Journal of Nonlinear Modeling and Analysis
Volume 5, Number 1, March 2023, 24–53
http://jnma.ca; http://jnma.ijournal.cn
DOI:10.12150/jnma.2023.24

Dynamics of a Deterministic and Stochastic Susceptible-exposed-infectious-recovered Epidemic Model*

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Abstract We investigate a susceptible-exposed-infectious-recovered (SEIR) epidemic model with asymptomatic infective individuals. First, we formulate a deterministic model, and give the basic reproduction number $\mathcal{R}_0$. We show that the disease is persistent, if $\mathcal{R}_0 > 1$, and it is extinct, if $\mathcal{R}_0 < 1$. Then, we formulate a stochastic version of the deterministic model. By constructing suitable stochastic Lyapunov functions, we establish sufficient criteria for the extinction and the existence of ergodic stationary distribution to the model. As a case, we study the COVID-19 transmission in Wuhan, China, and perform some sensitivity analysis. Our numerical simulations are carried out to illustrate the analytic results.

Keywords Asymptomatic infective individual, Extinction, Persistence, Stationary distribution.

MSC(2010) 92D30, 34D05, 60H10.

1. Introduction

It is well-known that mathematical modeling has become a powerful tool in studying dynamic behaviors and predicting the spreading trend of diseases [2,4,8,12,18]. The establishment of an appropriate epidemic model can clearly describe the transmission mechanism of infectious diseases, and then we analyze it and find effective measures for epidemic control. In 1927, Kermack and Mckendrick [14] first proposed the SIR epidemic model in which the population is separated into three mutually exclusive stages of infection: susceptible, infective and recovered individuals according to their status related to the disease with numbers at the time t denoted by $S(t)$, $I(t)$ and $R(t)$ respectively. Moreover, the basic reproduction number which determines the persistence or extinction of the disease is also described. The SIR model provides a sound theoretical basis for the use of mathematical models to study infectious diseases.

Following the idea of Kermack and Mckendrick, many realistic models have been proposed to investigate the transmission dynamics of infectious diseases (see,

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*The authors were partially supported by the National Natural Science Foundation of China (Grant Nos. 12201499, A010704), Chinese Universities Scientific Fund (Grant Nos. 2452021064, 2452022364) and Qinling National Forest Ecosystem Research Station.

e.g., [3, 25, 34, 36]). For some diseases (e.g., tuberculosis, influenza, measles), on adequate contact with an infective individual, a susceptible individual becomes infected, but it has not been infective yet. This individual remains in the exposed class for a certain latent period before becoming infective [7]. Thus, in [19], the SEIR model was proposed to further consider the exposed individuals. As a basis, the SEIR model has multiple variants with different degrees of complexity, including those admitting controls, i.e., different kinds of incidence rates, constant and feedback vaccination and treatment controls or those involving several interacting patches associated with different towns or regions (see [3, 28, 32, 35, 39] and the references therein). In the reality, for some infectious diseases (e.g., COVID-19), since the strong concealment of the asymptomatic infective individuals is verified, the existence of these individuals has made the control of disease more difficult. Therefore, it is important to take into account the asymptomatic infective individuals in the SEIR model. We assume that any individual can move between the classes according to the following graph.

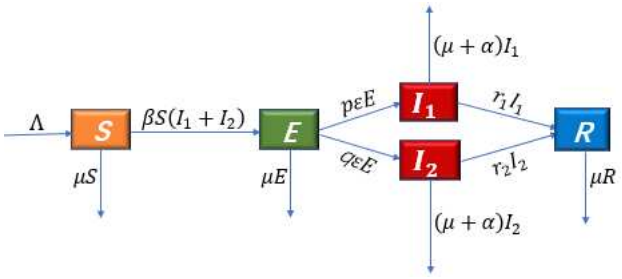

Figure 1. Transfer diagram of the model

In Figure 1, $I_1(t)$ is the number of the infective individuals, which are diagnosed and symptomatic, and $I_2(t)$ is the number of the infective individuals, which are diagnosed but asymptomatic. Thus, the model can be written as a system of differential equations with the form

$$\begin{cases} \dfrac{dS}{dt} = \Lambda - \beta S(I_1 + I_2) - \mu S, \\ \dfrac{dE}{\mathrm{d}t} = \beta S(I_1 + I_2) - (\epsilon + \mu)E, \\ \dfrac{dI_1}{dt} = p\epsilon E - (\mu + \alpha + r_1)I_1, \\ \dfrac{dI_2}{dt} = q\epsilon E - (\mu + \alpha + r_2)I_2, \\ \dfrac{dR}{dt} = r_1 I_1 + r_2 I_2 - \mu R. \end{cases} \tag{1.1}$$

The biological interpretations of the parameters are shown as the table below.