

Editorial

Mathematical Modeling and Dynamic Analysis of Complex Biological Systems

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From microscopic to macroscopic levels, mathematical and computational modeling of biological systems has gained increased importance over the years, as it allows getting insight into the system structure and a better understanding of the interplay between complex phenomena. The applications are numerous and include genetic regulatory networks, metabolic networks, ecosystems, bioeconomic systems, and epidemics.

The aim of this special issue is to present a collection of recent results in the above-mentioned areas of research, either at the conceptual (theoretical) level or in view of challenging applications in environmental sciences and the medical or biopharmaceutical sectors.

This special issue features 7 contributions as follows.

The paper titled “The Silent Cooperator: An Epigenetic Model for Emergence of Altruistic Traits in Biological Systems” explores how a cooperative behavior can be established in a spatially distributed population system. I. Hashem et al. present a simple model that captures two concepts from genetics which can explain how evolution overcomes the emergence problem, i.e., the establishment of an initial cluster of sufficient size to allow for a high frequency of intracooperator interactions. The first concept is that a gene may not express its phenotype except under specific environmental conditions, rendering it to be a “silent” gene. The second key idea is that a neutral gene, i.e., one that does not harm or improve an organism survival chances, can still spread through a population if it is physically near to another

gene that is positively selected. These two established genetic concepts, silent genes and genetic hitchhiking, could explain how a simple cooperative trait emerges in a biological system.

In their paper titled “Analytical Reduction of Nonlinear Metabolic Networks Accounting for Dynamics in Enzymatic Reactions,” C. L. Zazueta et al. consider nonlinear metabolic models where metabolic fluxes vary over time depending on the intracellular concentrations. Such metabolic models must be reduced and simplified so as to be calibrated and analyzed. Reducing these models of large dimension down to a model of smaller dimension is very challenging, especially when dealing with nonlinear metabolic rates. The authors propose a rigorous approach to reduce metabolic models using quasi steady state reduction based on Tikhonov’s Theorem. It is assumed that the metabolic network can be represented with Michaelis-Menten enzymatic reactions, with two time scales in the reactions, and that the system is excited with a continuous slowly varying input so that the system is never at steady state. The analysis proves that the metabolites which can accumulate reach higher concentrations than the fast metabolites.

An important class of biological networks, so-called bipartite, are characterized by two families of nodes, which can have interconnections between the two families, but not inside the same family. Gene-protein, host-pathogen, and predator-prey interactions are the basis of bipartite biological networks. Visualization is a powerful tool to explore and analyze bipartite networks, but the most common plots, such

as the bipartite graph and the interaction matrix, become confusing when working with large-size realistic biological networks. In the paper titled “A Structural Approach to Disentangle the Visualization of Bipartite Biological Networks,” J. Garcia-Algarra et al. have developed two new visualization ways that exploit the structural properties of the network to improve readability. Using a technique called k-core decomposition, which identifies groups of nodes that share connectivity properties, it is possible to build a plot based on information reduction, called polar plot, and another plot, called Ziggurat plot, which takes the groups as elementary blocks for spatial distribution. These plots provide two complementary views of the internal network structure. Their applications are described, as well as the underlying software which is provided in open source.

Citrus Huanglongbing (HLB), also known as citrus greening, is one of the most devastating diseases of citrus worldwide. In the paper titled “Dynamical Behavior of a Novel Impulsive Switching Model for HLB with Seasonal Fluctuations,” S. Gao et al. study a new model for the spread and control of HLB with seasonal fluctuations. Switching coefficients and switching control schemes are considered in this model, which represent the effect of pesticide spraying at specific times as well as the removal rate of infected symptomatic trees. The main purpose of the paper is to study the effects of switching control schemes on the dynamics of the model with periodic environment. The numerical results indicate that Spring and Autumn are the most effective seasons for spraying insecticide, and Winter is the optimum season for removing infected trees.

After a disease outbreak, recovered individuals constitute a large immune population. However, their immunity is waning in the long term and they may become susceptible again. Meanwhile, their immunity can be boosted by repeated exposure to the pathogen, which is linked to the density of infected individuals present in the population. In “Temporal Evolution of Immunity Distributions in a Population with Waning and Boosting,” M. V. Barbarossa et al. consider a hybrid system of equations of SIRS type, in which the immune population is structured by the level of immunity, whereas the susceptible and the infective populations are nonstructured. The authors investigate how different boosting mechanisms result in different immunity distributions. For a low average number of secondary infections, the solution converges to an endemic equilibrium for all the boosting mechanisms. In the situation of periodic disease outbreaks, the waveforms of immunity distributions are studied and visualized. The numerical results show that, observing the immune distribution or the dynamic of the immune population over time, one can reconstruct the underlying boosting mechanism.

In “Dynamical Analysis of Approximate Solutions of HIV-1 Model with an Arbitrary Order,” Asma et al. generalize an AIDS/HIV model to a fractional order system. The Laplace-Adomian decomposition method is applied to solve this fractional order HIV model, and the convergence of the method is discussed. It is shown, via simulation, that the proposed method is capable of computing approximate solutions with only a few terms.

It is well known that the harvest effort has a strong dynamic impact on predator-prey systems, which play a significant role in bioeconomic management. C. Liu et al. in their paper “Modeling and Dynamic Analysis in a Hybrid Stochastic Bioeconomic System with Double Time Delays and Lévy Jumps” introduce a predator-prey model incorporating two time delays, one representing a maturation delay of the prey and the other reflecting the fact that predator reproduction is not instantaneous but can be affected by a gestation delay. In addition, the prey and predator populations can be influenced by environmental stochastic fluctuations, which are modeled in the form of Gaussian white noises and Levy jumps. The authors first analyze the deterministic model, then its stochastic extension. Rigorous mathematical analysis of the models is provided, e.g., existence of solution, Hopf bifurcation, and stochastic stability. Finally, numerical simulations are carried out to show combined dynamic effects of double time delays and Levy jumps on the population dynamics. The sustainable development of commercially harvested population can be indirectly achieved by formulating relevant policy to regulate economic interest within some appropriate ranges.

Conflicts of Interest

The editors declare that they have no conflicts of interest regarding the publication of this special issue.

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