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Fish-hook bifurcation branch in a spatial heterogeneous epidemic model with cross-diffusion

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ABSTRACT

In this paper, we consider the following strongly coupled epidemic model in a spatially heterogeneous environment with Neumann boundary condition:

$$\begin{cases} \Delta S + bS - (m + k(S+I))S - \beta(x)SI = 0, & x \in \Omega, \\ \Delta((1 + c\theta(x)S)I) + \rho bI - (m + k(S+I))I - \delta I + \beta(x)SI = 0, & x \in \Omega, \\ \partial_{\mathbf{n}} S = \partial_{\mathbf{n}} I = 0, & x \in \partial\Omega, \end{cases}$$

where $\Omega \subset \mathbb{R}^n$ is a bounded domain with smooth boundary $\partial\Omega$; b, m, k, c and δ are positive constants; $\beta(x) \in C(\bar{\Omega})$ and $\theta(x)$ is a smooth positive function in $\bar{\Omega}$ within $\partial_{\mathbf{n}}\theta(x) = 0$ on $\partial\Omega$. The main result is that we have derived the set of positive solutions (endemic) and the structure of bifurcation branch: after assuming that the natural growth rate $a := b - m$ of S is sufficiently small, the disease-induced death rate δ is slightly small, and the cross-diffusion coefficient c is sufficiently large, we show that the model admits a bounded branch Γ of positive solutions, which is a monotone **S**-type or fish-hook-shaped curve with respect to the bifurcation parameter δ. One of the most interesting findings is that the multiple endemic steady-states are induced by the cross-diffusion and the spatial heterogeneity of environments together.

1. Introduction

Since the pioneering work of Shigesada, Kawasaki and Teramoto [1], the strongly coupled elliptic system has received increasing attention. Many scholars have studied population models with cross-diffusion terms from various mathematical viewpoints [2–19]. For the existence of positive stationary solutions to cross-diffusion systems, by using the methods of the bifurcation theory and Lyapunov–Schmidt reduction,

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Kuto [12] studied a Lotka–Volterra predator–prey system with cross-diffusion and found that spatial heterogeneity could cause the bifurcation branch to form a bounded fish-hook curve; Wang and Li [16,17] studied the cooperative systems with cross-diffusion and obtained an unbounded fish-hook-shaped global bifurcation.

In the case where the coefficients of cross-diffusion are spatially homogeneous, some researchers paid their attention to the effect of cross-diffusion on the spread of epidemic diseases from various aspects, including the global existence of solutions and positive steady state problems [13,20–25]. However, little attention has been paid to the positive stationary solution of the epidemic model with cross-diffusion and the spatial heterogeneity of the environment.

In this paper, based on the model in [26], and motivated by [10–12,15–17,27], we will focus on the following cross-diffusion epidemic model in a spatially heterogeneous environment:

$$\begin{cases} \tau\partial_t S = \Delta S + bS - (m + k(S+I))S - \beta(x)SI, & x \in \Omega,\ t > 0, \\ \partial_t I = \Delta((1 + c\theta(x)S)I) + \rho bI - (m + k(S+I))I - \delta I + \beta(x)SI, & x \in \Omega,\ t > 0, \\ \partial_{\mathbf{n}} S = \partial_{\mathbf{n}} I = 0, & x \in \partial\Omega,\ t > 0, \\ S(x,0) = S_0(x) \geq 0, \qquad I(x,0) = I_0(x) \geq 0, & x \in \Omega, \end{cases} \tag{1}$$

where $S(x,t)$ and $I(x,t)$ represent the density of the susceptible and the infectious in the same habitat Ω, respectively. τ, b, m, k, c and δ are positive constants. b and m are the constant birth and death rates, $a := b - m > 0$ the natural growth rate of the susceptible, $(b-m)/k$ carrying capacity, $\delta > 0$ the disease-induced death rate. $\rho \in [0,1]$ is the reduction of growth rate due to the disease, and $\rho = 0$ means that the infectious lose their reproducing ability while $\rho = 1$ indicates that they experience no reduction in reproductive fitness. $\beta(x)SI$ is called the mass action (or density-dependent incidence). $\beta(x)$ is the disease transmission rate. τ indicates a degree of inactivity of the susceptible. The habitat Ω is a bounded domain in $\mathbb{R}^n$ with smooth boundary $\partial\Omega$; $\mathbf{n}$ is the outward unit normal vector on $\partial\Omega$ and $\partial_{\mathbf{n}} = \partial/\partial\mathbf{n}$. In addition, we require that $\beta(x), S_0(x), I_0(x) \in C(\bar{\Omega})$, and $\theta(x)$ is a smooth positive function in $\bar{\Omega}$ with $\partial_{\mathbf{n}}\theta(x) = 0$ on $\partial\Omega$. In what follows, we always assume that $a > b(1-\rho)$, i.e., $b\rho - m > 0$.

It should be emphasized that the nonlinear diffusion $c\Delta(\theta(x)SI)$ in the second equation of model (1) yields an important term from both pure mathematical and ecological aspects (see [2] for the ecological background). It is usually referred to as the cross-diffusion term, which was first proposed to model the inter- and intra-specific influence on the competitive population system by Shigesada et al. [1]. From the ecological viewpoint, cross-diffusion expresses that the population flux of a given subpopulation is affected by the presence of other subpopulations [13]. In an epidemiological perspective, the diffusion of individuals may be connected with other things, such as escaping high infection risks [23]. One can see that

$$\Delta\Big(c\theta(x)SI\Big) = c\nabla \cdot [\theta(x)S\nabla I + I\nabla(\theta(x)S)],$$

where $\theta(x)$ is known as the cross-diffusion pressure, which means a tendency that I diffuses to the low density region of $\theta(x)S$, and moreover the tendency depends not only on the population pressure of S but also on the heterogeneity of the environments. In the homogeneous case that $\theta(x)$ is a positive constant, model (1) involves an escape tendency such that infectious I diffuses from high density area of susceptible S towards low-density area of S. In the heterogeneous case when $\theta(x)$ is a positive function, the term $\Delta(c\theta(x)SI)$ describes a situation in which infectious I diffuses to the low-value area of $\theta(x)S$, and the cross-diffusion coefficient c represents the sensitivity of the infectious I to population pressure from the susceptible S. In this sense, $\theta(x)$ yields a certain environment function which indicates an easiness of escape tendency of the infectious.

Furthermore, we can see that the diffusive flux of the infectious I is

$$\mathbf{J} = -\nabla\Big((1 + c\theta(x)S)I\Big) = -cI\nabla\Big(\theta(x)S\Big) - \Big(1 + c\theta(x)S\Big)\nabla I, \tag{2}$$