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# A vector–host epidemic model with spatial structure and age of infection

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## ABSTRACT

In this paper we study a diffusive age structured epidemic model with disease transmission between vector and host populations. The dynamics of the populations are described by reaction–diffusion equations, with infection age structure of the host population incorporated to account for incubation periods. The disease is transmitted between vector and host populations in crisscross fashion. The existence of solutions of the model is studied by operator semigroup methods, and the asymptotic behavior of the solution is investigated.

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## 1. Introduction

The objective of this paper is to analyze a spatial vector–host epidemic model. The model accounts for the random movement of the vector and host population in geographic regions, and the infection age-structure of the infected host population. Many diseases are transmitted to human by vectors, such as mosquito-borne diseases malaria, dengue, Zika and bug-borne Chagas. Such diseases are transmitted in a crisscross fashion: infected vectors transmit the disease to susceptible hosts, while susceptible vectors become infected through interactions with infected hosts. Crisscross models for the circulation of diseases between vectors and hosts have been proposed and studied by many researchers in the past. For example, in [1,2] the authors studied the spread of malaria, and in [3–5] the authors studied the spread of Chagas disease by crisscross models.

The vector and host populations are assumed to be confined in non-coincidental geographic regions. In particular we assume that the region of the vector population is contained in the region of the host population. The dispersal of individuals inside the regions is described by spatial diffusion terms with different diffusion

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rates for vector and host populations. We note that diffusion has been used to model the spatio-temporal spread of disease by a variety of authors [6–10].

After the susceptible hosts are infected with the disease, they are usually asymptomatic for a certain amount of time before becoming symptomatic and infectious. The incubation or non-infectious period of many vector–host diseases is appreciable longer than the time it takes for an individual to travel from one place to another. Indeed an outbreak in one locale could spread silently and globally via infected travelers, only be recognized days or even weeks later [11]. In order to incorporate the incubation period of the disease into the model, the host population is assumed to be structured by disease age [12]. We note that the theory of age-structured population models has been well-developed recently [13,14]. Epidemic models with diffusion and age-structure are studied in [15–18]. For a review of diffusive age-structured models, we refer the readers to [19].

Our goal is to understand how an infectious disease arises and spreads through vector–host populations in a geographical setting. Our model formulation assumes that diffusion describes the movement of individuals, both vectors and hosts, within this geographical region. This assumption is an idealization, since the movement of both vectors and hosts, particularly hosts, may be extremely complex. We argue, however, that the geographical spread of an epidemic, particularly from an initial small local outbreak, can be modeled by random diffusive processes. In this context diffusion indirectly models the average spatial spread of the underlying micro-biologic infectious agent (viral, bacterial, parasitic), rather than the local-time movement of hosts and vectors. The infectious agent exists within the host and vector populations, and is not modeled directly. Reaction–diffusion mechanisms indirectly describe the way this infectious agent spreads in space and time within these populations.

Our paper is organized as follows: we propose the vector–host model in the next section, which includes a system of reaction–diffusion equations for the vector population and a system with diffusion and age-structure for the host population; in Section 3, we study the global existence of solution of the model using analytic semigroup to represent solutions of the diffusive age-structured equation; in Section 4, we investigate the asymptotic behavior of the solution and prove that the solution always converges to the steady state.

## 2. The model

We assume that infected hosts are initially located in a small area of much larger host habitat. Essentially the infected hosts act as vectors introducing the disease to the region. This input corresponds to the disembarkation of infected travelers from a ship, plane or other means of conveyance. We also assume that the vector and host habitats are non-coincident with the vector habitat being a smaller sub-region of the larger host habitat. Recent works on the transmission of disease between species with non-coincident habitats include [20–22]. A salient feature of our consideration will be a noninfectious period of asymptomatic incubation of the virus in host. The incubation period complicates any effort to prophylactically screen for the infection at points of embarkation and disembarkation. We assume that the virus has no deleterious effect on the vectors and that the vectors become immediately infective upon contact with infected infectious hosts with no period of incubation. The virus is assumed to be non-lethal and of relatively short duration in the host and for this reason demographic considerations for the hosts will not be included in the model.

We assume that our host population remain confined to a geographic region  $\Omega \subset \mathbb{R}^2$ . In particular we assume that  $\Omega$  is a bounded domain in  $\mathbb{R}^2$  with smooth boundary  $\partial\Omega$ . The vector population is assumed to inhabit and remain confined to a bounded subdomain  $\Omega_* \subset \Omega$ , where  $\partial\Omega_*$  is smooth with  $\partial\Omega \cap \partial\Omega_* = \emptyset$ . The time-evolving spatial dependent density of the total vector population is denoted by  $T_v(x, t)$ . We assume that the vector population disperses by means of Fickian diffusion with flux term  $-d_1(x)\nabla T_v$  and further require that  $d_1(x) \geq d$  for a positive number  $d_*$ . The confinement of the vector population to  $\Omega_*$  translates as the Neumann boundary condition  $d_1(x)\partial T_v/\partial\eta = 0$  for  $x \in \partial\Omega_*$ , where  $\eta$  denotes the unit outward

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