



EDITORIAL

Introduction to the Special Issue on Advances in Mathematical Modeling: Numerical Approaches and Simulation for Computational Biology

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1 Introduction

Mathematical modeling has become an essential tool for understanding the complexity of biological systems, providing a quantitative framework for describing, analyzing, and predicting processes that operate across multiple spatial and temporal scales [1]. From the dynamics of infectious diseases and cellular populations to tumor-immune interactions, mathematical models enable systematic investigation of the mechanisms and dynamic behavior underlying biological and disease processes [2]. In parallel, advances in numerical analysis, scientific computing, optimization, and data-driven methods have substantially expanded the range of biological problems that can be addressed through simulation [3,4]. These developments are particularly important when analytical solutions are unavailable or when nonlinearities, stochastic effects, spatial heterogeneity, time delays, and complex interactions complicate the analysis of biological systems.

Despite this progress, the reliable simulation of biological systems continues to present significant mathematical and computational challenges. Numerical approaches must provide accurate and reliable approximations while appropriately representing the underlying biological dynamics. At the same time, biological applications increasingly require the integration of uncertainty, multiscale processes, and strategies for optimizing interventions [3]. Emerging computational approaches, including structure-preserving discretizations [5], stochastic and delay formulations [6], finite element methods [7], optimal control techniques [8], and physics-informed neural networks [9], provide new opportunities to address these challenges and connect mathematical theory more closely with biologically and clinically relevant applications.

Against this background, this Special Issue highlights recent developments at the intersection of mathematical modeling, numerical computation, and computational biology, bringing together eleven contributions covering infectious-disease and epidemic dynamics, stochastic and delay differential models, structure-preserving numerical methods, biomechanical and patient-specific finite element modeling, biological resource allocation and optimal control, biofluid dynamics, and computational oncology. These studies demonstrate how mathematical analysis and computational simulation can complement one another in investigating complex biological phenomena, evaluating intervention and control strategies, preserving biologically relevant model properties, and developing computational frameworks for realistic biological systems.

2 Contributions

The author-provided keywords across the eleven contributions are summarized in the word cloud shown in Fig. 1, while the Sankey diagram in Fig. 2 illustrates the principal methodological themes and their associations with the individual contributions. As several studies integrate multiple approaches, individual contributions may be associated with more than one methodological theme.

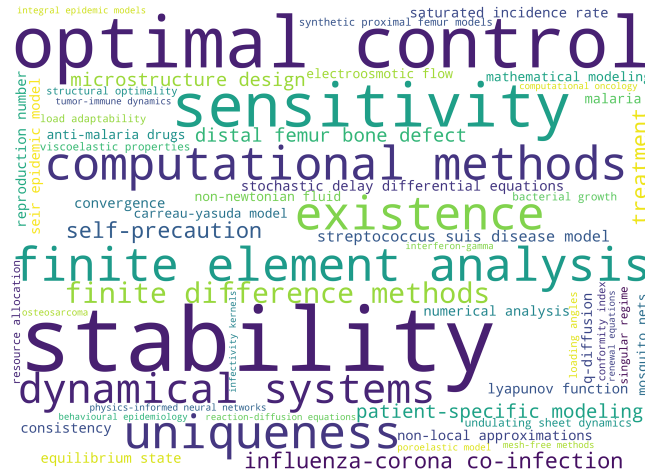


Figure 1: Word cloud of author-provided keywords across the eleven contributions.

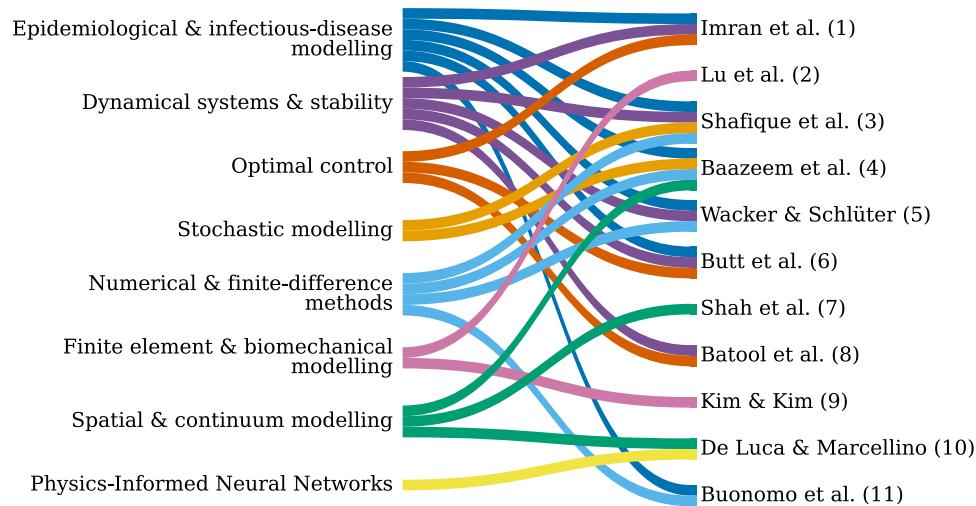


Figure 2: Methodological themes and their associations across the eleven contributions.

The individual contributions are summarized below:

Imran et al. (1) developed an extended SEIR model to study the joint transmission dynamics of influenza and coronavirus infections, incorporating treatment, hospitalization, and co-infection. The authors established key epidemiological properties, including non-negativity, boundedness, well-posedness, equilibrium states, and the basic reproduction number. Sensitivity analysis was used to identify influential parameters, while optimal control was applied to investigate strategies for reducing disease transmission and intervention costs. The study provided a mathematical framework for understanding and controlling influenza-coronavirus co-infection.

Lu et al. (2) investigated scaffold designs for reconstructing traumatic distal femur defects using patient-specific computational modeling. A three-dimensional finite element model incorporating realistic femoral geometry and material distribution was used to compare an intact femur with defect models reconstructed using nine microstructure scaffolds and two solid scaffolds under single-leg stance loading. The results showed that scaffold geometry and pillar dimensions affected fixation stability, with the metal solid scaffold providing the most stable fixation. The study also showed that appropriately designed microstructure scaffolds could satisfy the required biomechanical criteria.

Shafique et al. (3) formulated a stochastic delay differential equation model to study the dynamics of *Streptococcus suis* infection in pig populations. The model was analyzed for positivity, boundedness, equilibria, reproduction number, and parameter sensitivity. To overcome limitations of conventional stochastic numerical methods, the authors developed a stochastic non-standard finite difference method that avoided numerical negativity, unboundedness, inconsistency, and instability. The proposed method exhibited unconditional convergence toward the model's true states, demonstrating the importance of preserving biologically meaningful properties in stochastic delay models.

Baazeem et al. (4) studied a stochastic SEIR epidemic model with q-diffusion and a general incidence function. They proposed a computational scheme for the resulting stochastic partial differential equations using a compact spatial discretization together with an extension of the Euler-Maruyama method. The spatial scheme achieved sixth-order accuracy, while stability and consistency were established in the mean-square sense. Numerical comparisons with existing methods demonstrated improved performance, and the inclusion of q-diffusion provided a means of representing spatial-temporal disease dynamics beyond classical diffusion formulations.

Wacker and Schlüter (5) re-investigated a time-continuous model of untreated HIV infection and developed a non-standard finite difference method for its numerical solution. They established non-negativity, boundedness of selected solution components, global-in-time existence, uniqueness, equilibrium states, and stability properties of the continuous model. The proposed discretization preserved important properties of the original model, including non-negativity, boundedness, equilibria, and their stability. Linear convergence of the numerical formulation toward the continuous solution was also established.

Butt et al. (6) developed a nonlinear mathematical model for malaria transmission involving human and mosquito populations. The authors determined the basic reproduction number and investigated disease-free and endemic equilibria and their stability, while sensitivity analysis identified influential parameters associated with malaria transmission. The model was extended to include antimalarial treatment, larvicides, and insecticide-treated mosquito nets within an optimal control framework. The results showed how coordinated use of these interventions could reduce malaria transmission while limiting intervention costs.

Shah et al. (7) investigated a self-propelled undulating sheet in a non-Newtonian electrolyte solution confined within a wavy channel under electroosmotic effects. The fluid was modeled using the Carreau-Yasuda model, while the electroosmotic body force was obtained from the Poisson-Boltzmann equation. Under the Stokes flow regime, a fourth-order ordinary differential equation for the stream function was solved to study the sheet's propulsion and energy dissipation. The analysis examined the combined effects of electroosmosis and the viscoelastic properties of the surrounding fluid on the motion of the sheet. The findings also had relevance to biological propulsion and the design of artificial microswimmers for biomedical applications.

Batool et al. (8) studied resource allocation in *Escherichia coli* under cold stress using a dynamical model involving metabolic precursors, ribosomes, and the cold-shock protein CspA. Steady-state analysis identified temperature-dependent locally stable equilibria, showing how cellular allocation changed with

temperature. Growth maximization was then formulated as an optimal control problem using Pontryagin's Maximum Principle. The resulting strategies exhibited bang-bang and singular control structures and provided a quantitative description of the trade-off between cold-shock adaptation, resource allocation, and bacterial growth.

Kim and Kim (9) investigated regional structural optimality and load adaptability in a two-dimensional synthetic proximal femur model under varying loading angles. Three finite element model configurations were analyzed by varying hip-contact and muscle-force directions, with the proximal femur divided into regions of interest to examine local structural behavior. The femoral head and greater trochanter exhibited high conformity, whereas the femoral neck showed consistently lower conformity. The authors also demonstrated that model resolution and region size influenced predictive accuracy and stability, providing a quantitative framework for studying regional load adaptation.

De Luca and Marcellino (10) developed an extended physics-informed neural network framework for osteosarcoma tumor-immune dynamics by introducing interferon-gamma as a fifth biological variable. The model coupled five biological fields with mechanical tissue response through Biot's poroelastic theory in a two-dimensional domain. Four initial macrophage distributions were examined to study their influence on immune-tumor interactions and macrophage depletion. Numerical stability was achieved across all scenarios, with total loss values ranging from 0.056 to 0.158 and mechanical loss values below 3.2×10^{-5} . The results indicated that macrophage localization near tumor boundaries enhanced early immune-tumor contact, while curriculum learning and adaptive loss weighting were used to address temporal stiffness associated with rapid interferon-gamma decay.

Finally, Buonomo et al. (11) introduced EPITIME, a computational framework for two classes of integral epidemic models, namely an age-of-infection model and an information-dependent behavioural model. The modular MATLAB/Python environment was based on structure-preserving non-standard finite difference discretizations and included validation, reproducibility, performance assessment, and graphical interface tools. Depending on the model, the schemes preserved properties such as positivity, monotonicity, boundedness, final-size behavior, invariant regions, and equilibrium and threshold structures, with first-order convergence established. The framework was demonstrated through epidemic simulations, reconstruction of an infectivity kernel from COVID-19 incidence data, and behavioral dynamics under different memory kernels. Performance, scalability, and computational complexity were also analyzed, including comparisons with quadrature-based approaches.

3 Conclusion

The papers in this Special Issue illustrate the use of mathematical models and numerical methods in addressing different problems in biology and biomedicine. The contributions combine mathematical analysis with computation to study model behavior, assess numerical reliability, examine intervention and control strategies, and investigate biological and biomechanical processes. These studies also demonstrate the use of different computational approaches for addressing the mathematical and biological features of the problems considered.

The studies presented here also indicate how developments in numerical analysis can contribute to the study of biological systems that involve nonlinear behavior, uncertainty, spatial effects or complex interactions. At the same time, the applications considered in this Special Issue highlight the value of considering mathematical analysis, numerical implementation, and biological interpretation together in the study of biological systems. Future work in these areas may build on the mathematical and computational approaches presented here and explore their application to other biological and biomedical problems. We

hope that the work presented in this Special Issue will be useful to researchers working on related problems in mathematical and computational biology.

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List of Contributions

1. Imran M, McKinney B, Butt AIK. SEIR mathematical model for influenza-corona co-infection with treatment and hospitalization compartments and optimal control strategies. *Comput Model Eng Sci.* 2025;142(2):1899–931. doi:10.32604/cmes.2024.059552.
2. Lu HT, Hsu CC, Jian QQ, Chen WT. Biomechanical study of different scaffold designs for reconstructing a traumatic distal femur defect using patient-specific computational modeling. *Comput Model Eng Sci.* 2025;142(2):1883–98. doi:10.32604/cmes.2025.057675.
3. Shafique U, Raza A, Baleanu D, Nasir K, Naveed M, Siddique AB, et al. Computational modeling of *Streptococcus suis* dynamics via stochastic delay differential equations. *Comput Model Eng Sci.* 2025;143(1):449–76. doi:10.32604/cmes.2025.061635.
4. Baazeem A, Arif MS, Nawaz Y, Abodayeh K. Modeling and simulation of epidemics using q-diffusion-based SEIR framework with stochastic perturbations. *Comput Model Eng Sci.* 2025;143(3):3463–89. doi:10.32604/cmes.2025.066299.
5. Wacker B, Schlüter JC. A time-continuous model for an untreated HIV-infection and a novel non-standard finite-difference-method for its discretization. *Comput Model Eng Sci.* 2025;144(2):2191–229. doi:10.32604/cmes.2025.067397.
6. Butt AIK, Ismaeel T, Khan S, Imran M, Ahmad W, Abdulrashid I, et al. Investigating the role of antimalarial treatment and mosquito nets in malaria transmission and control through mathematical modeling. *Comput Model Eng Sci.* 2025;144(3):3463–92. doi:10.32604/cmes.2025.069277.
7. Shah RA, Asghar Z, Li C, Ardekani A, Ali N. Non-Newtonian electroosmotic flow effects on a self-propelled undulating sheet in a wavy channel. *Comput Model Eng Sci.* 2025;145(1):753–78. doi:10.32604/cmes.2025.069177.
8. Batool S, Imran M, McKinney B. Optimal resource allocation in a bacterial growth model under cold stress and temperature. *Comput Model Eng Sci.* 2026;146(3):30. doi:10.32604/cmes.2026.079067.
9. Kim J, Kim JJ. Assessment of regional structural optimality in a 2D synthetic proximal femur model under varying loading angles. *Comput Model Eng Sci.* 2026;147(2):27. doi:10.32604/cmes.2026.079665.
10. De Luca P, Marcellino L. Physics-informed neural networks for osteosarcoma tumor-immune dynamics. *Comput Model Eng Sci.* 2026;147(3):27. doi:10.32604/cmes.2026.082664.
11. Buonomo B, Messina E, Panico C, Pezzella M, Zanghirati G. EPITIME: a computational framework for integral epidemic models with structure-preserving discretizations. *Comput Model Eng Sci.* 2026;148(3):27. doi:10.32604/cmes.2026.084828.

References

1. Lashin SA, Ivanov RA, Matushkin YG. Mathematical and computational modeling of biosystems at different levels of organization. *Vavilov J Genet Breed*. 2026;30(3):502–14. doi:10.18699/vjgb-26-21.
2. Thurley K, Wolf J. Editorial overview: mathematical modeling of disease processes. *Curr Opin Syst Biol*. 2025;42:100554. doi:10.1016/j.coisb.2025.100554.
3. Banga JR, Fernandez Villaverde A. Mechanistic dynamic modelling of biological systems: the road ahead. *Curr Opin Syst Biol*. 2025;42:100553. doi:10.1016/j.coisb.2025.100553.
4. Roquemen-Echeverri V, Mosquera-Lopez C. Recent advancements and applications of physics-informed machine learning in biomedical research. *Curr Opin Biomed Eng*. 2025;35:100612. doi:10.1016/j.cobme.2025.100612.
5. Hoang MT, Ehrhardt M. Differential equation models for infectious diseases: mathematical modeling, qualitative analysis, numerical methods and applications. *SeMA J*. 2026;83:435–70. doi:10.1007/s40324-025-00404-9.
6. Babasola O, Omondi EO, Oshinubi K, Imbusi NM. Stochastic delay differential equations: a comprehensive approach for understanding biosystems with application to disease modelling. *AppliedMath*. 2023;3(4):702–21. doi:10.3390/appliedmath3040037.
7. Hoang P, Guccione J. Finite element modeling in left ventricular cardiac biomechanics: from computational tool to clinical practice. *Bioengineering*. 2025;12(9):913. doi:10.3390/bioengineering12090913.
8. Sun G-Q, He R, Hou L-F, Luo X, Gao S, Chang L, et al. Optimal control of spatial diseases spreading in networked reaction-diffusion systems. *Phys Rep*. 2025;1111:1–64. doi:10.1016/j.physrep.2025.01.005.
9. Zhao A, Fattahi D, Hu X. Physics-informed neural networks for physiological signal processing and modeling: a narrative review. *Physiol Meas*. 2025;46(7):07TR02. doi:10.1088/1361-6579/adf1d3.