

Editorial

Preface for the Special Issue on Dynamical Models of Biology and Medicine

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Mathematical and computational modeling approaches in biological and medical research are experiencing rapid growth globally. This special issue intends to catch a glimpse of this exciting phenomenon. Areas covered include general mathematical methods and their applications in biology and medicine, with an emphasis on work related to mathematical and computational modeling of the complex dynamics observed in biological and medical research. Specifically, there are fourteen rigorously reviewed papers included in this special issue. These papers cover several timely topics in classical population biology, fundamental biology and modern medicine.

There are four papers in the general area of computational biology dealing with modeling liquid-solid-porous media seepage coupling, bacterial cell-to-cell communication, representation and characterization of DNA sequences and protein sequences, respectively. The work of Bai Li and Xiaoyang Li [1] demonstrates the importance of microcirculation load in a hemodynamic model and their model offers a possibility for the simulation of the dynamic adjustment process of the human circulation system, which may also generate clinical applications. The work of Chun Li et al. [2] presented a cell-based descriptor vector based on the idea of “piecewise function” to numerically characterize the DNA sequence. The utility of their approach was fully illustrated by the examination of phylogenetic analysis on four datasets. In another paper by Chun Li et al. [3], the authors constructed a high dimensional vector to characterize protein sequences. The application of their method on two datasets and the identification of DNA-binding proteins suggested the potential for their user-friendly method. Most noteworthy is the data-validated delay differential equation modeling work of Maria Barbarossa and Christina Kuttler [4] on bacteria communication in continuous cultures. They observed that for a certain choice of parameter values, the model system presented stability switches with respect to the delay. On the other hand, when the delay was set to zero, a Hopf bifurcation might occur with respect to one of the negative feedback parameters. This delay differential model system is capable of explaining and predicting the biological observations.

There are also four papers in the general area of mathematical ecology. The work of Zejing Xing et al. [5] deals with the coexistence of multiple populations species in the context of intraguild predation (IPG). IPG is an ecological phenomenon, which occurs when one predator species attacks another predator species with which it competes for a shared prey species. Their study shows that it is possible for the coexistence of three species aided by the influence of environmental noise. The other three papers involve deterministic differential equation models. The paper by Bing Li et al. [6] studies a simple but non-smooth switched harvest model. The authors established that when the net reproductive number for the predator was greater than unity, the system was capable of generating

rich dynamics. In addition to positive equilibrium due to the effects of the switched harvest, the model generated a saddle-node bifurcation, a limit cycle, and the coexistence of a stable equilibrium and an unstable circled inside limit cycle and a stable circled outside limit cycle. When the net reproductive number was less than unity, a backward bifurcation from a positive equilibrium occurred. In another paper, Wei Wang et al. [7] proposed a dynamic model describing the cultivation and flocculation of a microorganism that used two distinct nutrients (carbon and nitrogen). Their model also exhibited rich dynamics, including the existence of possibly five positive equilibria and the possibility of backward and forward bifurcations. In addition, the authors obtained some interesting global stability results of the positive equilibrium. While the aforementioned ecological modeling papers are theoretical, the paper by Michael Stemkovski et al. [8] focused on the validation of a model for green algae (*Raphidocelis Subcapitata*) growth and the implications for a coupled dynamical system with *Daphnia Magna*. They collected longitudinal data from three replicate population experiments of *R. subcapitata*. These data together with statistical model comparison tests and uncertainty quantification techniques allowed the authors to compare the performance of four models: The Logistic model, the Bernoulli model, the Gompertz model, and a discretization of the Logistic model.

There are five papers in the general area of mathematical medicine. In the paper by Urszula Ledzewicz and Helen Moore [9], a mathematical model for the treatment of chronic myeloid leukemia (CML) through a combination of tyrosine kinase inhibitors and immunomodulatory therapies was analyzed as a dynamical system for the case of constant drug concentrations. The model exhibited a variety of behaviors which resembled the chronic, accelerated and blast phases typical of the disease. This work provided qualitative insights into the system which should be useful for understanding the interaction between CML and the therapies considered here. In the paper by Sara Manzano et al. [10], the authors extended an existing mechano-electrochemical computational model and employed the extended model to analyze and quantify the effects of obesity on the articular cartilage of the femoral hip.

Their results suggested that people with obesity should undergo preventive treatments for osteoarthritis to avoid homeostatic alterations and, subsequent, tissue deterioration. Combination antiviral drug therapy improves the survival rates of patients chronically infected with hepatitis B virus by controlling viral replication and enhancing immune responses. To address the trade-off between the positive and negative effects of the combination therapy, Jonathan Forde et al. [11] investigated an optimal control problem for a delay differential equation model of immune responses to hepatitis virus B infection.

Their results indicated that the high drug levels that induced immune modulation rather than suppression of virological factors were essential for the clearance of hepatitis B virus. In the paper by Shinji Nakaoka et al. [12], the authors developed some mathematical models for the inflammation process using ordinary differential equations and delay differential equations. They investigated the complex microbial community dynamics via transcription factors, protease and extracellular cytokines. They found that large time delays in the activation of immune responses on the dynamics of those bacterial populations led to the onset of oscillations in harmful bacteria and immune activities. The mathematical model suggested the possible annihilation of time-delay-driven oscillations by therapeutic drugs. The paper by Javier Baez and Yang Kuang [13] was motivated and based on clinical data. They proposed and validated a novel type of mathematical model of androgen resistance development in prostate cancer patients under intermittent androgen suppression therapy. More specifically, they formulated and analyzed two mathematical models that aimed to forecast future levels of prostate-specific antigen (PSA). While these models were simplifications of an existing model, they fit data with similar accuracy and improved forecasting results. Their findings suggested that including more realistic mechanisms of androgen dynamics in a two-population model may improve androgen resistance timing prediction.

Last but not the least; this special issue also included a paper on modeling the distribution of wildfires by Jonathan Martin and Thomas Hillen [14]. Their model was based on detailed physical

processes. They systematically discussed the use and measurement of their model in fire spread, fire management and fire breaching.

While authors of these papers deal with very different modeling questions, they are all well motivated by specific applications in biology and medicine and employ innovative mathematical and computational methods to study their complex model dynamics. We hope that these papers provide timely case studies that will inspire many more additional mathematical modeling efforts in biology and medicine.

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