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Stochastic stability and instability of an epidemic model with relapse

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A B S T R A C T

In this paper, we present a stochastic epidemic model with relapse. First, we prove global positivity of solutions. Then we discuss stability of the disease-free equilibrium state and we show extinction of epidemics using Lyapunov functions. Furthermore we show persistence of the disease under some conditions on parameters of the model. Our numerical simulations confirm the analytical results.

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1. Introduction

The whole world is devoted to avoid the outbreaks of epidemics. Investigation of qualitative properties of epidemic models has become a focus in applied mathematics. Some infectious diseases confer temporal or permanent immunity. This kind of diseases can be modeled by *SIR* or *SIRS* models [\[4,14,15\].](#page--1-0) For some other diseases recovered individuals may relapse with reactivation of latent infection and revert back to the infective class. These types of diseases are modeled by *SIRI* models which consist of systems with three compartments: susceptibles, infectives, and removed, labeled by *S*, *I* and *R*. In such models, susceptibles become infectious, then are removed with temporary immunity and then become infectious again. This recurrence of disease is an important feature of some animal and human diseases, for example tuberculosis including human and bovine and herpes [\[3,27\].](#page--1-0) In [\[23\]](#page--1-0) an epidemic model with relapse, which incorporates bilinear incidence rate and constant total population, was formulated by Tudor $[23]$. This system was extended to include nonlinear incidence functions by Moreira and Wang [\[22\].](#page--1-0) Blower [\[3\]](#page--1-0) developed a compartmental model for genital herpes, assuming standard incidence for the disease transmission and constant recruitment rate. A more general SIRI model, formulated as an integro-differential system with the fraction *P*(*t*) of recovered individuals remaining in the recovered class, *t* time units after the recovery expressed in an abstract form has been proposed and analyzed by van den Driessche and Zou [\[24\],](#page--1-0) certain threshold stability results being obtained by particularizing *P*(*t*). See also van den Driessche et al. [\[25\]](#page--1-0) for an analysis of a related SEIRI model. For other works see [\[8,19,28\]](#page--1-0) and the references therein. A deterministic SIRI disease can be modeled as follows [\[26\]:](#page--1-0)

 $\dot{S} = \mu - \beta SI - \mu S$, $\dot{I} = \beta SI - (\lambda + \mu)I + \gamma R,$ (1) $\dot{R} = \lambda I - (\mu + \nu)R$.

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The parameters are positive constants. The constant μ is the recruitment rate of susceptibles corresponding to births and immigration, which we suppose equal to the natural death rate of population. The parameter $β$ is the disease transmission coefficient, λ is the recovery rate and γ denotes the rate by which no-infectious individuals are reverted to the infectious state. The parameter

$$
\mathcal{R}_0 = \frac{\beta}{\mu + \lambda - \frac{\lambda \gamma}{\mu + \gamma}}
$$
 (2)

is the basic reproduction number of system [\(1\).](#page-0-0) It is the average number of secondary transmissions of a single infectious individual in a fully susceptible population. The deterministic model [\(1\)](#page-0-0) has been discussed by Vargas-de-León in [\[26\];](#page--1-0) where the following behaviors of model solutions according to the value of the threshold \mathcal{R}_0 were shown:

(i). If \mathcal{R}_0 < 1, system [\(1\)](#page-0-0) has a unique free-disease equilibrium $E_0(1, 0, 0)$ which is globally asymptotically stable. (ii). If $\mathcal{R}_0 > 1$, in addition to E_0 , system [\(1\)](#page-0-0) has a unique positive equilibrium point $E^*(S^*, I^*, R^*)$ such that

$$
S^* = \frac{1}{\mathcal{R}_0}, \quad I^* = \frac{\mu}{\beta} (\mathcal{R}_0 - 1), \quad R^* = \frac{\mu \lambda}{\beta (\mu + \gamma)} (\mathcal{R}_0 - 1).
$$
 (3)

Moreover, E^* is globally asymptotically stable.

In this work, we consider a stochastic epidemic model, which regards the disease transmission rate involved in the previous deterministic model [\(1\),](#page-0-0) to change randomly by $β = β + σ dB(t)/dt$, where $σ$ is the standard deviation of the noise. The resulting model can be described by the system as follows

$$
dS = (\mu - \beta SI - \mu S)dt - \sigma S dB(t),
$$

\n
$$
dI = (\beta SI - (\lambda + \mu)I + \gamma R)dt + \sigma S dB(t),
$$

\n
$$
dR = (\lambda I - (\mu + \gamma)R)dt.
$$
\n(4)

The effect of the environmental noise on epidemic models [\[6,9,16–18\]](#page--1-0) has been studied intensively. For instance, Gray et al. [\[9\]](#page--1-0) formulated a stochastic version of the classical SIS epidemic model with constant population size. The authors proved uniqueness and positivity of solution. They also gave conditions for extinction and persistence of the disease in the population. Chen and Kang [\[5\]](#page--1-0) presented analysis, for a stochastic SIS epidemic model, on both its almost sure exponential stability and its *p*th moment exponential stability. Then, they gave conditions for the persistence in the mean and also established the existence of a stationary distribution. Lahrouz et al. [\[16\]](#page--1-0) also introduced noise into the SIRS epidemic model with saturated incidence by perturbing the transmission rate. They carried out a detailed analysis on asymptotic stability both almost surely and in *p*th moment. Lin and Jiang [\[18\]](#page--1-0) proposed a perturbed SIR model by white noise. Sufficient conditions for the disease to extinct exponentially, existence of a stationary distribution and asymptotic stability properties were also obtained. However, to the best of our knowledge, there are no results about the stochastic SIRI model (4) with relapse. The rest of the paper is organized as follows. In the next section , we introduce some definitions and needed results throughout the paper. In [Section](#page--1-0) 3, we show positivity and boundedness of solutions of the stochastic model (4) with positive initial condition. [Section](#page--1-0) 4 is devoted to study the disease extinction both in probability and almost surely. In [Section](#page--1-0) 5, we study persistence of the epidemic. The analytical results are illustrated with the help of numerical examples. Finally, we close the paper with discussions and future directions.

2. Preliminaries on stochastic stability

In this section, for completeness of the presentation, we begin by recalling some definitions and theorems about equilibrium states of a stochastic differential equations. For the definition of stability we will use those introduced in [\[20\]](#page--1-0) (see also [\[12\]\)](#page--1-0). Consider the following *d*-dimensional stochastic system:

$$
dX(t) = F(t, X(t))dt + G(t, X(t))dB(t),
$$
\n(5)

where $F(t, X)$ is a function in \mathbb{R}^d defined in $[t_0, +\infty[\times \mathbb{R}^d]$ and $G(t, X)$ is an $d \times m$ matrix, *F* and *G* are locally Lipschitz functions in *X* and $B = {B(t)}_{t>0}$ is an *d*-dimensional Wiener process. We assume that $X = 0$ is a solution of the system (5).

Definition 2.1. The trivial solution $X \equiv 0$ of system (5) is said to be:

1. stochastically stable (or stable in probability) if for every $\varepsilon > 0$

$$
\lim_{x_0\to 0} \mathcal{P}(\sup_{t\geq 0} |X(t,x_0)| > \varepsilon) = 0,
$$

where *X*(*t*, *x*₀) denotes the solution of system (5) with initial condition *X*(0) = *x*₀. Otherwise, it is said to be stochastically unstable (or not stable in probability).

2. globally asymptotically stable (or stochastically asymptotically stable in the large) if it is stochastically stable and for all $x_0 \in \mathbb{R}^d$

$$
\mathcal{P}\left(\lim_{t\to+\infty}X(t,x_0)=0\right)=1.
$$

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