GLOBAL ANALYSIS FOR SPREAD OF AN INFECTIOUS DISEASE VIA HUMAN TRANSPORTATION

YUKIHIKO NAKATA∗ AND GERGEY RÓST†

Abstract. We investigate the global dynamics of epidemic models describing disease transmission dynamics between two regions, which are connected via bidirectional or unidirectional human transportation. We define regional reproduction numbers and the basic reproduction number by constructing a next generation matrix. If two regions are connected via bidirectional transportation, the basic reproduction number $R_0$ characterizes the existence of equilibria as well as the global dynamics. The disease free equilibrium always exists and it is globally asymptotically stable if $R_0 < 1$, while for $R_0 > 1$ an endemic equilibrium occurs which is globally asymptotically stable. If the two regions are connected via unidirectional transportation, the disease free equilibrium always exists, but for $R_0 > 1$ two endemic equilibria can appear. In this case, the regional reproduction numbers determine which one of the two is globally asymptotically stable. We illustrate the stability regions of equilibria in a parameter plane and discuss how human transportation between regions influences the spread of the disease.

Key words. Asymptotically autonomous system; Global asymptotic stability; Lyapunov functional; Transport-related infection;

1. Introduction. The recent examples of SARS (WHO [20]) and influenza A (H1N1) (Khan et al. [7]) outbreaks highlighted the importance of the role of global human transportation network on the spread of infectious diseases around the world. This motivated a number of authors to propose and analyze various epidemic models concerning mostly with the dispersal of the infected individuals (see Arino [1], Arino and van den Driessche [2], Ruan et al. [12], Wang and Zhao [19] and the references therein). However, during long distance travel, such as intercontinental flights, a single infected individual may cause several additional infections (Wagner et al. [18]). Therefore, to properly describe the spread of the disease between different regions, connected by human transportation system, we need to take into account the transmission dynamics during the travel.

This phenomena, that individuals may contract the disease while traveling from one region to another, was modeled in Cui et al. [4] by a system of ordinary differential equations based on the standard SIS epidemic model. For this model, Takeuchi et al. [16] proved several analytical results regarding local and global stability of equilibria and uniform persistence of the disease. One of the interesting properties of this model is that there is a parameter region such that the disease dies out in the absence of travel, but the disease persists and becomes endemic if we allow human transportation. Liu et al. [8] noted that the previously proposed models [4,9,16] implicitly used the assumption that the transportation between regions occur instantaneously. In some situations (for example in the case of influenza) the duration of the travel can be comparable to the duration of the infectious period. Furthermore, due to the possibility of new infections occurring during the travel, the number of infected passengers should be a dynamical variable. Based on such considerations, Liu et al. [8] introduced an SIS-type epidemic model that incorporates the time needed to complete the travel and also the possibility of infection during this time. The main results of [8] are the global asymptotic stability of the disease free equilibrium if the basic reproduction number $R_0$ is less than one, and the uniform persistence of the disease if $R_0 > 1$. In this latter case there exists a unique endemic equilibrium which is locally asymptotically stable. In a subsequent paper, Nakata [11] proved the global asymptotic stability of this endemic equilibrium by constructing a Lyapunov functional. Both [8] and [11] assumed that the regions are identical sharing

∗Basque Center for Applied Mathematics, Mazarredo, 14 E-48009 Bilbao, Spain (nakata@bcamath.org)
†Bolyai Institute, University of Szeged, H-6720 Szeged, Aradi vértanúk tere 1., Hungary (rost@math.u-szeged.hu)
the same parameter values. In reality, diseases frequently spread between regions which have very different characteristics (for example, from countries with high population density to countries with lower density, from rural areas to cities or vice versa).

In order to model this phenomenon, here we consider different population sizes and different dispersal rates for each region. This generalization of the previous model ([8], [11]) is more suitable to study the impact of transport-related infections on the disease dynamics in distinct regions connected by human transportation. Furthermore, we examine the effect of unidirectional and bidirectional transport between different regions to evaluate intervention strategies with travel restrictions, when infection is possible during travel.

The paper is organized as follows. In the next section we formulate the model which leads to a nonlinear system of delay differential equations. Using the asymptotic convergence of population sizes we derive a limit system with constant total population in each region. We use these reproduction numbers when discussing the existence and global stability of equilibria for both the bidirectional and the unidirectional cases in the following sections. Section 4 contains the main results. We prove that the disease free equilibrium is globally asymptotically stable if \( R_0 < 1 \) and, by constructing a Lyapunov functional, a unique positive equilibrium is globally asymptotically stable if \( R_0 > 1 \). Using the theory of asymptotically autonomous semiflows, we extend the global asymptotic stability results from the limit system to the original model. By determining the stability regions in the parameter space, we gain further insight into the relation of human transportation and disease dynamics. We discuss in details the case of unidirectional transportation in Section 5. Finally, we offer a discussion on the interpretation of the results and their implications.

2. Model formulation. Consider two distinct regions. For \( j \in \{1, 2\} \), denote by \( S_j(t) \) and \( I_j(t) \) the numbers of susceptible and infected individuals at time \( t \) in region \( j \), respectively. Let \( A_j \) be the recruitment rate, \( d_j \) the natural death rate and \( \delta_j \) the recovery rate of the infected individuals in region \( j \). We use standard incidence \( \beta_j S_j I_j / (S_j + I_j) \), where \( \beta_j \) is the disease transmission coefficient in region \( j \). Then we obtain the following basic SIS epidemic model:

\[
\frac{dS_j(t)}{dt} = A_j - d_j S_j(t) - \frac{\beta_j S_j(t) I_j(t)}{S_j(t) + I_j(t)} + \delta_j I_j(t),
\]

\[
\frac{dI_j(t)}{dt} = \frac{\beta_j S_j(t) I_j(t)}{S_j(t) + I_j(t)} - (d_j + \delta_j) I_j(t)
\]

for \( j \in \{1, 2\} \). We assume that, for \( j \in \{1, 2\} \), \( A_j, \beta_j \) and \( d_j \) are positive and \( \delta_j \) is nonnegative. Following [8], we incorporate transportation, assuming that individuals do not die or recover during travel. We denote by \( s_{kj}(\theta, t) \) and \( i_{kj}(\theta, t) \) the density of susceptible and infective individuals who left region \( k \) at time \( t \) and spent \( \theta \leq \tau \) time in transportation to region \( j \), where \( \tau \in (0, \infty) \) is the time required to complete a one-way travel. Let \( n_{kj}(\theta, t) = s_{kj}(\theta, t) + i_{kj}(\theta, t) \). Thus, \( \int_{\theta_2}^{\theta_1} n_{kj}(\theta, t - \theta) d\theta \) is the number of individuals who left region \( k \) in the time interval \( [t - \theta_1, t - \theta_2] \), where \( \tau \geq \theta_1 \geq \theta_2 \geq 0 \). In particular, for \( \theta_1 = \tau \) and \( \theta_2 = 0 \), this gives the total number of individuals who are being in travel from region \( k \) to \( j \) at time \( t \). Assume that susceptible and infected individuals leave region \( k \) to region \( j \) at a per capita rate \( \alpha_{kj} \in (0, \infty) \). Considering the rates susceptible and infected individuals leave region \( k \) to \( j \) at time \( t_s \), we obtain that

\[
(2.1) \quad s_{kj}(0, t_s) = \alpha_{kj} S_k(t_s) \text{ and } i_{kj}(0, t_s) = \alpha_{kj} I_k(t_s).
\]
Then the disease dynamics in the transportation from region \( k \) to region \( j \) is governed by

\[
\begin{align*}
\frac{\partial}{\partial \theta} s_{kj}(\theta, t_s) &= -\gamma_j \frac{i_{kj}(\theta, t_s)}{i_{kj}(\theta, t_s) + s_{kj}(\theta, t_s)} s_{kj}(\theta, t_s), \\
\frac{\partial}{\partial \theta} i_{kj}(\theta, t_s) &= \gamma_j \frac{i_{kj}(\theta, t_s)}{i_{kj}(\theta, t_s) + s_{kj}(\theta, t_s)} s_{kj}(\theta, t_s),
\end{align*}
\]

where \( \gamma_j \in (0, \infty) \) is the transmission rate during travel. Let us define \( N_j(t) := S_j(t) + I_j(t) \) for \( j \in \{1, 2\} \). Then

\[
n_{kj}(\theta, t_s) = s_{kj}(\theta, t_s) + i_{kj}(\theta, t_s) = \alpha_{kj}(S_k(t_s) + I_k(t_s)) = \alpha_{kj} N_k(t_s) \text{ for any } \theta \geq 0.
\]

From (2.2b) we obtain that

\[
\frac{\partial}{\partial \theta} i_{kj}(\theta, t_s) = \gamma_j i_{kj}(\theta, t_s) \left( 1 - \frac{i_{kj}(\theta, t_s)}{\alpha_{kj} N_k(t_s)} \right),
\]

which is a logistic equation. Using (2.1) as an initial condition, we solve (2.3) explicitly to obtain

\[
\begin{align*}
s_{kj}(\tau, t_s) &= \alpha_{kj} \frac{i_k(t_s)}{e^{-\frac{\gamma_j}{\alpha_k} S_k(t_s) + I_k(t_s)}} N_k(t_s), \\
i_{kj}(\tau, t_s) &= \alpha_{kj} N_k(t_s) - s_{kj}(\tau, t_s) = \frac{\alpha_{kj} e^{-\frac{\gamma_j}{\alpha_k} S_k(t_s)}}{e^{-\frac{\gamma_j}{\alpha_k} S_k(t_s) + I_k(t_s)}} N_k(t_s),
\end{align*}
\]

where \( s_{kj}(\tau, t_s) \) and \( i_{kj}(\tau, t_s) \) are the population densities of susceptible and infective individuals arriving to region \( j \) from \( k \) at time \( t_s + \tau \). Therefore, the respective population densities at time \( t \) become \( s_{kj}(\tau, t - \tau) \) and \( i_{kj}(\tau, t - \tau) \). Consequently, we obtain the following model:

\[
\begin{align*}
\frac{dS_j(t)}{dt} &= A_j - (d_j + \alpha_{jk}) S_j(t) - \frac{\beta_j S_j(t) I_j(t)}{S_j(t) + I_j(t)} + \delta_j I_j(t) + s_{kj}(\tau, t - \tau), \\
\frac{dI_j(t)}{dt} &= \frac{\beta_j S_j(t) I_j(t)}{S_j(t) + I_j(t)} - (d_j + \delta_j + \alpha_{jk}) I_j(t) + i_{kj}(\tau, t - \tau),
\end{align*}
\]

for \( j, k \in \{1, 2\} \) and \( j \neq k \). One can see that the transport-related infection model formulated in Liu et al. [8] is a special case of the system (2.5).

2.1. Asymptotically autonomous system. To analyze the dynamics of (2.5) it is convenient to consider a system which is described in terms of \( N \) and \( I \) instead of \( S \) and \( I \). As an equivalent system to (2.5) one can obtain

\[
\begin{align*}
\frac{dN_j(t)}{dt} &= A_j - (d_j + \alpha_{jk}) N_j(t) + \alpha_{kj} N_k(t - \tau), \\
\frac{dI_j(t)}{dt} &= I_j(t) \left\{ \beta_j - (d_j + \delta_j + \alpha_{jk}) - \frac{\beta_j}{N_j(t) I_j(t)} \right\} + i_{kj}(\tau, t - \tau)
\end{align*}
\]

for \( j, k \in \{1, 2\} \) and \( j \neq k \), where now

\[
i_{kj}(\tau, t - \tau) = \frac{\alpha_{kj} e^{-\frac{\gamma_j}{\alpha_k} I_k(t - \tau)}}{1 + \frac{\alpha_{kj}}{\alpha_k N_j(t - \tau)} I_k(t - \tau)}.
\]
We denote by \( C = C([−\tau, 0], \mathbb{R}^2) \) the Banach space of continuous functions mapping the interval \([−\tau, 0]\) into \(\mathbb{R}^2\) equipped with the sup-norm. The nonnegative cone of \( C \) is defined as \( C_+ = C([−\tau, 0], \mathbb{R}_+^2) \). We define a set, which only contains strictly positive functions, as
\[
G := \{ \phi \in C_+: \phi_1(\theta) > 0, \phi_2(\theta) > 0 \text{ for } s \in [−\tau, 0] \}.
\]
Due to the biological interpretation, we consider initial conditions for (2.6a) as positive. However, we restrict the initial function of (2.6a) to the function in \( G \) to define (2.7) for \( t > 0 \).

**Remark 2.1.** For any nonnegative initial function system (2.6a) generates strictly positive solution. However, we restrict the initial function of (2.6a) to the function in \( G \) to define (2.7) for \( t \in (0, \tau] \).

We prove the following result for (2.6a).

**Lemma 2.1.** There exists a unique positive equilibrium \((N_1, N_2)\) of (2.6a), where
\[
(2.8) \quad \begin{pmatrix} N_1 \\ N_2 \end{pmatrix} := \begin{pmatrix} d_1 + \alpha_{12} & -\alpha_{21} \\ -\alpha_{12} & d_2 + \alpha_{21} \end{pmatrix}^{-1} \begin{pmatrix} A_1 \\ A_2 \end{pmatrix},
\]
The positive equilibrium is asymptotically stable.

**Proof.** We define \( x_j(t) := N_j(t) - N_j \) for \( j \in \{1, 2\} \). We obtain
\[
\frac{d}{dt} x_1(t) = -(d_1 + \alpha_{12}) x_1(t) + \alpha_{21} x_2(t - \tau),
\]
\[
\frac{d}{dt} x_2(t) = -(d_2 + \alpha_{21}) x_2(t) + \alpha_{12} x_2(t - \tau).
\]
Since \( d_1 \) and \( d_2 \) are positive and \((d_1 + \alpha_{12})(d_2 + \alpha_{21}) > \alpha_{12} \alpha_{21}\), condition (16) in Suzuki and Matsunaga [15, Example 2, p. 1384] holds. Thus the zero solution of (2.9) is asymptotically stable.

We can consider (2.6b) as a system of non-autonomous delay differential equations with non-autonomous terms \( N_j(t) \) for \( j \in \{1, 2\} \), which are governed by system (2.6a). In the following, using Lemma 2.1, we derive a limiting system of (2.6b). For \( j, k \in \{1, 2\} \) and \( j \neq k \) we define a positive function
\[
f_{kj}(I) := \frac{\alpha_{kj} e^{\beta_{kj} \tau}}{1 + e^{\frac{\beta_{kj} \tau}{N_k}}} I, \text{ for } I \in [0, \infty),
\]
where \( N_k \) is the positive equilibrium of (2.6a) given as in (2.8). By Lemma 2.1 one can obtain
\[
\lim_{t \to +\infty} \left( i_{kj}(\tau, t - \tau) - f_{kj}(I_{kj}(t - \tau)) \right) = 0.
\]
Then we find that system (2.6b) is asymptotically autonomous with the following limiting system of delay differential equations:
\[
(2.10) \quad \frac{dI_j(t)}{dt} = I_j(t) \left\{ \beta_j - (d_j + \delta_j + \alpha_{jk}) - \frac{B_{kj}}{N_j} I_j(t) \right\} + f_{kj}(I_k(t - \tau)),
\]
for \( j, k \in \{1, 2\} \) and \( j \neq k \). To obtain information on the long-term behavior of solutions of (2.6b) we analyze global stability of system (2.10) and apply the theory of asymptotically autonomous systems [3, 10, 17] in Sections 4 and 5.
3. The basic reproduction number. We define and give an explicit formula for a basic reproduction number $R_0$ for (2.6). In absence of the inflow into a region due to the transportation, we define regional reproduction numbers as

\[
R_j := \frac{\beta_j}{d_j + \delta_j + \alpha_{jk}}
\]

for $j \in \{1, 2\}$, $k \neq j$. If we introduce a single infective into a fully susceptible region $j$, it will generate $R_j$ new infectives in this region in the expected sojourn time. Let us consider the expected number of infective individuals appeared in region $k$ due to the transportation by a typical infective individual introduced into region $j$: the probability of moving out from $I_j$ by means of travel is $\frac{\alpha_{jk}}{d_j + \delta_j + \alpha_{jk}}$, and the expected number of infected individuals who arrive at region $j$ if the travel was started with a single infective is $e^{-\gamma_{jk}}\tau$ (this follows from the linear part of (2.3)). Taking the product of these two numbers, for $j, k \in \{1, 2\}$ and $j \neq k$ we define

\[
r_{jk} := \frac{\alpha_{jk} e^{-\gamma_{jk}} \tau}{d_j + \delta_j + \alpha_{jk}}.
\]

Then we define a next generation matrix for (2.6) by

\[
M := \begin{pmatrix} R_1 & r_{21} \\ r_{12} & R_2 \end{pmatrix}.
\]

We define the basic reproduction number as the spectral radius of $M$ and denote it by $R_0$. We give an explicit expression for $R_0$.

**Proposition 3.1.** It holds that

\[
R_0 = \frac{1}{2} \left\{ (R_1 + R_2) + \sqrt{(R_1 - R_2)^2 + 4r_{12}r_{21}} \right\}.
\]

If $\alpha_{12} = 0$ or $\alpha_{21} = 0$, then

\[
R_0 = \max \{R_1, R_2\}.
\]

**Proof.** The eigenvalues of $M$ are roots of the equation

\[
(R_1 - \lambda)(R_2 - \lambda) - r_{12}r_{21} = 0.
\]

The roots of this quadratic equation can be computed as

\[
\lambda_{1,2} = \frac{1}{2} \left\{ (R_1 + R_2) \pm \sqrt{(R_1 - R_2)^2 + 4r_{12}r_{21}} \right\}.
\]

Since the larger root gives $R_0$, we get (3.3). We obtain (3.4) from (3.3) with $\alpha_{12} = 0$ or $\alpha_{21} = 0$. \[\Box\]

4. Disease transmission dynamics: bidirectional transportation. In this section we consider a situation in which two regions are connected to each other via bidirectional transportation. Thus we assume that

\[
\alpha_{jk} \in (0, \infty) \text{ for } j, k \in \{1, 2\} \text{ and } j \neq k.
\]

We prove that (2.6) admits a unique endemic equilibrium if and only if $R_0 > 1$ while there always exists a disease free equilibrium. Performing global stability analysis we show that $R_0$ works as a threshold quantity to determine which equilibrium is globally asymptotically stable.
4.1. Existence of equilibria. In order to prove the existence of the endemic equilibrium, we introduce a relation between the basic reproduction number and regional reproduction numbers.

**Proposition 4.1.** (A) For

\[ r_{12}r_{21} \in (0, 1), \]

the following statements hold:

(A1) \( R_0 < 1 \) if and only if

\[ r_{12}r_{21} < (1 - R_1)(1 - R_2) \text{ for } \max \{R_1, R_2\} \in (0, 1). \]

(A2) \( R_0 = 1 \) if and only if

\[ r_{12}r_{21} = (1 - R_1)(1 - R_2) \text{ for } \max \{R_1, R_2\} \in (0, 1). \]

(A3) \( R_0 > 1 \) if and only if either

\[ r_{12}r_{21} > (1 - R_1)(1 - R_2) \text{ for } \max \{R_1, R_2\} \in (0, 1). \]

or

\[ \max \{R_1, R_2\} \geq 1. \]

(B) If

\[ r_{12}r_{21} \geq 1, \]

then \( R_0 > 1 \) for any \( (R_1, R_2) \in (0, \infty) \times (0, \infty). \)

**Proof.** (A) We only prove statement (A3), statements (A1) and (A2) can be shown in a similar way. Assume (4.2). If we suppose (4.6), then

\[ R_0 > \frac{1}{2} \left\{ (R_1 + R_2) + \sqrt{(R_1 - R_2)^2} \right\} = \max \{R_1, R_2\} \geq 1. \]

From (3.3), \( R_0 > 1 \) if and only if

\[ \sqrt{(R_1 - R_2)^2 + 4r_{12}r_{21}} > 2 - (R_1 + R_2). \]

If \( \max \{R_1, R_2\} < 1 \), we can square both hand sides to obtain the equivalent inequality \( r_{12}r_{21} > (1 - R_1)(1 - R_2) \), as in (4.5). Therefore, both (4.5) and (4.6) imply \( R_0 > 1 \). For the other direction, suppose \( R_0 > 1 \). Then either (4.6) or \( \max \{R_1, R_2\} < 1 \) holds. In the latter case, we obtain \( r_{12}r_{21} > (1 - R_1)(1 - R_2) \) from (4.8) and thus (4.5) holds.

(B) Assume that (4.7) holds. Then from (3.3) we get \( R_0 > 1 \). The proof is complete. □

In Figure 4.2 for visualizing the dependency of \( R_0 \) on \( R_1 \) and \( R_2 \), we plot the condition (4.4) in the \((R_1, R_2)\) parameter plane by fixing \( r_{12} \) and \( r_{21} \) such that (4.2) holds.

Next we consider the existence of equilibria of (2.6). We define

\[ g_j(z) := \beta_j - (d_j + \delta_j + \alpha_{jk}) - \frac{\beta_j}{N_j}z \text{ for } z \in [0, \infty) \]

for \( j, k \in \{1, 2\} \) and \( j \neq k \) and

\[ h_1(x,y) := g_1(x) + f_{21}(y), \quad h_2(x,y) := g_2(y) + f_{12}(x). \]
In the following we study the solution of

\begin{equation}
0 = h_1(x,y) = h_2(x,y) \text{ for } (x,y) \in [0,\infty) \times [0,\infty).
\end{equation}

**Proposition 4.2.** For (4.9) there always exists a trivial solution \((0,0)\). There exists a unique solution, where both components are strictly positive, if and only if \(R_0 > 1\).

**Proof.** Clearly \((0,0)\) is always a solution of (4.9). For the existence of the positive solution, we show that (4.9) defines two curves having a unique intersection in the first quadrant if and only if \(R_0 > 1\). We define \(y^\ast := \lim_{y \to +\infty} f_{21}(y)\). One easily proves that \(y^\ast < 0\) and that \(f_{21}(y)\) is monotone increasing on \([0,\infty)\) with range \([0,y^\ast)\). Therefore, it is a bijection and thus invertible on this domain: there exists an inverse function of \(f_{21}\) such that 

\[ f_{21}^{-1} : [0,y^\ast) \to [0,\infty). \]

We define

\[ x_\ast(R_1) := \max \left\{ 0, N_1 \left( 1 - \frac{1}{R_1} \right) \right\}. \]

We see that \(g_1(x_\ast(R_1)) = 0\), \(\lim_{x \to +\infty} g_1(x) = -\infty\) and \(g_1(x)\) is monotone decreasing for \(x \in [x_\ast(R_1),\infty)\). We can find a unique \(x^\ast\) such that 

\[ -g_1(x^\ast) = y^\ast \]

and denote it by \(x^\ast\). Then we define a function \(G_1 : [x_\ast(R_1),x^\ast) \to [0,\infty)\) as

\[ G_1(x) := f_{21}^{-1}(-g_1(x)), \]

which is a continuous and monotone increasing function such that

\begin{equation}
G_1(x_\ast(R_1)) = 0 \text{ and } \lim_{x \to x^\ast} G_1(x) = +\infty.
\end{equation}

The graph of \(G_1\) is the zero level set of \(h_1\), i.e.,

\begin{equation}
h_1(x,G_1(x)) = 0.
\end{equation}

Similarly, we see that \(f_{12}(0) = 0\), and \(\lim_{x \to +\infty} f_{12}(x) < \infty\) and \(f_{12}(x)\) is monotone increasing for \(x \in [0,\infty)\). We define

\[ y_\ast(R_2) := \max \left\{ 0, N_2 \left( 1 - \frac{1}{R_2} \right) \right\}, \]

One can prove that \(g_2(y)\) is monotone decreasing on \([y_\ast(R_2),\infty)\) with range \((-\infty,0]\). Therefore, it is a bijection and thus invertible on this domain: there exists an inverse function of \(g_2\) such that \(g_2^{-1} : (-\infty,0] \to [y_\ast(R_2),\infty)\). We define \(y^\ast := g_2^{-1}\left( -\lim_{x \to +\infty} f_{12}(x) \right) < \infty\). Then we define a function \(G_2 : [0,\infty) \to [y_\ast(R_2),y^\ast)\) as

\[ G_2(x) := g_2^{-1}(-f_{12}(x)), \]

which is a continuous and monotone increasing function such that

\begin{equation}
G_2(0) = y_\ast(R_2) \text{ and } \lim_{x \to +\infty} G_2(x) = y^\ast.
\end{equation}

The graph of \(G_2\) is the zero level set of \(h_2\), i.e.,

\begin{equation}
h_2(x,G_2(x)) = 0.
\end{equation}

Consequently, intersections of the curves are given as a solution of the equation \(G_1(x) = G_2(x)\). For proving the existence of the solution we divide the proof into two cases.
Case 1: max \( \{ R_1, R_2 \} > 1 \) holds. From (4.10), (4.12) and monotonicity of \( G_2 \), it holds that
\[
G_1(x_*(R_1)) = 0 \leq y_*(R_2) = G_2(0) \leq G_2(x_*(R_1)).
\]

We have that either \( x_*(R_1) > 0 \) or \( y_*(R_2) > 0 \). Therefore, we obtain that \( G_1(x_*(R_1)) < G_2(x_*(R_1)) \). On the other hand, there exists \( x_0 \in (x_*, x^*) \) such that \( G_1(x_0) > G_2(x_0) \), since \( \lim_{x \to +\infty} G_2(x) = y^* \) and \( \lim_{x \to -\infty} G_1(x) = +\infty \) from (4.10) and (4.12). By the continuity, there must be an \( \bar{x} \in (x_*(R_1), x^*) \) such that \( G_1(\bar{x}) = G_2(\bar{x}) \) (see Figure 4.1. (a), (b) and (c)).

Case 2: max \( \{ R_1, R_2 \} \leq 1 \) holds. In this case, by (4.5) we have that \( x_*(R_1) = 0 \) and that \( y_*(R_2) = 0 \). Then \( G_1(0) = G_2(0) = 0 \). We compute the slope of \( G_1 \) and \( G_2 \) at zero to determine the existence of the intersection. By differentiation of (4.11) and evaluating at zero we obtain
\[
G_1'(0) = \frac{g_1'(0)}{f_{21}'(0)} = \frac{1 - R_1}{r_{21}}. \tag{4.14}
\]

Similarly, from (4.13), we get that
\[
G_2'(0) = \frac{r_{12}}{1 - R_2} \quad \text{(whenever } R_2 < 1), \tag{4.15}
\]
and in the case \( R_2 = 1 \) the graph of \( G_2 \) is tangential to the \( y \)-axis at 0. If max \( \{ R_1, R_2 \} \leq 1 \) but \( R_0 > 1 \), then from Proposition 4.1, either (4.7) holds or (4.2) and (4.6) hold. In any case we get \( G_1'(0) < G_2'(0) \) (where \( G_2'(0) = +\infty \) when \( R_2 = 1 \)). Hence there is some \( x_1 > 0 \) such that \( G_1(x_1) < G_2(x_1) \). Since we have that \( \lim_{x \to +\infty} G_2(x) = y^* < +\infty \) and \( \lim_{x \to -\infty} G_1(x) = +\infty \) from (4.10) and (4.12), there exists \( x_0 \) such that \( G_1(x_0) > G_2(x_0) \). By the continuity, there must be an \( \bar{x} \in (x_*, x^*) \) such that \( G_1(\bar{x}) = G_2(\bar{x}) \) (see Figure 4.1. (d)).

For the uniqueness of \( \bar{x} \), we examine the convexity properties of \( G_1 \) and \( G_2 \). Using implicit differentiation of \( h_1(x, y) = 0 \) and using that
\[
\frac{\partial^2 h_1(x, y)}{\partial y \partial x} = \frac{\partial^2 h_1(x, y)}{\partial x \partial y} = 0,
\]
we obtain
\[
0 = \frac{\partial^2 h_1(x, y)}{\partial x^2} + \frac{\partial^2 h_1(x, y)}{\partial y^2} G'_1(x)^2 + \frac{\partial h_1(x, y)}{\partial y} G''_1(x).
\]
Simple calculations show that \( \frac{\partial^2 h_1(x, y)}{\partial x^2} < 0 \), \( \frac{\partial^2 h_1(x, y)}{\partial y^2} < 0 \) and \( \frac{\partial h_1(x, y)}{\partial y} > 0 \). Hence, it follows that
\[
G''_1(x) = -\frac{\partial^2 h_1(x, y)}{\partial x^2} + \frac{\partial^2 h_1(x, y)}{\partial y^2} G'_1(x)^2 > 0.
\]
On the other hand, analogous calculations give \( G''_2(x) < 0 \). By these convexity properties we deduce that there is a unique positive solution \( \bar{x} \) of \( G_1(x) = G_2(x) \). Therefore, there exists a unique endemic equilibrium if \( R_0 > 1 \).

Finally, we assume that \( R_0 \leq 1 \) holds. Then either (4.3) or (4.4) in Proposition 4.1 holds, which gives \( G_1'(0) \geq G_2'(0) \) from (4.14) and (4.15). The convexity properties of \( G_1 \) and \( G_2 \) show that there is no positive solution of \( G_1(x) = G_2(x) \). Therefore, there does not exist any endemic equilibrium if \( R_0 \leq 1 \). The proof is complete. \( \square \)
For $R_0 > 1$ we denote by $(I_{1+}, I_{2+})$ the unique positive solution of (4.9). We obtain the following result on the existence of equilibria of (2.6).

**Theorem 4.3.** For (2.6) there always exists the disease free equilibrium given as

$$(N_1, N_2, 0, 0).$$

A unique endemic equilibrium given as

$$(N_1, N_2, I_{1+}, I_{2+})$$

exists if and only if $R_0 > 1$.

**Proof.** We obtain the first and second components of equilibria from Lemma 2.1. Since the third and fourth components of equilibria of (2.6) are determined by (4.9), from Proposition 4.2, we obtain the conclusion. □

From Theorem 4.3, one can easily obtain the existence of equilibria of (2.10).

**Theorem 4.4.** For (2.10) there always exists the trivial equilibrium $(0, 0)$. A unique positive equilibrium given as $(I_{1+}, I_{2+})$ exists if and only if $R_0 > 1$.

**4.2. Global dynamics analysis.** For (2.6b) and (2.10) we consider the same initial conditions as

$$ (I_1(\theta), I_2(\theta)) = \phi(\theta) $$
for $\theta \in [-\tau, 0]$, where $\phi \in C_a$. We denote by $\hat{\zeta}$ a function which is identically zero, i.e., $\phi(\theta) = 0$ for $\theta \in [-\tau, 0]$. In the following we assume

$$\phi \in C_+ \setminus \{\hat{\zeta}, \hat{\varrho}\}.$$  

The proof of the following lemma is straightforward thus omitted.

**Lemma 4.5.** Both (4.2b) and (2.10) have respective unique non-negative solutions $(I_1(t), I_2(t))$ defined for all $t > 0$ which are bounded. It holds that $I_j(t) > 0$, $j = \{1, 2\}$ for $t > \tau$, thus $(I_1, I_2) \in G$ for $t > 2\tau$.

**Remark 4.1.** For (4.2b) and (2.10) if $\hat{\zeta} = (0, 0)$ then it follows that $(I_1(t), I_2(t)) = (0, 0)$ for $t > 0$, thus $(I_1, I_2) = (\hat{\zeta}, \hat{\varrho})$ for $t > 0$.

We analyze the global stability of the trivial equilibrium of (2.10).

**Theorem 4.6.** The trivial equilibrium of (2.10) is globally asymptotically stable for $R_0 < 1$ and it is unstable for $R_0 > 1$.

**Proof.** We define

$$I_j := \beta_j - (d_j + \delta_j + \alpha_{jk}) \text{ for } j, k \in \{1, 2\} \text{ and } j \neq k.$$  

By linearizing (2.10) at the trivial equilibrium we obtain that

$$\frac{d}{dt} y(t) = B_1 y(t) + B_2 y(t - \tau),$$  

where $y(t) \in \mathbb{R}^2$ and

$$B_1 := \begin{pmatrix} l_1 & 0 \\ 0 & l_2 \end{pmatrix}, \quad B_2 := \begin{pmatrix} 0 & \alpha_{21} e^{\gamma_2 \tau} \\ \alpha_{12} e^{\gamma_1 \tau} & 0 \end{pmatrix}.$$  

Since (4.18) is a cooperative and irreducible system, from Smith [13, Chapter 5, Corollary 5.2] the stability of the trivial equilibrium is equivalent to that for

$$\frac{d}{dt} y(t) = (B_1 + B_2) y(t).$$  

One can show from a straightforward calculation that the trivial equilibrium of (4.19) is asymptotically stable if $R_0 < 1$ and it is unstable if $R_0 > 1$. Hence we obtain the conclusion on the stability of the trivial equilibrium of (2.10). Next we prove the global attractivity. From (2.10) we obtain that

$$\frac{d}{dt} \begin{pmatrix} I_1(t) \\ I_2(t) \end{pmatrix} \leq B_1 \begin{pmatrix} I_1(t) \\ I_2(t) \end{pmatrix} + B_2 \begin{pmatrix} I_1(t - \tau) \\ I_2(t - \tau) \end{pmatrix}.$$  

Since for $R_0 < 1$ we have that $\lim_{t \to +\infty} y(t) = (0, 0)$ for (4.18), using the standard comparison argument as in Smith [13, Chapter 5, Corollary 2.4] we conclude that $\lim_{t \to +\infty} I_j(t) = 0$ for $j \in \{1, 2\}$. Thus the trivial equilibrium is globally attractive. \[\square\]

Next we analyze the global stability of the positive equilibrium of (2.10). For the proof we employ Lyapunov’s direct method. For the construction of the Lyapunov functional we let

$$g(z) := z - 1 - \ln z \text{ for } z \in (0, +\infty).$$  

One can see that $g(z)$ has the global minimum at $z = 1$ with $g(1) = 0$. The following elementary Lemma is taken from Nakata [11, Lemma 2.4], which we use to prove the global asymptotic stability.
Lemma 4.7. For any $x, y \in (0, \infty)$ it holds that
\begin{equation}
\left( \frac{x}{y} - \frac{f_{kj}(x)}{f_{kj}(y)} \right) \left( \frac{f_{kj}(x)}{f_{kj}(y)} - 1 \right) \geq 0
\end{equation}
and
\begin{equation}
g \left( \frac{x}{y} \right) - g \left( \frac{f_{kj}(x)}{f_{kj}(y)} \right) \geq 0
\end{equation}
for $j, k \in \{1, 2\}$ and $j \neq k$.

Theorem 4.8. The positive equilibrium of (2.10) is globally asymptotically stable for $R_0 > 1$.

Proof. From the equilibrium condition of (2.10), it holds that
\[ \beta_j - (d_j + \delta_j + \alpha_{jk}) = \frac{\beta_j I_{j+}}{N_j} - \frac{f_{kj}(I_{k+})}{I_{k+}}. \]
Then from (2.10) we obtain that
\begin{equation}
\frac{dI_{j}(t)}{dt} = \frac{\beta_j I_{j+}}{N_j} I_j - I_j - f_{kj}(I_k(t-\tau)) - f_{kj}(I_{k+}) \frac{I_j(t)}{I_{j+}}
\end{equation}
for $j, k \in \{1, 2\}$ and $j \neq k$. For $(\phi_1, \phi_2) \in G$ we consider the following functional defined as
\begin{equation}
U(\phi_1, \phi_2) := \sum_{j,k \in \{1,2\}, j \neq k} \left( \frac{I_{j+}}{f_{kj}(I_{k+})} g \left( \frac{\phi_j(0)}{I_{j+}} \right) + \int_{-\tau}^{0} g \left( \frac{f_{kj}(\Phi_k(s))}{f_{kj}(I_{k+})} \right) ds \right).
\end{equation}
By Lemma 4.5 there exists $t_0$ such that $(I_{j+}, I_{k+}) \in G$ for $t \geq t_0 > 2\tau$. We differentiate $U$ with respect to $t$ along the solution of (4.22). For the convenience we drop $+$ from the notations. It holds that
\begin{equation}
\frac{d}{dt} \left( g \left( \frac{I_j(t)}{I_{j+}} \right) \right) = \frac{1}{I_j} \left( 1 - \frac{I_j}{I_{j+}} \right) \left\{ \frac{\beta_j I_{j+}}{N_j} I_j \left( 1 - \frac{I_j(t)}{I_{j+}} \right) + f_{kj}(I_k) \left( \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} - \frac{I_j(t)}{I_{j+}} \right) \right\}
\end{equation}

\begin{align}
&= -\frac{\beta_j I_{j+}}{N_j} \left( 1 - \frac{I_j(t)}{I_{j+}} \right)^2 + f_{kj}(I_k) \left( 1 - \frac{I_j}{I_{j+}} \right) \left( \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} - \frac{I_j(t)}{I_{j+}} \right). \\
&= \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} - \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} - \ln \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} + \ln \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)}.
\end{align}

Furthermore,
\begin{equation}
\frac{d}{dt} \int_{t-\tau}^{t} g \left( \frac{f_{kj}(I_k(s))}{f_{kj}(I_k)} \right) ds = g \left( \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} \right) - g \left( \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} \right)
\end{equation}

\begin{align}
&= \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} - \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} - \ln \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} + \ln \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)}.
\end{align}

We define
\begin{align}
C_{jk}(t) &:= \left( 1 - \frac{I_j}{I_{j+}} \right) \left( \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} - \frac{I_j(t)}{I_{j+}} \right) \\
&+ \left( \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} - \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)} \right) - \ln \frac{f_{kj}(I_k(t))}{f_{kj}(I_k)} + \ln \frac{f_{kj}(I_k(t-\tau))}{f_{kj}(I_k)}
\end{align}
for \( j,k \in \{1,2 \} \) and \( j \neq k \). Then from (4.24) and (4.25) we obtain that
\[
(4.26) \quad \frac{d}{dt} U(I_{1t}, I_{2t}) = \sum_{j=1}^{2} \left\{ -\frac{\beta_j t^2}{N_j f_k_j(I_k)} \left( 1 - \frac{I_j(t)}{I_j} \right)^2 \right\} + \sum_{j,k \in \{1,2\}, j \neq k} C_{jk}(t).
\]

Now we determine the sign of \( C_{jk}(t) \).
\[
C_{jk}(t) = \left( \frac{f_k_j(I_k(t-\tau))}{f_k_j(I_k)} - \frac{I_j(t)}{I_j} \right) - \left( \frac{\tau}{I_j} - 1 \right) \ln \left( \frac{f_k_j(I_k(t-\tau))}{f_k_j(I_k)} + 1 \right).
\]

Therefore, using (4.21) in Lemma 4.7, we obtain that
\[
\sum_{j,k \in \{1,2\}, j \neq k} C_{jk}(t) = \sum_{j,k \in \{1,2\}, j \neq k} \left\{ g \left( \frac{f_j(I_j(t))}{f_k(I_k)} \right) - g \left( \frac{I_j(t)}{I_k} \right) - g \left( \frac{I_j(t)}{I_k} \right) \right\} \leq 0.
\]

Consequently it holds that \( \frac{d}{dt} U(I_{1t}, I_{2t}) \leq 0 \) for \( t \geq t_0 \).

If \( \langle I_{1t}, I_{2t} \rangle \) is the function identically equal to \( \langle I_1, I_2 \rangle \), then it is obvious that it follows that \( \langle I_{1t}, I_{2t} \rangle = \langle I_1, I_2 \rangle \) for \( t > t_0 \). Thus we assume that \( \langle I_{1t}, I_{2t} \rangle \) is not the function identically equal to \( \langle I_{1t}, I_{2t} \rangle \). Then there exists \( c > 0 \) such that \( c = U(I_{1t}, I_{2t}) \). We define
\[
G_c := \{ \phi \in G | U(\phi) \leq c \}.
\]

We see that \( G_c \) is closed and positively invariant. Thus the closure of \( G_c \) is itself and \( G_c \) contains \( \langle I_{1t}, I_{2t} \rangle \) for all \( t \geq t_0 \). Since \( U \) is continuous on \( G_c \), \( U \) is a Lyapunov functional on \( G_c \) [6, Chapter 5.3]. We define the set
\[
\Sigma := \{ (\phi_1, \phi_2) \in G_c : \frac{d}{dt} U(\phi_1, \phi_2) = 0 \}.
\]

We obtain
\[
\Sigma = \{ (\phi_1, \phi_2) : \phi_j(0) = \phi_j(-\tau) = I_j, \ j \in \{1,2\} \}.
\]

Let \( L \) be the largest subset in \( \Sigma \) that is invariant with respect to (2.10). From the invariance, \( L \) consists of only the function identically equal to \( \langle I_1, I_2 \rangle \). Then, by LaSalle’s invariance principle [6, Theorem 3.1], we conclude that the solution tends to the positive equilibrium of (2.10). Since for every solution we can choose \( c \), the positive equilibrium is globally attractive. The stability of the equilibrium follows from [6, Section 5, Corollary 3.1], if we define \( a(\cdot) \) as
\[
a(\phi_1(0), \phi_2(0)) := \sum_{j,k \in \{1,2\}, j \neq k} \left( \frac{I_j}{f_k(I_k)} g \left( \frac{\phi_j(0)}{I_j} \right) \right).
\]
Hence the positive equilibrium is globally asymptotically stable. □

Finally, we extend the global stability results in Theorems 4.6 and 4.8 to the original system (2.6) by applying theory of asymptotic autonomous systems [17, Theorem 4.1].

**Theorem 4.9.** For (2.6) the following statements hold. The disease free equilibrium is globally asymptotically stable if \( R_0 > 1 \) and it is unstable if \( R_0 > 1 \). For \( R_0 > 1 \), the endemic equilibrium is globally asymptotically stable.

**Proof.** We first show that the stability properties of (2.6) is as same as of (2.10). Let

\[ N(t) := (N_1(t), N_2(t)) \text{ and } I(t) := (I_1(t), I_2(t)). \]

We define functions \( F : \mathbb{R}^2 \to \mathbb{R}^2 \) and \( H : \mathbb{R}^4 \to \mathbb{R}^2 \) as right hand side of (2.6), i.e., (2.6) can be written as

\[
\frac{d}{dt} N(t) = F(N(t), N(t - \tau)), \\
\frac{d}{dt} I(t) = H(N(t), N(t - \tau), I(t), I(t - \tau)).
\]

To analyze stability of (2.6) we apply the principle of linearized stability [5, Chapter VII, Theorem 6.8]. For an equilibrium \( (N, I) \) of (2.6) we define

\[
A := \begin{pmatrix} D_1 F(N, N) & 0 \\ D_1 H(N, N, I, I) & D_3 H(N, N, I, I) \end{pmatrix}, \\
B := \begin{pmatrix} D_2 F(N, N) & 0 \\ D_2 H(N, N, I, I) & D_4 H(N, N, I, I) \end{pmatrix}.
\]

We define

\[
D(\lambda) := \det \left( \lambda E - A - Be^{-\lambda \tau} \right),
\]

where \( E \) is the identity matrix. Then for an equilibrium \( (N, I) \) the characteristic equation is

(4.27) \[ D(\lambda) = 0. \]

We define

\[
D_1(\lambda) := \det \left( \lambda E - D_1 F(N, N) - D_2 F(N, N) e^{-\lambda \tau} \right), \\
D_2(\lambda) := \det \left( \lambda E - D_3 H(N, N, I, I) - D_4 H(N, N, I, I) e^{-\lambda \tau} \right).
\]

Then it follows that

\[ D(\lambda) = D_1(\lambda)D_2(\lambda). \]

From Lemma 2.1 we know that every root of \( D_1(\lambda) \) has negative real part. Thus (4.27) has a root in the right half complex plane if and only if

(4.28) \[ D_2(\lambda) = 0 \]

has a root in the right half complex plane. We can write

\[ \frac{d}{dt} I(t) = H(N, N, I(t), I(t - \tau)) \]

as (2.10). Then one can see that (4.28) is also the characteristic equation of (2.10). Therefore the stability of (2.10) is equivalent to that of (2.6). Finally, from Theorems 4.6 and 4.8,
we obtain the statements on stability of both the disease free equilibrium and the endemic equilibrium of (2.6).

Next we prove the global attractivity of equilibria of (2.6b) by applying [17, Theorem 4.1]. Since we have the boundedness of solutions from Lemma 4.5, one can show that forward orbits of (2.6b) are precompact thus the \( \omega \)-limit sets are not empty, see e.g. Smith [14, Chapter 5]. Consider first the case \( R_0 < 1 \). From Theorem 4.6 and Remark 4.1 the basin of attraction of the trivial equilibrium of (2.10) is \( C_+ \). Hence the \( \omega \)-limit set of every forward orbit of (2.6b) intersects the basin of attraction. By [17, Theorem 4.1], we can conclude that every solution of (2.6b) converges to \( (0,0) \). Now suppose \( R_0 > 1 \). We prove the global attractivity of the endemic equilibrium of (2.6). To apply [17, Theorem 4.1] we exclude the possibility that the \( \omega \)-limit set of a forward orbit of (2.6b) contains \( (\bar{0},\bar{0}) \). Suppose the contrary, then there is a solution \((\bar{I}_1(t),\bar{I}_2(t))\) of (2.6b) such that

\[
\lim_{t \to \infty} (\bar{I}_1(t),\bar{I}_2(t)) = (0,0).
\]

Since, from Lemma 2.1, it holds that \( \lim_{t \to \infty} N_j(t) = N_j \) for \( j \in \{1,2\} \), for any \( \varepsilon > 0 \) and \( j,k \in \{1,2\}, j \neq k \) there exists sufficiently large \( T \) such that

\[
\frac{1}{1 + \frac{\varepsilon}{N_j(t-\tau)} I_k(t-\tau)} > 1 - \varepsilon \quad \text{and} \quad R_j \frac{I_j(t)}{N_j(t)} < \varepsilon \quad \text{for} \ t > T.
\]

For \( t > T \), from (2.6b) we find the estimate

\[
\frac{dI_j(t)}{dt} > I_j(t) \left( d_j + \delta_j + \alpha_{jk} \right) \left( R_j - 1 - \varepsilon \right) + \left( 1 - \varepsilon \right) \alpha_{kj} e^{\beta_j \tau} I_k(t-\tau)
\]

for \( j,k \in \{1,2\}, j \neq k \). For \( j \in \{1,2\} \) if \( R_j > 1 \), then, choosing sufficiently small \( \varepsilon \), we see that \( I_j(t) \) is nondecreasing, which contradicts to (4.29). Hence we focus on the case when \( \max\{R_1,R_2\} \leq 1 \). We introduce the notation

\[
a_j^\varepsilon := \left( d_j + \delta_j + \alpha_{jk} \right) \left( R_j - 1 - \varepsilon \right) \quad \text{and} \quad b_j^\varepsilon := \left( 1 - \varepsilon \right) \alpha_{kj} e^{\beta_j \tau}
\]

for \( j,k \in \{1,2\}, j \neq k \). With this notation (4.30) can be written as

\[
\frac{dI_j(t)}{dt} > a_j^\varepsilon I_j(t) + b_j^\varepsilon I_k(t-\tau).
\]

Let

\[
V(I_{1,2}) := -a_2^\varepsilon \left( I_1(t) + b_1^\varepsilon \int_{t-\tau}^t I_2(s)ds \right) + b_1^\varepsilon \left( I_2(t) + b_2^\varepsilon \int_{t-\tau}^t I_1(s)ds \right).
\]

We note that \( a_j^\varepsilon < 0 \). Differentiating \( V \), the delayed terms and the coefficients of \( I_2(t) \) cancel out, and we obtain

\[
\frac{d}{dt} V(I_{1,2}) = I_1(t) \left( b_1^\varepsilon b_2^\varepsilon - a_1^\varepsilon a_2^\varepsilon \right).
\]

From Proposition 4.1 (A3), \( R_0 > 1 \) implies \( b_1^0 b_2^0 - a_1^0 a_2^0 > 0 \), therefore for sufficiently small \( \varepsilon \), \( b_1^\varepsilon b_2^\varepsilon - a_1^\varepsilon a_2^\varepsilon > 0 \) also holds. Thus \( V \) is nondecreasing, on the other hand, for positive solutions \( V(I_{1,2}) > 0 \). Since we assume (4.29), which leads to that \( \lim_{t \to \infty} V(I_{1,2}) = 0 \), we obtain a contradiction. Thus the \( \omega \)-limit set of every forward orbit of (2.6b) does not contain \( (0,0) \). Then by [17, Theorem 4.1] every solution of (2.6) converges to the endemic equilibrium. \( \square \)
4.3. The stability boundary in a two-parameter plane. From Theorem 4.9 we can conclude that the condition

\( R_0 = 1 \)  

is a threshold condition for the existence and global stability of equilibria. We fix \( r_{12} \) and \( r_{21} \) such that (4.2) holds. We define

\[
\xi(R_1) := 1 - \frac{r_{12}r_{21}}{1 - R_1} \text{ for } R_1 \in (0, 1 - r_{12}r_{21}).
\]  

Then from (4.4) the threshold condition (4.31) can be expressed as

\[ R_2 = \xi(R_1), \]

which we call the stability boundary in the \((R_1, R_2)\)-parameter plane. For visualization of the stability boundary we plot this curve in Figure 4.2. One can see that the stability boundary separates the parameter plane into two distinct regions. From Proposition 4.1 we can determine that the region above the stability boundary is the global stability region of the endemic equilibrium whereas the region below the stability boundary is the global stability region of the disease free equilibrium. One can easily prove that the stability region of the disease free equilibrium is smaller than the region, \( \{(R_1, R_2) | R_1 \leq 1 \text{ and } R_2 \leq 1\} \) as shown in Figure 4.2.

Thus, as in [8, 9, 16], it is possible that both regional reproduction numbers are less than one, but the disease is endemic in both regions. If we fix \( r_{12} \) and \( r_{21} \) such that (4.7) holds, then, from Proposition 4.1, \( R_0 > 1 \) holds for any value of regional reproduction numbers. Thus the endemic equilibrium is globally asymptotically stable everywhere in the \((R_1, R_2)\)-parameter plane. In this case the transport-related infection has enough potential to spread the disease in both regions although regional reproduction numbers are arbitrary small.

5. Disease transmission dynamics: unidirectional transportation. In this section we assume that two regions are connected via unidirectional transportation. Without loss of generality we assume that individuals move towards region 1 from region 2, but the opposite way is inhibited. Thus we assume that

\[ \alpha_{12} = 0 \text{ and } \alpha_{21} \in (0, \infty). \]

5.1. Existence of equilibria. For the convenience of the notation, for \( j \in \{1, 2\} \) we define

\[
T_j := \left(1 - \frac{1}{R_j}\right)N_j.
\]

For \( R_2 > 1 \) we define a quadratic polynomial function for \( I \in [0, \infty) \) as

\[
\eta(I) := I(d_1 + \delta_1) \left( R_1 - 1 - \frac{R_1}{N_1} I \right) + f_{21}(T_2).
\]

**Proposition 5.1.** If \( R_2 > 1 \) then

\[
I^* := \frac{(R_1 - 1) + \sqrt{(R_1 - 1)^2 + 4 \frac{R_1}{N_1} f_{21}(T_2)}}{2R_1} N_1
\]
is a unique positive solution of $\eta(I) = 0$. Furthermore one has

\[
\eta(I) = \begin{cases} 
> 0 & \text{for } I \in [0, I^*), \\
= 0 & \text{for } I = I^*, \\
< 0 & \text{for } I \in (I^*, \infty). 
\end{cases}
\]

Proof. We see that the coefficient of $I^2$ of $\eta$ is negative with $\eta(0) = f_{21}(I_2) > 0$. Since $\eta$ is a quadratic function, there exists a unique positive solution of $\eta(I) = 0$ and obtain (5.3) as a unique positive solution. Since we have $\eta(0) > 0$, it is easy to get (5.4). The proof is complete. $\square$

We formulate results on the existence of equilibria in terms of regional reproduction numbers.

**Theorem 5.2.** For (2.6) the following statements hold.

(i). There always exists the disease free equilibrium, which is given as $(N_1, N_2, 0, 0)$.

(ii). There exists an endemic equilibrium for only region 1, which is given as $(N_1, N_2, I_1, 0)$, if and only if $R_1 > 1$.

(iii). There exists an endemic equilibrium for both regions, which is given as $(N_1, N_2, I^*, I_2)$, if and only if $R_2 > 1$.

Proof. By Lemma 2.1 we obtain the first and second components of equilibria. We omit the proofs of (i) and (ii), since they are straightforward. Assume $R_2 > 1$. Then we see that the positive equilibrium of the second component of (2.6b) is $I_2$. To find an equilibrium of the first component of (2.6b) we consider the equation $\eta(I) = 0$. Since from Proposition 5.1 $I = I^*$ is a unique positive solution of $\eta(I) = 0$, we obtain the equilibrium. $\square$

We introduce the result on the existence of equilibria of (2.10) without the proof, since it follows in a straightforward manner from Theorem 5.2.

**Theorem 5.3.** For (2.10) the following statements hold.
(i) There always exists the trivial equilibrium \((0,0)\).
(ii) There exists a boundary equilibrium given as \((I_1,0)\) if and only if \(R_1 > 1\).
(iii) There exists a positive equilibrium given as \((I^*,I_2)\) if and only if \(R_2 > 1\).

### 5.2. Global dynamics analysis

For \((2.6b)\) and \((2.10)\) we consider the initial conditions as \(I_1(0) = I_1^0 \in \mathbb{R}_+\) and \(I_2(\theta) = \phi_2(\theta)\) for \(\theta \in [-\tau,0]\), where \(\phi_2 \in C([-\tau,0], \mathbb{R}_+)\). We assume that \(\phi_2(0) > 0\).

**Lemma 5.4.** Both \((2.6b)\) and \((2.10)\) have respective unique non-negative solutions \((I_1(t), I_2(t))\) defined for all \(t > 0\) which are bounded. It holds that \(I_1(t) > 0\) for \(t > \tau\) and that \(I_2(t) > 0\) for \(t > 0\).

**Remark 5.1.** If \(\phi_2(0) = 0\) then \(I_2(t) = 0\) for \(t > 0\). If \(I_1^0 = 0\) and \(\phi_2 = \hat{0}\) then \(I_j(t) = 0\) for \(j \in \{1, 2\}\) and \(t > 0\).

First, we analyze the the global dynamics of \((2.10)\).

**Theorem 5.5.** For \((2.10)\) the following statements hold.

(i) The trivial equilibrium is globally asymptotically stable if \(\max \{R_1, R_2\} < 1\) and it is unstable if \(\max \{R_1, R_2\} > 1\).

(ii) The boundary equilibrium is globally asymptotically stable if \(R_1 > 1 > R_2\) and it is unstable if \(R_2 > 1\).

(iii) The positive equilibrium is globally asymptotically stable if \(R_2 > 1\).

**Proof.** To analyze stability of \((2.10)\) we apply the principle of linearized stability [5, Chapter VII, Theorem 6.8]. For an equilibrium \((I_1, I_2)\) we have the characteristic equation

\[
\left\{ \beta_1 - (d_1 + \delta_1) - \frac{2\beta_1}{N_1}I_1 - \lambda \right\} \left\{ \beta_2 - (d_2 + \alpha_2) - \frac{2\beta_2}{N_2}I_2 - \lambda \right\} = 0.
\]

Thus roots are computed as

\[
\lambda_j = \beta_j \left( 1 - \frac{1}{R_j} - 2\frac{I_j}{N_j} \right)
\]

for \(j \in \{1, 2\}\). Then it is easy to obtain (i) and (ii). For the positive equilibrium we get

\[
\lambda_1 = \beta_1 \left( 1 - \frac{1}{R_1} - 2\frac{I^*}{N_1} \right)
\]

and \(\lambda_2 = -\beta_2 \left( 1 - \frac{1}{R_2} \right) < 0\). From \((5.2)\) and \(\eta(I^*) = 0\) we obtain

\[
1 - \frac{1}{R_1} - 2\frac{I^*}{N_1} < 1 - \frac{R_1}{R_1} - \frac{I^*}{N_1} = -\frac{f_{21}(I_2)}{I^*R_1(d_1 + \delta_1)} < 0.
\]

Thus \(\lambda_1 < 0\). Hence every root has negative real part and thus the equilibrium is asymptotically stable. Next we prove the global attractivity of equilibria. First, we assume that \(R_2 < 1\) holds. It is easy to prove that the trivial equilibrium of the second component of \((2.10)\) is globally attractive. Then the first component of \((2.10)\) is asymptotically autonomous with the following limit equation

\[
\frac{dT_1(t)}{dt} = T_1(t) \left\{ \beta_j - (d_1 + \delta_1) - \frac{\beta_1}{N_1}T_1(t) \right\}.
\]

with \(T_1(0) = T_1^0 \in \mathbb{R}_+\). If \(R_1 < 1\) then every solution of \((5.5)\) converges to the trivial equilibrium. Thus the basin of attraction of the trivial equilibrium is \(\mathbb{R}_+\) and the \(\omega\)-limit set of the
forward orbit of the first component of (2.10) intersects the basin of attraction. By [17, Theorem 4.1], it holds that every solution of (2.10) converges to the trivial equilibrium, thus we get (i). For \( R_1 > 1 \) one can see that every solution of (5.5) with \( I_1(t) \in \mathbb{R}_+ \setminus \{0\} \) converges to the positive equilibrium. By standard comparison theorem, it holds that \( I_1(t) > I_1(t) \) where \( I_1(t) \) is a solution of (2.10). Thus the \( \omega \)-limit set of any forward orbit of the first component of (2.10) does not contain 0 and it intersects the basin of attraction. Hence, by [17, Theorem 4.1], we obtain (ii). Finally, assume \( R_2 > 1 \). One can see that the positive equilibrium of the second component of (2.10) is globally attractive. Then the first component of (2.10) is asymptotically autonomous with the following limit equation

\[
\frac{dI_1(t)}{dt} = \eta(I_1(t)).
\]

(5.6)

with \( I_1(0) = I_1^0 \in \mathbb{R}_+ \). From (5.4) in Proposition 5.1, every solution of (5.6) converges to the positive equilibrium. Similarly we can apply [17, Theorem 4.1] to obtain (iii). \( \square \)

Similar as in the proof of Theorem 4.9 we obtain the global stability results for (2.6). We omit the proof.

**Theorem 5.6.** For (2.6) the following statements hold.

(i). The disease free equilibrium is globally asymptotically stable if \( \max\{R_1, R_2\} < 1 \) and it is unstable if \( \max\{R_1, R_2\} > 1 \).

(ii). The endemic equilibrium for only region 1 is globally asymptotically stable if \( R_1 > 1 \) and it is unstable if \( R_2 > 1 \).

(iii). The endemic equilibrium for both regions is globally asymptotically stable if \( R_2 > 1 \).

**5.3. The stability boundary in a two-parameter plane.** We assumed that (5.1) holds, which implies that there is only one-way transportation from region 2 to region 1. Thus we have that \( R_0 = \max\{R_1, R_2\} \) from Proposition 3.1. From Theorem 5.6, we can say that the basic reproduction number determines the complete eradication of the disease from both regions: if \( R_0 < 1 \) then the disease free equilibrium is globally asymptotically stable whereas if \( R_0 > 1 \) then there exists one endemic equilibrium which is globally asymptotically stable. In order to determine the endemic equilibrium that is globally asymptotically stable, regional reproduction numbers seem to be a helpful indicator. To visualize the results in Theorems 5.2 and 5.6 like in Section 4.3, choosing regional reproduction numbers as two free parameters, we express respective stability regions of equilibria in the \((R_1, R_2)\)-parameter plane in Figure 5.1. One can easily see that if the reproduction number for region 2 exceeds one, then both region becomes endemic, even if reproduction number for region 1 is less than one. This illustrates the impact of the unidirectional transportation from region 2 to region 1 on the disease transmission dynamics.

**6. Discussion.** We have formulated an epidemic model, based on an SIS epidemic model, describing disease transmission dynamics between two regions. The regions are connected via bidirectional or unidirectional human transportation. It is assumed that the disease is transmitted not only within a region but also in the human transportation connecting two regions as in [4]. We generalize the model developed in [8] which allows us to consider different characters of regions, such as population size and transportation rate. In Sections 4 and 5, we analyzed the existence and global stability of equilibria of the model using the basic reproduction number and regional reproduction numbers defined in Section 3. For the proof of the global stability of equilibria, we first analyze the limit system (2.10) and show that the long term behavior of the original system (2.6) is determined by the limit system (2.10) applying the theory of asymptotic autonomous systems [17].

We have considered two types of human transportation, namely bidirectional or unidirectional transportation. For both modes, we can conclude that the basic reproduction number
determines if the disease is completely eradicated: the disease free equilibrium is globally stable if $R_0 < 1$ and it is unstable if $R_0 > 1$. If two regions are connected via bidirectional transportation, there exists a unique endemic equilibrium that is globally asymptotically stable for $R_0 > 1$, see Theorem 4.9. On the other hand, if two regions are connected via unidirectional transportation, it is possible that there exist two endemic equilibria for $R_0 > 1$. Using the regional reproduction numbers we determined the endemic equilibrium that is globally asymptotically stable, see Theorem 5.6. Thus for the case of bidirectional transportation the basic reproduction number works as a threshold parameter to determine the disease dynamics, whereas for the case of unidirectional transportation regional reproduction numbers seem to be helpful indicators to determine which equilibrium is globally asymptotically stable.

For both transportation modes we defined the stability boundary in the $(R_1, R_2)$-parameter plane. Comparing Figures 4.2 and 5.1 one can easily understand that the model shows different disease transmission dynamics if we change the type of transportation. For bidirectional transportation it is possible that both regional reproduction numbers are less than one but the disease is endemic in both regions. This is consistent with the findings in [4, 16] where a transport-related infection model is formulated by a system of ordinary differential equations. For unidirectional transportation, we found that the system admits an endemic equilibrium, where region 1 is endemic and region 2 is disease free, which does not exist for the case of bidirectional transportation. The model for the case of unidirectional transportation may be associated with a disease prevention policy by inhibiting the human transportation from region 1 to region 2. Our analysis suggests that inhibiting the transportation makes a new equilibrium, where region 1 is endemic and region 2 is disease free. From Figure 5.1, one can see that the condition $R_2 < 1$ makes region 2 disease free. Furthermore, if we decrease $R_1$ so
that $R_1 < 1$ then the disease will be completely eradicated from both regions. Thus it is suggested that it is possible to control the disease dynamics by decreasing regional reproduction numbers after starting the disease prevention policy.

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