

Research Article

A HYBRID STRUCTURE FOR INFLUENZA DISEASE MODEL ALONG SPECIAL CASES

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Abstract

In this study, stochastic artificial neural network (ANN) methods backed by Levenberg-Marquardt back-propagation (LMBP), also known as ANN-LMBP (hybrid model), are used to numerically simulate the influenza disease system (IDS). The stiff ordinary differential system is built with three classes: susceptible s(t), infected i(t), and recovered r(t). For the purpose of solving three different IDS variations, the hybrid model was used to do the numerical computations. In order to reduce mean square error (MSE) from data-based reference solutions, the generated numerical solutions through the hybrid model for solving the IDS have been given. An extensive analysis is presented using the correlation studies, MSE information to observe the correctness, efficiency, competence, and proficiency of the created computing paradigm hybrid model. The value and significance of hybrid model are supported by comparisons of the findings.

Keywords: ANN, LMBP, IDS, MSE, Efficiency, Competence, Proficiency.

INTRODUCTION

There are multiple deadly viral diseases, including influenza, which mostly affects the upper respiratory tract, including the nose, throat, and bronchi. This disease can occasionally damage the lungs at low or high rates. Influenza is not a fatal illness with a high likelihood of recovery. It gets better in 1-2 weeks without any medical treatment. For people who are older or who have major medical conditions such as diabetes, lung disease, cancer, heart disease, or renal issues, influenza represents a serious risk [1]. Such individuals may develop pneumonia and other serious primary illnesses as a result of the infection. The greater rates of respiratory contagions have an impact on the annual epidemic rate of influenza, which ranges from 5 to 15%. The annual epidemic rate is estimated to be between 3 and 5 million, whereas the estimated number of fatalities is between 400,000 and 500,000 [2]. Numerous epidemiological issues are represented by an autonomous ordinary differential system of equations, which implies that the system parameters' predictions are not time-dependent. The variables in these systems represent recoverable, infected, disease-spreading, and susceptible sub-populations. The researchers [3] offer a multi-step variant of the differential transform strategy to solve the IDS with nonlinear plane. Another scholar [4] offer a mathematical illustration of the SIQR IDS nonlinear plane with a flawed quarantine procedure. A numerical strategy was put forth in [5] for solving a fractional-order IDS nonlinear plane. [6] Developed a multiobjective optimization-based method for allocating patients based on the pandemic influenza epidemic. The scholars observed two avian influenza epidemic systems incorporating fractal-fractional derivatives with Mittag-Leffler and power memory [7].

For the simulation of influenza epidemics, this [8] introduced an epidemic fractional order model. The dynamics of infection and virus-induced apoptosis in the development of an influenza vaccine based on cell culture were examined by [9]. The effect of media attention on the dynamics of human influenza transmission was covered via [10]. A net flow model for the distribution of influenza shots under a supply constraint in healthcare was described in [11]. Genetic algorithms were used in [12] to explore vaccination-based optimal solutions for epidemic influenza. The researchers presented the applications of the optimal regulator to the co-infection of influenza pneumonia with antiviral drug conflict [13]. The study's goal is to resolve the IDS as it is represented mathematically in [14, 15] by hybridization. The hybrid model was used to compute the numerical performances for three different IDS variations. Using the data-based reference solutions has made it possible to compare the results. Using the hybrid model and the reference dataset of Adams' findings, a comparison is made.

The following items make up the work that is being given:

- A novel integrated design is offered that utilizes an • intelligent computing scheme through specially created hybrid model to identify IDS solutions.
- The reference Adams dataset provides access to the planned hybrid model for various transmission and contact rate values (s) for the IDS.
- The results closely matching those obtained using the dataset of the Adams findings improve the value and worth of the created hybrid model for solving the IDS.
- The hybrid model for addressing the IDS is improved by the presentation through comparative examinations of the metrics based on MSE and correlation.

Related work: The most recent and advanced biological system models include: mosquito dispersal in heterogeneous

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environments [16], plant virus propagation model [17], dynamical study of a nonlinear corneal shape model [18], HIV infection spread system involving CD4+ T cells [19], soft tissue and micro vessel studies via a nonlinear reactive transport model [20], and the nonlinear HIV infection system of latently infected cells [21]. Speech emotion recognition [22], COVID-19 diagnosis [23], atrial fibrillation detection [24], classification of brain tumors based on MR images [25], and COVID-19 detection from chest radiography pictures [26] are all examples of the application of ANNs in biological fields. Other than the bio-informatics studies, the use of neural networks has been reported in a wide range of fields, such as the peristaltic motion of a third-grade fluidic study in a planar channel [27], environmental economic systems [28], a multifractional order singular system [29], a singular Thomas-Fermi model [30], a model of heat conduction in the human head [31], functional differential models [32], higher order nonlinear singular models [33], heart disease prediction system [34]. All of these examples serve as inspiration for authors to investigate and test neural networks in order to address IDS along its special cases.

METHODOLOGY

The hybrid model methodology is presented in two parts for the IDS numerical findings.

- The necessary descriptions are given in order to create the data for hybrid model execution using the most recent numerical techniques.
- Running hybrid model in order to solve the IDS and provide an approximation for each variation.

Figure1 depicts a step-by-step workflow diagram of the method used to solve the influenza illness system; Step 1 presents an overview of the issue, Step 2 presents a mathematical model of the, Step 3 presents a procedural block for hybrid model, and Step 4 presents the simulation results and their interpretation. The dataset for various scenarios of IDS is developed or generated in the first stage using Adams' numerical approach for solving differential equation systems. In the "ND Solve" function, the "Adams" algorithm is used, with the stoppage and execution tolerances set to default values. The performance in the remaining portions of the study is also compared using the IDS data. In order to approximate the solution dynamics of IDS, the NN multi-layer structure explain the model working. The 'Matlab' software is used to apply the appropriate testing statistics, hidden neurons, learning schemes, and authentication data. The parameter settings used for solving IDS are listed in Table 1.



Table 1. Setting of parameters for execution of hybrid model

Index	Settings
Maximum Epochs for Learning	500
Fitness goal, i.e., MSE	0
Adaptive parameter, i.e., mu	0.005
Decreeing factor for the mu	0.1
Increasing factor for the mu	10
Maximum of mu	10^{10}
Validation fail count	6
Minimum performance gradient	10^{-07}
Number of hidden Neuron	10
Training and testing samples70%	
Testing and validation samples30%	
Sample selection	Arbitrary
Input, output and hidden layers	Single for all three
Solver for dataset generation	Adams method
Adams solver equation and stoppage parameter	Default

The LMB procedure's parameter settings are listed in Table 1, and because even a small variation, change, or adjustment could lead to subpar performance, i.e., premature convergence, these settings will be carefully implemented following significant numerical testing and experience.

EMPERICAL RESULTS AND ANALYSIS

The resolution of three IDS situations using the suggested hybrid model is presented graphically in this section. These cases based on the IDS are presented by taking the values of β to be numerical format along the gap of 20. Whereas the values of the other are $\mu = 0.02$, $\gamma = 0.5 \sigma = 0.05$, $\alpha = 73$, $\mu =$ 0.02, and $\delta = 1$. The initial conditions are r1 = 0.8, r2 = 0.1, r3= 0.04, and r4 = 0.06. The reported results for the system mathematical influenza disease model with 10 neurons using the suggested hybrid model in the range [0, 1] with step size 0.01 are 70% for the training data and 30% for the testing and validation data. In Figure 2, specifically in cases1 to 3, the MSE values are calculated for the testing states, best curve, and validation are supplied to answer each scenario of the IDS. At epochs 37, 93 and 206 the best performance values for each instance are presented. These values are around $1.057 \times 10-08$, 3.465 ×10-09 and 3.935 ×10-09, respectively. These plotted results demonstrate the hybrid model convergence in answering all cases and scenarios in the IDS model. The findings that coincide demonstrate the validity of the hybrid model strategy that was developed to solve the IDS.



Figure 1. The proposed framework

Figure 2. MSE performance for the hybrid model to solve the IDS

Conclusion

The work that is being presented is related to creating a hybrid model for the biological influenza disease utilizing graphical format. For each case of the mathematical influenza illness system, the suggested hybrid model is adjusted by using 10 hidden neurons, 70% training data, and 30% validation or testing data. By implementing the overlap of the obtained and reference database-based Adams results, the hybrid model excellence, brilliance, perfection, and accuracy are verified. For all of the three IDS cases, the values of the performance using the MSE and convergence are given for training, best curve, and testing. Additionally, the precision and correctness graphical are determined using the numerical and representations of the convergence plots, MSE indices. Future research on the fluid dynamic system, biological nonlinear models, information security models, and other crucially important related studies can all benefit from the other fields rather than medical.

Conflict of interest

The authors confirm that there is no conflict of interest involve with any parties in this research study.

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