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Research article

A stochastic computational scheme for the computer epidemic virus with delay effects

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Abstract: This work aims to provide the numerical performances of the computer epidemic virus model with the time delay effects using the stochastic Levenberg-Marquardt backpropagation neural networks (LMBP-NNs). The computer epidemic virus model with the time delay effects is categorized into four dynamics, the uninfected $S(x)$ computers, the latently infected $L(x)$ computers, the breaking-out $B(x)$ computers, and the antivirus PC's aptitude $R(x)$. The LMBP-NNs approach has been used to numerically simulate three cases of the computer virus epidemic system with delay effects. The stochastic framework for the computer epidemic virus system with the time delay effects is provided using the selection of data with 11%, 13%, and 76% for testing, training, and verification together with 15 neurons. The proposed and data-based Adam technique is overlapped to execute the LMBP-NNs method's exactness. The constancy, authentication, precision, and capability of the LMBP-NNs scheme are perceived with the analysis of the state transition measures, regression actions, correlation performances, error histograms, and mean square error measures.

Keywords: computer epidemic virus model; delay; neural networks; nonlinear; Levenberg-Marquardt backpropagation
Mathematics Subject Classification: 60H35, 92B20

1. Introduction

A computer virus is an undesirable database that has the potential to make copies, disrupt operations, and steal user's sensitive information. The general virus sources are separated from the unknown emails or damaged relationships by clicking the virus-infected files and removable storage policies. An infected computer through the virus is considered dangerous for the user's secrecy. A decade ago, the Crypto locker virus was first released and spread through email attachments. The user's file is encoded and cannot use statistics. The hackers made thirty million dollars in 3 months. One of the famous, popular, and virulent computer viruses named "I Love You" was recognized for 22 years. The email attachments were the reason the virus spread. The earnings of this program were 15 billion dollars. The quick spreading virus is recognized as My Doom which had been infected by all emails around 25%, and the hackers earned lots. A few more dangerous computer viruses are Stuxnet and Storm worm. Recently, a vital query was, how the viruses attack computers and Laptops? A few vital signs have been considered to examine the contaminated-based nodes. The system does not perform, gets slow clicks icons, and switches off shortly. The default browser homepage changes the hidden icons through the firewall and desktop. Mishra et al. [1] proposed a mathematical computer virus system to consider different forms. Sayed et al. [2] presented a partial differential system with the virus spread. Peng et al. [3] studied the numerous subclasses based on the computers using the recovered, susceptible, and exposed. The computer system is used to the immunity that the antivirus software. Rey [4,5] designed a critical assessment of mathematical systems with improvements of the alternative complexities along with the infected, susceptible, and recovered models. In another study, Rey et al. [6] discussed a new technique that analyzes the widely disseminated computer virus utilizing the discrete range. Xu et al. [7] provided the virus spreading using the network nodes in the limited form of the antivirus ability. Sanchez et al. [8,9] proposed a mathematical model based on the coronavirus SITR dynamical model and nervous stomach nonlinear system. Khan [10] created a mathematical model for SEIRS that incorporates the drawbacks of the SIR method. Khan et al. [10] studied a propagating computer population system. Fatima et al. [11] provided a structure based on the investigation of preserving the computer virus system with a dormant period of isolation. Mishra et al. [12] explored the SEIQRS mathematical framework for virus spreading using computer networks to pro the numerical finding Bist [13] studied different features of mathematical systems to analyze the computer viruses along with malware replication using different schemes. Oztürk et al. [14] investigated an updated SIR version of the system to estimate the malware results. Amador et al. [15] analyzed the SIRS system with the spread of malware dynamics based on the warning signs. Umar et al. [16–19] proposed various biological models and numerical performances. Lanz et al. [20] discussed the SEI1I2QR system to authenticate the infective performances of the system. Bukola et al. [21] designed and examined the SIRS system with the status of bug-free asymptotically constant. Arif et al. [22–23] considered the dynamical structure of the stochastic virus system using the computer population and different computational performances. The coronavirus dynamics with the delay strategies, e.g., travel restrictions, quarantine, and extended breaks to control the infectious disease spread, are proposed [24,25].

These investigations aim to provide the numerical performances of the computer epidemic virus model with the time delay effects using the stochastic Levenberg-Marquardt backpropagation neural networks (LMBP-NNs). The stochastic LMBP-NNs approach has never been used to illustrate the dynamics of a computer epidemic virus system with delay effects. On the other hand, stochastic solvers have been designated to solve various complex, nonlinear, and stiff dynamical systems. To mention some of the applications are food chain systems [26], the coronavirus dynamical model [27], HIV infection system [28], singular thermal explosion theory model [29], eye surgery system [30], differential model of the smoking model [31], and singular model [32]. The novel study features are signified as:

- A nonlinear computer epidemic virus model with the time delay effects is presented numerically.
- Three cases of the computer virus epidemic system with the delay effects have been numerically stimulated using the LMBP-NNs scheme.
- The exactness of the LMBP-NNs solver is performed based on the overlapping of the proposed and data-based reference Adam method.
- The consistency of the LMBP-NNs solver is authenticated by using the absolute error (AE) performances of the computer virus epidemic system with the delay effects.
- The state transitions (STs) measures, regression actions, correlation performances, error histograms (EHs), and mean square error (MSE) measures are provided using the LMBP-NNs solver for the computer epidemic virus system with the delay effects.

The other paper parts are organized as follows: Section 2 shows the computer epidemic virus model. The designed network structure is shown in Section 3. Section 4 narrates the results simulations. Conclusions are discussed in the final Section.

2. Mathematical model

This section performs the mathematical structure of the computer epidemic virus system with the delay effects. The system is categorized into four dynamics, the uninfected S(x) computers, the latently infected L(x) computers, the breaking-out B(x) computers and the antivirus PC's aptitude R(x). The mathematical structure of the computer virus epidemic system with the delay effects along with the initial conditions (ICs) is given as [33]:

$$\begin{cases} \dfrac{dS(x)}{dx} = \mu - \beta S(x-\tau)L(x-\tau) + B(x-\tau)e^{-\mu x} - \mu S(x) & S(0)=c_1, \\ \dfrac{dL(x)}{dx} = \beta S(x-\tau)L(x-\tau) + B(x-\tau)e^{-\mu x} - (\varepsilon+\mu)L(x) & L(0)=c_2, \\ \dfrac{dB(x)}{dx} = \varepsilon L(x) - rB(x) - \mu B(x) & B(0)=c_3, \\ \dfrac{dR(x)}{dx} = rB(x) - \alpha R(x) - \mu R(x) & R(0)=c_4. \end{cases} \tag{1}$$

The parameter based on the computer epidemic virus dynamical model with the time delay effects is tabulated in Table 1, while the flow illustrations are provided in Figure 1.

Table 1. Detailed parameters of the computer dynamical epidemic virus system with the delay effects.

Parameters	Details
μ	Recruitment and disinterest rate based on the new and old PCs in the database
β	Bilinear form of the incidence ratio based on the uninfected and latently infected PCs
ε	Latently infected rate with breaking-out PCs
μ	Natural rate of mortality with infectious PCs
r	Breaking-out rate of PC to get the antivirus aptitude
α	Antivirus ability rate of those who hold PC with viruses
τ	Delay term
x	Time
c_1, c_2, c_3, c_4	ICs

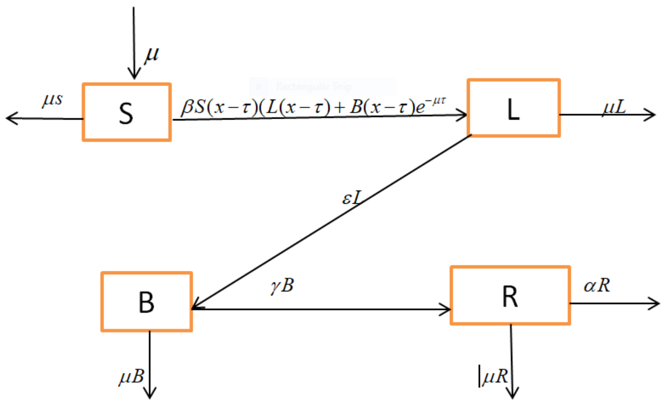


Figure 1. Flow map of the computer epidemic virus dynamical model with the time delay effects.

3. Methodology: LMBP-NNs scheme

In this section, the structure of the LMBP-NNs scheme is presented to the computer dynamical epidemic virus system with the delay effects by using the necessary performances of the procedure along with its implementation. Figure 2 shows the optimization performances of the multi-layer stochastic process based on the LMBP-NNs technique. The stochastic framework of the computer epidemic virus model with the time delay effects is provided using data selection with 11%, 13% and 76% for testing, training and verification. Fifteen numbers of neurons have been used in this study to solve the delay differential model.

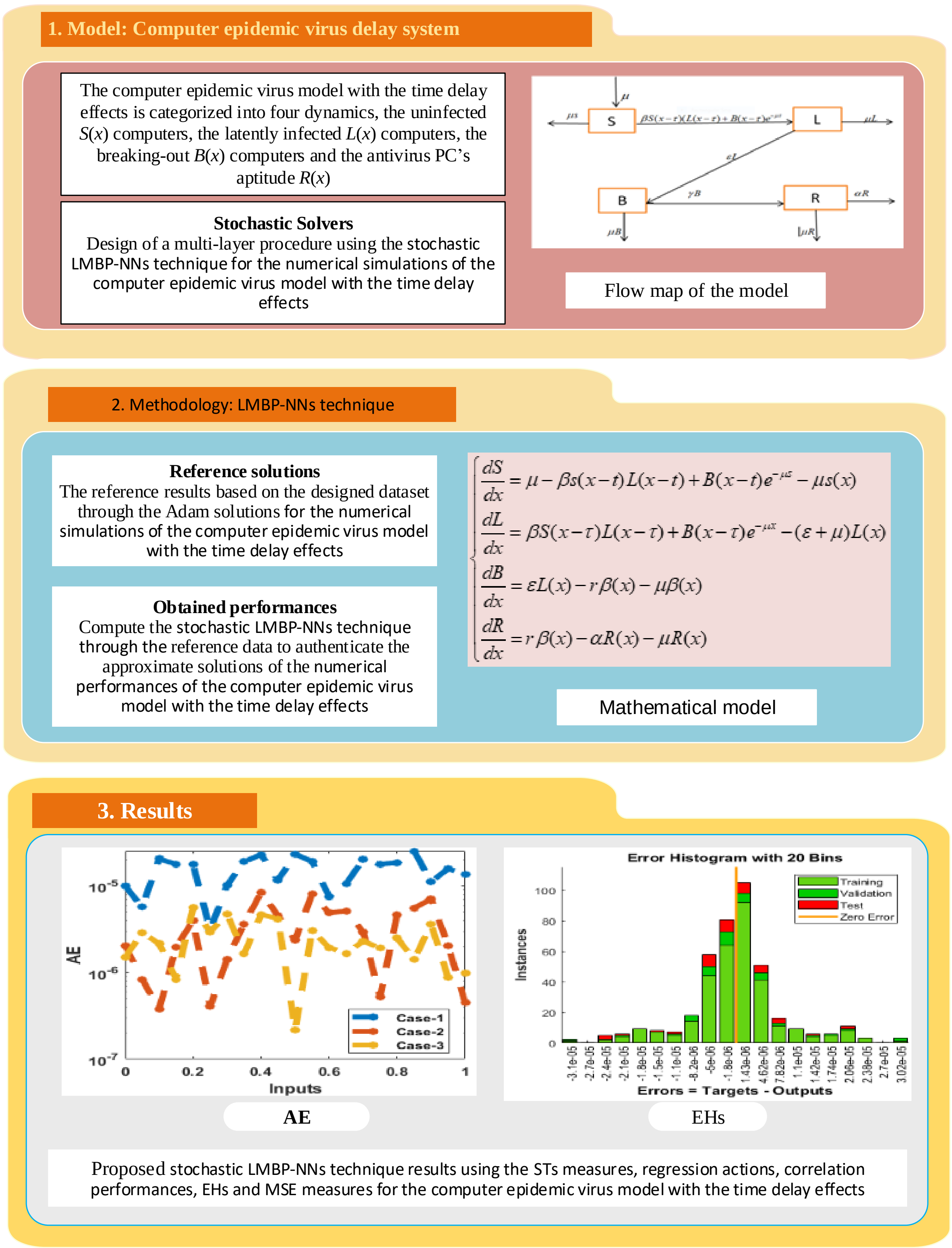


Figure 2. Numerical LMBP-NNs technique for the numerical simulations of the model.

The setting of the parameters based on the LMBP-NNs procedure is specified to the computer dynamical epidemic virus system with the delay effects provided in Table 2. The slight alteration and variation can conclude the poor performances, i.e., untimely convergence. Consequently, these options will be carefully included after substantial numerical trial and expertise. The LMB algorithms implementation process and necessary additional theoretical details are shown in [34,35].

Table 2. Parameter settings to execute the LMBP-NNs procedure.

Index	Settings
Verification data	76%
Fitness goal (MSE)	0
Test data	11%
Maximum learning iterations	680
Decreasing mu term	0.2
Selection of statics	Random
Maximum mu values	10^{10}
Output/input/ hidden layers	Single
Dataset generation	Adam scheme
Adaptive parameter (mu)	0.003
Train data	13%
Increasing mu terms	9
Hidden neurons	15
Fail of authentication count	6
Minimum gradient values	10^{-8}
Adam solver Execution of Adam method and terminating criteria	Default

4. Methodology: MWNN-GA-ASA scheme

This section presents the solutions to the dynamical form of the mathematical model. These types of mathematical dynamical models have been reported in various studies [36–38]. The numerical results of the computer epidemic virus of the time delay system using the LMBP-NNs scheme are shown in this section. The mathematical form of each case is shown as:

Case 1: Consider $\mu = 0.5$, $\beta = 0.35$, $\varepsilon = 0.2$, $\tau = 0.15$, $\alpha = 0.4$, $r = 0.4$, $c_1 = 0.4,$ $c_2 = 0.3,$ $c_3 = 0.2$ and $c_4 = 0.1$ is given in Eq (1) as:

$$\begin{cases} \dfrac{dS(x)}{dx} = 0.5 - 0.35S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.5S(x) & S(0) = 0.4, \\ \dfrac{dL(x)}{dx} = 0.35S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.7L(x) & L(0) = 0.3, \\ \dfrac{dB(x)}{dx} = 0.2L(x) - 0.9B(x) & B(0) = 0.2, \\ \dfrac{dR(x)}{dx} = 0.4B(x) - 0.9R(x) & R(0) = 0.1. \end{cases}$$

Case 2: Consider $\mu = 0.5$, $\beta = 0.6$, $\varepsilon = 0.2$, $\tau = 0.15$, $\alpha = 0.4$, $r = 0.4$, $c_1 = 0.4,$ $c_2 = 0.3,$ $c_3 = 0.2$ and $c_4 = 0.1$ is given in Eq (1) as:

$$\begin{cases} \dfrac{dS(x)}{dx} = 0.5 - 0.6S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.5S(x) & S(0) = 0.4 \\ \dfrac{dL(x)}{dx} = 0.6S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.7L(x) & L(0) = 0.3, \\ \dfrac{dB(x)}{dx} = 0.2L(x) - 0.9B(x) & B(0) = 0.2, \\ \dfrac{dR(x)}{dx} = 0.4B(x) - 0.9R(x) & R(0) = 0.1. \end{cases}$$

Case 3: Consider $\mu = 0.5$, $\beta = 0.9$, $\varepsilon = 0.2$, $\tau = 0.15$, $\alpha = 0.4$, $r = 0.4$, $c_1 = 0.4$, $c_2 = 0.3$, $c_3 = 0.2$ and $c_4 = 0.1$ is given in Eq (1) as:

$$\begin{cases} \dfrac{dS(x)}{dx} = 0.5 - 0.9S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.5S(x) & S(0) = 0.4, \\ \dfrac{dL(x)}{dx} = 0.9S(x-0.15)L(x-0.15) + B(x-0.15)e^{-0.5x} - 0.7L(x) & L(0) = 0.3, \\ \dfrac{dB(x)}{dx} = 0.2L(x) - 0.9B(x) & B(0) = 0.2, \\ \dfrac{dR(x)}{dx} = 0.4B(x) - 0.9R(x) & R(0) = 0.1. \end{cases}$$

The solutions to the computer epidemic virus system with the delay effects using the LMBP-NNs scheme are provided for three variations based on the ICs. The output, hidden, and input layer construction is presented in Figure 3.

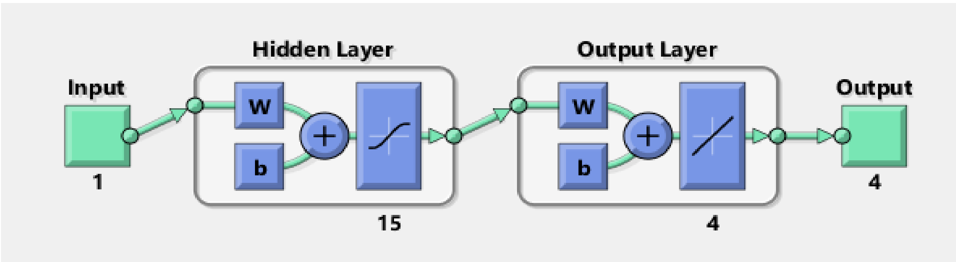


Figure 3. Hidden input and output layers construction for the computer epidemic model.

In Figures 4–6, the LMBP-NNs technique is used to draw the numerical representations of three distinct variants based on the ICs for the computer virus epidemic system with the delay effects. The STs measures and best assessment values are derived in Figures 4 and 5. The STs performances and MSE measures for the best curves, verification, and training are presented for three different variations based on the ICs. These precise results based on the computer virus epidemic model with the delay effects are derived at epochs 42, 17, and 53, measured as 1.2145×10^{-10}, 2.9103×10^{-11} and 1.3341×10^{-10}, respectively. The performances of the gradient operators have been reported in Figure 4 based on the computer virus epidemic system with the delay effects. These gradient operator performances have been provided as 6.9708×10^{-8}, 7.3422×10^{-8}, and 9.9456×10^{-8}. These graphical plot representations indicate the convergence of the LMBP-NNs scheme of the computer epidemic virus system. Figure 5 validates the fitting cure design to perform the numerical simulations of the computer virus epidemic system with the delay effects. The graphical curve plots compare the results for each case of the model. The error plots through the training, verification, and testing performances have been indicated in the computer virus epidemic model with the delay effects using the LMBP-NNs procedure. The EHs illustrations and the regression measures have been presented in Figure 5 using the computer virus epidemic system using the LMBP-NNs procedure. The EHs values have been presented as 1.43×10^{-6}, 2.68×10^{-7} and 2.08×10^{-6} for each model variation using the LMBP-NNs procedure. The regression plot illustrations are reported in Figure 6 to indicate the correlation measures. It is observed that the correlation measures are reported as 1 for individual cases of the model. The testing, training, and authentication plots label the exactness of the LMBP-NNs procedure to indicate the numerical simulations of the model using the LMBP-NNs procedure. The convergence plots obtained through the MSE measures using the testing, validation, training, epochs, and complexity are provided in Table 3 for the computer epidemic virus model using the LMBP-NNs procedure.

Table 3. Designed LMBP-NNs procedure for the computer epidemic virus model with the time delay effects.

Case	MSE			Gradient	Mu	Iterations	Performance	Time
	Testing	Training	Endorsement					
1	1.04×10^{-10}	6.88×10^{-11}	1.21×10^{-10}	9.97×10^{-8}	1×10^{-10}	42	6.89×10^{-11}	03
2	3.09×10^{-11}	4.67×10^{-12}	2.91×10^{-11}	7.34×10^{-8}	1×10^{-11}	17	4.68×10^{-12}	02
3	1.28×10^{-10}	6.11×10^{-11}	1.33×10^{-10}	9.95×10^{-8}	1×10^{-10}	53	6.11×10^{-11}	04

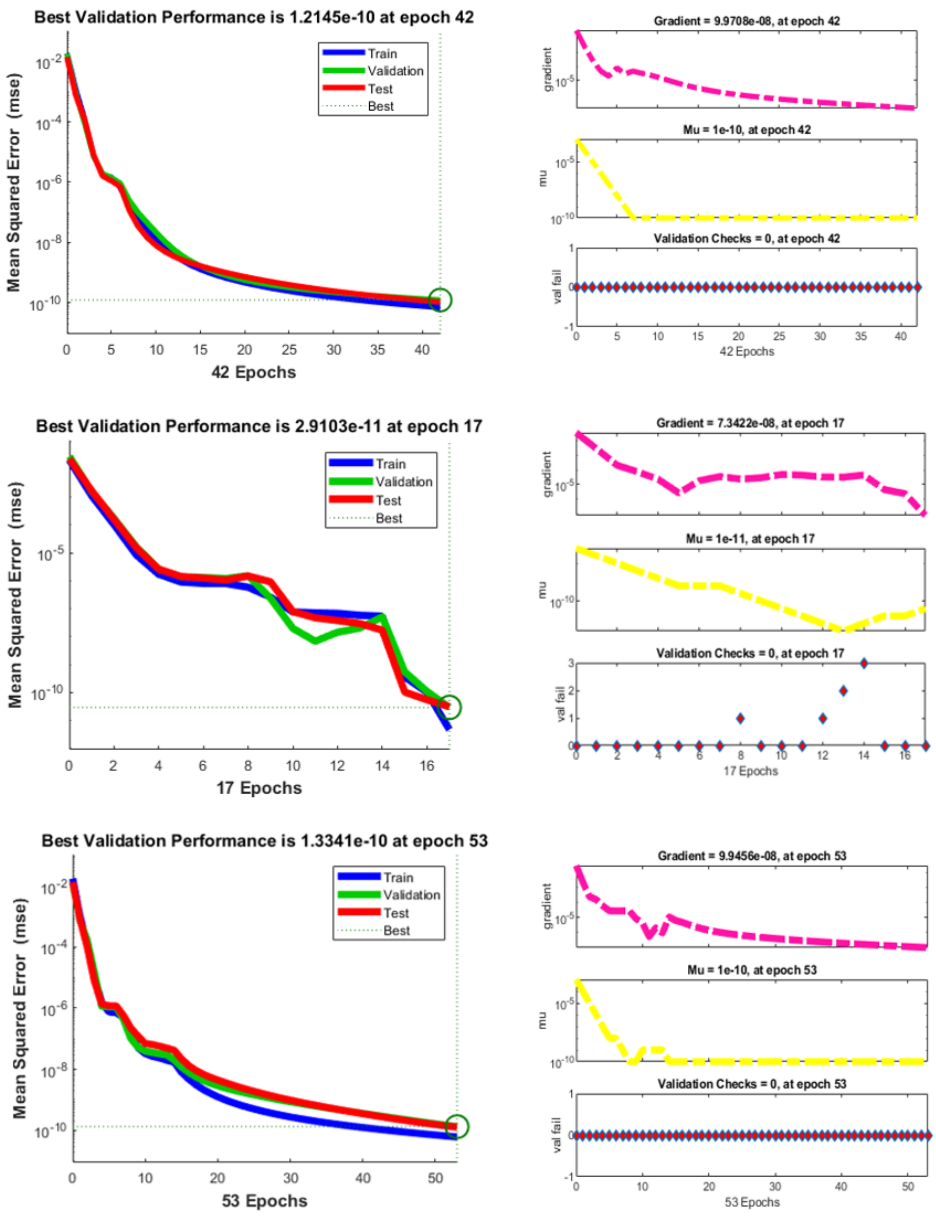


Figure 4. MSE measures and STs performances for the computer epidemic virus model with the time delay effects using the LMBP-NNs procedure.

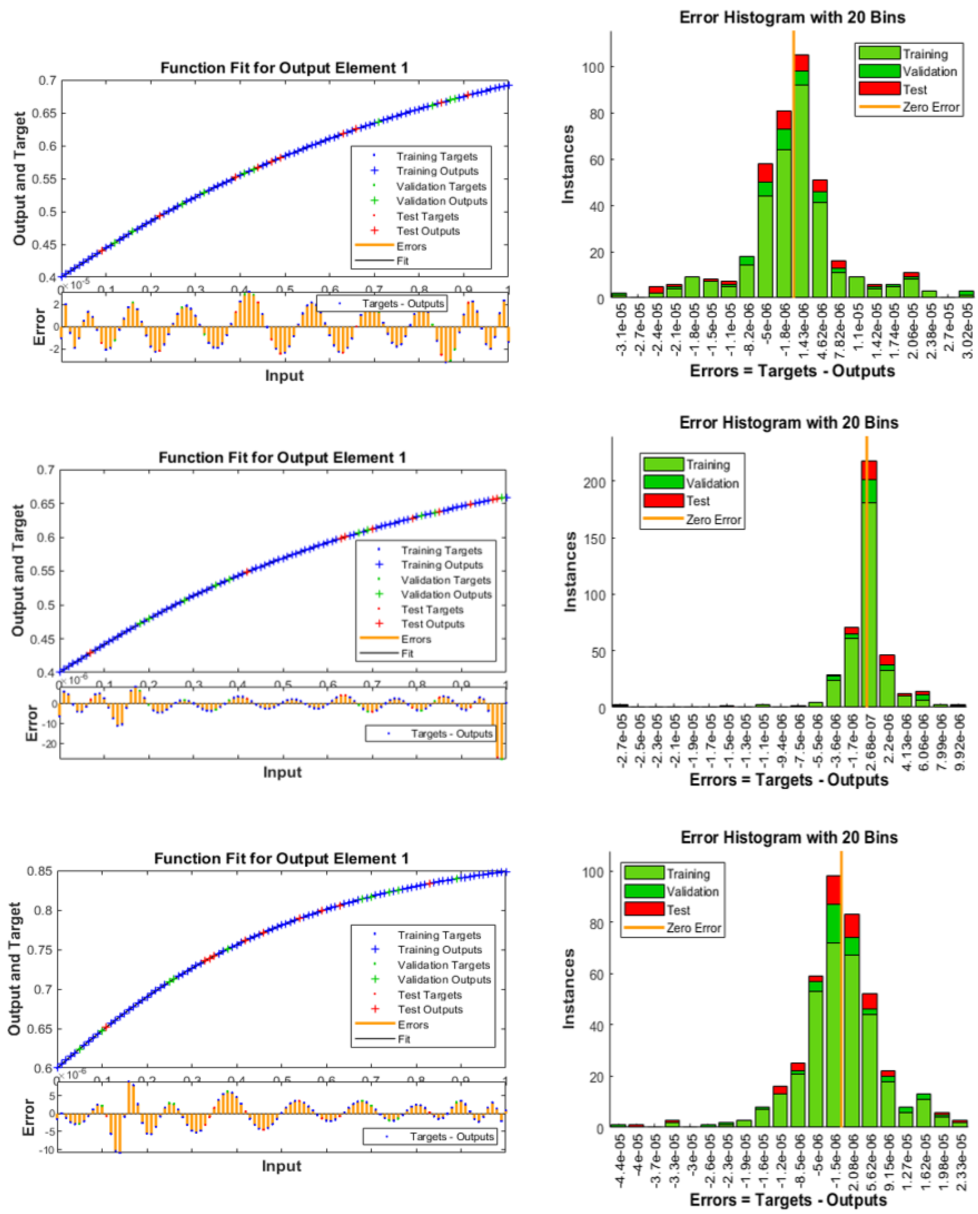
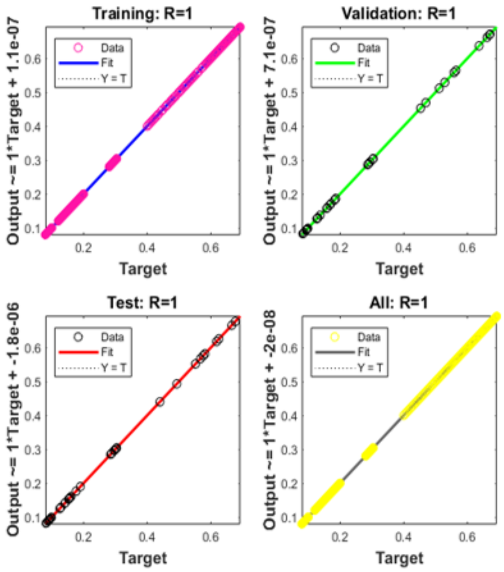
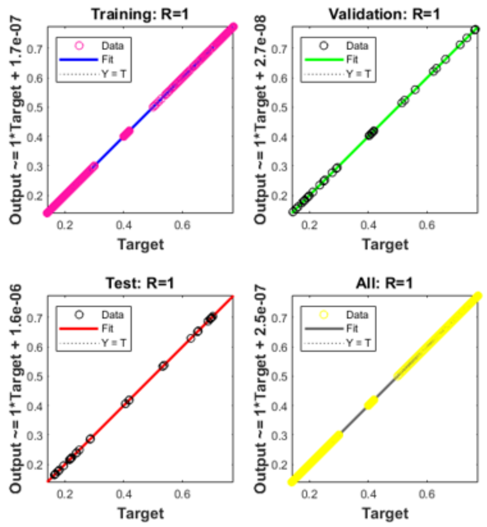


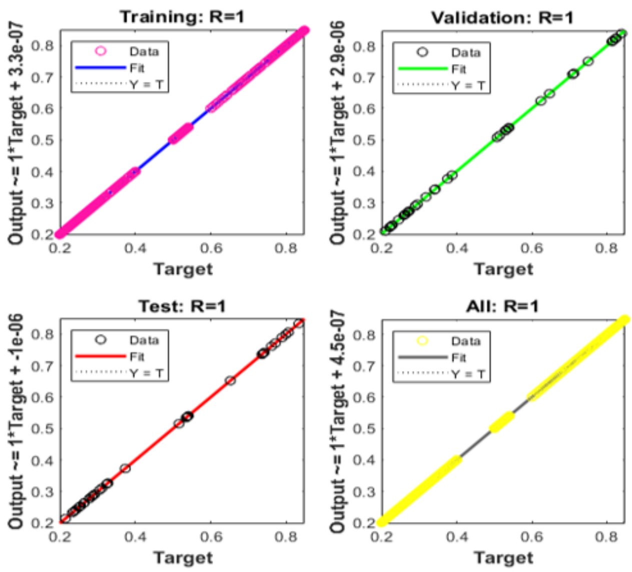
Figure 5. EHs and results for the computer epidemic virus model with the time delay effects using the LMBP-NNs procedure.



(a) Regression: **Case 1**



(b) Regression: **Case 2**



(c) Regression: **Case 3**

Figure 6. Regression plots for computer virus epidemic system with the delay effects using the LMBP-NNs procedure.

The performance outcomes and absolute error (AE) values from three validation, testing, and training cases utilizing the LMBP-NNs approach are shown in Figures 7 and 8. These plots indicate the correctness of the LMBP-NNs scheme for the computer epidemic virus system with the time delay effects. Figure 7 shows the comparison values through the achieved and reference results for solving the computer virus epidemic system with the delay effects. The matching of the obtained, and reference results provides the correctness of LMBP-NNs scheme for the computer epidemic virus model. The

AE measures for the LMBP-NNs stochastic approach using three different cases of the model are derived in Figure 8. The computer epidemic virus model with the time delay effects is categorized into four dynamics, the uninfected S(x) computers, the latently infected L(x) computers, the breaking-out B(x) computers, and the antivirus PC's aptitude R(x). The AE for the uninfected PC's S(x) is derived as 10^{-5} to 10^{-6}, 10^{-5} to 10^{-7}, and 10^{-5} to 10^{-8} for individual cases of the computer epidemic virus model. The AE performances for the latently infected L(x) computers are derived as 10^{-5} to 10^{-6}, 10^{-6} to 10^{-7}, and 10^{-6} to 10^{-8} for cases 1–3. The AE values for the breaking-out PC's B(x) are performed as 10^{-5} to 10^{-6}, 10^{-6} to 10^{-7}, and 10^{-5} to 10^{-7}. Similarly, the AE measures for the antivirus PC's ability R(x) are performed as 10^{-5} to 10^{-8}, 10^{-6} to 10^{-8} and 10^{-5} to 10^{-7} for individual cases of the computer epidemic virus model. These precise and accurate measures indicate the correctness of the LMBP-NNs scheme for the computer epidemic virus model with the time delay effects.

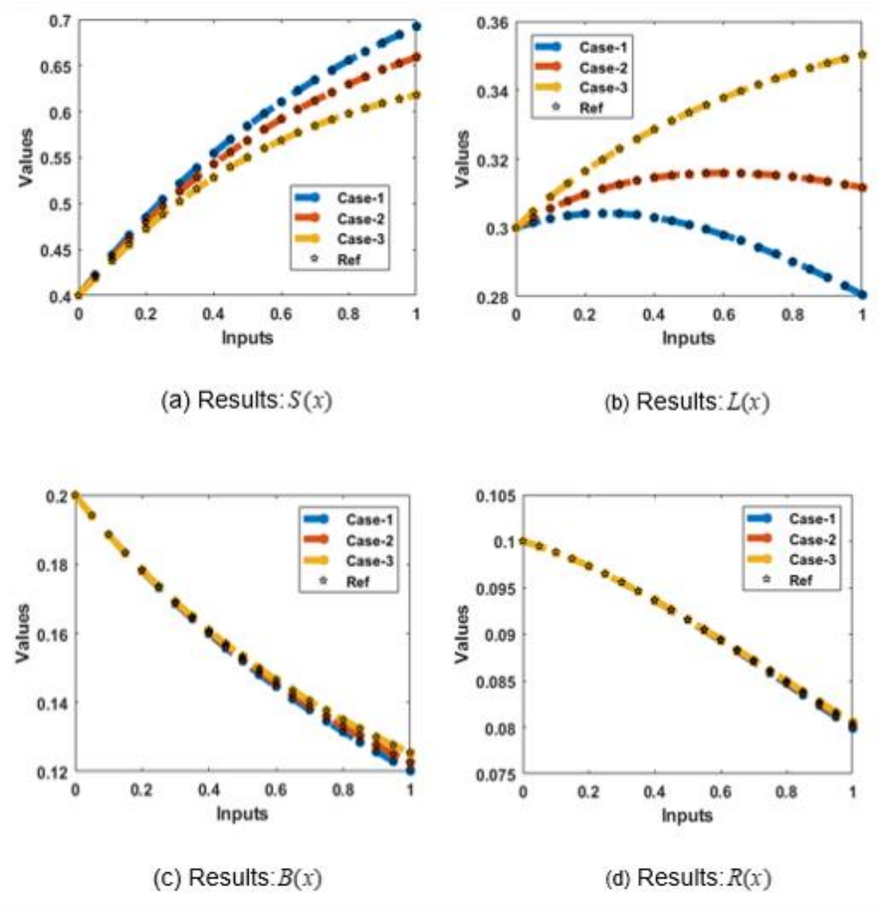


Figure 7. Comparison performances for the computer epidemic virus model with the time delay effects.

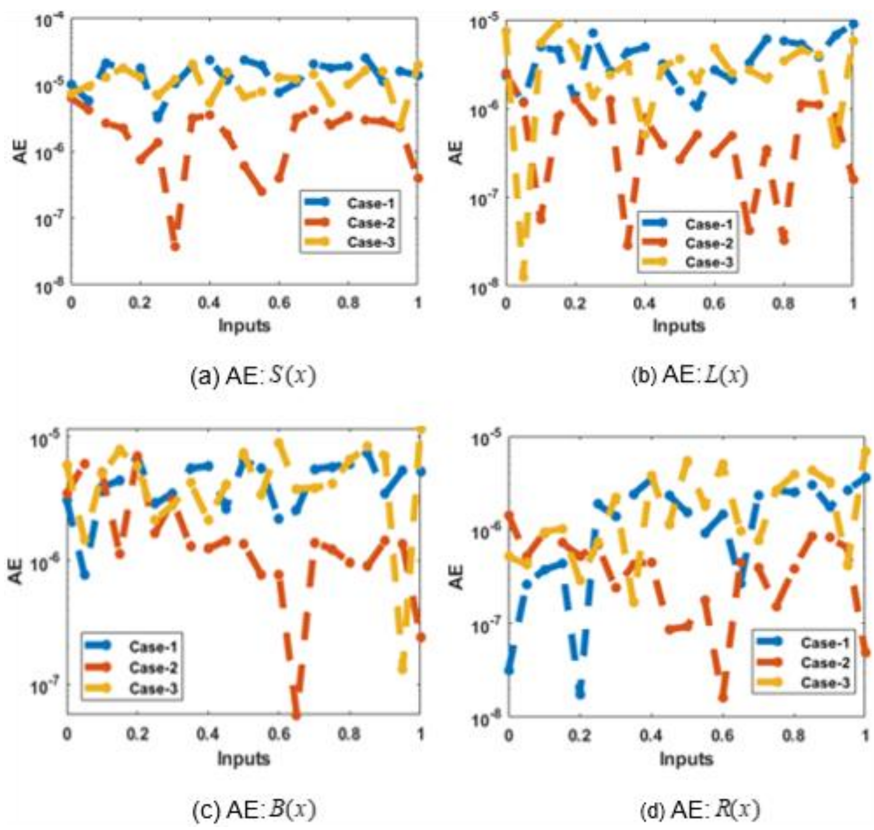


Figure 8. AE values for the computer epidemic virus model with the time delay effects.

5. Conclusions

This study aims to solve the computer epidemic virus model with the time delay effects using the Levenberg-Marquardt backpropagation neural networks. The mathematical form of the model is categorized into four dynamics, the uninfected S(x) computers, the latently infected L(x) computers, the breaking-out B(x) computers, and the antivirus PC's aptitude R(x). Finally, a few concluding remarks of the current study are presented as follows:

- A nonlinear computer epidemic virus model with the time delay effects has been numerically solved.
- The computer epidemic virus model's delay factors complicate the dynamic system. To numerically formulate the computer epidemic virus model with delay effects, the stochastic approach based on Levenberg-Marquardt backpropagation neural networks is one of the appropriate options.
- The stochastic framework for the computer virus epidemic model with the delay effects has been provided using data selection with 11%, 13%, and 76% for testing, training, and verification.
- Fifteen hidden neurons have been used to solve the computer virus epidemic model with the delay effects.
- Stochastic LMBP-NNs procedure's exactness has been performed by overlapping the proposed and data-based reference Adam method.
- The AE values are provided in suitable measures, which are performed as 10^{-4} to 10^{-7} for each category of the computer virus epidemic system with the delay effects.

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Conflict of interest

All authors declare that there are no potential conflicts of interest.

References

1. B. K. Mishra, D. Saini, Mathematical models on computer viruses, *Appl. Math. Comput.*, **187** (2007), 929–936. https://doi.org/10.1016/j.amc.2006.09.062
2. A. M. El-Sayed, A. A. Arafa, M. Khalil, A. Hassan, A mathematical model with memory for propagation of computer virus under human intervention, *Prog. Fract. Differ. Appl.*, **2** (2016), 105–113. https://doi.org/10.18576/pfda/020203
3. M. Peng, X. He, J. Huang, T. Dong, Modeling computer virus and its dynamics, *Math. Probl. Eng.*, **2013** (2013), 842614. https://doi.org/10.1155/2013/842614
4. A. M. del Rey, Mathematical modeling of the propagation of malware: a review, *Security Comm. Networks*, **8** (2015), 2561–2579. https://doi.org/10.1002/sec.1186
5. A. M. del Rey, A SIR e-Epidemic model for computer worms based on cellular automata, In: *Advances in artificial intelligence*, Berlin: Springer, 2013, 228–238. https://doi.org/10.1007/978-3-642-40643-0_24
6. A. M. del Rey, G. R. Sánchez, A discrete mathematical model to simulate malware spreading, *Int. J. Mod. Phys. C*, **23** (2012), 1250064. https://doi.org/10.1142/S0129183112500647
7. Y. Xu, J. Ren, Propagation effect of a virus outbreak on a network with limited anti-virus ability, *Plos One*, **11** (2016), e0164415. https://doi.org/10.1371/journal.pone.0164415
8. Y. G. Sánchez, Z. Sabir, J. L. Guirao, Design of a nonlinear SITR fractal model based on the dynamics of a novel coronavirus (COVID-19), *Fractals*, **28** (2020), 2040026. https://doi.org/10.1142/S0218348X20400265
9. Y. G. Sánchez, Z. Sabir, H. Günerhan, H. M. Baskonus, Analytical and approximate solutions of a novel nervous stomach mathematical model, *Discrete Dyn. Nat. Soc.*, **2020** (2020), 5063271. https://doi.org/10.1155/2020/5063271
10. M. S. S. Khan, A computer virus propagation model using delay differential equations with probabilistic contagion and immunity, 2014, arXiv:1410.5718.
11. U. Fatima, M. Ali, N. Ahmed, M. Rafiq, Numerical modeling of susceptible latent breaking-out quarantine computer virus epidemic dynamics, *Heliyon*, **4** (2018), e00631. https://doi.org/10.1016/j.heliyon.2018.e00631
12. B. K. Mishra, N. Jha, SEIQRS model for the transmission of malicious objects in computer network, *Appl. Math. Model.*, **34** (2010), 710–715. https://doi.org/10.1016/j.apm.2009.06.011
13. A. S. Bist, Mathematical approaches for computer virus, *Int. J. Eng. Sci. Res. Technol.*, **1** (2012), 429–431.
14. Y. Öztürk, M. Gülsu, Numerical solution of a modified epidemiological model for computer viruses, *Appl. Math. Model.*, **39** (2015), 7600–7610. https://doi.org/10.1016/j.apm.2015.03.023

15. J. Amador, J. R. Artalejo, Stochastic modeling of computer virus spreading with warning signals, *J. Frankl. Inst.*, **350** (2013), 1112–1138. https://doi.org/10.1016/j.jfranklin.2013.02.008
16. M. Umar, Z. Sabir, M. A. Z. Raja, Intelligent computing for numerical treatment of nonlinear prey-predator models, *Appl. Soft Comput.*, **80** (2019), 506–524. https://doi.org/10.1016/j.asoc.2019.04.022
17. M. Umar, F. Amin, H. A. Wahab, D. Baleanu, Unsupervised constrained neural network modeling of boundary value corneal model for eye surgery, *Appl. Soft Comput.*, **85** (2019), 105826. https://doi.org/10.1016/j.asoc.2019.105826
18. M. Umar, Z. Sabir, M. A. Z. Raja, H. M. Baskonus, S. W. Yao, E. Ilhan, A novel study of Morlet neural networks to solve the nonlinear HIV infection system of latently infected cells, *Results Phys.*, **25** (2021), 104235. https://doi.org/10.1016/j.rinp.2021.104235
19. M. Umar, Z. Sabir, M. A. Z. Raja, Y. G. Sánchez, A stochastic numerical computing heuristic of SIR nonlinear model based on dengue fever, *Results Phys.*, **19** (2020), 103585. https://doi.org/10.1016/j.rinp.2020.103585
20. A. Lanz, D. Rogers, T. L. Alford, An epidemic model of malware virus with quarantine, *J. Adv. Math. Comput. Sci.*, **33** (2019), 1–10.
21. O. Bukola, A. O. Adetunmbi, T. T. Yusuf, An SIRS model of virus epidemic on a computer network, *J. Adv. Math. Comput. Sci.*, **17** (2016), 1–12. https://doi.org/10.9734/BJMCS/2016/24816
22. M. S. Arif, A. Raza, W. Shatanawi, M. Rafiq, M. Bibi, A stochastic numerical analysis for computer virus model with vertical transmission over the internet, *Comput. Mater. Con.*, **61** (2019), 1025–1043. https://doi.org/10.32604/cmc.2019.08405
23. M. S. Arif, A. Raza, M. Rafiq, M. Bibi, J. N. Abbasi, A. Nazeer, et al., Numerical simulations for stochastic computer virus propagation model, *Comput. Mater. Con.*, **61** (2019), 61–77. https://doi.org/10.32604/cmc.2020.08595
24. E. F. D. Goufo, Y. Khan, Q. A. Chaudhry, HIV and shifting epicenters for COVID-19, an alert for some countries, *Chaos Soliton. Fract.*, **139** (2020), 110030. https://doi.org/10.1016/j.chaos.2020.110030
25. N. Faraz, Y. Khan, E. D. Goufo, A. Anjum, A. Anjum, Dynamic analysis of the mathematical model of COVID-19 with demographic effects, *Z. Naturforsch. C*, **75** (2020), 389–396. https://doi.org/10.1515/znc-2020-0121
26. Z. Sabir, Stochastic numerical investigations for nonlinear three-species food chain system, *Int. J. Biomath.*, **15** (2022), 2250005. https://doi.org/10.1142/S179352452250005X
27. M. Umar, Z. Sabir, M. A. Z. Raja, M. Shoaib, M. Gupta, Y. G. Sánchez, A stochastic intelligent computing with neuro-evolution heuristics for nonlinear SITR system of novel COVID-19 dynamics, *Symmetry*, **12** (2020), 1628. https://doi.org/10.3390/sym12101628
28. M. Umar, Z. Sabir, F. Amin, J. L. Guirao, M. A. Z. Raja, Stochastic numerical technique for solving HIV infection model of CD4+ T cells, *Eur. Phys. J. Plus*, **135** (2020), 403. https://doi.org/10.1140/epjp/s13360-020-00417-5
29. Z. Sabir, Neuron analysis through the swarming procedures for the singular two-point boundary value problems arising in the theory of thermal explosion, *Eur. Phys. J. Plus*, **137** (2022), 638. https://doi.org/10.1140/epjp/s13360-022-02869-3

30. B. Wang, J. F. Gomez-Aguilar, Z. Sabir, M. A. Z. Raja, W. F. Xia, H. Jahanshahi, et al., Numerical computing to solve the nonlinear corneal system of eye surgery using the capability of Morlet wavelet artificial neural networks, *Fractals*, **2022** (2022), 2240147. https://doi.org/10.1142/S0218348X22401478
31. T. Saeed, Z. Sabir, M. S. Alhodaly, H. H. Alsulami, Y. G. Sánchez, An advanced heuristic approach for a nonlinear mathematical based medical smoking model, *Results Phys*., **32** (2022), 105137. https://doi.org/10.1016/j.rinp.2021.105137
32. Z. Sabir, H. A. Wahab, Evolutionary heuristic with Gudermannian neural networks for the nonlinear singular models of third kind, *Phys. Scr.*, **96** (2021), 125261. https://doi.org/10.1088/1402-4896/ac3c56
33. A. Raza, U. Fatima, M. Rafiq, N. Ahmed, I. Khan, K.S. Nisar, et al., Mathematical analysis and design of the nonstandard computational method for an epidemic model of computer virus with delay effect: application of mathematical biology in computer science, *Results Phys.*, **21** (2021), 103750. https://doi.org/10.1016/j.rinp.2020.103750
34. K. Mukdasai, Z. Sabir, M. A. Z. Raja, R. Sadat, M. R. Ali, P. Singkibud, A numerical simulation of the fractional order Leptospirosis model using the supervise neural network, *Alex. Eng. J.*, **61** (2022), 12431–12441. https://doi.org/10.1016/j.aej.2022.06.013
35. T. Botmart, Z. Sabir, M. A. Z. Raja, M. R. Ali, R. Sadat, A. A. Aly, et al., A hybrid swarming computing approach to solve the biological nonlinear Leptospirosis system, *Biomed. Signal Proces.*, **77** (2022), 103789. https://doi.org/10.1016/j.bspc.2022.103789
36. M. De la Sen, S. Alonso-Quesada, A. Ibeas, On the stability of an SEIR epidemic model with distributed time-delay and a general class of feedback vaccination rules, *Appl. Math. Comput*., **270** (2015), 953–976. https://doi.org/10.1016/j.amc.2015.08.099
37. Q. Gao, J. Zhuang, Stability analysis and control strategies for worm attack in mobile networks via a VEIQS propagation model, *Appl. Math. Comput.*, **368** (2020), 124584. https://doi.org/10.1016/j.amc.2019.124584
38. H. Zhou, S. Shen, J. Liu, Malware propagation model in wireless sensor networks under attack-defense confrontation, *Comput. Commun*., **162** (2020), 51–58. https://doi.org/10.1016/j.comcom.2020.08.009