



Editorial

Editorial: Mathematical foundations in biological modelling and simulation

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An excellent tool for comprehending the various mechanisms pertaining to biology is mathematical modeling and simulation. It aids in our comprehension of how to preserve ecosystems, halt the spread of infectious diseases, and ensure sustainability in the context of biosystems. Presenting some mathematical modeling and numerical research pertaining to issues in ecology, epidemiology, and evolutionary biology is the goal of this special issue.

We gather a total of seven research papers in this special issue by researchers with a variety of backgrounds and from diverse fields of mathematical modeling. All the research papers are focused on problems related to biology, especially ecology and epidemiology. This special issue covered a variety of fields related to mathematical modeling and simulation, which can be classified mainly into three aspects: epidemic modeling, evolutionary game dynamics, and ecological modeling.

First the special issue starts with a mathematical model that has multiple disease stages [1]. The model considers a general incidence rate, functions for death and immigration rates in all populations. It is shown that the eradication of the disease is impossible due to the constant flow of infected people. An example of a mathematical model of HIV/AIDS, where the population is divided into four stages of disease progression is presented to show the theoretical results and numerical simulations. Noffel and Dobrovolny used a mathematical model to fit data from challenge studies of respiratory syncytial virus (RSV) in healthy adults to quantify the effect of defective viral genomes (DVGs) [2]. It was found that the late onset of DVGs and prolonged DVG detection are associated with lower infection rates and higher clearance rates. This result is important for the potential use of DVGs as a therapeutic. Luebben et al. [3], studied different vaccination strategies that could have been implemented for the COVID-19 pandemic. A demographic epidemiological mathematical model based on differential equations was constructed to investigate the optimality of a variety of vaccination strategies under

limited vaccine supply. The mathematical model takes into account demographic risk factors such as age, comorbidity status and social contacts of the population. Numerical simulations were used to evaluate strategies. The results show the importance of designing an optimal vaccination strategy in order to save human lives.

Simelane et al. [4] presents the analysis of a nonlinear fractional model of tungiasis dynamics that considers the impact of public health education. The infected population is split into two subgroups; infected but unaware and infected but aware. The analysis shows that tungiasis can be contained when the reproduction number is less than one. Using numerical simulations, it is observed that public health education and treatment can reduce numbers of tungiasis-infected individuals. In the context of biological processes related to microbial food-web, Albargi et al [5] present a four-dimensional mathematical model for the anaerobic mineralization of phenol in a two-step microbial food-web. The model considers the concentrations of hydrogen and phenol. They considered a general class of nonlinear growth kinetics, instead of Monod kinetics. The stability analysis is carried out and it is shown that the system can have up to four steady states. Numerical simulations validating the obtained results are provided. In the context of population dynamics, Kadelka presents a very important topic related to epidemics such as contact networks. A new method to expand a given contact matrix to populations stratified by binary attributes with a known level of homophily is presented [6]. Moreover, using an epidemiological model, the effect that homophily can have on model dynamics is presented. A Python source code accounts for the presence of homophily with respect to binary attributes in contact patterns is provided. Finally, Sultana et al. [7], constructed a new mathematical model to investigate the effect of the introduction of an exposed stage for cats who become infected with the *T. gondii* parasite, but that are not still able to produce oocysts in the environment. The model considers a time delay to represent the duration of the exposed stage. The authors found conditions such that the toxoplasmosis disease becomes extinct. Numerical simulations are carried out to observe the impact that the time delay has on the dynamics of toxoplasmosis dynamics.

In conclusion, seven full length research articles related to a variety of biological processes are presented in this special issue in the context of mathematical modeling and simulation of various topics related to life sciences. We express our gratitude to every researcher who accepted our invitations and made contributions to this special edition. We appreciate the support on this topic from the MBE editorial team and all the referees.

References

1. M. C. Gómez, F. A. Rubio, E. I. Mondragón, Qualitative analysis of generalized multistage epidemic model with immigration, *Math. Biosci. Eng.*, **20** (2023), 15765–15780. <https://doi.org/10.3934/mbe.2023702>
2. Z. Noffel, H. M. Dobrovolny, Quantifying the effect of defective viral genomes in respiratory syncytial virus infections, *Math. Biosci. Eng.*, **20** (2023), 12666–12681. <https://doi.org/10.3934/mbe.2023564>
3. G. Luebben, G. González-Parra, B. Cervantes, Study of optimal vaccination strategies for early COVID-19 pandemic using an age-structured mathematical model: A case study of the USA, *Math. Biosci. Eng.*, **20** (2023), 10828–10865. <https://doi.org/10.3934/mbe.2023481>

4. S. M. Simelane, P. G. Dlamini, F. J. Osaye, G. Obaido, B. Ogbukiri, K. Aruleba, et al., Modeling the impact of public health education on tungiasis dynamics with saturated treatment: Insight through the Caputo fractional derivative, *Math. Biosci. Eng.*, **20** (2023), 7696–7720. <https://doi.org/10.3934/mbe.2023332>
5. A. H. Albargi, M. El Hajji, Mathematical analysis of a two-tiered microbial food-web model for the anaerobic digestion process, *Math. Biosci. Eng.*, **20** (2023), 6591–6611. <https://doi.org/10.3934/mbe.2023283>
6. C. Kadelka. Projecting social contact matrices to populations stratified by binary attributes with known homophily, *Math. Biosci. Eng.*, **20** (2023), 3282–3300. <https://doi.org/10.3934/mbe.2023154>
7. S. Sultana, G. González-Parra, A. J. Arenas, Dynamics of toxoplasmosis in the cat's population with an exposed stage and a time delay, *Math. Biosci. Eng.*, **19** (2022), 12655–12676. <https://doi.org/10.3934/mbe.2022591>



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