



Preface

Special Issue: Mathematical modeling and analysis of social and ecological determinants for the dynamics of infectious diseases and public health policies

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Mathematical modeling of infectious diseases dynamics is a powerful tool that has been used to study the driving and adaptive mechanisms of how diseases spread, predict the future course of an outbreak, and evaluate the effectiveness of control strategies of an epidemic. Through this special issue, we seek to collect cutting-edge articles that optimize and identify the cost-effectiveness of public health interventions including vaccination, drug treatment, and other control strategies. Interdisciplinarity and data-driven mathematical modeling approaches are the key in these articles which not only address public health challenges for a wide range of infectious diseases but also help in developing and advancing policies to prevent, detect, and control infectious diseases in resource-limited settings. Investigations of model features and mechanisms, including qualitative or quantitative analysis of model dynamics, parameter sensitivity analysis, intensive data analysis for parameterization and for patterns from model outputs, and numerical schemes for complex model simulations will provide a deeper understanding of disease dynamics and reliable prediction for disease transmissions. Temporal and spatial components, age and stage structures, different transmission mechanisms within and between humans and vectors, environmental factors, pertaining to the adaptive biological systems will be explored. The authors present their work on a range of topics such as modeling and control of COVID-19, Zika virus, invasive nontyphoidal *Salmonella* (iNTS), hepatitis C virus (HCV), human papillomavirus (HPV), a multi-host human-rodent model for plague, and the impacts of literacy and social media on the dynamics of infectious diseases. Finally, a review paper on

quantitative characterization of animal social organization with applications for epidemiological modeling is provided.

He et al. presented a stochastic discrete-time epidemic model to evaluate the risk of COVID-19 resurgence by analyzing the data from the beginning of the outbreak to the second wave in these three places. They discovered that to prevent the occurrence of a future wave, timely screening and detection are needed to identify infected cases in the early stage of infection. When infected cases appear, various measures such as contact tracing and quarantine should be followed to reduce the size of the susceptible population in order to mitigate the COVID-19 outbreak. Borowiak et al. focused on using mathematical models to evaluate strategies to suppress the spread of the virus on campus, specifically in dorms and in classrooms. For dorms, they show that giving students single rooms rather than double rooms could substantially reduce virus spread. For classrooms, they show that moving classes with size above some cutoff online could make the basic reproduction number $R_0 < 1$, preventing a widespread epidemic. Sharma et al. used their model to fit available data for some European countries. A more detailed model with two different subclasses of susceptible individuals was introduced to study the influence of social interaction on disease progression. They used the coefficient of social interaction K to characterize the level of social contacts in comparison with complete lockdown ($K = 0$) and the absence of lockdown ($K = 1$). The fitting of data shows that the actual level of this coefficient in some European countries is about 0.1, characterizing a slow disease progression. A slight increase of this value in the autumn can lead to a strong epidemic burst.

Yue et al. established a Zika virus model and investigated the transmission dynamics of the Zika virus with two types of harvesting: proportional harvesting and constant harvesting. They find that the proportional harvesting strategy can eliminate the virus when the basic reproduction number R_0 is less than 1, but the constant harvesting strategy may control the virus whether the basic reproduction number is less than 1 or not. Epidemiologically, they find that increasing harvesting may stimulate an increase in the number of virus infections at some point, and harvesting can postpone the peak of disease transmission with the mortality of mosquitoes increasing. Endo and Nishiura reanalyzed surveillance data of Zika virus infection during the outbreak on Yap island. Likelihood-based Bayesian inference was used to gauge the age and geographically dependent force of infection and age-dependent reporting rate, with unobservable variables imputed by the data augmentation method. Their results suggest a high degree of heterogeneity in the Yap epidemic. The symptomatic ratio in dengue cases is known to correlate with age, and their findings presumably indicate a similar tendency in Zika virus disease.

Zhuo et al. developed and analyzed a stage-progression compartmental model to study the emerging invasive nontyphoidal *Salmonella* (iNTS) epidemic in sub-Saharan Africa. The results indicate that the asymptomatic HIV+ adults without antiretroviral therapy (ART) serve as the driving force of infection for the iNTS epidemic. Their study indicates that the most effective strategies to reduce iNTS mortality in the studied population are to improve the ART coverage among high-risk HIV+ adults and reduce malnutrition among children.

Chatterjee et al. presented a mathematical model to study the dynamics of hepatitis C virus (HCV) disease with the aim to control the disease. Impulse periodic dosing with varied rate and time intervals is adopted for cost-effective disease control for finding the proper dose and dosing interval for the control of HCV disease.

Zhang et al. formulated a mathematical model to explore the transmission dynamics of human papillomavirus (HPV). They conducted sensitivity analysis to identify the factors that markedly affected HPV infection rates and proposed an optimal control problem to minimize vaccination and screening costs.

Rai et al. investigated the combined impacts of literacy and social media on the dynamics of infectious

diseases spreading through direct contact. The dissemination of awareness among literate people also suppresses the prevalence of limit cycle oscillations and drives the system to the disease-free zone. Their results evoke that media and education play a tremendous role in mounting awareness among the population leading to the elimination of the disease in society.

Chen and Yuan established a new multi-host mathematical model to reflect the transmission dynamics of plague with wild rodents, commensal rodents, and human beings, in which the roles of different species will no longer be at the same level. They analyzed the biological implications of the zoonotic model and then studied some biological hypotheses that had never been proposed or verified before.

Finally, in a review paper, Voelkl introduced network analysis as a tool to characterize the social organization of animal groups and populations. Then he focused on the application of this method for epidemiological modeling, specifically the prediction of spreading patterns of pathogens in livestock and its potential for informing targeted surveillance and planning of intervention measures.

The variety of mathematical model- and data-driven biological results makes this issue a significant contribution in mathematical biology, in particular for the dynamics of infectious diseases and public health policies. We hope that the readers will find useful information for their own research and training others in the methods discussed in this special issue. 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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