A nonlocal spatial model for Lyme disease ☆

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Abstract

This paper is devoted to the study of a nonlocal and time-delayed reaction–diffusion model for Lyme disease with a spatially heterogeneous structure. In the case of a bounded domain, we first prove the existence of the positive steady state and a threshold type result for the disease-free system, and then establish the global dynamics for the model system in terms of the basic reproduction number. In the case of an unbound domain, we obtain the existence of the disease spreading speed and its coincidence with the minimal wave speed. At last, we use numerical simulations to verify our analytic results and investigate the influence of model parameters and spatial heterogeneity on the disease infection risk.
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Keywords: Lyme disease; Basic reproduction number; Disease-free dynamics; Global stability; Propagation phenomena

1. Introduction

Lyme disease is a worldwide vector-borne infection caused by the spriochete bacterium *Borrelia burgdorferi*, whose primary vector in North America is the black-legged tick (also known as Ixodes scapularis). The black-legged tick normally has a two-year life cycle including three feeding stages: larva, nymph and adult. In those stages, ticks could acquire blood meals from a variety of hosts like rodents and mammals. In particular, larvae and nymphs mainly feed on white-footed mouse *Peromyscus leucopus*, and adult ticks obtain blood meals almost exclusively

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from the white-tailed deer *Odocoileus virginianus* [3]. Since nymphs are too tiny (less than 2 mm) to detect, humans may carry Lyme disease through the bites of infectious nymphs. For more biological discussions about the infection of Lyme disease, we refer to [1,22,19,14,29,13] and references therein.

To understand the invasion of Lyme disease, many mathematical modeling efforts are made through investigating the tick and host populations dynamics [11,21,9,25,18]. More specifically, Caraco et al. [4] proposed a reaction–diffusion model to study the effects of the tick's stage structure on the spatial expansion of Lyme disease in the northeast United States. The global dynamics and the spreading speed were obtained in [37] for the spatial model of [4]. To take the climate changes into account, Ogden et al. [23,24] presented simulation models, Wu et al. [33] established a temperature-driven map of the basic reproduction number of Lyme disease in Canada, and Zhang and Zhao [34] modified the model in [4] to a reaction–diffusion system with seasonality and studied its global dynamics and propagation phenomena. Note that the spatially homogeneous environment is basically assumed in these works, but the spatial heterogeneity is also vital. Geographic variations of food resources and climates could limit the activity and the population size of ticks and hosts. Biological studies [2,15] show that spatial patterns of the disease are highly linked to the spatial configurations coupled with dispersal by vertebrates like mice. Furthermore, there are few mathematical models incorporating the spatial variation to estimate the Lyme disease risk. The patch models presented in [2,12] considered the tick population dynamics with the dispersal of ticks on vertebrate hosts among multiple habitats, or between woodland and pasture, both of which are based on the assumption that the interactions are homogeneous in every habitat. To formulate a continuous-time model of Lyme disease including spatially dependent parameters, Wang and Zhao [32] took the model of Carco et al. [4] as a basis and adapted it in the following aspects:

(a) allow a spatial-dependent carrying capacity of hosts (mice), spatial-dependent diffusion rates of hosts and disease transmission coefficients;
(b) consider the influence of deers on disease transmissions;
(c) replace the random mobility of ticks in [4] with nonlocal terms to reveal the spatial movements of larvae, nymphs and adult ticks determined by their hosts (mice or deers).

Indeed, they proposed a nonlocal reaction–diffusion model and introduced the basic reproduction number R_0 of Lyme disease and revealed that R_0 can be a threshold value to describe the extinction and persistence of Lyme disease evolution under some appropriate assumptions. They also obtained a threshold result on the global dynamics in the case where the host diffusion rates and the carrying capacity of mice are constants.

The purpose of the present paper is to adopt the nonlocal spatial model in [32] by incorporating the self-regulation mechanism for the tick population as discussed in [3], and to study the spatial dynamics of Lyme disease while keeping the spatially heterogeneous structure of the model system. To be specific, we consider the Lyme disease transmission in a bounded habitat $\Omega \subset \mathbb{R}^2$ with a smooth boundary $\partial\Omega$. Let $\Gamma(t, x, y, D)$ be the Green function associated with the linear parabolic equation:

$$\frac{\partial u}{\partial t} = \nabla \cdot (D(x)\nabla u), \ t > 0, x \in \Omega,$$

$$\frac{\partial u}{\partial \nu} = 0, \ t > 0, x \in \partial\Omega,$$