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# Stationary distribution and extinction of a stochastic SEIR epidemic model with standard incidence

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## HIGHLIGHTS

- A stochastic SEIR epidemic model with standard incidence is studied.
- We establish sufficient conditions for the existence of ergodic stationary distribution.
- Our result does not depend on the positive endemic equilibrium $E^*$.
- We establish sufficient conditions for extinction of the disease.

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## ABSTRACT

In this paper, we consider a stochastic SEIR epidemic model with standard incidence. By constructing suitable stochastic Lyapunov functions, we establish sufficient conditions for the existence of ergodic stationary distribution to the model. Our result does not depend on the positive endemic equilibrium $E^*$ of the deterministic system, which improves the previous result to a greater extent. Moreover, we also establish sufficient conditions for extinction of the disease.

## 1. Introduction

Recently, mathematical models have been revealed as a powerful tool to understand the dynamic spread of infectious diseases since the pioneer work of Kermack and McKendrick [1], which provides useful control measures (see e.g. [2,3]). From then on, much attention has been paid to the epidemic models in order to monitoring and curbing the spread of some human diseases. Many authors have made an important progress on SIR epidemic models (see e.g. [1,2,4]), where $S$, $I$ and $R$ denote the fractions of the susceptible, the infective and the recovered hosts in the population, respectively. SIR models assume that the disease has no latent period. However, for some diseases, such as hepatitis B, hepatitis C and AIDS, sometimes has to be passed before an infected individual becomes infectious. Hence an extra class, the class of the exposed

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hosts ($E$), should be introduced in the system, where $E$ denotes the fraction of the exposed population. The model is called SEIR (susceptible–exposed–infected–removed) model, and SEIR models are studied by many scholars (see e.g. [5–7]). The deterministic SEIR model with standard incidence can be expressed as follows

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \dfrac{\beta SI}{N} - \mu S, \\ \dfrac{dE}{dt} = \dfrac{\beta SI}{N} - (\varepsilon + \mu)E, \\ \dfrac{dI}{dt} = \varepsilon E - (\gamma + \mu + \alpha)I, \\ \dfrac{dR}{dt} = \gamma I - \mu R, \end{cases} \tag{1.1}$$

where $N = S+E+I+R$ denotes the number of total population individuals; $\Lambda$ is the birth rate; $\beta$ denotes the average number of adequate contacts; $\mu$ is the natural death rate of $S, E, I$ and $R$, respectively; $\varepsilon$ is the rate at which the exposed individuals become infectious; $\gamma$ represents the recovery rate of infective individuals; $\alpha$ denotes the additional disease caused rate suffered by the infectious individuals. The parameters involved in system (1.1) are positive constants. In system (1.1), the basic reproduction number is $R_0 = \frac{\beta\varepsilon}{(\varepsilon+\mu)(\gamma+\mu+\alpha)}$ which determines the epidemic occurs or not. If $R_0 < 1$, system (1.1) has a unique disease-free equilibrium $E_0 = (S_0, 0, 0, 0) = (\frac{\Lambda}{\mu}, 0, 0, 0)$ and it is a global attractor in the invariant set $\Gamma$. This shows that the disease will die out and the entire population will be susceptible. If $R_0 > 1$, then model (1.1) has two equilibria: a disease-free equilibrium $E_0$ and an endemic equilibrium $E^* = (S^*, E^*, I^*, R^*)$, $E_0$ is unstable and $E^*$ is a global attractor in the interior of $\Gamma$ provided $\alpha = 0$, where $\Gamma = \{(S, E, I, R) : S > 0, E > 0, I > 0, R > 0, S + E + I + R \le \frac{\Lambda}{\mu}\}$. This means that the disease will prevail and persist in a population.

On the other hand, in the real world, biological populations are always affected by the environmental noise (see e.g. [8–15]). For human disease related epidemics, the nature of epidemic growth and spread is random due to the unpredictability in person-to-person contacts [16]. Therefore the variability and randomness of the environment is fed through the state of the epidemic [17]. And in epidemic dynamics, stochastic models may be a more appropriate way of modeling epidemics in many circumstances (see e.g. [18–21]). For example, stochastic models are able to take care of randomness of infectious contacts occurring in the latent and infectious periods [22]. It also has been verified that some stochastic epidemic models can provide an additional degree of realism in comparison with their deterministic counterparts (see e.g. [8,23–32]). Especially, Allee et al. [8] pointed out that stochastic model should suit the question of disease extinction better. Herwaarden et al. [24] suggested that an endemic equilibrium in a deterministic model can disappear in its corresponding stochastic system due to stochastic fluctuations. And Näsell [25] formulated stochastic models to show that some stochastic models are a better approach to describe epidemics for a large range of realistic parameter values in comparison with their deterministic counterparts.

There are different approaches used in the literature to introduce random perturbations into population models, both from a mathematical and biological perspective [30,33]. In this paper, we follow the approach used in Mao et al. [12] and assume that the parameters involved in the model always fluctuate around some average value due to continuous fluctuations in the environment. Following this approach, we study a stochastic SEIR epidemic model with standard incidence where we assume that the environmental noise is proportional to the variables. Some authors (see e.g. [34,35]) have stated that this approach is reasonable and well justified biologically. For $\Delta t$ small, it is appropriate to model $X = (S, E, I, R)^T$ as a Markov process with the following specifications (see [36])

$$\begin{aligned} &\mathbb{E}[S(t+\Delta t) - S(t)|X = x] \approx \left[\Lambda - \frac{\beta SI}{N} - \mu S\right]\Delta t,\ \mathbb{E}[E(t+\Delta t) - E(t)|X = x] \approx \left[\frac{\beta SI}{N} - (\varepsilon+\mu)E\right]\Delta t, \\ &\mathbb{E}[I(t+\Delta t) - I(t)|X = x] \approx [\varepsilon E - (\gamma+\mu+\alpha)I]\Delta t,\ \mathbb{E}[R(t+\Delta t) - R(t)|X = x] \approx [\gamma I - \mu R]\Delta t \end{aligned}$$

and

$$\begin{aligned} &Var[S(t+\Delta t) - S(t)|X = x] \approx \sigma_1^2 S^2 \Delta t,\ Var[E(t+\Delta t) - E(t)|X = x] \approx \sigma_2^2 E^2 \Delta t, \\ &Var[I(t+\Delta t) - I(t)|X = x] \approx \sigma_3^2 I^2 \Delta t,\ Var[R(t+\Delta t) - R(t)|X = x] \approx \sigma_4^2 R^2 \Delta t. \end{aligned}$$

More formally, corresponding to system (1.1), we consider the following stochastic system

$$\begin{cases} dS = \left[\Lambda - \dfrac{\beta SI}{N} - \mu S\right]dt + \sigma_1 S dB_1(t), \\ dE = \left[\dfrac{\beta SI}{N} - (\varepsilon+\mu)E\right]dt + \sigma_2 E dB_2(t), \\ dI = [\varepsilon E - (\gamma+\mu+\alpha)I]dt + \sigma_3 I dB_3(t), \\ dR = [\gamma I - \mu R]dt + \sigma_4 R dB_4(t), \end{cases} \tag{1.2}$$

where $B_1(t), B_2(t), B_3(t)$ and $B_4(t)$ are standard one-dimensional independent Brownian motion, $\sigma_i^2 > 0$ are the intensity of the white noise, $i = 1, 2, 3, 4$. Other parameters are the same as in system (1.1).