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Preface

Special issue: Spatial dynamics for epidemic models with dispersal of organisms and heterogenity of environment

Guest Editors: Arnaud Ducrot, Shigui Ruan and Zhi-Cheng Wang

In the study of transmission dynamics of infectious diseases, there is an increasing interest on employing mathematical models with spatial effects. It is well-known that environment heterogeneity and spatial-temporal movement of organisms have a profound impact on the dynamics of epidemic models. It is therefore very important to investigate the dynamics of epidemic models with spatial effects. This special issue of Mathematical Biosciences and Engineering is devoted to the studies on the spatial dynamics of epidemic models involving movement of organisms and heterogeneity of environment. It contains 14 peer-reviewed papers and covers a very broad spectrum of topics in the area of epidemic models with heterogenous environment.

Some studies concentrate on classical epidemic models such as SIRS epidemic models with ratio-dependent incidence rate (Zhang et al.), edge-based SEIR models for sexually transmitted diseases (Huo et al.); reaction-diffusion SIS epidemic models with linear source (Suo and Li); and diffusive SIS epidemic models with saturated incidence rate (Wang et al.). Some authors focus on models derived from studying specific diseases. Ratchford and Wang formulate a multi-group multi-scale mathematical model to study the between-host and within-host dynamics of cholera; Huang et al. analyze a HBV model which incorporates the spatial variations of free antibody, virus-antibody complexes, and free virus; Qiang et al. propose a dynamic model of pathogenesis of Kawasaki disease.

Some infectious diseases spread gradually in space, so fixed domains are not suitable to describe the gradual expanding process. In this issue, some authors use epidemic models with free boundaries to characterize such a gradual spreading process. Ding et al. are concerned with the free boundary problem for a reaction-diffusion SIRI model with relapse and bilinear incidence rate; Zhao et al. investigate the effect of small advection on the propagation dynamics of epidemic models with free boundary. In considering the impact of changing habitats on disease control, Pu and Lin study a diffusive SIS epidemic model with periodically evolving domain. Lupica et al. examine the effects of some different structures of information on the dynamics of vaccine uptake in absence of the infection; Zhu et al. consider a class of reaction-diffusion SVIR model which includes the factors of disease relapse and vaccination. Moreover, Lin et al. estimate the spreading speeds in diffusive epidemic models with nonlocal delays, nonlinear incidence rate and constant recruitment rate; Hsu et al. focus on the existence and stability of traveling wavefronts for competitive-cooperative systems with three species. The variety of mathematical and biological results makes this issue a significant contribution in mathematical biology, in particular on spatial dynamics of biological and epidemiological models. We hope that the readers will find useful information for their own research. We would like to thank all authors for their valuable contributions and all referees for their great efforts and valuable comments. Finally, we thank the Editor-in-Chief of MBE, Professor Yang Kuang, and the Editor Assistant, for their professional and technical support and for making this special issue possible.

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