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Numerical Study of Computer Virus Reaction Diffusion Epidemic Model

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Abstract: Reaction–diffusion systems are mathematical models which link to several physical phenomena. The most common is the change in space and time of the meditation of one or more materials. Reaction–diffusion modeling is a substantial role in the modeling of computer propagation like infectious diseases. We investigated the transmission dynamics of the computer virus in which connected to each other through network globally. The current study devoted to the structure-preserving analysis of the computer propagation model. This manuscript is devoted to finding the numerical investigation of the reaction–diffusion computer virus epidemic model with the help of a reliable technique. The designed technique is finite difference scheme which sustains the important physical behavior of continuous model like the positivity of the dependent variables, the stability of the equilibria. The theoretical analysis of the proposed method like the positivity of the approximation, stability, and consistency is discussed in detail. A numerical example of simulations yields the authentication of the theoretical results of the designed technique.

1 Introduction

Computer viruses are automated programs that, against the users' wish, make copies of themselves to spread to new targets and as a result infect the computers [1]. With the accelerated advancement of modern technologies, the internet has assimilated into each part of our life, which is a great help for us, as well as it also poses a serious problem to individual and corporate computer systems through cyber-attacks [2]. A lot of effort has been dedicated to studying how to avoid harmful actions. To control effectively the diffusion of computer viruses, it is very crucial to figure out the ways that nasty codes

propagate over the Internet. In order to minimize the threat of virus spread, various strategies can be proposed by using epidemic models. In 2018, Ali et al. [3] studied the Padé approximation method to describe the propagation of a computer virus via the SEIR model. Due to the compelling analogy between a computer virus and a biological virus, some classic computer virus epidemic models, such as SIRS, SIS, SIR, SLB, SEIR, delayed, and stochastic models were proposed and studied. In epidemics, the most common fatal infectious diseases are measles, malaria, HIV/AIDS, tuberculosis, influenza, etc., determine the individual mechanisms and environmental conditions that have contributed to their spread. Epidemic modeling helps to identify the specific areas of virus spread and also predict effective preventives and creative measures to control it [4]. Mishra et al. [5] presented various mathematical models on computer viruses. In 2017, Kumar [6] developed a SIRA dynamical model of the computer virus. In 2008, Doud et al. [7] proposed computer virus plans and discovery methods by using different delays. In 2015, Ebenezer et al. [8] presented the SIER mathematical model by the use of local and global sense dynamics of computer bugs productivity. In 2019, Ozdemir et al. [9] proposed the SEIR-KS model of fractional order model for computer virus transmission. In 2015, Oztürk et al. [10] presented the mathematical modeling of an improved version of the SIR model. Rey [11] investigated the dynamics of computer virus spread in the system of networks. In 2019, Lanz et al. [12] proposed the SEI_1I_2QR model in which they examine types of malware acquired based on infection symptoms treatment. In 2016, Xu et al. [13] presented the SEIR model to discuss the spread of malware in the presence of anti-virus capacity. In 2016, Liu et al. [14] represented the SIQR model by utilizing two delays strategy. In 2008, Yuan et al. [15] described the SEIR model by use of three crucial networking environmental factors. In 2012, Yang et al. [16] suggested the SLBS model in which explains the prohibition of malware on the internet. In 2020, Dubey et al. [17] studied the analytically schemes for malware spread through the network and proposed the CVP model. In 2020, Arif et al. [18] investigated the stochastic dynamics of the computer propagation model by using the different numerical techniques in which focus on the structure-preserving method. In our opinion, the epidemic models for computer viruses can help to better understanding how the viruses diffuse on networks. In this study, we extend a computer virus epidemic model by placing a diffusion term. We determine the conditions under which epidemics are likely to occur. The computer virus has a latent period, during which individuals are exposed to a computer virus but are not yet infectious. An infected computer which is in latency, will not infect other computers immediately; however, it still can be infected [19]. In this study, the following reaction–diffusion computer virus epidemic model is proposed for numerical analysis which is an extended form of the model given by Persaei et al. [20].

$$\frac{\partial S}{\partial t} = d_1 \frac{\partial^2 S}{\partial x^2} + \delta - \beta S(L + B) + \gamma_1 L + \gamma_2 B - \delta S, \tag{1}$$

$$\frac{\partial L}{\partial t} = d_2 \frac{\partial^2 L}{\partial x^2} + \beta S(L + B) - \gamma_1 L - \acute{\alpha} L - \delta L, \tag{2}$$

$$\frac{\partial B}{\partial t} = d_3 \frac{\partial^2 B}{\partial x^2} + \acute{\alpha} L - \gamma_2 B - \delta B. \tag{3}$$

with initial conditions

$S(x, 0) = \mathcal{F}_1(x) \geq 0, \, L(x, 0) = \mathcal{F}_2(x) \geq 0, \, B(x, 0) = \mathcal{F}_3(x) \geq 0,$

and homogenous Neumann boundary conditions. Where $S(x, t)$ represents the class of uninfected computers, $L(x, t)$ represents latent computers and $B(x, t)$ represents the seizing computers at time t. The constant rate of connecting external computers with internet and disconnecting internal computers from internet is denoted by δ. β is the constant rate of infection and the term $\beta S(L + B)$ is the percentage of internal computers infected at time t. $\acute{\alpha}$ is the constant rate of latent computer breakout. Latent computers are cured at the constant rate of γ_1, while breaking out computers are cured at the constant rate of γ_2. d_1, d_2, d_3 are

constant rate of diffusion. All these parameters used in this model are positive. It is observed that the variables of interest of the proposed computer virus model are the computer populations. Now it is the basic need for the solution of system (Eqs. (1)–(3)) to be positive as values of unknown variables involved are taken as absolute [21]. In the present era, several positivity persevering numerical techniques are proposed by various authors because many dynamical continuous systems require the positive solution [22,23]. The current work is dedicated to designing and analyzing a finite difference algorithm which retains the positive solution of the state variables of the continuous system for the solution of computer virus epidemic model (Eqs. (1)–(3)). This manuscript is sectioned as follows. The reproductive number and equilibrium points of the system under study is explained in Section 2. In Section 3, a numerical algorithm is designed to solve the computer virus epidemic system. In the same section, the theoretical analysis of the proposed technique is performed. It is shown that the designed numerical technique is capable of retaining the positivity of the solution. The stability and consistency of the proposed algorithm are also authenticated in this section. Section 4 is devoted to the computation results. The simulations are justified the theoretical results of the designed method.

2 Equilibria of the Model

The model Eqs. (1)–(3) admits two equilibrium points, VFE (virus free equilibrium) $= E_0 = (1,\ 0,\ 0)$, and the CVE (computer virus endemic equilibrium point) $= E_1 = (S_1,\ L_1,\ B_1)$.

where, $S_1 = \dfrac{1}{\Re_0} = \dfrac{(\gamma_2 + \delta)(\acute{\alpha} + \gamma_1 + \delta)}{\beta(\acute{\alpha} + \gamma_2 + \delta)}$, $L_1 = \dfrac{(\Re_0 - 1)(\gamma_2 + \delta)}{\Re_0(\acute{\alpha} + \gamma_2 + \delta)}$, $B_1 = \dfrac{\acute{\alpha}(\Re_0 - 1)}{\Re_0(\acute{\alpha} + \gamma_2 + \delta)}$, and reproductive

number of the model is $\Re_0 = \dfrac{\beta(\acute{\alpha} + \gamma_2 + \delta)}{(\gamma_2 + \delta)(\acute{\alpha} + \gamma_1 + \delta)}$.

3 Numerical Modeling

Divide $[0, L] \times [0, T]$ into $M^2 \times N$ with step sizes $h = \dfrac{L}{M}$ and $k = \dfrac{T}{N}$. Grid points are

$$x_j = jh, \qquad j = 0, 1, 2, \ldots, M,$$

$$t_n = nk, \qquad n = 0, 1, 2, \ldots, N,$$

S_j^n, L_j^n and B_j^n are denoted as finite difference approximations of $S(jh, nk)$, $L(jh, nk)$ and $B(jh, nk)$ respectively.

Take Eq. (1)

$$\frac{S_j^{n+1} - S_j^n}{k} = d_1 \frac{S_{j-1}^{n+1} - 2S_j^{n+1} + S_{j+1}^{n+1}}{h^2} + \delta - \beta S_j^{n+1}\left(L_j^n + B_j^n\right) + \gamma_1 L_j^n + \gamma_2 B_j^n - \delta S_j^{n+1},$$

$$S_j^{n+1} - S_j^n = d_1 k \frac{S_{j-1}^{n+1} - 2S_j^{n+1} + S_{j+1}^{n+1}}{h^2} + \delta k - \beta k S_j^{n+1}\left(L_j^n + B_j^n\right) + \gamma_1 k L_j^n + \gamma_2 k B_j^n - \delta k S_j^{n+1}$$

$$S_j^{n+1} - S_j^n = \lambda_1\left(S_{j-1}^{n+1} - 2S_j^{n+1} + S_{j+1}^{n+1}\right) + \delta k - \beta k S_j^{n+1}\left(L_j^n + B_j^n\right) + \gamma_1 k L_j^n + \gamma_2 k B_j^n - \delta k S_j^{n+1},$$

$$-\lambda_1\left(S_{j-1}^{n+1} + S_{j+1}^{n+1}\right) + S_j^{n+1}\left(1 + 2\lambda_1 + \beta k\left(L_j^n + B_j^n\right) + \delta k\right) = S_j^n + \delta k + \gamma_1 k L_j^n + \gamma_2 k B_j^n, \tag{4}$$

Similarly we have from Eq. (2) and Eq. (3) simultaneously.

$$-\lambda_2 \left(L_{j-1}^{n+1} + L_{j+1}^{n+1}\right) + L_j^{n+1}(1 + 2\lambda_2 + (\acute{\alpha} + \gamma_1 + \delta)k) = L_j^n + \beta k S_j^n \left(L_j^n + B_j^n\right), \tag{5}$$

$$-\lambda_3 \left(B_{j-1}^{n+1} + B_{j+1}^{n+1}\right) + B_j^{n+1}(1 + 2\lambda_3 + (\gamma_2 + \delta)k) = B_j^n + \acute{\alpha} L_j^n. \tag{6}$$

where $\lambda_1 = \dfrac{d_1 k}{h^2}$, $\lambda_2 = \dfrac{d_2 k}{h^2}$ and $\lambda_3 = \dfrac{d_3 k}{h^2}$.

3.1 Consistency of the Proposed Scheme

This section is concerned about the verification of the proposed scheme to be consistent. For this,

$$Ł_S = \frac{S_j^{n+1} - S_j^n}{k} - d_1 \frac{S_{j-1}^{n+1} - 2S_j^{n+1} + S_{j+1}^{n+1}}{h^2} - \delta + \beta S_j^{n+1}\left(L_j^n + B_j^n\right) - \gamma_1 L_j^n - \gamma_2 B_j^n + \delta S_j^{n+1} \tag{7}$$

$$S_j^{n+1} = S_j^n + k\frac{\partial S}{\partial t} + \frac{k^2}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^3}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots \tag{8}$$

$$\begin{aligned}
S_{j+1}^{n+1} = {}& S_j^n + k\frac{\partial S}{\partial t} + h\frac{\partial S}{\partial x} + \frac{k^2}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{h^2}{2!}\frac{\partial^2 S}{\partial x^2} + 2hk\frac{\partial S}{\partial t}\frac{\partial S}{\partial x} + \frac{k^3}{3!}\frac{\partial^3 S}{\partial t^3} + \frac{h^3}{3!}\frac{\partial^3 S}{\partial x^3} \\
& + 3\frac{h^2 k}{3!}\frac{\partial^3 S}{\partial x^2 \partial t} + 3\frac{hk^2}{3!}\frac{\partial^3 S}{\partial x \partial t^2}.
\end{aligned} \tag{9}$$

$$\begin{aligned}
S_{j-1}^{n+1} = {}& S_j^n + k\frac{\partial S}{\partial t} - h\frac{\partial S}{\partial x} + \frac{k^2}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{h^2}{2!}\frac{\partial^2 S}{\partial x^2} - 2hk\frac{\partial S}{\partial t}\frac{\partial S}{\partial x} + \frac{k^3}{3!}\frac{\partial^3 S}{\partial t^3} - \frac{h^3}{3!}\frac{\partial^3 S}{\partial x^3} \\
& + 3\frac{h^2 k}{3!}\frac{\partial^3 S}{\partial x^2 \partial t} - 3\frac{hk^2}{3!}\frac{\partial^3 S}{\partial x \partial t^2}.
\end{aligned} \tag{10}$$

By putting all these definitions' in Eq. (7), we have

$$\begin{aligned}
Ł_S = {}& \frac{k}{k}\left(\frac{\partial S}{\partial t} + \frac{k}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^2}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots\right) - \frac{d_1 h^2}{h^2}\left(\frac{\partial^2 S}{\partial x^2} + k\frac{\partial^3 S}{\partial x^2 \partial t} + \cdots\right) - \delta + \beta\left(L_j^n + B_j^n\right) \\
& \left(S_j^n + k\frac{\partial S}{\partial t} + \frac{k^2}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^3}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots\right) - \gamma_1 L_j^n - \gamma_2 B_j^n + \delta\left(S_j^n + k\frac{\partial S}{\partial t} + \frac{k^2}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^3}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots\right) \\
= {}& \frac{\partial S}{\partial t} - d_1\frac{\partial^2 S}{\partial x^2} - \delta + \beta S_j^n\left(L_j^n + B_j^n\right) - \gamma_1 L_j^n - \gamma_2 B_j^n + \delta S_j^n - \frac{d_1 h^2}{12}\frac{\partial^4 S}{\partial x^4} \\
& + k\left(\beta\left(\left(L_j^n + B_j^n\right) + \delta\right)\frac{\partial S}{\partial t} - d_1\frac{\partial^3 S}{\partial x^2 \partial t} + \frac{1}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^2}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots\right), \\
= {}& -\frac{d_1 h^2}{12}\frac{\partial^4 S}{\partial x^4} + k\left(\beta\left(\left(L_j^n + B_j^n\right) + \delta\right)\frac{\partial S}{\partial t} - d_1\frac{\partial^3 S}{\partial x^2 \partial t} + \frac{1}{2!}\frac{\partial^2 S}{\partial t^2} + \frac{k^2}{3!}\frac{\partial^3 S}{\partial t^3} + \cdots\right) \to 0 \text{ as } h^2 \to 0, \ k \to 0.
\end{aligned}$$

Similarly we can check for $Ł_L$ and $Ł_B$ i.e.,

$$Ł_L = -\frac{d_2 h^2}{12}\frac{\partial^4 L}{\partial x^4} + k\left((\acute{\alpha} + \gamma_1 + \delta)\frac{\partial L}{\partial t} - d_2\frac{\partial^3 L}{\partial x^2 \partial t} + \frac{1}{2!}\frac{\partial^2 L}{\partial t^2} + \frac{k^2}{3!}\frac{\partial^3 L}{\partial t^3} + \cdots\right) \to 0 \text{ as } h^2 \to 0, \ k \to 0.$$

$$L_B = -\frac{d_3 h^2}{12}\frac{\partial^4 B}{\partial x^4} + k\left((\gamma_2 + \delta)\frac{\partial B}{\partial t} - d_2\frac{\partial^3 B}{\partial x^2 \partial t} + \frac{1}{2!}\frac{\partial^2 B}{\partial t^2} + \frac{k^2}{3!}\frac{\partial^3 B}{\partial t^3} + \cdots\right) \to 0 \; as \; h^2 \to 0, \; k \to 0.$$

Hence our proposed scheme is consistent and first order accurate in time and second order accurate in space.

3.2 Stability of Proposed Scheme

In this section, we will use von Neumann stability criteria to show our proposed implicit scheme from Eqs. (4)–(6) is unconditionally stable. For this purpose, we will introduce the following terms,

$S_j^n = \psi(t)e^{ijh}$, $S_j^{n+1} = \psi(t + \Delta t)e^{ijh}$, $S_{j+1}^{n+1} = \psi(t + \Delta t)e^{i(j+\Delta j)h}$

And $S_{j-1}^{n+1} = \psi(t + \Delta t)e^{i(j-\Delta j)h}$

Put all these terms in Eq. (4), we have

$-\lambda_1\left(\psi(t + \Delta t)e^{i(j+\Delta j)h} + \psi(t + \Delta t)e^{i(j-\Delta j)h}\right) + \psi(t + \Delta t)e^{ijh}\left(1 + 2\lambda_1 + \beta k \; c_j^n + \delta k\right) = \psi(t)e^{ijh},$

where $c_j^n = \left(L_j^n + B_j^n\right).$

$\psi(t + \Delta t)\left(-\lambda_1\left(e^{i(j+\Delta j)h} + e^{i(j-\Delta j)h}\right) + e^{ijh}\left(1 + 2\lambda_1 + \beta k \; c_j^n + \delta k\right)\right) = \psi(t)e^{ijh},$

After proper calculation and rearranging terms, we have

$$\frac{\psi(t + \Delta t)}{\psi(\Delta t)} = \frac{1}{\left(1 + 4\lambda_1 \sin^2\frac{\Delta jh}{2} + \beta k \; c_j^n + \delta k\right)},$$

Take absolute value on both sides, we have the following inequality,

$$\left|\frac{\psi(t + \Delta t)}{\psi(\Delta t)}\right| = \left|\frac{1}{\left(1 + 4\lambda_1 \sin^2\frac{\Delta jh}{2} + \beta k \; c_j^n + \delta k\right)}\right| < 1. \tag{11}$$

By using similar process for Eq. (5), and Eq. (6) simultaneously we have, we have

$$\left|\frac{\psi(t + \Delta t)}{\psi(\Delta t)}\right| = \left|\frac{1}{\left(1 + 4\lambda_2 \sin^2\frac{\Delta jh}{2} + (\acute{\alpha} + \gamma_1 + \delta)k\right)}\right| < 1, \tag{12}$$

and

$$\left|\frac{\psi(t + \Delta t)}{\psi(\Delta t)}\right| = \left|\frac{1}{\left(1 + 4\lambda_3 \sin^2\frac{\Delta jh}{2} + (\gamma_2 + \delta)k\right)}\right| < 1. \tag{13}$$

Inequalities from Eqs. (11)–(13) are showing that our proposed implicit scheme is unconditionally stable by using von Neumann stability analysis.

3.3 Positivity

Theorem 1: For any positive k and h, S^n, L^n and B^n appertaining the to the Eqs. (4)–(6) are positive for all $n = 0, 1, \ldots$

Proof: We will use m-matrix theory and mathematical induction to show our scheme preserve positivity. For this purpose rewrite Eqs. (4)–(6) in vector form, as

$$GS^{n+1} = S^n + +\delta k + \gamma_1 kL^n + \gamma_2 kB^n, \tag{14}$$

$$HL^{n+1} = L^n + \beta kS_j^n\left(L_j^n + B_j^n\right), \tag{15}$$

$$IB^{n+1} = B^n + \acute{\alpha}L^n. \tag{16}$$

If $\bar{Q}$ represents any of G, H or I, where these are all real square matrices, then $\bar{Q}$ can be written in general form as

$$\bar{Q} = \begin{pmatrix} q_3 & q_1 & 0 & & 0 & 0 & 0 \\ q_2 & q_3 & q_2 & \cdots & 0 & 0 & 0 \\ 0 & q_2 & q_3 & & 0 & 0 & 0 \\ & \vdots & & \ddots & & \vdots & \\ 0 & 0 & 0 & & q_3 & q_1 & 0 \\ 0 & 0 & 0 & \cdots & q_2 & q_3 & q_2 \\ 0 & 0 & 0 & & 0 & q_2 & q_3 \end{pmatrix}$$

The off-diagonal and diagonal entries of G are $g_1 = -2\lambda_1$, $g_2 = -\lambda_1$ and $g_3 = 1 + 2\lambda_1 + \beta k\left(L_j^n + B_j^n\right) + \delta k)$. The off-diagonal and diagonal entries of H are $h_1 = -2\lambda_2$, $h_2 = -\lambda_2$ and $h_3 = 1 + 2\lambda_2 + (\acute{\alpha} + \gamma_1 + \delta)k$. The off-diagonal and diagonal entries of I are $i_1 = -2\lambda_3$, $i_2 = -\lambda_2$ and $i_3 = 1 + 2\lambda_3 + (\gamma_2 + \delta)k$.

Thus G, H, I are m-matrices.

This implies G, H, I are non-singular matrices. So Eqs. (14)–(16) can be written as

$$S^{n+1} = G^{-1}(S^n + \delta k + \gamma_1 kL^n + \gamma_2 kB^n), \tag{17}$$

$$L^{n+1} = H^{-1}(L^n + \beta kS_j^n\left(L_j^n + B_j^n\right)), \tag{18}$$

$$B^{n+1} = I^{-1}(B^n + \acute{\alpha}L^n). \tag{19}$$

Suppose that S^n, L^n, $B^n > 0$, $\Rightarrow$ $S^n + \delta k + \gamma_1 kL^n + \gamma_2 kB^n > 0, L^n + \beta kS_j^n\left(L_j^n + B_j^n\right) > 0$, and $B^n + \acute{\alpha}L^n > 0$.

Also G, H, I are m-matrices. This guarantees that all the entries of G^{-1}, H^{-1}, I^{-1} are positive. The product of two positive matrices is also positive.

$\Rightarrow$ R.H.S of Eqs. (17)–(19) are > 0.

So S^{n+1}, L^{n+1}, B^{n+1} are also positive.

Hence our proposed implicit scheme preserve positivity.

4 Numerical Example and Simulations

In this section, we demonstrate a numerical example and simulations for the application of proposed structure preserving technique. For this we consider the following initial conditions,

$$S(x,0) = \begin{cases} 0.5x, & 0 \le x < 0.5 \\ 0.5(1-x), & 0.5 \le x \le 1 \end{cases}, \quad L(x,0) = \begin{cases} 0.2x, & 0 \le x < 0.5 \\ 0.2(1-x), & 0.5 \le x \le 1 \end{cases}$$

$$B(x,0) = \begin{cases} 0.2x, & 0 \le x < 0.5 \\ 0.2(1-x), & 0.5 \le x \le 1 \end{cases},$$

4.1 CVF Point

First we discuss the simulations of proposed structure preserving method at CVF point. For the CVF point we take the following values of parameters involved in the model so that the value of $\Re_0$ is less than one.

$$d_1 = 0.01, \; d_2 = 0.01, \; d_3 = 0.01, \; \alpha = 0.6, \; \delta = 0.1, \; \beta = 0.3, \; \gamma_1 = 0.1, \; \gamma_2 = 0.3$$

Figs. 1–3 demonstrate the numerical solution of model by implementing the proposed technique at the VFE point. It is given that the VFE point of the computer virus model is $(1,0,0)$. This point is stable when the reproductive number values are less than one. So it is concluded that the computer virus epidemic model under study possesses two main properties, positive solution, and stability of both equilibria. It is evident from Figs. 1–3 that the simulation results are with the good agreement of theorem 1. The proposed structure-preserving technique retains positive solutions and stability of the CVF point. The graphs of susceptible, latent, and breaking out computers shows the convergence towards VFE point $(1,0,0)$.
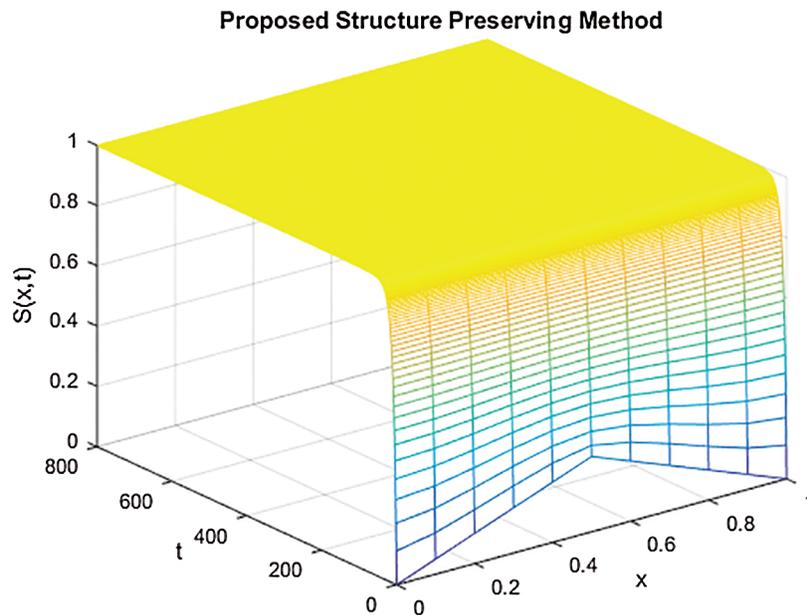

Figure 1: The solution graphs of susceptible computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$

4.2 CVE Point

Now we present the simulations of proposed structure preserving method at CVE point. For the CVE point we use the following values of parameters involved in the model so that the value of $\Re_0$ is greater than one.

$$d_1 = 0.01, \; d_2 = 0.01, \; d_3 = 0.01, \; \alpha = 0.3, \; \delta = 0.1, \; \beta = 0.4, \; \gamma_1 = 0.1, \; \gamma_2 = 0.3.$$

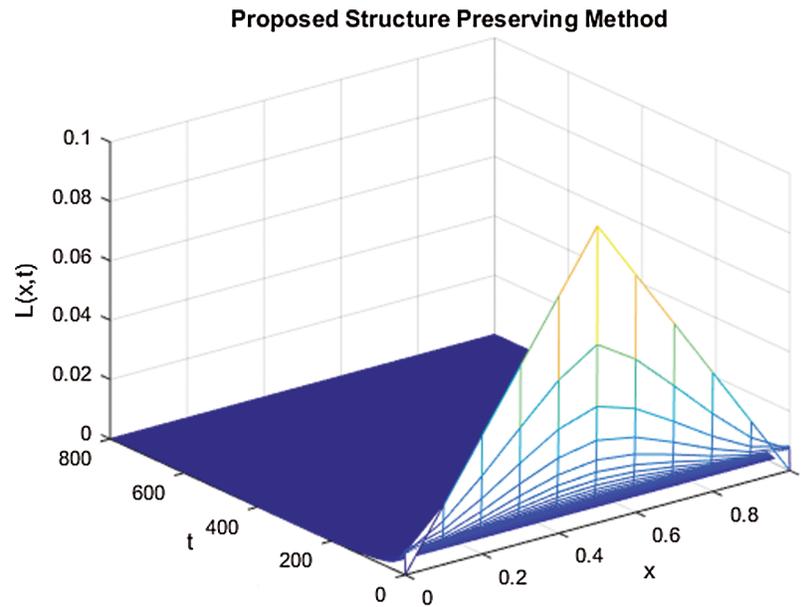**Proposed Structure Preserving Method**

Figure 2: The solution graphs of latent computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$
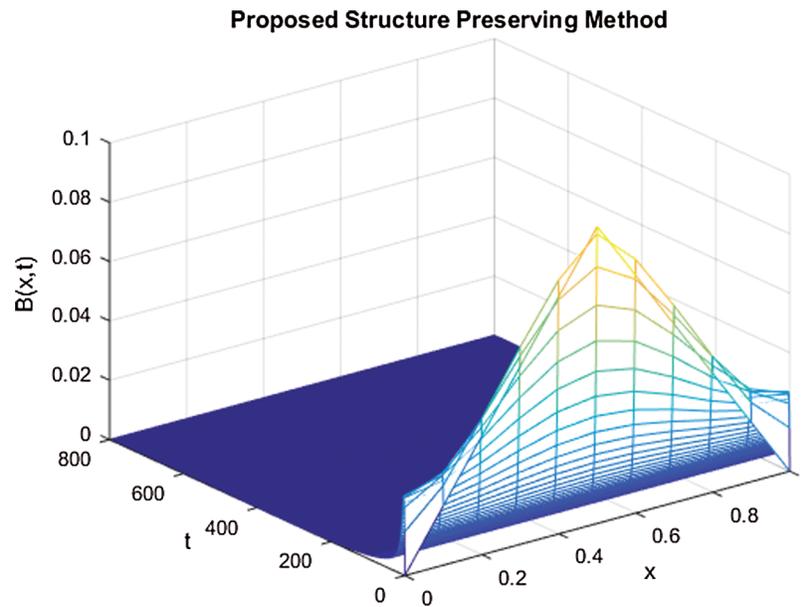
Proposed Structure Preserving Method

Figure 3: The solution graphs of breaking out computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$

Figs. 4–6 describe the graphical solution of the system by using the proposed technique at CVE point. The CVE point is stable when the reproductive number values are greater than one. It is clearly shown from the Figs. 4–6 that the proposed structure-preserving numerical technique sustains the positive behavior of the solution of continuous system. Also, this method preserves the stability of the CVF point. It is validated from

the solution graphs of susceptible, latent and breaking out computers in above figures as the sketches in these figures show the convergence towards CVE point (S_*, L_*, B_*).
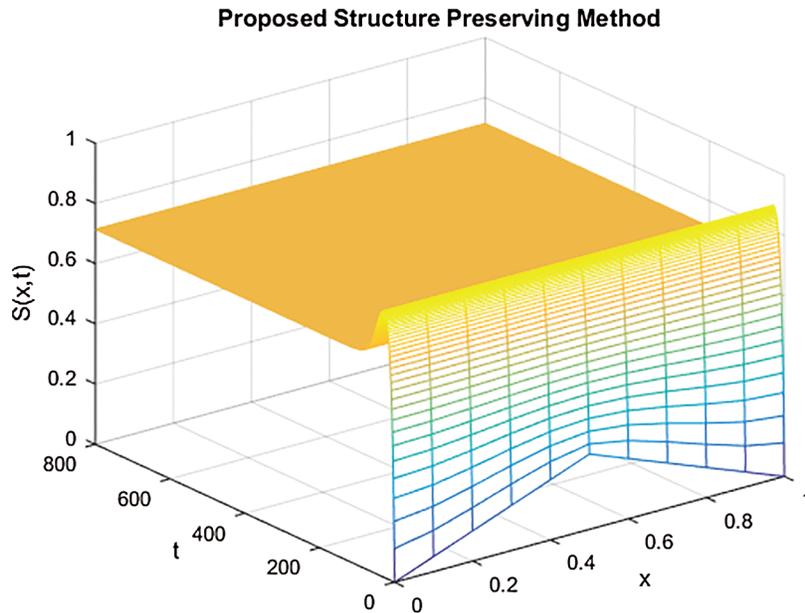
Proposed Structure Preserving Method

Figure 4: The solution graphs of susceptible computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$
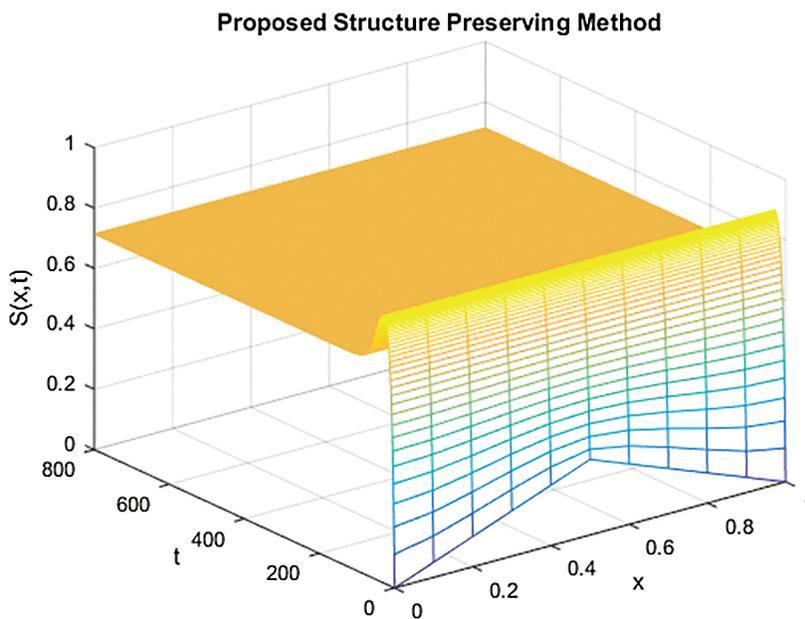
Proposed Structure Preserving Method

Figure 5: The solution graphs of latent computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$
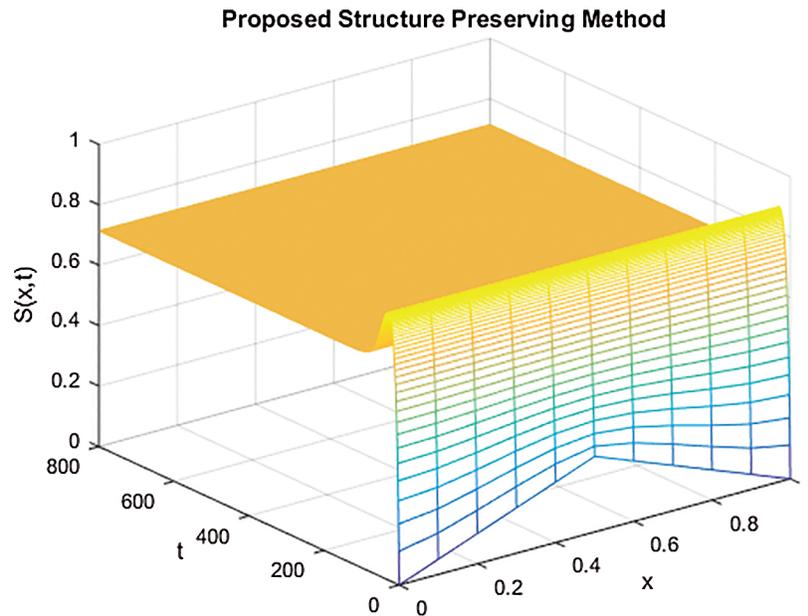
Figure 6: The solution graphs of breaking out computers representing the behavior of proposed structure preserving technique with values of step sizes $h = 0.1$ and $k = 0.8$

5 Conclusion

In this paper, we propose an extended reaction–diffusion epidemic model of computer virus dynamics for the numerical investigation. An efficient and reliable numerical technique is designed which preserves the stability of equilibria and positivity of the approximation. The stability, consistency, and positivity of the proposed algorithm are shown mathematically and are validated graphically with the help of a numerical example. The proposed algorithm can be used for the solution of reaction–diffusion models like predator-prey models, chemical reaction models and infectious disease models. In future work, we shall extend the modeling of a computer virus in the computer population in the well-known notations like fractional and stochastic fractional-order derivatives [24–26].

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

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