



EDITORIAL

Introduction to the Special Issue on Mathematical Aspects of Computational Biology and Bioinformatics-II

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1 Summary

Mathematical modeling has become a cornerstone in understanding the complex dynamics of infectious diseases and chronic health conditions. With the advent of more refined computational techniques, researchers are now able to incorporate intricate features such as delays, stochastic effects, fractional dynamics, variable-order systems, and uncertainty into epidemic models. These advancements not only improve predictive accuracy but also enable deeper insights into disease transmission, control, and policy-making.

Tashfeen et al. [1] developed a delay-based mathematical model for typhoid transmission caused by *Salmonella typhi*, emphasizing how time delays affect disease dynamics and pattern formation. The model includes equilibrium and stability analysis, with numerical simulations using Euler, RK-4, and Non-Standard Finite Difference (NSFD) methods. Among these, the NSFD method effectively preserved key properties like positivity, boundedness, and stability, outperforming traditional schemes. The study highlights the limitations of conventional methods and suggests extending the model to fractional, stochastic, and fuzzy frameworks.

Shafique et al. [2] proposed a deterministic and stochastic delayed model for bacterial meningitis, structured through four compartments: susceptible, carrier, infected and recovered. The study emphasizes the significance of delay effects in disease persistence and extinction, supported by rigorous mathematical analysis of equilibrium points, reproduction number, and stability. Standard numerical schemes like Euler-Maruyama and stochastic Runge-Kutta failed to preserve essential biological properties. In contrast, the stochastic non-standard finite difference (NSFD) method, robust under delay and perturbation, successfully maintained positivity, boundedness, and biological realism, validated through stability theorems and numerical simulations.

Sweilam et al. [3] proposed two hybrid variable-order fractional models for cancer dynamics using the Grünwald-Letnikov approximation. The study focused on the existence, uniqueness, and stability of the model, introducing the Caputo proportional constant-based Adams-Bashforth fifth-step method (CPC-AB5SM) for numerical simulation. Compared with generalized Runge-Kutta methods, their approach revealed novel system behaviors, demonstrating higher accuracy and efficiency. The piecewise modeling strategy offered new insights into dynamic system properties, previously unobserved in classical



and standard fractional-order frameworks, highlighting the potential for future extensions to optimal control problems.

Efil et al. [4] examined the long-term impact of COVID-19 on individuals with preexisting conditions such as cancer, heart disease, and diabetes by formulating two ODE-based models. Stability analysis and sensitivity analysis were employed to assess the effect of key parameters like smoking, obesity, and heredity. The study underscored that the fear of visiting healthcare centers during the pandemic may lead to late diagnoses and worsening of chronic conditions. Results indicated a strong link between diabetes and heart disease and revealed that COVID-19 exacerbates these ailments by disrupting routine healthcare. The authors emphasized increased public awareness and regular medical check-ups as crucial steps to mitigate future health crises.

Arif et al. [5] proposed a novel Hybrid SIR-Fuzzy model that enhances traditional epidemic modeling by incorporating fuzzy logic to account for uncertainties in parameter estimation, especially in the transmission rate. The study emphasizes the need for models that can effectively handle imprecise or incomplete data in real-world scenarios. Equilibrium analysis and sensitivity studies under three different cases highlight the model's flexibility and accuracy. A robust numerical scheme was developed and shown to outperform conventional forward Euler methods in stability and convergence. Simulation results demonstrated how the model adapts to dynamic epidemic behaviors and can guide more informed public health decisions by considering contextual factors like population density and healthcare infrastructure.

Omame et al. [6] developed a stochastic model to study the co-dynamics of COVID-19 and viral hepatitis B, emphasizing the epidemiological impact of vaccine booster doses. The model incorporates logistic growth and saturated incidence functions and is calibrated using real COVID-19 data from Pakistan. Using stochastic calculus, the authors established conditions for the existence of unique global solutions, stationary distributions in the sense of ergodicity, and disease extinction. The estimated stochastic threshold is given by $R_0^S = 3.0651$. Numerical experiments indicate that increasing both primary and booster vaccination rates substantially decreases infection levels across all compartments, including those co-infected. The study also examines the role of stochastic white noise intensities, suggesting avenues for future research such as the inclusion of time-dependent contact rates, asymptomatic classes, and more realistic assumptions involving quadratic Levy noise and variable diffusion rates.

Yildirim et al. [7] proposed a numerical scheme based on Pell-Lucas polynomials (PLPs) and the collocation method to solve a fractional-order HIV/AIDS epidemic model that incorporates a treatment compartment. The model divides the population into five classes: susceptible individuals (S), HIV-positive (I), full-blown AIDS without treatment (A), treated individuals (T), and those who have modified their sexual behavior (R). The fractional model is transformed into a nonlinear algebraic system using PLPs at specific collocation points. Error analysis based on the residual function confirms the method's reliability, even in the absence of an exact solution. Numerical experiments conducted for various fractional orders ($p = 1, 0.95, 0.9, 0.85$) over the interval $[0, 200]$ days demonstrate the accuracy and efficiency of the method. Results show that the infectious and AIDS compartments eventually vanish, and that increasing the polynomial degree N reduces the error significantly. The approach is computationally efficient, particularly in MATLAB, and is well-suited for solving similar epidemic models due to its simplicity and low cost.

Together, these studies underscore the richness and diversity of mathematical modeling techniques applied to infectious and chronic diseases. Whether through delay differential equations, fractional calculus, stochastic modeling, or fuzzy systems, each work contributes to the growing toolkit for understanding complex biological systems. Such models not only aid in predicting disease outcomes but also support the development of more effective intervention strategies and public health policies.

Conflicts of Interest: The authors declare no conflicts of interest to report regarding the present study.

References

1. Tashfeen M, Dayan F, Ur Rehman MA, Abdeljawad T, Mukheimer A. A dynamical study of modeling the transmission of typhoid fever through delayed strategies. *Comput Model Eng Sci.* 2024;141(2):1419–46. doi:10.32604/cmes.2024.053242.
2. Shafique U, Al-Shamiri MM, Raza A, Fadhal E, Rafiq M, Ahmed N. Numerical analysis of bacterial meningitis stochastic delayed epidemic model through computational methods. *Comput Model Eng Sci.* 2024;141(1):311–29. doi:10.32604/cmes.2024.052383.
3. Sweilam N, Al-Mekhlafi S, Ahmed A, Alsheri A, Abo-Eldahab E. Numerical treatments for crossover cancer model of hybrid variable-order fractional derivatives. *Comput Model Eng Sci.* 2024;140(2):1619–45. doi:10.32604/cmes.2024.047896.
4. Efil FN, Qureshi S, Gokbulut N, Hosseini K, Hincal E, Soomro A. Aggravation of cancer, heart diseases and diabetes subsequent to COVID-19 Lockdown via mathematical modeling. *Comput Model Eng Sci.* 2024;140(1):485–512. doi:10.32604/cmes.2024.047907.
5. Arif MS, Abodayeh K, Nawaz Y. A hybrid SIR-fuzzy model for epidemic dynamics: a numerical study. *Comput Model Eng Sci.* 2024;139(3):3417–34. doi:10.32604/cmes.2024.046944.
6. Omame A, Abbas M, Baleanu D. A stochastic model to assess the epidemiological impact of vaccine booster doses on COVID-19 and viral hepatitis B co-dynamics with real data. *Comput Model Eng Sci.* 2024;138(3):2973–3012. doi:10.32604/cmes.2023.029681.
7. Yıldırım G, Yüzbaşı Ş. A collocation technique via pell-lucas polynomials to solve fractional differential equation model for HIV/AIDS with treatment compartment. *Comput Model Eng Sci.* 2024;141(1):281–310. doi:10.32604/cmes.2024.052181.