Threshold dynamics in a time-delayed epidemic model with dispersal

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1. Introduction

The dynamics of infectious diseases is an important research area in mathematical epidemiology. Some commonly studied types are SIR models where a disease spreads through contact and a population is divided among three classes: susceptible, infective and recovered. In many studies, the goal is to understand the key factors in disease transmission (see, for example, [2,3,7,8]) and this often includes (but is not limited to) determining a threshold condition for the persistence and extinction of the disease. The basic reproduction number, \( R_0 \), is the expected number of new infected individuals from one typical infected individual. Hence, \( R_0 \) is a threshold: the disease goes extinct when \( R_0 < 1 \); while it persists in the population when \( R_0 > 1 \).

Many diseases such as influenza, measles and sexually transmitted diseases are easily spread between countries, regions or cities due to travel. This population dispersal is an important aspect to consider when studying the spread of a disease. We consider a disease transmission model with population dispersal among \( n \) patches, as in papers such as [1,13]. As in [4], the population demographic is described by

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

where \( N \) is the (non-constant) size of a population, \( B(N) \) is the birth rate of the population and \( \mu \) is its death rate.

In ordinary differential equation models, the duration of the infectious period is described by the negative exponential distribution (see, for example, [8]). Here we assume that individuals have a constant length of infection \( \tau \) which gives rise to delay differential equations. This new feature of the standard patch model is studied in [14] using a typical example of the function \( B(N) \) found in biological literature. In that work, \( B(N)/N \) is a linear function which simplifies the analysis. Our purpose in the current paper is to extend the results in [14] to the general function \( B(N)/N \) and numerically investigate the impact of the other typical functions (where \( B(N)/N \) is nonlinear) on the basic reproduction number.

In the following section, the model is established and preliminary results are given. Section 3 is devoted to establishing the basic reproduction number and the threshold dynamics for the model with the general birth rate function. In the fourth section, we use numerical simulations for some typical functions \( B(N)/N \) to illustrate the effect of dispersal. A discussion of the main results and the examples is provided in the fifth section, and the proofs of the main analytical results are given in the last section.

2. The model

In this section, we present an epidemic model with population dispersal and infection period, which is based on [14].

Let \( S_i, I_i \) and \( R_i \) denote the density of susceptible, infective and recovered individuals in patch \( i \). The population size, \( N_i \), is therefore given by \( N_i = S_i + I_i + R_i \) and we assume that the demographic structure is described by

\[
\frac{dN_i(t)}{dt} = B_i(N_i(t))N_i(t) - \mu_i N_i(t),
\]

where \( B_i \) is the per capita birth rate and \( \mu_i \) the per capita death rate. Birth rate functions satisfy the following conditions:
When the patches are connected, the dynamics of disease transmission is described by

\[
\begin{align*}
\frac{dS_1}{dt} &= B_1(N_1(t))N_1(t) - (\mu_1 + d_1)S_1(t) - k_1S_1(t)I_1(t) + d_2S_2(t), \\
\frac{dS_2}{dt} &= B_2(N_2(t))N_2(t) - (\mu_2 + d_2)S_2(t) - k_2S_2(t)I_2(t) + d_1S_1(t), \\
\frac{dI_1}{dt} &= k_1S_1(t)I_1(t) - (\mu_1 + r_1 + b_1)I_1(t) + b_2I_2(t), \\
\frac{dI_2}{dt} &= k_2S_2(t)I_2(t) - (\mu_2 + r_2 + b_2)I_2(t) + b_1I_1(t), \\
\frac{dR_1}{dt} &= r_1I_1(t) - (\mu_1 + c_1)R_1(t) + c_2R_2(t), \\
\frac{dR_2}{dt} &= r_2I_2(t) - (\mu_2 + c_2)R_2(t) + c_1R_1(t),
\end{align*}
\]

(2.1)

where \( k_i \) is the disease transmission coefficient and \( r_i \) is the recovery rate of infected individuals, with \( i = 1, 2 \). Migration of susceptible individuals from the first patch to the second is given by \( d_1 \), while migration from the second patch to the first is given by \( d_2 \). Similarly, \( b_1, b_2, c_1, c_2 \) describe the migration of infective individuals and recovered individuals, respectively. As in [14], we assume that disease-related death is negligible compared to the natural death rate, which is the case with many epidemics.

We assume that the length of infection for all infectious individuals is the constant \( \tau \), and that the number of individuals recovered due to treatment per unit is proportional to the number of infectious individuals. Let \( a \) be the infection age and let \( I_i(a, t) \) be the density of infected individuals at time \( t \) with respect to infection age \( a \) in the \( i \)th patch. Then the force of infection in patch \( i \) at time \( t \) is

\[
k_i \int_0^\tau I_i(a, t) da
\]

and (2.1) can be modified as

\[
\begin{align*}
\frac{dS_1}{dt} &= B_1(N_1(t))N_1(t) - (\mu_1 + d_1)S_1(t) - \lambda_1(t)S_1(t) + d_2S_2(t), \\
\frac{dS_2}{dt} &= B_2(N_2(t))N_2(t) - (\mu_2 + d_2)S_2(t) - \lambda_2(t)S_2(t) + d_1S_1(t), \\
\frac{dI_1}{dt} &= \lambda_1(t)S_1(t) - (\mu_1 + r_1 + b_1)I_1(t) + b_2I_2(t), \\
\frac{dI_2}{dt} &= \lambda_2(t)S_2(t) - (\mu_2 + r_2 + b_2)I_2(t) + b_1I_1(t), \\
\frac{dR_1}{dt} &= r_1I_1(t) - (\mu_1 + c_1)R_1(t) + c_2R_2(t), \\
\frac{dR_2}{dt} &= r_2I_2(t) - (\mu_2 + c_2)R_2(t) + c_1R_1(t),
\end{align*}
\]

(2.2)

with initial conditions given by

\[
\begin{align*}
S_i(0) &= S_i^0 > 0, \\
R_i(0) &= R_i^0 > 0, & i = 1, 2, \\
I_i(0, 0) &= \iota_i(a) > 0, & 0 < a \leq \tau, & i = 1, 2.
\end{align*}
\]

Let \( P_i(t) = \int_0^\tau I_i(a, t) da \) be the total density of infected members at time \( t \) in the \( i \)th patch. Define

\[
B = \begin{bmatrix} -\mu_1 - r_1 - b_1 & b_2 \\ b_1 & -\mu_2 - r_2 - b_2 \end{bmatrix}, \\
(b_1(a)) := \exp(Ba), \\
Q_i(t) := k_1S_i(t)P_i(t),
\]

and

\[
\gamma_i(t) := r_iP_i(t) + b_1(\tau)Q_1(t - \tau) + b_2(\tau)Q_2(t - \tau), & i = 1, 2.
\]

By integrating along the characteristics, Wang and Zhao [14] derived the following time-delayed model:

\[
\begin{align*}
\frac{dS_1}{dt} &= B_1(N_1(t))N_1(t) - (\mu_1 + d_1)S_1(t) - Q_1(t) + d_2S_2(t), \\
\frac{dS_2}{dt} &= B_2(N_2(t))N_2(t) - (\mu_2 + d_2)S_2(t) - Q_2(t) + d_1S_1(t), \\
\frac{dP}{dt} &= Q(t) - \exp(B\tau)Q(t - \tau) + BP(t), \\
\frac{dR_1}{dt} &= \gamma_1(t) - (\mu_1 + c_1)R_1(t) + c_2R_2(t), \\
\frac{dR_2}{dt} &= \gamma_2(t) - (\mu_2 + c_2)R_2(t) + c_1R_1(t),
\end{align*}
\]

(2.3)

for \( t > \tau \), with initial functions satisfying

\[
P(t) = \int_0^t \exp(-B\tau)Q(s)ds.
\]

Eq. (2.3) is an autonomous functional differential equation system defined on \( C(0, \infty, \mathbb{R}_+^6) \). After a time translation, we will consider, without loss of generality, (2.3) on \( C([-\tau, 0], \mathbb{R}_+^6) \) under the condition

\[
P(0) = \int_{-\tau}^0 \exp(-B\tau)Q(s)ds.
\]

Assume that each \( B_i(N_i)N_i \) extends to a \( C^1 \) function \( G_i(N_i) \) on \( [0, \infty) \) with \( G_i(0) \geq 0 \). Let \( u(t) = (S(t), P(t), R(t)) \) be a continuous function from \( [-\tau, \sigma] \) to \( \mathbb{R}_+^6 \) for some \( \sigma > 0 \). For each \( t \in [0, \sigma] \), we define \( u \in C([-\tau, 0], \mathbb{R}_+^6) \) by \( u_i(s) = u(t + s) \) for all \( s \in [-\tau, 0] \). Set

\[
X := \left\{ (S, P, R) \in C([-\tau, 0], \mathbb{R}_+^6) : P(0) = \int_{-\tau}^0 \exp(-B\tau)Q(s)ds \right\}.
\]

By the standard theory of functional differential equations (see [6]), for any \( \phi \in C([-\tau, 0], \mathbb{R}_+^6) \) there exists a unique solution \( u(t, \phi) \) of system (2.3) satisfying \( u_0 = \phi \), which is defined on its maximal interval of existence \( [0, \sigma_\phi] \). It was shown in [14] that for any \( \phi \in X \), \( u(t, \phi) \) is (componentwise) non-negative on \( [0, \sigma_\phi] \), \( u_i(\phi) \in X \), \( \forall t \in [0, \sigma_\phi] \), and

\[
P(t) = \int_{t-\tau}^t \exp(B(t-s))Q(s)ds = \int_{-\tau}^0 \exp(-B\tau)Q(t + s)ds,
\]

(2.4)

for all \( t \in [0, \sigma_\phi] \).

3. Threshold dynamics

In addition to (B1)–(B3), we further make the following assumptions on \( B_i(N_i) \).

(H) \( \mu_i, k_i, b_i, i = 1, 2 \) are positive constants; \( d_i \) and \( c_i \) are non-negative constants for \( i = 1, 2 \).

Define

\[
X_L := \left\{ \phi = (\phi_1, \ldots, \phi_L) \in X : \sum_{l=1}^L \phi_l(0) \leq L \right\}, \quad \forall L \geq 0.
\]

Lemma 3.1. Let (H) hold. Then there exists an \( L' \) such that for any \( L > L' \) the set \( X_L \) is positively invariant for solution maps of (2.3), and every solution \( u(t, \phi) \) of (2.3) with \( \phi \in X \) eventually enters into \( [0, L'] \).
Proof. By (2.3), we have
\[
\begin{aligned}
dN_1 &= (B_1(N_1) - \mu_1)N_1 - d_1S_1 + d_2S_2 - b_1P_1 + b_2P_2 - c_1R_1 + c_2R_2, \\
dN_2 &= (B_2(N_2) - \mu_2)N_2 - d_2S_2 + d_1S_1 - b_2P_2 + b_1P_1 - c_2R_2 + c_1R_1.
\end{aligned}
\]
Let \(N = N_1 + N_2\). Since \(B_1(N_1)\) is continuous and \(\mu_1 > B_1(\infty)\), there exists an \(L_1\) such that \(\mu_1 > B_1(N_1)\) for all \(N_1 > L_1\). Similarly, there exists an \(L_2\) such that \(\mu_2 > B_2(N_2)\) for all \(N_2 > L_2\). Set \(L = L_1 + L_2\) and
\[
m = \min(B_1(L_1) - \mu_1, B_2(L_2) - \mu_2) > 0.
\]
Then,
\[
\begin{aligned}
d\frac{d}{dt}(N_1 + N_2) &= (B_1(N_1) - \mu_1)N_1 + (B_2(N_2) - \mu_2)N_2 \leq mn,
\end{aligned}
\]
for all \(N > L\).

Thus, the standard comparison theorem completes the proof. \(\square\)

Let \(\Phi(t) : X \rightarrow X\) be the solution semiflow associated with (2.3). This means that \(\Phi(t)\phi = \phi(t)\), \(\phi \in X, t \geq 0\). By Lemma 3.1, solutions of (2.3) are ultimately bounded and uniformly bounded. It then follows that the semiflow \(\Phi(t)\) is point dissipative on \(X\) and \(\Phi(t) : X \rightarrow X\) is compact for each \(t > \tau\). By [5, Theorem 3.8], \(\Phi(t)\) admits a global attractor that attracts every bounded set in \(X\).

In order to find the disease-free equilibrium, which is needed for the basic reproduction number, we consider
\[
\begin{aligned}
dS_1 &= B_1(S_1)S_1 - (\mu_1 + d_1)S_1 + d_2S_2, \\
dS_2 &= B_2(S_2)S_2 - (\mu_2 + d_2)S_2 + d_1S_1.
\end{aligned}
\]
Let \(F : \mathbb{R}^2 \rightarrow \mathbb{R}^2\) be defined by the right-hand side of (3.1) and \(S = (S_1, S_2)\). Clearly, \(F\) is continuously differentiable and \(F(0) = 0\). Recall that \(G_i(N) = B_i(N_i)/N_i, \forall N_i > 0, i = 1, 2\). Then the Jacobian \(DF(S)\) is given by
\[
DF(S) = \begin{bmatrix}
G_1(S_1) - (\mu_1 + d_1) & d_2 \\
d_1 & G_2(S_2) - (\mu_2 + d_2)
\end{bmatrix}.
\]
Since the off-diagonal elements of \(DF(S)\) are positive, \(F\) is cooperative for every \(S \in \mathbb{R}^2\). Note also that \(DF(S)\) is irreducible. Let \(\alpha \in (0, 1)\) and \(S \in \text{int}(\mathbb{R}^2)\). Then the following holds
\[
\begin{aligned}
\alpha B_1(S_1)S_1 - \alpha(\mu_1 + d_1)S_1 + d_2S_2 > \alpha B_1(S_1)S_1 - (\mu_1 + d_1)S_1 + d_2S_2, \\
\alpha B_2(S_2)S_2 - \alpha(\mu_2 + d_2)S_2 + d_1S_1 > \alpha B_2(S_2)S_2 - (\mu_2 + d_2)S_2 + d_1S_1.
\end{aligned}
\]
Thus, \(F\) is strongly subhomogeneous on \(\mathbb{R}^2\).

Recall that the stability modulus of a square matrix \(M\), denoted by \(s(M)\), is defined by
\[
s(M) := \max \{\text{Re}\lambda : \lambda \text{ is an eigenvalue of } M\}.
\]
In order for (3.1) to admit a positive equilibrium, we need to assume that
\[
(B4) \; s(DF(0)) > 0.
\]

By Lemma 3.1, as applied to the constant initial data \(\phi(0) = (S(0), 0, 0)\), \(\forall t \in [-\tau, 0]\), solutions of (3.1) are ultimately bounded. It then follows from [15, Corollary 3.2] that (3.1) admits a unique positive equilibrium \(S^* = (S_1^*, S_2^*)\) and that \(S^*\) is globally asymptotically stable for \(S \in \mathbb{R}^2 \setminus \{0\}\). Thus, \(E_0 = (S_1^*, S_2^*, 0, 0, 0)\) is a disease-free equilibrium of (2.3).

As in [14], we first determine the basic reproduction number, which is the average number of secondary cases an infected individual will cause in a population. Assume that the population is near the disease-free equilibrium \(E_0\). Then it follows from (2.4) that
\[
\begin{aligned}
P_1(t) &= k_1S_1 \int_0^t b_1(a)P_1(t-a)da + k_2S_2 \int_0^t b_2(a)P_2(t-a)da, \\
P_2(t) &= k_1S_1 \int_0^t b_1(a)P_1(t-a)da + k_2S_2 \int_0^t b_2(a)P_2(t-a)da.
\end{aligned}
\]
Set
\[
\begin{bmatrix}
P_1(t) \\
P_2(t)
\end{bmatrix} = \begin{bmatrix}
k_1S_1 \int_0^t b_1(a)da \\
k_2S_2 \int_0^t b_2(a)da
\end{bmatrix} \begin{bmatrix}
k_1S_1 \int_0^t b_1(a)da \\
k_2S_2 \int_0^t b_2(a)da
\end{bmatrix}.
\]

Since \(U\) is a positive matrix, its spectral radius \(\rho(U)\) is a simple eigenvalue with a positive eigenvector (see, e.g., [9]). Let \(\Psi = (\psi_1, \psi_2)\) be an initial distribution of infected members in the patches during the infection period, where \(\psi_1, \psi_2\) are constants. Set
\[
F = \begin{bmatrix}
k_1S_1 & 0 \\
0 & k_2S_2
\end{bmatrix}.
\]
Thus, \(F\) is the rate of infective individuals in the two patches. In [14], it was concluded that \(\rho(U)\) is the probability that an infective person initially in patch \(j\) at infection age zero is in patch \(i\) at infection age \(a\). Then \(U^{\Psi} = \int_0^t \exp(B)F\Psi da\) gives the number of infective individuals in the patches at the end of an infection period. As in [12,14], \(U\) is called the next infection matrix and \(\rho(U)\) is defined as the basic reproduction number \(R_0\) of (3.1). Clearly, \(R_0\) depends on the infection period \(\tau\).

Our first result shows that the disease is uniformly persistent in the case where \(R_0 > 1\).

Theorem 3.1. Let (H) hold. If \(R_0 > 1\), then the disease is uniformly persistent in the sense that there is a positive number \(c\) such that for any \(\phi \in X \times \phi(0) > 0\) and \(\phi_2(0) > 0\), the solution \((S(t, \phi), P(t, \phi), R(t, \phi))\) of (2.3) satisfies \(\inf_{t \rightarrow \infty} P_1(t, \phi) = c\), \(i = 1, 2\).

The subsequent result indicates that the disease dies out if \(R_0 < 1\), provided that the initial size of the infected population is relatively small.

Theorem 3.2. Let (H) hold. If \(R_0 < 1\), then for every \(L \gg L\), there exists a \(\varepsilon = (\varepsilon > 0\) such that for any \(\phi \in X\), with \(\phi_1(0), \phi_2(0) \in (0, \varepsilon)\), the solution \((S(t, \phi), P(t, \phi), R(t, \phi))\) of (2.3) converges to \(E_0\) as \(t \rightarrow \infty\).

The proofs of Theorems 3.1 and 3.2 are given in the Appendix.

4. Examples

In this section, we analyze the effect of population dispersal on the spread of the disease. In doing this we must consider the behavior of the disease when the patches are isolated and compare this to how they are connected. In epidemiology the basic reproduction number \(R_0\) characterizes this disease spread; if \(R_0 > 1\) then the disease will persist and if \(R_0 < 1\) the infection will die out in the long term. Therefore, for a given model, we can calculate a basic reproduction number as if the patches were disconnected and we can calculate the actual reproduction number when the dispersal parameters \((b_i, c_i, d_i)\) are non-zero.

First we consider the disconnected system 0:}
and
\[ \frac{dS_i}{dt} = B_i(N_i)N_2 - \mu S_i(t) - Q_i(t), \]
\[ \frac{dP_i}{dt} = Q_i(t) - e^{-(\mu_1 + r_1)t}Q_i(t - \tau) - (\mu_2 + r_2)P_i(t), \]
\[ \frac{dR_i}{dt} = r_2P_i(t) + e^{-(\mu_1 + r_1)t}Q_i(t - \tau) - \mu R_i(t), \]
\[ N_2(t) = S_2(t) + R_2(t) + P_2(t), \quad t \geq 0. \]

(4.2)

As in the proof of Lemma 3.1, by the properties of \( B_i(N_i) \), there exists a unique \( L_i > 0 \) such that \( B_i(L_i) = \mu_i \). Therefore, \( E_{0i} = (L_i, 0, 0) \), \( i = 1, 2 \), is the disease-free equilibrium for patch \( i \). Let \( R_{0i} \) be the basic reproduction number for patch \( i \). By similar arguments as those for model (2.3), it then follows that
\[ R_{0i} = k_iS_i \int_0^\infty e^{-(\mu_1 + r_1)s}Q_i(s)ds, \]
and that \( R_{0i} > 1 \) implies that the disease is uniformly persistent in the isolated patch \( i \). The next result shows that, for an isolated patch, the disease dies out if \( R_{0i} < 1 \).

**Theorem 4.1.** Let the two patches be isolated. If \( R_{0i} < 1 \), then every solution \((S_i(t), P_i(t), R_i(t))\) with \( P_i(0) > 0 \) converges to \( E_{0i} \).

**Proof.** We consider patch 1 since the proof for patch 2 is similar. It follows from (4.1) that
\[ \frac{dN_1}{dt} = (B_1(N_1) - \mu_1)N_1(t), \]
for an isolated patch. Therefore, as in the proof of Lemma 3.1 and as noted earlier,
\[ N_1(t) \rightarrow L_1 \quad \text{as} \quad t \rightarrow \infty. \]

Since \( R_{01} < 1 \), we can choose \( \epsilon > 0 \) small enough such that
\[ R_{01}^\epsilon := k_1(L_1 + \epsilon)\frac{1 - \exp(-1) - (\mu_1 + r_1)}{\mu_1 + r_1} < 1. \]

We can choose \( t > 0 \) large enough such that
\[ S_1(t) < L_1 + \epsilon \quad \text{for} \quad t \geq \tilde{t}. \]

Since
\[ P_1(t) = \int_0^\infty e^{-(\mu_1 + r_1)s}Q_1(s)ds = \int_0^\infty e^{-(\mu_1 + r_1)s}Q_1(t + s)ds, \quad \forall t \geq 0, \]
it follows that
\[ P_1(t) < k_1(S_0 + \epsilon) \int_0^\infty e^{-(\mu_1 + r_1)t}P_1(t - \delta)dt, \quad \forall t \geq \tilde{t} + \tau. \]

Fix a \( \delta > 0 \) such that \( P_1(t) < \tilde{\delta} \) for \( \tilde{t} + \tau < t \leq \tilde{t} + 2\tau \). By an induction argument similar to that in the proof of Theorem 3.2, it follows that
\[ P_1(t) < (R_{01}^\epsilon)^\delta \tilde{\delta}, \quad \forall t \geq \tilde{t} + (n + 1)\tau, \quad n \geq 0. \]

Since \( R_{01} < 1 \), we have \( P_1(t) \rightarrow 0 \) as \( t \rightarrow \infty \). By using the theory of chain transitive sets, we further obtain that \((S_1(t), R_1(t)) \rightarrow (L_1, 0) \) as \( t \rightarrow \infty \). □

In order to perform numerical simulations, we must choose a specific birth function. As in [4], we consider the following examples of birth rate functions which are found in biological literature:

**C1** \( B_1(N_1) = H_1e^{-\lambda N_1} \) with \( A_1 > 0, H_1 > 0 \).

**C2** \( B_1(N_1) = \frac{P_1}{N_1^m} \) with \( p_1 > 0, q_1 > 0, m_1 > 0 \).

**C3** \( B_1(N_1) = \frac{A_1}{N_1} + H_1 \) with \( A_1 > 0, H_1 > 0 \).

In [14] the birth rate function (C3) is used both in the proofs of the theorems in the previous section and in the numerical examples. Those simulations suggest that dispersal is often very important. There are cases where different levels of dispersal cause ‘switches’ in \( R_0 \) being less than or larger than one. There are even cases where low and high dispersal have \( R_0 > 1 \) while a moderate dispersal has \( R_0 < 1 \). This may be due to the birth rate function; since \( B_i(N_i)N_i = A_i + H_iN_i \) is a linear function, the number of births is proportional to the number of individuals with no saturation.

The function \( G_i(N_i) = B_i(N_i)N_i \) behaves differently for large \( N_i \) in cases (C1), (C2) and (C3). For (C3), \( G_i(N_i) \) is unbounded. For (C1), \( G_i(N_i) \) tends to zero as \( N_i \rightarrow \infty \). And for (C2), \( G_i(N_i) \) tends to the constant \( p_1 \) when we take \( m_1 = 1 \). Depending on the type of function used, it can lead to significant changes in the numerical modeling of a population.

In this project, we use the birth rate functions (C1) and (C2) for simulations. The objective is to find some interesting and representative dynamical behavior over several examples. It is also important to pay careful attention to the dispersal parameters since they characterize the patch environment. We first consider systems (4.1) and (4.2) with birth rate function (C1).

Systems (4.1) and (4.2) are isolated patches; that is, there is no dispersal between the patches. With the birth function (C1), the disease-free equilibrium for each is given by \( E_{01} = (S_{01}, 0, 0) \) and \( E_{02} = (S_{02}, 0, 0) \), where \( S_{0i} = \frac{1}{\lambda_i} \ln(H_1/\mu_i) \), i.e., \( S_{02} = \frac{1}{\lambda_2} \ln(H_2/\mu_2) \). Thus, the basic reproduction number is given by
\[ R_{0i} = \ln \left( \frac{H_1}{\mu_i} \right) k_i(1 - \exp(-1) - (\mu_1 + r_1)) \frac{1}{A_1(\mu_1 + r_1)}. \]

In the following examples, comparisons are made between the disease behavior in the isolated patches and in the connected system:

\[ \frac{dS_i}{dt} = H_iN_i(t)e^{-\lambda_iN_i} - (\mu_i + d_i)S_i(t) - Q_i(t) + d_iS_i(t), \]
\[ \frac{dQ_i}{dt} = H_iN_i(t)e^{-\lambda_iN_i} - (\mu_i + d_i)Q_i(t) - Q_i(t), \]
\[ \frac{dP_i}{dt} = Q(t) - \exp(Bt)Q(t - \tau) + B(t), \]
\[ \frac{dR_i}{dt} = \gamma_i(t) - (\mu_i + c_i)R_i(t) + c_iR_i(t), \]
\[ N_i(t) = S_i(t) + R_i(t) + P_i(t), \quad i = 1, 2. \]

In these examples, we fix \( A_1 = 0.2, A_2 = 0.3, H_1 = 2.6, H_2 = 2.0 \). As in [14], we take the delay \( \tau = 1 \), the constant death rate to be \( \mu_i = \mu_2 = 0.2 \) and the treatment rates to be \( r_1 = r_2 = 0 \). We set \( c_1 = c_2 = 0 \) for computational simplicity. This means that recovered individuals do not travel after their recovery. However, for the susceptible and infective patches, set \( d_1 = d_2 = d \) and \( b_1 = b_2 = 0.01d \). This means that individuals travel between the patches but that 99% of infected individuals cannot travel to screening and regulations while the other 1% represents the failure of control regulations. The parameter \( k_i \) is the transmission coefficient in patch \( i \) and we adjust both \( k_i \) and \( d \) in these simulations. The initial data used here are: \( S_i(0) = 1.5, S_{0i}(0) = 1.2, R_i(0) = 0.5, R_{0i}(0) = 0.3, P_i(0) = 0.8, P_{0i}(0) = 0.6 \) for \( \theta \in [-\tau, 0] \). We note that the long-term behavior of these solutions does not change when many other (positive) initial data are used.

**Example 1.** \( k_1 = 0.05, k_2 = 0.05 \).

The reproduction numbers for the isolated patches can be calculated by formula (4.5). We have that \( R_{01} = 0.581 \) and \( R_{02} = 0.348 \). Each is below 1 so the disease will die out over time and the disease-free equilibria \( E_{01} \) and \( E_{02} \) are globally asymptotically sta-
ble. From an epidemiological standpoint, $1 > R_{01} > R_{02}$ means that the disease will last longer in patch 1 than in patch 2. This is explained by the parameters of the birth rate functions; in patch 1 the per capita birth rate is higher than in patch 2. When these patches are connected, the disease-free equilibrium $(S_1', S_2')$ and $R_0$ can be calculated numerically. For $d = 0.5$, we find that $(S_1', S_2') = (11.25, 9.58)$ and that $R_0 = 0.509$. This means that the disease will also die out for a low transmission coefficient when the patches are connected.

For $d = 5$, a much higher dispersion, $R_0 = 0.478$ which is a little lower but not much different. There is a change in value of the disease-free equilibrium; now, $(S_1', S_2') = (10.64, 10.41)$ and this is reasonable due to the large increase in dispersal between the patches. This change, however, is not very significant since we are much more concerned with the basic reproduction number. In this case, the disease does not persist in isolated patches and does not persist when the patches are connected for both low and high dispersal. This is a typical result, observed here for both low and high levels of dispersal.

**Example 2.** $k_1 = 0.05, k_2 = 0.13$.

Here the disease transmission coefficient $k_2$ is larger than in our first example. This means that the disease spreads more easily in patch 2 than in patch 1. This is reflected by the reproduction numbers; $R_{01} = 0.581$ and $R_{02} = 0.904$. Thus, the disease will not persist in either patch. For the connected system, however, $R_0 = 1.13$ when $d = 0.5$. Here, dispersal facilitates persistence and the relative levels of infected individuals is quite small. Note that the size of the infected population converges to a constant fairly quickly.

For $d = 5$, $R_0 = 1.20$ which is not much of a change. But the size of the infected populations in each patch has grown considerably. This result, illustrated in Fig. 1, shows that dispersal can allow a disease to persist when it would not in each isolated patch. However, it appears that, for this choice of birth rate function, the value of $d$ is not very important.

**Example 3.** $k_1 = 0.13, k_2 = 0.05$.

In this example, $R_{01} = 1.51$ and $R_{02} = 0.348$. The introduction of low dispersal, $d = 0.5$, yields $R_0 = 1.32$. In this case, dispersal promotes persistence of the disease. For $d = 5$, the reproduction number $R_0 = 1.22$ and although it has decreased, it is still larger than one. As in the previous example the size of the epidemic populations in each patch has grown significantly with the larger value of $d$ (see Fig. 2).

It appears that dispersal does not affect $R_0$ very much but does affect epidemic population sizes for the birth rate function (C1). We now consider the following epidemic model with birth rate function (C2):

$$\frac{dS_1}{dt} = \frac{p_1}{q_1 + N_1} - (\mu_1 + d_1)S_1(t) - Q_1(t) + d_2S_2(t),$$

$$\frac{dS_2}{dt} = \frac{p_1}{q_1 + N_1} - (\mu_2 + d_2)S_2(t) - Q_2(t) + d_1S_1(t),$$

$$\frac{dP}{dt} = Q(t) - \exp(Bl)Q(t - \tau) + BP(t),$$

$$\frac{dR_1}{dt} = \gamma_1(t) - (\mu_1 + c_1)R_1(t) + c_2R_2(t),$$

$$\frac{dR_2}{dt} = \gamma_2(t) - (\mu_2 + c_2)R_2(t) + c_1R_1(t),$$

(4.7)

$$N_i(t) = S_i(t) + R_i(t) + P_i(t), \quad i = 1, 2.$$  

It then follows that $S_{01} = \frac{p_1}{q_1} - q_1$, $S_{02} = \frac{p_2}{q_2} - q_2$, and the basic reproduction number is given by

$$R_0 = k_i(p_i - q_i\mu_i)\left(1 - \exp\left(-\left(\mu_i + r_i\right)\tau\right)\right) \frac{1}{\mu_i(\mu_i + r_i)}.$$  

(4.8)

We now look at two examples. Set $p_1 = 1.6, p_2 = q_1 = q_2 = 1.0$.

**Example 4.** $k_1 = 0.10, k_2 = 0.10$.

Here we have the same transmission coefficient in each patch. The reproduction numbers for the isolated patches are $R_{01} = 0.634$ and $R_{02} = 0.363$. Therefore, patch 1 is not as good as patch 2 from an epidemiological standpoint. The disease does not persist in either patch, though, since each reproduction number is less than one. When $d = 0.5$, the reproduction number for the connected system is $R_0 = 0.518$. If the dispersal is increased significantly, for example $d = 5$, then we have $R_0 = 0.499$. As in example 1, there is not much of a change. In fact, for $d = 0.5$, $(S_1, S_2) = (5.72, 5.29)$ and, for $d = 5$, $(S_1, S_2) = (5.53, 5.48)$. This is similar to the first example because a higher dispersion seems to lead to the equilibriums of each patch becoming closer to equal as dispersion increases.
Example 5. $k_1 = 0.20, k_2 = 0.10$.

Now the transmission coefficient in patch 1 is twice that of patch 2. Without dispersal, $R_{01} = 1.27$ and $R_{02} = 0.363$ so the disease is persistent in one patch and not in the other. Introducing a low level of dispersion, $d = 0.5$, the overall reproduction number is $R_0 = 1.04$. This means that the disease is persistent but the size of the endemic populations may be quite small. See, for example, the left plot in Fig. 3.

To contrast this, we find that a high dispersal, $d = 5$, causes a major change. Now $R_0 = 0.980$ and through numerical simulations, we confirm that the disease will die out over time. The convergence is slower since the value of $R_0$ is so close to one. The right plot of Fig. 3 illustrates this phenomenon.

5. Discussion

In this project, we analyzed an epidemic model proposed in [14] to simulate the dynamics of disease transmission when the population is dispersed among patches. This model, which incorporates a constant infection period, uses dispersal to represent the movements of hosts between areas. Using the assumptions that the death rates, disease transmission coefficients, the treatment rates and the migration rates are constant for infected individuals, this model becomes a time-delayed differential system. As in [14], we define the basic reproduction number $R_0$.

This model uses the standard nonlinear birth function $B(N)$ discussed in [4]. We have proven that for two patches the disease is uniformly persistent if $R_0 > 1$ and the disease cannot invade if $R_0 < 1$, provided that the initial size of the infected population is relatively small. The choice of the function $B(N)$ for numerical simulations is very important; here, we use two common nonlinear birth functions different from the simulations in [14] where $B(N) = A + HN$, a linear function. Examples 1 through 3 suggest that dispersal is not very significant when the birth function $B(N) = H \exp(-AN)$ is used since only small changes in the reproduction number is shown with low and high dispersal rates. Examples 4 and 5 suggest that dispersal is somewhat significant for models with $B(N) = \frac{\phi_N}{\phi_F}$. Indeed, the last example shows a case where larger levels of dispersal cause the disease to go extinct. In [14] examples are used to illustrate that dispersal can both help eliminate or promote disease transmission, so this agrees with those conclusions.

In [14], the linearity of $B(N)N$ allowed for an explicit calculation of the disease-free equilibrium. This simplified the numerical simulations and made it easier to plot $R_0$ versus $d$. For more complicated birth rate functions, these more illustrative techniques are more difficult (and sometimes impossible) to employ. In future work, it would be interesting to expand on the simulations here with the other birth functions or by further adjusting the relative values of death rates $\mu_i$ and infection period $\tau$. Since $R_0$ depends on $\tau$, we can also further study the effect of $\tau$ on the global dynamics of the model system. From a theoretical standpoint, future work could include an age-structure in this model through death rates, infection force or migration rates and a generalization to more than two patches.

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Appendix. Proofs of the main results

Proof of Theorem 3.1. As in [14], we use persistence theory. Note that a form for the function $B_i(N_i)$ is not assumed. Instead, the function $G_i(N_i) = B_i(N_i)N_i$ is used. We established earlier that the solution semiflow $\Phi(t)$ of (2.3) has a global attractor on $X$. Define

$$X_0 := \{\phi \in X : \phi_i(0) > 0, \phi_4(0) > 0\}, \quad dX_0 := X \setminus X_0.$$  

Let $(S(t, \phi), P(t, \phi), R(t, \phi))$ be a solution of (2.3) with $\phi \in X$. We claim that if $P_i(0, \phi) > 0$ for some $i$, then $S_i(t, \phi) > 0, \forall t > 0$. Indeed, we see from (2.3) that

$$\frac{dS_i(t)}{dt} \geq - (\mu_i + d_i + k_i P_i(t)) S_i(t), \quad \forall t \geq 0.$$
It then follows that if $S_t(t_0) > 0$ for some $t_0 > 0$, then $S_t(t) > 0$, $\forall t \geq t_0$. In the case where $S_0(0, \phi) > 0$, we have $S_t(\phi) > 0$, $\forall t \geq 0$. In the case where $S_0(0, \phi) = 0$, we see from (2.3) that $\delta(0, \phi) > 0$ since $N_0(0, \phi) \neq P_0(0, \phi) = 0$. Thus, $S_t(\phi) > 0$ for all sufficiently small $t_0 > 0$, which implies that $S_t(\phi) > 0$, $\forall t > 0$. In view of the above claim and (2.4), we see that $X_0$ is positively invariant for $\Phi(t)$. Note that

$$\partial X_0 = \{ \phi \in X : \phi_3(0) = 0 \text{ or } \phi_4(0) = 0 \},$$

which is relatively closed in $X$. Let $L \in (L^*, \infty)$ be fixed. Then Lemma 3.1 implies that every solution of (2.3) enters $[0, L]^6$ ultimately. Define

$$M_0 := \{ \phi \in X : \Phi(t)\phi \in \partial X_0, \forall t \geq 0 \}.$$

Since $b_1, b_2 > 0$ imply that $\exp(Ba) > 0$, assume that $(S_0(\phi), P_0(\phi), R_0(\phi)) = \phi$. Then

$$M_0 = \{ \phi \in X : P(t, \phi) = 0, \forall t \geq 0 \}.$$

Set

$$U_t = \left[ k_1(S_1 - \epsilon) \int_{0}^{t} b_1(a)da \right] k_2(S_2 - \epsilon) \int_{0}^{t} b_2(a)da.$$

Since $\rho(U_t)$ is continuous in $\epsilon$, we can restrict $\epsilon > 0$ small enough such that $U_t$ is positive and $\rho(U_t) > 1$. Now consider the following system:

$$\frac{du_1}{dt} = b_1(u_1 + \eta)u_1 - (\mu_1 + d_1 + k_1\lambda)u_1(t) + d_2u_2(t),$$

$$\frac{du_2}{dt} = b_2(u_2 + \eta)u_2 - (\mu_2 + d_2 + k_2\lambda)u_2(t) + d_1u_1(t),$$

where $\eta > 0$ is a small number. Arguing as before, (6.1) satisfies the conditions of [[15], Corollary 3.2] and, as such, it admits an equilibrium $(u'_1(\eta), u'_2(\eta))$ which is globally asymptotically stable. Moreover, since this system is a perturbation of (3.1), we have that $(u'_1(\eta), u'_2(\eta)) \rightarrow (S'_1, S'_2)$ as $\eta \rightarrow 0$. By the implicit function theorem, we choose $\eta = \eta(e)$ to be small enough so that $u'_1(\eta) > S'_1 - e$, $i = 1, 2$. It follows that every positive solution $(u_1(t), u_2(t))$ of (6.1) satisfies $u_1(t) > S'_1 - e$, $i = 1, 2$ for all large $t$. We define

$$M_i := r_i + L(b_1(\tau)k_1 + b_2(\tau)k_2),$$

and consider

$$\frac{dw_1(t)}{dt} = \delta M_1 - (\mu_1 + c_1)w_1 + c_2w_2,$$

$$\frac{dw_2(t)}{dt} = \delta M_2 - (\mu_2 + c_3)w_2 + c_1w_1.$$ 

This is a linear, non-homogeneous system. The origin is globally asymptotically stable for the corresponding homogeneous system and it is easy to show that the particular solution of (6.2) is a constant which tends to zero as $\delta \rightarrow 0$. Therefore, (6.2) has a globally asymptotically stable equilibrium $(w_1(\delta), w_2(\delta))$ which satisfies $(w_1(\delta), w_2(\delta)) \rightarrow (0, 0)$ as $\delta \rightarrow 0$. Thus, we can fix $\delta$ with $0 < \delta < \frac{\epsilon}{2}$ such that $w_1(\delta), w_2(\delta) < \frac{\epsilon}{2}, i = 1, 2$. It then follows that every positive solution of (6.2) satisfies $w_1(t) < \frac{\epsilon}{2}, i = 1, 2$ for large $t$. We now have the following claim.

**Claim.** $\limsup_{t \rightarrow \infty} \max\{P_1(t, \phi), P_2(t, \phi)\} \geq 0$ for any $\phi \in X_0$.

Assume, by way of contradiction, that the claim does not hold for some $\phi \in X_0$. Then $P_1(t) = P_2(t) < \frac{\epsilon}{2}, i = 1, 2$ for all large $t$. Since solutions of (2.3) are ultimately bounded, we have that $Q_i(t) \leq k_iS_0(\phi) < k_i\lambda < k_i\lambda 0\eta, i = 1, 2$ for large $t$. It then follows that $\gamma_i(t) \leq \delta M_1, i = 1, 2$, for large $t$, and hence

$$\frac{dR_1(t)}{dt} \leq \delta M_1 - (\mu_1 + c_1)R_1 + c_2R_2,$$

$$\frac{dR_2(t)}{dt} \leq \delta M_2 - (\mu_2 + c_3)R_2 + c_1R_1.$$ 

By the comparison theorem for cooperative systems (see, e.g., [9]), we have $R_1(t) \leq W(t) < \frac{\epsilon}{2}, i = 1, 2$ for large $t$. It follows that for all large $t$,

$$N_i(t) \leq S_1(t) + \eta, \quad i = 1, 2,$$

and

$$B_i(N_i(t)) \leq S_1(t) + \eta, \quad i = 1, 2.$$

Therefore, we see that for large $t$,

$$\frac{dS_1(t)}{dt} > B_i(S_1(t) + \eta)S_1(t) - (\mu_1 + d_1 + k_1\lambda)S_1(t) + d_2S_2(t),$$

$$\frac{dS_2(t)}{dt} > B_i(S_2(t) + \eta)S_2(t) - (\mu_2 + d_2 + k_2\lambda)S_2(t) + d_1S_1(t).$$

By the comparison theorem, it follows that $S_i(t) > u_i(t) > S'_1 - e$, $i = 1, 2$, for all large $t$. Thus, (2.4) implies that there is a $t_0 > 0$ such that for all $t \geq t_0$,

$$P_i(t) < k_i(S'_1 - e) \int_{0}^{t} b_1(a)P_i(t - a)da + k_2(S'_2 - e) \int_{0}^{t} b_2(a)P_2(t - a)da,$$

$$P_2(t) > k_i(S'_1 - e) \int_{0}^{t} b_2(a)P_1(t - a)da + k_2(S'_2 - e) \int_{0}^{t} b_2(a)P_2(t - a)da.$$ 

Let $\nu = (v_1, v_2)^T$ be a positive right eigenvector of $U_t$ with respect to $\rho(U_t)$. Choose $l > 0$ small enough such that $lV_l < \min(P_l(t) : t \leq t_0 + t) \lt t < t_0 + t$ for $i = 1, 2$. Then the following inequality is true:

$$IV_l < P_i(t), \quad i = 1, 2, \quad \forall t \geq t_0.\tag{6.5}$$

To see this, we set

$$t_1 = \inf\{t \in [t_0, \infty) : lV_l = P_i(t) \text{ or } lV_2 = P_2(t)\}.$$ 

Clearly, $t_1 > t_0 + t$. Then $lV_l < P_i(t), i = 1, 2, \quad \forall t < t_0 + t 1$ and $lV_l = P_i(t) \text{ or } lV_2 = P_2(t)$. But, we see from (6.4) that

$$P_1(t) > k_i(S'_1 - e)lV_l \int_{0}^{t} b_1(a)da + k_2(S'_2 - e)lV_2 \int_{0}^{t} b_2(a)da = \rho(U_t)lV_1,\tag{6.6}$$

$$P_2(t) > k_i(S'_1 - e)lV_l \int_{0}^{t} b_2(a)da + k_2(S'_2 - e)lV_2 \int_{0}^{t} b_2(a)da = \rho(U_t)lV_2,$$

which contradicts $lV_l = P_i(t) \text{ or } lV_2 = P_2(t)$. Thus, (6.5) holds.

Now suppose that for some $n \geq 1$,

$$\rho^n(U_t)lV_l < P_i(t), \quad i = 1, 2, \quad \forall t \geq t_0 + (n - 1)t.\tag{6.6}$$

We want to prove that

$$\rho^n(U_t)lV_l \leq P_i(t), \quad i = 1, 2, \quad \forall t \geq t_0 + nt.\tag{6.7}$$

By (6.4) and (6.6) we have that

$$\rho^n(U_t)lV_l < P_i(t_0 + nt), \quad i = 1, 2.$$
Let \( \nu = (v_1, v_2) \) be a positive right eigenvector of \( V_r \) associated with \( \rho(V_r) \). Choose \( \xi_3 > 0 \) small enough such that
\[
\xi_3(v_i t_i + b_1(\tau_1)k_1 t_i + b_2(\tau_2)k_2 t_i) < \xi_2, \quad \xi_3 v_i < \xi_1/2, \quad i = 1, 2. 
\]
(6.11)

Let \( T_3 = T_3(L) := \max\{T_1, T_2\} + \tau \) and \( W := \text{diag}(k_1, k_2, k_3) \). Then there exists \( \xi = \xi(L) > 0 \) such that for every solution \((P_1(t), P_2(t))\) of the linear system
\[
dP(t) = (W + B)P(t), \quad t \geq 0, \quad P(0) = P_0(0) \in [0, \xi]^2,
\]
with \( (P_0(t), P_1(t)) \in [0, \xi]^2 \), we have \( P_1(< \xi, 1) = 1, 2 \) for all \( t \in [0, 2T_3] \). For a given \( \phi \in X_2 \), with \( (\phi_0(0), \phi_1(0)) \in [0, \xi]^2 \), we let \((S(t), P(t), R(t)) = (S(t, \phi), P(t, \phi), R(t, \phi)) \) by (2.3) and (6.8), we then have
\[
dP(t) = d(S(t), P(t)) \leq (W + B)P(t), \quad \forall t \geq 0. 
\]

Since \( P(0) \in [0, \xi]^2 \), the comparison principle implies that
\[
P_i(t) < \xi, \quad \forall t \in [0, 2T_3], \quad i = 1, 2.
\]
(6.12)

We further claim that (6.12) holds for all \( t \geq 0 \). If the claim is not true, then there exists a \( T_3 = T_3(\phi) > 2T_3 \) such that \( P_i(t) < \xi, i = 1, 2 \), and \( P_i(T_3) = \xi, j = 1, 2 \). It follows from (2.3) and (6.11) that
\[
\frac{dR_i(t)}{dt} \leq \xi, \quad \frac{dR_j(t)}{dt} \leq \xi, \quad \forall t \in T_3.
\]
(6.13)

By the comparison principle and the properties of system (6.10), we have \( R_i(t) < \xi, i = 1, 2, \) for all \( t \in [T_3, T_4] \). It follows from (2.3) that
\[
\frac{dS(t)}{dt} \leq \xi, \quad \forall t \in [T_3, T_4]. 
\]
(6.14)

By the comparison principle and the properties of system (6.9), we obtain \( S_i(t) \leq \xi, i = 1, 2, \) for all \( t \in [T_1, T_2] \). Hence, (2.4) implies that for any \( t \in [T_2, T_4] \), there hold
\[
P_i(t) < k_3(S_1 + \epsilon)\int_0^t b_1(\tau_1)P_i(t - \tau_1)da + k_2(S_2 + \epsilon)\int_0^t b_2(\tau_2)P_i(t - \tau_2)da,
\]
(6.15)

It then follows that
\[
P_i(t) < k_3(S_1 + \epsilon)\int_0^t b_1(\tau_1)P_i(t - \tau_1)da + k_2(S_2 + \epsilon)\int_0^t b_2(\tau_2)P_i(t - \tau_2)da,
\]
for all \( t \in [T_2, T_4] \). Since \( \rho(V_r) < 1 \), we obtain \( P_i(t) < \xi v_i \) for all \( i = 1, 2 \). Hence (6.15) holds for all \( t \geq 2T_3 \). By an induction argument similar to that in the proof of Theorem 3.1, it follows that \( P_i(t) < \rho^2(V_r)\xi v_i, \forall t \geq 2T_3 + \nu t, \) for all \( n \geq 0, 1, 2, \) which implies that \( \lim_{t \to \infty} P_i(t) = 0, \forall t = 1, 2 \). By the theory of chain transitive sets (see, e.g., [16, Theorem 1.2.1]), as argued in [13, Theorem 2.2], we further obtain that \( S_i(t), R_i(t) \to (S_1, S_1, 0) \) as \( t \to \infty \), in the case where \( \phi_0(0), \phi_1(0) \in [0, \xi]^2 \).
References