Fatal Disease and Demographic Allee Effect: Population Persistence and Extinction

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Disease Transmission

- Transmission of disease is influenced by aggregation patterns in the host population as well as its social organization and behavioral traits (Anderson and May 1979, Hilker 2009, etc).

- Disease incidence (new infection per unit time)
  - Density-dependent (mass action) transmission assumes that effective contact rate between susceptible and infective individuals increases linearly with population size.
  - Frequency-dependent (standard incidence or proportional mixing) assumes the number of contacts between susceptible and infective individuals is independent of population size.
Allee Effect (Critical Depensation)

- The phenomenon that populations benefit from large population sizes (due to high success rates in finding mating partners, predator dilution or reduction in inbreeding, etc).
- At low densities, populations experience positive density dependence as they have difficulties in maintaining social functioning, for example.
- If the Allee effect is strong (respectively, weak) the population growth rate is negative (reduced) at low densities.
Allee Effect In Real Populations

- **Saiga Antelopes** (*Saiga tatarica*): One of the world’s most rapidly declining species, their numbers falling by 95% in just 15 years.

- **Polar Bear** (*Ursus maritimus*): Polar bears were listed as threatened in 2008 by Dirk Kempthorne, an Interior Secretary under then-President George W. Bush, because of an alarming loss of summer sea ice in recent decades and climate models indicating the trend will continue.

- **African Wild dog** (*Lycaon pictus*)
- **Island Fox** (*Urocyon littoralis*)
- **Atlantic cod** (*Gadus morhua*)
Demographic Equation

\[
\frac{dp}{dt} = r(1 - p)(p - u)p
\]
Question

If a healthy host population at the disease-free equilibrium is subject to an Allee effect, can a small number of infected individuals with a fatal disease drive the total population to extinction?
SI Epidemic Model

(Hilker et al., Am. Nat. 2009)

\[
\begin{align*}
\frac{dp}{dt} &= r(1 - p)(p - u)p - \alpha i, \\
\frac{di}{dt} &= [ -A + (\sigma - 1)p - \sigma i ] i,
\end{align*}
\]

(2.4)

\[A = \alpha + d + ru.\]
In Model (2.4), we take initial conditions

\[ 0 < i(0) < p(0) < 1. \quad (3.1) \]

**Theorem 3.1.** The solution \((p(t), i(t))\) of (2.4) and (3.1) satisfies the inequalities

\[ 0 < i(t) < p(t) \text{ for all } t > 0. \]
As in [16], we introduce the critical host population density for disease establishment, the disease threshold,

\[ P_T = \frac{A}{\sigma - 1}, \quad (3.2) \]

and the basic reproductive ratio,

\[ R_0 = \frac{\sigma}{A + 1}. \]
Local Stability

**Theorem 3.2.** If \( P_T > 1 \), then \((1, 0)\) is locally asymptotically stable and the disease goes extinct.
Theorem 3.3. If

\[ 0 < u < P_T < 1 \]  \quad (3.3)

and

\[ \max_{u < u < P_T} \{ r(1 - y)(y - u)y \} > \frac{\alpha(\sigma - 1)}{\sigma} (1 - P_T), \]  \quad (3.4)

then for any solution of Model (2.4) with \( p(0) \geq u + \varepsilon_0 \) for some \( \varepsilon_0 > 0 \), there exists a \( \delta > 0 \) depending only on \( \varepsilon_0 \) and a time \( T = T(\varepsilon_0, i(0)) \) such that

\[ i(t) \geq \delta \text{ for all } t \geq T(\varepsilon_0, i(0)). \]  \quad (3.5)
Theorem 3.4. If $0 < P_T < \min\{1, u\}$ and

$$\max_{u \leq y \leq 1} \left\{ r(1 - y)(y - u)y - \frac{\alpha(\sigma - 1)}{\sigma}(y - P_T) \right\} \leq \varepsilon \quad (3.8)$$

for some sufficiently small $\varepsilon > 0$, then every solution of Model (2.4) with $1 - \delta < p(0) \leq 1$ for any $\delta > 0$ sufficiently small and $i(0) > 0$ satisfies:

$$p(t) \to 0 \text{ and } i(t) \to 0 \text{ as } t \to \infty.$$ 

Condition (3.8) holds whenever the $p$–nullcline, $\Gamma_p$, is below the $i$–nullcline, $\Gamma_i$, of Model (2.4) (see Figure 2).
Stability of Endemic Equilibrium

Let

\[ F(x) = \frac{d}{dx} \left[ r(1 - x)(x - u)x \right]. \]

**Theorem 7.1.** If \( 0 < u < P_T < 1 \), then Model (2.4) has a unique stationary point

\( (\bar{p}, \bar{i}) \) with \( P_T < \bar{p} < 1, \bar{i} > 0 \),

and \( (\bar{p}, \bar{i}) \) is locally asymptotically stable if

\[ F(\bar{p}) < (\sigma - 1)(\bar{p} - P_T). \] (7.1)
Conclusion (single patch)

- Studies of systems that exhibit the Allee mechanism seem to be focused on the role of the Allee effect at small population densities.
- In combination with a fatal infectious disease, we prove that a small perturbation to the disease-free equilibrium can lead to the catastrophic extinction of the host population.
- We prove that when there is an Allee effect in the host demographics and a fatal disease invades the host population, then the Allee threshold is effectively increased (Deredec and Couchamp, 2006).
\begin{align*}
\frac{dp_j}{dt} &= r_j (1 - p_j) (p_j - u_j) p_j - \alpha_j i_j + \delta \sum_{k \in \Omega} (L_{jk} p_k - L_{kj} p_j), \\
\frac{di_j}{dt} &= [-A_j + (\sigma_j - 1) p_j - \sigma_j i_j] i_j + \delta \sum_{k \in \Omega} (L_{jk} i_k - L_{kj} i_j), 
\end{align*}
\tag{2.1}

where on each patch $j \in \Omega$, $A_j = \alpha_j + d_j + r_j u_j$, $\delta$ is the non-negative diffusion coefficient for the total population, the Allee threshold $u_j \in (0, 1)$ and $L_{jk}$ is the degree of movement from patch $k$ to patch $j$. We make the following additional assumptions:

(A1) The matrix $L = (L_{jk})$ is nonnegative and irreducible.

This means that $L_{jk} \geq 0$ for all $j, k \in \Omega$, and that for any $j, k \in \Omega$ there exists a sequence $j_1, j_2, \ldots, j_t$ such that

$$L_{jj_1} > 0, L_{j_1j_2} > 0, \ldots, L_{j_{t-1}j_t} > 0, L_{j_tk} > 0.$$ 

We shall also impose throughout this paper the initial conditions:

(A2)

$$0 < i_j(0) < p_j(0) < 1 \quad \text{for all} \quad j \in \Omega. \quad (2.2)$$
Initial Conditions

Theorem 3.1. The solution \( \left( \vec{p}(t), \vec{i}(t) \right) \) of (2.1) satisfies the inequalities

\[
0 < i_j(t) < p_j(t) < 1 \text{ for all } t > 0 \text{ and } j \in \Omega.
\]  

(3.1)
Disease-Free Equilibrium Points

The set of disease-free equilibrium points of the single patch model without diffusion, Model (2.3), are

\[(p_{0j}, i_{0j}) = (0, 0), (p_{1j}, i_{1j}) = (u_j, 0) \text{ and } (p_{2j}, i_{2j}) = (1, 0).\]

The corresponding disease-free equilibrium (DFE) points of the diffusion-linked \(n\)-patch model, Model (2.1), are

\[\overline{\mathbf{o}} = (0, 0, 0, ..., 0, 0),\]

\[\left(\overline{\mathbf{u}}, \overline{\mathbf{0}}\right) = (u_1, u_2, ..., u_n, 0, 0, ..., 0)\]

and

\[\left(\overline{\mathbf{1}}, \overline{\mathbf{0}}\right) = (1, 1, ..., 1, 0, 0, ..., 0).\]

In Model (2.3), \((p_{0j}, i_{0j})\) is locally asymptotically stable. Furthermore, any solution of Model (2.3) with \(p_j(0) < u_j\) satisfies:

\[p_j(t) \downarrow 0 \text{ as } t \to \infty.\]

Consequently, under weak diffusion in Model (2.1), \(\overline{\mathbf{0}}\) is locally asymptotically stable and any solution with \(p_j(0) < u_j\) for each patch \(j \in \Omega\) satisfies:

\[\left(p_1(t), p_2(t), ..., p_n(t), i_1(t), i_2(t), ..., i_n(t)\right) \to \overline{\mathbf{0}} \text{ as } t \to \infty.\]
Theorem 4.1 (Population Extinction). In Model (2.1), assume that

\[ 0 < p_j(0) < u = \min_{1 \leq i \leq n} \{u_i\} \text{ for all } j \in \Omega. \]

Then the solution

\[ \left( \overrightarrow{p}(t), \overrightarrow{i}(t) \right) \]

satisfies

\[ p_j(t) < u - \varepsilon \text{ for all } t > 0 \text{ and } j \in \Omega, \]

where \( \varepsilon > 0 \) is sufficiently small. Moreover,

\[ \sum_{j \in \Omega} p_j(t) \leq Ce^{-\gamma t} \]

where \( C \) and \( \gamma \) are positive constants. Hence,

\[ \left( \overrightarrow{p}(t), \overrightarrow{i}(t) \right) \to \overrightarrow{0} \text{ as } t \to \infty. \]
Population Extinction: Single Patch

Using the single patch model with no diffusion, Model (2.3), Friedman and Yakubu showed that population extinction is possible on each local patch \( j \in \Omega \) whenever \( p_j(0) > u_j \). In particular, Friedman and Yakubu proved that in Model (2.3), if

\[
R_{0j} = \frac{\sigma_j - 1}{A_j} > 1, \quad \frac{1}{R_{0j}} < u_j
\]

and

\[
\max_{y_j \leq y \leq 1} \left\{ r_j(1 - y_j)(y_j - u_j)y_j - \frac{\alpha_j(\sigma_j - 1)}{\sigma_j} (y_j - \frac{1}{R_{0j}}) \right\} \leq \varepsilon_j
\]

for some sufficiently small \( \varepsilon_j > 0 \), then every solution of Model (2.3) with \( p_j(0) = 1 \) and \( i_j(0) > 0 \) satisfies:

\[
p_j(t) \to 0 \text{ and } i_j(t) \to 0 \text{ as } t \to \infty.
\]
To obtain a similar population extinction result for the diffusion-linked $n$-patch model, we let

$$R_0^j = \frac{\sigma_j - 1}{A_j + \delta \sum_{k \in \Omega} L_{kj}}$$

for each $j, k \in \Omega$.

Hence, $R_0^j < R_0$ (that is, $R_0^j > 1$ implies $R_0 > 1$ and $R_0 < 1$ implies $R_0^j < 1$) and $\lim_{\delta \to 0} R_0^j = R_0$. First, we obtain a local stability result.

**Theorem 4.2.** If

$$R_0^j > 1 \text{ for all } j \in \Omega,$$

then the DFE, $\left( \overrightarrow{1}, \overrightarrow{0} \right)$, is unstable.
The Jacobian matrix evaluated at \((\bar{T}, \bar{\sigma})\) is

\[
J(\bar{T}, \bar{\sigma}) = \begin{pmatrix}
\delta L_{21} & \delta L_{12} & -\alpha_1 & 0 \\
\delta L_{11} & \delta L_{12} & -\alpha_2 & 0 \\
0 & -\alpha_1 & 0 & \delta L_{12} \\
0 & -\alpha_2 & 0 & \delta L_{21}
\end{pmatrix}
\]

For \(j \in \{1, 2\}\), let \(m_j = -n_j(1 - u_j) - \delta L\) and \(n_j = -A_j + \sigma_j - 1 - \delta L\), where \(L_{21} = L_{12} = L\). Then the eigenvalues of \(J(\bar{T}, \bar{\sigma})\) are the roots of the characteristic equations

\[
\lambda^2 - \lambda(n_1 + n_2) + n_1n_2 - (\delta L)^2 = 0
\]

and

\[
\lambda^2 - \lambda(n_1 + n_2) + n_1n_2 - (\delta L)^2 = 0.
\]

The largest eigenvalue is

\[
\frac{(n_1 + n_2) + \sqrt{(n_1 - n_2)^2 + 4(\delta L)^2}}{2}
\]

which is easily seen to be larger than

\[
\max_{j=1,2}(-A_j + \sigma_j - 1).
\]

Hence, if we denote by \(R_0\) the basic reproduction number for the migration-linked Model (2.1), then

\[
R_0 > 1 \text{ if } \max_{j=1,2} R_{0j} > 1. \quad (4.5)
\]
When the number of patches is \( n \), then the eigenvalues of \( J(T, T) \) are the roots of the characteristic equations,

\[
M = \begin{vmatrix}
    m_1 - \lambda & \delta L_{12} & \delta L_{13} & \cdots & \delta L_{1n} \\
    \delta L_{12} & m_2 - \lambda & \delta L_{23} & \cdots & \delta L_{2n} \\
    \cdots & \cdots & \cdots & \cdots & \cdots \\
    \delta L_{1n} & \delta L_{2n} & \cdots & m_n - \lambda \\
\end{vmatrix} = 0
\]

and

\[
N = \begin{vmatrix}
    n_1 - \lambda & \delta L_{12} & \delta L_{13} & \cdots & \delta L_{1n} \\
    \delta L_{12} & n_2 - \lambda & \delta L_{23} & \cdots & \delta L_{2n} \\
    \cdots & \cdots & \cdots & \cdots & \cdots \\
    \delta L_{1n} & \delta L_{2n} & \cdots & n_n - \lambda \\
\end{vmatrix} = 0
\]

where for each \( j \in \Omega \), \( m_j = -r_j(1 - u_j) - \delta \sum_{k \in \Omega} L_{kj} \) and \( n_j = -A_j + \sigma_j - 1 - \delta \sum_{k \in \Omega} L_{kj} \). The zeros of \( M \) are all negative, but the zeros of \( N \),

\[ \lambda_1, \lambda_2, \ldots, \lambda_n, \delta, \]

may be positive or negative or zero. If

\[
\max_{j \in \Omega} \lambda_{j, \delta} < 0 \quad \text{then} \quad R_\delta < 1,
\]

and if

\[
\max_{j \in \Omega} \lambda_{j, \delta} > 0 \quad \text{then} \quad R_\delta > 1.
\]

When \( \delta \) is small, one can easily compute that

\[
\max_{j \in \Omega} \lambda_{j, \delta} = \max_{j \in \Omega} \{ \lambda_{j, 0} + \delta L_j \} + O(\delta^2),
\]

where \( \lambda_{j, \delta} = -A_j + \sigma_j - 1 \) and \( \delta = \sum_{k \in \Omega} L_{kj} \). Hence,

\[
R_\delta > 1 \quad \text{if} \quad \max_{j \in \Omega} R_{kj} \geq 1. \quad (4.6)
\]

This means that \( \delta \) - migration increases the chance of "instability". For \( n = 2 \), (4.6) holds for all \( \delta > 0 \) (see (4.5)), and we conjecture that (4.6) holds for all \( \delta > 0 \) and arbitrary \( \Omega \in \{ 1, 2, 3, \ldots \} \).
Theorem 4.3 (Host Population Extinction). In Model (2.1), assume that
\[ R_\delta > 1, \]
and, for any \( l \in \Omega, \) if \( u < y_l < 1 \) and \( 0 < y_j < 1 \) for all \( j \in \Omega, \ j \neq l, \) then
\[ \sum_{j \in \Omega} \left\{ r_j (1 - y_j) (y_j - u_j) y_j - \frac{\alpha_j (\sigma_j - 1)}{\sigma_j} (y_j - P_{T_j}) \right\} < 0. \tag{4.7} \]

Then every solution of Model (2.1),
\[ \left( \hat{p}(t), \hat{i}(t) \right) \to \bar{0} \text{ as } t \to \infty, \]
provided \( \left( \hat{p}(0), \hat{i}(0) \right) \) does not lie on either the (local) stable or center mani-
folds of \( \left( \hat{1}, \bar{0} \right). \)
We first consider the disease-free model (2.3). That is,

\[ \frac{dp_j}{dt} = r_j(1 - p_j)(p_j - u_j)p_j + \delta \sum_{k \in \Omega} (L_{jk}p_k - L_{kj}p_j). \quad j \in \Omega. \] (5.1)
Host Population Persistence (No Infected)

Theorem 5.1 (Population Persistence). In Model (5.1), assume
\[ \bar{u} < p_j(0) < 1 \text{ for all } j \in \Omega. \]

Then the model solution
\[ (p_1(t), p_2(t), \ldots, p_n(t)) \]
satisfies
\[ \bar{u} + \varepsilon < p_j(t) \text{ for all } t > 0 \text{ and } j \in \Omega, \]
where \( \varepsilon > 0 \) is sufficiently small and \( \bar{u} = \max_{1 \leq i \leq n} \{ u_i \} \).

Hence, in the absence of the disease, the diffusion-linked population persists uniformly whenever each initial local patch population exceeds the biggest Allee threshold.
Disease Persistence

By Theorem 5.2, each Patch \( j \in \Omega \) is either low-risk or high-risk at high densities whenever \( R_\delta > 1 \) and condition (5.3) holds. In the next theorem, to prove persistence of the infected individuals, we assume in addition to (5.3) that

\[
(\sigma_j - 1)u > A_j \text{ for all } j \in \Omega. \tag{5.4}
\]

**Theorem 5.3 (Disease Persistence).** In Model (2.1), if

\[ R_\delta > 1. \]

\[ \bar{u} + \varepsilon < r_j(0) \leq 1 \text{ for all } j \in \Omega, \]

\[ \sum_{i \in \Omega} i_i(0) > 0, \]

and conditions (5.3), (5.4) are satisfied, then the solution

\[ \left( \overrightarrow{p}(t), \overrightarrow{i}(t) \right) \]

satisfies

\[ \sum_{i \in \Omega} i_i(t) \leq \text{(constant)} > 0 \text{ for all } t \geq 0. \]
SI Epidemic PDE Model

Instead of the discrete set of compartments,
\[ \left( \overline{p}(t), \overline{i}(t) \right) , \]
we now consider a continuum
\[ (p(x, t), i(x, t)) \]
where \( x \) varies in a bounded domain \( G \) in \( \mathbb{R}^n \) with boundary \( \partial G \). In this case, the movement among compartments is replaced by the dispersion operator
\[ \Delta = \sum_{j=1}^{n} \frac{\partial^2}{\partial x_j^2}, \]
where \( x = (x_1, x_2, ..., x_n) \). Thus, we have
\[
\begin{cases}
\frac{\partial p}{\partial t} - \Delta p &= r(x)(1 - p)(p - u(x))p - \alpha(x)i \\
\frac{\partial i}{\partial t} - \Delta i &= -A(x) + (\sigma(x) - 1)p - \sigma(x)i 
\end{cases} \tag{6.1}
\]
where \( p = p(x, t) \), \( i = i(x, t) \), \( A(x) = \alpha(x) + d(x) + r(x)u(x) \) and \( 0 < u(x) < 1 \). We assume no-flux boundary conditions. That is,
\[
\frac{\partial p}{\partial \nu} = \frac{\partial i}{\partial \nu} = 0 \text{ on } \partial G, \ t > 0, \tag{6.2}
\]
where \( \nu \) is the outward normal, and prescribes the initial conditions
\[
p(x, 0) = p_0(x), \ i(x, 0) = i_0(x) \text{ for } x \in \overline{G}. \tag{6.3}
\]
SI PDE Model Assumptions

- We assume no-flux boundary conditions. That is,

$$\frac{\partial p}{\partial \nu} = \frac{\partial i}{\partial \nu} = 0 \text{ on } \partial G, \ t > 0,$$  \hspace{1cm} (6.2)

where $\nu$ is the outward normal, and prescribes the initial conditions

$$p(x, 0) = p_0(x), \ i(x, 0) = i_0(x) \text{ for } x \in \overline{G}. \hspace{1cm} (6.3)$$

- We assume that

$$0 \leq i_0(x) \leq p_0(x) \leq 1 \text{ for } x \in \overline{G}, \hspace{1cm} (6.4)$$

that the functions

$r, u, \alpha, d, \sigma, i_0$ and $p_0$

are in a Hölder class $C^\alpha(G)$, that $\partial G$ is in $C^{2+\alpha}$, and that

$$\frac{\partial p_0}{\partial \nu} = \frac{\partial i_0}{\partial \nu} = 0 \text{ on } \partial G.$$

- Then by standard theory of parabolic PDEs, there exists a unique solution of (6.1)-(6.3) for all $t > 0$ with

$$D_t p, \ D^2_i p, \ D_t i \text{ and } D^2_i i$$

$\alpha-$Hölder continuous in $x$ and $(\alpha/2)-$Hölder continuous in $t$, uniformly in $G \times [t_0, T]$ for any $0 < t_0 < T < \infty$, and $p, i$ are continuous for $x \in \overline{G}$ and $t \geq 0$. 


Theorem 6.1. If

\[ 0 < i_0(x) < p_0(x) < 1 \quad \text{for } x \in \overline{G} \]

then the solution \((p(x,t), i(x,t))\) of (6.1) satisfies the inequalities

\[ 0 < i(x,t) < p(x,t) < 1 \quad \text{for } x \in \overline{G}, \ t > 0. \]
Theorem 6.2 (Host Population Extinction). In Model (6.1), assume that
\[ 0 < p_0(x) < \underline{u} \text{ for all } x \in \overline{G}. \]
Then the solution
\[ (p(x, t), i(x, t)) \]
satisfies
\[ p(x, t) < \underline{u} - \varepsilon \text{ for all } t > 0 \text{ and some } \varepsilon > 0, \]
and
\[ p(x, t) \leq Ce^{-\gamma t} \text{ for all } x \in \overline{G} \text{ and } t > 0, \]  \hspace{1cm} (6.6)
where \( C \) and \( \gamma \) are positive constants. Hence,
\[ (p(x, t), i(x, t)) \to \underline{0} \text{ as } t \to \infty. \]
We denote the DFE of (6.1), the solution of

\[ p(x, t) = 1 \text{ and } i(x, t) = 0 \]

by (1, 0). We consider the case when (1, 0) is not stable in the following sense. There exists a neighborhood \( V_{\varepsilon_0} \) of (1, 0) defined by

\[ V_{\varepsilon_0} \equiv \{ 1 - \varepsilon_0 < p(x) < 1, \ 0 < i(x) < \varepsilon_0 \text{ for all } x \in G \} \quad (6.7) \]

for some small \( \varepsilon_0 > 0 \) and initial condition \((p_0(x), i_0(x)) \notin V_{\varepsilon_0}\) such that

\[ (p_0, i_0) \in V_\delta \text{ for some small } \delta > \varepsilon_0, \text{ and } (p(x, t), i(x, t)) \notin V_{\varepsilon_0} \forall t > 0. \quad (6.8) \]

The next theorem is similar to Theorem 4.3. As in the remark following the statement of Theorem 4.3, we shall assume that

\[ \frac{\sigma(x)}{A(x)} \text{ and } \frac{\alpha(x)}{r(x)} \quad (6.9) \]

are sufficiently large and, in particular,

\[ P_T(x) \equiv \frac{A(x)}{\sigma(x) - 1} < \mu \quad (6.10) \]
Theorem 6.3 (Host Population Extinction). Under conditions (6.9) and (6.10), if $(p_0, i_0)$ is as in (6.8),

Then the solution of (6.1),

$(p(x, t), i(x, t))$,

satisfies

\[ \max_{x \in \mathcal{D}} p(x, t) \to 0 \text{ as } t \to \infty. \]
SI PDE: Disease-Free System

Theorem 6.4 (Population Persistence). In Model (6.1), if \( i_0(x) \equiv 0 \) and
\[ i_0(x) \equiv 0, \quad p_0(x) > \bar{u} + \varepsilon \text{ for all } x \in \mathcal{G} \text{ and } \varepsilon > 0, \]
then the model solution
\[ (p(x, t), i(x, t)) \]
satisfies
\[ \bar{u} + \varepsilon < p(x, t) \text{ for all } x \in \mathcal{G}, \ t > 0. \]
Theorem 6.5 (Host Population Persistence). In Model (6.1),
\[ i_0(x) \geq 0, \ p_0(x) > \overline{u} + \varepsilon \text{ for all } x \in \overline{G}, \ \varepsilon > 0, \quad (6.13) \]
and
\[ \min_{x \in \overline{G}} [r(x)(1 - y)(y - u(x))y - a(x)y]_{y=\overline{u}+\varepsilon} > 0. \quad (6.14) \]

Then the model solution \((p(x, t), i(x, t))\)
satisfies
\[ \overline{u} + \varepsilon < p(x, t) \text{ for all } x \in \overline{G}, \ t > 0. \]
In order to establish persistence of the infected population, we introduce the function

\[ I(t) \equiv \int_G u(x,t) \, dx \]

and the condition

\[ (\sigma(x) - 1) \cdot \bar{u} > A(x) \text{ for all } x \in \overline{G}. \tag{6.15} \]

**Theorem 6.6 (Disease Persistence).** In Model (6.1), under conditions (6.13)-(6.15), if

\[ I(0) > 0, \]

then

\[ I(t) \geq \varepsilon_0 \text{ for all } t \text{ sufficiently large and some positive constant } \varepsilon_0. \]
Single Patch SI Model


- If a healthy stable host population at the disease-free equilibrium is subject to an Allee effect, can a small number of infected individuals with a fatal disease cause the host population to go extinct?
High Risk In All Patches
High Risk Vrs Low Risk Patches

![Graphs showing the comparison between high risk and low risk patches.](image-url)
Conclusion

- We used mathematical theorems to link Allee effect in host demographics, spatial heterogeneity, habitat connectivity, and rates of movement to host population persistence or extinction.
- At high densities, migration from a low (respectively, high) risk patch to a high (respectively, low) risk patch can save an endangered species from local patch extinction.
- At high densities, migration of the total population between high risk patches leads to the extinction of the total population.
Thank You!