compartment. A few numerical simulations are shown in Section 4 to confirm the theoretical findings. Section 5 presents a conclusion based on the findings.

2. Preliminaries

In this section, we outline certain notations and fundamental results pertaining to system (2), which serve as the foundation for a more in-depth exploration of its dynamics. We consider the following n-dimensional stochastic differential equation:

$$dx(t) = f(x(t), t)dt + g(x(t), t)dB(t) \; for \; t \geq t_0.$$

Denote by $C^{\{2,1\}}(R^n \times [t_0, \infty); R_+)$ the family of all nonnegative functions $P(x, t)$ defined on $R^n \times [t_0, \infty)$ such that they are continuously twice differentiable with respect to x and once with respect to t. We also introduce the differential operator defined in (21).

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

If L acts on a function $P \in C^{\{2,1\}}(R_n \times [t_0, \infty); R_+)$, then

$$LP(x,t) = P_t(x,t) + P_x(x,t)f(x,t) + \frac{1}{2}\, trace[g^T(x,t)P_{xx}(x,t)g(x,t)],$$

where $P_t = \frac{\partial P}{\partial t}, P_x = (\frac{\partial P}{\partial x_1}, \ldots, \frac{\partial P}{\partial x_n})$ and $P_{xx} = \left(\frac{\partial^2 P}{\partial x_i \partial x_j}\right)_{\{n\times n\}}$.

From Ito's formula, if $x(t) \in R_n$, then

$$dP(x(t),t) = LP(x(t),t)\, dt + P_x(x(t),t)g(x(t),t)dB(t).$$

3. Extinction analysis

This section will analyze the factors leading to the extinction of the infectious diseases identified in system 2, particularly in the context of a white noise stochastic disturbance.

Theorem 3.1

If $\sigma_2 > \frac{\beta}{2(\gamma+\mu+\alpha)}$, then two infectious diseases of system (2) go to extinction almost surely $(a.s,)$.

Proof:

Applying Ito's formula to the system (2), we have

$$d\, lnI(t) = \left[\frac{\beta S}{1 + b_1 S + b_2 I} - (\gamma + \mu + \alpha) - \sigma_2^2 \frac{S^2}{2(1 + b_1 S + b_2 I)}\right] dt + \sigma_2 \frac{S}{1 + b_1 S + b_2 I} dB\_2(t).$$

Integrating both side from 0 to t, we have

$$ln\, I(t) = ln\, I(0) - \frac{\sigma_2^2}{2} \int_0^t \left(\frac{S(\tau)}{1+b_1 S(\tau)+b_2 I(\tau)} - \frac{\beta}{\sigma_2^2}\right)^2 d\tau + \frac{\beta^2}{2\sigma_2^2}\, t + M(t) - (\gamma + \mu + \alpha)t.$$

Here,

$$M(t) = \int_0^t \sigma_2 \frac{S(\tau)}{1+b_1 S(\tau)+b_2 I(\tau)}\, dB(\tau).$$

The function $M(t)$ is also known as the local continuous martingale with $M(0) = 0$, and by the following Lemma (3.1), we have

$$lim_{\{t\to\infty\}} \frac{M(t)}{t} = 0.$$

Therefore,

$$\frac{lnI(t)}{t} \leq \frac{lnI(0)}{t} + \frac{\beta^2}{2}\sigma_2^2 + \frac{M(t)}{t} - (\gamma + \mu + \alpha).$$

Taking the limit superior of both sides of, we have

$$lim_{\{t\to\infty\}} sup \frac{I(t)}{t} \leq \frac{\beta^2}{2\sigma_2^2} - (\gamma + \mu + \alpha) < 0 \text{ if } \sigma_2 > \frac{\beta}{2(\gamma+\mu+\alpha)}.$$

Therefore, if $\sigma_2 > \frac{\beta}{2(\gamma+\mu+\alpha)}$, then $lim_{\{t\to\infty\}}\, I(t) = 0$. This completes the proof.

Lemma 3.1

From the strong law of large numbers for martingales (21), let $(S(t), I(t))$ be a solution of system (2) with non-negative initial value $(S(0), I(0))$, then

$$lim_{\{t\to+\infty\}}\frac{1}{t}\int_0^t \sigma\frac{S(\tau)I(\tau)}{1+b_1S(\tau)+b_2I(\tau)}\,dB(\tau)=0,$$

$$lim_{\{t\to+\infty\}}\frac{1}{t}\int_0^t \sigma\ S(\tau)I(\tau)\,dB(\tau)=0.$$

4. Numerical validation

In this section, we will conduct numerical simulations utilizing R software to demonstrate the extinction of infectious disease on the system (2). The numerical approach derived from Milstein's higher order technique (22) implemented on the stochastic system (2) under consideration is provided by

$$S_{j+1}=S_j+S_j[\left(\lambda-\frac{\beta S_jI_j}{1+b_1S_j+b_2\,I_j}-\mu S_j-\gamma I_j\right)\Delta t+\sigma_1\zeta_j\sqrt{(\Delta t)}+\frac{1}{2}\sigma_1^2\Delta t(\zeta_j^2-1)\,],$$

$$I_{j+1}=I_j+I_j[(\frac{\beta S_jI_j}{1+b_1S_j+b_2\,I_j}-(\gamma+\mu+\alpha)I_j)\Delta t+\sigma_2\epsilon_j\sqrt{(\Delta t)}+\tfrac{1}{2}\sigma_2^2\Delta t(\epsilon_j^2-1)\,].$$

where ζ_j and ϵ_j are two independent Gaussian random variables of normal distribution $N(0,1)$ for $j=1,2,\ldots,n$. All numerical simulations reported here are carried out with the choice of time stepping $\Delta t=0.01$. In this section, we always take the following parameter values: $\mu=0.1,\gamma=0.1,\alpha=0.1,b\_1=0.7,b\_2=0.7,\lambda=0.2$.

(1a) **(1b)**

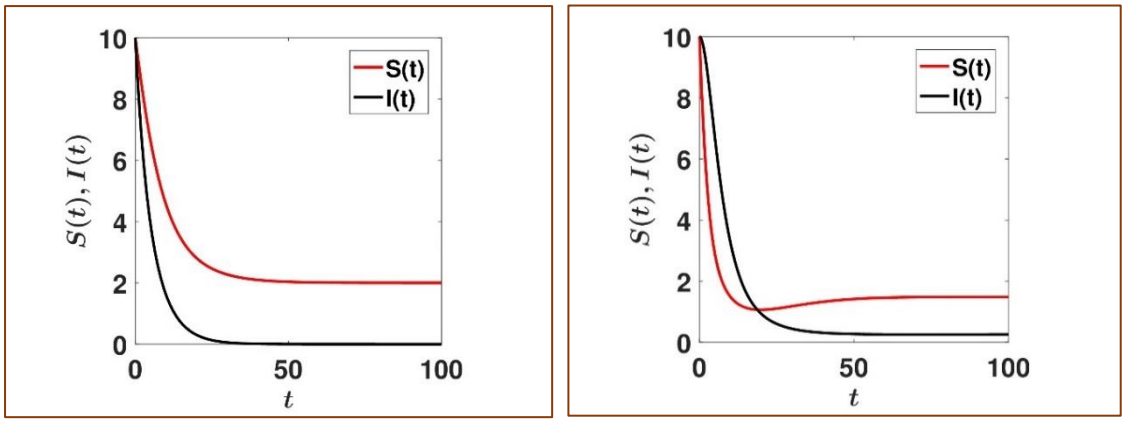

Figure 1: Snapshots of contour pictures of the time evolution of susceptible and infected compartment in the system (1). Figure shows (a) disease free state for $\beta=0.15$ and (b) endemic state for $\beta=0.45$ for the parameter values: $\mu=0.1,\gamma=0.1,\alpha=0.1,b_1=0.7,b_2=0.7,\lambda=0.2$.

(2a) **(2b)**

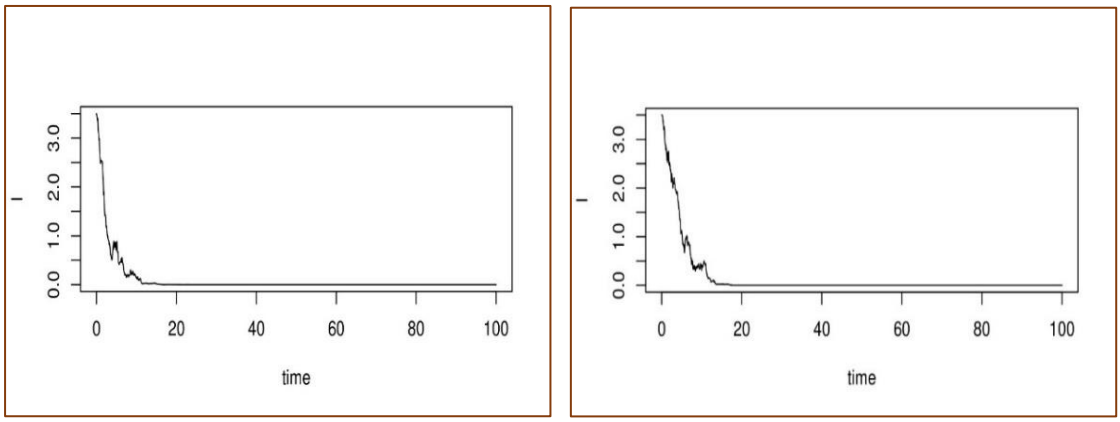

Figure 2: Figure shows stochastic time series of infected compartment of system (2) for (a) $\sigma_1 = \sigma\_2 = 0.5, \beta = 0.15$ and (b) $\sigma_1 = \sigma_2 = 0.8, \beta = 0.15$. Other parameter values are as same as figure-1.

(3a) **(3b)**

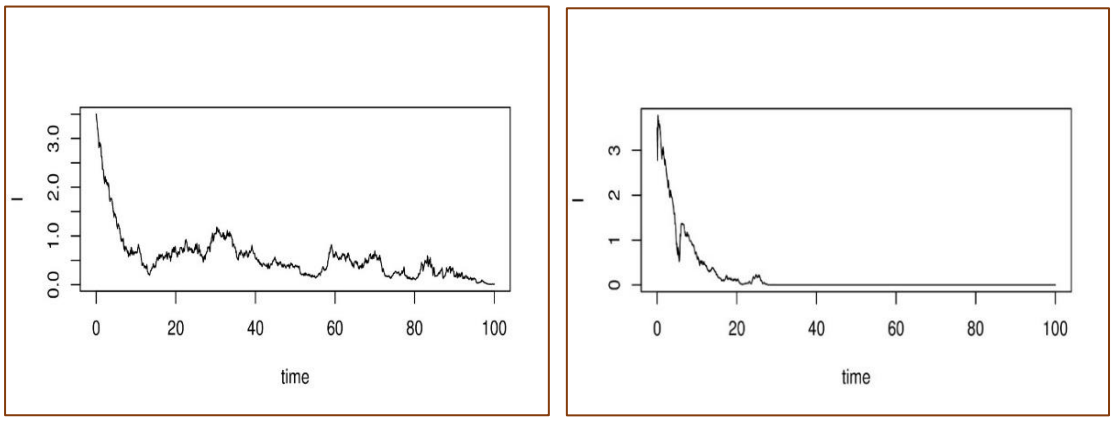

Figure 3: Figure shows stochastic time series of infected compartment of system (2) for (a) $\sigma_1 = \sigma_2 = 0.5, \beta = 0.45$ and (b) $\sigma_1 = \sigma_2 = 2.1, \beta = 0.45$. Other parameter values are as same as figure-1.

To utilize our findings, derived in Section 3, the initial numerical time series is generated for the deterministic system (1) with the above-mentioned parameter values (See figure 1). In this illustration, we depict time series of disease-free equilibrium $(S, 0)$ for $\beta = 0.15$ and endemic equilibrium (S, I) for $\beta = 0.45$. Moreover, we display several numerical time series simulation findings for the system (2) to demonstrate the influence of noise on the system dynamics. keeping fix the parameter $\beta = 0.15$, we see that the disease goes to extinction almost surely for the stochastic model (2), for $\sigma_2 < \frac{\beta}{2(\gamma+\mu+\alpha)}$ (see fig 2a ($\sigma\_i = 0.5, i = 1,2$)) or $\sigma_2 > \frac{\beta}{2(\gamma+\mu+\alpha)}$ (see fig 2b ($\sigma\_i = 0.8, i = 1,2$)).

Finally, keeping fix the parameter β at 0.45, we see that the disease go to extinction almost surely for the stochastic model (2), for $\sigma_2 < \frac{\beta}{2(\gamma+\mu+\alpha)}$ (see fig 2a ($\sigma\_i = 0.5, i = 1,2$)) or $\sigma_2 > \frac{\beta}{2(\gamma+\mu+\alpha)}$ (see fig 2b ($\sigma\_i = 2.1, i = 1,2$)).

5. Conclusion

Epidemic models of the SI type have garnered significant interest in research over an extended period. Recently, the primary emphasis has shifted towards exploring potential control mechanisms through the use of stochastic differential equations. Stochastic modelling serves as a robust and effective approach for addressing the complexities of highly nonlinear natural phenomena. In light of this, the deterministic model has been expanded into a stochastic differential equation model by integrating multiplicative noise components. In this study, we have derived the conditions for stochastic extinction. Our findings indicate that substantial white noise stochastic disturbances can result in the extinction of epidemics.

6. Data availability

There is no data associated with this paper.

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