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On the global stability of a delayed epidemic model with transport-related infection

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ABSTRACT

We study the global dynamics of a time delayed epidemic model proposed by Liu et al. (2008) [J. Liu, J. Wu, Y. Zhou, Modeling disease spread via transport-related infection by a delay differential equation, Rocky Mountain J. Math. 38 (5) (2008) 1525–1540] describing disease transmission dynamics among two regions due to transport-related infection. We prove that if an endemic equilibrium exists then it is globally asymptotically stable for any length of time delay by constructing a Lyapunov functional. This suggests that the endemic steady state for both regions is globally asymptotically stable regardless of the length of the travel time when the disease is transferred between two regions by human transport.

1. Introduction

Population dispersal by human transportation currently plays an important role in the spread of infectious disease around the world. SARS (severe acute respiratory syndrome) spread along the routes of international air travel and infection was carried to many places [1]. Khan et al. [2] pointed out a correlation between inter-regional spread of a novel influenza A (H1N1) virus and travelers. From these observations a number of authors have proposed epidemic models describing disease transmission dynamics among multiple locations due to the population dispersal (see [3–6] and the references therein).

Cui et al. [7] have proposed an epidemic model which models a phenomenon where individuals in a population suffer from diseases and possibly become infected during the movement between two regions. The model is given as a system of ordinary differential equations based on an SIS epidemic model. Takeuchi et al. [8] analyzed local and global stability of equilibria as well as uniform persistence of the system. They found that there is a possibility of endemic situation due to the transport-related infection. However, as pointed out by Liu et al. [9] the epidemic models proposed in [7,10,8] implicitly assumed that the transportation between two regions occurs instantaneously. This motivated Liu et al. [9] to rigorously describe the disease transmission dynamics during the transportation by introducing the time needed to complete the use of the transportation. They assumed that it takes $\tau$ units of time to complete one-way transport between two regions. They obtained the following delay differential equations:

\[
\begin{align*}
\frac{dS_1(t)}{dt} &= A - dS_1(t) - \frac{\beta S_1(t)I_1(t)}{S_1(t) + I_1(t)} + \delta I_1(t) - \alpha S_1(t) + s_{21}(\tau, t - \tau), \\
\frac{dI_1(t)}{dt} &= \frac{\beta S_1(t)I_1(t)}{S_1(t) + I_1(t)} + i_{21}(\tau, t - \tau) - (d + \delta + \alpha)I_1(t), \\
\frac{dS_2(t)}{dt} &= A - dS_2(t) - \frac{\beta S_2(t)I_2(t)}{S_2(t) + I_2(t)} + \delta I_2(t) - \alpha S_2(t) + s_{12}(\tau, t - \tau), \\
\frac{dI_2(t)}{dt} &= \frac{\beta S_2(t)I_2(t)}{S_2(t) + I_2(t)} + i_{12}(\tau, t - \tau) - (d + \delta + \alpha)I_2(t),
\end{align*}
\] (1.1)
with
\[
S_{21}(\tau, t - \tau) = \frac{\alpha e^{-\gamma \tau} S_2(t - \tau)}{e^{-\gamma \tau S_2(t - \tau) + S_2(t - \tau)}} (S_2(t - \tau) + I_2(t - \tau)),
\]
\[
i_{21}(\tau, t - \tau) = \frac{\alpha I_2(t - \tau)}{e^{-\gamma \tau S_2(t - \tau) + S_2(t - \tau)}} (S_2(t - \tau) + I_2(t - \tau)),
\]
\[
S_{12}(\tau, t - \tau) = \frac{\alpha e^{-\gamma \tau} S_1(t - \tau)}{e^{-\gamma \tau S_1(t - \tau) + S_1(t - \tau)}} (S_1(t - \tau) + I_1(t - \tau)),
\]
\[
i_{12}(\tau, t - \tau) = \frac{\alpha I_1(t - \tau)}{e^{-\gamma \tau S_1(t - \tau) + S_1(t - \tau)}} (S_1(t - \tau) + I_1(t - \tau)).
\]

Here \(S_j(t)\) and \(I_j(t)\) denote the numbers of susceptible and infected individuals at time \(t\) in region \(j\), respectively, where \(j \in \{1, 2\}\). \(A\) is the total number of newborns per unit time, \(d\) is the natural death rate and \(\delta\) is the recovery rate. Disease is transmitted by \(\beta S_j I_j / (S_j + I_j)\), where \(\beta\) is the disease transmission coefficient in each region. Susceptible and infected individuals leave a region towards another region at a per capita rate \(\alpha\). Thus the numbers of susceptible and infected individuals leaving region \(j\) per unit time are given by \(\alpha S_j(t)\) and \(\alpha I_j(t)\), respectively. \(S_{kj}(\tau, t - \tau)\) and \(I_{kj}(\tau, t - \tau)\) for \(j, k \in \{1, 2\}\) and \(j \neq k\) denote the numbers of susceptible and infected individuals arriving in region \(j\) from region \(k\) per unit time at time \(t\). They leave region \(j\) at time \(t - \tau\) and spend \(\tau\) units of time in transportation, where disease transmission occurs. We denote by \(\gamma\) the transmission coefficient in the transportation. It is assumed that every parameter is positive.

Following [9], we explain how to derive \(S_{kj}(\tau, t - \tau)\) and \(I_{kj}(\tau, t - \tau)\) for \(j, k \in \{1, 2\}\) and \(j \neq k\). We denote by \(S_{kj}(\theta, t)\) and \(I_{kj}(\theta, t)\) the numbers of susceptible and infected individuals leaving region \(k\) per unit time at time \(t\) and spend \(\theta\) units of time in transportation to region \(j\), where \(\theta \in [0, \tau]\). Then considering the number of susceptible and infected individuals leaving region \(k\) to \(j\) per unit time at time \(t - \tau\) we obtain that
\[
S_{kj}(0, t - \tau) = \alpha S_{kj}(t - \tau) \quad \text{and} \quad I_{kj}(0, t - \tau) = \alpha I_{kj}(t - \tau).
\]

We assume that the individuals in the population do not die in the transportation. Then the disease dynamics in the transportation from region \(k\) to \(j\) can be described as
\[
\frac{\partial}{\partial \theta} S_{kj}(\theta, t - \tau) = -\gamma I_{kj}(\theta, t - \tau) S_{kj}(\theta, t - \tau),
\]
\[
\frac{\partial}{\partial \theta} I_{kj}(\theta, t - \tau) = \gamma I_{kj}(\theta, t - \tau) S_{kj}(\theta, t - \tau),
\]
where \(\gamma\) is the transmission coefficient in the transportation. Since it holds that
\[
S_{kj}(\theta, t - \tau) + I_{kj}(\theta, t - \tau) = \alpha(S_1(t - \tau) + I_1(t - \tau)) \quad \text{for any } \theta \in [0, \tau]
\]
we obtain that
\[
\frac{\partial}{\partial \theta} I_{kj}(\theta, t - \tau) = \gamma I_{kj}(\theta, t - \tau) \left\{ 1 - \frac{I_{kj}(\theta, t - \tau)}{\alpha(S_1(t - \tau) + I_1(t - \tau))} \right\}.
\]

By solving (1.4) using (1.2) as the initial condition, we obtain the expression for \(I_{kj}(\tau, t - \tau)\). Then it is easy to see that (1.3) gives the expression for \(S_{kj}(\tau, t - \tau)\).

Liu et al. [9] identified the basic reproduction number \(R_0\) and analyzed the stability property of the equilibria and uniform persistence of the system; the basic reproduction number is given as
\[
R_0 := \frac{\beta + \alpha e^{\gamma \tau}}{d + \delta + \alpha}.
\]

(1.1) always has a disease-free equilibrium. They proved that the disease-free equilibrium is globally asymptotically stable if \(R_0 < 1\). If \(R_0 > 1\) then (1.1) admits a unique endemic equilibrium. By analyzing an associated characteristic equation they proved that the endemic equilibrium is locally asymptotically stable if \(R_0 > 1\) [9, Theorem 4.1]. Moreover, by the uniform persistence theorem [11], they obtained that the disease eventually persists if \(R_0 > 1\) [9, Theorem 4.2].

However, the problem of global stability of the endemic equilibrium remains unsolved. Stability analysis for epidemic models is helpful for obtaining insight into the disease transmission dynamics. Global stability of equilibria, in particular, makes the model dynamics clear and enhances our understanding of the mathematical models. In this paper we prove that the endemic equilibrium is globally asymptotically stable if \(R_0 > 1\). Our proof is based on constructing a Lyapunov functional and using LaSalle’s invariance principle. Our mathematical results suggest that, when the infectious disease is transferred between two regions by human transportation, the endemic steady state is globally asymptotically stable regardless of the length of the travel time if the basic reproduction number exceeds 1.

The paper is organized as follows. In the next section, first, we discuss the global dynamics of the total populations in both regions and show that a unique positive equilibrium is globally asymptotically stable. Using this result we obtain a limit system for (1.1). Constructing a Lyapunov functional for this reduced system, we prove that an unique positive equilibrium of the system is globally asymptotically stable if \(R_0 > 1\) in Theorem 2.6. This implies that the endemic equilibrium of (1.1) is also globally asymptotically stable if \(R_0 > 1\). In Section 3, we offer a discussion.
2. Global stability of the endemic equilibrium

To investigate the dynamics of (1.1), we set a suitable phase space. We denote by \( C = C([-\tau, 0], \mathbb{R}) \) the Banach space of continuous functions mapping the interval \([-\tau, 0]\) into \( \mathbb{R} \) equipped with the sup-norm. The nonnegative cone of \( C \) is defined as \( C_+ = C([-\tau, 0], \mathbb{R}_+) \). From the biological meanings, the initial conditions for (1.1) are

\[
S_1(\theta) = \phi_1(\theta), \quad I_1(\theta) = \phi_2(\theta), \quad S_2(\theta) = \psi_1(\theta), \quad I_2(\theta) = \psi_2(\theta), \quad \theta \in [-\tau, 0],
\]

where \( \phi_i, \psi_i \in C_+, i = 1, 2 \).

**Lemma 2.1** (See [9, Lemmas 2.1 and 2.2]). The solution of (1.1) with initial conditions (2.1) is nonnegative for all \( t > 0 \). Moreover, there exist \( M > 0 \) and \( T > 0 \) such that \( S_i(t) \leq M \) and \( I_i(t) \leq M \) for \( i = 1, 2 \) and \( t \geq T \).

First, we consider the global dynamics of total populations in both regions. Let us define

\[
N_j(t) := S_j(t) + I_j(t), \quad j \in \{1, 2\}.
\]

Then from (1.1) and (2.1) we have

\[
\frac{dN_j(t)}{dt} = A - (d + \alpha)N_j(t) + \alpha N_i(t - \tau) \quad \text{for} \ j, k \in \{1, 2\} \text{ and } j \neq k
\]

with the initial conditions \( N_j(\theta) = \phi(\theta) \) and \( N_i(\theta) = \psi(\theta) \) for \( \theta \in [-\tau, 0] \), where \( \phi = \phi_1 + \phi_2 \) and \( \psi = \psi_1 + \psi_2 \). We prove that (2.2) has a unique positive equilibrium which is globally asymptotically stable.

**Lemma 2.2.** (2.2) has a unique positive equilibrium which is globally asymptotically stable.

**Proof.** Since the equilibrium satisfies

\[
\begin{pmatrix} N_1 \\ N_2 \end{pmatrix} = \left( \begin{array}{cc} d + \alpha & -\alpha \\ -\alpha & d + \alpha \end{array} \right)^{-1} \left( \begin{array}{c} A \\ 1 \end{array} \right)
\]

we easily obtain the existence of the unique positive equilibrium.

Let us consider the asymptotic stability of the equilibrium. We define

\[
G_N = \{(\phi, \psi) \in C([-\tau, 0], \mathbb{R}^2_+)|\phi(\theta) \geq 0, \psi(\theta) \geq 0, \theta \in [-\tau, 0], \phi(0) > 0, \psi(0) > 0\}.
\]

\( \overline{G}_N \), which is the closure of \( G_N \), is positively invariant for (2.2).

We denote by \( (N^*, N^*) \) the positive equilibrium of (2.2). Consider the following functional defined on \( G_N \):

\[
\begin{equation}
L(N_1, N_2) = \sum_{j=1}^{2} g \left( \frac{N_j(t)}{N^*} \right) + \alpha \sum_{j=1}^{2} \int_{t-\tau}^{t} g \left( \frac{N_j(s)}{N^*} \right) ds,
\end{equation}
\]

where

\[
g(x) = x - 1 - \ln x \quad \text{for} \ x \in (0, +\infty)
\]

and \( N_j(t), j = 1, 2 \), is any solution of (2.2). It is clear that \( L \) is continuous on \( G_N \) and that for any \( (\phi, \psi) \in \partial G_N \) (the boundary of \( G_N \)), the limit \( l(\phi, \psi) = \lim_{(\phi, \psi) \to (\phi, \psi) \in \partial G_N} L(\phi, \psi) \), \( (\phi, \psi) \in G_N \), exists or is \( +\infty \). We consider the time derivative of \( L(N_1, N_2) \) along the solution of (2.2).

First of all, we see that

\[
\frac{d}{dt} \left[ \frac{N_j(t)}{N^*} \right] = \frac{1}{N^*} \left( 1 - \frac{N^*}{N_j(t)} \right) \left( A - (d + \alpha)N_j(t) + \alpha N_i(t - \tau) \right).
\]

Then, from \( A = (d + \alpha)N^* - \alpha N^* \), it follows that

\[
\frac{d}{dt} \left[ \frac{N_j(t)}{N^*} \right] = (d + \alpha) \left( 1 - \frac{N^*}{N_j(t)} \right) \left( 1 - \frac{N_j(t)}{N_j(t)} \right) + \alpha \left( 1 - \frac{N^*}{N_j(t)} \right) \left( \frac{N_i(t - \tau)}{N^*} - 1 \right)
\]

\[
= (d + \alpha) \left( 2 - \frac{N_j(t)}{N_j} - \frac{N^*}{N_j(t)} \right) + \alpha \left( \frac{N_i(t - \tau)}{N^*} - 1 - \frac{N_i(t - \tau)}{N_j(t)} + \frac{N^*}{N_j(t)} \right).
\]

It follows that

\[
\frac{d}{dt} \int_{t-\tau}^{t} g \left( \frac{N_j(s)}{N^*} \right) ds = g \left( \frac{N_j(t)}{N^*} \right) - g \left( \frac{N_j(t - \tau)}{N^*} \right)
\]

\[
= \frac{N_j(t)}{N^*} - \ln \left( \frac{N_j(t)}{N^*} \right) - \frac{N_j(t - \tau)}{N^*} + \ln \left( \frac{N_j(t - \tau)}{N^*} \right).
\]
Therefore, we obtain that
\[
\dot{L}_{(2,2)}(N_1, N_2) = \sum_{j=1}^{2} \left\{ (d + \alpha) \left( 2 - \frac{N_j(t)}{N^*} - \frac{N^*}{N_j(t)} \right) + \alpha \left( -2 + \frac{N_j(t)}{N^*} + \frac{N^*}{N_j(t)} \right) \right\} \\
+ \alpha \left\{ \left( -\frac{N_2(t - \tau)}{N_1(t)} + 1 + \ln \frac{N_2(t - \tau)}{N_1(t)} \right) + \left( -\frac{N_1(t - \tau)}{N_2(t)} + 1 + \ln \frac{N_1(t - \tau)}{N_2(t)} \right) \right\} \\
= d \sum_{j=1}^{2} \left( 2 - \frac{N_j(t)}{N^*} - \frac{N^*}{N_j(t)} \right) - \alpha \left\{ g \left( \frac{N_2(t - \tau)}{N_1(t)} \right) + g \left( \frac{N_1(t - \tau)}{N_2(t)} \right) \right\}.
\]

Hence we obtain that
\[
\dot{L}_{(2,2)}(N_1, N_2) \leq 0.
\] (2.4)

From (2.3) and (2.4), the positive equilibrium is stable.

Let us define that
\[
E := \{ (\phi, \psi) \in \mathbb{C}_N | l(\phi, \psi) < +\infty, \dot{L}_{(2,2)}(\phi, \psi) = 0 \}
\]
and that \( M \) is the largest subset in \( E \) that is invariant with respect to (2.2). Then, we see that
\[
E = \{ (\phi, \psi) \in \mathbb{C}_N | \phi(0) = \phi(-\tau) = \psi(0) = \psi(-\tau) = N^* \}.
\]

Consider any initial function \((\phi, \psi) \in M\). Then it holds that \((N_{1t}, N_{2t}) \in M \subset E\), where \(N_{1t}(\theta) = N_1(t + \theta)\) and \(N_{2t}(\theta) = N_2(t + \theta)\) through \((0, \phi, \psi)\). Hence, \(M = \{N^*, N^*\}\). By an extension of LaSalle’s invariance principle [12, Lemma 3.1], any solution tends to \(M\) (see also [13,14]). Hence, the positive equilibrium is globally asymptotically stable. \( \Box \)

**Remark 2.3.** Suzuki and Matsunaga [15] established the necessary and sufficient conditions for asymptotic stability of a class of linear delay differential equations. Their result is applicable to (2.2) and it also yields Lemma 2.2 [15, Example 2].

Next using the result in Lemma 2.2 we derive a limit system of (1.1). We denote by \((N^*, N^*)\) the unique positive equilibrium of (2.2). Since \(S_j(t) = N_j(t) - I_j(t), j \in \{1, 2\}, (1.1)\) has the following limit system:
\[
\frac{dI_j(t)}{dt} = I_j(t) \left\{ \beta - (d + \delta + \alpha) - \frac{\beta}{N^*}I_j(t) \right\} + G(I_k(t - \tau)) \quad \text{for} \ j, k \in \{1, 2\} \text{ and } j \neq k,
\] (2.5)

where
\[
G(I) := \frac{\alpha e^{\tau I}}{1 + e^{\tau I/N^*}} \quad \text{for} \ I \in [0, +\infty).
\]

From now on we consider the reduced system (2.5) in order to understand the asymptotic behavior of the solution of (1.1) (see [16,17]).

Liu et al. [9] proved that (1.1) has a unique endemic equilibrium if and only if \(R_0 > 1\). We denote the endemic equilibrium by \((S^*, I^*, I^*)\) where every component is strictly positive. Then it is easy to prove that \((I^*, I^*)\) is a unique positive equilibrium of (2.5) if and only if \(R_0 > 1\). We study the global stability of the positive equilibrium of (2.5) in order to establish the global stability of the endemic equilibrium of (1.1).

We give an elementary result to prove the global asymptotic stability of the endemic equilibrium. Let us define
\[
g(x) := x - 1 - \ln x \quad \text{for} \ x \in (0, +\infty).
\]

**Lemma 2.4.** Let us assume that \(R_0 > 1\). Then it holds that
\[
\left( \frac{I_j(t)}{I^*} - \frac{G(I_j(t))}{G(I^*)} \right) \left( \frac{G(I_j(t))}{G(I^*)} - 1 \right) \geq 0
\] (2.6)

and
\[
g \left( \frac{I_j(t)}{I^*} \right) - g \left( \frac{G(I_j(t))}{G(I^*)} \right) \geq 0
\] (2.7)

for \( j \in \{1, 2\} \).
Proof. Direct computation gives

\[
\left( \frac{l_j(t)}{I^*} - \frac{G(l_j(t))}{G(I^*)} \right) \left( \frac{G(l_j(t))}{G(I^*)} - 1 \right) = \frac{G(l_j(t))}{I^*} \left( \frac{l_j(t)}{G(l_j(t))} \right) \left( 1 - \frac{I^*}{G(I^*)} \right) \frac{1}{G(I^*)} (G(l_j(t)) - G(I^*))
\]

\[
= \frac{G(l_j(t))}{G(I^*)} \left( \frac{l_j(t)}{G(l_j(t))} \right) \left( 1 - \frac{I^*}{G(I^*)} \right) (G(l_j(t)) - G(I^*))
\]

for \( j \in \{1, 2\} \). Since \( G(I) \) and \( \frac{I}{G(I)} \) are monotone increasing functions we obtain (2.6). (2.6) implies that

\[
\begin{cases}
\frac{l_j(t)}{I^*} \leq \frac{G(l_j(t))}{G(I^*)} < 1 & \text{for } l_j(t) < I^*, \\
\frac{l_j(t)}{I^*} = \frac{G(l_j(t))}{G(I^*)} = 1 & \text{for } l_j(t) = I^*, \\
\frac{l_j(t)}{I^*} \geq \frac{G(l_j(t))}{G(I^*)} > 1 & \text{for } l_j(t) > I^*.
\end{cases}
\]

Then (2.7) holds. The proof is complete. \( \square \)

Remark 2.5. The property of (2.7) in Lemma 2.4 is also found in [18, 19] and it is used to analyze global dynamics of epidemic models having a nonlinear incidence rate.

We prove the global asymptotic stability of the positive equilibrium of (2.5).

Theorem 2.6. Let us assume that there exists \( \theta_0 \in [-\tau, 0] \) such that \( \phi_2(\theta_0) + \psi_2(\theta_0) > 0 \). Let \( R_0 > 1 \). Then the positive equilibrium of (2.5) is globally asymptotically stable.

Proof. Since there exists a unique positive equilibrium of (2.5) it holds that

\[
\beta - (d + \delta + \alpha) = \frac{\beta I^*}{N^*} - \frac{G(I^*)}{I^*}.
\]

Then (2.5) becomes the following:

\[
\frac{dl_j(t)}{dt} = l_j(t) \left( \frac{\beta I^*}{N^*} - \frac{G(I^*)}{I^*} \right) - \frac{\beta l_j(t)^2}{N^*} + G(l_k(t - \tau))
\]

\[
= \frac{\beta}{N^*} l_j(t) \left( I^* - l_j(t) \right) + G(l_k(t - \tau)) - G(I^*) \frac{l_j(t)}{I^*} \quad \text{for } j \in \{1, 2\} \text{ and } j \neq k.
\] (2.8)

We define

\[
G = \{(\phi_2, \psi_2) \in C([-\tau, 0], \mathbb{R}^2_+) | \phi_2(\theta) \geq 0, \psi_2(\theta) \geq 0, \theta \in [-\tau, 0], \phi_2(0) > 0, \psi_2(0) > 0 \}.
\]

\( \overline{G} \), the closure of \( G \), is positively invariant for (2.8). Moreover, there exists an \( \epsilon > 0 \) such that every solution \((l_1(t), l_2(t))\) of (1.1) with \( \phi_2(\theta_0) + \psi_2(\theta_0) > 0 \) for some \( \theta_0 \in [-\tau, 0] \) satisfies \( \liminf_{t \to +\infty} l_j(t) \geq \epsilon \) (see [9, Theorem 5.1]). This implies that \( G \) is also positively invariant for (2.8).

Consider the following functional defined on \( G \):

\[
U(l_1, l_2) = \frac{l^*}{G(I^*)} \sum_{j=1}^{2} g \left( \frac{l_j(t)}{I^*} \right) + \sum_{j=1}^{2} \int_{t-\tau}^{t} g \left( \frac{G(l_j(s))}{G(I^*)} \right) ds,
\] (2.9)

where \( l_j(t), j \in \{1, 2\} \), are any solutions of (2.8). Then it is clear that \( U \) is continuous on \( G \) and that for any \( (\phi, \psi) \in \partial G \) (the boundary of \( G \)), the limit \( \ell(\phi, \psi) = \lim_{(\phi, \psi) \to (\phi, \psi) \in \partial G} U(\Phi, \Psi), (\Phi, \Psi) \in G \) is \( +\infty \).

We consider the time derivative of \( U \) along the solution of (2.8). First, we see that

\[
\frac{d}{dt} \left[ g \left( \frac{l_j(t)}{I^*} \right) \right] = \frac{1}{I^*} \left( 1 - \frac{I^*}{l_j(t)} \right) \left( \frac{\beta}{N^*} l_j(t)^2 \left( 1 - \frac{l_j(t)}{I^*} \right) + G(I^*) \left( \frac{G(l_k(t - \tau))}{G(I^*)} - \frac{l_j(t)}{I^*} \right) \right)
\]

\[
= -\frac{\beta l^*_j}{N^*} \left( 1 - \frac{l_j(t)}{I^*} \right)^2 + \frac{G(I^*)}{I^*} \left( 1 - \frac{l_j(t)}{l_j(t)} \right) \left( \frac{G(l_k(t - \tau))}{G(I^*)} - \frac{l_j(t)}{I^*} \right)
\]

\[
= -\frac{\beta l^*_j}{N^*} \left( 1 - \frac{l_j(t)}{I^*} \right)^2 + \frac{G(I^*)}{I^*} \left( \frac{G(l_k(t - \tau))}{G(I^*)} - \frac{l_j(t)}{l_j(t)} \right) \left( 1 - \frac{l_j(t)}{l_j(t)} \right) + \left( 1 - \frac{l_j(t)}{l_j(t)} \right) \frac{G(I^*)}{I^*} + 1 \). \] (2.10)
Next it follows that
\[
\frac{d}{dt} \int_{t-	au}^{t} g \left( \frac{G(l_j(s))}{G(l^*)} \right) ds = g \left( \frac{G(l_j(t))}{G(l^*)} \right) - g \left( \frac{G(l_j(t-	au))}{G(l^*)} \right) = \frac{G(l_j(t))}{G(l^*)} - \ln \left( \frac{G(l_j(t))}{G(l^*)} \right) - \frac{G(l_j(t-	au))}{G(l^*)} + \ln \left( \frac{G(l_j(t-	au))}{G(l^*)} \right).
\]
(2.11)

From (2.10) and (2.11) we obtain that
\[
\dot{U}(t_1, t_2) = \frac{B l^*}{N^*} \frac{I^*}{G(l^*)} \sum_{j=1}^{2} \left( 1 - \frac{l_j(t)}{l^*} \right)^2 + C(t),
\]
(2.12)

where
\[
C(t) = \sum_{j,k=1;2}^{l^*} \left( \frac{G(l_k(t-	au))}{G(l^*)} - \frac{l_j(t)}{l^*} - \frac{l^*}{l_j(t)} \frac{G(l_k(t-	au))}{G(l^*)} + 1 \right) + \sum_{j=1}^{2} \left\{ - \ln \left( \frac{G(l_j(t))}{G(l^*)} \right) + \ln \left( \frac{G(l_j(t-	au))}{G(l^*)} \right) \right\}.
\]

We compute \( C(t) \) as follows:
\[
C(t) = \sum_{j,k=1;2}^{l^*} \left( \frac{G(l_k(t-	au))}{G(l^*)} - \frac{l_j(t)}{l^*} - \frac{l^*}{l_j(t)} \frac{G(l_k(t-	au))}{G(l^*)} + 1 \right) + \sum_{j=1}^{2} \left\{ - \ln \left( \frac{G(l_j(t))}{G(l^*)} \right) + \ln \left( \frac{G(l_j(t-	au))}{G(l^*)} \right) \right\} = 2 \sum_{j=1}^{2} \left\{ - \ln \left( \frac{G(l_j(t))}{G(l^*)} \right) + \ln \left( \frac{l_j(t)}{l^*} \right) + \ln \left( \frac{l^*}{l_j(t)} \frac{G(l_k(t-	au))}{G(l^*)} \right) \right\} = 2 \sum_{j=1}^{2} \left\{ g \left( \frac{G(l_j(t))}{G(l^*)} \right) - g \left( \frac{l_j(t)}{l^*} \right) \right\} - \sum_{j,k=1;2}^{l^*} \frac{G(l_k(t-	au))}{G(l^*)}.
\]

Then, from (2.7) in Lemma 2.4, we see that \( C(t, \tau) \leq 0 \). Therefore, we obtain
\[
\dot{U}(t_1, t_2) \leq 0
\]
from (2.12).

Let us define that \( E = \{ (\phi_2, \psi_2) \in \mathcal{G} | (\phi_2, \psi_2) < +\infty, \dot{U}(t_1, t_2) = 0 \} \) and that \( M \) is the largest subset in \( E \) that is invariant with respect to (2.8). Then, we see that
\[
E = \{ (\phi_2, \psi_2) \in \mathcal{G} | \phi_2(0) = \psi_2(0) = \phi_2(-\tau) = \psi_2(-\tau) = l^* \}.
\]
Consider any initial function \((\phi_2, \psi_2) \in M\). Then it holds that \((l_1, l_2) \in M \subset E\), where \( l_k(\theta) = l(t + \theta), j = 1, 2 \) through \((0, \phi, \psi)\). Hence, \( M = \{ (l^*, l^*) \} \). By an extension of LaSalle’s invariance principle [12, Lemma 3.1], any solution tends to \( M \) (see also [13,14]) and hence, the positive equilibrium \((l^*, l^*)\) of (2.5) is globally asymptotically stable. \(\square\)

3. Discussion

In this paper, we have studied the global dynamics of a delayed epidemic model (1.1) proposed by Liu et al. [9]. The model describes disease transmission dynamics due to transport-related infection [7,10,8] and captures the time needed to complete the use of the transportation.
Liu et al. [9] established that the disease-free equilibrium of (1.1) is globally asymptotically stable if $R_0 < 1$ and that (1.1) admits a unique endemic equilibrium, which is locally asymptotically stable, if $R_0 > 1$. However, the problem of the global stability of the endemic equilibrium remained unsolved and was an open problem.

For this problem, we considered the global dynamics of the limit system (2.5). (2.5) is derived from (1.1) using that the positive equilibrium of (2.2) is asymptotically stable. Constructing a Lyapunov functional and using LaSalle’s invariance principle for the reduced system, we prove that the positive equilibrium of (2.5) is globally asymptotically stable if $R_0 > 1$ (Theorem 2.6). This implies that the endemic equilibrium of (1.1) is also globally asymptotically stable if $R_0 > 1$. The mathematical result suggests that, when the disease is endemic, in a situation where two regions are connected to each other by transportation, the endemic steady state is globally asymptotically stable regardless of the length of the travel time. However, one can see that in (1.1) it is assumed that the two regions share an identical parameter set. It may be necessary to consider two different population sizes and different dispersal rates in order to discuss precisely the impact of the transport-related infection on the disease dynamics. We leave this to future work.

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References

[1] WHO, Severe acute respiratory syndrome (SARS): status of the outbreak and lessons for the immediate future. Geneva, May 20, 2003.
[2] K. Khan, J. Arino, W. Hu, P. Raposo, J. Sears, F. Calderon, C. Heidebrecht, M. Macdonald, J. Liauw, A. Chan, M. Gardam, Spread of a novel influenza a (H1N1) virus via global airline transportation, N. Engl. J. Med. 361 (2) (2009) 212–214.
[3] S. Ruan, W. Wang, S.A. Levin, The effect of global travel on the spread of SARS, Math. Biosci. Eng. 3 (1) (2006) 205–218.
[4] W. Wang, X.-Q. Zhao, An epidemic model in a patchy environment, Math. Biosci. 190 (1) (2004) 97–112.
[5] J. Arino, P. van den Driessche, A multi-city epidemic model, Math. Popul. Stud. 10 (3) (2003) 175–193.
[6] J. Arino, Diseases in metapopulations, in: Modeling and Dynamics of Infectious Diseases, in: Ser. Contemp. Appl. Math. CAM, vol. 11, Higher Ed. Press, Beijing, 2009, pp. 64–122.
[7] J. Cui, Y. Takeuchi, Y. Saito, Spreading disease with transport-related infection, J. Theoret. Biol. 239 (3) (2006) 376–390.
[8] Y. Takeuchi, X. Liu, J. Cui, Global dynamics of SIS models with transport-related infection, J. Math. Anal. Appl. 329 (2) (2007) 1460–1471.
[9] J. Liu, J. Wu, Y. Zhou, Modeling disease spread via transport-related infection by a delay differential equation, Rocky Mountain J. Math. 38 (5) (2008) 1525–1540.
[10] X. Liu, Y. Takeuchi, Spread of disease with transport-related infection and entry screening, J. Theoret. Biol. 242 (2) (2006) 517–528.
[11] J.K. Hale, P. Waltman, Persistence in infinite-dimensional systems, SIAM J. Math. Anal. 20 (2) (1989) 388–395.
[12] Y. Saito, T. Hara, W. Ma, Necessary and sufficient conditions for permanence and global stability of a Lotka–Volterra system with two delays, J. Math. Anal. Appl. 236 (2) (1999) 534–556.
[13] J.K. Hale, S.M. Verduyn Lunel, Introduction to Functional-Differential Equations, in: Applied Mathematical Sciences, vol. 99. Springer-Verlag, New York, 1993.
[14] J.P. LaSalle, The Stability of Dynamical Systems, Society for Industrial and Applied Mathematics, Philadelphia, Pa., 1976, with an appendix: “Limiting equations and stability of nonautonomous ordinary differential equations” by Z. Artstein, Regional Conference Series in Applied Mathematics.
[15] M. Suzuki, H. Matsunaga, Stability criteria for a class of linear differential equations with off-diagonal delays, Discrete Contin. Dyn. Syst. 24 (4) (2009) 1381–1391.
[16] K. Mischaikow, H. Smith, H.R. Thieme, Asymptotically autonomous semiflows: chain recurrence and Lyapunov functions, Trans. Amer. Math. Soc. 347 (5) (1995) 1669–1685.
[17] C.-C. Carlos, H.R. Thieme, Asymptotically autonomous epidemic models, in: Mathematical Population Dynamics: Analysis of Heterogeneity I. Theory of Epidemics, vol. I, Wuerz Publishing, 1995, pp. 33–50.
[18] Y. Enatsu, Y. Nakata, Y. Muroya, Global stability of SIR epidemic models with a wide class of nonlinear incidence rates and distributed delays, Discrete Contin. Dyn. Syst. Ser. B 15 (1) (2011) 61–74.
[19] Y. Nakata, Global dynamics of a viral infection model with a latent period and Beddington–DeAngelis response, Nonlinear Anal. TMA 74 (9) (2011) 2929–2940.