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EDITORIAL

Introduction to the Special Issue on Recent Developments on Computational Biology-I

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In modern time, experts started to use interdisciplinary properties with the development of technology and science. Thus, these disciplines provide more sophisticated properties of real-world problems. In this sense, some models need to be investigated by using revised and modified traditional methods. The first discipline is the applied sciences such as physics, engineering, mechanics, electricity, biology, economy and mathematical applications [1–5]. In this stage, many methods [5–10] are developed and modified. To uncover the deep properties of problems is to use the main properties of such interdisciplinary properties. Furthermore, works conducted on such mathematical models including non-local operators, partial, ordinary and integer order have introduced a deeper investigation of problems for experts. By using technological tools, experts may observe more realistic and exact results of models.

In response to the call for papers, 24 submissions have been received. All submissions have been reviewed by at least three experts in the field. Finally, 6 papers have been accepted for publication in this special issue, all of which are of high quality and well representative of the areas covered by this special issue. This corresponds to an acceptance rate of 33.3%.

The published papers in this special issue are herein briefly studied as follows:

In [11], the authors studied a new fractional operator, COVID-19 by using different numerical techniques and the time fractional parameters. The mechanical characteristics of the fractional order model have been identified. The uniqueness and existence have been established by them. The model's Ulam-Hyers stability analysis has been found. In order to justify the theoretical results, numerical simulations are carried out for the presented method in the range of fractional order to show the implications of fractional and fractal orders. They applied very effective numerical techniques to obtain the solutions of the model and simulations. Also, they presented the conditions of existence for a solution to the proposed epidemic model and calculated the reproduction number in certain state Conditions of the analyzed dynamic system. In [12], authors constructed an epidemic model with fuzzy parameters. Since the classical epidemic model does not elaborate on the successful interaction of susceptible and infective people, the constructed fuzzy epidemic model discusses the more detailed versions of the interactions between infective and susceptible people. The next-generation matrix approach was employed to find the reproduction number of a deterministic model. The sensitivity analysis and local stability analysis of the system are also provided. For solving the fuzzy epidemic model, a numerical scheme is constructed which consists of three-time levels. The numerical scheme has an advantage over the existing forward Euler scheme for determining the conditions of getting the positive solution. The established scheme also has an advantage over existing non-standard finite difference methods in terms of order of accuracy. The stability of the scheme for the considered fuzzy model is also provided. From the plotted results, it can be observed that susceptible people decay by rising interaction parameters. In [13], authors focused on three types of biological systems: the dengue fever disease model, the COVID-19 virus model, and the transmission of Tuberculosis model. The new technique of creating the integration matrix for the Bernoulli wavelets was applied. Also, the novel method proposed in this paper is called as the Bernoulli wavelet collocation scheme (BWCM). All three models are in the form system of coupled ordinary differential equations without an exact solution. These systems are converted into a system of algebraic equations using the Bernoulli wavelet collocation scheme. The numerical wave distributions of these governing models are obtained by solving the algebraic equations via the Newton-Raphson method. The results obtained from the developed strategy are compared to several schemes such as the Runge Kutta method, and ND solver in mathematical software. The convergence analysis is discussed through theorems. The newly implemented Bernoulli wavelet method improves the accuracy and converges when it is compared with the existing methods in the literature. In [14], authors presented a restricted SIR mathematical model to analyze the evolution of a contagious infectious disease outbreak (COVID-19) using available data. The new model focuses on two main concepts: first, it can present multiple waves of the disease, and second, it analyzes how far an infection can be eradicated with the help of vaccination. The stability analysis of the equilibrium points for the suggested model is initially investigated by identifying the matching equilibrium points and examining their stability. The basic reproduction number is calculated, and the positivity of the solutions is established. Numerical simulations are performed to determine if it is multipeak and evaluate vaccination's effects. In addition, the proposed model is compared to the literature already published and the effectiveness of vaccination has been recorded.

In [15], authors have demonstrated that the transmission is not truly homogeneous via various data sets showing the prevalence of numerous viral diseases. Two examples are the spread of Spanish flu and COVID-19. The aim of this research is to develop a comprehensive nonlinear stochastic model having six cohorts relying on ordinary differential equations via piecewise fractional differential operators. Firstly, the strength number of the deterministic case is carried out. Then, for the stochastic model, they show that there is a critical number RS 0 that can predict virus persistence and infection eradication. Because of the peculiarity of this notion, an interesting way to ensure the existence and uniqueness of the global positive solution characterized by the stochastic COVID-19 model is established by creating a sequence of appropriate Lyapunov candidates. A detailed ergodic stationary distribution for the Stochastic COVID-19 model is provided. Our findings demonstrate a piecewise numerical technique to generate simulation studies for these frameworks. The collected outcomes leave no doubt that this conception is a revolutionary doorway that will assist mankind in good perspective nature.

In [16], authors considered the COVID-19 model in which the population by dividing into five compartments. The present model presents the population's diffusion effects on all susceptible, exposed, infected, isolated, and recovered compartments. The reproductive number, which has a key role in the infectious models, is discussed. The equilibrium points and their stability are presented. For numerical simulations, finite difference (FD) schemes like nonstandard finite difference (NSFD), forward in time central in space (FTCS), and Crank Nicolson (CN) schemes are implemented. Some core characteristics of schemes like stability and consistency are calculated.

In [17], authors constructed a stochastic fractional framework of measles spreading mechanisms with dual medication immunization considering the exponential decay and Mittag-Leffler kernels.

In this approach, the overall population was separated into five cohorts. Furthermore, the descriptive behavior of the system was investigated, including prerequisites for the positivity of solutions, invariant domain of the solution, presence and stability of equilibrium points, and sensitivity analysis. They included a stochastic element in every cohort and employed linear growth and Lipschitz criteria to show the existence and uniqueness of solutions. Several numerical simulations for various fractional-orders and randomization intensities are illustrated.

In [18], the transmission dynamics of the Omicron variant of COVID-19 using SEIQIcRVW and SQIRV models, considering the delay in converting susceptible individuals into infected ones was examined by the authors. The significant delays eventually resulted in the pandemic's containment. To ensure the safety of the host population, this concept integrates quarantine and the COVID-19 vaccine. They have investigated the stability of the proposed models. The fundamental reproduction number influences stability conditions. According to our findings, asymptomatic cases considerably impact the prevalence of Omicron infection in the community. The real data of the Omicron variant from Chennai, Tamil Nadu, India, is used to validate the outputs.

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