An epidemic model in a patchy environment

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Abstract

An epidemic model is proposed to describe the dynamics of disease spread among patches due to population dispersal. We establish a threshold above which the disease is uniformly persistent and below which disease-free equilibrium is locally attractive, and globally attractive when both susceptible and infective individuals in each patch have the same dispersal rate. Two examples are given to illustrate that the population dispersal plays an important role for the disease spread. The first one shows that the population dispersal can intensify the disease spread if the reproduction number for one patch is large, and can reduce the disease spread if the reproduction numbers for all patches are suitable and the population dispersal rate is strong. The second example indicates that a population dispersal results in the spread of the disease in all patches, even though the disease can not spread in each isolated patch.

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1. Introduction

Many epidemic models have been proposed and studied to understand mechanism of disease transmission (see, for example, [1,3,12] and the references cited therein). One of the most
important subjects in this field is to obtain a threshold that determines the persistence and extinction of a disease. Reproduction numbers for ordinary differential equation models were investigated by Diekmann et al. [6,7], Hyman and Li [15], and van den Driessche and Watmough [19]. Reproduction numbers for SIS epidemiological models with delays were studied by Cooke and van den Driessche [4], Hethcote and van den Driessche [13]. The thresholds for the uniform persistence and extinction of a disease in epidemic models with delays were also considered recently by Thieme [18], Zhao and Zou [23], Wang and Ma [20]. Reproduction number and persistence in an endemic model with many infection stages were proposed and studied by Feng and Thieme [8,9].

Communicable diseases such as influenza and sexual diseases can be easily transmitted from one country (or one region) to other countries (or other regions). Thus, it is important to consider the effect of population dispersal on spread of a disease. Hethcote [11] proposed an epidemic model with population dispersal between two patches. Brauer and van den Driessche [2] proposed a model with immigration of infectives. In this paper, we consider a disease transmission model with population dispersal among \( n \) patches. We assume that demographic structure is described by the following equation:

\[
N' = B(N)N - \mu N,
\]

where \( N \) is the number of a population, \( B(N) \) is the birth rate of the population, and \( \mu \) is its death rate. This type of demographic structure with variable population size was proposed by Cooke et al. [5]. We adopt it here as a basis to develop an epidemic model with population dispersal.

We consider SIS type of disease transmission. The population is divided into two classes: susceptible individuals and infectious individuals. Susceptible individuals become infective after contact with infective individuals. Infective individuals return to susceptible class when they are recovered. Gonorrhea and other sexually transmitted diseases or bacterial infections exhibit this phenomenon. We denote the numbers of susceptible individuals at time \( t \) by \( S(t) \) and the numbers of infective individuals at time \( t \) by \( I(t) \). If there is no population dispersal among patches, i.e., the patches are isolated, we suppose that the population dynamics in \( i \)th patch is governed by

\[
\begin{align*}
S'_i &= B_i(N_i)N_i - \mu_i S_i - \beta_i S_i I_i + \gamma_i I_i, \\
I'_i &= \beta_i S_i I_i - (\mu_i + \gamma_i)I_i,
\end{align*}
\]

where \( S_i \) is the number of susceptible individuals in patch \( i \), \( I_i \) the number of infective individuals in patch \( i \), \( N_i = S_i + I_i \) is the number of the population in patch \( i \), \( B_i(N_i) \) is the birth rate of the population in the \( i \)th patch, \( \beta_i \) is the disease transmission coefficient, \( \mu_i \) is the death rate of the population in the \( i \)th patch, and \( \gamma_i \) is the recovery rate of infective individuals in the \( i \)th patch. Here, we adopt mass action incidence rate for convenience. Our method also applies to standard incidence rate. Following [5], we assume that \( B_i(N_i) \) satisfy the following basic assumptions for \( N_i \in (0, \infty) \):

(A1) \( B_i(N_i) > 0 \), \( i = 1, 2, \ldots, n \);

(A2) \( B_i(N_i) \) is continuously differentiable with \( B'_i(N_i) < 0 \), \( i = 1, 2, \ldots, n \);

(A3) \( \mu_i > B_i(\infty) \), \( i = 1, 2, \ldots, n \).
As mentioned in [5], the following three types of birth functions $B_i(N_i)$ can be found in the biological literature:

(B1) $B_i(N_i) = b_i e^{-a_i N_i}$ with $a_i > 0$, $b_i > 0$;

(B2) $B_i(N_i) = \frac{p_i}{q_i + N_i}$ with $p_i$, $q_i$, $m > 0$;

(B3) $B_i(N_i) = \frac{A_i}{N_i} + c_i$ with $A_i > 0$, $c_i > 0$.

When the patches are connected, we suppose that the dynamics of those individuals is governed by the following model:

\[
\begin{align*}
S_i' &= B_i(N_i)N_i - \mu_i S_i - \beta_i S_i I_i + \gamma_i I_i + \sum_{j=1}^{n} a_{ij} S_j, \quad 1 \leq i \leq n, \\
I_i' &= \beta_i S_i I_i - (\mu_i + \gamma_i) I_i + \sum_{j=1}^{n} b_{ij} I_j, \quad 1 \leq i \leq n,
\end{align*}
\]

where $a_{ii}$, $b_{ii}$, $1 \leq i \leq n$, are non-positive constants, $a_{ij}$ and $b_{ij}$ with $i \neq j$ are non-negative constants. $-a_{ii} \geq 0$ represents the emigration rate of susceptible individuals in the $i$th patch, $-b_{ii} \geq 0$ represents the emigration rate of infective individuals in the $i$th patch, $a_{ij}$, $j \neq i$, represents the immigration rate of susceptible individuals from $j$th patch to $i$th patch, and $b_{ij}$, $j \neq i$, the immigration rate of infective individuals from $j$th patch to $i$th patch. For simplicity, we neglect death rates and birth rates of the individuals during the dispersal process. Thus, we have

\[
\sum_{j=1}^{n} a_{ji} = 0, \quad \sum_{j=1}^{n} b_{ji} = 0, \quad \forall \ 1 \leq i \leq n.
\]

We further assume that the $n$ patches cannot be separated into two groups such that there is no immigration of susceptible and infective individuals from first group to second group. Mathematically, this means that two $n \times n$ matrices $(a_{ij})$ and $(b_{ij})$ are irreducible (see, e.g., [16, Appendix A]). Note that system (1.2) indicates that the population can have different demographic structures and different infection forces among different patches, $a_{ij} \neq b_{ij}$ implies that we also consider the variation of the dispersal rates of susceptible individuals and infective individuals.

The remaining parts of this paper is organized as follows. In the next section, we establish a threshold between the extinction and persistence of the disease. In Section 3, the results are applied to the model with the patch number being 2. Section 4 gives a brief discussion of main results.

2. Threshold dynamics

In order to find the disease-free equilibrium of (1.2), we consider

\[
S_i' = B_i(S_i)S_i - \mu_i S_i + \sum_{j=1}^{n} a_{ij} S_j, \quad i = 1, \ldots, n.
\]
If \( z \) is a non-negative constant, we define an auxiliary matrix
\[
M(z) = \begin{bmatrix}
B_1(z) - \mu_1 + a_{11} & a_{12} & \cdots & a_{1n} \\
a_{21} & B_2(z) - \mu_2 + a_{22} & \cdots & a_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
a_{n1} & a_{n2} & \cdots & B_n(z) - \mu_n + a_{nn}
\end{bmatrix}.
\]

This matrix is used to prove the existence and the uniqueness of a positive equilibrium in (2.1) and is different from the standard Jacobian matrix.

Recall that the stability modulus of an \( n \times n \) matrix \( M \), denoted by \( s(M) \), is defined by
\[
s(M) := \max \{ \text{Re} \lambda : \lambda \text{ is an eigenvalue of } M \}.
\]

Note that \( M(z) \) is irreducible and has non-negative off-diagonal elements. By [16, Theorem A.5], it then follows that \( s(M(z)) \) is a simple eigenvalue of \( M(z) \) with a (componentwise) positive eigenvector.

Let \( F : \mathbb{R}_+^n \to \mathbb{R}^n \) be defined by the right-hand side of (2.1). Clearly, \( F \) is cooperative and \( DF(S) \) is irreducible for every \( S \in \mathbb{R}_+^n \). For any \( x \in (0, 1) \) and \( S = (S_1, \ldots, S_n) \in \text{int}(\mathbb{R}_+^n) \), there holds
\[
\alpha S_i B_i(xS) - \mu_i xS_i + \sum_{j=1}^n a_{ij} xS_j > \alpha \left[ B_i(S_i)S_i - \mu_i S_i + \sum_{j=1}^n a_{ij} S_j \right], \quad i = 1, 2, \ldots, n.
\]

Thus \( F \) is strongly sublinear on \( \mathbb{R}_+^n \) (see, e.g., [22]). It then follows that for any \( S_0 \in \mathbb{R}_+^n \), the unique solution \( S(t, S_0) \) of (2.1) satisfying \( S(0, S_0) = S_0 \) exists globally on \([0, \infty)\) and \( S(t, S_0) \geq 0, \forall t \geq 0 \). We further claim that (2.1) admits a bounded positive solution. Indeed, in view of (A3), we can choose a sufficiently large real number \( K > 0 \) such that \( B_i(K) < \mu_i, \ i = 1, 2, \ldots, n \). Let \( \bar{v} = (\bar{v}_1, \ldots, \bar{v}_n) \) be a positive eigenvector associated with \( s(M(K)) \). Then \( V(t) = (V_1(t), \ldots, V_n(t)) = e^{s(M(K))t} \bar{v} \) is a positive solution of the linear ordinary differential system \( V' = M(K)V \). Let \( \Sigma(t) = \sum_{i=1}^n V_i(t) = e^{s(M(K))t} \sum_{i=1}^n \bar{v}_i. \) By the first equation in (1.3), it easily follows that \( \Sigma'(t) \leq a \Sigma(t), \forall t \geq 0 \), where \( a = \max \{ B_i(K) - \mu_i : 1 \leq i \leq n \} < 0 \). Thus \( \lim_{t \to \infty} \Sigma(t) = 0 \), and hence \( s(M(K)) < 0 \). Choose \( l > 0 \) large enough such that \( l \bar{v}_i > K, \ i = 1, 2, \ldots, n \). Set \( x(t) \equiv l\bar{v} \). If we rewrite (2.1) as \( \dot{x} = F(S) \), it is easy to see that
\[
\dot{x}(t) = 0 > s(M(K))x(t) = M(K)x(t) > F(x(t)), \quad \forall t \geq 0,
\]
where (A2) is used. By the standard comparison theorem (see, e.g., [16, Theorem B.1]), it follows that:
\[
0 < S(t, l\bar{v}) \leq x(t) = l\bar{v}, \quad \forall t \geq 0.
\]
Consequently, \( S(t, l\bar{v}) \) is a bounded positive solution of (2.1). In order for (2.1) to admit a positive equilibrium, we need to assume that
\[
(A4) \quad s(M(0)) > 0.
\]

By [22, Corollary 3.2], it then follows that (2.1) has a unique positive equilibrium \( S^* = (S_1^*, S_2^*, \ldots, S_n^*) \) and \( S^* \) is globally asymptotically stable for \( S \in \mathbb{R}_+^n \setminus \{0\} \). Thus, \( E_0 = (S_1^*, S_2^*, \ldots, S_n^*, 0, \ldots, 0) \) is a disease-free equilibrium of (1.2).
Define

\[
M_1 = \begin{bmatrix}
\beta_1 S_1^* - \mu_1 - \gamma_1 + b_{11} & b_{12} & \cdots & b_{1n} \\
b_{21} & \beta_2 S_2^* - \mu_2 - \gamma_2 + b_{22} & \cdots & b_{2n} \\
\cdots & \cdots & \cdots & \cdots \\
b_{n1} & b_{n2} & \cdots & \beta_n S_n^* - \mu_n - \gamma_n + b_{nn}
\end{bmatrix}.
\]

Clearly, \( M_1 \) is irreducible and has non-negative off-diagonal elements. Then \( s(M_1) \) is a simple eigenvalue of \( M_1 \) with a positive eigenvector (see, e.g., [16, Theorem A.5]).

According to the concepts of next generation matrix and reproduction number presented in [6,19], we define

\[
F := \begin{bmatrix}
\beta_1 S_1^* & 0 & \cdots & 0 \\
0 & \beta_2 S_2^* & \cdots & 0 \\
\cdots & \cdots & \cdots & \cdots \\
0 & 0 & \cdots & \beta_n S_n^*
\end{bmatrix}
\]

and

\[
\Psi := \begin{bmatrix}
-\mu_1 - \gamma_1 + b_{11} & b_{12} & \cdots & b_{1n} \\
b_{21} & -\mu_2 - \gamma_2 + b_{22} & \cdots & b_{2n} \\
\cdots & \cdots & \cdots & \cdots \\
b_{n1} & b_{n2} & \cdots & -\mu_n - \gamma_n + b_{nn}
\end{bmatrix}.
\]

Set \( R_0 := \rho(F \Psi^{-1}) \), where \( \rho \) represents the spectral radius of the a matrix. Then \( R_0 \) is called the reproduction number for (1.2). Note that \( M_1 = F - \Psi \). Thus, the following observation is implied by the proof of [19, Theorem 2] with \( J_1 = M_1 \).

**Lemma 2.1.** There hold two equivalences:

\[
R_0 > 1 \iff s(M_1) > 0, \quad R_0 < 1 \iff s(M_1) < 0. \tag{2.3}
\]

By [19, Theorem 2], the disease-free equilibrium \( E_0 \) is locally asymptotically stable if \( R_0 < 1 \) and is unstable if \( R_0 > 1 \). We will show that \( R_0 \) is a threshold parameter for the uniform persistence and extinction of the disease, which is more general.

To investigate the global dynamics of (1.2), we first show that (1.2) admits a compact, positively invariant set which absorbs all forward orbits in \( \mathbb{R}^{2n}_+ \), and hence (1.2) has a global compact attractor on \( \mathbb{R}^{2n}_+ \) (see, e.g., [10, Theorem 3.4.8]). For convenience, we denote the positive solution \((S_1(t), \ldots, S_n(t), I_1(t), \ldots, I_n(t))\) of (1.2) by \((S(t), I(t))\).

**Lemma 2.2.** Let (A1)–(A4) hold. Then there is an \( N^* > 0 \) such that every forward orbit in \( \mathbb{R}^{2n}_+ \) of (1.2) eventually enters into \( G := \{ (S, I) \in \mathbb{R}^{2n}_+ : \sum_{i=1}^n (S_i + I_i) \leq N^* \} \), and \( G \) is positively invariant for (1.2).
Proof. Let \( N = \sum_{i=1}^{n} N_i, N_t = S_t + I_t. \) By (1.2) and (1.3), we have
\[
N' = \sum_{i=1}^{n} (B_i(N_i) - \mu_i)N_i. \tag{2.4}
\]
If \( B_i(0+) < \mu_i, i = 1, 2, \ldots, n, \) then there exists an \( \alpha > 0 \) such that \( N'(t) \leq -\alpha N(t), \forall t \geq 0, \) and hence, Lemma 2.2 holds for any positive number \( N^*. \) Otherwise, we partition \( \{1, 2, \ldots, n\} \) into two sets \( P_1 \) and \( P_2 \) such that
\[
B_i(0+) > \mu_i, \quad \forall i \in P_1, \\
B_i(0+) \leq \mu_i, \quad \forall i \in P_2.
\]
Without loss of generality, we suppose that \( P_1 = \{1, \ldots, m\} \) and \( P_2 = \{m + 1, \ldots, n\}. \) For \( i \in P_1, \) since \( B_i(0+) > \mu_i \) and \( B_i(\infty) < \mu_i, \) (A2) implies that there is a unique \( k_i > 0 \) such that \( B_i(k_i) - \mu_i = 0. \) It follows from (A3) that there is an \( N_0 > 0 \) such that
\[
(B_i(N) - \mu_i)N < -\sum_{j=1}^{m} k_j B_j(0+) - 1, \quad \forall N \geq N_0, \quad i = 1, 2, \ldots, n.
\]
Let \( N^* = nN_0. \) By the definition of \( N, \) it is easy to see that \( N \geq N^* \) implies \( N_0 > 0 \) for some \( 1 \leq i_0 \leq n. \) It then follows from (2.4) that
\[
N'(t) \leq \sum_{j=1}^{m} B_j(0+)k_j + (B_i(0) - \mu)N_0 < -1, \quad \text{if} \quad N(t) \geq N^*,
\]
which implies that \( G \) is positively invariant and every forward orbit enters into \( G \) after a certain time. \( \Box \)

In the case where the susceptible and infective individuals in each patch have the same dispersal rate, we have the following result on the global attractivity of \( E_0. \)

Theorem 2.1. Let (A1)–(A4) hold and \( R_0 < 1. \) If \( a_{ij} = b_{ij} \) for \( i = 1, \ldots, n, \) \( j = 1, \ldots, n, \) then \( E_0 \) is globally attractive for \( (S_0, I_0) \in (R_+^n \setminus \{0\}) \times R_+^n. \)

Proof. Let us consider a non-negative solution \( (S(t), I(t)) \) of (1.2). We wish to show that
\[
\lim_{t \to \infty} I(t) = 0. \tag{2.5}
\]
By (1.2), we have
\[
N'_i = B_i(N_i)N_i - \mu_i N_i + \sum_{j=1}^{n} a_{ij}N_j, \quad i = 1, \ldots, n. \tag{2.6}
\]
By the afore-mentioned conclusion for (2.1), (2.6) admits a unique positive equilibrium \( S^* \) which is globally asymptotically stable for \( N \in R_+^n \setminus \{0\}. \) It then follows that for any \( \epsilon > 0, \) there holds \( N(t) = S(t) + I(t) < S^* + \epsilon, \) where \( \epsilon = (\epsilon, \ldots, \epsilon) > 0, \) when \( t \) is sufficiently large. Thus, if \( t \) is sufficiently large, we have
\[
I'_i < \beta_i(S_i^* + \epsilon)I_i - (\mu_i + \gamma_i)I_i + \sum_{j=1}^{n} b_{ij}I_j, \quad \forall 1 \leq i \leq n. \tag{2.7}
\]
It then suffices to show that positive solutions of the following auxiliary system:

\[
I'_i = \beta_i(S'_i + \epsilon)I_i - (\mu_i + \gamma_i)I_i + \sum_{j=1}^{n} b_{ij}I_j, \quad 1 \leq i \leq n
\]

(2.8)
tend to zero as \( t \) goes to infinity. Let \( M_2 \) be the matrix defined by

\[ M_2 = \text{diag}(\beta_1, \beta_2, \ldots, \beta_n). \]

Since \( s(M_1) < 0 \) and \( s(M_1 + \epsilon M_2) \) is continuous for small \( \epsilon \), we can fix an \( \epsilon > 0 \) small enough such that \( s(M_1 + \epsilon M_2) < 0 \). As a consequence, solutions of (2.8) tend to zero as \( t \) goes to infinity, which implies (2.5).

For any \((S_0, I_0) \in R^n_+ \times R^n_+ \) with \( S_0 \neq 0 \), we have \( N_0 = S_0 + I_0 \in R^n_+ \setminus \{0\} \). By the global attractivity of \( S^* \) for system (2.6), it then follows that \( \lim_{t \to \infty} S(t) = \lim_{t \to \infty}(N(t) - I(t)) = S^* - 0 = S^* \). □

If the susceptible and infective individuals have different dispersal rates, by using the arguments in obtaining the unique positive equilibrium of (2.1) or by [19, Theorem 2], we see that (A1)–(A4) and \( R_0 < 1 \) imply that the disease-free equilibrium is locally asymptotically stable. This means that a positive solution \((S(t), I(t))\) of (1.2) satisfies \( I(t) \to 0 \) as \( t \to \infty \) if its initial position is near to the disease-free equilibrium. Here, we give a little more general result where it is only needed that the values of infective individuals are small.

**Theorem 2.2.** Let (A1)–(A4) hold and \( R_0 < 1 \). Then there exists \( \delta > 0 \) such that for every \((S(0), I(0)) \in G \) with \( I_i(0) < \delta, \quad i = 1, 2, \ldots, n \), the solution \((S(t), I(t))\) of (1.2) satisfies

\[
\lim_{t \to \infty}(S'(t), I(t)) = (S^*, 0).
\]

**Proof.** Let us consider an auxiliary system

\[
S'_i = B_i(S_i)S_i - \mu_i S_i + (B_i(0+) + \gamma_i)\epsilon + \sum_{j=1}^{n} a_{ij}S_j, \quad i = 1, \ldots, n,
\]

(2.9)
where \( \epsilon > 0 \) is a small constant to be determined. By (A4) and the previous analysis of system (2.1), we can restrict \( \epsilon \) small enough such that (2.9) admits a unique positive equilibrium \( S^*(\epsilon) \) which is globally asymptotically stable. Let \( S(t, N^*) \) be the solution of (2.9) through \((N^*, \ldots, N^*)\) at \( t = 0 \). Select \( T(\epsilon) > 0 \) such that

\[
S(t, N^*) < S^*(\epsilon) + \bar{\epsilon}, \quad \forall t \geq T(\epsilon);
\]

where \( \bar{\epsilon} = (\epsilon, \ldots, \epsilon) \). Define a matrix \( M_1(\epsilon) \) by

\[
\begin{bmatrix}
\beta_1S'_1(\epsilon) - \mu_1 - \gamma_1 + b_{11} & b_{12} & \cdots & b_{1n} \\
b_{21} & \beta_2S'_2(\epsilon) - \mu_2 - \gamma_2 + b_{22} & \cdots & b_{2n} \\
\vdots & \vdots & \ddots & \vdots \\
b_{n1} & b_{n2} & \cdots & \beta_nS'_n(\epsilon) - \mu_n - \gamma_n + b_{nn}
\end{bmatrix}.
\]

Since \( M_1(0) = M_1 \) and \( s(M_1(\epsilon) + \epsilon M_2) \) is continuous for small \( \epsilon \), we can now restrict \( \epsilon \) small enough such that \( s(M_1(\epsilon) + \epsilon M_2) < 0 \). Let \( v = (v_1, \ldots, v_n) \) be a positive eigenvector associated with \( s(M_1(\epsilon) + \epsilon M_2) \). Choose \( k > 0 \) small enough such that \( kv < \bar{\epsilon} \).
Now, we define another auxiliary system
\[ I_t' = \beta_i N^* I_t - (\mu_i + \gamma_i) I_t + \sum_{j=1}^{n} b_{ij} I_j, \quad i = 1, \ldots, n. \] (2.10)

Let \( I(t, \delta) \) be the solution of (2.10) through \((\delta, \ldots, \delta)\) at \( t = 0 \). We restrict \( \delta > 0 \) small enough such that
\[ I(t, \delta) < kv, \quad \forall t \in [0, T(\epsilon)]. \] (2.11)

Let \((S(t), I(t))\) be a non-negative solution of (1.2) with \((S(0), I(0)) \in G\) and \( I_i(0) < \delta, \quad i = 1, 2, \ldots, n\). We claim that \( I(t) \leq kv, \forall t \geq 0 \). Suppose not. By the comparison principle and (2.11), there exist a \( q, 1 \leq q \leq n \), and a \( T_1 > T(\epsilon) \) such that
\[ I(t) \leq kv \quad \text{for} \quad 0 \leq t \leq T_1, \]
\[ I_q(T_1) = kvq, \quad I_q(t) > kvq \quad \text{for} \quad 0 < t - T_1 < 1. \] (2.12)

Notice that for \( 0 \leq t \leq T_1 \), we have
\[ S_t' < B_i(S_t)S_t - \mu_i S_t + (B(0^+) + \gamma_i)\epsilon + \sum_{j=1}^{n} a_{ij} S_j, \quad i = 1, \ldots, n. \] (2.13)

It follows from the comparison principle that \( S(T_1) < S^*(\epsilon) + \epsilon \). Hence, for \( 0 \leq t - T_1 < 1 \), we have
\[ I_t' < \beta_i(S_t^*(\epsilon) + \epsilon)I_t - (\mu_i + \gamma_i) I_t + \sum_{j=1}^{n} b_{ij} I_j, \quad i = 1, \ldots, n. \]

Since \( I(T_1) \leq kv \), the comparison principle implies that
\[ I(t) < kve^{(M_1(\epsilon) + M_2)(t - T_1)} \quad \text{for} \quad 0 \leq t - T_1 < 1 \]
and hence,
\[ I_q(t) < kvq e^{(M_1(\epsilon) + M_2)(t - T_1)} < kvq \quad \text{for} \quad 0 < t - T_1 < 1, \]
which contradicts to (2.12). This proves the claim.

Now, (2.13) holds for all \( t \geq 0 \) due to the claim, and hence, the comparison principle implies that \( S(t) < S^*(\epsilon) + \epsilon, \forall t \geq T(\epsilon) \). By a similar argument as above, it then follows that
\[ I(t) < kve^{(M_1(\epsilon) + M_2)(t - T(\epsilon))}, \quad \forall t > T(\epsilon). \]

Consequently, \( I(t) \to 0 \) as \( t \to \infty \).

Let \( \Phi(t) : R^+_1 \to R^+_n \) be the solution semiflow of (1.2), that is, \( \Phi(t)(S_0, I_0) = (S(t), I(t)) \) is the solution of (1.2) with \((S(0), I(0)) = (S_0, I_0)\). Given \((S_0, I_0) \in G \) with \( S_0 \neq 0 \) and \( I_0 < \delta, i = 1, \ldots, n \), it easily follows that \( S(t) \in \text{int}(R^+_n) \), \( \forall t > 0 \). Let \( \omega = \omega(S_0, I_0) \) be the omega limit set of \( \Phi(t)(S_0, I_0) \). Since \( I(t) \to 0 \) as \( t \to \infty \), there holds \( \omega = \tilde{\omega} \times \{0\} \). We claim that, by contradiction, \( \tilde{\omega} = \{0\} \). Then \( \lim_{t \to \infty} (S(t), I(t)) = (0, 0) \). By assumption (A4), we can choose a small \( \eta > 0 \) such that \( s(M(0) - \eta E) > 0 \), where \( E = \text{diag}(1, \ldots, 1) \). It follows that there exists a \( \overline{t} > 0 \) such that \( B_i(N(t)) - \beta_i I(t) \geq B_i(0^+) - \eta \) for \( \forall t \geq \overline{t}, \quad i = 1, \ldots, n \). Then \( S(t) = (S_1(t), \ldots, S_n(t)) \) satisfies
\[ S'_i(t) > (B_i(0+) - \eta)S_i - \mu_iS_i + \sum_{j=1}^{n} a_{ij}S_j, \quad \forall t \geq i, \quad i = 1, \ldots, n. \] (2.14)

Let \( w = (w_1, \ldots, w_n) \) be a positive eigenvector of \( M(0) - \eta E \) associated with the eigenvalue \( s(M(0) - \eta E) \). Choose a small number \( \varepsilon > 0 \) such that \( S(i) > \varepsilon w \). Then the comparison theorem implies that

\[ S(t) \geq \varepsilon w e^{(M(0) - \eta E)(t-i)}, \quad \forall t \geq i \]

and hence \( \lim_{t \to \infty} S_i(t) = \infty, \quad i = 1, 2, \ldots, n \), a contradiction.

It is easy to see that
\[ \phi(t)|_{\omega}(S, 0) = (\Phi(t)S, 0), \]
where \( \Phi(t) \) is the solution semiflow of system (2.1). By [14, Lemma 2.1], \( \omega \) is an internal chain transitive set for \( \Phi(t) \), and hence, \( \hat{\omega} \) is an internal chain transitive set for \( \Phi(t) \). Since \( \hat{\omega} \neq \{0\} \) and \( S^* \) is globally asymptotically stable for (2.1) in \( R^n_+ \setminus \{0\} \), we have \( \hat{\omega} \cap W^u(S^*) \neq \emptyset \). By [14, Theorem 3.1 and Remark 4.6], we then get \( \hat{\omega} = S^* \). This proves \( \omega = \{(S^*, 0)\} \). Consequently, \( (S(t), I(t)) \to (S^*, 0) \) as \( t \to \infty \). \( \square \)

It is easy to see that the eigenvalues of \( M_1 \) are also the eigenvalues of the Jacobian matrix of (1.2) at \( E_0 \). It follows that \( E_0 \) is unstable if \( R_0 > 1 \). The following result shows that \( R_0 > 1 \) actually implies that model (1.2) admits at least one endemic equilibrium and the disease is uniformly persistent.

**Theorem 2.3.** Let (A1)-(A4) hold and \( R_0 > 1 \). Then (1.2) admits at least one (componentwise) positive equilibrium, and there is a positive constant \( \varepsilon \) such that every solution \( (S(t), I(t)) \) of (1.2) with \( (S(0), I(0)) \in R^n_+ \times int(R^n_+) \) satisfies

\[ \liminf_{t \to \infty} I_i(t) \geq \varepsilon, \quad i = 1, 2, \ldots, n. \]

**Proof.** Define

\[
\begin{align*}
X &= \{(S_1, \ldots, S_n, I_1, \ldots, I_n) : S_i \geq 0, \quad I_i \geq 0, \quad i = 1, 2, \ldots, n\}, \\
X_0 &= \{(S_1, \ldots, S_n, I_1, \ldots, I_n) \in X : I_i > 0, \quad i = 1, 2, \ldots, n\}, \\
\partial X_0 &= X \setminus X_0.
\end{align*}
\]

It then suffices to show that (1.2) is uniformly persistent with respect to \( (X_0, \partial X_0) \).

First, by the form of (1.2), it is easy to see that both \( X \) and \( X_0 \) are positively invariant. Clearly, \( \partial X_0 \) is relatively closed in \( X \). Furthermore, system (1.2) is point dissipative(see Lemma 2.2). Set

\[ M_0 = \{(S(0), I(0)) : (S(t), I(t)) \text{ satisfies } (1.2) \text{ and } (S(t), I(t)) \in \partial X_0, \forall t \geq 0\}. \]

We now show that

\[ M_0 = \{(S, 0) : S \geq 0\}. \] (2.15)

Assume \( (S(0), I(0)) \in M_0 \). It suffices to show that \( I(t) = 0, \forall t \geq 0 \). Suppose not. Then there exist an \( i_0, 1 \leq i_0 \leq n, \) and a \( t_0 \geq 0 \) such that \( I_{i_0}(t_0) > 0 \). We partition \( \{1, 2, \ldots, n\} \) into two sets \( Q_1 \) and \( Q_2 \) such that
$I_i(t_0) = 0, \quad \forall i \in Q_1,$
$I_i(t_0) > 0, \quad \forall i \in Q_2.$

$Q_1$ is non-empty due to the definition of $M_5$. $Q_2$ is non-empty since $I_i(t_0) > 0$. For any $j \in Q_1$, we have

$$I'_i(t_0) \geq b_{ji}I_i(t_0) > 0.$$ 

It follows that there is an $\epsilon_0 > 0$ such that $I_i(t) > 0$, $j \in Q_1$ for $t_0 < t < t_0 + \epsilon_0$. Clearly, we can restrict $\epsilon_0 > 0$ small enough such that $I_i(t) > 0$, $i \in Q_2$ for $t_0 < t < t_0 + \epsilon_0$. This means that $(S(t), I(t)) \not\in \partial X_0$ for $t_0 < t < t_0 + \epsilon_0$, which contradicts the assumption that $(S(0), I(0)) \in M_5$. This proves (2.15).

It is clear that there are two equilibria $(0, 0)$ and $(S^*, 0)$ in $M_5$. Choose $\eta > 0$ small enough such that $s(M_1 - \eta M_2) > 0$. Let us consider a perturbed system of (2.1)

$$S'_i = B_i(S_i + \epsilon_i)S_i - (\mu_i + \beta_i \epsilon_i)S_i + \sum_{j=1}^{N} a_{ij}S_j, \quad i = 1, \ldots, n. \quad (2.16)$$

First, as in our previous analysis of system (2.1), we can restrict $\epsilon_1 > 0$ small enough such that (2.16) admits a unique positive equilibrium $S^*(\epsilon_1)$ which is globally asymptotically stable. By the implicit function theorem, it follows that $S^*(\epsilon_1)$ is continuous in $\epsilon_1$. Thus, we can further restrict $\epsilon_1$ small enough such that $S^*(\epsilon_1) > S^* - \eta$. Let us consider an arbitrary positive solution $(S(t), I(t))$ of (1.2). We now claim that

$$\limsup_{t \to \infty} \max_i \{I_i(t)\} > \epsilon_1.$$ 

Suppose, for the sake of contradiction, that there is a $T > 0$ such that $I_i(t) \leq \epsilon_1$, $i = 1, 2, \ldots, n$, for all $t \geq T$. Then for $t \geq T$, we have

$$S'_i \geq B_i(S_i + \epsilon_i)S_i - (\mu_i + \beta_i \epsilon_i)S_i + \sum_{j=1}^{N} a_{ij}S_j, \quad i = 1, \ldots, n. \quad (2.17)$$

Since the equilibrium $S^*(\epsilon_1)$ of (2.16) is globally asymptotically stable and $S^*(\epsilon_1) > S^* - \eta$, there is a $T_1 > 0$ such that $S(t) \geq S^* - \eta$ for $t \geq T + T_1$. As a consequence, for $t > T + T_1$, there holds

$$I'_i \geq \beta_i(S_i^* - \eta)I_i - (\mu_i + \gamma_i)I_i + \sum_{j=1}^{n} b_{ij}I_j, \quad i = 1, \ldots, n. \quad (2.18)$$

Since the matrix $M_1 - \eta M_2$ has a positive eigenvalue $s(M_1 - \eta M_2)$ with a positive eigenvector, it is easy to see that $I_i(t) \to \infty$ as $t \to \infty$, $i = 1, 2, \ldots, n$, which leads to a contradiction.

Note that $S^*$ is globally asymptotically stable in $R_+^n \setminus \{0\}$ for system (2.1). By the above-mentioned claim, it then follows that $(0, 0)$ and $E_0$ are isolated invariant sets in $X$, $W^s((0, 0)) \cap X_0 = \emptyset$, and $W^u(E_0) \cap X_0 = \emptyset$. Clearly, every orbit in $M_5$ converges to either $(0, 0)$ or $E_0$, and $(0, 0)$ and $E_0$ are acyclic in $M_5$. By [17, Theorem 4.6] (see also [14, Theorem 4.3 and Remark 4.3], for a stronger repelling property of $\partial X_0$), we conclude that system (1.2) is uniformly persistent with respect to $(X_0, \partial X_0)$. By [21, Theorem 2.4], system (1.2) has an equilibrium $(\bar{S}, \bar{T}) \in X_0$. Then $\bar{S} \in R_+^n$ and $\bar{T} \in int(R_+^n)$. We further claim that $\bar{S} \in R_+^n \setminus \{0\}$. Suppose that $\bar{S} = 0$. By the second equation in (1.3), we then get $0 = -\sum_{i=1}^{n} (\mu_i + \gamma_i)\bar{T}_i$, and hence $\bar{T}_i = 0$, $i = 1, 2, \ldots, n$, a contradiction. By the first equation in (1.2) and the irreducibility of the cooperative matrix $(a_{ij})$, it follows that $\bar{S} = S(t, \bar{S}, \bar{T}) \in int(R_+^n)$, $\forall t > 0$. Then $(\bar{S}, \bar{T})$ is a componentwise positive equilibrium of (1.2). □
3. Application to two patches

In the case where the patch number \( n \) is 2, the assumption (1.3) is equivalent to that \( a_{12} = -a_{22}, \ a_{21} = -a_{11}, \ b_{12} = -b_{22}, \ b_{21} = -b_{11}, \) and hence, (1.2) reduces to

\[
\begin{align*}
S'_1 &= B_1(N_1)N_1 - (\mu_1 - a_{11})S_1 - \beta_1S_1I_1 + \gamma_1I_1 - a_{22}S_2, \\
I'_1 &= \beta_1S_1I_1 - (\mu_1 + \gamma_1 - b_{11})I_1 - b_{22}I_2, \\
S'_2 &= B_2(N_2)N_2 - (\mu_2 - a_{22})S_2 - \beta_2S_2I_2 + \gamma_2I_2 - a_{11}S_1, \\
I'_2 &= \beta_2S_2I_2 - (\mu_2 + \gamma_2 - b_{22})I_2 - b_{11}I_1,
\end{align*}
\]

where \( a_{ii} \) and \( b_{ii}, \ 1 \leq i \leq 2, \) are negative constants. Assume that

\[ (A5) \quad B_i(0+) > \mu_i, \quad \forall 1 \leq i \leq 2. \]

It then follows that \( s(M(0)) > 0. \) Let \((S'_1, S'_2)\) be the positive solution of the following system:

\[
\begin{align*}
B_1(S_1)S_1 - (\mu_1 - a_{11})S_1 - a_{22}S_2 &= 0, \\
B_2(S_2)S_2 - (\mu_2 - a_{22})S_2 - a_{11}S_1 &= 0.
\end{align*}
\]

Now \( M_1 \) becomes

\[
\begin{bmatrix}
\beta_1S'_1 + b_{11} - \mu_1 - \gamma_1 & -b_{22} \\
-b_{11} & \beta_2S'_2 + b_{22} - \mu_2 - \gamma_2
\end{bmatrix}.
\]

Its characteristic equation is \( \lambda^2 - h_1\lambda + h_2 = 0 \) where

\[
\begin{align*}
h_1 &= \beta_1S'_1 + \beta_2S'_2 + b_{11} + b_{22} - \gamma_1 - \gamma_2 - \mu_1 - \mu_2, \\
h_2 &= \beta_1S'_1\beta_2S'_2 - b_{11}b_{22} - \beta_1S'_1(\mu_2 + \gamma_2 - b_{22}) \\
&\quad - \beta_2S'_2(\mu_1 + \gamma_1 - b_{11}) + (\mu_1 + \gamma_1 - b_{11})(\mu_2 + \gamma_2 - b_{22}).
\end{align*}
\]

It is easy to see that

\[
s(M_1) = \frac{h_1 + \sqrt{h_1^2 - 4h_2}}{2}. \tag{3.4}
\]

Then \( R_0 > 1 \) if and only if \( h_1 \geq 0 \) or

\[
\begin{cases}
h_1 < 0, \\
1 + \frac{\beta_1S'_1\beta_2S'_2 - b_{11}b_{22}}{(\mu_1 + \gamma_1 - b_{11})(\mu_2 + \gamma_2 - b_{22})} < \frac{\beta_1S'_1}{\mu_1 + \gamma_1 - b_{11}} + \frac{\beta_2S'_2}{\mu_2 + \gamma_2 - b_{22}}.
\end{cases} \tag{3.5}
\]

\( h_1 \geq 0 \) means that the total infection force of two patches overpasses the sum of recovery rates, death rates and emigration rates of infectives in the two patches. \( \frac{\beta_1S'_1}{\mu_1 + \gamma_1 - b_{11}} \) can be viewed as a reproduction number at the first patch, and \( \frac{\beta_2S'_2}{\mu_2 + \gamma_2 - b_{22}} \) a reproduction number at the second patch. \( \frac{\beta_1S'_1\beta_2S'_2 - b_{11}b_{22}}{(\mu_1 + \gamma_1 - b_{11})(\mu_2 + \gamma_2 - b_{22})} \) represents the quantity that new infectives minus moving infectives during the interval of product of infection periods in two patches. Thus, the second inequality of (3.5) can be interpreted as the sum of reproduction numbers in the two patches is stronger than 1 plus the net
value that the numbers of new infectives minus moving infectives during the interval of product of infection periods in two patches.

The conditions clearly show the effect of population dispersal on the spread of the disease. In order to be specific, we choose the birth rates $B_i$ of the population as

$$B_i(N_i) = \frac{r_i}{N_i} + c_i, \quad c_i < \mu_i, \quad 1 \leq i \leq 2.$$ 

Then (3.1) reduces to

$$S'_i = r_i + c_i I_i - (\mu_i - c_i - a_{1i}) S_i - \beta_i S_i I_i + \gamma_i I_i - a_{2i} S_i,$$

$$I'_i = \beta_i S_i I_i - (\mu_i + \gamma_i - b_{1i}) I_i - b_{2i} I_i,$$

$$S'_2 = r_2 + c_2 I_2 - (\mu_2 - c_2 - a_{22}) S_2 - \beta_2 S_2 I_2 + \gamma_2 I_2 - a_{11} S_1,$$

$$I'_2 = \beta_2 S_2 I_2 - (\mu_2 + \gamma_2 - b_{22}) I_2 - b_{11} I_1.$$ 

(3.6)

In this case $(S'_1, S'_2)$ can be given explicitly as

$$S'_1 = \frac{r_2 a_{22} - \mu_2 r_1 + c_2 r_1 + r_1 a_{22} - \mu_2 \mu_1 + \mu_2 c_1 + \mu_2 a_{11} + c_2 \mu_1 - c_2 c_1 - c_2 a_{11} + \mu_1 a_{22} - c_1 a_{22}}{-\mu_1 r_2 + c_1 r_2 + a_{11} r_2 + a_{11} r_1},$$

$$S'_2 = \frac{r_2 a_{22} - \mu_2 r_1 + c_2 r_1 + r_1 a_{22} - \mu_2 \mu_1 + \mu_2 c_1 + \mu_2 a_{11} + c_2 \mu_1 - c_2 c_1 - c_2 a_{11} + \mu_1 a_{22} - c_1 a_{22}}{-\mu_1 r_2 + c_1 r_2 + a_{11} r_2 + a_{11} r_1}.$$ 

(3.7)

In the absence of population dispersal between two patches, i.e., $a_{11} = a_{22} = b_{11} = b_{22} = 0$, (3.6) becomes

$$S'_1 = r_1 + c_1 I_1 - (\mu_1 - c_1) S_1 - \beta_1 S_1 I_1 + \gamma_1 I_1,$$

$$I'_1 = \beta_1 S_1 I_1 - (\mu_1 + \gamma_1) I_1,$$

(3.8)

and

$$S'_2 = r_2 + c_2 I_2 - (\mu_2 - c_2) S_2 - \beta_2 S_2 I_2 + \gamma_2 I_2,$$

$$I'_2 = \beta_2 S_2 I_2 - (\mu_2 + \gamma_2) I_2.$$ 

(3.9)

Set

$$R_{01} := \frac{\beta_1 r_1}{(\mu_1 - c_1)(\mu_1 + \gamma_1)},$$ 

(3.10)

$$R_{02} := \frac{\beta_2 r_2}{(\mu_2 - c_2)(\mu_2 + \gamma_2)}.$$ 

(3.11)

It is well known that $R_{01}$ is a reproduction number of the disease in the first patch and $R_{02}$ is a reproduction number of the disease in the second patch.

Let $(f_1, f_2)$ be the vector field defined by system (3.8). Then, for the Dulac function $D(S_1, I_1) := \frac{1}{S_1 I_1}$, there holds

$$\frac{\partial (f_1)}{\partial S_1} + \frac{\partial (f_2)}{\partial I_1} = - r_1 S_1^2 I_1 - \frac{c_1 + \gamma_1}{S_1^2 I_1} < 0.$$ 

Thus, (3.8) does not have a limit cycle. Then it is easy to see that the disease will disappear in the first patch if $R_{01} < 1$ and there is an endemic equilibrium in (3.8) which is globally asymptotically stable if $R_{02} > 1$. Similarly, the disease will disappear in the second patch if $R_{02} < 1$ and there is an
endemic equilibrium in (3.9) which is globally asymptotically stable if $R_{02} > 1$. Based upon these results, we can present two examples that illustrate the effect of population dispersal on the spread of disease.

**Example 3.1.** Suppose $r_1 = r_2 = r$, $c_1 = c_2 = c$, $\mu_1 = \mu_2 = \mu$, $\gamma_1 = \gamma_2 = \gamma$, $a_{11} = a_{22} = b_{11} = b_{22} = -\theta$ in (3.6). This means that we assume that two patches have the same demographic structure and the same recovery rate for the disease. In this way, it is easier to find the effect of the variance of the contact rates in two patches and the population dispersal rate on the disease spread. Then, it is easy to obtain $S_1^{*} = S_2^{*} = \frac{r}{\mu - c}$. It follows from (3.4) that

$$2s(M_1) = \frac{r(\beta_1 + \beta_2)}{\mu - c} - 2\theta - 2(\mu + \gamma) + \sqrt{\frac{r^2(\beta_2 - \beta_1)^2}{(\mu - c)^2} + 4\theta^2}.$$  \text{(3.12)}

If the two patches are isolated, the discussions above show that the disease will be persistent in the first patch if

$$R_{01} = \frac{r\beta_1}{(\mu - c)(\mu + \gamma)} > 1$$

and the disease will disappear in the first patch if $R_{01} < 1$. Further, the disease will be persistent in the second patch if

$$R_{02} = \frac{r\beta_2}{(\mu - c)(\mu + \gamma)} > 1$$

and the disease will disappear in the second patch if $R_{02} < 1$.

Assume that the disease spreads in each isolated patch, i.e., $R_{0i} > 1$, $i = 1, 2$. Notice that

$$\sqrt{\frac{r^2(\beta_2 - \beta_1)^2}{(\mu - c)^2} + 4\theta^2 > 2\theta}, \text{ if } \beta_1 \neq \beta_2.$$ 

By (3.12), we have $s(M_1) > 0$, and hence $R_0 > 1$. It follows that the disease also spreads in both patches when population dispersal occurs.

Now, we suppose that the disease dies out in each isolated patch, i.e., $R_{0i} < 1$, $i = 1, 2$. Note that

$$2s(M_1) = (\mu + \gamma) \left[ R_{01} + R_{02} - 2 + \frac{(R_{01} - R_{02})^2}{\sqrt{(R_{01} - R_{02})^2 + 4\theta^2/((\mu + \gamma)^2 + 2\theta/(\mu + \gamma))}} \right] < 0$$

and hence $R_0 < 1$. Thus, the disease dies also out in the two patches when population dispersal occurs.

Let us consider the other cases. Fix $r = c = \gamma = 1$, $\mu = 2$, $\beta_2 = 1$. By means of Maple software, we see that $s(M_1) > 0$ (i.e., $R_0 > 1$) for all $\theta > 0$ if $\beta_1 \geqslant 5$ (see Fig. 1), Thus, the disease spreads in both patches when population dispersal occurs. Since $R_{01} \geqslant 5/3$ and $R_{02} = 1/3$, we see that the population dispersal intensifies the disease spread. If $3 < \beta_1 < 5$, We find that there is a $\theta_0 > 0$ such that $s(M_1) > 0$ (i.e., $R_0 > 1$) for all $0 < \theta < \theta_0$ and $s(M_1) < 0$ (i.e., $R_0 < 1$) for all $\theta > \theta_0$ (see Fig. 2). Hence, the disease will disappear in both patches if the population dispersal rate is large. Since $1 < R_{01} < 5/3$ and $R_{02} = 1/3$, we see that the population dispersal reduces the disease spread and is beneficial to disease control.
Example 3.2. We consider the case where susceptible individuals and infective individuals in each patch have the same dispersal rate, but the population has different birth rates and different contact rates in different patches. Fix $r_1 = 1$, $r_2 = 5$, $c_1 = c_2 = 1$, $\mu_1 = \mu_2 = 2$, $\gamma_1 = \gamma_2 = 0$, $a_{11} = b_{11} = 0.3$, $a_{22} = b_{22} = -0.3k$, $\beta_1 = 1.5$, $\beta_2 = 0.1$ in (3.6), where $k$ is a positive constant. In the absence of population dispersal, it is easy to see that the reproduction numbers in the two patches are $R_{01} = 0.75$, $R_{02} = 0.25$. Thus, the disease dies out in each patch when they are isolated. If the population dispersal occurs, by calculating the $h_i$ defined in (3.3) we have

$$h_1 = \frac{-14.9 + 20.1k}{13.0 + 3.0k} - \frac{0.9(k + 8.486078811)(k + 2.513921189)}{13.0 + 3.0k},$$

$$h_2 = \left(\frac{3.0}{13.0 + 3.0k} - 2.3\right)\left(\frac{6.8}{13.0 + 3.0k} - 0.3k - 2\right) - 0.09k.$$
By numerical calculations, we obtain
\[
\begin{align*}
    h_1 &< 0 \quad \text{for all } k > 0, \\
    h_2 &> 0 \quad \text{if } k < 0.7138728627, \\
    h_2 &< 0 \quad \text{if } k > 0.7138728627.
\end{align*}
\]

It then follows that \( R_0 > 1 \) when \( k > 0.7138728627 \). Thus, the disease will spread in the two patches if \( k > 0.7138728627 \), although the disease cannot spread in any patch when they are isolated.

4. Discussions

In this paper, we have proposed an epidemic model in order to simulate the dynamics of disease transmission under the influence of a population dispersal among patches. The population dispersal among patches can be interpreted as the movement that people travel or migrate from one city to another city or from one country to another country. In order to be more realistic, we have incorporated more general demographic structure, proposed in [5], into the model and incorporated both the difference of demographic structure and disease transmission among different patches and the difference between the dispersal rates of susceptible individual and the dispersal rates of infective individuals, which simulates the process of disease control. We establish a threshold above which the disease is uniformly persistent and below which disease-free equilibrium is locally attractive, and globally attractive when both susceptible and infective individuals in each patch have the same dispersal rate. We have also applied our result to a specific demographic structure. For this special case, we have constructed two examples to show that population dispersal can both intensify and reduce the spread of disease in patches. In the first example, we consider a case where the disease spreads in one patch and cannot spread in the other patch when they are isolated. We have shown that the population dispersal leads to the disease spread in both patches if the reproduction number for one patch is large. We have also shown that the disease dies out in the two patches if the reproduction numbers for two patches are suitable and the population dispersal rate is strong. In the second example, we suppose that susceptible individuals and infective individuals in each patch have the same dispersal rate, but the population has different birth rates and different contact rates in different patches. We have shown that a population dispersal results in the spread of the disease in all patches, even though the disease cannot spread in each isolated patch.

It will be interesting to consider the global stability of an endemic equilibrium of the model under the influence of population dispersal among patches. This seems to be a difficult problem since the dimension of the model is higher. We leave this for future investigations.

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