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ANALYSIS OF A SUSCEPTIBLE-EXPOSED-INFECTED EPIDEMIC MODEL WITH RANDOM PERTURBATION AND VARYING POPULATION SIZE*†

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Abstract

In this paper, we study a type of susceptible-exposed-infected (SEI) epidemic model with varying population size and introduce the random perturbation of the constant contact rate into the SEI epidemic model due to the universal existence of fluctuations. Under some moderate conditions, the density of the exposed and the infected individuals exponentially approaches zero almost surely are derived. Furthermore, the stochastic SEI epidemic model admits a stationary distribution around the endemic equilibrium, and the solution is ergodic. Some numerical simulations are carried out to demonstrate the efficiency of the main results.

Keywords varying population size; random perturbation; SEI epidemic model; stationary distribution

2000 Mathematics Subject Classification 60H10

1 Introduction

The dynamical properties of infectious diseases around daily life of each human being have already played an important role in better understanding of the epidemic models and the control of infectious diseases. The control of infectious diseases always becomes a vital theme in the field of the epidemiology when the health situation of human being is taken into account. The classical assumption of the epidemic models is that the diseases spread in short duration with their limited effects on the mortality. Apparently, the epidemic models with a fixed population size do not work well with the fast immigration and emigration around the nowadays communities. There have been a number of studies on the threshold of the epidemic

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models, for instance, Zhao *et al.* [1], Zhao and Jiang [2], Liu and Chen [3], Liu and Wei [4] and the related references therein, in which the basic assumption that the population has a fixed size with the constant birth rate and the mortality is not valid any more. The modified epidemic models have therefore been proposed and studied in the recent years, Li and Jin [5,6], Kim and Lin [7], Wei and Liu [8] and the related contributions, for example.

We would like to mention the work by Kim and Lin [7], in which they proposed a deterministic Susceptible-Exposed-Infected epidemic model with varying population size as follows:

$$\begin{aligned}
\dot{S}(t) &= bN(t) - \lambda\frac{S(t)}{N(t)}E(t) - dS(t),\\
\dot{E}(t) &= \lambda\frac{S(t)}{N(t)}E(t) - rE(t) - (d+\alpha_1)E(t),\\
\dot{I}(t) &= rE(t) - kI(t) - (d+\alpha_2)I(t),
\end{aligned} \tag{1}$$

where $S(t)$ is the density of the susceptible individuals to the disease, $E(t)$ represents the members who are exposed (that is, in the latent period) and $I(t)$ denotes the density of the individuals who are infected; b and d are the natural birth rate and the disease-free death rate, respectively; $\frac{\lambda SE}{N}$ is a standard incidence rate where λ is the effective constant contact rate, which is the average number of contacts of the exposed per unit time; The constant k denotes the segregate rate of the infected individuals; α_1 and α_2 are the rates related to death caused by disease respectively; The transition rate from the exposed individuals to the infected individuals is denoted by r. All parameters in model (1) are assumed to be nonnegative and $b>0$, $r>0$.

Based on model (1), in this paper, we set a new variable $N(t) = S(t)+E(t)+I(t)$ as the total population size at time t, the change rate of which is governed by $\dot{N}(t) = (b-d)N(t) - \alpha_1 E(t) - (k+\alpha_2)I(t)$. Let

$$x(t) = \frac{S(t)}{N(t)}, \quad y(t) = \frac{E(t)}{N(t)}, \quad z(t) = \frac{I(t)}{N(t)}, \tag{2}$$

then model (1) thus becomes:

$$\begin{aligned}
\dot{x}(t) &= b - bx(t) - (\lambda-\alpha_1)x(t)y(t) + (k+\alpha_2)x(t)z(t),\\
\dot{y}(t) &= \lambda x(t)y(t) - (b+r+\alpha_1)y(t) + \alpha_1 y^2(t) + (k+\alpha_2)y(t)z(t),\\
\dot{z}(t) &= ry(t) - (k+\alpha_2+b)z(t) + \alpha_1 y(t)z(t) + (k+\alpha_2)z^2(t).
\end{aligned} \tag{3}$$

Obviously, the feasible region of model (3) is $\Gamma = \{(x(t),y(t),z(t)) \in \mathbb{R}^3_+ \,|\, x(t)+y(t)+z(t) = 1\}$. We can compute the disease-free equilibrium and the basic reproduction number of model (3) respectively as $P_0(x,y,z) = (1,0,0)$ and $R_0 = \frac{\lambda}{r+\alpha_1+d}$. We easily show that $P_0(1,0,0)$ is globally asymptotically stable in the region Γ if $R_0 < 1$.