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EDITORIAL

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

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The special issue presents new mathematical and computational approaches, to investigate some core problems of the computational biological sciences. This topic presents a huge interest from both theoretical and applied viewpoints.

The content of this special issue was focused mainly to debate a wide range of the theory and applications of integer-order and fractional-order derivatives and fractional-order integrals in different directions of mathematical biology. Several interdisciplinary groups reported their related results.

However, after the referee process, only 15 high quality papers were accepted to be part of this special issue.

The manuscript by Li et al. debated the interesting topic of Cherenkov radiation: A stochastic differential model driven by Brownian motions. The result of the GEANT4 simulation is compared with the numerical solution of the corresponding stochastic partial differential equations, which shows that the stochastic partial differential equation can simulate the corresponding process.

The paper by Gokbulut et al. discussed reducing the range of cancer risk on BI-RADS 4 subcategories via mathematical modelling. The model showed that the percentages of parameters play an important role in the diagnosis of BI-RADS 4 subcategories. All things considered, with the assistance of the most effective parameters, the range of cancer risks in BI-RADS 4 subcategories will decrease.

The authors Ejaz et al. debated the stability analysis of the predator-prey system with consuming resource and disease in predator species. It is applied for solving presently modified eco-epidemiological mathematical model with and without diffusion. They also run a computer simulation to determine the effectiveness of the proposed numerical scheme.

A contemporary topic, namely the numerical computational heuristic through Morlet wavelet neural network for solving the dynamics of nonlinear SITR COVID-19 was investigated by Sabir et al. The detail of each class of the SITR nonlinear COVID-19 system is discussed. The obtained outcomes of the SITR system are compared with the Runge-Kutta results to check the perfection of the designed method. The statistical analysis is performed using different measures for 30 independent runs as well as 15 variables to authenticate the consistency of the proposed method. The plots of the absolute

error, convergence analysis, histogram, performance measures, and boxplots are also provided to find the exactness, dependability and stability of the MWNN-GA-ASA.

Behar et al. presented their original work on the ResNet50-based effective model for breast cancer classification using histopathology image. The result illustrated state-of-the-art performance of the proposed model with the highest training, validation and test accuracies as 99.70%, 99.24% and 99.24%, respectively. Classification accuracy is increased by 0.66% and 0.2% when compared with similar recent studies on training and test data results. Average precision and F1 score have also improved, and the receiver operating characteristic (RoC) area has been achieved to 99.1%. Thus, a reliable, accurate and consistent CNN model based on pre-built ResNet50 architecture has been developed.

Assessing medical screening and isolation measures based on a numerical method for the COVID-19 epidemic model in Japan was very well depicted by Chen et al. They found that the transmission rates were related to the age structure ratio, PCR test index, and isolation efficiency. Both isolation measures and PCR test medical screening can effectively reduce the number of infected cases based on the simulation results. However, the strategy of increasing PCR test medical screening would encounter a bottleneck effect on the virus control when the index reached 0.3. The effectiveness of the policy would decrease and the basic reproduction number reached the extreme value at 0.6. This study gave a feasible combination for isolation and PCR test by simulation. The isolation intensity could be adjusted to compensate for the insufficiency of PCR test to control the pandemic.

The sensitivity analysis of COVID-19 in the Mediterranean island was performed by Savasan et al. It is concluded that the studied part of the island is late for the control of the disease via the vaccine. This can be explained by two main reasons; vaccinating the people that are not in mobility most of the time (aged people and people with chronic diseases) and getting the vaccine late. The results showed that this rate and distribution of vaccines would not be enough to control the pandemic on the island.

Another interesting contribution on the near future perspective of ESBL-producing *Klebsiella pneumoniae* strains using mathematical modeling was communicated by Bagkur et al. According to the study, in approximately seventy months, ESBL-producing K. pneumoniae strains will exceed non-ESBL K. pneumoniae strains. As a result, the analyses showed that hospital admissions and people infected with non-ESBL or ESBL-producing K. pneumoniae have the highest rate of spreading the infections. In addition, it was observed that the use of antibiotics plays a major role in the spread of ESBL-producing K. pneumoniae compared to other risk factors such as in-hospital transmissions. As a matter of course, recoveries from Klebsiella infections were seen to be the most effective way of limiting the spread. It can be concluded from the results that although the use of antibiotics is one of the most effective factors in the development of the increasing ESBL-producing K. pneumoniae, regulation of antibiotic use policy could be a remedial step together with effective infection control measures. Such steps may hopefully lead to decreased morbidity and mortality rates as well as improved medical costs.

In addition, the fractional analysis of dynamical novel COVID-19 by semi-analytical technique is the contribution of Iqbal et al. The proposed fractional-order scheme for solving the COVID-19 fractional-order model possesses some salient features like producing closed-form semi-analytical solutions, fast convergence and non-dependence on the discretization of the domain. Several graphical presentations have demonstrated the dynamical behaviors of subpopulations involved in the underlying fractional COVID-19 model. The successful application of the scheme presented in this work reveals new horizons of its application to several other fractional-order epidemiological models.

The research article entitled numerical solutions of a novel designed prevention class in the HIV nonlinear model was designed by Sabir et al. The optimization performances through GA-ASA are accessed by presenting an error-based fitness function designed for all the classes of the HIPV model and its corresponding initial conditions represented with nonlinear systems of ODEs. To check the exactness of the proposed stochastic scheme, the comparison of the obtained results and Adams numerical results is performed. For the convergence measures, the learning curves are presented based on the different contact rate values. Moreover, the statistical performances through different operators indicate the stability and reliability of the proposed stochastic scheme to solve the novel designed HIPV model.

The paper entitled the solution of modified Bergman minimal blood glucose-insulin model using Caputo-Fabrizio fractional derivative, by Dubey et al. represents a nice application based on fractional calculus techniques. It is clear from the obtained results and their graphical representation that the obtained results of modified Bergman's minimal model are better than Bergman's model.

An interesting approach on a binomial model approach: comparing the R_0 values of SARS-CoV-2 rRT-PCR data from laboratories across Northern Cyprus is due to Sultanoglu et al. They calculated that the median values of the NEU DESAM COVID-19 laboratory and other laboratories performing the SARS-CoV-2 rRT-PCR on air passengers during the studied period to be 0.96 and 1.29, respectively, compared to Northern Cyprus median value which was 0.99. The rRT-PCR screening results from the NEU DESAM COVID-19 laboratory were closely aligned with the screening results of Northern Cyprus whereas the screening results reported by other laboratories were not fit with the regional pattern. This study also aimed to point out the importance of the rRT-PCR screening procedure since asymptomatic positive SARS-CoV-2 cases entery to Northern Cyprus was inhibited and this prevented the spread of the disease within the population.

Abolaban has presented an interesting work entitled modeling dysentery diarrhea using statistical period prevalence. The fractional model showed smaller discrepancies compared to the integer-order model when the models were fitted and validated with the actual cases of infected humans. Qualitative theory for the existence and uniqueness of the solutions was extensively explored, and the stability of equilibria was investigated. The most influential parameters were found via forward sensitivity indices. This multidisciplinary research shows and explains the results of numerical simulations applied to a biological issue.

Besides, we remark on the research paper talking on the fractional mathematical model of tumour invasion and metastasis by Veeresha et al. The obtained results confirm that the considered method is very efficient and highly methodical to analyze the behaviors of the system of fractional order differential equations.

Finally, the dynamical transmission of the coronavirus model with analysis and simulation by Farman et al. is another valuable piece of this special issue. Some numerical results are presented which show the effect of parameter estimation and different step sizes on our obtained solutions at the real data of some countries to check the actual behavior of COVID-19 in different countries.

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