Mathematical Biosciences and Engineering

Preface

Special issue: Resource explicit population models

Guest editors: Yang Kuang, Angela Peace and Hao Wang

As human activities continue to alter environmental balances and nutrient cycles, it is becoming vital to understand how these changes can impact the environment and population dynamics. Biological processes depend explicitly on energy and elemental resources. This special issue presents timely biological and mathematical findings where resources quantities are explicitly incorporated into models that deepen our understanding of population dynamics. In this issue authors further the field as they shed light on the mathematical and physical properties in diverse biological systems spanning from controlled chemostat-type chambers to aquatic environments to terrestrial landscapes and cancer growth.

Controlled growth chambers such as chemostats have proven to be useful both empirically and theoretically to model microorganism systems. De Leenheer et al. present a two species chemostat model that investigates the interplay between corporation and cheating dynamics under a shared nutrient resource. Here, they show the possibility for the cooperator to outcompete the cheater if it can evolve important traits (i.e. uptake rate function, yield constant). Tsai and Wang also consider a two species chemostat model, however they incorporate light, as well as inorganic carbon limitation, which is often neglected in models. Here parameter scenarios can yield competitive exclusion or the co-existence of both species. Almocera et al. present chemostat models of microbial food web in the presence of parasitic fungi. Here, they explore the interesting interplay between small grazers and large phytoplankton, which only becomes available to grazers in the presence of parasitic fungi.

A number of authors include creative modifications to chemostat-type chambers to further explore the influence of resources on population dynamics. Yao presents a model with a turbidostat, which is a modified chemostat with feedback controlled dilution rates. The dynamics of a turbidostat model with Contois growth rate and a time delay are analyzed. Hsu et al. consider a self-cycling fermenter growth chamber. This hybrid system includes batch phases followed by partial draining and refilling with fresh medium once resources decrease bellow threshold values. Here, they use impulsive differential equations with state-dependent impulses to model the growth of a single population on two limiting essential resources in a self-cycling fermentor. Loladze presents additional extensions to the classical chemostat models by considering an iterative-chemostat with feedbacks between the supply of nutrients and biotic parameters. He uses an iterative-continuous modeling framework that retains the structure of classical ecological models within each iteration but accounts for nutrient feedbacks between iterations.

Many of these manuscripts in this special issue use the resource explicit modeling framework of Biological Stoichiometry, the study of the balance of energy and multiple chemical elements in living organisms. Stoichiometric modeling, a relatively young branch of mathematical biology, has been greatly expanded in recent decades, and population models inspired by biological stoichiometry have produced complex but strikingly realistic dynamical behaviors. A majority of stoichiometric modeling has been devoted to aquatic systems of planktonic primary producers and grazers. Several authors pursue this traditional setting with biological and mathematical advances to traditional models including extension with seasonality, spatial gradients, eco-toxicity, algae blooms, as well as stochastic and discrete modeling approaches.

Asik et al. present a stoichiometric producer-grazer model subject to seasonal variations in the producer's light-dependent carrying capacity. Such seasonal forcing can lead to complicated population dynamics, including periodic and quasi-periodic solutions. Song et al. also incorporate a seasonally driven light intensity into a stoichiometric producer model in order to predict and control harmful algal blooms. Ji et al. use a stochastic approach to explore algal booms with the formulation of a discrete Markov chain model that incorporates the effects of environmental random fluctuations and a time delay for nutrient microbial decomposition. Rana et al. extends a mechanistically formulated stoichiometric producer-grazer model to be spatially heterogeneous. Here, spatially tracking free nutrient yields qualitatively different behavior than previous works. Hassan et al. investigate concurrent stoichiometric and toxicological stressors in producer-grazer systems. Model analysis elucidates important consequences to toxicological dynamics under high nutrient conditions. Chen et al. formulate a discrete stoichiometric tritrophic food-chain model. Comparing their model to a corresponding continuous model they found the models can exhibit qualitatively different behaviors with the same parameter sets and discretization enlarges the parameter ranges for the existence of chaotic dynamics.

Alongside these more traditional aquatic applications, stoichiometric models have been implemented into resource-consumer dynamics in the terrestrial realm. Zhou et al. explore the effects of stoichiometric constraints on grassland ecosystems, incorporating both aboveground and belowground interactions. They formulate a regrowth-herbivore model and explore the effects of nutrition and light intensity on the dynamics of plant and herbivore biomass. Pell et al. explicitly incorporate nutrients into plant host-pathogen models that consider the dynamics of nutrient-limited virus production. Including nutrient mediated viral production into plant-pathogen interactions is used to untangle how nutrients impact pathogen dynamics. The iterative-continuous chemostat based models presented by Loladze has additional applications in terrestrial settings where seasonal leaf production and decomposition can be viewed as an iteratively continuous.

Often models with biological applications are motivated by observed phenomenon and functions are mechanistically formulated. An alternative approach, if one has the luxury of a quality data set, is to motivate model formulation with specific data and fitting techniques. A number of authors here use rich data sets to fit resource explicit models of populations dynamics. Phan et al. present cell population models within prostate cancer patients under intermittent androgen suppression therapy in order to study the treatment of resistance development. By comparing models driven by data they investigate the interplay and tradeoffs between available data and model complexity. The plant-pathogen systems developed by Pell et al. are also motivated and fit to a rich data set of virion production across nutrient gradients. Finally, the seasonal algal bloom model by Song et al. is validated with times series data of algal densities in the Bohai Sea.

Swain and Fagan construct a bacterial metabolic model with three trade-offs to uncover how substrate availability influences growth rate and to explain certain complex phenomena in modern- and paleo-ecosystems. This paper focuses on the dependence of bacterial physiological aspect on nutrients and substrates.

The biological and mathematical directions contained in this special issue shed light on how essential elements and resources and their interactions shape population dynamics across a wide variety of systems. These studies highlight the importance of explicitly incorporating resources in population dynamics as they often play vital roles in the predictive power of biological models.