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Analysis on an SEIR Epidemic Model with Logistic Death Rate of Virus Mutation

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Abstract In this paper, we propose an SEIR epidemic model with Logistic death rate of virus mutation. By means of the direct Lyapunov method and the LaSalle's Invariance Principle, the global stability of the disease-free equilibrium is proved. Using algebraic method to construct Lyapunov function, the global stability of the endemic equilibrium is proved. In addition, numerical simulations are done and the influence of parameters in the model on disease transmission is analyzed.

Keywords virus mutation; logistic death rate; global stability; algebraic method

MR(2010) Subject Classification 34A30; 34D05; 34D20; 34D23

1. Introduction

People have been using the infectious disease dynamics method to study the spread of infectious diseases and predict the epidemic disease trend of each arrival. There are many research results on the stability of infectious disease models with bilinear incidence and standard incidence [1–3]. In [4,5], the authors studied the epidemiological models of SI and SVEI with bilinear incidence and by using algebraic approach, they obtained the global asymptotic stability of the disease-free equilibrium and the endemic equilibrium. If there is a virus mutation in the transmission process of infectious diseases, it is easy to cause the diseases out of control. Such as bird flu virus (H7N9), hepatitis B and other diseases. Therefore, the process of studying virus of genetic variation will help to understand diseases and control diseases spread. For infectious diseases with virus mutation, their infectivity is different and the cure methods are different. In [6, 7], the authors studied the global stability of the epidemic model under the conditions of competition and coexistence. In [8, 9], the authors studied the variant epidemic model and discussed the branching problem of model. Korobeinikov studied the SEIR epidemic model of a variety of different virus infections and obtained the global stability of the model [10]. In [11–13], the authors analyzed the virus mutation model with bilinear incidence and discussed the stability of equilibrium points. In the process of spread of infectious diseases, the virus mutation will have a certain impact on the prevention and control of the diseases. Therefore, studying the

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model of virus mutation can better understand transmission rules of the infectious diseases in order to provide theoretical guidance for making preventive measures. In this paper, we consider that the virus of entering susceptible individuals will enter latent period, then some of the latent individuals are transformed into infected individuals. At the same time, the virus is mutated in this process. The infected individuals are divided into the infected individuals before virus mutation and the infected individuals after virus mutation. They are all contagious and spread diseases at standard incidence rate. Based on the previous articles [11–13], we will establish an SEIR epidemic model with Logistic death rate of virus mutation.

The organization of this paper is as follows: In Section 1, we will establish an SEIR epidemic model. In Section 2, we will prove the global stability of the disease-free equilibrium and endemic equilibrium. In Section 3, we will do numerical simulations and analyze the influence of parameters in the model on disease transmission. Finally, we will make a summary for this article.

2. Model description

The virus will mutate during the process of infection and the mutated virus patients are contagious. In this section, we will establish an SEIR epidemic model with Logistic death rate of virus mutation as follows:

$$\begin{cases} \dfrac{\mathrm{d}S(t)}{\mathrm{d}t} = \mu N(t) - \frac{\beta_1 S(t) I_1(t)}{N(t)} - \frac{\beta_2 S(t) I_2(t)}{N(t)} - (d + \frac{\mu N(t)}{K}) S(t), \\ \dfrac{\mathrm{d}E(t)}{\mathrm{d}t} = \frac{\beta_1 S(t) I_1(t)}{N(t)} + \frac{\beta_2 S(t) I_2(t)}{N(t)} - \varepsilon E(t) - (d + \frac{\mu N(t)}{K}) E(t), \\ \dfrac{\mathrm{d}I_1(t)}{\mathrm{d}t} = \varepsilon E(t) - (k_1 + \delta) I_1(t) - (d + \frac{\mu N(t)}{K}) I_1(t), \\ \dfrac{\mathrm{d}I_2(t)}{\mathrm{d}t} = \delta I_1(t) - k_2 I_2(t) - (d + \frac{\mu N(t)}{K}) I_2(t), \\ \dfrac{\mathrm{d}R(t)}{\mathrm{d}t} = k_1 I_1(t) + k_2 I_2(t) - (d + \frac{\mu N(t)}{K}) R(t). \end{cases} \tag{2.1}$$

In model (2.1), the total population $N(t)$ is divided into five compartments $S(t), E(t), I_1(t)$, $I_2(t)$ and $R(t)$ with $N(t) = S(t)+E(t)+I_1(t)+I_2(t)+R(t)$. These variables $S(t), E(t), I_1(t), I_2(t)$ and $R(t)$ represent the number of the susceptible, the exposed, the infected individuals before virus mutation, the infected individuals after virus mutation and the recovered, respectively. Here parameters μ, d, β_1, β_2 and K are positive constants, and δ, ε, k_1 and k_2 are non-negative constants. μ is the birth rate coefficient of the total population, and d is the natural death rate. β_1 is the infection rate coefficient of infected individuals before virus mutation, β_2 is the infection rate coefficient of infected individuals after virus mutation. K is the carrying capacity. δ is the rate that infected individuals before virus mutation becomes infected individuals after virus mutation. ε is the coefficient of the latent individuals becoming infected individuals before virus mutation. k_1 is the rate of recovery infected individuals before virus mutation, k_2 is the rate of recovery infected individuals after virus mutation. In addition, $d + \dfrac{\mu N(t)}{K}$ is the Logistic

death rate of the population [14].

In model (2.1), total population $N(t) = S(t) + E(t) + I_1(t) + I_2(t) + R(t)$ satisfies

$$N'(t) = (\mu - d - \frac{\mu N(t)}{K})N(t).$$

Obviously, $N(t)$ is bounded above as $\mu > d, t \to \infty$. Otherwise, $N(t) \to 0$ as $\mu < d, t \to \infty$, the result is not in accordance with the actual situation.

Let $s(t) = \frac{S(t)}{N(t)}, e(t) = \frac{E(t)}{N(t)}, i_1(t) = \frac{I_1(t)}{N(t)}, i_2(t) = \frac{I_2(t)}{N(t)}, r(t) = \frac{R(t)}{N(t)}$ and $s(t) + e(t) + i_1(t) + i_2(t) + r(t) = 1$. Then model (2.1) turns out to be

$$\begin{cases} \dfrac{\mathrm{d}s(t)}{\mathrm{d}t} = \mu - \mu s(t) - \beta_1 s(t) i_1(t) - \beta_2 s(t) i_2(t), \\ \dfrac{\mathrm{d}e(t)}{\mathrm{d}t} = \beta_1 s(t) i_1(t) + \beta_2 s(t) i_2(t) - (\varepsilon + \mu) e(t), \\ \dfrac{\mathrm{d}i_1(t)}{\mathrm{d}t} = \varepsilon e(t) - (k_1 + \delta + \mu) i_1(t), \\ \dfrac{\mathrm{d}i_2(t)}{\mathrm{d}t} = \delta i_1(t) - (k_2 + \mu) i_2(t), \\ \dfrac{\mathrm{d}r(t)}{\mathrm{d}t} = k_1 i_1(t) + k_2 i_2(t) - \mu r(t). \end{cases} \tag{2.2}$$

Note that the variable $r(t)$ does not appear in the first and fourth equations of system (2.2), hence we only need to consider the subsystem of system (2.2) as follows:

$$\begin{cases} \dfrac{\mathrm{d}s(t)}{\mathrm{d}t} = \mu - \mu s(t) - \beta_1 s(t) i_1(t) - \beta_2 s(t) i_2(t), \\ \dfrac{\mathrm{d}e(t)}{\mathrm{d}t} = \beta_1 s(t) i_1(t) + \beta_2 s(t) i_2(t) - (\varepsilon + \mu) e(t), \\ \dfrac{\mathrm{d}i_1(t)}{\mathrm{d}t} = \varepsilon e(t) - (k_1 + \delta + \mu) i_1(t), \\ \dfrac{\mathrm{d}i_2(t)}{\mathrm{d}t} = \delta i_1(t) - (k_2 + \mu) i_2(t). \end{cases} \tag{2.3}$$

For system (2.3), we get that $\mathrm{n}(t) = s(t) + e(t) + i_1(t) + i_2(t)$ satisfies

$$\mathrm{n}'(t) = \mu - \mu \mathrm{n}(t) - k_1 i_1(t) - k_2 i_2(t),$$

which implies $\mathrm{n}'(t) \le \mu - \mu \mathrm{n}(t)$, thus $\limsup_{t \to \infty} \mathrm{n}(t) \le 1$ only if $\mathrm{n}(0) \le 1$.

It is easy to know that the set

$$D = \{(s(t), e(t), i_1(t), i_2(t)) \in \mathbb{R}^4_+ : s(t) + e(t) + i_1(t) + i_2(t) \le 1\} \tag{2.4}$$

is a positively invariant set. Therefore, we will consider the global stability of system (2.3) on the set D .

3. Existence and stability of equilibrium points

3.1. Existence of equilibrium points

In this subsection, we determine the existence of the equilibrium points of system (2.3). It is straightforward to obtain disease-free equilibrium $p_0 = (s^0, e^0, i_1^0, i_2^0) = (1, 0, 0, 0)$.

The stability of p_0 can be described by using the next generation operator method [15]. According to the notation in [15], the Jacobian matrices F (of new infection terms) and V (of remaining transition terms) are given, respectively [16]. We have

$$F = \begin{pmatrix} 0 & \beta_1 & \beta_1 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \quad V = \begin{pmatrix} \varepsilon+\mu & 0 & 0 \\ -\varepsilon & k_1+\delta+\mu & 0 \\ 0 & -\delta & k_2+\mu \end{pmatrix}.$$

V^{-1} is given by

$$V^{-1} = \begin{pmatrix} \frac{1}{\varepsilon+\mu} & 0 & 0 \\ \frac{\varepsilon}{(\varepsilon+\mu)(\delta+k_1+\mu)} & \frac{1}{\delta+k_1+\mu} & 0 \\ \frac{\delta\varepsilon}{(\varepsilon+\mu)(k_2+\mu)(\delta+k_1+\mu)} & \frac{\delta}{(k_2+\mu)(\delta+k_1+\mu)} & \frac{1}{k_2+\mu} \end{pmatrix}.$$

Thus

$$FV^{-1} = \begin{pmatrix} \frac{\beta_1\varepsilon(k_2+\mu)+\beta_2\delta\varepsilon}{(\varepsilon+\mu)(k_2+\mu)(\delta+k_1+\mu)} & \frac{\beta_1(k_2+\mu)+\beta_2+\delta}{(\delta+k_1+\mu)(k_2+\mu)} & \frac{\beta_2}{k_2+\mu} \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}.$$

Therefore, the basic reproductive number for system (2.3) is

$$R_0 = \frac{\beta_1\varepsilon(k_2+\mu)+\beta_2\delta\varepsilon}{(\varepsilon+\mu)(k_2+\mu)(\delta+k_1+\mu)}. \tag{3.1}$$

Now we turn to discuss a possible endemic equilibrium point $p_1 = (s^*, e^*, i_1^*, i_2^*)$ in the interior of the feasible region D . Here $s^*, e^*, i_1^*, i_2^* > 0$ satisfy the following equilibrium equations:

$$\mu - \mu s^*(t) - \beta_1 s^*(t) i_1^*(t) - \beta_2 s^*(t) i_2^*(t) = 0, \tag{3.2}$$

$$\beta_1 s^*(t) i_1^*(t) + \beta_2 s^*(t) i_2^*(t) - (\varepsilon+\mu) e^*(t) = 0, \tag{3.3}$$

$$\varepsilon e^*(t) - (k_1+\delta+\mu) i_1^*(t) = 0, \tag{3.4}$$

$$\delta i_1^*(t) - (k_2+\mu) i_2^*(t) = 0. \tag{3.5}$$

From (3.5), endemic equilibrium point (s^*, e^*, i_1^*, i_2^*) must satisfy

$$i_2^* = \frac{\delta i_1^*}{\mu+k_2}. \tag{3.6}$$

According to (3.2), (3.4) and (3.6) we get

$$s^* = \frac{\mu}{\mu + \beta_1 i_1^* + \beta_2 \frac{\delta i_1^*}{\mu+k_2}}, \quad e^* = \frac{(\mu+k_1+\delta) i_1^*}{\varepsilon}. \tag{3.7}$$

Substituting s^*, e^*, i_2^* into (3.3), we obtain i_1^* .

$$i_1^* = \frac{\varepsilon\mu\beta_1(\mu+k_2) + \varepsilon\delta\mu\beta_2 - \mu(\varepsilon+\mu)(\mu+k_2)(\delta+k_1+\mu)}{(\varepsilon+\mu)(\mu+k_2)(\delta+k_1+\mu)(\beta_1+\frac{\beta_2\delta}{\mu+k_2})} = \frac{\mu(R_0-1)}{\beta_1+\frac{\beta_2\delta}{\mu+k_2}}. \tag{3.8}$$

According to (3.6)–(3.8), we obtain the following Theorem 3.1.

Theorem 3.1 *When $R_0 \leq 1$, system (2.3) has only a disease-free equilibrium p_0. When $R_0 > 1$, the system (2.3) has endemic equilibrium p_1 in addition to the disease-free equilibrium p_0.*

3.2. Global stability of the disease-free equilibrium point

In this subsection, by means of the direct construction Lyapunov method and the LaSalle's Invariance Principle to prove global asymptotical stability of the disease-free equilibrium p_0.

Theorem 3.2 *If $R_0 \leq 1$, then the disease-free equilibrium p_0 is globally asymptotically stable.*

Proof Consider the following Lyapunov function

$$V(s,e,i_1,i_2) = s - 1 - \ln s + e + \frac{\beta_1(\mu+k_2)+\beta_2\delta}{(\mu+k_1+\delta)(\mu+k_2)}i_1 + \frac{\beta_2}{\mu+k_2}i_2.$$

The derivative of V along solutions of system (2.3) is

$$\begin{aligned}
\frac{\mathrm{d}V}{\mathrm{d}t}\Big|_{(2.3)} =& -\mu(s+\frac{1}{s}-2)+\beta_1 i_1-(\varepsilon+\mu)e+\frac{\beta_1(\mu+k_2)+\beta_2\delta}{(\mu+k_1+\delta)(\mu+k_2)}\varepsilon e-\\
&\frac{\beta_1(\mu+k_2)+\beta_2\delta}{\mu+k_2}i_1+\frac{\beta_2\delta}{\mu+k_2}i_1\\
=& -\mu(s+\frac{1}{s}-2)-(\varepsilon+\mu)e+\frac{\beta_1(\mu+k_2)+\beta_2\delta}{(\mu+k_1+\delta)(\mu+k_2)}\varepsilon e\\
=& -\mu(s+\frac{1}{s}-2)-(\varepsilon+\mu)\big(1-\frac{\beta_1(\mu+k_2)+\beta_2\delta}{(\varepsilon+\mu)(\mu+k_1+\delta)(\mu+k_2)}\varepsilon\big)e\\
=& -\mu(s+\frac{1}{s}-2)-(\varepsilon+\mu)\big(1-\frac{\beta_1\varepsilon(k_2+\mu)+\beta_2\delta\varepsilon}{(\varepsilon+\mu)(k_2+\mu)(\delta+k_1+\mu)}\big)e\\
=& -\mu(s+\frac{1}{s}-2)-(\varepsilon+\mu)(1-R_0)e.
\end{aligned}$$

Obviously, $s+\frac{1}{s} \geq 2$. When $R_0 \leq 1$, we obtain $\frac{\mathrm{d}V}{\mathrm{d}t}|_{(2.3)} \leq 0$. Denote

$$\begin{aligned}
M =& \{(s,e,i_1,i_2)|\frac{\mathrm{d}V}{\mathrm{d}t}|_{(2.3)}=0\}\\
=& \{(s,e,i_1,i_2)|s=1,e=0,i_1=i_1(0)\exp(-(\mu+k_1+\delta)t),i_2=i_2(0)\exp(-(\mu+k_2)t)\}.
\end{aligned}$$

Here $i_1 = i_1(0)\exp(-(\mu+k_1+\delta)t) \to 0$ $(t \to +\infty)$, $i_2 = i_2(0)\exp(-(\mu+k_2)t) \to 0$ $(t \to +\infty)$. Thus, p_0 is the only largest positive invariant subset of M . Therefore, by the LaSalle's Invariance Principle [17], the disease-free equilibrium p_0 is globally asymptotically stable on the set D when $R_0 \leq 1$. □

3.3. Global stability of the endemic equilibrium point

In this subsection, we use algebraic method [4] to prove the global asymptotical stability of the endemic equilibrium p_1.

Theorem 3.3 *If $R_0 > 1$, then the endemic equilibrium p_1 is globally asymptotically stable.*

Proof We define a Lyapunov function

$$V(s,e,i_1,i_2) =(s-s^*-s^*\ln\frac{s}{s^*})+a_1(e-e^*-e^*\ln\frac{e}{e^*})+a_2(i_1-i_1^*-i_1^*\ln\frac{i_1}{i_1^*})+$$
$$a_3(i_2-i_2^*-i_2^*\ln\frac{i_2}{i_2^*}), \tag{3.9}$$

where $a_j>0$ $(j=1,2,3)$ are left unspecified. For simplicity, denote

$$y_0=\frac{s}{s^*},\ y_1=\frac{e}{e^*},\ y_2=\frac{i_1}{i_1^*},\ y_3=\frac{i_2}{i_2^*}$$

then the derivative of function $V(s,e,i_1,i_2)$ along solutions of system (2.3) is given by

$$\begin{aligned}\frac{\mathrm{d}V}{\mathrm{d}t}|_{(2.3)} =&(1-\frac{1}{y_0})(\mu-\mu y_0s^*-\beta_1y_0y_2s^*i_1^*-\beta_2y_0y_3s^*i_2^*)+a_1(1-\frac{1}{y_1})(\beta_1y_0y_2s^*i_1^*+\\ &\beta_2y_0y_3s^*i_2^*-(\varepsilon+\mu)y_1e^*)+a_2(1-\frac{1}{y_2})(\varepsilon y_1e^*-(\mu+k_1+\delta)y_2i_1^*)+\\ &a_3(1-\frac{1}{y_3})(\delta y_2i_1^*-(\mu+k_2)y_3i_2^*)\\ =&C-\mu s^*y_0-(a_1(\varepsilon+\mu)e^*-a_2\varepsilon e^*)y_1-(a_2(\mu+k_1+\delta)i_1^*-a_3\delta i_1^*-\beta_1s^*i_1^*)y_2-\\ &(a_3(\mu+k_2)i_2^*-\beta_2s^*i_2^*)y_3-(\beta_1s^*i_1^*-a_1\beta_1s^*i_1^*)y_0y_2-(\beta_2s^*i_2^*-a_1\beta_2s^*i_2^*)y_0y_3-\\ &\mu\frac{1}{y_0}-a_1\beta_1s^*i_1^*\frac{y_0y_2}{y_1}-a_1\beta_2s^*i_2^*\frac{y_0y_3}{y_1}-a_2\varepsilon e^*\frac{y_1}{y_2}-a_3\delta i_1^*\frac{y_2}{y_3}\\ \triangleq&G(y_0,y_1,y_2,y_3)\end{aligned}$$

where $C=\mu+\mu s^*+a_1(\varepsilon+\mu)e^*+a_2(\mu+k_1+\delta)i_1^*+a_3(\mu+k_2)i_2^*$. Next, we construct the function set

$$\Gamma=\Big\{y_0,y_1,y_2,y_3,y_0y_2,y_0y_3,\frac{1}{y_0},\frac{y_0y_2}{y_1},\frac{y_0y_3}{y_1},\frac{y_1}{y_2},\frac{y_2}{y_3}\Big\}.$$

There are at most three groups associated with Γ such that the product of all functions within each group is unity. The three groups are, respectively,

$$\{y_0,\frac{1}{y_0}\};\ \ \{\frac{1}{y_0},\frac{y_0y_2}{y_1},\frac{y_1}{y_2}\};\ \ \{\frac{y_1}{y_2},\frac{y_0y_3}{y_1},\frac{y_2}{y_3},\frac{1}{y_0}\}.$$

Further, according to the above groups, we define function

$$\begin{aligned}H(y_0,y_1,y_2,y_3)=&-b_1(y_0+\frac{1}{y_0}-2)-b_2(\frac{1}{y_0}+\frac{y_0y_2}{y_1}+\frac{y_1}{y_2}-3)-\\ &-b_3(\frac{y_1}{y_2}+\frac{y_0y_3}{y_1}+\frac{y_2}{y_3}+\frac{1}{y_0}-4)\end{aligned}$$

with the coefficients b_j $(j=1,2,3)$ left unspecified.

We would like to determine suitable parameters $a_j>0$ $(j=1,2,3)$ and $b_j\geq 0$ $(j=1,2,3)$ such that $G(y_0,y_1,y_2,y_3)=H(y_0,y_1,y_2,y_3)$. Due to the terms $y_1,\ y_2,\ y_3,\ y_0y_2$ and y_0y_3 of function G do not appear in function H, first the coefficients of the terms $y_1,\ y_2,\ y_3,\ y_0y_2$ and

y_0y_3 are all equal to zero in function G, then it follows that

$$\begin{cases} a_1(\varepsilon+\mu)e^* - a_2\varepsilon e^* = 0, \\ a_2(\mu+k_1+\delta)i_1^* - a_3\delta i_1^* - \beta_1 s^* i_1^* = 0, \\ a_3(\mu+k_2)i_2^* - \beta_2 s^* i_2^* = 0, \\ \beta_1 s^* i_1^* - a_1\beta_1 s^* i_1^* = 0, \\ \beta_2 s^* i_2^* - a_1\beta_2 s^* i_2^* = 0. \end{cases} \tag{3.10}$$

Notice that s^*, e^*, i_1^* and i_2^* satisfy that the functions at the right hand side of system (2.3) equal to zero, and it follows from (3.10) that a_1, a_2 and a_3 can be uniquely determined as

$$a_1 = 1, a_2 = \frac{\varepsilon+\mu}{\varepsilon}, a_3 = \frac{\beta_2 s^*}{\mu+k_2}.$$

Consequently, the Lyapunov function (3.9) is specified. Function G is in turn given as

$$\begin{aligned} G(y_0,y_1,y_2,y_3) =& C - \mu s^* y_0 - \mu\frac{1}{y_0} - a_1\beta_1 s^* i_1^* \frac{y_0y_2}{y_1} - a_1\beta_2 s^* i_2^* \frac{y_0y_3}{y_1} - a_2\varepsilon e^* \frac{y_1}{y_2} - \\ & a_3\delta i_1^* \frac{y_2}{y_3} \triangleq \tilde{G}(y_0,y_1,y_2,y_3). \end{aligned}$$

Further, letting $\tilde{G}(y_0,y_1,y_2,y_3) = H(y_0,y_1,y_2,y_3)$ and comparing the coefficients of the like terms between them yields

$$b_1 = \mu s^*,\ b_2 = \beta_1 s^* i_1^*,\ b_3 = \frac{\beta_2\delta s^* i_1^*}{\mu+k_2}. \tag{3.11}$$

So function $H(y_0,y_1,y_2,y_3)$ is also uniquely determined, the derivative of the Lyapunov function is given by

$$\begin{aligned} \frac{\mathrm{d}V}{\mathrm{d}t}|_{(2.3)} =& -b_1(y_0 + \frac{1}{y_0} - 2) - b_2(\frac{1}{y_0} + \frac{y_0y_2}{y_1} + \frac{y_1}{y_2} - 3) - \\ & b_3(\frac{y_1}{y_2} + \frac{y_0y_3}{y_1} + \frac{y_2}{y_3} + \frac{1}{y_0} - 4), \end{aligned}$$

where $b_j > 0$ $(j = 1,2,3)$ are determined by (3.11). According to the relation between the arithmetic and the associated geometric means, we have $\mathrm{d}V/\mathrm{d}t|_{(2.3)} \le 0$ and the equality holds if and only if $y_0 = 1$ and $y_1 = y_2 = y_3$, that is $s = s^*$ and $e/e^* = i_1/i_1^* = i_2/i_2^*$. It can be easily verified that the largest invariant set of system (2.3) on the set $\{(s,e,i_1,i_2) \in \mathbb{R}_+^4 : s = s^*, e/e^* = i_1/i_1^* = i_2/i_2^*\}$ is the singleton $\{p_1\}$. Therefore, by the LaSalle's Invariance Principle [17], it follows that the endemic equilibrium p_1 of system (2.3) is globally stable in the feasible region D when it exists. □

According to Theorem 3.2, the disease-free equilibrium p_0 is globally stable. From Theorem 3.3, we can see that when $R_0 > 1$, the endemic equilibrium p_1 is globally stable. Therefore, it can be determined that there is no Hopf-branching in the SEIR epidemic model with virus mutation.

4. Numerical simulation

In this section, some numerical results of system (2.3) are presented for supporting the analytic results obtained above. The parameter values in Table 1 are derived from [11–14]. Here

we choose initial value $s(0) = 0.7, e(0) = 0.6, i_1(0) = 0.5, i_2(0) = 0.4$.

β_1	β_2	ε	k_1	k_2	δ	R_0	Figure
0.0005	0.0016	0.04	0.0666	0.1428	0.05	0.0011	1
0.0005	0.0016	0.04	[0,1]	[0,1]	0.05	Variation	2
0.7	0.6	0.4	0.0666	0.1428	0.05	3.0418	3
0.7	0.6	0.9	0.0666	0.1428	0.05	3.4220	4
0.7	0.6	0.4	0.0666	0.1428	0.9	2.1932	5
0.7	0.6	0.4	0.2	0.1428	0.05	1.8824	6
0.7	0.6	0.4	0.0666	0.5	0.05	2.7701	7

Table 1 Values of parameters

Here we assume $\mu = 0.1$, we can get from the above Table 1 as follows:

(1) $\mu = 0.1, \beta_1 = 0.0005, \beta_2 = 0.0016, \varepsilon = 0.04, k_1 = 0.0666, k_2 = 0.1428, \delta = 0.05$ then $R_0 = 0.0011 < 1$. According to Theorem 3.2, we know that the disease-free equilibrium p_0 is globally asymptotically stable (see Figure 1).

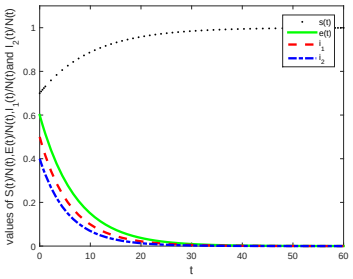

Figure 1 The disease-free equilibrium p_0 is globally stable

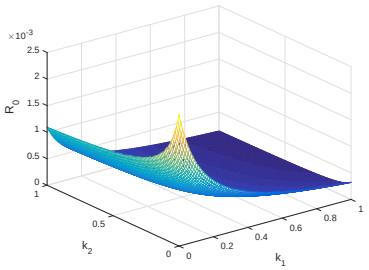

Figure 2 The relationship between the parameters and R_0

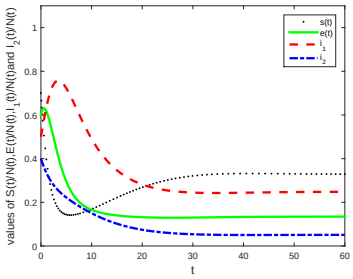

Figure 3 The endemic equilibrium p_1 is globally stable

In the following, we study the relationship between R_0 and the rate k_1 of the recovery rate before mutation, the rate k_2 of the recovery rate after mutation on system (2.3) by numerical analysis (see Figure 2).

(2) $\mu = 0.1, \beta_1 = 0.7, \beta_2 = 0.6, \varepsilon = 0.4, k_1 = 0.0666, k_2 = 0.1428, \delta = 0.05$ then $R_0 = 3.0418 > 1$. According to Theorem 3.3, we know that the endemic equilibrium p_1 is globally stable (see Figure 3).

(3) If parameter $\varepsilon = 0.9$ and other parameters are the same as Figure 3, then $R_0 = 3.4220 > 1$ (see Figure 4). If parameter $\delta = 0.9$ and other parameters are the same as Figure 3, then $R_0 = 2.1932 > 1$ (see Figure 5). If parameter $k_1 = 0.2$ and other parameters are the same as Figure 3, then $R_0 = 1.8824 > 1$ (see Figure 6). If parameter $k_2 = 0.5$ and other parameters are the same as Figure 3, then $R_0 = 2.7701 > 1$ (see Figure 7). According to Theorem 3.3, we know that the endemic equilibrium p_1 is globally stable.

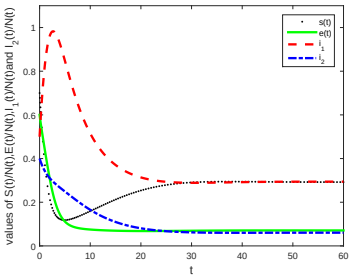

Figure 4 This is the change in ε

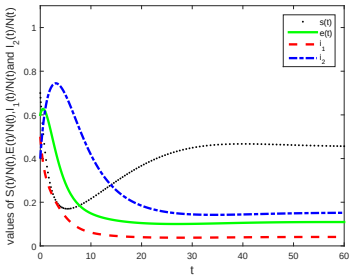

Figure 5 This is the change in δ

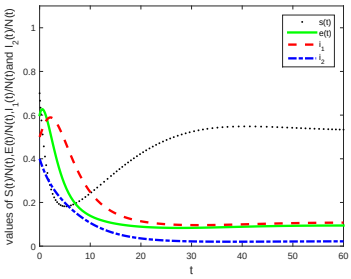

Figure 6 This is the change in k_1

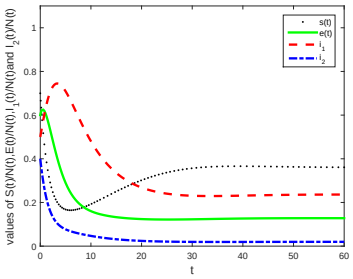

Figure 7 This is the change in k_2

From Figures 3 and 4, it can be seen that the rate ε of the latent individuals becoming infected individuals before virus mutation increases to 2.25 times the original value, then the infected individuals before virus mutation i_1 increases to 1.19 times the original value, the infected individuals after virus mutation i_2 increases to 1.19 times the original value.

From Figures 3 and 5, it can be seen that the rate δ of infected individuals before virus mutation becoming infected individuals after virus mutation increases to 18 times the original value, then infected individuals before virus mutation i_1 reduces to 6 times the original value, infected individuals after virus mutation i_2 increases to 2.97 times the original value.

From Figures 3 and 6, it can be seen that the rate k_1 of recovery before virus mutation increases to 3 times the original value, then infected individuals before virus mutation i_1 reduces to 2.3 times the original value, infected individuals after virus mutation i_2 reduces to 2.32 times the original value.

From Figures 3 and 7, it can be seen that the rate k_2 of recovery after virus mutation increases

to 3.5 times the original value, then infected individuals before virus mutation i_1 reduces to 1.05 times the original value, infected individuals after virus mutation i_2 reduces to 2.59 times the original value.

5. Summary

In this paper, an SEIR epidemic model with Logistic death rate of virus mutation is studied. By constructing the Lyapunov function using algebraic methods, the global stability of the endemic equilibrium p_1 is presented. Through numerical simulation, it can be found that the recovery rate k_1 before the mutation and the recovery rate k_2 after the mutation have the greatest influence on results of system (2.3) (see Figures 2, 6 and 7). Therefore, by strengthening health, epidemic prevention and raising medical standards, the value of k_1 and k_2 can be increased to control the outbreak of the disease from its root.

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