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Global Dynamics of an SEIS Epidemic Model with Transport-related Infection and Exposed

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Abstract: Some analytical results are given for an SEIS model that describes the propagation of a disease in a population of individuals who travel between two cities. This model is to understand the effect of the exposed and infective individuals' transport on disease spread. Transportation among regions is one of the main factors which affect the outbreak of disease. The basic reproduction number $R_{0\gamma}$ is given. If $R_{0\gamma} \leq 1$, there only exists the disease-free equilibrium and it is globally asymptotically stable which implies the disease will go to extinction. If $R_{0\gamma} > 1$, the disease-free equilibrium is unstable, the endemic equilibrium appears and is locally asymptotically stable, the system is permanent. It is shown that the disease is endemic in the sense of permanence if and only if $R_{0\gamma} > 1$. Sufficient conditions are established for global asymptotic stability of the endemic equilibrium. Computer observation shows that the endemic equilibrium is globally asymptotically stable if $R_{0\gamma} > 1$ even if the additional condition is invalid. This will be left in our future work. Our results discover the effect of the transport of the exposed and infective people on disease spread.

Keywords: Epidemiology, Permanence, Global stability, Endemic equilibrium.

1. INTRODUCTION

Epidemiology is the study of the spread of disease, in space and time, with the objective to trace factors that are responsible for, or contribute to their occurrence. A theory of epidemics was derived by W.O.Kermack, a chemist, and A.G. Mckendrick, a physician, who worked at the Royal College of Surgeons in Edinburgh between 1900 and 1930. They introduced and used many novel mathematical ideas in studies of populations [1]. One important result of theirs is that an infection determines a threshold size for the susceptible population, above which an epidemic will propagate. Their theoretical epidemic threshold is observed in practice, and it measures to what extent a real population is vulnerable to spread of an epidemic. The propagation of infection is modelled to determine what aspects of a population might be controlled to reduce the risk of an epidemic [2,3,4].

There are many factors that lead to the dynamics of an infectious disease of humans. They include such a human behavior as population dislocations, living style, sexual practices, rising international travel. Population dispersal, as a common phenomenon in human society, may cause many diseases such as influenza, foot-and mouth disease, HIV and SARS etc. Since the first AIDS cases were reported in the United States in June 1981, the number of cases and deaths among persons with AIDS increased rapidly during the 1980s followed by substantial declines in new cases and deaths in the late 1990s. In 2003, SARS began in Guangdong province of China, however, it broke out at last in almost all parts of China and some other cities in the world due to dispersal (Wang and Ruan, 2004, [5]). Recently, some epidemic models have been proposed to understand the spread dynamics of infectious disease.

Rvachev and Longini used a discrete time difference equations in a continuous state space to study the global spread of influenza [6,7]. Sattenspiel and Dietz (1995) introduced a model with travel between populations [8].

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They proceeded to an identification of the parameters in the case of the transmission of measles in the Caribbean island of Dominica, and numerically studied the behavior of the model. Sattenspiel and Herring (1998) considered the same type of model but applied to travel between populations in the Canadian subartic, which can be thought of as a closed population where travel is easily quantified [9]. Recently, the same authors (Sattenspiel and Herring 2003) formulated a model that includes quarantine, and applied it to data of the 1918-1919 influenza epidemic in central Canada [10]. Wang and Mulone (2003) and Wang and Zhao (Wang and Zhao 2004) have also recently formulated and discussed other models for the spread of a disease among two patches and *n* patches [11-13]. In 2003, Arino and Van den Driessche have also formulated a mobility model for residents of *n* cities (or discrete geographical regions) who may travel between them to study the spatial spread of infectious [14].

All these investigations ignore the possibility for the individuals to become infective during travel. In paper [15], Cui, Takeuchi and Saito have proposed the following SIS epidemic to understand the effect of transport-related infection on disease spread for the first time.

$$\begin{cases} \dfrac{dS_1}{dt} &= a - bS_1 - \dfrac{\beta S_1 I_1}{S_1 + I_1} + dI_1 - \alpha S_1 + \alpha S_2 - \dfrac{\gamma\alpha S_2 I_2}{S_2 + I_2}, \\ \dfrac{dI_1}{dt} &= \dfrac{\beta S_1 I_1}{S_1 + I_1} + \dfrac{\gamma\alpha S_2 I_2}{S_2 + I_2} - (c + d + \alpha) I_1 + \alpha I_2, \\ \dfrac{dS_2}{dt} &= a - bS_2 - \dfrac{\beta S_2 I_2}{S_2 + I_2} + dI_2 - \alpha S_2 + \alpha S_1 - \dfrac{\gamma\alpha S_1 I_1}{S_1 + I_1}, \\ \dfrac{dI_2}{dt} &= \dfrac{\beta S_2 I_2}{S_2 + I_2} + \dfrac{\gamma\alpha S_1 I_1}{S_1 + I_1} - (c + d + \alpha) I_2 + \alpha I_1. \end{cases} \tag{1.1}$$

Considering entry screening and exit screening to detect infected individuals, Liu and Takeuchi [16] proposed an SIQS model to studied the effect of transport-related infection and entry screening.Mathematically, Cui, Takeuchi and Saito mainly stuied local asymptotical stability of model (1.1) and the endemic equilibrium was proved to be asymptotically stable with an additional condition besides the condition its existence. Subsequently, Takeuchi et al [17]. studied further the global dynamics of model (1.1). They prove the endemic equilibrium is locally asymptotically stable if it exists, but the global stabilities of equilibria, include disease-free equilibrium and endemic equilibrium, still required additional condition besides the condition its existence. Liu and Takeuchi [16], the global stability of equilibria remains unsolved.

Many diseases (e.g. Tuberculosis, Measles, AIDS, SARS etc.) have incubation period. The disease will incubate inside the host for a period of time before the host becomes infectious. A susceptible individual first goes through a latent period (often called the exposed or in the class E) after infection before becoming infectious. The models obtained by the compartmental approach are said to be SEI models or SEIS models, respectively, depending on whether the patient is cured or not. In fact, the spread of disease is profoundly influenced by the exposed individuals' movement. Because the exposed individuals has no any symptoms, they have more chances on contact with others. In this paper, we will study the effect of transport-related infection and exposed individuals' movement via mathematical analysis. Our results show that the disease will develop to become endemic as the travel of exposed or infective individuals.

The paper is organized as follows. In Section 2, we will construct an SEIS epidemic model with transport-related infection and give explicit fomulas of basic reproductive number, equilibria. Section 3 deals with the global stability of the disease-free equilibrium. In section 4, we will discuss the local stability of endemic equilibrium by using Routh-Hurwitz Criterion. Permanence of the SEIS model in section 2 is settled in Section 5. We will give some sufficient conditions for global stability of endemic equilibrium in section 6. In the final section, we will discuss our results and give some numerical simulations.

2. MODEL FORMULATION

We consider a model with state variables S_i, E_i, I_i and N_i that represent the number of susceptible, exposed, infected individuals and total population in city i, respectively ($i = 1, 2$). The basic assumptions underlying the dynamics of the system are as follows:

- We assume that both cites are identical.
- All newborns, denoted by a, join into the susceptible class per unit time.
- Natural death rate for susceptible individuals is a constant per capita rate b.
- Disease is transmitted with the standard form incidence rate $\beta S_i I_i/N_i$, $i = 1, 2$, within city i. β is the probability per unit time of transmitting the infection of between two individuals taking part in a contact.
- We may assume that a susceptible individual first goes through a latent period (and is said to become exposed or in the class E) after infection, before becoming infectious.
- ε is the rate constant at which the exposed individuals become infective, so that $\frac{1}{\varepsilon}$ is the mean latent period.
- Susceptible, exposed and infected individuals of every city i leave for city j ($i \neq j$, $i, j = 1, 2$) at a per capita rate α. We assume that two cities are connected by the direct transport such as airplanes or trains etc.
- When the individuals in city i travel to city j, disease is transmitted with the incidence rate $\gamma_1(\alpha S_i)(\alpha I_i)/(\alpha S_i + \alpha I_i) = \gamma_1 \alpha S_i I_i/N_i$ with a transmission rate $\gamma_1\alpha$.
- When the exposed individuals in city i travel to city j, there is $\gamma_2\alpha E_i$ becoming infectious per unit time.
- The rate constant for recovery is denoted by d, so that $\frac{1}{d}$ is the mean infective period. We omit the mortality induced disease (For this model with the mortality induced disease, this issue would be left as our future consideration).
- We suppose that individuals who are travelling do not give birth and do not take death. Further we assume that infected individuals do not recover during travel.

These assumptions lead to a model of the form:

$$\begin{cases} \dfrac{dS_1}{dt} &= a - bS_1 - \dfrac{\beta S_1 I_1}{S_1 + E_1 + I_1} + dI_1 - \alpha S_1 + \alpha S_2 - \dfrac{\gamma_1 \alpha S_2 I_2}{S_2 + E_2 + I_2}, \\ \dfrac{dE_1}{dt} &= \dfrac{\beta S_1 I_1}{S_1 + E_1 + I_1} + \dfrac{\gamma_1 \alpha S_2 I_2}{S_2 + E_2 + I_2} - bE_1 - \varepsilon E_1 - \alpha E_1 + \alpha E_2 - \gamma_2 \alpha E_2, \\ \dfrac{dI_1}{dt} &= \varepsilon E_1 - (b+d) I_1 - \alpha I_1 + \alpha I_2 + \gamma_2 \alpha E_2, \\ \dfrac{dS_2}{dt} &= a - bS_2 - \dfrac{\beta S_2 I_2}{S_2 + E_2 + I_2} + dI_2 - \alpha S_2 + \alpha S_1 - \dfrac{\gamma_1 \alpha S_1 I_1}{S_1 + E_1 + I_1}, \\ \dfrac{dE_2}{dt} &= \dfrac{\beta S_2 I_2}{S_2 + E_2 + I_2} + \dfrac{\gamma_1 \alpha S_1 I_1}{S_1 + E_1 + I_1} - bE_2 - \varepsilon E_2 - \alpha E_2 + \alpha E_1 - \gamma_2 \alpha E_1, \\ \dfrac{dI_2}{dt} &= \varepsilon E_2 - (b+d) I_2 - \alpha I_2 + \alpha I_1 + \gamma_2 \alpha E_1, \\ N_1 &= S_1 + E_1 + I_1, N_2 = S_2 + E_2 + I_2. \end{cases} \tag{2.1}$$

By biological point of view, since the term αS_i and αE_i represent the susceptible and exposed individuals leaving city i and $\gamma_1\alpha S_i I_i/N_i$ and $\gamma_2\alpha E_i$ denote individuals in αS_i and αE_i becoming infected and infectious during travel from city i to j, respectively. Hence, $\alpha S_i - \gamma_1\alpha S_i I_i/N_i$ and $\alpha E_i - \gamma_2\alpha E_i$ should be nonnegative. Therefore, we always suppose that $0 \le \gamma_i \le 1$ $(i = 1, 2)$ in the following discussion.

The point $P_0 = (\frac{a}{b},0,0,\frac{a}{b},0,0)$ is the disease-free equilibrium of (2.1), and it exists for all nonnegative values of the parameters. According to the concept of next generation matrix (Diekmann et al., 1990, [18]) and reproduction number presented in van den Driessche and Watmough (2002, [19]), we define

$$F = \begin{pmatrix} 0 & 0 & \beta & \gamma_1\alpha \\ 0 & 0 & \gamma_1\alpha & \beta \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} b+\alpha+\varepsilon & -\alpha(1-\gamma_2) & 0 & 0 \\ -\alpha(1-\gamma_2) & b+\alpha+\varepsilon & 0 & 0 \\ -\varepsilon & -\gamma_2\alpha & b+d+\alpha & -\alpha \\ -\gamma_2\alpha & -\varepsilon & -\alpha & b+d+\alpha \end{pmatrix}$$

Hence the reproduction number for (2.1) is

$$R_{0\gamma} = \rho(FV^{-1}) = \frac{(\beta+\gamma_1\alpha)(\varepsilon+\gamma_2\alpha)}{(b+\varepsilon+\gamma_2\alpha)(b+d)}.$$

When $R_{0\gamma} > 1$, (2.1) has the unique positive equilibrium P_+ $(S^*, E^*, I^*, S^*, E^*, I^*)$, where

$$\begin{aligned} S^* &= \frac{a}{b}\frac{1}{R_{0\gamma}}, \\ E^* &= \frac{b+d}{\varepsilon+\gamma_2\alpha I^*}, \\ I^* &= \frac{a(\varepsilon+\gamma_2\alpha)}{b(b+d+\varepsilon+\gamma_2\alpha)}\left(1-\frac{1}{R_{0\gamma}}\right). \end{aligned} \tag{2.2}$$

Obviously, $S^* + E^* + I^* = \frac{a}{b}$. It is easy to prove the following theorem.

Theorem 2.1: When $R_{0\gamma} \le 1$, then system (2.1) only has the disease-free equilibrium P_0 and when $R_{0\gamma} > 1$, then system (2.1) has the unique endemic equilibrium P_+ except for P_0

3. GLOBAL STABILITY OF P_0

In this section, we show that the disease-free equilibrium is globally stable as long as $R_{0\gamma} \le 1$, and is unstable if $R_{0\gamma} > 1$. We process this as two steps. We first prove its local stability and instability then global stability.

Theorem 3.1: If $R_{0\gamma} \le 1$, then P_0 is global asymptotically stable. If $R_{0\gamma} > 1$, then P_0 is unstable

Proof: The Jacobian matrix at P_0 for the right hand side of (2.1) is given by

$$J(P_0) = \begin{pmatrix} A & B \\ B & A \end{pmatrix}$$

where

$$A = \begin{pmatrix} -(b+\alpha) & 0 & -\beta + d \\ 0 & -(b+\varepsilon+\alpha) & \beta \\ 0 & \varepsilon & -(b+d+\alpha) \end{pmatrix}$$

and

$$B = \begin{pmatrix} \alpha & 0 & -\gamma_1\alpha \\ 0 & \alpha(1-\gamma_2) & \gamma_1\alpha \\ 0 & \gamma_2\alpha & \alpha \end{pmatrix}.$$

The eigenvalues of $J(P_0)$ are identical to those of $A + B$ and $A - B$, where

$$A + B = \begin{pmatrix} -b & 0 & -\beta + d - \gamma_1\alpha \\ 0 & -(b+\varepsilon+\gamma_2\alpha) & \beta + \gamma_1\alpha \\ 0 & \varepsilon + \gamma_2\alpha & -(b+d) \end{pmatrix}$$

and

$$A - B = \begin{pmatrix} -(b+2\alpha) & 0 & -\beta + d + \gamma_1\alpha \\ 0 & -(b+\varepsilon+2\alpha-\gamma_2\alpha) & \beta - \gamma_1\alpha \\ 0 & \varepsilon - \gamma_2\alpha & -(b+d+2\alpha) \end{pmatrix}.$$

Because there is only one non-zero element in the first column for $A+B$ and $A-B$, which are both negative, we may reduce the question of whether the eigenvalues of the following two 2×2 matrixes have negative real part.

$$J_1 = \begin{pmatrix} -(b+\varepsilon+\gamma_2\alpha) & \beta+\gamma_1\alpha \\ \varepsilon+\gamma_2\alpha & -(b+d) \end{pmatrix}, \quad J_2 = \begin{pmatrix} -(b+\varepsilon+2\alpha-\gamma_2\alpha) & \beta-\gamma_1\alpha \\ \varepsilon-\gamma_2\alpha & -(b+d+2\alpha) \end{pmatrix}$$

It is easy to verify that $tr\,(J_i) < 0$ and $\det\,(J_i) > 0$ when $R_{0\gamma} < 1$. When $R_{0\gamma} > 1$, $\det\,(J_1) < 0$ implies J_1 has at lease one eigenvalue with positive real part. Hence, P_0 is locally asymptotically stable if $R_{0\gamma} < 1$ and P_0 is unstable if $R_{0\gamma} > 1$. Next, we will discuss the global stability of P_0 under the condition $R_{0\gamma} \le 1$. We next prove global stability of the disease-free equilibrium.

Consider the following Liapunov function

$$V(t) = E_1 + E_2 + \frac{b+\varepsilon+\gamma_2\alpha}{\varepsilon+\gamma_2\alpha}(I_1 + I_2).$$

Its derivative along the solutions of system (2.1) is

$$V'(t) = (\beta+\gamma_1\alpha)\left(\frac{S_1 I_1}{S_1+E_1+I_1} + \frac{S_2 I_2}{S_2+E_2+I_2}\right) - \frac{(b+\varepsilon+\gamma_2\alpha)(b+d)}{\varepsilon+\gamma_2\alpha}(I_1+I_2).$$

If $R_{0\gamma} < 1$, then

$$V'(t) \le \left[(\beta+\gamma_1\alpha) - \frac{(b+\varepsilon+\gamma_2\alpha)(b+d)}{\varepsilon+\gamma_2\alpha}\right](I_1+I_2) \le 0.$$

If $R_{0\gamma} = 1$, then

$$V'(t) = -(\beta+\gamma_1\alpha)\left[\frac{I_1(E_1+I_1)}{S_1+E_1+I_1} + \frac{I_2(E_2+I_2)}{S_2+E_2+I_2}\right] \le 0.$$

When $R_{0\gamma} \le 1$, we set

$$\begin{aligned} L &= \{(S_1,E_1,I_1,S_2,E_2,I_2) : V'(t) = 0\} \\ &= \{(S_1,E_1,I_1,S_2,E_2,I_2) : I_1 = 0, I_2 = 0\} \end{aligned}$$

Restricting system (2.1) on the set L, we easily obtain that $\lim_{t\to\infty} E_i(t) = 0$ and $\lim_{t\to\infty} S_i(t) = \frac{a}{b}$. Therefore, $M = \{P_0\}$ is the largest positively invariant subset of L. By Liapunov-LaSalle theorem, P_0 is global asymptotically stable provided $R_{0\gamma} \le 1$. This completes the proof of this theorem.

Remark 3.1: Theorem 3.1 completely determines the global dynamics of (2.1) when $R_{0\gamma} \le 1$. Its epidemiological implication is that the sum of the exposed and the infectious subclasses in the population vanishes over time so the disease dies out in both two cities . In Section 5, we show that the disease is permanent when $R_{0\gamma} > 1$.

4. LOCAL STABILITY OF P_+

We have shown that there exists a positive endemic equilibrium if and only if $R_{0\gamma} > 1$ in Section 2. In this section, we prove that if the endemic equilibrium exits, it is always locally asymptotically stable.

Consider matrix

$$Q = \begin{pmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & a_{32} & a_{33} \end{pmatrix}. \tag{4.1}$$

Denote $Q_1 = a_{11}a_{22} - a_{12}a_{21}$, $Q_2 = a_{22}a_{33}$¡$a_{23}a_{32}$ and $Q_3 = a_{11}a_{33}$. For convenience, we state Routh-Hurwitz criterion for this kind of matrix.

Lemma 4.1: Let $A_1 = -\text{tr}(Q)$, $A_2 = Q_1 + Q_2 + Q_3$ and $A_3 = -\det(Q)$, then each eigenvalue of Q has negative real part if and only if

1. $A_1 > 0$,
2. $A_3 > 0$,
3. $A_1A_2 - A_3 > 0$.

The characteristic polynomial of matrix Q is

$$\lambda^3 + A_1\lambda^2 + A_2\lambda + A_3 = 0.$$

Calculating $A_1\, A_2 - A_3$ directly, we get

$$\begin{aligned} A_1A_2 - A_3 &= -(a_{11} + a_{22} + a_{33})(Q_1 + Q_2 + Q_3) + \det(Q) \\ &= -a_{11}(Q_1 + Q_3) - a_{22}(Q_1 + Q_2 + Q_3) - a_{33}(Q_2 + Q_3) \\ &\quad + a_{13}a_{21}a_{32} \text{ ¡ } a_{11}a_{22}a_{33}. \end{aligned}$$

Remark 4.1: $a_{ii} < 0$, $Q_i > 0 (i = 1; 2; 3)$ and $a_{13}a_{21}a_{32} - a_{11}a_{22}a_{33} > 0$ imply that $A_1A_2 - A_3 > 0$.

Theorem 4.1: If $R_{0\gamma} > 1$, the endemic equilibrium P_+ of the system (2.1) is locally asymptotically stable.

Proof: The matrix of the linearization of the system (2.1) at the equilibrium $P_+(S^*, E^*, I^*, S^*, E^*, I^*)$ is

$$J(P_+) = \begin{pmatrix} A & B \\ B & A \end{pmatrix} \tag{4.2}$$

where

$$A = \begin{pmatrix} -\frac{\beta I^*(E^*+I^*)}{(S^*+E^*+I^*)^2} - (b+\alpha) & \frac{\beta S^* I^*}{(S^*+E^*+I^*)^2} & -\frac{\beta S^*(S^*+E^*)}{(S^*+E^*+I^*)^2} + d \\ \frac{\beta I^*(E^*+I^*)}{(S^*+E^*+I^*)^2} & -\frac{\beta S^* I^*}{(S^*+E^*+I^*)^2} - (b+\varepsilon+\alpha) & \frac{\beta S^*(S^*+E^*)}{(S^*+E^*+I^*)^2} \\ 0 & \varepsilon & -(b+d+\alpha) \end{pmatrix}$$

and

$$B = \begin{pmatrix} -\frac{\gamma_1\alpha I^*(E^*+I^*)}{(S^*+E^*+I^*)^2} + \alpha & \frac{\gamma_1\alpha S^* I^*}{(S^*+E^*+I^*)^2} & -\frac{\gamma_1\alpha S^*(S^*+E^*)}{(S^*+E^*+I^*)^2} \\ \frac{\gamma_1\alpha I^*(E^*+I^*)}{(S^*+E^*+I^*)^2} & -\frac{\gamma_1\alpha S^* I^*}{(S^*+E^*+I^*)^2} + \alpha(1-\gamma_2) & \frac{\gamma_1\alpha S^*(S^*+E^*)}{(S^*+E^*+I^*)^2} \\ 0 & \gamma_2\alpha & \alpha \end{pmatrix}.$$

By (2.2), we can write A and B the following forms

$$A = \begin{pmatrix} -\beta\left(1-\frac{1}{R_{0\gamma}}\right)^2 k - (b+\alpha) & \beta\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k & -\beta\left(\frac{1}{R_{0\gamma}} - \frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k\right) + d \\ \beta\left(1-\frac{1}{R_{0\gamma}}\right)^2 k & -\beta\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k - (b+\varepsilon+\alpha) & \beta\left(\frac{1}{R_{0\gamma}} - \frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k\right) \\ 0 & \varepsilon & -(b+d+\alpha) \end{pmatrix}$$

and

$$B=\begin{pmatrix} -\gamma_1\alpha\left(1-\frac{1}{R_{0\gamma}}\right)^2 k+\alpha & \gamma_1\alpha\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k & -\gamma_1\alpha\left(\frac{1}{R_{0\gamma}}-\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k\right) \\ \gamma_1\alpha\left(1-\frac{1}{R_{0\gamma}}\right)^2 k & -\gamma_1\alpha\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k+\alpha(1-\gamma_2) & \gamma_1\alpha\left(\frac{1}{R_{0\gamma}}-\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k\right) \\ 0 & \gamma_2\alpha & \alpha \end{pmatrix}.$$

where $k=\frac{\varepsilon+\gamma_2\alpha}{b+d+\varepsilon+\gamma_2\alpha}<1$. Similar to the proof of Theorem 3.1, to calculate the eigenvalues of $J(P_+)$ is equivalent to calculate the eigenvalues of matrix $A+B$ and $A-B$, where

$$A+B=\begin{pmatrix} a_{11} & a_{12} & a_{13} \\ a_{21} & a_{22} & a_{23} \\ 0 & a_{32} & a_{33} \end{pmatrix} \text{ and } A-B=\begin{pmatrix} b_{11} & b_{12} & b_{13} \\ b_{21} & b_{22} & b_{23} \\ 0 & b_{32} & b_{33} \end{pmatrix}.$$

Here, elements of $A+B$ are

$$a_{11}=-(\beta+\gamma_1\alpha)(1-\tfrac{1}{R_{0\gamma}})^2 k-b,$$

$$a_{12}=(\beta+\gamma_1\alpha)\tfrac{1}{R_{0\gamma}}(1-\tfrac{1}{R_{0\gamma}})k,$$

$$a_{13}=-(\beta+\gamma_1\alpha)\left(\tfrac{1}{R_{0\gamma}}-\tfrac{1}{R_{0\gamma}}\left(1-\tfrac{1}{R_{0\gamma}}\right)k\right)+d,$$

$$a_{21}=(\beta+\gamma_1\alpha)\left(1-\tfrac{1}{R_{0\gamma}}\right)^2 k,$$

$$a_{22}=-(\beta+\gamma_1\alpha)\tfrac{1}{R_{0\gamma}}\left(1-\tfrac{1}{R_{0\gamma}}\right)k-(b+\varepsilon+\gamma_2\alpha),$$

$$a_{23}=(\beta+\gamma_1\alpha)\left(\tfrac{1}{R_{0\gamma}}-\tfrac{1}{R_{0\gamma}}(1-\tfrac{1}{R_{0\gamma}})k\right),$$

$$a_{32}=\varepsilon+\gamma_2\,\alpha$$

$$a_{33}=-(b+d),$$

and elements of $A-B$ are

$$b_{11}=-(\beta-\gamma_1\alpha)(1-\tfrac{1}{R_{0\gamma}})^2 k-(b+2\alpha),$$

$$b_{12}=(\beta-\gamma_1\alpha)\tfrac{1}{R_{0\gamma}}(1-\tfrac{1}{R_{0\gamma}})k,$$

$$b_{13}=-(\beta-\gamma_1\alpha)\left(\tfrac{1}{R_{0\gamma}}-\tfrac{1}{R_{0\gamma}}\left(1-\tfrac{1}{R_{0\gamma}}\right)k\right)+d,$$

$$b_{21}=(\beta-\gamma_1\alpha)\left(1-\tfrac{1}{R_{0\gamma}}\right)^2 k,$$

$$b_{22} = -(\beta - \gamma_1\alpha)\frac{1}{R_{0\gamma}}\left(1-\frac{1}{R_{0\gamma}}\right)k - (b+\varepsilon+2\alpha-\gamma_2\alpha),$$

$$b_{23} = (\beta - \gamma_1\alpha)\left(\frac{1}{R_{0\gamma}} - \frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k\right),$$

$$b_{32} = \varepsilon + \gamma_2\,\alpha$$

$$b_{33} = -(b+d+2\alpha),$$

Firstly, using Lemma 4.1, we prove that each eigenvalue of $\boldsymbol{A} + B$ has negative real part. The process is as follows.

(I) Obviously, $A_1 = -tr\,(A+B) = -(a_{11} + a_{22} + a_{33}) > 0$ by $R_{0\gamma} > 1$.

(II) Calculating the determinant of $A + B$, i.e

$$A_3 = -\det(A+B) = -\begin{vmatrix} -b & 0 & 0 \\ a_{21} & -(\beta+\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k-(b+\varepsilon+\gamma_2\alpha) & (\beta+\gamma_1\alpha)(\frac{1}{R_{0\gamma}}-(1-\frac{1}{R_{0\gamma}})k) \\ 0 & \varepsilon+\gamma_2\alpha & -(b+d) \end{vmatrix}$$

$$= b[(b+d)(\beta+\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k + (b+d)(b+\varepsilon+\gamma_2\alpha)$$

$$-(\varepsilon+\gamma_2\alpha)(\beta+\gamma_1\alpha)(\frac{1}{R_{0\gamma}} - (1-\frac{1}{R_{0\gamma}})k)]$$

$$> b[(b+d)(b+\varepsilon+\gamma_2\alpha) - (\varepsilon+\gamma_2\alpha)(\beta+\gamma_1\alpha)\frac{1}{R_{0\gamma}}] = 0$$

(III) In the following, we will prove that $A_1 A_2 - A_3 > 0$. By Remark 4.1, we only need show that

$$Q_1 > 0,\ Q_2 > 0,\ Q_3 > 0,\ -a_{11}a_{22}a_{33} + a_{13}a_{21}a_{32} > 0. \tag{4.3}$$

It is clear that $Q_3 = a_{11}\,a_{33} > 0$. Hence, we divided into the following parts for proving (4.3).

(i) Claim $Q_1 > 0$.

$$Q_1 = \begin{vmatrix} -b & -(\varepsilon+\gamma_2\alpha) \\ (\beta+\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2 k & -(\beta+\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k-(b+\varepsilon+\gamma_2\alpha) \end{vmatrix}$$

$$= b[(\beta+\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k + (b+\varepsilon+\gamma_2\alpha)] + (\beta+\gamma_1\alpha)(\varepsilon+\gamma_2\alpha)(1-\frac{1}{R_{0\gamma}})^2 k > 0.$$

(ii) Claim $Q_2 > 0$.

$$Q_2 = a_{22}a_{33} - a_{23}a_{32}$$

$$= (b+d)(\beta+\gamma_1\alpha)\frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k + (b+d)(b+\varepsilon+\gamma_2\alpha)$$

$$-(\beta+\gamma_1\alpha)(\varepsilon+\gamma_2\alpha)\frac{1}{R_{0\gamma}} + (\varepsilon-\gamma_2\alpha)(\beta+\gamma_2\alpha)\frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k > 0$$

(iii) Claim $J = -a_{11}a_{22}a_{33} + a_{13}a_{21}a_{32} > 0$

$$J = [(\beta + \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2 k + b][(\beta + \gamma_1\alpha)\tfrac{1}{R_{0\gamma}}(1 - \tfrac{1}{R_{0\gamma}})k + (b + \varepsilon + \gamma_2\alpha)][b + d]$$
$$+(\varepsilon + \gamma_2\alpha)(\beta + \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2 k[-(\beta + \gamma_1\alpha)(\tfrac{1}{R_{0\gamma}} - \tfrac{1}{R_{0\gamma}}(1 - \tfrac{1}{R_{0\gamma}})k) + d]$$
$$> (\beta + \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2 k(b + \varepsilon + \gamma_2\alpha)(b + d)$$
$$-(\beta + \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2 k(\varepsilon + \gamma_2\alpha)(\beta + \gamma_1\alpha)\tfrac{1}{R_{0\gamma}} = 0.$$

By(i)-(iii), we know that (4.3) is valid which implies $A_1 A_2 - A_3 > 0$. From parts (I) – (III), we can conclude that the real parts of all eigenvalues of $A + B$ are negative.

Next we check $A - B$ as follows. It is obvious that $b_{ii} < 0$ as $R_{0\gamma} > 1$ and $0 \le \gamma_i \le 1 (i = 1, 2)$. Similarly, we separate into three parts as follows.

(I') Obviously, $A_1 = -\mathrm{tr}(A - B) = -(b_{11} + b_{22} + b_{33}) > 0$.

(II') Validate $A_3 = -\det(A - B) > 0$. Adding the second and third rows to the first row then the first column multiplied by -1 to the second and third column respectively, we obtain

$$A_3 = -\begin{vmatrix} -(b+2\alpha) & 0 & 0 \\ b_{21} & -(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k-(b+\varepsilon+2\alpha-\gamma_2\alpha) & (\beta-\gamma_1\alpha)(\frac{1}{R_{0\gamma}}-(1-\frac{1}{R_{0\gamma}})k) \\ 0 & \varepsilon-\gamma_2\alpha & -(b+d+2\alpha) \end{vmatrix}$$

$$= b[(b + 2\alpha)(\beta + d + 2\alpha)((\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k + (b + \varepsilon + 2\alpha - \gamma_2\alpha)$$
$$- (\varepsilon - \gamma_2\alpha)(\beta - \gamma_1\alpha)(\tfrac{1}{R_{0\gamma}} - (1 - \tfrac{1}{R_{0\gamma}})k)]$$

$A_3 > 0$ is equivalent to

$$\xi = (b + d + 2\alpha)((\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k + (b + \varepsilon + 2\alpha - \gamma_2\alpha))$$
$$-(\varepsilon - \gamma_2\alpha)(\beta - \gamma_1\alpha)(\tfrac{1}{R_{0\gamma}} - (1 - \tfrac{1}{R_{0\gamma}})k) > 0$$

$\xi > 0$ can be shown as the following four cases.

Case 1: $\beta - \gamma_1\alpha \ge 0,\ \varepsilon - \gamma_2\alpha \ge 0$

$$\xi > (b + \varepsilon + 2\alpha - \gamma_2\alpha)(b + d + 2\alpha) - (\varepsilon - \gamma_2\alpha)(\beta - \gamma_1\alpha)\tfrac{1}{R_{0\gamma}}$$
$$\ge (b + \varepsilon + \gamma_2\alpha)(b + d) - (\varepsilon + \gamma_2\alpha)(\beta + \gamma_1\alpha)\tfrac{1}{R_{0\gamma}} = 0.$$

Case 2: $\beta - \gamma_1\alpha \ge 0,\ \varepsilon - \gamma_2\alpha < 0$

$$\xi > (\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k(b + d + 2\alpha) + (\varepsilon - \gamma_2\alpha)(\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k$$
$$= (\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k(b + d + 2\alpha + \varepsilon - \gamma_2\alpha) > 0.$$

Case 3: $\beta - \gamma_1\alpha < 0,\ \varepsilon - \gamma_2\alpha \ge 0$

$$\xi \ge (\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k(b + d + 2\alpha + \varepsilon - \gamma_2\alpha)$$
$$+ (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha)$$
$$\ge -\alpha(b + d + 2\alpha + \varepsilon - \gamma_2\alpha) + (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha)$$
$$= (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha) - \alpha d > 0.$$

Case 4: $\beta - \gamma_1\alpha < 0,\ \varepsilon - \gamma_2\alpha < 0$

$$\begin{aligned}\xi &= (\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k(b + d + 2\alpha + \varepsilon - \gamma_2\alpha)\\ &\quad + (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha) - (\varepsilon - \gamma_2\alpha)(\beta - \gamma_1\alpha)\ \tfrac{1}{R_{0\gamma}}\\ &\geq -\gamma_1\alpha(b + d + 2\alpha + \varepsilon - \gamma_2\alpha) + (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha) - \gamma_1\gamma_2\alpha_2\\ &\geq -\alpha(b + d + 2\alpha + \varepsilon) + (b + d + 2\alpha)(b + \varepsilon + 2\alpha - \gamma_2\alpha)\\ &= (b + d + 2\alpha)(b + \varepsilon + \alpha - \gamma_2\alpha) - \alpha\varepsilon > 0\end{aligned}$$

By **Case 1-Case 4**, it is clear that $A_3 > 0$.

(III')In the following, we will prove that $A_1A_2 - A_3 > 0$. By Remark 4.1, we only need show that

$$Q_1 > 0,\ Q_2 > 0,\ Q_3 > 0,\ -b_{11}b_{22}b_{33} + b_{13}b_{21}b_{32} > 0 \tag{4.4}$$

It is clear that $Q_3 = b_{11}b_{33} > 0$. Hence, we divided into the following three parts for proving (4.4).

(i') Claim $Q_1 > 0$.

$$\begin{aligned}Q_1 &= b_{11}b_{22} - b_{12}b_{21}\\ &= \begin{vmatrix} -(b+2\alpha) & -(\varepsilon-\gamma_2\alpha)\\ (\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2 k & -(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})k-(b+\varepsilon+2\alpha-\gamma_2\alpha)\end{vmatrix}\\ &= (b - 2\alpha)((\beta - \gamma_1\alpha)(1 - \tfrac{1}{R_{0\gamma}})k(b + \varepsilon + 2\alpha - \gamma_2\alpha))\\ &\quad + (\beta - \gamma_1\alpha)(\varepsilon - \gamma_2\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2 k.\end{aligned}$$

$Q_1 > 0$ can be shown as the following three cases.

Case 1: $(\beta - \gamma_1\alpha)(\varepsilon - \gamma_2\alpha) \geq 0$, it is obvious that $Q_1 > 0$.

Case 2: $\beta - \gamma_1\alpha > 0$, $\varepsilon - \gamma_2\alpha < 0$

$$\begin{aligned}Q_1 &> (\beta - \gamma_1\alpha)\ (1 - \tfrac{1}{R_{0\gamma}})k(b + 2\alpha) + (\beta - \gamma_1\alpha)\ (\varepsilon - \gamma_2\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2k\\ &\geq (\beta - \gamma_1\alpha)\ (1 - \tfrac{1}{R_{0\gamma}})k(b + \varepsilon + 2\alpha - \gamma_2\alpha) \geq 0.\end{aligned}$$

Case 3: $\beta - \gamma_1\alpha < 0$, $\varepsilon - \gamma_2\alpha > 0$

$$\begin{aligned}Q1 &\geq (b + 2\alpha)(b + \epsilon + 2\alpha - \gamma_1\alpha - \gamma_2\alpha)\\ &\quad +(\beta - \gamma_1\alpha)(\varepsilon - \gamma_2\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2k\\ &> (b + 2\alpha)(b + \epsilon) - \gamma_1\alpha(\epsilon - \gamma_2\alpha)(1 - \tfrac{1}{R_{0\gamma}})^2k > 0.\end{aligned}$$

Therefore, we can obtain $Q_1 > 0$ from *Case 1-Case 3*.

(ii') Claim $Q_2 > 0$.

$$\begin{aligned}Q_2 &= b_{22}b_{33} - b_{23}b_{32}\\ &= (b + d + 2\alpha)(\beta - \gamma_1\alpha)\ \tfrac{1}{R_{0\gamma}}\ (1- \tfrac{1}{R_{0\gamma}})\ k + (\beta + \varepsilon + 2\alpha - \gamma_2\alpha))\\ &\quad -(\beta - \gamma_1\alpha)(\varepsilon - \gamma_2\alpha)(\tfrac{1}{R_{0\gamma}} - \tfrac{1}{R_{0\gamma}}(1 - \tfrac{1}{R_{0\gamma}})k).\end{aligned}$$

$Q_2 > 0$ can be shown as the following three cases.

Case 1: $(\beta - \gamma_1\alpha)(\varepsilon - \gamma_2\alpha) \leq 0$, it is obvious that $Q_2 > 0$.

Case 2: $\beta - \gamma_1\alpha > 0,\ \ \varepsilon - \gamma_2\alpha > 0$

$$\begin{aligned} Q_2 &> (b+d+2\alpha)(b+\varepsilon+2\alpha-\gamma_2\alpha) - (\beta-\gamma_1\alpha)(\varepsilon-\gamma_2\alpha)\ \frac{1}{R_{0\gamma}} \\ &> (b+d)(b+\varepsilon+\gamma_2\alpha) - (\beta+\gamma_1\alpha)(\varepsilon+\gamma_2\alpha)\ \frac{1}{R_{0\gamma}} = 0 \end{aligned}$$

Case 3: $\beta - \gamma_1\alpha < 0,\ \varepsilon - \gamma_2\alpha < 0$

$$\begin{aligned} Q_2 &= (\beta-\gamma_1\alpha)\frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k(b+d+2\alpha+\varepsilon-\gamma_2\alpha) \\ &\quad + (b+d+2\alpha)(b+\varepsilon+2\alpha-\gamma_2\alpha) - (\beta-\gamma_1\alpha)(\varepsilon-\gamma_2\alpha)\ \frac{1}{R_{0\gamma}} \\ &> -\gamma_1\alpha(b+d+2\alpha+\varepsilon-\gamma_2\alpha) + (b+d+2\alpha)(b+\varepsilon+2\alpha-\gamma_2\alpha) - \gamma_1\gamma_2\alpha^2 \\ &\geq -\alpha(b+d+2\alpha+\varepsilon) + (b+d+2\alpha)(b+\varepsilon+\alpha) > 0. \end{aligned}$$

Therefore, we can obtain $Q_2 > 0$ from *Case* 1-*Case* 3.

(iii') Claim $f = -b_{11}b_{22}b_{33} + b_{13}b_{21}b_{32} > 0$, i.e.

$$\begin{aligned} f &= [(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k + (b+2\alpha)][(\beta-\gamma_1\alpha)\ \frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k \\ &\quad + (b+\varepsilon+2\alpha-\gamma_2\alpha)](b+d+2\alpha) \\ &\quad -(\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k[(\beta-\gamma_1\alpha)(\frac{1}{R_{0\gamma}} - \frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k) - d] > 0 \end{aligned}$$

$f > 0$ can be shown as the following four cases.

Case 1: $\beta - \gamma_1\alpha \geq 0,\ \varepsilon - \gamma_2\alpha \geq 0$

$$\begin{aligned} f &> (\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k(b+\varepsilon+2\alpha-\gamma_2\alpha)(b+d) \\ &\quad -(\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k(\beta-\gamma_1\alpha)\ \frac{1}{R_{0\gamma}} \\ &\geq (\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k[(b+\varepsilon+\gamma_2\alpha)(b+d) - (\varepsilon+\gamma_2\alpha)(\beta+\gamma_1\alpha)\ \frac{1}{R_{0\gamma}}] = 0 \end{aligned}$$

Case 2: $\beta - \gamma_1\alpha \geq 0,\ \varepsilon - \gamma_2\alpha < 0$

$$\begin{aligned} f &> (\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k(b+\varepsilon+2\alpha-\gamma_2\alpha)d + d(\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k \\ &= d(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k(b+2\varepsilon+2\alpha-2\gamma_2\alpha) \geq 0 \end{aligned}$$

Case 3: $\beta - \gamma_1\alpha < 0,\ \varepsilon - \gamma_2\alpha \geq 0$

$$\begin{aligned} f &> \alpha\varepsilon(d+\alpha) - (\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k[(\beta-\gamma_1\alpha)\ \frac{1}{R_{0\gamma}} - d] \\ &> \alpha\varepsilon(d+\alpha) - (\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k[-d-\alpha] \\ &> \alpha\varepsilon(d+\alpha) - \gamma_1\alpha(\varepsilon-\gamma_2\alpha)(1-\frac{1}{R_{0\gamma}})^2k[d+\alpha] > 0 \end{aligned}$$

Case 4: $\beta - \gamma_1\alpha < 0,\ \varepsilon - \gamma_2\alpha < 0$

Since

$$-(\varepsilon-\gamma_2\alpha)(\beta-\gamma_1\alpha)(1-\frac{1}{R_{0\gamma}})^2k[(\beta-\gamma_1\alpha)(\frac{1}{R_{0\gamma}} - \frac{1}{R_{0\gamma}}(1-\frac{1}{R_{0\gamma}})k) - d] > 0,$$

it is clear that $f > 0$.

By (i')-(iii'), we know that (4.4) is valid which implies $A_1A_2 - A_3 > 0$. From parts (I') – (III'), we can conclude that the real parts of all eigenvalues of $A - B$ are negative. Generally speaking, each eigenvalue of $J(P_+)$ has negative real part. Hence, P_+ is locally asymptotically stable. This completes the proof.

5. PERMANENCE

In this section, we investigate the permanence of system (2.1). We will prove that the system (2.1) is permanent if $R_{0\gamma} > 1$.

Theorem 5.1: There exists an $M > 0$ such that for any solution $(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t))$ of (2.1) with initial values $S_i(0) \geq 0$, $E_i(0) \geq 0$, $I_i(0) \geq 0$ for $i = 1, 2$ satisfies $S_i(t) \leq M$, $E_i(t) \leq M$ and $I_i(t) \leq M$ $(i = 1, 2)$ for large enough t.

Proof: Let $L(t) = S_1(t) + E_1(t) + I_1(t) + S_2(t) + E_2(t) + I_2(t)$. Since

$$L'|_{(2.1)}(t) = 2a - bL(t),$$

it is easy to verify that there exists $t_1 > 0$ such that $L(t) \leq \frac{2a}{b} + \epsilon \triangleq M$ for any $\epsilon > 0$ as $t \geq t_1$. Then $S_i(t) \leq L(t) \leq M$, $E_i(t) \leq L(t) \leq M$, and $I_i(t) \leq L(t) \leq M$ for $t \geq t_1$. The proof is complete.

Theorem 5.2: If $R_{0\gamma} > 1$, then there exists an $\eta > 0$ such that every solution $(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t))$ of (2.1) with initial values $S_i(0) \geq 0$, $E_i(0) \geq 0$, $I_i(0) > 0$ for $i = 1, 2$ satisfies

$$\liminf_{t\to\infty} S_i(t) \geq \eta, \liminf_{t\to\infty} E_i(t) \geq \eta, \liminf_{t\to\infty} I_i(t) \geq \eta, i = 1, 2.$$

Proof: We will use the result of Thieme in [Theorem 4.6, 18] to prove it. Define

$$X = \{(S_1, E_1, I_1, S_2, E_2, I_2) : S_i \geq 0, E_i \geq 0, I_i \geq 0, i = 1, 2\}$$
$$X_0 = \{(S_1, E_1, I_1, S_2, E_2, I_2)\ _2\ X : I_i > 0, i = 1, 2\}.$$
$$\partial X_0 = X_n \backslash X_0$$

In the following, we will show that (2.1) is uniformly persistent with respect to $(X_0, \partial X_0)$.

Obviously, X is positively invariant with respect to system (2.1). If $S_i(0) \geq 0$, $E_i(0) \geq 0$ and $I_i(0) > 0$ for $i = 1, 2$, then $S_i(t) > 0$, $E_i(t) > 0$ and $I_i(t) > 0$ for all $t > 0$. Since $I_i'(t) \geq -(b + d + \alpha) I_i(t)$ and $I_i(0) > 0$, we have $I_i(t) \geq I_i(0)\, e^{-(b+d+\alpha)t} > 0$. Thus, X_0 is also positively invariant. Furthermore, by Theorem 5.1, there exists a compact set B in which all solutions of (2.1) initiated in X will enter and remain forever after. The compactness condition $(C_{4.2})$ in Thieme (1993 [20]) is easily verified for this set B. Denote

$$M_\partial = \{(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) :$$
$$(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t)) \in \partial X_0, t \geq 0\}.$$

We now show that

$$M_\partial = \{(S_1, E_1, 0, S_2, E_2, 0) : S_i \geq 0, E_i \geq 0\}. \tag{5.1}$$

Suppose that $(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) \in M_\partial$. It suffices to show $I_i(t) = 0$ for any $t \geq 0$ and $i = 1, 2$. If it is not true, then there exists a $t_0 \geq 0$ such that $I_1(t_0) > 0$ or $I_2(t_0) > 0$. Without loss of generality, we may assume $I_1(t_0) > 0$ then $I_2(t_0) = 0$. Otherwise, $(S_1(t_0), E_1(t_0), I_1(t_0), S_2(t_0), E_2(t_0), I_2(t_0)) \in X_0$ contradicts to $(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) \in M_\partial$. By the sixth equation of (2.1), we have

$$I'_2(t_0) = \varepsilon\, E_2(t_0) + \alpha I_1(t_0) + \gamma_2 \alpha E_1(t_0) > 0$$

Combining with $I_1(t_0)$, it follows that there exists a $\delta > 0$ small enough such that $I_1(t) > 0$ and $I_2(t) > 0$ for all $t \in (t_0, t_0 + \delta)$. Hence,

$$(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t)) \in X_0$$

in $(t_0, t_0 + \delta)$. This is a contradiction with

$$(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) \in M_\partial.$$

This proves (5.1).

Denote

$$\Omega = \bigcup\{\omega(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) : (S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0)) \in X\}$$

where $\omega(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0))$ is the omega limit set of the solutions of system (2.1) starting in $(S_1(0), E_1(0), I_1(0), S_2(0), E_2(0), I_2(0))$. Restricting system (2.1) on M_∂ gives

$$\begin{cases} \dfrac{dS_1}{dt} &= a-(b+\alpha)S_1+\alpha S_2, \\ \dfrac{dE_1}{dt} &= -(b+\varepsilon+\alpha)E_1+\alpha(1-\gamma_2)E_2, \\ \dfrac{dS_2}{dt} &= a-(b+\alpha)S_2+\alpha S_1, \\ \dfrac{dE_2}{dt} &= -(b+\varepsilon+\alpha)E_2+\alpha(1-\gamma_2)E_1. \end{cases} \tag{5.2}$$

It is easy to verify that system (5.2) has an unique equilibrium $(\frac{a}{b},0,\frac{a}{b},0)$. Thus $(\frac{a}{b},0,0,\frac{a}{b},0,0)$ is the unique equilibrium of system (2.1) in M_∂. It is easy to check that $(\frac{a}{b},0,\frac{a}{b},0)$ is locally asymptotically stable. This implies that $(\frac{a}{b},0,\frac{a}{b},0)$ is globally asymptotically stable for (5.2) is a linear system. Therefore $\Omega = \{P_0\}$. And P_0 is a covering of Ω, which is isolated and is acyclic (since there exists no solution in M_∂ which links P_0 to itself). Finally, the proof will be done if we show P_0 is a weak repeller for X_0, i.e.

$$\limsup_{t\to\infty} dist((S_1(t),E_1(t),I_1(t),S_2(t),E_2(t),I_2(t)),P_0) > 0,$$

where $(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t))$ is an arbitrarily solution with initial value in $\boldsymbol{X}_0$. By Leenheer and Smith (2003, Proof of Lemma 3.5, [21]), we need only prove $W^s(P_0) \cap X_0 = \phi$ where $W^s(P_0)$ is the stable manifold of P_0. Suppose it is not true, then there exists a solution $(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t))$ in X_0, such that

$$S_i(t) \to \frac{a}{b}, E_i(t) \to 0, I_i(t) \to 0 \quad \text{as} \quad t \to \infty. \tag{5.3}$$

Since $R_{0\gamma} = \frac{(\beta+\gamma_1\alpha)(\varepsilon+\gamma_2\alpha)}{(b+\varepsilon+\gamma_2\alpha)(b+d)} > 1$ which is equivalent to $\frac{\beta+\gamma_1\alpha}{b+d} > \frac{b+\varepsilon+\gamma_2\alpha}{\varepsilon+\gamma_2\alpha}$. Thus, we can choose $\delta > 0$, $\rho_1 > 0$ and $\rho_2 > 0$ such that

$$\frac{\beta+\gamma_1\alpha}{b+d}\cdot\frac{a-b\delta}{a+b\delta} > \frac{\rho_2}{\rho_1} > \frac{b+\varepsilon+\gamma_2\alpha}{\varepsilon+\gamma_2\alpha}.$$

For $\delta > 0$, by (5.3) there exists $T > 0$ such that

$$\frac{a}{b} - \delta < S_i(t) < \frac{a}{b} + \delta, 0 \le E_i(t) < \delta, 0 < I_i(t) < \delta$$

for $t \ge T$ and $i = 1, 2$. Let

$$V(t) = \rho_1 (E_1(t) + E_2(t)) + \rho_2 (I_1(t) + I_2(t)).$$

The derivative of V along the solution $(S_1(t), E_1(t), I_1(t), S_2(t), E_2(t), I_2(t))$ is given by

$$\begin{aligned} V'(t) &= \rho_1(\beta + \gamma_1\alpha)\left[\tfrac{S_1 I_1}{S_1+E_1+I_1} + \tfrac{S_2 I_2}{S_2+E_2+I_2}\right] - \rho_1(b + \varepsilon + \gamma_2\alpha)(E_1 + E_2) \\ &\quad + \rho_2(\varepsilon + \gamma_2\alpha)(E_1 + E_2) - \rho_2(b + d)(I_1 + I_2) \\ &\ge \rho_1(\beta + \gamma_1\alpha)\ \tfrac{a-b\delta}{a+b\delta}\ (I_1 + I_2) - \rho_1(b + \varepsilon + \gamma_2\alpha)(E_1 + E_2) \\ &\quad + \rho_2(\varepsilon + \gamma_2\alpha)(E_1 + E_2) - \rho_2(b + d)(I_1 + I_2) \\ &= [\rho_1(\beta + \gamma_1\alpha)\ \tfrac{a-b\delta}{a+b\delta} - \rho_2(b + d)](I_1 + I_2) + [\rho_2(\varepsilon + \gamma_2\alpha) \\ &\quad - \rho_1(b + \varepsilon + \gamma_2\alpha)](E_1 + E_2) \ge \rho V(t) \end{aligned}$$

for all $t \ge T$, where

$$\rho = \min\left(\frac{\rho_1(\beta+\gamma_1\alpha)\frac{a-b\delta}{a+b\delta} - \rho_2(b+d)}{\rho_2}, \frac{\rho_2(\varepsilon+\gamma_2\alpha) - \rho_1(b+\varepsilon+\gamma_2\alpha)}{\rho_1} \right) > 0.$$

Hence $V(t) \to \infty$ as $t \to \infty$, which contradicts to the boundedness of $V(t)$. This completes the proof.

Remark 5.1: From Theorem 5.1 together with Theorem 3.1, we can claim that the basic reproduction number $R_{0\gamma}$ is a sharp threshold parameter which determines the outcome of disease. In other words, if $R_{0\gamma} \le 1$, the disease-free equilibrium P_0 is globally asymptotically stable so that the disease dies out, while if $R_{0\gamma} > 1$, the disease is permanent so that the disease remains endemic in the sense of permanence.

6. GLOBAL STABILITY OF P_+

Firstly, we give the following results which may be found in [22] for studying the global stability of P_+. Consider the following two systems

$$x'(t) = f(t, x) \tag{6.1}$$

$$x'(t) = g(y), \tag{6.2}$$

where f and g are continuous and locally Lipschitz on $x \in R^n$ and solutions exist for all time t. If $\lim_{t\to\infty} f(t, x) = g(x)$ uniformly for $x \in R^n$, then we called system (6.2) is *asymptotically autonomous limit system* of system (6.1).

Lemma 6.1: Let M be a locally asymptotically stable equilibrium of system (6.2) and Ω be the ω–limit set of a forward bounded solution $x(t)$ of system (6.1). If Ω contains a point y_0 such that the solution of system (6.2) $y(t) \to M$ $(t \to \infty)$ with $y(0) = y_0$, *then* $\Omega = \{M\}$ *i.e.* $x(t) \to M$ $(t \to \infty)$.

Corollary 6.1: If solutions of the system (6.1) are bounded and the equilibrium M of the limit system (6.2) is globally asymptotically stable, then any solution $x(y)$ of the system (6.1) satisfies $x(t) \to M$ $(t \to \infty)$.

By (2.1), N_1 and N_2 satisfies the following equation

$$\begin{aligned} N_1'(t) &= a-(b+\alpha)N_1(t)+\alpha N_2(t), \\ N_2'(t) &= a-(b+\alpha)N_2(t)+\alpha N_1(t). \end{aligned} \tag{6.3}$$

It easy to check that system (6.3) has an unique equilibrium $(\frac{a}{b},\frac{a}{b})$ which is globally stable. Hence, the differential system (2.1) is asymptotically autonomous to the following system:

$$\begin{cases} \dfrac{dE_1}{dt} = \beta\frac{b}{a}(\frac{a}{b}-E_1-I_1)I_1+\gamma_1\alpha\frac{b}{a}(\frac{a}{b}-E_2-I_2)I_2-(b+\varepsilon+\alpha)E_1+\alpha(1-\gamma_2)E_2, \\ \dfrac{dI_1}{dt} = \varepsilon E_1-(b+d+\alpha)I_1+\alpha I_2+\gamma_2\alpha E_2, \\ \dfrac{dE_2}{dt} = \beta\frac{b}{a}(\frac{a}{b}-E_2-I_2)I_2+\gamma_1\alpha\frac{b}{a}(\frac{a}{b}-E_1-I_1)I_1-(b+\varepsilon+\alpha)E_2+\alpha(1-\gamma_2)E_1, \\ \dfrac{dI_2}{dt} = \varepsilon E_2-(b+d+\alpha)I_2+\alpha I_1+\gamma_2\alpha E_1. \end{cases} \tag{6.4}$$

Furthermore, we easily know that the set

$$\Gamma=\left\{(E_1,I_1,E_2,I_2): 0\le E_i\le\frac{a}{b}, 0\le I_i\le\frac{a}{b}, i=1,2\right\}.$$

is positively invariant.

Theorem 6.1: Suppose that

$$\begin{aligned} &|\beta-\gamma_1\alpha|\left\{9|\beta-\gamma_1\alpha|+4(b+d+2\alpha)+6|\beta+\varepsilon-\gamma_1\alpha-\gamma_2\alpha|\right\} \\ &< 4(b+d+2\alpha)(b+\varepsilon+2\alpha-\gamma_2\alpha)-(\beta+\varepsilon-\gamma_1\alpha-\gamma_2\alpha)^2. \end{aligned} \tag{6.5}$$

The endemic equilibrium point $P_+(S^*, E^*, I^*, S^*, E^*, I^*)$ is globally asymptotically stable on X_0 for $R_{0\gamma}>1$.

Proof. By Theorem 5.1 and Corollary 6.1, we only need show that the equilibrium (E^*, I^*, E^*, I^*) of system (6.4) is globally asymptotically stable in Γ for global stability of P_+. Let us consider the function:

$$V(t)=\frac{1}{2}\left\{(E_1(t)-E_2(t))^2+(I_1(t)-I_2(t))^2\right\}$$

The time derivative of $V(t)$ along solutions of (6.4) becomes

$$\begin{aligned} V'(t) &= (E_1-E_2)(E_1'-E_2')+(I_1-I_2)(I_1'-I_2') \\ &= (E_1-E_2)\{(\beta-\gamma_1\alpha)\tfrac{b}{a}[(\tfrac{a}{b}-E_1-I_1)I_1-(\tfrac{a}{b}-E_2-I_2)I_2] \\ &\quad -(b+\varepsilon+2\alpha-\gamma_2\alpha)(E_1-E_2)\} \\ &\quad +(I_1-I_2)\{(\varepsilon-\gamma_2\alpha)(E_1-E_2)-(b+d+2\alpha)(I_1-I_2)\} \end{aligned}$$

$$= -(b + \varepsilon + 2\alpha - \gamma_2\alpha)(E_1 - E_2)^2 - (b + d + 2\alpha)(I_1 - I_2)^2$$
$$+(\beta + \varepsilon - \gamma_1\alpha - \gamma_2\alpha)(E_1 - E_2)(I_1 - I_2)$$
$$-(\beta - \gamma_1\alpha)\, \tfrac{b}{a} (E_1 - E_2)[(E_1I_1 - E_2I_2) + (I_1^2 - I_2^2)]$$

Note that

$$|E_1I_1 - E_2I_2| \le |E_1I_1 - E_1I_2| + |E_1I_2 - E_2I_2| \le \tfrac{a}{b} (|I_1 - I_2| + |E_1 - E_2|)$$

and

$$|I_1^2 - I_2^2| \le 2\tfrac{a}{b}\; |I_1 - I_2|$$

which gives the following

$$V'(t) \le -(b + \varepsilon + 2\alpha - \gamma_2\alpha - |\beta - \gamma_1\alpha|)(E_1 - E_2)^2 - (b + d + 2\alpha)(I_1 - I_2)^2$$
$$+(|\beta + \varepsilon - \gamma_1\alpha - \gamma_2\alpha| + 3|\beta - \gamma_1\alpha|)|E_1 - E_2||I_1 - I_2|.$$

The above quadratic form is negative definite if and only if

$$|\beta - \gamma_1\alpha| < b + \varepsilon + 2\alpha - \gamma_2\alpha$$

and

$$(|\beta + \varepsilon - \gamma_1\alpha - \gamma_2\alpha| + 3|\beta - \gamma_1\alpha|)^2 < 4(b + \varepsilon + 2\alpha - \gamma_2\alpha - |\beta - \gamma_1\alpha|)(b + d + 2\alpha)$$

It is easy to check that the above conditions are satisfied if and only if (6.5) is satisfied. Hence we can find some positive constant λ satisfying

$$V'(t) \le -\lambda\ \{(E_1 - E_2)^2 + (I_1 - I_2)^2\}.$$

which shows that for any solution $(E_1(t), I_1(t), E_2(t), I_2(t))$ of (6.4), we have

$$\lim_{t\to\infty}\left(E_1(t) - E_2(t)\right) = 0, \quad \lim_{t\to\infty}\left(I_1(t) - I_2(t)\right) = 0.$$

By Lyapunov's theorem, we know that $\omega(x) \bigcap R_+^4$ is contained in the set $\{x \in R_+^4 : \dot{V} = 0\} = \{(E_1, I_1, E_2, I_2) \in R_+^4 :$ $E_1, I_1 = I_2\}$. Here $\omega(x)$ is ω–limit set of the solution $(E_1(t), I_1(t), E_2(t), I_2(t))$ of (6.4) with initial value in R_+^4. On the set $W = \{(E_1, I_1, E_2, I_2) \in R_+^4 : E_1 = E_2, I_1 = I_2\}$, we now consider the following system for $E = E_i$ and $I = I_i (i = 1, 2)$ i.e.

$$\begin{cases} \dfrac{dE}{dt} = (\beta + \gamma_2\alpha)\dfrac{b}{a}\left(\dfrac{a}{b} - E - I\right)I - (b + \varepsilon + \gamma_1\alpha)\, E \triangleq f(E, I) \\[2ex] \dfrac{dI}{dt} = (\varepsilon + \gamma_2\alpha)E - (b + d)\, I \triangleq g\,(E, I). \end{cases} \tag{6.6}$$

It is trivial that the equilibrium (E^*, I^*) of system (6.6) is locally asymptotically stable and the equilibrium (0, 0) is unstable as $R_{0\gamma} > 1$. Take Dulac's function $B = \frac{1}{I}$, since

$$\frac{\partial}{\partial E}\left(\frac{f}{I}\right) + \frac{\partial}{\partial I}\left(\frac{g}{I}\right) = -(\beta + \gamma_1\alpha)\frac{b}{a} - \frac{b + \varepsilon + \gamma_2\alpha}{I} - \frac{(\varepsilon + \gamma_2\alpha)E}{I^2} < 0$$

then there is no periodic solution of (6.6). Thus, (E^*, I^*) of system (6.6) is globally asymptotically stable. This shows that the endemic equilibrium P_+ of system (2.1) is globally asymptotically stable. This completes the proof.

Remark 6.1: Unfortunately, we are unable yet to prove the global stability of the endemic equilibrium when it exists. Numerical simulation shows that the additional condition (6.5) is just sufficient. We will explore global stability of P_+ if it exists in near future.

7. DISCUSSION

In this paper, we have formulated a compartmental SEIS epidemic model with transport-related infection. We derived an explicit formula for the reproductive number $R_{0\gamma}$. From Theorems 3.1, 4.1, 5.1 and 6.1, we know that when the reproduction number $R_{0\gamma} \le 1$, disease eradication in both cities is possible. However, when $R_{0\gamma} > 1$, the disease will always exist in both cities in the sense of permanence, which means the number of infected individuals independent of initial value will ultimately remain above a positive level. If we neglect the movement of individuals, that is, consider the case $\alpha = 0$, then (2.1) is reduced to a very well known SEIS model

$$\begin{cases} \dfrac{dS}{dt} & = a - bS - \dfrac{\beta SI}{S+E+I} + dI, \\ \dfrac{dE}{dt} & = \dfrac{\beta SI}{S+E+I} - bE - \varepsilon E, \\ \dfrac{dI}{dt} & = \varepsilon E - (b+d)I. \end{cases} \tag{7.1}$$

Above model has been analyzed many times in the past and the basic reproduction number is give below

$$R_0 = \frac{\beta\varepsilon}{(b+\varepsilon)(b+d)}.$$

When $R_0 \le 1$, the disease-free equilibrium of system (7.1) is GAS. When $R_0 > 1$, the endemic equilibrium of system (7.1) is GAS. Comparing $R_{0\gamma}$ and R_0, we see that $R_{0\gamma} > R_0$ for $\gamma_1 + \gamma_2 > 0$ as $\alpha > 0$. Even if the disease dies out separately in two cities in the absence of transport-related infection, it is possible that the disease will cause endemic disease due to transport-related infection.

Now we consider the coexistence steady state $P_+ (S^*, E^*, I^*, S^*, E^*, I^*)$ when the disease is endemic in both cities. It is easy to check that

$$\frac{\partial S^*}{\partial \gamma_i} < 0, \quad \frac{\partial I^*}{\partial \gamma_i} > 0, \, (i = 1, 2).$$

This implies that at the steady state the total number of susceptible individuals in both cities decreases with the increase of γ_i, while one of infected individuals increases with the increase of γ_i.

Since we know that the endemic equilibrium P_+ of (2.1) is LAS and system (2.1) is permanent if $R_{0\gamma} > 1$. The global asymptotic stability results of P_+ are obtained for the model (2.1) with certain condition (6.5). Computer observations suggest that the endemic equilibrium is still GAS when (6.5) is invalid (see Figure 1 and Figure 2).

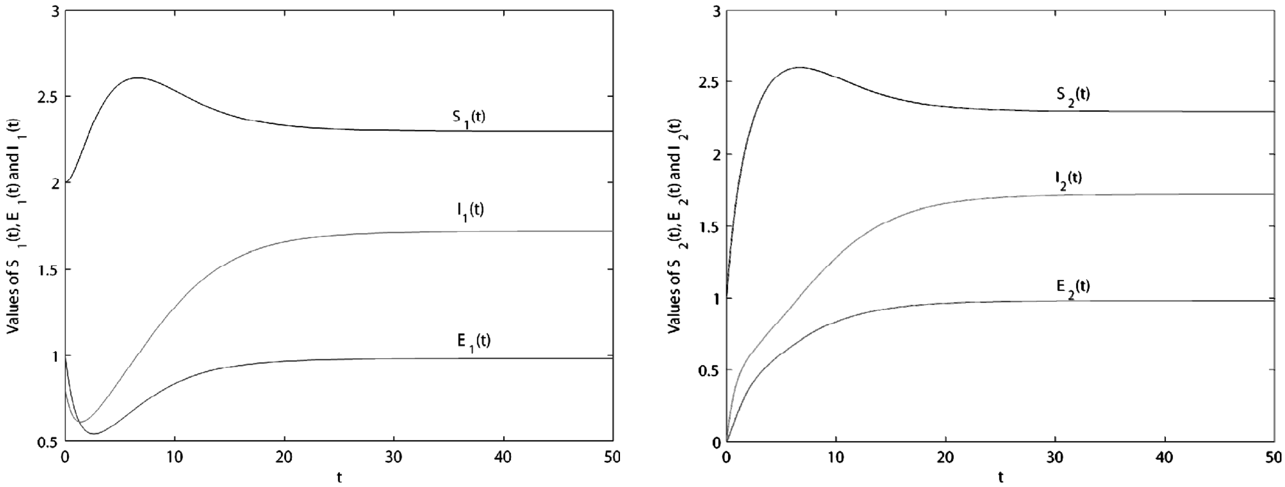

Figure 1: The Left Figure Shows that Movement Paths of S_1, E_1 and I_1 as functions of time t. The Right Figure Shows that Movement Paths of S_2, E_2 and I_2 as Functions of Time t. Here, $a = 1$, $b = 0.2$, $d = 0.2$, $\beta = 0.8$, $\alpha = 0.1$, $\gamma_1 = 0.8$, $\gamma_2 = 1$ and $\varepsilon = 0.3$. We have $R_{0\gamma} = 2.1778 > 1$ and $\eta = 1.2964 > 0$. Initial Data are (2,1,0.8,1,0,0). The Endemic Equilibrium is GAS

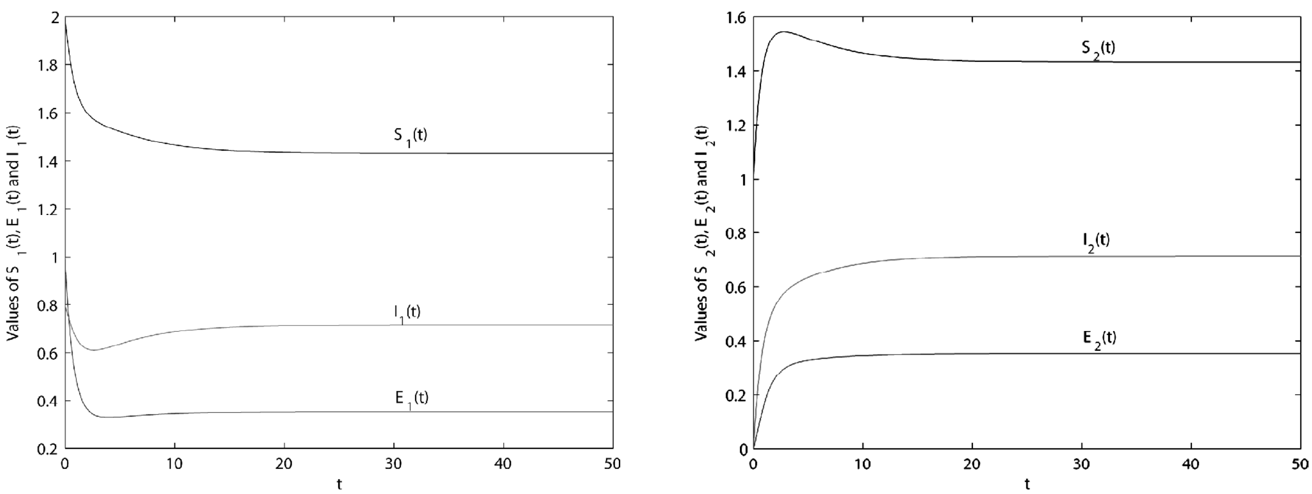

Figure 2: The Left Figure Shows that Movement Paths of S_1, E_1 and I_1 as Functions of Time t. The Right Figure Shows that Movement Paths of S_2, E_2 and I_2 as Functions of Time t. Here, $a = 1$, $b = 0.4$, $d = 0.044$, $\beta = 0.8$, $\alpha = 0.4$, $\gamma_1 = 0.8$, $\gamma_2 = 1$ and $\varepsilon = 0.5$. We have $R_{0\gamma} = 1.7463 > 1$ and $\eta = 0$. Initial Data are (2,1,0.8,1,0,0). The Endemic Equilibrium is GAS

Conjecture: The endemic point P_+ of (2.1) is globally asymptotically stable if it exists.

About Figure 1 and Figure 2, we give some simple biological meaning. For convenience, we denote

$$\begin{aligned}\eta = &|\beta-\gamma_1\alpha|\{9|\beta-\gamma_1\alpha|+4(b+d+2\alpha)+6|\beta+\varepsilon-\gamma_1\alpha-\gamma_2\alpha|\}\\ &-4(b+d+2\alpha)(b+\varepsilon+2\alpha-\gamma_2\alpha)+(\beta+\varepsilon-\gamma_1\alpha-\gamma_2\alpha)^2.\end{aligned}$$

Hence, $\eta < 0$ is equivalent to (6.5). From Figure 1 and Figure 2, we take initial value (2,1,0.8,1,0,0), which means there is no patient in city 2 at time 0. But the disease is still developed to become endemic in city 2 by exposed and infected individuals' movement.

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