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GLOBAL STABILITY OF AN SEIR MODEL WITH INFECTIOUS FORCE IN LATENT AND INFECTED

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Abstract. This paper considers an SEIR model with infectious force in latent and infected. By means of Lyapunov function and LaSalle's invariant set theorem, we proved the global asymptotically stable results of the disease-free equilibrium. It is then obtained the sufficient conditions for the global stability of the unique endemic equilibrium by the compound matrix theory. In addition, it is verified that there is phenomena of limit cycle according to simulations.

Keywords: SEIR model; Global stability; Lyapunov function; Numerical simulation.

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1. Introduction

Mathematical modeling for disease transmission in host population is of great practical value in predicting and controlling disease spread such as SARS [1], HIV/AIDS [2] and H1N1 influenza [3]. Many infectious diseases in nature incubate inside the hosts for a period of time

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before the hosts become infectious. Assume that the population size N is divided into four homogeneous classes: the susceptible S , the exposed (in the latent period) E , the infective I , and the recovered R . Xuezhi Li and Linlin Zhou [4] considered the global dynamics of an SEIR epidemic model with vertical transmission and the saturating contact. Chengjun Sun and Yinghen Hsieh [5] studied an SEIR model with varying population size and vaccination strategy. Na Yi *et al.* [6] studied the dynamical behaviors of an SEIR epidemic system with nonlinear transmission rate. Since there is a difference in relative measure of infectiousness between the exposed and the infected populations, the incidence rate between the susceptible fraction S and the infected fraction I should be different from that between the susceptible fraction with the exposed ones. Wang Lianhua *et al.* [13] studied an SEIR epidemic model with constant recruitment of susceptible and infective individuals, respectively, and proved the global asymptotical stable results of the endemic equilibrium. In this paper, we assume that all newborns are susceptible (no vertical transmission) and a uniform birthrate (Cholera, Hepatitis A are of this case) and will obtain the different results from the case in [13]. In the following paper, we firstly investigate the SEIR model by considering the infectious force both in latent period and infected period such as tuberculosis [7]

$$\begin{aligned}
 S' &= bN - dS - \beta_1 SI/N - \beta_2 SE/N, \\
 E' &= \beta_1 SI/N + \beta_2 SE/N - (\alpha + d)E, \\
 I' &= \alpha E - (\varepsilon + d)I, \\
 R' &= \varepsilon I - dR, \\
 N &= S + I + E + R.
 \end{aligned} \tag{1}$$

where the derivative d/dt is denoted by $'$. $b > 0$ is the rate for natural birth. $d > 0$ is the rate for natural death. The positive parameter α is the rate at which the exposed individuals become infective. $\varepsilon > 0$ is the rate for recovery. β_1 is the force of infection. β_2 denotes the relative measure of infectiousness for the asymptomatic class E . If $b - d \neq 0$, then the population would be naturally exponentially growing or decaying in the absence of the infectious disease. From biological considerations, we assume that $b = d \neq 0$, then there is an inflow of newborn

susceptible and the population size remains constant . For simplicity, we denote by

$$s = S/N, \quad e = E/N, \quad i = I/N, \quad r = R/N,$$

then

$$s' = S'/N - s(b - d), \quad e' = E'/N - e(b - d),$$

and $i' = I'/N - i(b - d)$. Since the variable R do not appear in the equations of S, E, I , we only need to consider the system:

$$\begin{aligned} s' &= b(1 - s) - \beta_1 si - \beta_2 se, \\ e' &= \beta_1 SI/N + \beta_2 SE/N - (\alpha + b)E, \\ i' &= \alpha e - (\varepsilon + b)i, \\ 1 &= s + e + i + r. \end{aligned} \tag{2}$$

It is easy to verify that all solutions of (2) initiating in set $D = \{(s, e, i) \in R_+^3 : 0 \leq s, e, i \leq 1\}$, where R_+^3 denotes the non-negative cone of R^3 , including its lower-dimensional faces. Therefore, D is positively invariant for (2). We consider the solutions of (2) in D below.

2. Dynamic analysis

It is easy to visualize that the system (2) always has a disease-free equilibrium $E_0(1, 0, 0)$. We first establish the following results for E_0 .

Theorem 1. *When $R_0 \leq 1$, the disease-free equilibrium E_0 is global asymptotically stable, and when $R_0 > 1$, E_0 is unstable , where $R_0 \leq \frac{\varepsilon\beta_2 + b\beta_2 + \alpha\beta_1}{(\varepsilon + b)(\alpha + b)}$.*

Proof. Consider the function

$$L = \frac{\varepsilon\beta_2 + b\beta_2 + \alpha\beta_1}{(\varepsilon + b)(\alpha + b)} e + \frac{\beta_1 i}{\varepsilon + b}.$$

Its derivative along the solutions to the system (2) is

$$L' = (\beta_1 i + \beta_2 e)(R_0 s - 1) \leq (\beta_1 i + \beta_2 e)(R_0 - 1) \leq 0.$$

Furthermore, $L' = 0$ only if $i = e = 0$. The maximum invariant set in $\{(s, e, i) \in D : L' = 0\}$ is the singleton $\{E_0\}$. The global stability of E_0 when $R_0 \leq 1$ follows from LaSalles Invariance

Principle (see [8]). By direct calculating, the determinant of $J(E_0)$ is $(\varepsilon + b)(\alpha + b)(1 - R_0) < 0$ when $R_0 > 1$, therefore E_0 is unstable. This completes the proof.

We can easily see that system (2) has a unique endemic equilibrium $E^*(s^*, e^*, i^*)$ if $R_0 > 1$ where

$$s^* = 1/R_0, \quad e^* = \frac{b(R_0 - 1)}{R_0(\alpha + b)(\varepsilon + b)}.$$

To demonstrate the local stability of E^* , we need the following lemma.

Lemma 1. (see [9], [10]) *Let M be a 3×3 real matrix. If $\text{tr}(M)$, $\det(M)$ and $\det(M^{[2]})$ are all negative, then all of the eigenvalues of M have negative real part.*

Theorem 2. *The unique endemic equilibrium E^* of (2) is locally asymptotically stable if $R_0 > 1$.*

Proof. The Jacobian matrix of the system (2) at a point E^* is

$$J(E^*) = \begin{bmatrix} -bR_0 & -\beta_2/R_0 & -\beta_1/R_0 \\ b(R_0 - 1) & \beta_2/R_0 - \alpha - b & \beta_1/R_0 \\ 0 & \alpha & -\varepsilon - b \end{bmatrix} \quad (3)$$

$$\text{tr}(J(E^*)) = bR_0 - \varepsilon - b - \frac{\alpha\beta_1}{R_0(\varepsilon + b)} < 0.$$

It follows from (3) that the determinant of $J(E^*)$ is given by

$$\det(J(E^*)) = -b(\varepsilon + b)(\alpha + b)(R_0 - 1) < 0.$$

The second additive compound matrix $J^{[2]}(E^*)$ of $J(E^*)$ is given by

$$J^{[2]}(E^*) = \begin{bmatrix} -bR_0 - \frac{\alpha\beta_1}{R_0}(\varepsilon + b) & \frac{\beta_1}{R_0} & \frac{\beta_1}{R_0} \\ \alpha & -bR_0 - \varepsilon - b & \frac{\beta_2}{R_0} \\ 0 & b(R_0 - 1) & -\frac{\alpha\beta_1}{R_0(\varepsilon + b)} - \varepsilon - b \end{bmatrix} \quad (4)$$

Direct calculations show that

$$\begin{aligned} \det(J^{[2]}(E^*)) &= -b(R_0 - 1)(b\beta_2 + \frac{\alpha\beta_1\beta_2}{R_0^2(\varepsilon + b)}) - \frac{b\alpha\beta_1}{R_0} - bR_0(\varepsilon + b)^2 \\ &\quad - (\frac{\alpha\beta_1}{R_0(\varepsilon + b)} + \varepsilon + b)(b^2R_0^2 + \frac{\alpha\beta_1}{\varepsilon + b}). \end{aligned}$$

Hence, the result follows Lemma 1. This completes the proof.

In the following, using the geometrical approach of Li and Muldowney in [11], we will present a sufficient condition for the global asymptotic stability of the unique endemic equilibrium E^* . Denote the interior of D by \mathring{D} .

Theorem 3. *The unique endemic equilibrium E^* of the system (2) is globally asymptotically stable in \mathring{D} , when $b + \alpha > 2\beta_2$*

Proof. We calculate easily E_0 is unstable when $b + \alpha > 2\beta_2$ and we can easy see that the system (2) satisfies the assumptions (H_1) and (H_2) (see [11]) in the interior of its feasible region D .

Let $x = (s, e, i)$ and $f(x)$ denote the vector field of (2). The Jacobian matrix associated with a general solution to (2) is

$$J(E) = \begin{bmatrix} -b - \beta_1 i - \beta_2 e & -\beta_2 s & -\beta_1 s \\ \beta_1 i + \beta_2 e & \beta_2 s - \alpha - b & \beta_1 s \\ 0 & \alpha & -\varepsilon - b \end{bmatrix}$$

and its second additive compound matrix is

$$J^{[2]}(E) = \begin{bmatrix} \beta_2 s - \beta_1 i - \beta_2 e - \alpha - 2b & \beta_1 s & \beta_1 s \\ \alpha & -\beta_1 i - \beta_2 e - \varepsilon - 2b & -\beta_2 s \\ 0 & \beta_1 i + \beta_2 e & \beta_2 s - \varepsilon - \alpha - 2b \end{bmatrix}$$

Set the function

$$P(x) = P(s, e, i) = \text{diag}(1, e/i, e/i),$$

Then the matrix $B = P_f P^{-1} + P J^{[2]} P^{-1}$ can be written in block form

$$B = \begin{bmatrix} B_{11} & B_{12} \\ B_{21} & B_{22} \end{bmatrix},$$

where

$$B_{11} = \beta_2 s - \beta_1 i - \beta_2 e - \alpha - 2b, \quad B_{21} = (\alpha e/i \quad 0)', \quad B_{12} = (\beta_1 s i/e \quad \beta_1 s i/e)$$

$$B_{22} = \begin{bmatrix} e'/e - i'/i - 2b - \varepsilon - \beta_1 i - \beta_2 e & -\beta_2 s \\ \beta_1 i + \beta_2 e & e'/e - i'/i - 2b - \varepsilon - \alpha \end{bmatrix},$$

Let (u, v, w) denote the vectors in $R^3 \cong R^{\frac{3}{2}}$, we select a norm in R^3 as

$$|(u, v, w)| = \max\{|u|, |v| + |w|\},$$

and let ρ denotes the Lonzinskii measure with respect to this norm. Using the method of estimating ρ in [11], we have $\rho(B) \leq \sup(g_1, g_2)$, where

$$g_1 = \rho_1(B_{11}) + |B_{12}|, \quad g_2 = |B_{21}| + \rho_1(B_{22})$$

$|B_{12}|$ and $|B_{21}|$ are matrix norms with respect to the l_1 vector norm, and ρ_1 denotes the Lonzinskii measure with respect to l_1 norm. More specifically,

$$\rho_1(B_{11}) = B_{11}, \quad |B_{21}| = \alpha e/i, \quad \text{and} \quad |B_{12}| = \beta_1 si/e$$

Rewriting (2), we get

$$\alpha e/i = i'/i + \varepsilon + b,$$

and

$$\beta_1 si/e = e'/e - \beta_2 s + \alpha + b.$$

Therefore

$$g_1 = e'/e - b - \beta_1 i - \beta_2 e, \quad g_2 = \max\{e'/e - b, e'/e - (\alpha + b - 2\beta_2 s)\}.$$

From the system (2), we have $0 < s < 1, e > 0, i > 0$.

We can choose \bar{t} large enough such that

$$g_1 < e'/e - b, \quad g_2 < e'/e - h, \quad \text{for } t > \bar{t},$$

where

$$b + \alpha > 2\beta_2, \quad h = \min\{\alpha + b - 2\beta_2, b\} > 0.$$

Therefore

$$\rho(B) \leq \sup(g_1, g_2) \leq e'/e - h, \quad \text{for } t > \bar{t}.$$

Along each solution $(s(t), e(t), i(t))$ of (2) with such that $((s(0), e(0), i(0)) \in K$, where K is the compact absorbing set, we have

$$\frac{1}{t} \int_0^t \rho(B) ds \leq \frac{1}{t} \log \frac{e(t)}{e(\bar{t})} + \frac{1}{t} \int_0^{\bar{t}} \rho(B) ds - h \frac{t - \bar{t}}{t}$$

which implies $\bar{q}_2 \leq -h/2 < 0$. This completes the proof.

3. Numerical simulations

From practical point of view, numerical solutions are very important beside analytical study. In this section, we apply the simulation to investigate the case of $b + \alpha < 2\beta_2$ and $R_0 > 1$. We choose the parameters of (2) as $\beta_1 = 0.28$ (see [6]), $\varepsilon = 0.5$ (see [12]), and $\alpha = 0.1$, $\beta_2 = 0.3$, $b = 0.002$, $(s(0), e(0), i(0)) = (0.8, 0.0001, 0.001)$. Then the unique endemic equilibrium $E^* = (0.29, 0.0139, 0.0028)$, $R_0 = 3.488 > 1$. Therefore, by Theorem 2, E^* is locally asymptotically stable, and by Theorem 1, the disease-free equilibrium $E_0(1, 0, 0)$ is unstable. The spectrum of Lyapunov exponents of the system (2) with respect to times is given in Fig.1, which shows that there exists limit cycle. To well see the dynamics, the phase portraits in susceptible-exposed-infective, susceptible-exposed, exposed-infective, and susceptible-infective are given in Fig. 2, 3, 4, and 5.

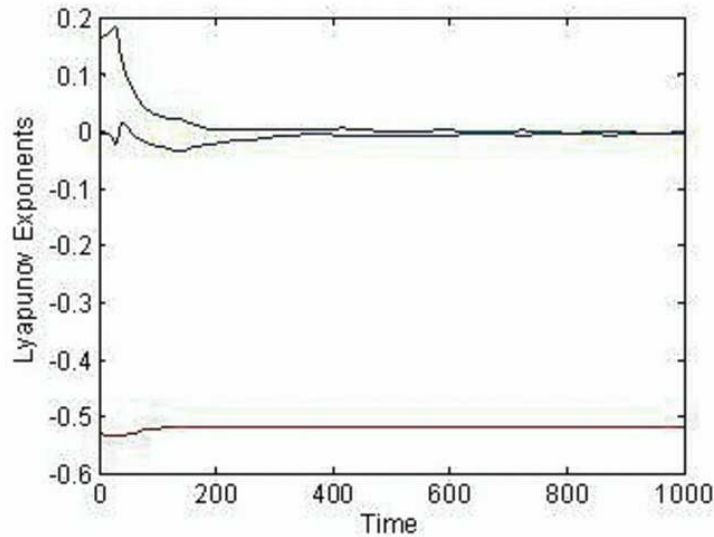


FIGURE 1. Lyapunov exponents of the system (2) with respect to times.

4. Conclusion

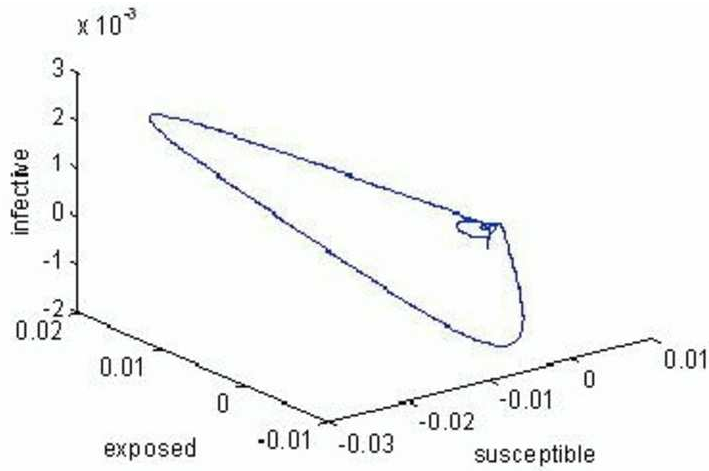


FIGURE 2. The phase portrait in susceptible-exposed-infective.

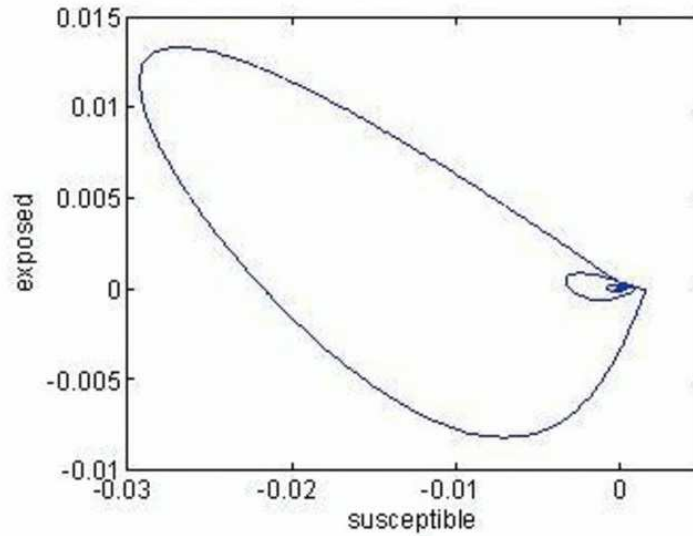


FIGURE 3. The phase portrait in susceptible-exposed.

In this paper, we discuss an SEIR epidemic model with infectious force in latent and infected and investigate the global dynamics of the reduced proportional system. The assumed conditions and results are different from the case in [13]. We obtain that the disease-free equilibrium E_0 is globally asymptotically stable when $R_0 \leq 1$. If and only if $R_0 > 1$, a unique endemic equilibrium E^* exists and is locally asymptotically stable. The unique endemic equilibrium is globally asymptotically stable when $R_0 > 1$ and $b + \alpha > 2\beta_2$. Without infectivity in latent, (1)

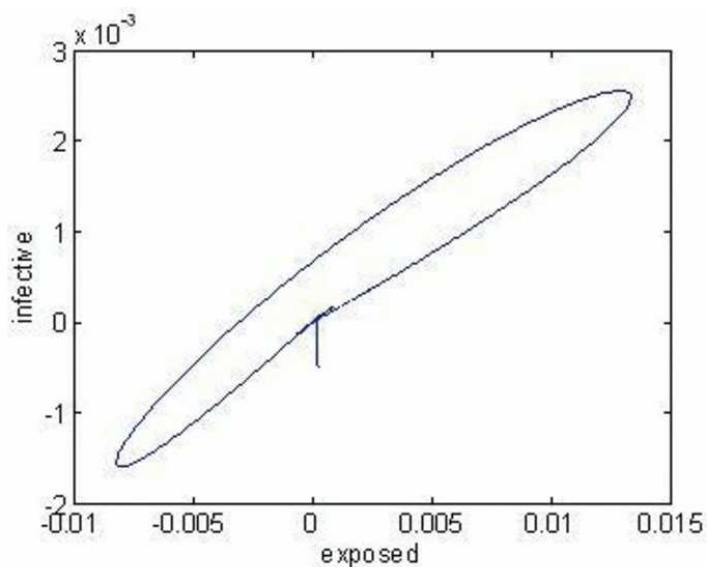


FIGURE 4. The phase portrait in exposed-infective.

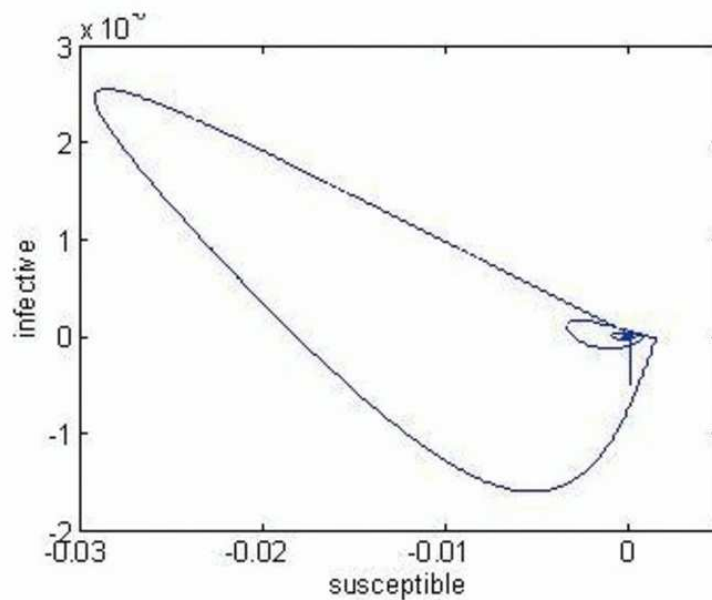


FIGURE 5. The phase portrait in susceptible-infective

becomes an SEIR model without infectious force in latent (see [6]). Finally, it is verified that there is phenomena of limit cycle according to simulations.

Conflict of Interests

The authors declare that there is no conflict of interests.

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