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Analysis of a Kind of Stochastic Dynamics Model with Nonlinear Function*

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Abstract In this paper, we establish stochastic differential equations on the basis of a nonlinear deterministic model and study the global dynamics. For the deterministic model, we show that the basic reproduction number $\Re_0$ determines whether there is an endemic outbreak or not: if $\Re_0 < 1$, the disease dies out; while if $\Re_0 > 1$, the disease persists. For the stochastic model, we provide analytic results regarding the stochastic boundedness, perturbation, permanence and extinction. Finally, some numerical examples are carried out to confirm the analytical results. One of the most interesting findings is that stochastic fluctuations introduced in our stochastic model can suppress disease outbreak, which can provide us some useful control strategies to regulate disease dynamics.

Keywords Nonlinear incidence, Stochastic differential equation, Stationary distribution, Permanence, Extinction.

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1. Introduction

Bilinear and standard incidences have been frequently used in many epidemic models [21]. Several different forms of incidences have been proposed by some researchers. Let $S(t)$ and $I(t)$ be the numbers of susceptible and infective individuals at time t, respectively. Capasso and Serio [4] introduced a saturated incidence $Sf(I)$ into epidemic models to study of the cholera epidemic spread in Bari in 1973. The nonlinear incidences of the forms $\beta I^p S^q$ and $\beta I^p S/(1 + aI^q)$ were proposed by Liu et al. [19]. Epidemic models with the incidence $\beta I^p S^q$ had also been studied in [14]. An SEIRS epidemic model with the saturation incidence $\beta SI/(1 + aS)$ was examined in [8]. Epidemic models with the incidence $\beta I^p S/(1 + aI^q)$ had been investigated in [28]. The nonlinear incidences of the form $\beta(I + \upsilon I^p)S$ proposed by van den Driessche and Watmough [7] was used in [29]. The more general forms of nonlinear incidence were considered in [27, 30]. In view of the fact that the transmission mechanism of many infectious diseases is not fully known, increasing attention has been paid to infectious disease models with nonlinear incidence in recent years. In [13], the global stability of a class of nonlinear epidemic models is considered.

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Stochastic models could be a more appropriate way of modeling epidemics in many circumstances [3,11,12,15–18,22,25,26,31,32]. For example, stochastic models are able to take care of randomness of infectious contacts occurring in the latent and infectious periods [17,18,26,31]. It also has been showed that some stochastic epidemic models can provide an additional degree of realism in comparison with their deterministic counterparts [2,6,9]. Many realistic stochastic epidemic models can be derived based on their deterministic formulations. Allen [1] provided a great introduction to the methods of the methods of derivation for various types of stochastic models including stochastic differential equation (SDE) epidemic models. Liu et al. [16] established a deterministic model of nonlinear incidence rate, and studied the global stability of the model by the basic reproduction number of the model. Then, a stochastic model is formulated on the basis of the deterministic model, and the perturbation, persistence and extinction of the stochastic model in the deterministic model are studied. Britton [2] gave an excellent survey on SDE epidemic models which presented the exact and asymptotic properties of a simple stochastic epidemic model, and was illustrated by studying effects of vaccination and inference procedures for important parameters such as the basic reproduction number and the critical vaccination coverage. Gray [9] formulated a SDE SIS epidemic model, and proved that the model has a unique global positive solution and established conditions for extinction and persistence of infectious individuals.

There are different possible approaches to including random effects in the model, and both of which are from a biological and mathematical perspective [20]. The general stochastic differential equation SIRS model introduced in this manuscript adopts the approach by Mao et al. [23], which has been pursued in [3, 11, 12, 15–18, 25, 26, 31, 32], and assume that the parameters involved in the model always fluctuate around some average value due to continuous fluctuation in the environment. Following their approach, we will focus on a SDE SIR model with nonlinear incidence rate.

The rest of this paper is organized as follows: In Section 2, we find deterministic models from the literature and describe the results of their deterministic models. Considering the methods mentioned above, a stochastic model is formulated on the basis of deterministic model. In Section 3, we first prove the existence of global positive solutions for stochastic models. Secondly, we prove the extinction of diseases. Thirdly, we prove the perturbation of disease-free equilibrium points and the existence of stationary distribution for stochastic models. Finally, we prove the persistence in mean. In Section 4, the numerical examples are carried out to illustrate the main theoretical results. In Sections 5, we provide a brief discussion and the summary of the main results.

2. Model description

2.1. The deterministic SIR model

In [13], Li et al. formulated a nonlinear deterministic epidemiological model in which the nonlinear incidence $Sf(I)$. The authors assume that $f(I)$ is a real locally Lipschitz function at least on $[0, +\infty)$ which satisfies the following conditions:

(i) $f(0) = 0, f(I) > 0$ for $I > 0$;

(ii) $f(I)/I$ is continuous and monotone nonincreasing for $I > 0$, and $\lim\limits_{I \to 0^+} f(I)/I$