



# The asymptotic behavior of a stochastic vaccination model with backward bifurcation



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## ABSTRACT

In this paper, we aim to explore the effect of environmental fluctuation on a deterministic vaccination model that exhibits backward bifurcation. First, we prove that the stochastic model admits a unique and global positive solution. Next, by investigating the asymptotic behavior of the stochastic model around the disease free equilibrium, we find that due to the influence of environmental fluctuation the disease dies out even though it may still persist for the deterministic model with backward bifurcation. We also estimate the probability distribution for the disease extinction time. Then, we derive sufficient conditions for the solution of the stochastic model to fluctuate around the endemic equilibrium, and thus we prove the ergodicity of the stochastic model. Our theoretical results are verified by computer simulations and numerical comparison results of the stochastic model and deterministic version is also given. Finally, numerical simulations of a stochastic reaction diffusion model with multiplicative noise are presented to illustrate the combined effects of spatial movement of individuals and environmental noise on the spread of disease.

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## 1. Introduction

Due to changes in meteorological conditions, variability within and between individuals, and other environmental factors [1], the research on the influence of environmental noise on epidemic models has attracted tremendous attention in recent years [2–5]. For human infectious diseases, the nature of epidemic growth and spread is inherently random owing to the unpredictability of individuals contacts [6,7]. Hence, the variability and stochasticity of the environment are fed through to the state of the epidemics [8,9]. Stochastic differential equation models could be a more appropriate way of modeling infectious diseases. Particularly, the stochastic vaccination models have been investigated under the assumption that the vaccinated individuals could not be infected [10–12] or the vaccinated individuals still could be infected [13,14] because of the partial effectiveness of the vaccine.

Actually, under the assumption of completely effectiveness of the vaccine, Zhao et al. [10] found that the conditions for extinction and persistence in the stochastic model were much weaker than in the corresponding deterministic model, and Lin et al. [11] studied the asymptotic stability of the stochastic SISV model and the existence of a stationary distribution. Taking the partial effectiveness of the vaccine into account, Tornatore et al. [13] constructed another version of stochastic vaccination model and analyzed the stability of the disease free equilibrium. Among most of these existing stochastic models, however, the corresponding deterministic models did not occur backward bifurcation. As it is known, when there exists

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a backward bifurcation in the deterministic model, the disease cannot eliminate even if the basic reproduction number is less than unity. Therefore, it is natural for us to consider whether introducing environmental noise can eliminate the disease in this case.

Motivated by the above consideration, we will fill this gap by including random fluctuation into a deterministic vaccination model [15] that exhibits backward bifurcation. Considering the partial effectiveness of the vaccine, Arino et al. [15] constructed the following deterministic model

$$\begin{cases} S'(t) = (1 - \alpha)\mu N - \mu S(t) - \beta \frac{S(t)I(t)}{N} - \varphi S(t) + \theta V(t) + \nu R(t), \\ I'(t) = \beta \frac{S(t)I(t)}{N} + \sigma \beta \frac{V(t)I(t)}{N} - (\mu + \gamma)I(t), \\ R'(t) = \gamma I(t) - (\mu + \nu)R(t), \\ V'(t) = \alpha \mu N + \varphi S(t) - (\mu + \theta)V(t) - \sigma \beta \frac{V(t)I(t)}{N}, \end{cases} \quad (1.1)$$

where  $S(t)$ ,  $I(t)$ ,  $R(t)$ ,  $V(t)$  denote the number of the susceptible, infective, recovered, and vaccinated individuals at time  $t$ , respectively. Here, the parameter  $\mu$  is the natural death rate of each state which is assumed to be equal to the birth rate,  $\beta$  is the transmission coefficient,  $\varphi$  is the vaccination rate,  $\theta$  is the waning rate of the vaccine,  $\gamma$  is the recovery rate, and  $\nu$  is the rate at which recovered individuals lose immunity. In addition, the parameter  $\alpha \in [0, 1]$  denotes the proportion of vaccination for the newborns, and  $\sigma \in [0, 1]$  measures the efficacy of the vaccine-induced protection against infection. Here,  $\sigma = 0$  means that the vaccine is completely effective in preventing infection, while  $\sigma = 1$  indicates that the vaccine is utterly ineffective. Since the total population  $N$  is constant, the system (1.1) can be rewritten in terms of proportions as

$$\begin{cases} S'(t) = (1 - \alpha)\mu - \mu S(t) - \beta S(t)I(t) - \varphi S(t) + \theta(1 - S(t) - I(t) - R(t)) + \nu R(t), \\ I'(t) = \beta S(t)I(t) + \sigma \beta(1 - S(t) - I(t) - R(t))I(t) - (\mu + \gamma)I(t), \\ R'(t) = \gamma I(t) - (\mu + \nu)R(t), \end{cases} \quad (1.2)$$

where  $S(t)$ ,  $I(t)$ ,  $R(t)$  denote the proportions in the susceptible, infective, and recovered states, respectively, and  $V(t) = 1 - S(t) - I(t) - R(t)$  is the proportion of the vaccinated individuals. Clearly, the model (1.2) always has a disease free equilibrium

$$E_0 = (S_0, 0, 0), \quad S_0 = \frac{\theta + \mu(1 - \alpha)}{\mu + \theta + \varphi}, \quad V_0 = 1 - S_0 = \frac{\varphi + \mu\alpha}{\mu + \theta + \varphi}.$$

Employing the next generation operator approach [15,16], the basic reproduction number of the system (1.2) is

$$R_v = \frac{\beta(S_0 + \sigma V_0)}{\mu + \gamma} = \frac{\beta(\mu + \theta + \sigma\varphi - \mu\alpha(1 - \sigma))}{(\mu + \gamma)(\mu + \theta + \varphi)}.$$

In terms of [15], there may occur a backward bifurcation of the deterministic model (1.2), and thus the disease free equilibrium  $E_0$  is locally stable instead of globally stable even if  $R_v < 1$ .

There are several possible ways to introduce random fluctuations in the epidemic models [17–20]. In general, one of the standard approaches is that the parameter involved in the model fluctuate around a mean value due to continuous fluctuations in the environment [21–24]. Instead, our basic approach is analogous to that of [25–27]. We assume that the environmental influence on the individuals is described by stochastic perturbations and it is proportional to each state  $S(t)$ ,  $I(t)$ ,  $R(t)$ . Then, we formulate the stochastic model by introducing the multiplicative noise terms into the deterministic system (1.2), which is used to model the interaction between the individuals and the environment. Hence, we arrive at a stochastic model as

$$\begin{cases} dS(t) = ((1 - \alpha)\mu - \mu S(t) - \beta S(t)I(t) - \varphi S(t) + \theta(1 - S(t) - I(t) - R(t)) + \nu R(t))dt + D_1 S(t) dW_1(t), \\ dI(t) = (\beta S(t)I(t) + \sigma \beta(1 - S(t) - I(t) - R(t))I(t) - (\mu + \gamma)I(t))dt + D_2 I(t) dW_2(t), \\ dR(t) = (\gamma I(t) - (\mu + \nu)R(t))dt + D_3 R(t) dW_3(t), \end{cases} \quad (1.3)$$

where  $W_1(t)$ ,  $W_2(t)$ ,  $W_3(t)$  are independent standard Brownian motions, and  $D_1$ ,  $D_2$ ,  $D_3$  are the intensities of the standard Gaussian white noises, respectively. Through investigating the stochastic model (1.3), we will show how the environmental noise affects the dynamics of the deterministic vaccination model (1.2) with backward bifurcation. Note that the model (1.1) assumes that individuals experience the same homogeneous environment and the population are well fixed. In reality, the environment in which a population lives is often heterogeneous making it necessary to distinguish the locations [28–30]. Thus we numerically investigate a stochastic reaction diffusion model with multiplicative noise to show the combined effects of spatial movements of individuals and environmental noise on disease spreading as a further remark.

The paper is organized as follows. The existence of the unique global positive solution is shown in Section 2. The asymptotic behavior of the stochastic model around the disease free equilibrium and the probability distribution for the disease extinction time are investigated in Section 3. Sufficient conditions for the solution of the stochastic model to fluctuate around the endemic equilibrium and the ergodicity of the stochastic model are analyzed in Section 4. Numerical comparison results of the stochastic model and deterministic version are presented in Section 5. A stochastic reaction diffusion model with multiplicative noise is further illustrated by computer simulations in Section 6. In Section 7, we give a brief conclusion.

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