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 higher 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)

$$\left.\begin{aligned} \frac{dp}{dt} &= r(1-p)(p-u)p - \alpha i, \\ \frac{di}{dt} &= \left[-A + (\sigma - 1)p - \sigma i\right] i, \end{aligned}\right\} (2.4)$$

$$A = \alpha + d + ru.$$

Initial Conditions

In Model (2.4), we take initial conditions

$$0 < i(0) < p(0) < 1. \qquad (3.1)$$

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

$$0 < i(t) < p(t) \text{ for all } t > 0.$$

Disease Threshold and R_0

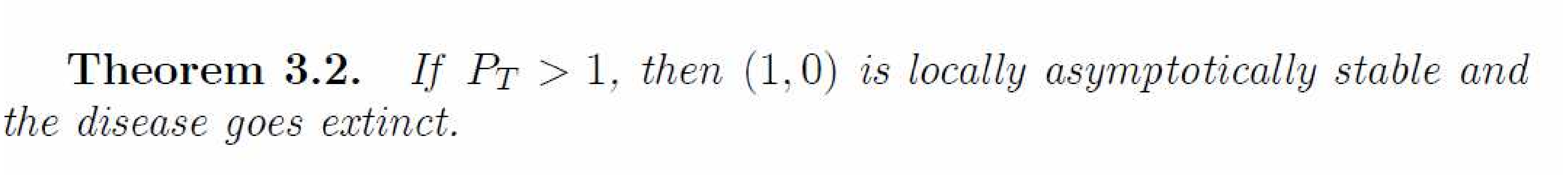
As in [16], we introduce the critical host population density for disease establishment, the disease threshold,

$$P_T = \frac{A}{\sigma - 1}, \qquad (3.2)$$

and the basic reproductive ratio,

$$\mathcal{R}_0 = \frac{\sigma}{A+1}.$$

Local Stability



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

Persistence

Theorem 3.3. *If*

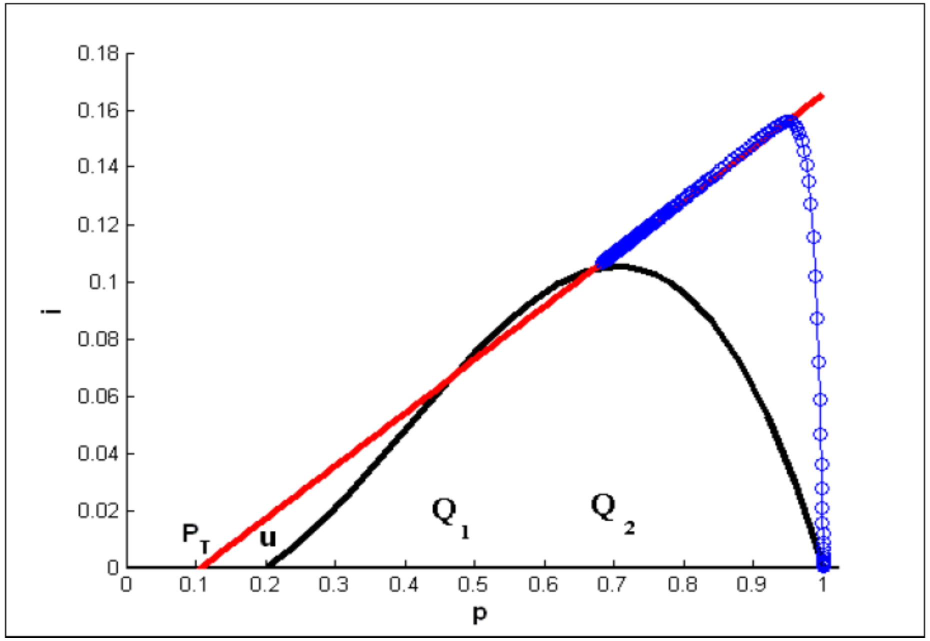
$$0 < u < P_T < 1 \tag{3.3}$$

and

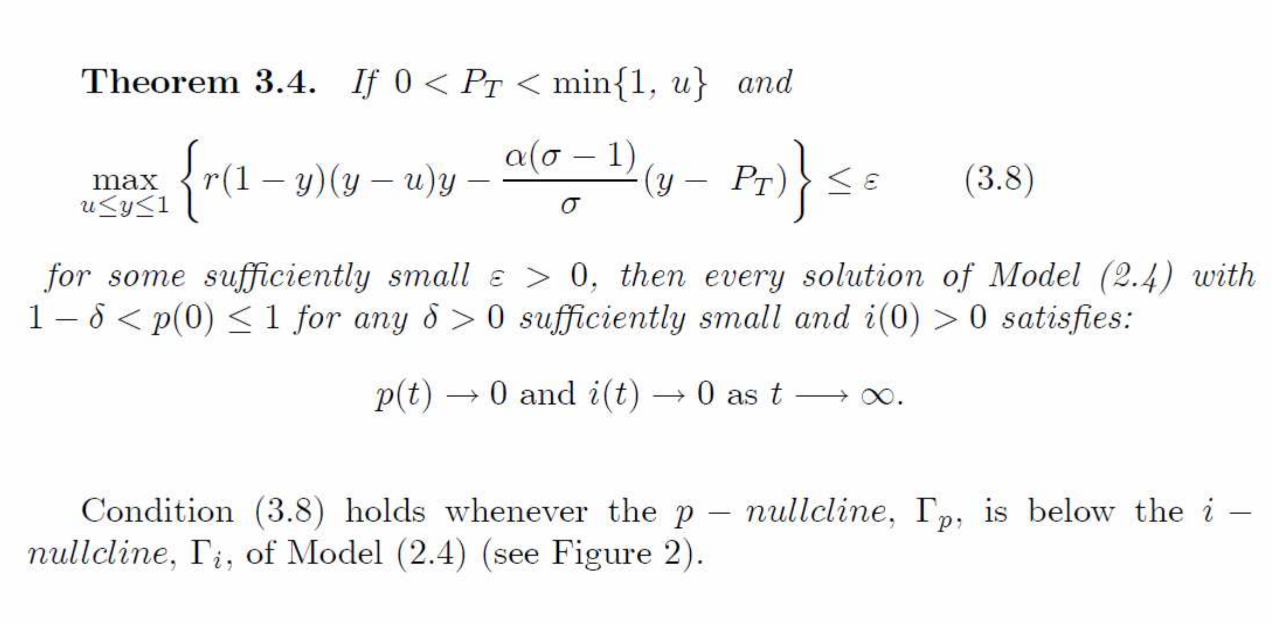
$$\max_{u<y<P_T} \{r(1-y)(y-u)y\} > \frac{\alpha(\sigma-1)}{\sigma}(1-P_T), \tag{3.4}$$

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* ε_0 *and a time* $T = T(\varepsilon_0, i(0))$ *such that*

$$i(t) \geq \delta \text{ for all } t \geq T(\varepsilon_0, i(0)). \tag{3.5}$$



Extinction



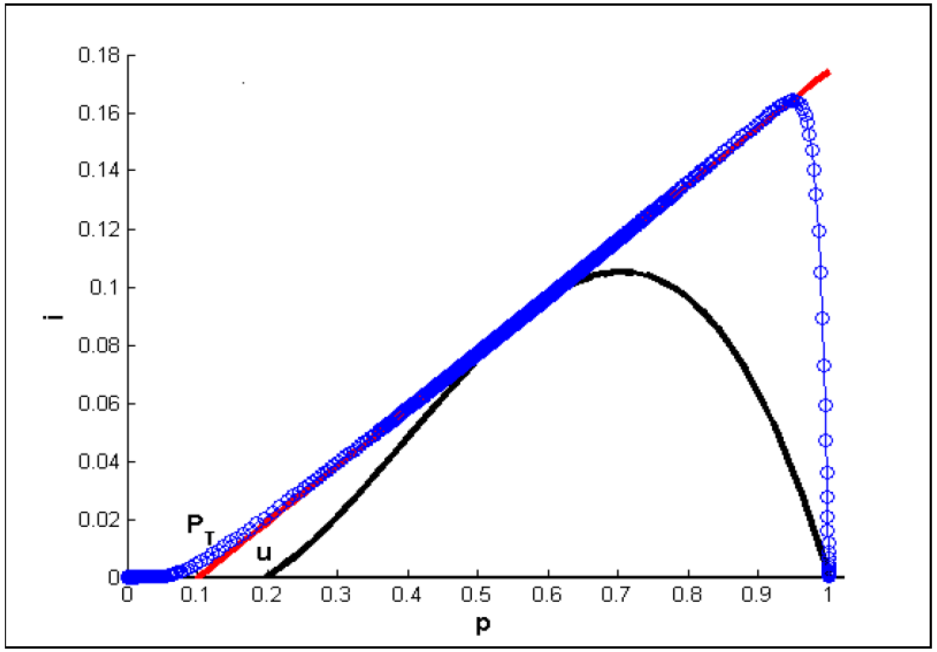
Theorem 3.4. *If* $0 < P_T < \min\{1,\, u\}$ *and*

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

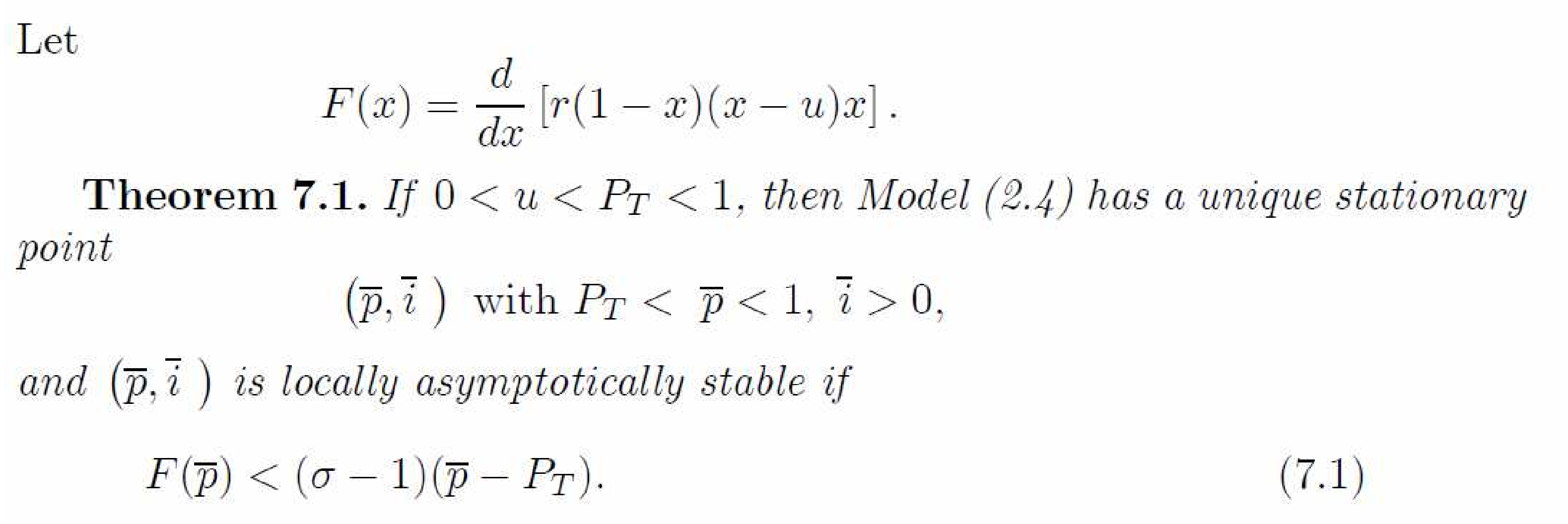
for some sufficiently small $\varepsilon > 0$, *then every solution of Model (2.4) with* $1 - \delta < p(0) \le 1$ *for any* $\delta > 0$ *sufficiently small and* $i(0) > 0$ *satisfies:*

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

Condition (3.8) holds whenever the $p - nullcline$, Γ_p, is below the $i - nullcline$, Γ_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*

$$(\overline{p}, \overline{i}\,) \text{ with } P_T < \overline{p} < 1,\ \overline{i} > 0,$$

and $(\overline{p}, \overline{i}\,)$ *is locally asymptotically stable if*

$$F(\overline{p}) < (\sigma - 1)(\overline{p} - P_T). \tag{7.1}$$

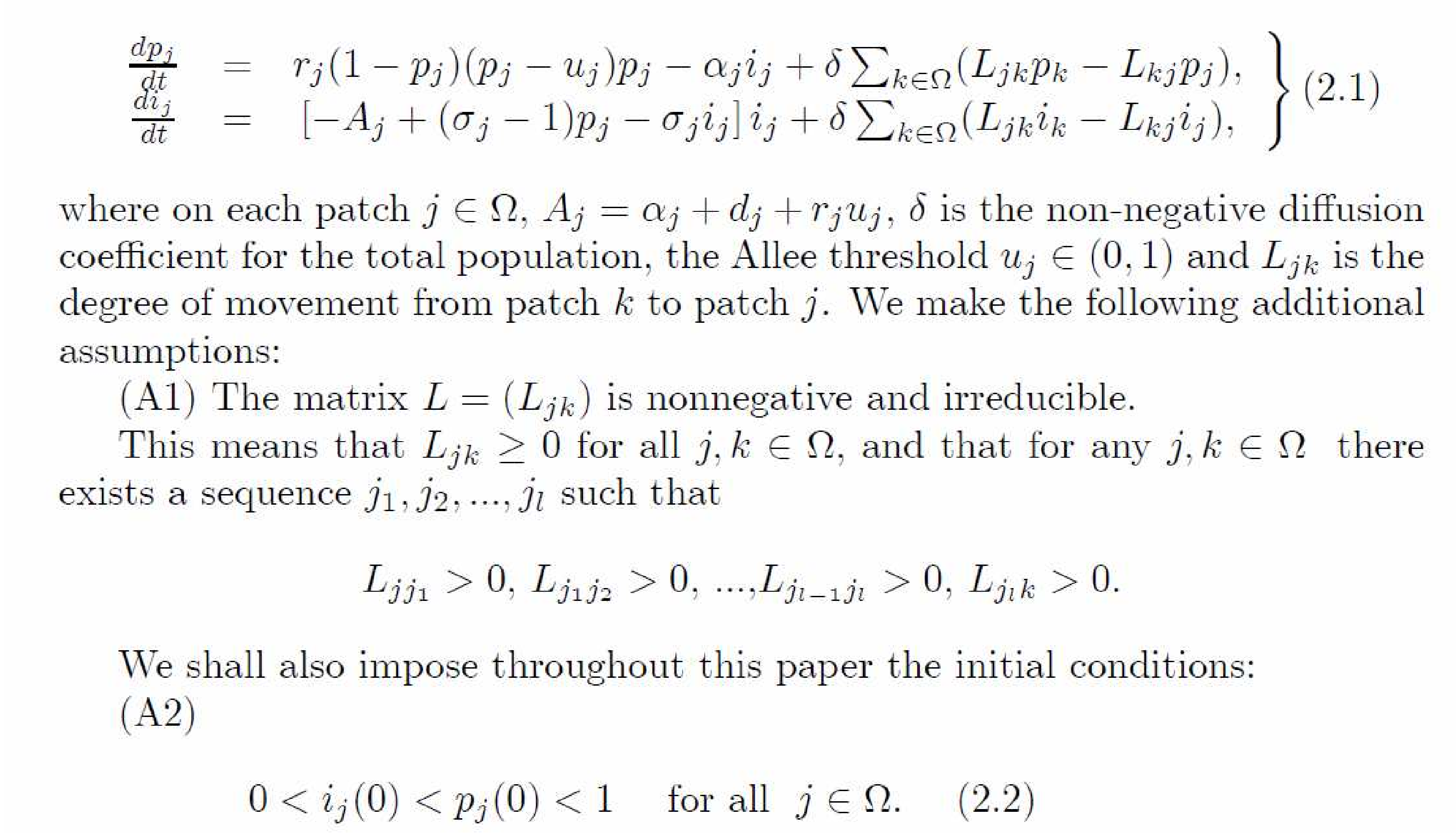
Conclusion (single patch)

- 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).

SI Epidemic Patch Model

Spatial heterogeneity, habitat connectivity and rates of movement play important roles in disease persistent and extinction (Allen et al. 2009, Yakubu and Castillo-Chavez 2002, Lloyd and May 2001).

SI Model In Patchy Environment



$$\left.\begin{aligned}\frac{dp_j}{dt} &= r_j(1-p_j)(p_j-u_j)p_j - \alpha_j i_j + \delta \textstyle\sum_{k\in\Omega}(L_{jk}p_k - L_{kj}p_j),\\ \frac{di_j}{dt} &= [-A_j + (\sigma_j - 1)p_j - \sigma_j i_j]\, i_j + \delta \textstyle\sum_{k\in\Omega}(L_{jk}i_k - L_{kj}i_j),\end{aligned}\right\} \quad (2.1)$$

where on each patch $j \in \Omega$, $A_j = \alpha_j + d_j + r_j u_j$, δ 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 $j_1, j_2, ..., j_l$ such that

$$L_{jj_1} > 0,\ L_{j_1j_2} > 0,\ ...,L_{j_{l-1}j_l} > 0,\ L_{j_lk} > 0.$$

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* $\left(\overrightarrow{p}(t), \overrightarrow{i}(t)\right)$ *of (2.1) satisfies the inequalities*

$$0 < i_j(t) < p_j(t) < 1 \text{ for all } t > 0 \text{ and } j \in \Omega. \qquad (3.1)$$

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

$$\overrightarrow{\mathbf{0}} = (0, 0, 0, 0, ..., 0, 0),$$

$$\left(\overrightarrow{u}, \overrightarrow{0}\right) = (u_1, u_2, ..., u_n, 0, 0, ..., 0)$$

and

$$\left(\overrightarrow{1}, \overrightarrow{0}\right) = (1, 1, ..., 1, 0, 0, ..., 0).$$

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:

$$p_j(t) \downarrow 0 \text{ as } t \longrightarrow \infty.$$

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

$$(p_1(t), p_2(t), ..., p_n(t), i_1(t), i_2(t), ..., i_n(t)) \rightarrow \overrightarrow{\mathbf{0}} \text{ as } t \longrightarrow \infty.$$

Population Extinction

Theorem 4.1 (Population Extinction). *In Model (2.1), assume that*

$$0 < p_j(0) < \underline{u} = \min_{1 \le i \le n} \{u_i\} \text{ for all } j \in \Omega.$$

Then the solution

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

satisfies

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

where $\varepsilon > 0$ *is sufficiently small. Moreover,*

$$\sum_{j \in \Omega} p_j(t) \le Ce^{-\gamma t}$$

where C *and* γ *are positive constants. Hence,*

$$\left(\overrightarrow{p}(t), \overrightarrow{i}(t)\right) \to \overrightarrow{\mathbf{0}} \text{ as } t \longrightarrow \infty.$$

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

$$\mathcal{R}_{0j} = \frac{\sigma_j - 1}{A_j} > 1, \ \frac{1}{\mathcal{R}_{0j}} < u_j$$

and

$$\max_{u_j \leq y_J \leq 1} \left\{ r_j(1 - y_J)(y_j - u_j)y_j - \frac{\alpha_j(\sigma_j - 1)}{\sigma_j}(y_j - \frac{1}{\mathcal{R}_{0j}}) \right\} \leq \varepsilon_j$$

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:

$$p_j(t) \to 0 \text{ and } i_j(t) \to 0 \text{ as } t \longrightarrow \infty.$$

R_0 in Patchy Environment

To obtain a similar population extinction result for the diffusion-linked $n-patch$ model, we let

$$\mathcal{R}_{0j}^{\delta} = \frac{\sigma_j - 1}{A_j + \delta \sum_{k\in\Omega} L_{kj}} \quad \text{for each } j, k \in \Omega.$$

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

Theorem 4.2. *If*

$$\mathcal{R}_{0j}^{\delta} > 1 \ \textit{for all} \ \ j \in \Omega,$$

then the DFE, $\left(\overrightarrow{1}, \overrightarrow{0}\right)$, *is unstable.*

Rδ

The Jacobian matrix evaluated at $\left(\vec{1}, \vec{0}\right)$ is

$$J_{\left(\overline{1},\overline{0}\right)} = \begin{pmatrix} -r_1(1-u_1)-\delta L_{21} & \delta L_{12} & -\alpha_1 & 0 \\ \delta L_{21} & -r_2(1-u_2)-\delta L_{12} & 0 & -\alpha_2 \\ 0 & 0 & -A_1+\sigma_1-1-\delta L_{21} & \delta L_{12} \\ 0 & 0 & \delta L_{21} & -A_2+\sigma_2-1-\delta L_{12} \end{pmatrix}.$$

For $j \in \{1,2\}$, let $m_j = -r_j(1-u_j)-\delta L$ and $n_j = -A_j+\sigma_j-1-\delta L$, where $L_{21} = L_{12} = L$. Then the eigenvalues of $J_{\left(\overline{1},\overline{0}\right)}$ are the roots of the characteristic equations

$$\lambda^2 - \lambda(m_1+m_2) + m_1 m_2 - (\delta L)^2 = 0$$

and

$$\lambda^2 - \lambda(n_1+n_2) + n_1 n_2 - (\delta L)^2 = 0.$$

The largest eigenvalue is

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

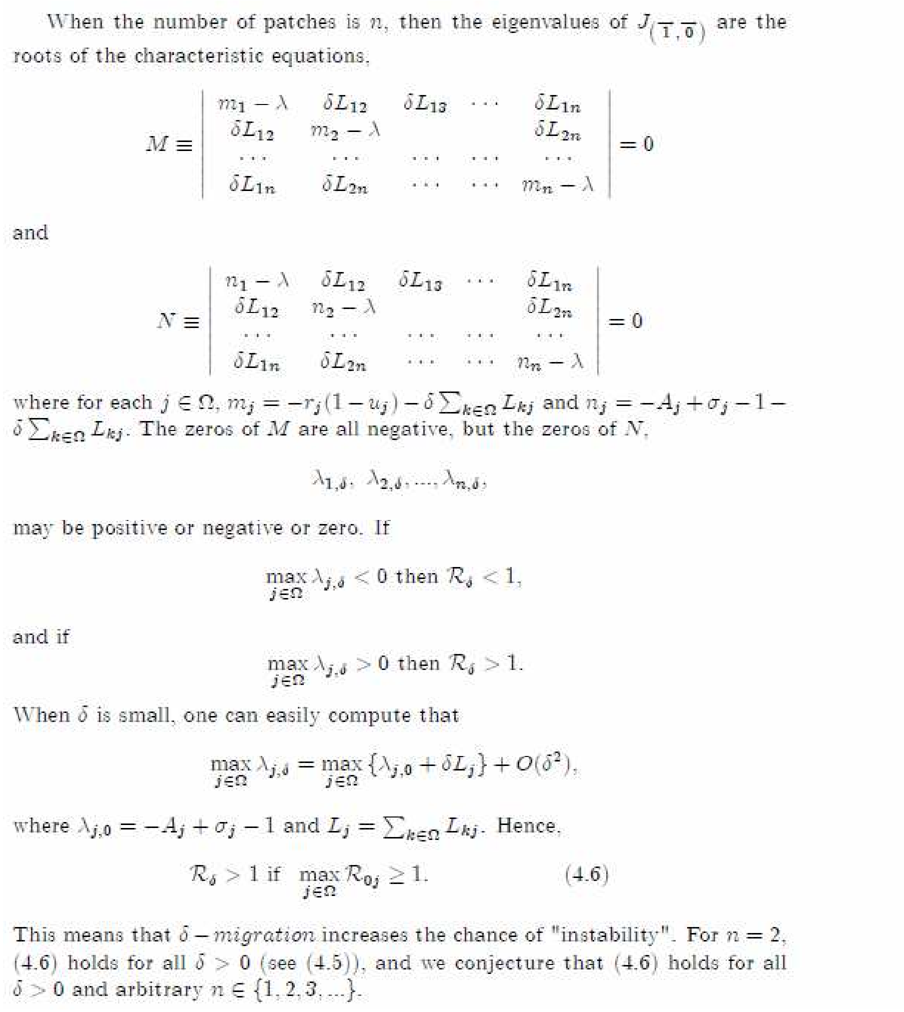
which is easily seen to be larger than

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

Hence, if we denote by $\mathcal{R}_\delta$ the basic reproduction number for the migration-linked Model (2.1), then

$$\mathcal{R}_\delta > 1 \text{ if } \max_{j=1,2} \mathcal{R}_{0j} > 1. \qquad (4.5)$$

R$^{\delta}$



When the number of patches is n, then the eigenvalues of $J_{(\overline{1},\overline{0})}$ are the roots of the characteristic equations,

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

and

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

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,

$$\lambda_{1,\delta},\ \lambda_{2,\delta}, \ldots, \lambda_{n,\delta},$$

may be positive or negative or zero. If

$$\max_{j\in\Omega} \lambda_{j,\delta} < 0 \text{ then } \mathcal{R}_\delta < 1,$$

and if

$$\max_{j\in\Omega} \lambda_{j,\delta} > 0 \text{ then } \mathcal{R}_\delta > 1.$$

When δ 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 $\lambda_{j,0} = -A_j + \sigma_j - 1$ and $L_j = \sum_{k\in\Omega} L_{kj}$. Hence,

$$\mathcal{R}_\delta > 1 \text{ if } \max_{j\in\Omega} \mathcal{R}_{0j} \geq 1. \qquad (4.6)$$

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 $n \in \{1, 2, 3, \ldots\}$.

Population Extinction

Theorem 4.3 (Host Population Extinction). *In Model (2.1), assume that*

$$\mathcal{R}_\delta > 1,$$

and, for any $l \in \Omega$, *if* $\underline{u} < y_l < 1$ *and* $0 < y_j < 1$ *for all* $j \in \Omega$, $j \neq l$, *then*

$$\sum_{j \in \Omega} \left\{ r_j(1 - y_j)(y_j - u_j)y_j - \frac{\alpha_j(\sigma_j - 1)}{\sigma_j}(y_j - P_{Tj}) \right\} < 0. \qquad (4.7)$$

Then every solution of Model (2.1),

$$\left(\overrightarrow{p}(t), \overrightarrow{i}(t)\right) \to \overrightarrow{\mathbf{0}} \text{ as } t \longrightarrow \infty,$$

provided $\left(\overrightarrow{p}(0), \overrightarrow{i}(0)\right)$ *does not lie on either the (local) stable or center manifolds of* $\left(\overrightarrow{1}, \overrightarrow{0}\right)$.

Disease-Free Sytem

We first consider the disease-free model (2.3). That is,

$$\frac{dp_j}{dt} = r_j(1 - p_j)(p_j - u_j)p_j + \delta \sum_{k\in\Omega}(L_{jk}p_k - L_{kj}p_j). \qquad j \in \Omega. \qquad (5.1)$$

Host Population Persistence (No Infected)

Theorem 5.1 (Population Persistence). *In Model (5.1), assume*

$$\overline{u} < p_j(0) < 1 \text{ for all } j \in \Omega.$$

Then the model solution

$$(p_1(t), p_2(t), ..., p_n(t))$$

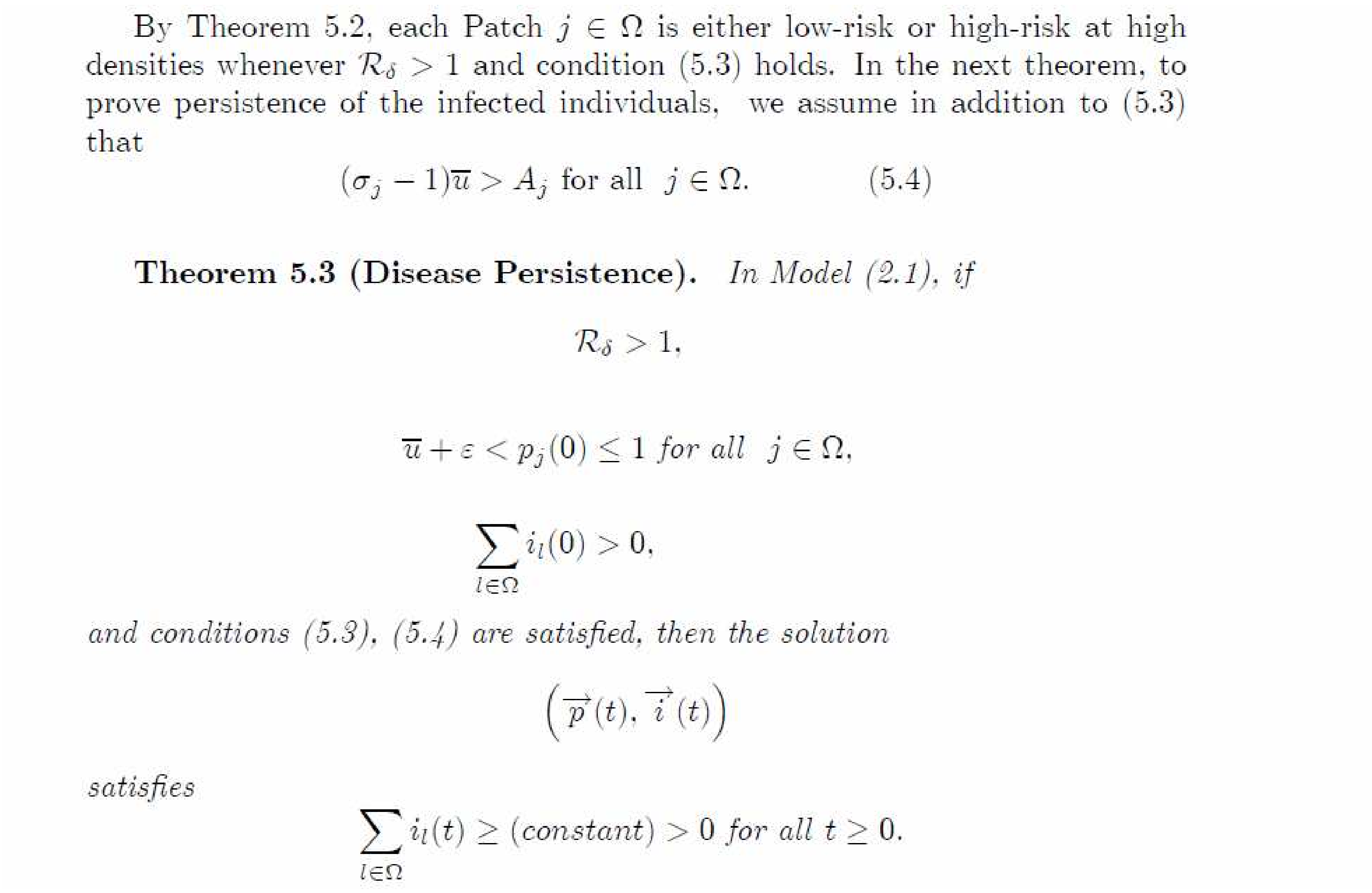
satisfies

$$\overline{u} + \varepsilon < p_j(t) \text{ for all } t > 0 \text{ and } j \in \Omega,$$

where $\varepsilon > 0$ *is sufficiently small and* $\overline{u} = \max_{1 \leq i \leq n} \{u_i\}$.

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 $\mathcal{R}_\delta > 1$ and condition (5.3) holds. In the next theorem, to prove persistence of the infected individuals, we assume in addition to (5.3) that

$$(\sigma_j - 1)\overline{u} > A_j \text{ for all } \; j \in \Omega. \qquad (5.4)$$

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

$$\mathcal{R}_\delta > 1,$$

$$\overline{u} + \varepsilon < p_j(0) \leq 1 \textit{ for all } \; j \in \Omega,$$

$$\sum_{l \in \Omega} i_l(0) > 0,$$

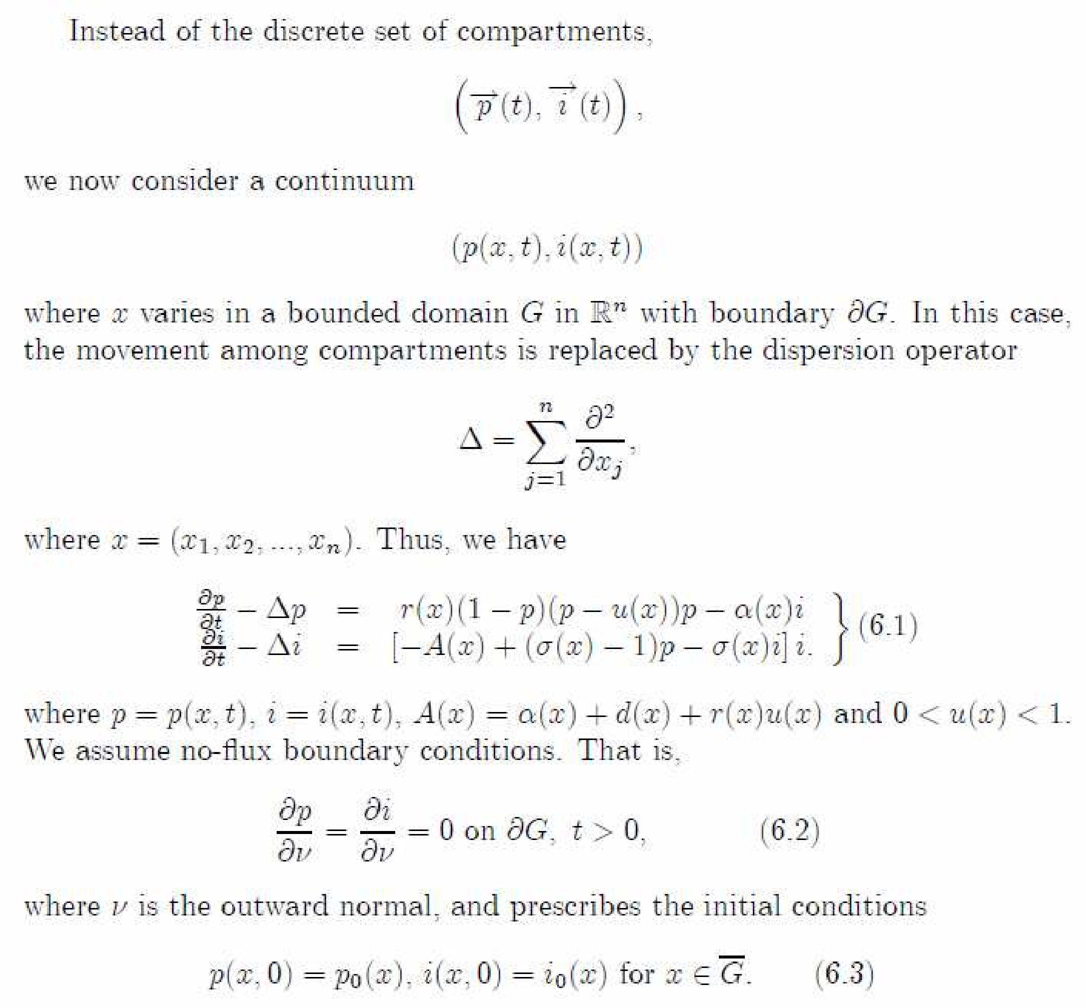
and conditions (5.3), (5.4) are satisfied, then the solution

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

satisfies

$$\sum_{l \in \Omega} i_l(t) \geq (constant) > 0 \textit{ for all } t \geq 0.$$

SI Epidemic PDE Model



Instead of the discrete set of compartments,

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

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 ∂G. In this case, the movement among compartments is replaced by the dispersion operator

$$\Delta = \sum_{j=1}^{n} \frac{\partial^2}{\partial x_j},$$

where $x = (x_1, x_2, ..., x_n)$. Thus, we have

$$\left.\begin{array}{rcl} \frac{\partial p}{\partial t} - \Delta p &=& r(x)(1-p)(p-u(x))p - \alpha(x)i \\ \frac{\partial i}{\partial t} - \Delta i &=& [-A(x) + (\sigma(x)-1)p - \sigma(x)i]\, i. \end{array}\right\} (6.1)$$

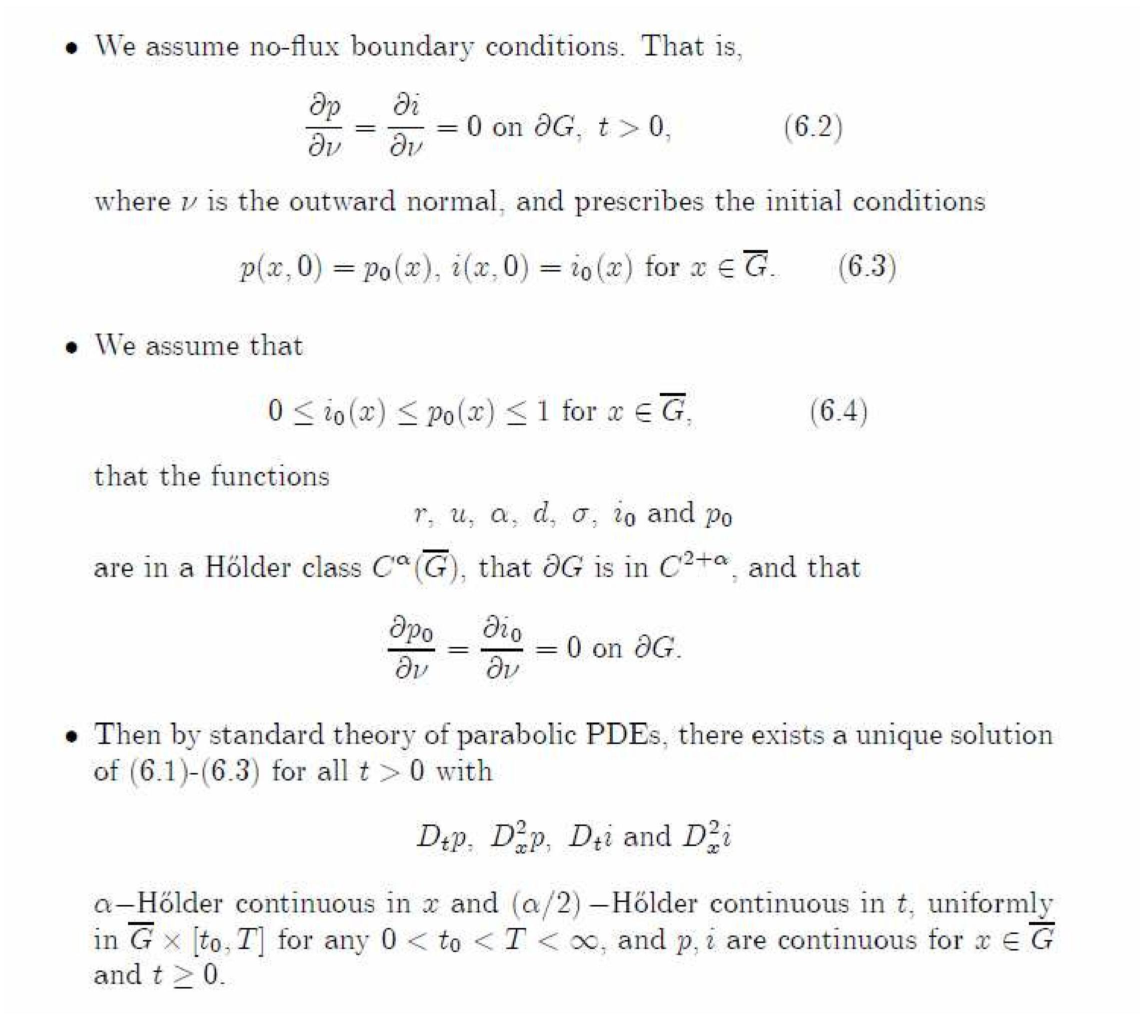
where $p = p(x,t)$, $i = i(x,t)$, $A(x) = \alpha(x) + d(x) + r(x)u(x)$ and $0 < u(x) < 1$. We assume no-flux boundary conditions. That is,

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

where ν is the outward normal, and prescribes the initial conditions

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

SI PDE Model Assumptions



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where ν is the outward normal, and prescribes the initial conditions

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

- We assume that

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

that the functions

$$r,\ u,\ \alpha,\ d,\ \sigma,\ i_0 \text{ and } p_0$$

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

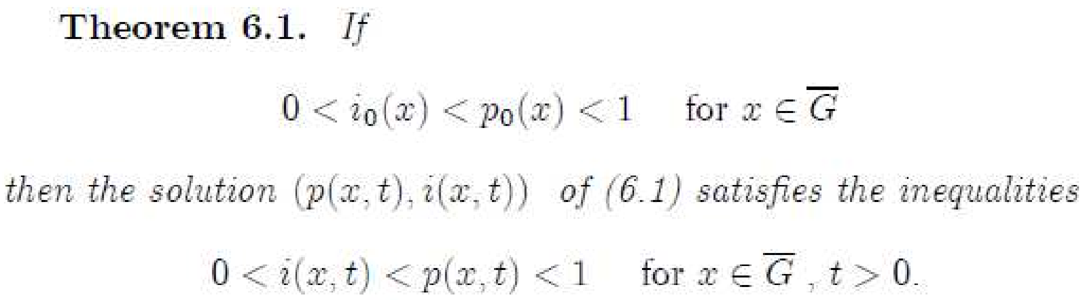
$$\frac{\partial p_0}{\partial \nu} = \frac{\partial i_0}{\partial \nu} = 0 \text{ on } \partial G.$$

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

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

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

SI PDE: Initial Conditions



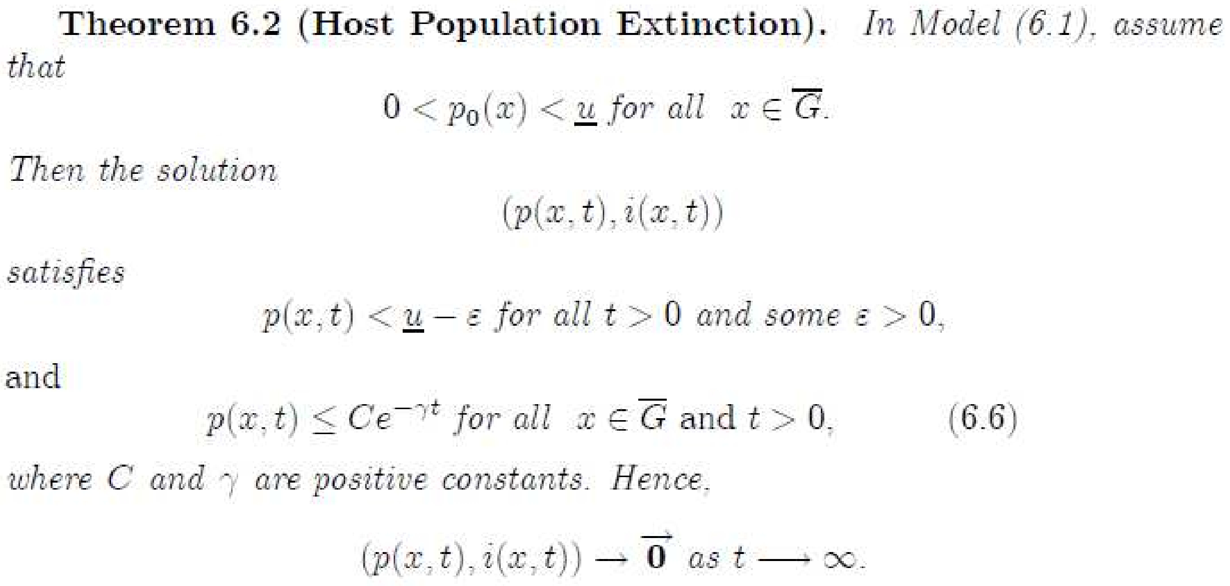
Theorem 6.1. *If*

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

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

$$0 < i(x,t) < p(x,t) < 1 \quad \text{for } x \in \overline{G}\ ,\ t > 0.$$

SI PDE: Population Extinction



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

$$p(x,t) \leq Ce^{-\gamma t} \text{ for all } x \in \overline{G} \text{ and } t > 0, \qquad (6.6)$$

where C *and* γ *are positive constants. Hence,*

$$(p(x,t), i(x,t)) \to \overrightarrow{\mathbf{0}} \text{ as } t \longrightarrow \infty.$$

SI PDE: DFE

We denote the DFE of (6.1), the solution of

$$p(x,t) \equiv 1 \text{ and } i(x,t) \equiv 0$$

by $(1,0)$. We consider the case when $(1,0)$ is not stable in the following sense. There exists a neighborhood V_{ε_0} of $(1,0)$ defined by

$$V_{\varepsilon_0} \equiv \{1-\varepsilon_0 < p(x) < 1,\ \ 0 < i(x) < \varepsilon_0 \text{ for all } \ x \in \overline{G}\} \tag{6.7}$$

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

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

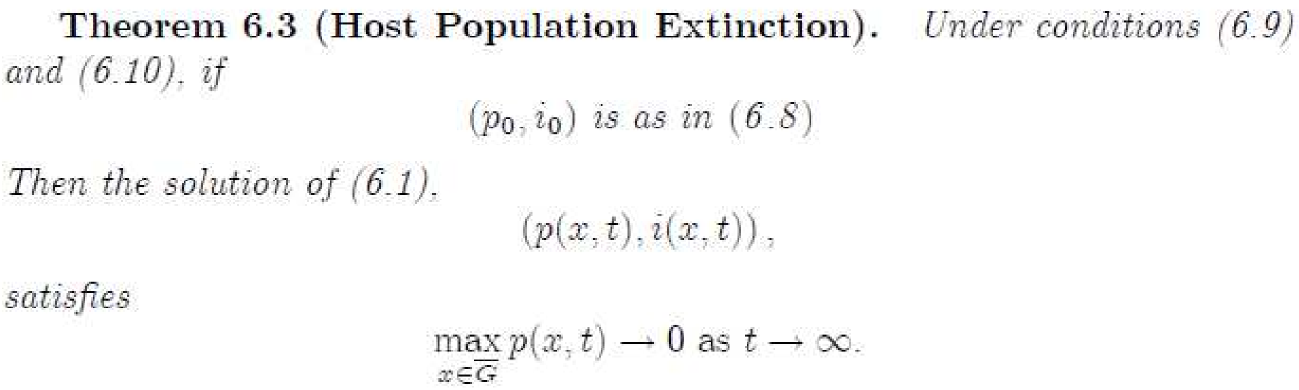
The next theorem is similar to Theorem 4.3. As in the remark following the statement of Theorem 4.3, we shall assume that

$$\frac{\sigma(x)}{A(x)} \text{ and } \frac{\alpha(x)}{r(x)} \tag{6.9}$$

are sufficiently large and, in particular,

$$P_T(x) \equiv \frac{A(x)}{\sigma(x)-1} < \underline{u} \tag{6.10}$$

SI PDE: Population Extinction



Theorem 6.3 (Host Population Extinction). *Under conditions (6.9) and (6.10), if*

$$(p_0, i_0) \text{ is as in } (6.8)$$

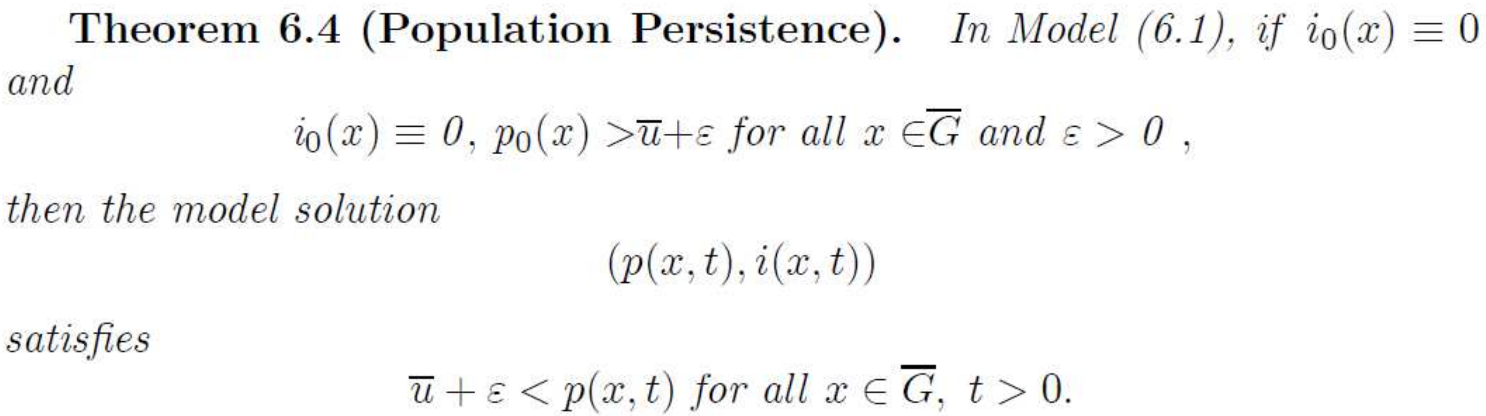
Then the solution of (6.1),

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

satisfies

$$\max_{x\in\overline{G}} p(x,t) \to 0 \text{ as } t \to \infty.$$

SI PDE: Disease-Free System



Theorem 6.4 (Population Persistence). *In Model (6.1), if* $i_0(x) \equiv 0$ *and*

$$i_0(x) \equiv 0,\ p_0(x) > \overline{u} + \varepsilon \text{ for all } x \in \overline{G} \text{ and } \varepsilon > 0\ ,$$

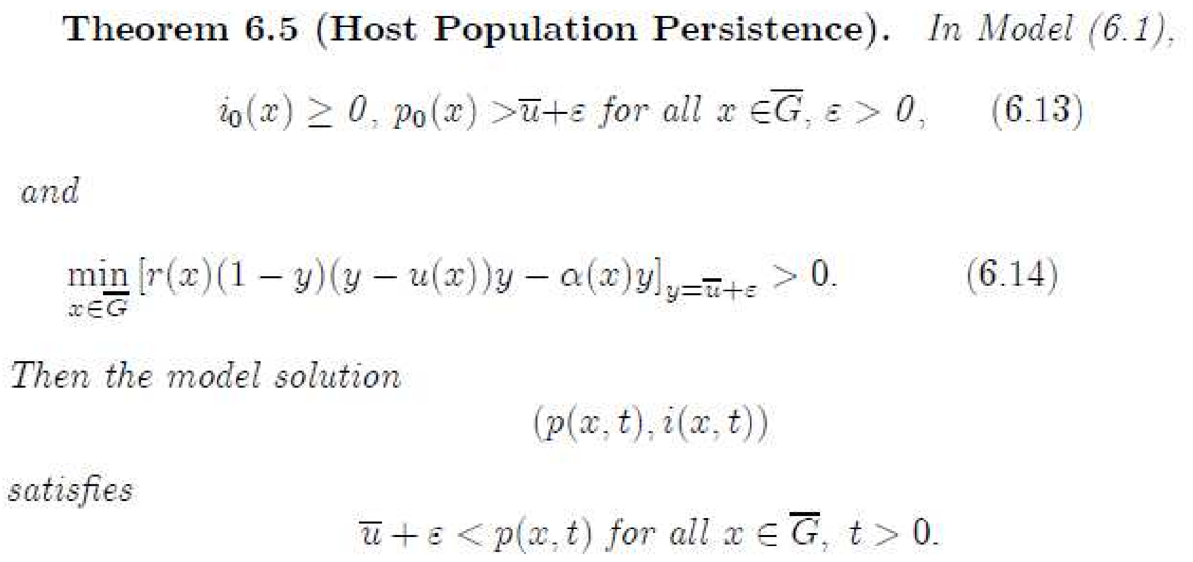
then the model solution

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

satisfies

$$\overline{u} + \varepsilon < p(x,t) \text{ for all } x \in \overline{G},\ t > 0.$$

SI PDE: Population Persistence



Theorem 6.5 (Host Population Persistence). *In Model (6.1),*

$$i_0(x) \geq 0,\ p_0(x) > \overline{u}+\varepsilon \text{ for all } x \in \overline{G},\ \varepsilon > 0, \qquad (6.13)$$

and

$$\min_{x \in \overline{G}} [r(x)(1-y)(y-u(x))y - \alpha(x)y]_{y=\overline{u}+\varepsilon} > 0. \qquad (6.14)$$

Then the model solution

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

satisfies

$$\overline{u}+\varepsilon < p(x,t) \text{ for all } x \in \overline{G},\ t > 0.$$

SI PDE: Disease Extinction

In order to establish persistence of the infected population, we introduce the function

$$I(t) \equiv \int_G i(x,t)dx$$

and the condition

$$(\sigma(x) - 1)\overline{u} > A(x) \text{ for all } x \in \overline{G}. \qquad (6.15)$$

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

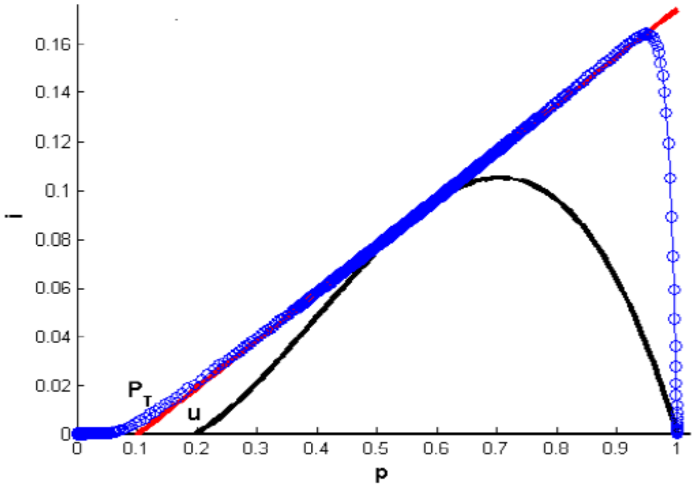
$$I(0) > 0,$$

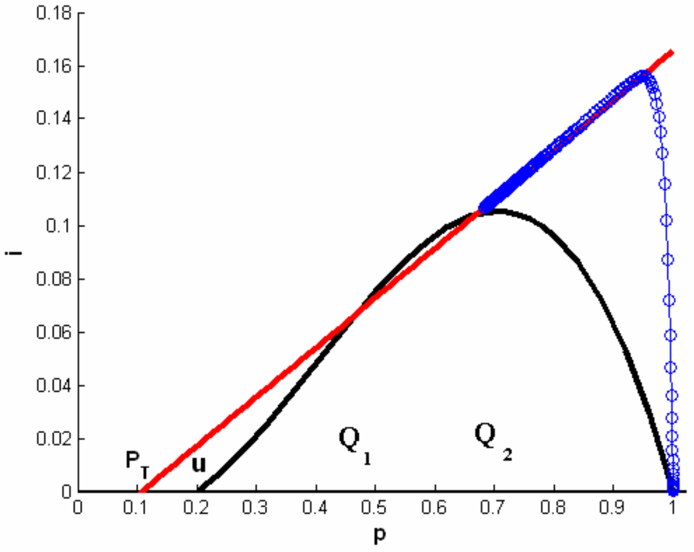
then

$$I(t) \geq \varepsilon_0 \text{ for all } t \text{ sufficiently large and some positive constant } \varepsilon_0.$$

Single Patch SI Model

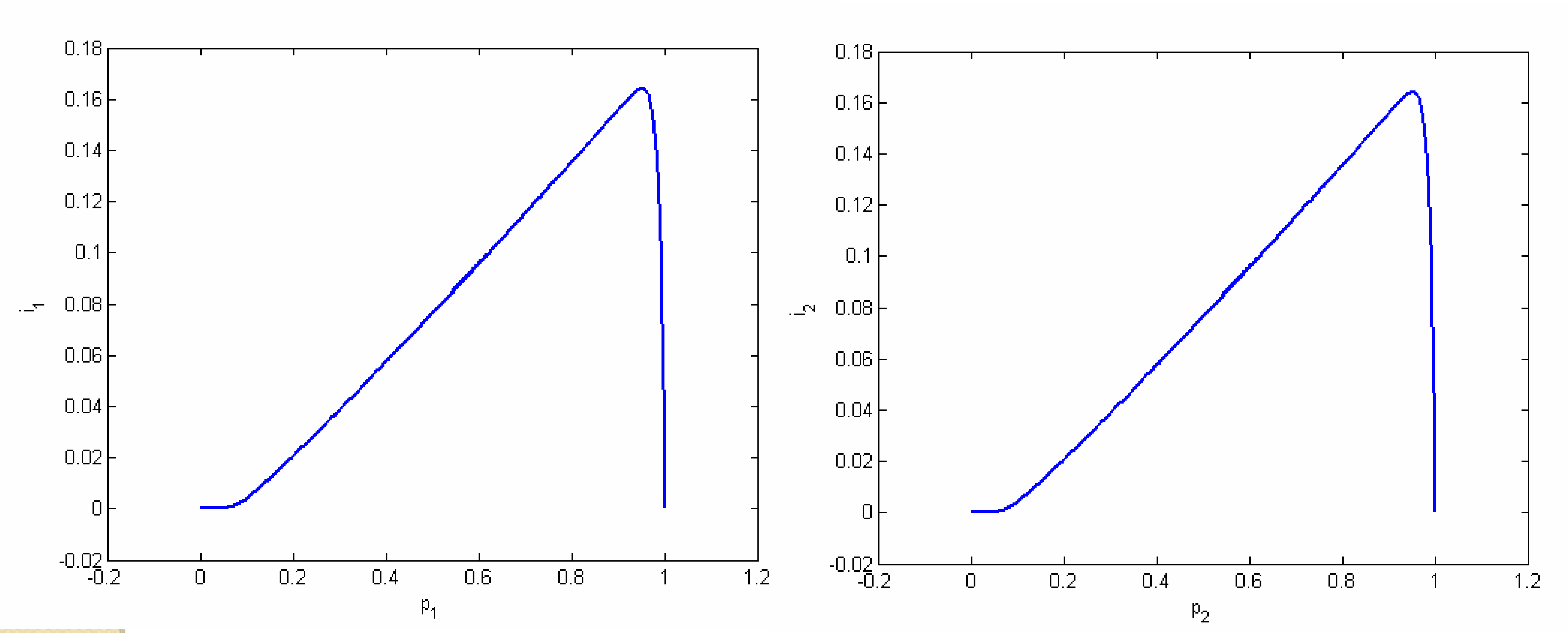
(A. Friedman and A.-A. Yakubu, JBD in press
11)



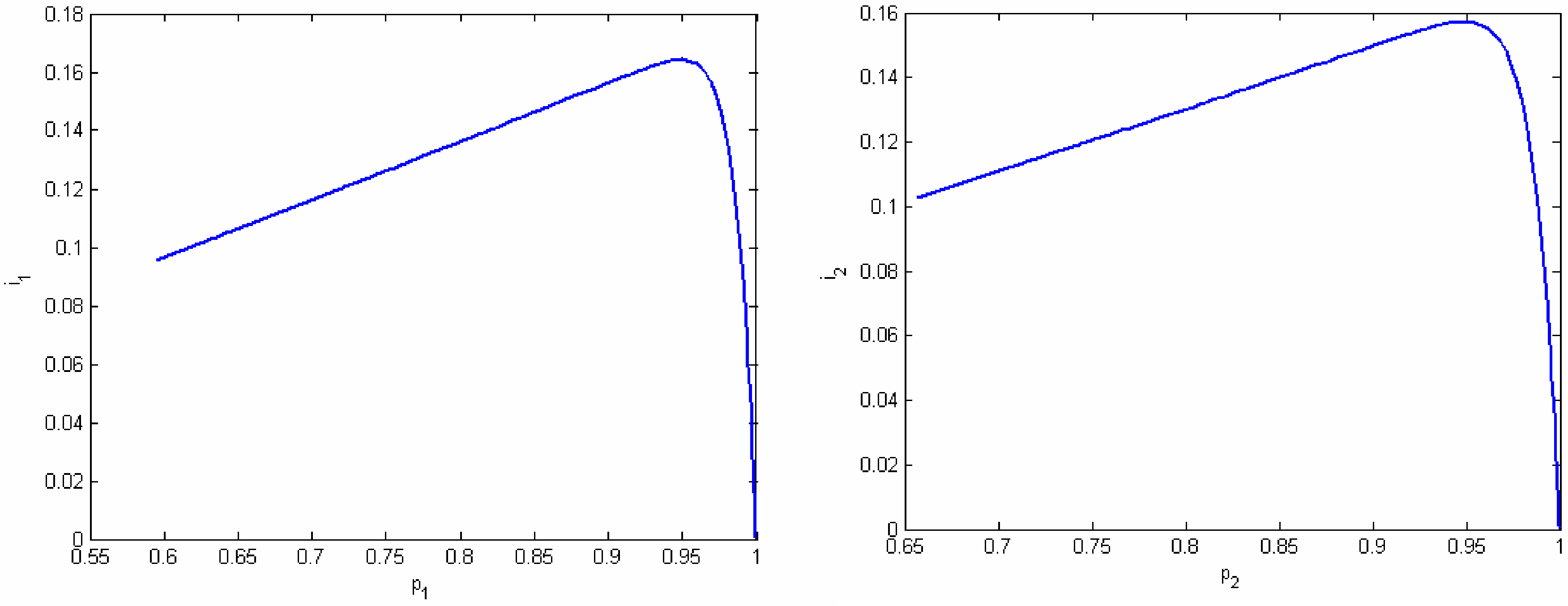


- If a healthy stable host population at the disease-free equilibrium is subject to an Allee effect, can a small number of infected individuals with a fatal disease cause the host population to go extinct?

High Risk In All Patches



High Risk Vrs Low Risk Patches



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!