Principal Eigenvalues and Basic Reproduction Numbers for Reaction-Diffusion Models

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A motivation example

To study the spatial spread of rabies among foxes, Murray, Stanley and Brown (1986) proposed the following model:

$$\begin{aligned}
\frac{\partial E}{\partial t} &= \beta IS - \sigma E - \left[b + (a-b)\frac{N}{K}\right] E, \\
\frac{\partial I}{\partial t} &= \frac{\partial}{\partial x}\left(D\frac{\partial I}{\partial x}\right) + \sigma E - \alpha I - \left[b + (a-b)\frac{N}{K}\right] I, \qquad (1.1) \\
\frac{\partial S}{\partial t} &= (a-b)S\left(1 - \frac{N}{K}\right) - \beta IS,
\end{aligned}$$

where S is the density of susceptible foxes, E is the density of infected but non-infectious foxes, I is the density of rabid foxes, $N = S + E + I$ is the total fox population.

D is the diffusion coefficient, a is the birth rate, b is the intrinsic death rate, and K is the environmental carrying capacity, β is the disease transmission coefficient, σ is the per capita rate of infected foxes becoming infectious, α is the disease-induced death rate of rabid fox, and x is the one dimensional space variable. The term $(a-b)N/K$ represents the death rate due to depletion of the food supply by all foxes. Moreover, $a > b$ is assumed to ensure sustainable population size.

For simplicity, we choose $\Omega = (0,1)$ and impose the Neumann boundary conditions for I:

$$\frac{\partial I}{\partial x}\Big|_{x=0} = \frac{\partial I}{\partial x}\Big|_{x=1} = 0. \tag{1.2}$$

We further assume that $D(x) \geq D_0$, $\forall x \in [0,1]$, for some constant $D_0 > 0$, $\beta(x)$ and $\alpha(x)$ are nonnegative continuous functions on $[0,1]$ with $\beta(x) \not\equiv 0$.

Linearize system (1.1) at the disease-free steady sate $(0, 0, K)$, we obtain the following equations for E and I:

$$\begin{aligned}
\frac{\partial E}{\partial t} &= -(\sigma + a)E + \beta(x)KI, \\
\frac{\partial I}{\partial t} &= \frac{d}{dx}\left(D(x)\frac{dI}{dx}\right) + \sigma E - (\alpha(x) + a)I, \qquad (1.3) \\
\frac{dI}{dx}\Big|_{x=0} &= \frac{dI}{dx}\Big|_{x=1} = 0.
\end{aligned}$$

Note that (1.3) is cooperative and hence, admits the comparison principle. However, the solution maps of (1.3) are not compact due to the lack of diffusion term in the E equation.

Let $E(t, x) = e^{\lambda t}E(x)$ and $I(t, x) = e^{\lambda t}I(x)$, we have the following eigenvalue problem:

$$
\begin{aligned}
&-(\sigma+a)E+\beta(x)KI=\lambda E,\ x\in(0,1),\\
&\frac{d}{dx}\left(D(x)\frac{dI}{dx}\right)+\sigma E-(\alpha(x)+a)I=\lambda I,\ x\in(0,1),\\
&\left.\frac{dI}{dx}\right|_{x=0}=\left.\frac{dI}{dx}\right|_{x=1}=0.
\end{aligned}
\tag{1.4}
$$

Question 1: Does the eigenvalue problem (1.4) have a principal eigenvalue? How can we determine the stability of $(0,0,K)$ for the nonlinear system (1.1)?

Note that we cannot use the Krein-Rutman theorem.

Question 2: How can we introduce and compute the basic reproduction number R_0 for system (1.1)?

Basic Reproduction Number R_0:

By definition, the basic reproduction number R_0 is the expected number of secondary cases produced, in a completely susceptible population, by a typical infective individual.

Diekmann, Heesterbeek and Metz (1990): Introduced next generation matrixes (operators).

van den Driessche and Watmough (2002): A computation formula of R_0 for autonomous compartmental models of ODEs.

Bacaer and Guernaoui (2006): Introduced an operator on the space of periodic functions.

Wang and Zhao (2008): Periodic compartmental models of ODEs.

Many calculations of R_0 for various autonomous and periodic epidemic models....

Allen, Bolker, Lou, and Nevai (2008): An SIS epidemic reaction-diffusion model.

Thieme (2009): Spectral bound and reproduction number for the infinite-dimensional population structure and time heterogeneity.

Wang and Zhao (2011): Introduced the next infection operator for a nonlocal and time-delayed reaction-diffusion model of dengue fever.

Lou and Zhao (2011): A nonlocal reaction-diffusion malaria model.

Mckenzie, Jin, Jacobsen, and Lewis (2012): An advection-diffusion-reaction population model.

Peng and Zhao (2012): A periodic reaction-diffusion SIS epidemic model.

Our purpose

1. To develop the theory of the principal eigenvalue for an elliptic eigenvalue problem associated with a linear parabolic cooperative system with some zero diffusion coefficients.

2. To establish the basic reproduction number and its computation formulae for reaction-diffusion epidemic models with compartmental structure.

The principal eigenvalue

Let Ω be a domain in $\mathbb{R}^l$ with the smooth boundary $\partial\Omega$, and ν be the unit normal vector on $\partial\Omega$. For a given integer $k > 0$, let $X = C(\overline{\Omega}, \mathbb{R}^k)$ and $X_+ = C(\overline{\Omega}, \mathbb{R}^k_+)$. Set $u_K = (u_1, \cdots, u_k)^T$ and

$$\nabla \cdot (d_K(x)\nabla u_K) = \operatorname{diag}\left(\nabla \cdot (d_1(x)\nabla u_1), \cdots, \nabla \cdot (d_k(x)\nabla u_k)\right).$$

Let $M(x)$ be a continuous $k \times k$ matrix-valued function of $x \in \overline{\Omega}$. We consider the following elliptic eigenvalue problem

$$\begin{aligned} &\nabla \cdot (d_K(x)\nabla u_K) + M(x)u_K = \lambda u_K, \qquad x \in \Omega, \\ &\frac{\partial u_i}{\partial \nu} = 0, \quad \forall\, 1 \le i \le k \text{ with } d_i > 0, \quad x \in \partial\Omega. \end{aligned} \tag{2.1}$$

For convenience, we set $L(\phi)(x) = \nabla \cdot (d_K(x)\nabla\phi(x))$, and let M denote the multiplication operator defined by $M(\phi)(x) = M(x)\phi(x)$.

Without loss of generality, we assume that

(D) There exists a number $d_0 > 0$ and an integer $1 \le i_1 < k$ such that $d_i(x) \ge d_0,\ \forall x \in \overline{\Omega},\ 1 \le i \le i_1$, and $d_{i_1+i}(x) = 0,\ \forall x \in \overline{\Omega},\ 1 \le i \le i_2 := k - i_1$.

Let $Y_1 = C(\overline{\Omega}, \mathbb{R}^{i_1})$ and $Y_2 = C(\overline{\Omega}, \mathbb{R}^{i_2})$. We split the cooperative matrix $M(x)$ into

$$M(x) = \begin{pmatrix} M_{11}(x) & M_{12}(x) \\ M_{21}(x) & M_{22}(x) \end{pmatrix},$$

where M_{11} is an $i_1 \times i_1$ matrix and M_{22} is an $i_2 \times i_2$ matrix. Set

$$\mathbf{u}_{i_1} = (u_1, \cdots, u_{i_1})^T, \quad \mathbf{u}_{i_2} = (u_{i_1+1}, \cdots, u_k)^T,$$
$$\nabla \cdot (\mathbf{d}_{i_1}(x)\nabla \mathbf{u}_{i_1}) = diag\left(\nabla \cdot (d_1(x)\nabla u_1), \cdots, \nabla \cdot (d_{i_1}(x)\nabla u_{i_1})\right).$$

Let $Q(t)$ be the solution semigroup on X associated with the linear parabolic system

$$\begin{aligned}
\frac{\partial \mathbf{u}_{i_1}}{\partial t} &= \nabla \cdot (\mathbf{d}_{i1}(x)\nabla \mathbf{u}_{i1}) + M_{11}(x)\mathbf{u}_{i_1} + M_{12}(x)\mathbf{u}_{i_2}, \\
\frac{\partial \mathbf{u}_{i_2}}{\partial t} &= M_{21}(x)\mathbf{u}_{i_1} + M_{22}(x)\mathbf{u}_{i_2}, \\
\frac{\partial \mathbf{u}_{i_1}}{\partial \nu} &= 0, \quad t > 0, \ \ x \in \partial\Omega.
\end{aligned} \tag{2.2}$$

It follows that $Q(t)$ is a positive C_0-semigroup on X, and its generator B can be written as

$$B = \begin{pmatrix} L_1 + M_{11} & M_{12} \\ M_{21} & M_{22} \end{pmatrix},$$

where $L_1(\mathbf{u}_{i_1})(x) := \nabla \cdot (\mathbf{d}_{i1}(x)\nabla \mathbf{u}_{i1})$.

Let $T_2(t)\phi_2(x) = e^{M_{22}(x)t}\phi_2(x)$. It then follows that

$$(\lambda I - M_{22})^{-1}\phi_2 = \int_0^\infty e^{-\lambda t}T_2(t)\phi_2 dt, \quad \forall \lambda > s(M_{22}),\ \phi_2 \in Y_2.$$

Thus, we can define an one-parameter family of linear operators:

$$\mathcal{L}_\lambda = L_1 + M_{11} + M_{12}(\lambda I - M_{22})^{-1}M_{21}, \quad \forall \lambda > s(M_{22}).$$

Theorem 2.1 Let (D) hold and assume that $M(x)$ is cooperative for all $x \in \overline{\Omega}$ and for any $\lambda > s(M_{22})$, there exists some $x_\lambda \in \Omega$ such that $M_{11}(x_\lambda) + M_{12}(\lambda I - M_{22})^{-1}M_{21}(x_\lambda)$ is irreducible. If there exist $\lambda_0 > s(M_{22})$ and $\phi_0 > 0$ in Y_1 such that $\mathcal{L}_{\lambda_0}\phi_0 \geq \lambda_0\phi_0$, then the following statements are valid:

(i) $s(B)$ is a geometrically simple eigenvalue of (2.1) with a positive eigenvector.

(ii) $s(B)$ is the unique $\lambda \in (s(M_{22}), \infty)$ with $s(\mathcal{L}_\lambda) = \lambda$.

(iii) $s(B)$ has the same sign as $s(\mathcal{L}_0)$ provided that $s(M_{22}) < 0$.

Outline of the proof

For any $\lambda > s(M_{22})$, let $T_\lambda(t)$ be the semigroup generated by $\mathcal{L}_\lambda$ and define $\mu(\lambda) := s(\mathcal{L}_\lambda)$.

Step 1. Prove that $\mu(\lambda) = \lambda$ has a unique solution $\lambda^* \geq \lambda_0$, and that λ^* is an eigenvalue of B with a positive eigenvector, and hence, $s(B) \geq \lambda^*$ and $s(B) \in \sigma(B)$.

Step 2. Prove that $\lambda I - B$ is semi-Fredholm for all $\lambda > \lambda^*$.

Step 3. Prove that $s(B) = \lambda^*$ by a way of contradiction and a preliminary result on semi-Fredholm operators.

Remark 2.1 Theorem 2.1 is still valid if the condition $\mathcal{L}_{\lambda_0}\phi_0 \geq \lambda_0\phi_0$ is replaced with a weaker assumption that $u(t,x) := e^{\lambda_0 t}\phi_0(x)$ is a sub-solution of the integral form of the linear system $u_t = \mathcal{L}_{\lambda_0}u$. This is because we only need these conditions to guarantee $\mu(\lambda_0) \geq \lambda_0$ in the proof of Theorem 2.1.

Corollary 2.1 Let (D) hold and assume that $M(x)$ is cooperative for all $x \in \overline{\Omega}$ and $M_{11}(x_0)$ is irreducible for some $x_0 \in \Omega$. If $s(L_1 + M_{11}) > s(M_{22})$, then three statements in Theorem 2.1 hold true.

Remark 2.2 If we replace $-L_1$ with uniformly elliptic operators of second order and use Dirichlet or Robin type boundary conditions in (2.1), then Theorem 2.1, Remark 2.1, and Corollary 2.1 are still valid.

Remark 2.3 If we replace $-L_1$ with spatially periodic and uniformly elliptic operators of second order and use the periodic boundary condition in (2.1) with $\Omega = \mathbb{R}$, then Theorems 2.1, Remark 2.1, and Corollary 2.1 are still valid.

Basic reproduction number R_0

Consider the reaction-diffusion epidemic model described by

$$\begin{aligned} \frac{\partial u_i}{\partial t} &= \nabla \cdot (d_i(x)\nabla u_i) + f_i(x,u), \quad 1 \le i \le n, \\ \frac{\partial u_i}{\partial \nu} &= 0, \quad \forall\, 1 \le i \le n \text{ with } d_i > 0, \quad t > 0,\ x \in \partial\Omega, \end{aligned} \tag{3.1}$$

where u_i is the density of a population in compartment i, $d_i(x)$ is the diffusion coefficient of population u_i, f_i is the reaction term in compartment i under the influences of demographic process and epidemic interactions, Ω is the spatial habitat in $\mathbb{R}^l$ with smooth boundary $\partial\Omega$, ν denotes the unit normal vector on $\partial\Omega$, and the no-flux boundary condition means that no individuals cross the boundary. We emphasize that some diffusion coefficients may be zero on Ω.

Let $u = (u_1, \ldots, u_n)^T$, with each $u_i \geq 0$, be the state of individuals in all compartments. We assume that they can be divided into two types: infected compartments, labeled by $i = 1, \ldots, m$, and uninfected compartments, labeled by $i = m+1, \ldots, n$. Define U_s to be the set of all disease-free states:

$$U_s := \{u \geq 0 : \ u_i = 0, \forall\, i = 1, \ldots, m\}.$$

Let $\mathcal{F}_i(x, u)$ be the input rate of newly infected individuals in the ith compartment, $\mathcal{V}_i^+(x, u)$ be the rate of transfer of individuals into compartment i by other means (for example, births, immigrations), and $\mathcal{V}_i^-(x, u)$ be the rate of transfer of individuals out of compartment i (for example, deaths and recovery). Thus, the model (3.1) can be rewritten as

$$\begin{aligned} &\frac{\partial u_i}{\partial t} = \nabla \cdot (d_i(x)\nabla u_i) + \mathcal{F}_i(x, u) - \mathcal{V}_i(x, u),\ 1 \leq i \leq n, \\ &\frac{\partial u_i}{\partial \nu} = 0,\ \forall\, 1 \leq i \leq n \text{ with } d_i > 0, \quad t > 0,\ x \in \partial\Omega, \end{aligned} \tag{3.2}$$

where $\mathcal{V}_i = \mathcal{V}_i^- - \mathcal{V}_i^+$.

We make the following assumptions:

(A1) For each $1 \leq i \leq n$, functions $\mathcal{F}_i(x,u), \mathcal{V}_i^+(x,u), \mathcal{V}_i^-(x,u)$ and $d_i(x)$ are nonnegative and continuous on $\overline{\Omega} \times \mathbb{R}_+^n$ and continuously differential with respect to u.

(A2) If $u_i = 0$, then $\mathcal{V}_i^- = 0$. In particular, if $u \in U_s$, then $\mathcal{V}_i^- = 0$ for $i = 1, \ldots, m$.

(A3) $\mathcal{F}_i = 0$ for $i > m$.

(A4) If $u \in U_s$, then $\mathcal{F}_i = \mathcal{V}_i^+ = 0$ for $i = 1, \ldots, m$.

Note that (A1) arises from the simple fact that each function denotes a directed non-negative transfer of individuals. Biologically, (A2) means that there is no transfer of individuals out of a compartment if the compartment is empty; (A3) indicates that there is no infection for uninfected compartments; (A4) implies that the population will remain free of disease if it is free of disease at the beginning.

We assume that system (3.2) admits a disease-free steady state

$$u^0 = (0, \dots, 0, u^0_{m+1}(x), \dots, u^0_n(x))^T,$$

where $u^0_i(x) > 0, m+1 \le i \le n$ for all $x \in \Omega$. Set

$$u_I = (u_1, \cdots, u_m)^T, \qquad d_I(x) = (d_1(x), \cdots, d_m(x))^T,$$
$$u_S = (u_{m+1}, \cdots, u_n)^T, \qquad d_S(x) = (d_{m+1}(x), \cdots, d_n(x))^T,$$

and

$$\nabla \cdot (d_I(x)\nabla u_I) = (\nabla \cdot (d_1(x)\nabla u_1), \cdots, \nabla \cdot (d_m(x)\nabla u_m))^T,$$
$$\nabla \cdot (d_S(x)\nabla u_S) = (\nabla \cdot (d_{m+1}(x)\nabla u_{m+1}), \cdots, \nabla \cdot (d_n(x)\nabla u_n))^T,$$
$$f_I(x,u) = (f_1(x,u), \cdots, f_m(x,u))^T,$$
$$f_S(x,u) = (f_{m+1}(x,u), \cdots, f_n(x,u))^T.$$

Let

$$M^0(x) := \left(\frac{\partial f_i(x, u^0(x))}{\partial u_j} \right)_{m+1 \le i,j \le n}.$$

For the linear reaction-diffusion system

$$\begin{aligned} \frac{\partial u_S}{\partial t} &= \nabla \cdot (d_S(x)\nabla u_S) + M^0(x)u_S, \\ \frac{\partial u_i}{\partial \nu} &= 0, \quad \forall\, m+1 \le i \le n \text{ with } d_i > 0, \quad t > 0, \end{aligned} \tag{3.3}$$

we make the following assumption to ensure u^0 is linearly stable in the disease-free space.

(A5) $M^0(x)$ is cooperative for all $x \in \overline{\Omega}$ and $\lambda^0(M^0) := s(\nabla \cdot (d_S\nabla) + M^0) < 0$.

By assumptions (A1)-(A4), we can set

$$D_u\mathcal{F}(x, u^0(x)) = \begin{pmatrix} F(x) & 0 \\ 0 & 0 \end{pmatrix}$$

and

$$D_u\mathcal{V}(x, u^0(x)) = \begin{pmatrix} V(x) & 0 \\ J(x) & -M^0(x) \end{pmatrix},$$

where $F(x)$ and $V(x)$ are two $m \times m$ matrices defined by

$$F(x) = \left(\frac{\partial \mathcal{F}_i(x, u^0(x))}{\partial u_j} \right)_{1 \le i,j \le m}$$

and

$$V(x) = \left(\frac{\partial \mathcal{V}_i(x, u^0(x))}{\partial u_j} \right)_{1 \le i,j \le m},$$

respectively, and $J(x)$ is an $(n-m) \times n$ matrix. Note that (A1) and (A4) imply that $F(x)$ is non-negative.

Set $X_1 := C(\overline{\Omega}, \mathbb{R}^m)$ and $X_1^+ := C(\overline{\Omega}, \mathbb{R}^m_+)$. Let $T(t)$ be the solution semigroup on X_1 associated with the following linear reaction-diffusion system

$$\begin{aligned} \frac{\partial u_I}{\partial t} &= \nabla \cdot (d_I(x)\nabla u_I) - V(x)u_I, \\ \frac{\partial u_i}{\partial \nu} &= 0, \quad \forall\, 1 \le i \le m \text{ with } d_i > 0. \end{aligned} \tag{3.4}$$

Note that the internal evolution of individuals in the infectious compartments due to deaths and movements among the compartments is dissipative, and exponentially decays in many cases because of the loss of infective members from natural mortalities and disease-induced mortalities. Thus, we assume that

(A6) $-V(x)$ is cooperative for each $x \in \overline{\Omega}$, and $\lambda^0(-V) := s(\nabla \cdot (d_I \nabla) - V) < 0$.

Now we assume that the state variables are near the disease-free steady state u^0. Then we introduce the distribution of initial infection described by $\phi(x)$. Under the synthetical influences of mobility, mortality and transfer of individuals in infected compartments, the distribution of those infective members as time evolves becomes $T(t)\phi(x)$. Thus, the distribution of new infection at time t is $F(x)T(t)\phi(x)$. Consequently, the distribution of total new infections is

$$\int_0^\infty F(x)T(t)\phi(x)dt.$$

Define

$$L(\phi)(x) := \int_0^\infty F(x)T(t)\phi dt = F(x)\int_0^\infty T(t)\phi dt.$$

Then L is a continuous and positive operator which maps the initial infection distribution ϕ to the distribution of the total infective members produced during the infection period. This motivates us to define $R_0 := r(L)$.

Let $B := \nabla \cdot (d_I \nabla) - V$. By using the theory developed by Thieme (2009), we can prove the following result.

Theorem 3.1 Let (A1)-(A6) hold. Then the following statements are valid:

(i) $R_0 - 1$ has the same sign as $\lambda^* := s(B + F)$.

(ii) If $R_0 < 1$, then u^0 is asymptotically stable for system (3.2).

Theorem 3.2 Let (A1)-(A6) hold. Assume that there exists $d_0 > 0$ such that $d_i(x) \geq d_0$ for all $1 \leq i \leq m$. If the elliptic eigenvalue problem

$$
\begin{aligned}
&-\nabla \cdot (d_I(x)\nabla\phi) + V(x)\phi = \mu F(x)\phi, \qquad x \in \Omega,\\
&\frac{\partial \phi}{\partial \nu} = 0, \quad x \in \partial\Omega.
\end{aligned}
$$

admits a unique positive eigenvalue μ_0 with a positive eigenfunction, then $R_0 = r(-FB^{-1}) = r(-B^{-1}F) = 1/\mu_0$.

Proof. Use the Krein-Rutman theorem and the perturbation theory for linear operators.

In the case where some $d_i(x)$ are identically zero, we can reduce the computation of R_0 to that of the principal eigenvalue of a lower dimensional elliptic eigenvalue problem under additional conditions.

Without loss of generality, we assume that $d_I(x) = (d_1(x), \ldots, d_m(x))$ satisfies (D) with $k = m$, and then use the notations $\mathbf{u}_{i_1}$, $\mathbf{u}_{i_2}$, and $\nabla \cdot (\mathbf{d}_{i_1}(x)\nabla \mathbf{u}_{i_1})$ in section 2. We split two $m \times m$ matrices $F(x)$ and $V(x)$ into

$$F(x) = \begin{pmatrix} F_{11}(x) & F_{12}(x) \\ F_{21}(x) & F_{22}(x) \end{pmatrix}, \quad V(x) = \begin{pmatrix} V_{11}(x) & V_{12}(x) \\ V_{21}(x) & V_{22}(x) \end{pmatrix},$$

where F_{11} and V_{11} are $i_1 \times i_1$ matrices, F_{22} and V_{22} are $i_2 \times i_2$ matrices, and $i_1 + i_2 = m$. Then we have the following result.

Theorem 3.3 Let (A1)-(A6) hold and assume that $s(-V_{22}) < 0$. Let $B_1 := \nabla \cdot (\mathbf{d}_{i_1} \nabla) - V_1$, where $V_1 := V_{11} - V_{12}V_{22}^{-1}V_{21}$. Then the following statements are valid:

(i) If $F_{12} = 0$ and $F_{22} = 0$, then $R_0 = r(-B^{-1}F) = r(-B_1^{-1}F_1)$, where $F_1 = F_{11} - V_{12}V_{22}^{-1}F_{21}$.

(ii) If $F_{21} = 0$ and $F_{22} = 0$, then $R_0 = r(-B^{-1}F) = r(-B_1^{-1}F_2)$, where $F_2 := F_{11} - F_{12}V_{22}^{-1}V_{21}$.

Remark 3.1 If we replace the nonzero diffusion terms $-\nabla \cdot (d_i(x)\nabla)$ with uniformly elliptic operators of second order and use Dirichlet or Robin type boundary conditions, then Theorems 3.1, 3.2 and 3.3 are still valid.

The following result shows that the reaction-diffusion epidemic model in a spatially homogenous habitat with the Neumann boundary condition admits the same basic reproduction number as its ODE counterpart.

Theorem 3.4 If each d_i is a positive constant for $1 \leq i \leq m$, and $F(x) = F$ and $V(x) = V$ are independent of $x \in \overline{\Omega}$, then $R_0 = r(FV^{-1})$.

Proof. Use the perturbation theory for linear operators and the uniqueness of the principal eigenvalue.

An application

Now let us return to the spatial model of rabies:

$$\begin{aligned}
\frac{\partial E}{\partial t} &= \beta(x) I S - \sigma E - \left[b + (a-b)\frac{N}{K} \right] E, \\
\frac{\partial I}{\partial t} &= \frac{\partial}{\partial x}\left(D(x)\frac{\partial I}{\partial x} \right) + \sigma E - \alpha(x) I - \left[b + (a-b)\frac{N}{K} \right] I, \quad (4.1) \\
\frac{\partial S}{\partial t} &= (a-b) S \left(1 - \frac{N}{K} \right) - \beta(x) I S,
\end{aligned}$$

subject to the boundary condition $\left.\frac{\partial I}{\partial x}\right|_{x=0} = \left.\frac{\partial I}{\partial x}\right|_{x=1} = 0.$

Note that system (4.1) admits a disease-free steady sate $(0, 0, K)$. Thus, the matrices F and V become

$$F(x) = \begin{pmatrix} 0 & \beta(x)K \\ 0 & 0 \end{pmatrix}, \qquad V(x) = \begin{pmatrix} \sigma + a & 0 \\ -\sigma & \alpha(x) + a \end{pmatrix}.$$

We first consider the elliptic eigenvalue problem:

$$\begin{aligned} &-(\sigma + a)E + \beta(x)KI = \lambda E, \ x \in (0,1), \\ &\frac{d}{dx}\left(D(x)\frac{dI}{dx}\right) + \sigma E - (\alpha(x) + a)I = \lambda I, \ x \in (0,1), \\ &\frac{dI}{dx}\Big|_{x=0} = \frac{dI}{dx}\Big|_{x=1} = 0. \end{aligned} \tag{4.2}$$

Lemma 4.1 Problem (4.2) has a principal simple eigenvalue λ^* with a positive eigenfunction.

Proof. First construct a sub-solution, and then use Theorem 2.1.

Let R_0 be the basic reproduction number of system (4.1), as defined in section 3. Then we have the following observation.

Lemma 4.2 Let μ_1 be the unique positive eigenvalue of the following eigenvalue problem:

$$-\frac{d}{dx}\left(D(x)\frac{d\phi}{dx}\right)+(\alpha(x)+a)\phi=\mu\frac{\sigma K\beta(x)}{\sigma+a}\phi, \quad x\in(0,1),$$
$$\frac{d\phi}{dx}\Big|_{x=0}=\frac{d\phi}{dx}\Big|_{x=1}=0,$$

with a positive eigenfunction. Then $R_0=1/\mu_1$.

Proof. Use Theorem 3.3 (i).

The subsequent result implies that R_0 is a threshold value for the local stability of the disease-free equilibrium $(0, 0, K)$ of system (4.1).

Theorem 4.1 The following statements are valid:

(i) If $R_0 < 1$, then the disease-free steady state $(0, 0, K)$ is asymptotically stable for (4.1).

(ii) If $R_0 > 1$, then there exists $\epsilon_0 > 0$ such that any positive solution of (4.1) satisfies
$\limsup_{t\to\infty} \|(E(t,\cdot), I(t,\cdot), S(t,\cdot)) - (0, 0, K)\| \geq \epsilon_0$.

To explore the influences of heterogeneous spatial infections and population diffusion, we compute R_0 numerically (see Lemma 4.2).

Case 1. $K = 0.98, a = 0.0027, \alpha = 0.2, \sigma = 0.0357, D = 0.137,$ and $\beta(x) = 0.2192(1 + c_1 \cos(\pi x))$.

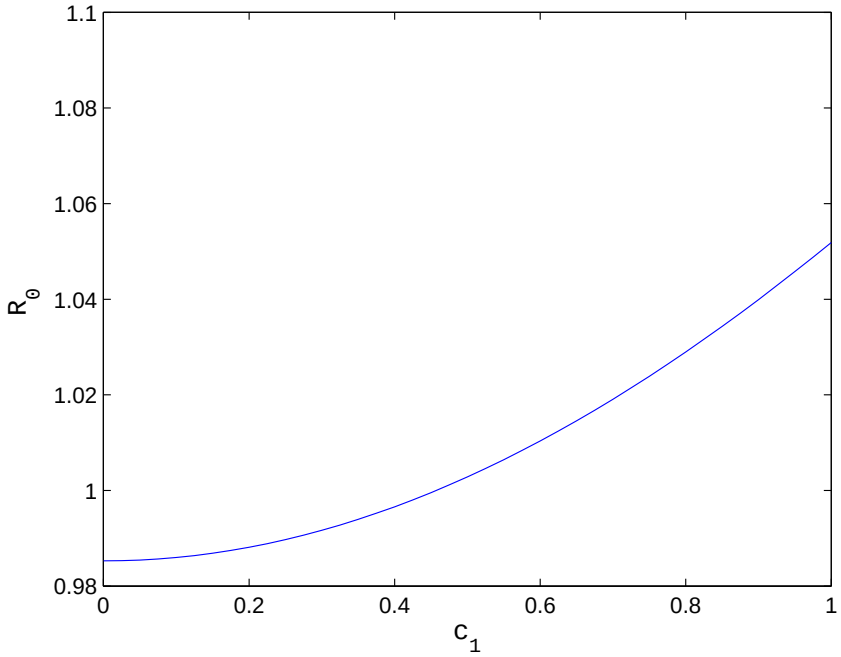

Figure: 1

R_0 is an increasing function of c_1. Thus, the spatially heterogenous infection can induce the persistence of disease.

Case 2. $K = 1.5, a = 0.0027, \beta = 0.2192(1 + \cos(\pi x)), \sigma = 0.0357, \alpha = 0.2(1 + \sin(\pi x))$ and $D = D_0(1 + \cos(\pi x))$.

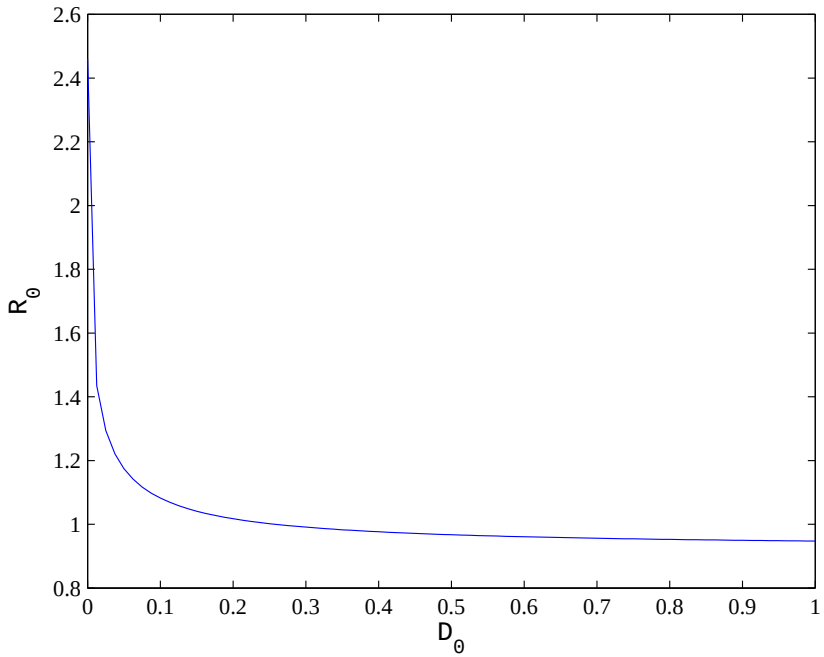

Figure: 2

R_0 decreases as D_0 increases.

Case 3. We consider the optimal vaccine strategy in spatially heterogenous environment. Fix

$$\beta(x) = 0.2192 \times 6x(1-x),$$

which has the highest infection coefficient at the center of spatial domain. Motivated by the fact that vaccine baits are distributed by aeroplane in practice, we suppose that the distribution of vaccine is described by

$$v_0(x) = \begin{cases} \frac{c_0}{L}, & \text{if} \quad 0 \le a_0 < a_0 + L \le 1, \\ 0, & \text{otherwise}, \end{cases}$$

where $c_0 > 0$ represents the total quantity of vaccine baits. With the introduction of vaccine, we assume that $\beta(x)$ is replaced by $\beta(x)(1-\eta(x))$, where $\eta(x)$ is the vaccine efficacy. For an illustrative purpose, we fix

$$\eta(x) = \frac{v_0(x)}{1+v_0(x)}.$$

We hope to minimize R_0 by selecting best a_0 and L for fixed c_0, which gives the optimal strategy of vaccine distribution.
Fixing $K = 3, a = 0.0027, \alpha = 0.2, \sigma = 0.0357$ and $D = 0.137$, numerical computations indicate that the minimum c_0 to drive R_0 below 1 is 0.18 where $a_0 = 0.23$ and $L = 0.54$ are chosen to obtain the lowest R_0 (see Figures 3 and 4).

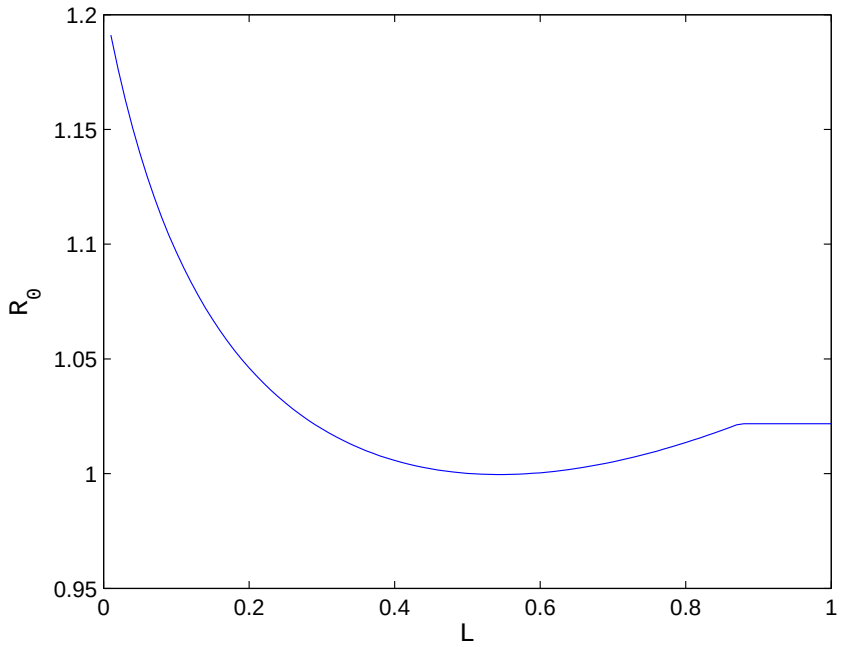

Figure: 3

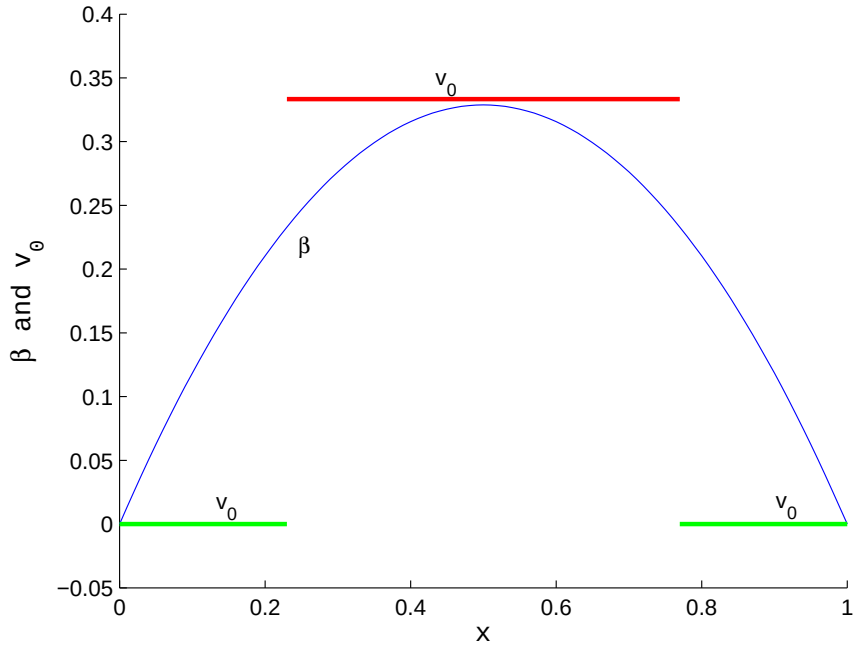

Figure: 4

Thank you!