The Global Dynamics for a Stochastic SIR Epidemic Model with Vaccination

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Abstract A new stochastic SIR epidemic model with vaccination is established and its dynamical behavior is analyzed. Considering the random effects of vaccination rates and mortality in this model, it is demonstrated that the extinction and persistence of the virus is only correlated with the threshold R_0^s. If $R_0^s < 1$, the disease dies out with probability one. And if $R_0^s > 1$, the disease is stochastic persistent in the means with probability one. In addition, the existence and uniqueness of a smooth distribution are proven using the Itôs formula, and the sufficiency criterion is obtained using the Lyapunov function. Finally, the accuracy and efficiency of the stochastic SIR epidemic model with vaccination in predicting disease transmission trends were verified through simulation. Unlike the singularity of stochastic perturbations in existing infectious disease models, the innovation of this paper is in the addition of multiple stochastic perturbations, especially distinguishing the stochastic perturbations of mortality under vaccination, which are used to study the dynamics of the model.

Keywords Vaccination, random disturbance, smooth distribution, Lyapunov function, stability

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1. Introduction

It is well known that infectious diseases have been the number one killer threatening human life and health. In particular, the spread of COVID-19 has caused great impact on human life and health in recent years. Thus, the prevention and control of infectious diseases have become urgent problems for all countries. And the analysis of infectious diseases requires the establishment of corresponding mathematical models. Therefore, studying how to develop a realistic mathematical model is of great practical significance. The use of mathematical models for the analysis of infectious diseases has yielded a wealth of results. For example, Wen considered that the disease has temporary immunity and proposed the SIR model [1]. And the author ingeniously constructed Lyapunov function to investigate the stabilization of the equilibrium point. In [1], it proved the stability problem related to the equilibrium point and obtained conclusions that when $R_0 < 1$, the disease-free equilibrium is globally asymptotically stable regardless of time delay. But when $R_0 > 1$, the endemic equilibrium is existent while the disease-free equilibrium gets

unstable. Peijiang Liu, Din Anwarud and Zenab [2] are devoted to the study of the dengue epidemic model. They used a randomly perturbed dengue fever model and information intervention factors. Qualitative analysis was conducted on the positive solutions of the model based on stochastic differential equations. By constructing Lyapunov functions, a basic recurrence number scheme is introduced to ensure the exponential stability.

With the development of biotechnology, experts found that vaccination can effectively slow down the diffusion of infectious diseases and thus reduce morbidity and mortality [3–5]. Therefore, vaccination has become an effective measure to prevent various infectious diseases. Over time, more experts are considering vaccination as a factor when studying infectious diseases [6–8]. In 2014, Chauhan S, Misra O P and Dhar J introduced vaccination rates in their original SIR model [9]. In this paper, the linear stability and global stability of the two models were addressed, and the existence of disease-free and epidemic equilibrium points of the two models were compared. It was analyzed that the local and global stability of the model is determined by the underlying reproduction number. Afterward, Maurício de Carvalho João P. S [10] introduced logistic growth into the SIR model and combined it with vaccination, studying the bifurcation issues of the model. Finally, a parameter space (R_0, p) was established to evaluate the proportion of vaccinated individuals necessary to eliminate the the disease and to conclude how the vaccination may affect the outcome of the epidemic. In 2023, the paper [11] further considered the reduction of vaccine costs and proposes several options of the stochastic SIR epidemics model with limited treatment. It demonstrated the efficiency of different vaccination strategies. Finally, a method was presented to obtain the optimal vaccination strategy that minimizes the cost functional. Afterwards, Changjin Xu investigated the infectious disease model, using COVID-19 as an example [12]. The study considered factors such as incubation times, vaccine effectiveness, and quarantine periods in the spread of the virus in symptomatically contagious individuals. Additionally, nonlinear analysis was employed to illustrate some findings concerning the ergodic aspect of the stochastic model.

Indeed, regardless of the infectious disease model utilized for analysis, white noise originating from real-life environments will inevitably impact the model to some extent. Din Anwarud developed and analyzed a random hepatitis B model considering propagation coefficient delay and CTL immune response categories through research. He investigated whether the model has a unique global solution and further analyzed the extinction and persistence of the disease. The research proved that the ergodic stationary distribution exists under certain conditions. From this, it can be inferred that white noise plays an important role in controlling infection [13]. Hence, the study of stochastic epidemic models becomes more relevant. Consequently, an increasing number of researchers have incorporated random disturbances into infectious disease models and analyzed various system properties such as stability [14–18]. For instance, in [19], Khan T et al. proposed a stochastic model for novel coronaviruses based on the assumption that only transmission rates fluctuate stochastically, and used Lyapunov functions to find conditions for extinction and persistence. The paper [28] provided insights into the impact of information campaigns on the spread of stochastic hepatitis. In [21], the authors also considered the random fluctuations in infection and recovery rates caused by environmental and weather variations. They proposed a stochastic infectious disease model that incorporates vaccination and saturation treatment. They then applied the random