Editorial

Editorial: Dynamics of Deterministic Models of Biological Systems

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Theoretical modeling of biological processes is an indispensable tool for mathematicians, biologists, and bioengineers to describe and predict the behavior of complex biological systems. In mathematics and computer science, deterministic systems are those in which future states are not influenced by randomness. Consequently, deterministic models consistently yield the same results given identical initial conditions. These models facilitate the precise calculation of future events without unpredictable influence of noise, allowing for confident predictions based on complete data.

In systems biology, models are predominantly deterministic, translating biological problems into systems of equations solvable through numerical simulations. These equations describe the dynamical interactions between biological units, elucidating various biological processes at different levels, from viruses to living organisms. The efficiency of quantitative modeling, including equation-based approaches, is closely related to the quality and abundance of data obtained for the system being modeled. Equation-based modeling not only integrates but also enhances traditional statistical inference methods.

This special issue compiles original contributions focusing on the analytical and numerical studies of difference and differential equations for modeling biological systems. The included papers explore various facets of equation-based modeling, examining their assumptions, strengths, weaknesses, and providing specific examples of simple models.

The issue comprises five contributions, all employing deterministic models to simulate biological dynamics in different contexts: neuron dynamics [1], viral infections [2], bone mineralization [3], cirrhosis evolution [4], and bacterial growth [5]. Three of these studies [1–3] utilize fractional-order difference [1] and differential [2, 3] equations, while two rely on integer-order differential equations [4, 5].

Recent years have seen a growing interest in the application of fractional-order calculus across vari-

ous fields, including physics, engineering, and biology. The dynamics of fractional-order systems have garnered attention due to the enhanced accuracy of fractional derivatives in various interdisciplinary contexts. One significant advantage of fractional-order systems over classical integer-order models is their infinite memory, which effectively describes the hereditary properties of neural networks. However, the dynamical behavior of fractional-order biological systems requires further investigation.

Vivekanandhan et al. [1] introduced a fractional-order Rulkov map to describe the synchronous dynamics of coupled neurons. Using traditional nonlinear dynamics tools such as phase space analysis, bifurcation diagrams, and Lyapunov exponents, they demonstrate various dynamical regimes, including silence, bursting, and chaotic firing. They also analyzed the stability of fixed points and investigated synchronization of two fractional-order Rulkov maps, concluding that complete synchronization is unattainable.

In another paper, Alzubaidi et al. [2] employed a fractional-order mathematical model to simulate the dynamics of mpox (formerly monkeypox), a disease caused by a virus of the variola family, which was declared a public health emergency of international concern from July 23, 2022 to May 11, 2023. Their simulations indicated that the new fractal-fractional operator provided deeper biological insights into the disease's dynamics.

The comparison of fractional-order and integer-order models was made by Agarwal et al. [3] in their study of bone mineralization, a complex process of depositing inorganic sediments onto an organic matrix. Modeling this process is crucial for assessing bone stability. Their simulations showed that minerals were detected as an earlier stage in the fractional-order model, a phenomenon not observed in the integer-order model.

Distinct from the aforementioned studies, the remaining two papers focus on deterministic models based on integer-order differential equations. Specifically, Ayala et al. [4] developed a mathematical model of cirrhosis, a disease for which there is currently no effective drug treatment. Instead, herbal remedies, particularly, a mixture of seven popular Mexican plants, are often helpful in curating this disease. The results of numerical simulations using their model with the plants' parameters showed good agreement with experiments carried out on rats with induced cirrhosis.

Lastly, Villa et al. [5] presented a mathematical model for the growth of microbial *Geobacter* cells. This model provided a comprehensive framework for optimizing the relationships among various variables influencing cellular function. The authors suggested that their model could serve as a theoretical basis for studying microbial growth and have practical applications in optimizing bacterial cultures for specific outcomes.

In conclusion, I believe this special issue will benefit computational biologists and researchers interested in applying mathematical tools to address real-world biological challenges.

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