Editorial

Advanced Nonlinear Dynamics of Population Biology and Epidemiology

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Modern biology and epidemiology have become more and more driven by the need of mathematical models and theory to elucidate general phenomena arising from the complexity of interactions on the numerous spatial, temporal, and hierarchical scales at which biological systems operate and diseases spread. Epidemic modeling and study of disease spread such as gonorrhea, HIV/AIDS, BSE, foot and mouth disease, measles, and rubella have had an impact on public health policy around the world which includes the United Kingdom, The Netherlands, Canada, and the United States. A wide variety of modeling approaches are involved in building up suitable models. Ordinary differential equation models, partial differential equation models, delay differential equation models, stochastic differential equation models, difference equation models, and nonautonomous models are examples of modeling approaches that are useful and capable of providing applicable strategies for the coexistence and conservation of endangered species, to prevent the overexploitation of natural resources, to control disease's outbreak, and to make optimal dosing polices for the drug administration, and so forth.

This special issue is concerned with the nonlinear dynamic modeling and related analysis of interacting populations and important epidemic diseases. All papers submitted to this special issue went through a thorough peer-refereeing process. Based on the reviewer's reports, we collect 50 original research articles by more than 100 active international researchers on differential equations. In the following, we briefly review each of the papers by highlighting the significance of the key contributions.

Twenty papers are concerned about the disease dynamics of differential equations on time scales. N. Wang et al. study the global stability of a multigroup SEIR epidemic model with general latency distribution and general incidence rate and define the basic reproduction number R_0 as the role of a threshold. L. Feng et al. present a mathematical model which combines the scale-free trait of Internet with the formation of P2P botnet and demonstrate that the model has a globally stable endemic equilibrium when the infection rate is greater than a critical value. C. Liu et al. establish a hybrid SIR vector disease model with incubation and show that there is a phenomenon of singularity inducing bifurcation as well as local stability switch around interior equilibrium when the economic interest increases forward zero. L. Qi et al. establish a mathematical model of schistosomiasis transmission under flood in Anhui province, China, and show that the disease-free equilibrium is locally asymptotically stable if the basic reproduction number is less than one, and the stability of the unique endemic equilibrium may be changed under some conditions even if the basic reproduction number is larger than one. J. Wang et al. analyze the impact of seasonal activity of psyllid on the dynamics of Huanglongbing (HLB) infection and establish a new model about HLB transmission and show that if $R_0 < 1$, the disease-free periodic solution is globally asymptotically stable while if $R_0 > 1$ the disease persists. F. Wang et al. present an estimating formula for hospital potential capacity and demonstrate that the formula is useful to estimate the basic reproduction number in epidemiology. The results may contribute to the improvement of decision-making in the allocation of medical resources and