Check for updates

OPEN ACCESS

EDITED BY Saurav Mallik, Harvard University, United States

REVIEWED BY Kasmika Borah, Cotton University, India Soumita Seth, Aliah University, India

*CORRESPONDENCE Raluca Eftimie Izaluca.eftimie@univ-fcomte.fr

RECEIVED 31 March 2023 ACCEPTED 30 May 2023 PUBLISHED 13 June 2023

CITATION

Eftimie R (2023) Editorial: Insights in mathematical biology 2022. *Front. Appl. Math. Stat.* 9:1197661. doi: 10.3389/fams.2023.1197661

COPYRIGHT

© 2023 Eftimie. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.

Editorial: Insights in mathematical biology 2022

Raluca Eftimie*

Laboratoire de Mathématiques de Besançon, Université de Franche-Comté, UMR CNRS 6623, Besançon, France

KEYWORDS

developments in mathematical biology, optimization, food production, neural networks and finite element, structured cell populations

Editorial on the Research Topic Insights in mathematical biology 2022

This Insights in Mathematical Biology Research Topic aimed to showcase some new developments and future research perspectives in the mathematical biology field. The three articles published in this topic are a very small sample of some of the current interests in mathematical biology, from the optimization of food production to the optimization of numerical simulations for complex mathematical models describing medical problems and the understanding of multi-scale molecular–cellular aspects in health and disease. These articles also emphasize some of the current approaches in mathematical biology that oppose single-scale vs. multi-scale models, simple vs. complex models, and fast vs. slow numerical simulations.

In the following, we briefly summarize these three papers.

O'Hare focused on maximizing food production in a sustainable manner. To investigate the competitive behavior between two different types of food producers (one where farmers harvest and make profit at the end of the season and a second one where farmers harvest and make profit continuously throughout the season), the author considered a simple individualbased framework. This framework was applied to 25 farms distributed on a spatial grid, which could interact with neighboring farms and produce food using either of the two food-producing systems. The interaction rule between the different farms was given by a simple algebraic equation that considered the distance between farms (which could belong to different farm networks: square grid, linear network, circular network, and random network) and the time since the farmers started to implement actions that could impact neighboring farms. The profit obtained by each farmer (calculated using an integral equation) depended on the running cost of each farmer to produce their crops, the price at which the crop is sold, and on the interaction rule between the different farms. The solution of this integral equation showed that the profit obtained through farming was calculated for all farms, and the results showed that profit depended on the farm's position in the landscape. Moreover, neighboring farms that produced similar crops could benefit from others' treatment of their crops, while neighboring farms that produced different crops had a negative impact on each other. The study also modeled the impact of connections between different farms (connections by a road or a river) and investigated the level of landscape pollution at various farms and how this was transported toward other connected farms. The toy individualbased model developed in this study to calculate the profit for each farmer (with its farm belonging to a spatially distributed network of farms) showed that even simple mathematical models could be used to generate new testable hypotheses for complex ecological problems. However, such toy models will have to be modified in the future to describe specific landscape

conditions, specific food producers, specific pollutants (pesticides) use, and their dispersion characteristics to neighboring farms.

Egberts et al. focused on a different type of optimization: the optimization of numerical simulations in the context of a very complex mathematical model for wound healing. The model, described by nine non-linear partial differential equations, focused on the spatio-temporal interactions between different cell types (fibroblasts, myofibroblasts), collagen, and chemicals during postburn tissue contraction. To improve the performance of the finite element numerical simulations of this 2D spatial model for cell- and tissue-scale dynamics of wound healing, the authors considered a feed-forward neural network (with two hidden layers) trained and then tested on 2D finite element simulations. The resulting optimized network was used to predict the wound boundary contraction and the total strain energy density. It was also suggested that the fast numerical simulations could be eventually integrated into medical practice through the development of apps that consider age-related parameters to predict wound contractures.

Hodgkinson et al. focused on a biological aspect underlying many medical problems: the molecular and cell-scale dynamics behind the regulation of cell cycle via a family of proteins called cyclin-dependent kinases and the p53 gene. The study presented two mathematical models described by integro-partial differential equations: the first one focused on the quantity of cyclins across cell cycle at the level of one single cell, and the second one focused on the role of cyclin, the p53 protein, and the mdm2 protein (which degrades p53) in cell-cycle dynamics at the level of wholecell populations. In the first model, the variables describing the amount of S-cyclin and M-cyclin in a cell (where the S-cyclins and M-cyclins denoted the cyclins synthesized in the S and M phases of cell cycle) depended on time and space. In the second model, the variables describing the densities of cells in the various phases of cell cycle (S, G, M) depended on time, cyclin level synthesized in various phases, cell damage level, and p53 and mdm2 levels. Numerical simulations (using a finite difference scheme together with a midpoint integration method for integrals) with the first model showed oscillatory dynamics between the S-cyclin and M-cyclin states. Numerical simulations with the second model (using a finite difference scheme based on a predictor-corrector MacCormack scheme for time integration and central differences for the spatial gradients) showed the distributions of cell populations in S and M phases across the (cyclin, damage) space and the distribution of the cell population in the G phase across the (cyclin, damage) space, the (p53, damage) space, and the (p53, mdm2) space for various parameter values. Due to the complexity of this second model in [2] and the computational limitations on the number of dimensions that could be simulated simultaneously at a resolution that could allow enough accuracy, this second model did not include any spatial cell structure. This is an open problem that will have to be addressed in the future.

In summary, the articles in this Research Topic highlight some of the current open problems in cell biology, medicine, and ecology. All these articles also mention the issue of parameterizing these models (either simple or complex) with real single-scale and multiscale data, which is mainly due to the lack of such data.

Author contributions

The author confirms being the sole contributor of this work and has approved it for publication.

Funding

RE acknowledges support from a French Agence Nationale de Recherche (ANR) grant number ANR-21-CE45-0025-01.

Conflict of interest

The author declares that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.