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Numerical modeling of susceptible latent breaking-out quarantine computer virus epidemic dynamics

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Abstract

This work is concerned with the numerical modeling of susceptible-latent-breakingout-quarantine-susceptible (SLBQRS) computer virus dynamics. The SLBQRS epidemic system is solved with three finite difference methods, one is proposed nonstandard finite difference (NSFD) method and the other two are well known forward Euler finite difference (FD) method and Runge-Kutta finite difference method of order 4 (RK-4). The proposed NSFD method preserves all the essential conditions of the continuous system while RK-4 method and forward Euler method fail to preserve some of its essential conditions like positivity, convergence to the true steady states of the continuous system. The convergence analysis of the proposed NSFD method is also performed. Bifurcation value of infection coefficient for the system is also find out.

Keywords: Computational mathematics, Computer science

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1. Introduction

Computer virus is a program which malignant for computer systems and disrupt the normal functionalities of the system and damages data files. Computer virus act like biological viruses which connects itself to a host computer, damages a program file, data file and operating system of that PC. It has the capacity to reproduce itself by attaching to other programs like epidemic disease. A virus will continue spreading the infection to other files and programs and affect the performance of any system. Viruses can be transmitted from computer to computer in many different ways and reproduce by mailing themselves to dozens of people in the inbox of host's mail address. It can also transmit by downloading any file from internet, network connections, floppy disk, and universal serial buses or by CDs. To study the prevention and control of the spread of virus in computers, epidemic models for computer virus dynamics are established in recent years [1, 2, 3, 4, 5, 6, 7, 8]. The spread of virus can be controlled by isolating the highly infected nodes. The isolation of infected files is a remedy to reduce the rapid transmission of virus in other computers.

In this work, we solved numerically the quarantined epidemic model with latent and breaking-out over the internet [1]. The term latent is referred for the infected computers with latent period to become infectious. The breaking-out are the infectious computer which are effected by the virus and are needed to be recovered. The quarantine is referred to the isolation method in which highly infected nodes are isolated from the network. This method helps to slow down the spread of virus. The main purpose of this article is to develop a numerical scheme for susceptible-latent-breakingout-quarantine-susceptible (SLBQRS) computer virus model which preserves the structure of continuous model. It is necessary for a numerical method to preserve all the necessary conditions possessed by the continuous model. For example, numerical scheme cannot justify negative values for the solution of computer virus epidemic model because negative value of susceptible computers is meaningless. Therefore, in order to study the actual behavior of epidemic computer virus dynamics at all points of the domain, it is necessary to solve continuous system with structure preserving numerical method. Nonstandard finite difference (NSFD) method introduced by Mickens [5] is an efficient structure preserving numerical method to solve dynamical systems [5, 9, 10, 11, 12, 13, 14]. This technique has also become a reliable technique to solve epidemic models [5, 12, 13, 14]. Because of reliability, efficiency and capability of preserving the structure of continuous system, we develop a NSFD scheme for the numerical solution of SLBQRS computer virus model.

The main motivation of this research is to develop the reliable positivity preserving numerical schemes for the continuous model for virus propagation in a computer network. In Section 2, stability of the model and its bifurcation analysis has been performed. Moreover, three finite difference numerical schemes for the continuous

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model are also presented and stability analysis of proposed NSFD scheme has been discussed. In Section 3, numerical experiment for all the FD schemes is performed, spectral radius has been calculated and effect of quarantine strategy has been observed. Sections 4 and 5 constitutes the relevant discussion and conclusion.

2. Materials and methods

2.1. Mathematical model

S: Susceptible computers at time t with no immunity.

L: Latent computers at time t.

B: Breaking out computers at time t.

Q: Quarantine computers at time t.

R: Recovered computers at time t with temporary immunity.

μ: Rate of connection of external computers and disconnection of internal computers to the internet.

λ: Rate of crashing of nodes because of virus attack.

β: Rate of infection.

α: Rate at which latent computers break-out.

η: Cured rate for breaking-out computers

γ: Rate at which breaking-out computers are quarantined.

δ: Cured rate of quarantined computers. Rate of recovery of infected computers in quarantined compartment.

ε: Rate at which recovered computers are susceptible again.

The assumptions on the spread of virus in computer node are illustrated in Fig. 1. The diffusion between model classes can be described by the system of differential equations.

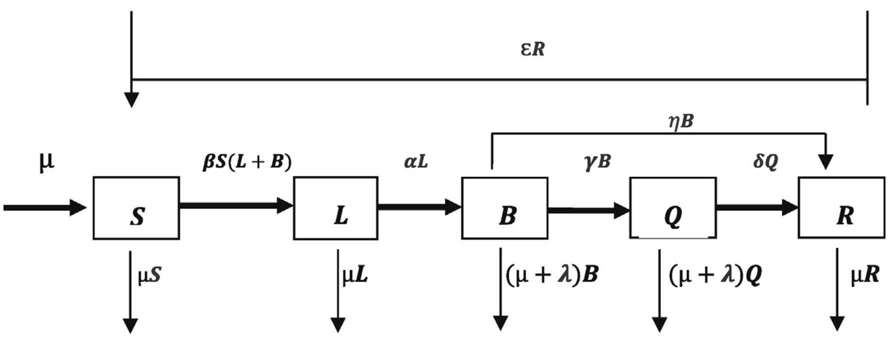

Fig. 1. State transition diagram for the flow of viruses in the SLBQRS model.

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The system of nonlinear differential equations for SLBQRS epidemic model [1] is given as

$$\left.\begin{aligned}
\frac{dS}{dt} &= \mu - \beta S(L+B) + \varepsilon R - \mu S \\
\frac{dL}{dt} &= \beta S(L+B) - (\mu+\alpha)L \\
\frac{dB}{dt} &= \alpha L - (\mu+\gamma+\eta+\lambda)B \\
\frac{dQ}{dt} &= \gamma B - (\mu+\lambda+\delta)Q \\
\frac{dR}{dt} &= \delta Q - (\mu+\varepsilon)R + \eta B
\end{aligned}\right\} \tag{1}$$

with initial conditions

$$S(0) = S_0 \geq 0,\ L(0) = L_0 \geq 0,\ B(0) = B_0 \geq 0,\ Q(0) = Q_0 \geq 0,\ R(0) = R_0 \geq 0$$

2.2. Analysis of the model

Two equilibrium points of the system (1) can be identified, one is virus free equilibrium (VFE) point and the other is viral equilibrium (VE) point. $\varepsilon_1(S_0, L_0, B_0, Q_0, R_0) = \varepsilon_1(1,0,0,0,0)$ is the virus free equilibrium point and viral point $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$, Where

$$S_* = \frac{(\mu+\alpha)(\mu+\gamma+\eta+\lambda)}{\beta(\mu+\alpha+\gamma+\eta+\lambda)}$$

$$L_* = \frac{(\mu+\gamma+\eta+\lambda)}{\alpha}B_*$$

$$Q_* = \frac{\gamma}{(\mu+\lambda+\delta)}B_*$$

$$R_* = \frac{\delta\gamma(\mu+\lambda+\delta)}{(\mu+\varepsilon)(\mu+\lambda+\delta)}B_* \quad \text{and}$$

$$B_* = \frac{\mu\alpha(\mu+\lambda+\delta)(\mu+\varepsilon)(1-\Re_0)}{\Re_0\alpha\gamma\delta\varepsilon(\mu+\lambda+\delta)[\Re_0\alpha\eta\varepsilon - \beta(\mu+\varepsilon)(\mu+\alpha+\gamma+\eta+\lambda)]}$$

where, $\Re_0 = \dfrac{\beta(\mu+\alpha+\gamma+\eta+\lambda)}{(\mu+\alpha)(\mu+\gamma+\eta+\lambda)}$

$\Re_0$ is a basic reproductive number which decides the existence of ε_1 point or ε_2 point. If $\Re_0 < 1$, then the system (1) has virus free point $\varepsilon_1(1,0,0,0,0)$ point and if $\Re_0 > 1$, then system has viral point $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$.

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2.3. Stability of the system

The variational matrix of the system (1) at equilibrium point $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$ [15] is given as

$$V = \begin{bmatrix} v_{11} & v_{12} & v_{13} & v_{14} & v_{15} \\ v_{21} & v_{22} & v_{23} & v_{24} & v_{25} \\ v_{31} & v_{32} & v_{33} & v_{34} & v_{35} \\ v_{41} & v_{42} & v_{43} & v_{44} & v_{45} \\ v_{51} & v_{52} & v_{53} & v_{54} & v_{55} \end{bmatrix}$$

Where,

$$\begin{aligned} v_{11} &= -\beta(L_* + B_*) - \mu,\ v_{12} = -\beta S_*,\ v_{13} = -\beta S_*, v_{14} = 0,\ v_{15} = \varepsilon,\ v_{21} \\ &= \beta(L_* + B_*),\ v_{22} = \beta S_* - (\mu + \alpha),\ v_{23} = \beta S_*,\ v_{24} = 0,\ v_{25} = 0,\ v_{31} = 0,\ v_{32} \\ &= \alpha,\ v_{33} = -(\mu + \gamma + \eta + \lambda), v_{34} = 0,\ v_{35} = 0,\ v_{41} = 0,\ v_{42} = 0,\ v_{43} = \gamma,\ v_{44} \\ &= -(\mu + \lambda + \delta),\ v_{45} = 0,\ v_{51} = 0,\ v_{52} = 0,\ v_{53} = \eta,\ v_{54} = \delta,\ v_{55} = -(\mu + \varepsilon) \end{aligned}$$

The characteristics equation of V is

$$\lambda^5 + p_1\lambda^4 + p_2\lambda^3 + p_3\lambda^2 + p_4\lambda + p_5 = 0$$

The expression for p_1, p_2, p_3, p_4 and p_5 are mentioned in [16].

The Routh-Hurwitz stability criteria gives $p_1 > 0,\ p_2 > 0, p_3 > 0, p_4 > 0,$ $p_5 > 0, p_1p_2p_3 - p_3^2 - p_1^2p_4 > 0$ and $(p_1p_4 - p_5)(p_1p_2p_3 - p_3^2 - p_1^2p_4) - p_5(p_1p_2 - p_3)^2 - p_1p_5^2 > 0.$

2.4. Bifurcation value of infection parameter β

The value for which the equilibrium point shifts from stable to unstable region is known as bifurcation value. By using the procedure given in [15], the bifurcation value of infection parameter β is computed. To compute the bifurcation value of β, $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$ is substituted in $v_{11}, v_{12}, v_{13}, \ldots$

$$\begin{aligned} v_{11} &= 0.0023255814 - 0.5542635659\beta,\ v_{12} = -0.1846153846,\ v_{13} \\ &= -0.1846153846,\ v_{14} = 0,\ v_{15} = 0.1,\ v_{21} \\ &= 0.5542635659\beta - 0.1023255814,\ v_{22} = -0.0153846154,\ v_{23} \\ &= 0.1846153846,\ v_{24} = 0,\ v_{25} = 0,\ v_{31} = 0,\ v_{32} = 0.1,\ v_{33} = -1.2,\ v_{34} \\ &= 0,\ v_{35} = 0,\ v_{41} = 0,\ v_{42} = 0,\ v_{43} = 0.1,\ v_{44} = -1.1,\ v_{45} = 0,\ v_{51} \\ &= 0,\ v_{52} = 0,\ v_{53} = 0.1,\ v_{54} = 0.1,\ v_{55} = -0.2 \end{aligned}$$

The Routh-Hurwitz stability method gives,

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$$p_1 = 0.5542635659\beta + 2.51305903399 = f_1(\beta)$$

$$p_2 = 1.4965116279\beta + 1.7752593918 = f_2(\beta)$$

$$p_3 = 1.2637209302\beta + 0.2140822898 = f_3(\beta)$$

$$p_4 = 0.3430891473\beta - 0.0366010733 = f_4(\beta)$$

$$p_5 = 0.0286\beta - 0.00528 = f_5(\beta)$$

$$p_1p_2p_3 - p_3^2 - p_1^2p_4 = 0.9428085623\beta^3 + 3.6321333525\beta^2 + 4.0477671072\beta + 1.1404136925 = f_6(\beta)$$

$$\begin{aligned}(p_1p_4 - p_5)\left(p_1p_2p_3 - p_3^2 - p_1^2p_4\right) - p_5(p_1p_2 - p_3)^2 - p_1p_5^2 \\ = 0.1596091866\beta^5 + 1.2959678523\beta^4 + 3.1240200856\beta^3 \\ + 2.4476684160\beta^2 + 0.2175268382\beta - 0.0036980863 = f_7(\beta)\end{aligned}$$

The above equations are solved for the bifurcation value of β. The point of equilibrium is shifted from stable to unstable equilibrium for the value $\beta = 0.18461538462$. The negative and large values of β are ignored. The equilibrium point is stable for the values greater than $\beta = 0.18461538462$ and is unstable for the values less than $\beta = 0.18461538462$.

2.5. Forward Euler finite difference method

Forward Euler method is a well-known time forward FD scheme which is explicit in nature. This FD scheme is developed for the system (1) as,

$$S^{n+1} = S^n + h(\mu - \beta S^n(L^n + B^n) + \varepsilon R^n - \mu S^n)$$

$$L^{n+1} = L^n + h(\beta S^n(L^n + B^n) + (\mu + \alpha)L^n)$$

$$B^{n+1} = B^n + h(\alpha L^n - (\mu + \gamma + \eta + \lambda)B^n)$$

$$Q^{n+1} = Q^n + h(\gamma B^n - (\mu + \lambda + \delta)Q^n)$$

$$R^{n+1} = R^n + h(\delta Q^n - (\mu + \varepsilon)R^n + \eta B^n)$$

2.6. RK-4 finite difference method

RK-4 is also a well-known time forward explicit FD scheme. RK-4 FD scheme for the system (1) is

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STEP-1

$$k_1 = h(\mu - \beta S^n(L^n + B^n) + \varepsilon R^n - \mu S^n)$$

$$m_1 = h(\beta S^n(L^n + B^n) + (\mu + \alpha)L^n)$$

$$n_1 = h(\alpha L^n - (\mu + \gamma + \eta + \lambda)B^n)$$

$$o_1 = h(\gamma B^n - (\mu + \lambda + \delta)Q^n)$$

$$p_1 = h(\delta Q^n - (\mu + \varepsilon)R^n + \eta B^n)$$

STEP-2

$$k_2 = h\left[\mu - \beta\left(S^n + \frac{k_1}{2}\right)\left\{\left(L^n + \frac{m_1}{2}\right) + \left(B^n + \frac{n_1}{2}\right)\right\} + \varepsilon\left(R^n + \frac{p_1}{2}\right) - \mu\left(S^n + \frac{k_1}{2}\right)\right]$$

$$m_2 = h\left[\beta\left(S^n + \frac{k_1}{2}\right)\left\{\left(L^n + \frac{m_1}{2}\right) + \left(B^n + \frac{n_1}{2}\right)\right\} + (\mu + \alpha)\left(L^n + \frac{m_1}{2}\right)\right]$$

$$n_2 = h\left[\alpha\left(L^n + \frac{m_1}{2}\right) - (\mu + \gamma + \eta + \alpha)\left(B^n + \frac{n_1}{2}\right)\right]$$

$$o_2 = h\left[\gamma\left(B^n + \frac{n_1}{2}\right) - (\mu + \lambda + \delta)\left(Q^n + \frac{o_1}{2}\right)\right]$$

$$p_2 = h\left[\delta\left(Q^n + \frac{o_1}{2}\right) - (\mu + \varepsilon)\left(R^n + \frac{p_1}{2}\right) + \eta\left(B^n + \frac{n_1}{2}\right)\right]$$

STEP-3

$$k_3 = h\left[\mu - \beta\left(S^n + \frac{k_2}{2}\right)\left\{\left(L^n + \frac{m_2}{2}\right) + \left(B^n + \frac{n_2}{2}\right)\right\} + \varepsilon\left(R^n + \frac{p_2}{2}\right) - \mu\left(S^n + \frac{k_2}{2}\right)\right]$$

$$m_3 = h\left[\beta\left(S^n + \frac{k_2}{2}\right)\left\{\left(L^n + \frac{m_2}{2}\right) + \left(B^n + \frac{n_2}{2}\right)\right\} + (\mu + \alpha)\left(L^n + \frac{m_2}{2}\right)\right]$$

$$n_3 = h\left[\alpha\left(L^n + \frac{m_2}{2}\right) - (\mu + \gamma + \eta + \lambda)\left(B^n + \frac{n_2}{2}\right)\right]$$

$$o_3 = h\left[\gamma\left(B^n + \frac{n_2}{2}\right) - (\mu + \lambda + \delta)\left(Q^n + \frac{o_2}{2}\right)\right]$$

$$p_3 = h\left[\delta\left(Q^n + \frac{o_2}{2}\right) - (\mu + \varepsilon)\left(R^n + \frac{p_2}{2}\right) + \eta\left(B^n + \frac{n_2}{2}\right)\right]$$

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STEP-4

$$k_4 = h[\mu + \beta(S^n + k_3)\{(L^n + m_3) + (B^n + n_3)\} + \varepsilon(R^n + p_3) - \mu(S^n + k_3)]$$

$$m_4 = h[\beta(S^n + k_3)\{(L^n + m_3) + (B^n + n_3)\} + (\mu + \alpha)(L^n + m_3)]$$

$$n_4 = h[\alpha(L^n + m_3) - (\mu + \gamma + \eta + \lambda)(B^n + n_3)]$$

$$o_4 = h[\gamma(B^n + n_3) - (\mu + \lambda + \delta)(Q^n + n_3)]$$

$$p_4 = h[\delta(Q^n + o_3) - (\mu + \varepsilon)(R^n + p_3) + \eta(B^n + n_3)]$$

Now,

$$S^{n+1} = S^n + \frac{1}{6}(k_1 + 2k_2 + 2k_3 + k_4)$$

$$L^{n+1} = L^n + \frac{1}{6}(m_1 + 2m_2 + 2m_3 + m_4)$$

$$B^{n+1} = B^n + \frac{1}{6}(n_1 + 2n_2 + 2n_3 + n_4)$$

$$Q^{n+1} = Q^n + \frac{1}{6}(o_1 + 2o_2 + 2o_3 + o_4)$$

$$R^{n+1} = R^n + \frac{1}{6}(p_1 + 2p_2 + 2p_3 + p_4)$$

2.6. Nonstandard finite difference method

Nonstandard FD method was developed firstly by Mickens [10] which overcomes the various problems such as the positivity concerning problem, boundedness and monotonicity etc. NSFD scheme has become very effective for solving epidemic systems as these systems possess properties like positivity boundedness etc. In this section, we design NSFD scheme for the system (1) with the help of the rules defined by Mickens [10].

$$\frac{S^{n+1} - S^n}{\phi(h)} = \mu - \beta S^{n+1}(L^n + B^n) + \varepsilon R^n - \mu S^{n+1}$$

$$S^{n+1} = S^n + \phi(h)\mu - \phi(h)\beta S^{n+1}(L^n + B^n) + \phi(h)\varepsilon R^n - \phi(h)\mu S^{n+1}$$

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$$S^{n+1} = \frac{S^n + \phi(h)\mu + \phi(h)\varepsilon R^n}{\phi(h)\beta(L^n + B^n) + \phi(h)\mu}$$

Similarly, we have

$$L^{n+1} = \frac{L^n + \phi(h)\beta S^n(L^n + B^n)}{1 + \phi(h)(\mu + \alpha)}$$

$$B^{n+1} = \frac{B^n + \phi(h)\alpha L^n}{1 + \phi(h)(\mu + \gamma + \eta + \lambda)}$$

$$Q^{n+1} = \frac{Q^n + \phi(h)\gamma B^n}{1 + \phi(h)(\mu + \lambda + \delta)}$$

$$R^{n+1} = \frac{R^n + \phi(h)\delta Q^n + \phi(h)\eta B^n}{1 + \phi(h)(\mu + \varepsilon)}$$

2.7. Convergence analysis

Consider

$$F = \frac{S + \phi(h)\mu + \phi(h)\varepsilon R}{\phi(h)\beta(L + B) + \phi(h)\mu},\; G = \frac{L + \phi(h)\beta S(L + B)}{1 + \phi(h)(\mu + \alpha)},$$
$$H = \frac{B + \phi(h)\alpha L}{1 + \phi(h)(\mu + \gamma + \eta + \lambda)},\; I = \frac{Q + \phi(h)\gamma B}{1 + \phi(h)(\mu + \lambda + \delta)},$$
$$J = \frac{R + \phi(h)\delta Q + \phi(h)\eta B}{1 + \phi(h)(\mu + \varepsilon)}$$

The Jacobian matrix at disease free equilibrium point $\varepsilon_1(S_0, L_0, B_0, Q_0, R_0)$ is

$$\mathscr{J}(S_0, L_0, B_0, Q_0, R_0) = \begin{bmatrix} \frac{\partial F}{\partial S} & \frac{\partial F}{\partial L} & \frac{\partial F}{\partial B} & \frac{\partial F}{\partial Q} & \frac{\partial F}{\partial R} \\ \frac{\partial G}{\partial S} & \frac{\partial G}{\partial L} & \frac{\partial G}{\partial B} & \frac{\partial G}{\partial Q} & \frac{\partial G}{\partial R} \\ \frac{\partial H}{\partial S} & \frac{\partial H}{\partial L} & \frac{\partial H}{\partial B} & \frac{\partial H}{\partial Q} & \frac{\partial H}{\partial R} \\ \frac{\partial I}{\partial S} & \frac{\partial I}{\partial L} & \frac{\partial I}{\partial B} & \frac{\partial I}{\partial Q} & \frac{\partial I}{\partial R} \\ \frac{\partial J}{\partial S} & \frac{\partial J}{\partial L} & \frac{\partial J}{\partial B} & \frac{\partial J}{\partial Q} & \frac{\partial J}{\partial R} \end{bmatrix}$$

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Where,

$$\frac{\partial F}{\partial S}=\frac{1}{[1+\phi(h)\beta(L_0+B_0)+\mu\phi(h)]},\ \frac{\partial F}{\partial L}=\frac{-[(S_0+\mu h+\varepsilon hR_0)(h\beta)]}{[1+\phi(h)\beta(L_0+B_0)+\mu\phi(h)]^2},$$
$$\frac{\partial F}{\partial B}=\frac{-[(S_0+\mu\phi(h)+\varepsilon\phi(h)R_0)(\phi(h)\beta)]}{[1+\phi(h)\beta(L_0+B_0)+\mu\phi(h)]^2},\ \frac{\partial F}{\partial Q}=0,\ \frac{\partial F}{\partial R}$$
$$=\frac{\varepsilon\phi(h)}{[1+\phi(h)\beta(L_0+B_0)+\mu\phi(h)]},\ \frac{\partial G}{\partial S}=\frac{[L+\phi(h)\beta(L_0+B_0)]}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial L}$$
$$=\frac{[1+\phi(h)\beta S_0]}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial B}=\frac{\phi(h)\beta S_0}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial Q}=0,\ \frac{\partial G}{\partial R}=0,\ \frac{\partial H}{\partial S}$$
$$=0,\ \frac{\partial H}{\partial L}=\frac{\alpha\phi(h)}{[1+\phi(h)(\mu+\gamma+\eta+\lambda)]},\ \frac{\partial H}{\partial B}=\frac{1}{[1+\phi(h)(\mu+\gamma+\eta+\lambda)]},\ \frac{\partial H}{\partial Q}$$
$$=0,\ \frac{\partial H}{\partial R}=0,\ \frac{\partial I}{\partial S}=0,\ \frac{\partial I}{\partial L}=0,\ \frac{\partial I}{\partial B}=\frac{\phi(h)\gamma}{[1+\phi(h)(\mu+\gamma+\delta)]},\ \frac{\partial I}{\partial Q}$$
$$=\frac{1}{[1+\phi(h)(\mu+\gamma+\delta)]},\frac{\partial I}{\partial R}=0,\frac{\partial J}{\partial S}=0,\ \frac{\partial J}{\partial L}=0,\ \frac{\partial J}{\partial B}$$
$$=\frac{\phi(h)\eta}{[1+\phi(h)(\mu+\varepsilon)]},\ \frac{\partial J}{\partial Q}=\frac{\phi(h)\delta}{[1+\phi(h)(\mu+\varepsilon)]},\ \frac{\partial J}{\partial R}=\frac{1}{[1+\phi(h)(\mu+\varepsilon)]}$$

If all the eigenvalues of the Jacobian matrix are less than 1, then the proposed NSFD scheme is stable for every time step. We prove this numerically by plotting the spectral radius (largest eigenvalue) for very large time step with the help of MATLAB in Fig. 2.

Now the Jacobian matrix for viral equilibrium point $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$ is

$$\mathscr{J}(S_*,L_*,B_*,Q_*,R_*)=\begin{bmatrix}\frac{\partial F}{\partial S}&\frac{\partial F}{\partial L}&\frac{\partial F}{\partial B}&\frac{\partial F}{\partial Q}&\frac{\partial F}{\partial R}\\ \frac{\partial G}{\partial S}&\frac{\partial G}{\partial L}&\frac{\partial G}{\partial B}&\frac{\partial G}{\partial Q}&\frac{\partial G}{\partial R}\\ \frac{\partial H}{\partial S}&\frac{\partial H}{\partial L}&\frac{\partial H}{\partial B}&\frac{\partial H}{\partial Q}&\frac{\partial H}{\partial R}\\ \frac{\partial I}{\partial S}&\frac{\partial I}{\partial L}&\frac{\partial I}{\partial B}&\frac{\partial I}{\partial Q}&\frac{\partial I}{\partial R}\\ \frac{\partial J}{\partial S}&\frac{\partial J}{\partial L}&\frac{\partial J}{\partial B}&\frac{\partial J}{\partial Q}&\frac{\partial J}{\partial R}\end{bmatrix}$$

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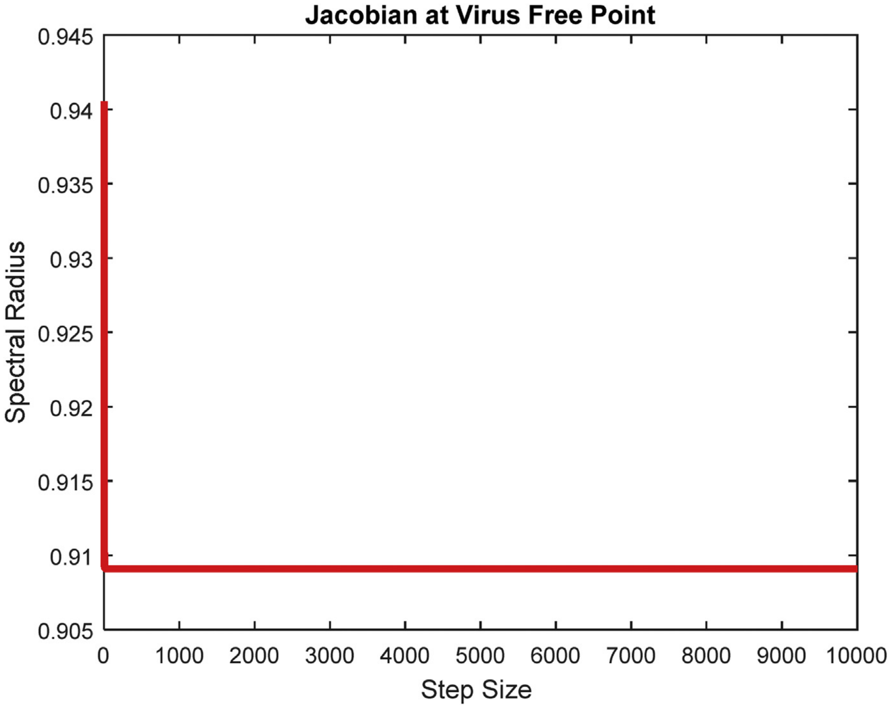

Fig. 2. The spectral radius of Jacobian matrix at virus free equilibrium point.

Where,

$$\frac{\partial F}{\partial S}=\frac{1}{[1+\phi(h)\beta(L_*+B_*)+\mu\phi(h)]},\ \frac{\partial F}{\partial L}=\frac{-[(S_*+\mu h+\varepsilon hR_*)(h\beta)]}{[1+\phi(h)\beta(L_*+B_*)+\mu\phi(h)]^2},\ \frac{\partial F}{\partial B}=\frac{-[(S_*+\mu\phi(h)+\varepsilon\phi(h)R_*)(\phi(h)\beta)]}{[1+\phi(h)\beta(L_*+B_*)+\mu\phi(h)]^2},\ \frac{\partial F}{\partial Q}=0,\ \frac{\partial F}{\partial R}=\frac{\varepsilon\phi(h)}{[1+\phi(h)\beta(L_*+B_*)+\mu\phi(h)]},\ \frac{\partial G}{\partial S}=\frac{[L+\phi(h)\beta(L_*+B_*)]}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial L}=\frac{[1+\phi(h)\beta S_*]}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial B}=\frac{\phi(h)\beta S_*}{[1+\phi(h)(\mu+\alpha)]},\ \frac{\partial G}{\partial Q}=0,\ \frac{\partial G}{\partial R}=0,\ \frac{\partial H}{\partial S}=0,\ \frac{\partial H}{\partial L}=\frac{\alpha\phi(h)}{[1+\phi(h)(\mu+\gamma+\eta+\lambda)]},\ \frac{\partial H}{\partial B}=\frac{1}{[1+\phi(h)(\mu+\gamma+\eta+\lambda)]},\ \frac{\partial H}{\partial Q}=0,\ \frac{\partial H}{\partial R}=0,\ \frac{\partial I}{\partial S}=0,\ \frac{\partial I}{\partial L}=0,\ \frac{\partial I}{\partial B}=\frac{\phi(h)\gamma}{[1+\phi(h)(\mu+\gamma+\delta)]},\ \frac{\partial I}{\partial Q}=\frac{1}{[1+\phi(h)(\mu+\gamma+\delta)]},\ \frac{\partial I}{\partial R}=0,\ \frac{\partial J}{\partial S}=0,\ \frac{\partial J}{\partial L}=0,\ \frac{\partial J}{\partial B}=\frac{\phi(h)\eta}{[1+\phi(h)(\mu+\varepsilon)]},\ \frac{\partial J}{\partial Q}=\frac{\phi(h)\delta}{[1+\phi(h)(\mu+\varepsilon)]},\ \frac{\partial J}{\partial R}=\frac{1}{[1+\phi(h)(\mu+\varepsilon)]}$$

In Fig. 3, spectral radius of Jacobian matrix at viral equilibrium point for each time step is plotted.

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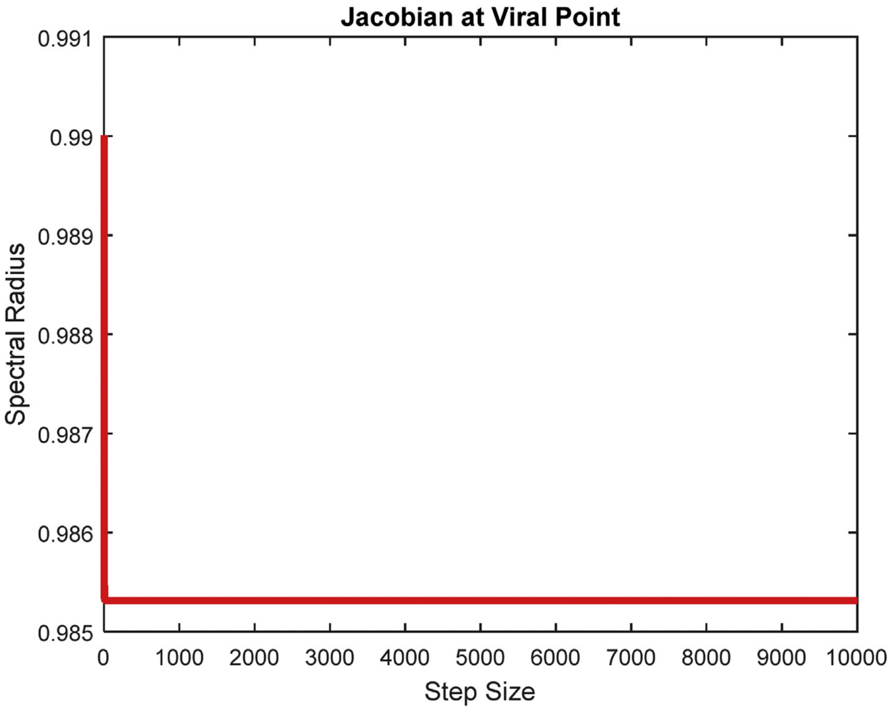

Fig. 3. The spectral radius of Jacobian matrix at viral equilibrium point.

3. Results

In this section, a numerical experiment is carried out for the validations of claims about positivity and unconditional convergence of proposed NSFD scheme. Simulations are presented to validate the results by using MATLAB. The values of parameters used in the experiment are given in Table 1. Table 2 shows that the system is stable for all the cases.

3.1. Spectral radius of Jacobian matrix

Fig. 2 demonstrate the spectral radius of Jacobian matrix at VFE point for the values of 'h', $0 < h \leq 10000$. At each value of h, the spectral radius remains less than 1.

Table 1. The parametric values.

Parameters	Values for disease free point	Values for viral point
μ	0.1	0.1
λ	0.9	0.9
β	0.01	0.2
α	0.1	0.1
η	0.1	0.1
γ	0.1	0.1
δ	0.1	0.1
ε	0.1	0.1

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Table 2. Stability of the system.

Cases	μ	λ	β	α	η	γ	δ	ε	p_1	p_2	p_3	p_4	p_5	k^*	l^*	Stable/Unstable
1	0.1	0.9	0.2	0.1	0.1	0.1	0.1	0.1	2.62	2.07	0.47	0.03	0.0004	2.10	0.16	Stable
2	0.1	0.9	0.2	0.1	0.1	0.3	0.1	0.1	2.82	2.35	0.53	0.03	0.0004	2.97	0.29	Stable
3	0.1	0.9	0.2	0.1	0.1	0.6	0.1	0.1	3.11	2.76	0.63	0.04	0.0004	4.68	0.60	Stable
4	0.1	0.9	0.2	0.1	0.1	0.9	0.1	0.1	3.41	3.18	0.74	0.05	0.0004	6.94	1.12	Stable

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Hence each eigen value of Jacobian at VFE point is less than 1 which verifies the fact that proposed NSFD scheme is convergent at each time step h.

In the similar way as above, Fig. 3 also proves the unconditional convergence at VE point.

3.2. Euler method at VFE point

Fig. 4 represents the graphs of breaking out and quarantine computers only using Euler method. Graphs (a) and (b) show that Euler method lose positivity property and shows negative values of breaking-out and quarantine computers. Negative values of breaking-out and quarantine computers are meaningless and are due to scheme dependent instabilities. Graphs (c) and (d) describe that Euler method overflow and diverges at $h = 2$.

3.3. RK-4 method at VFE point

The graphs (a)−(c) in Fig. 5 describe the virus free equilibrium point using RK-4 FD method. RK-4 FD method also produces negative values of latent and quarantined computers and finally diverges like Euler FD method.

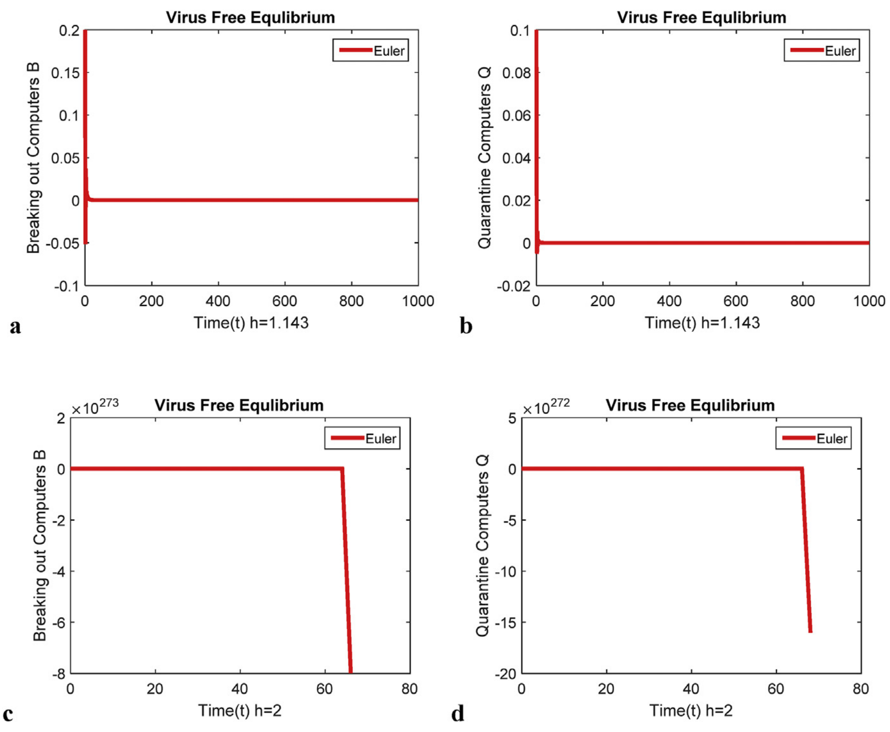

Fig. 4. Graphs (a) and (b) represent the breaking-out and quarantine computers respectively for virus free equilibrium using forward Euler method at $h = 1.143$ while graphs (c) and (d) represent the breaking-out and quarantine computers respectively for virus free equilibrium using forward Euler method at $h = 2$.

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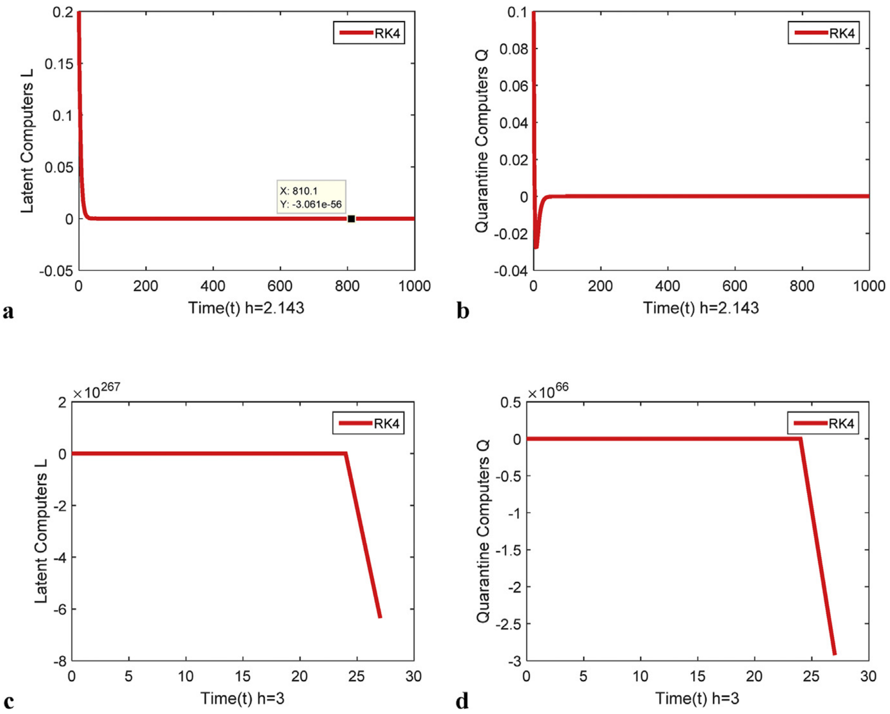

Fig. 5. Graphs (a) and (b) represent the latent and quarantine computers respectively for virus free equilibrium using RK-4 method at $h = 2.143$ while graphs (c) and (d) represent the latent and quarantine computers respectively for virus free equilibrium using RK-4 method at $h = 3$.

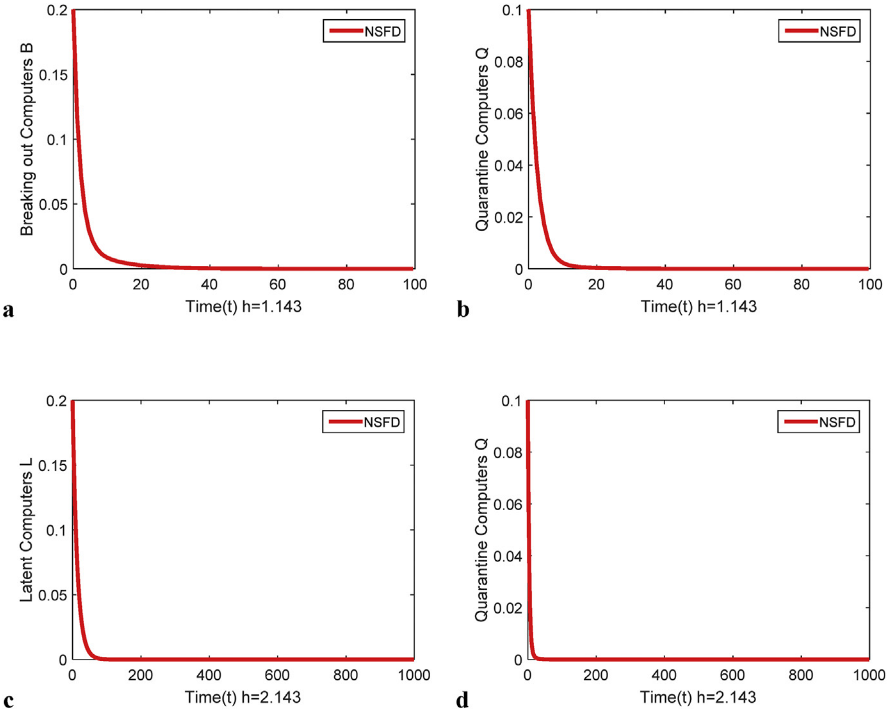

Fig. 6. Graphs (a) and (b) represent the breaking-out and quarantine computers respectively for virus free equilibrium using NSFD method at $h = 1.143$ while graphs (c) and (d) represent the latent and quarantine computers respectively for virus free equilibrium using NSFD method at $h = 2.143$.

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3.4. NSFD method at VFE point

Fig. 6 displays the graphs of breaking-out and quarantine computers at $h = 1.143$, graphs of latent and quarantine computers at $h = 2.143$ using proposed NSFD method. Graphs verify that the proposed NSFD method preserves the positivity property and its convergence to the equilibrium points.

In Fig. 7, graphs (a)−(e) describe the virus free equilibrium state at $h = 1000$ using proposed NSFD method. Graphs show that proposed NSFD method converges to virus free point $\varepsilon_1(1, 0, 0, 0, 0)$ even at very large time step $h = 1000$, showing that proposed NSFD method is independent of the step size h.

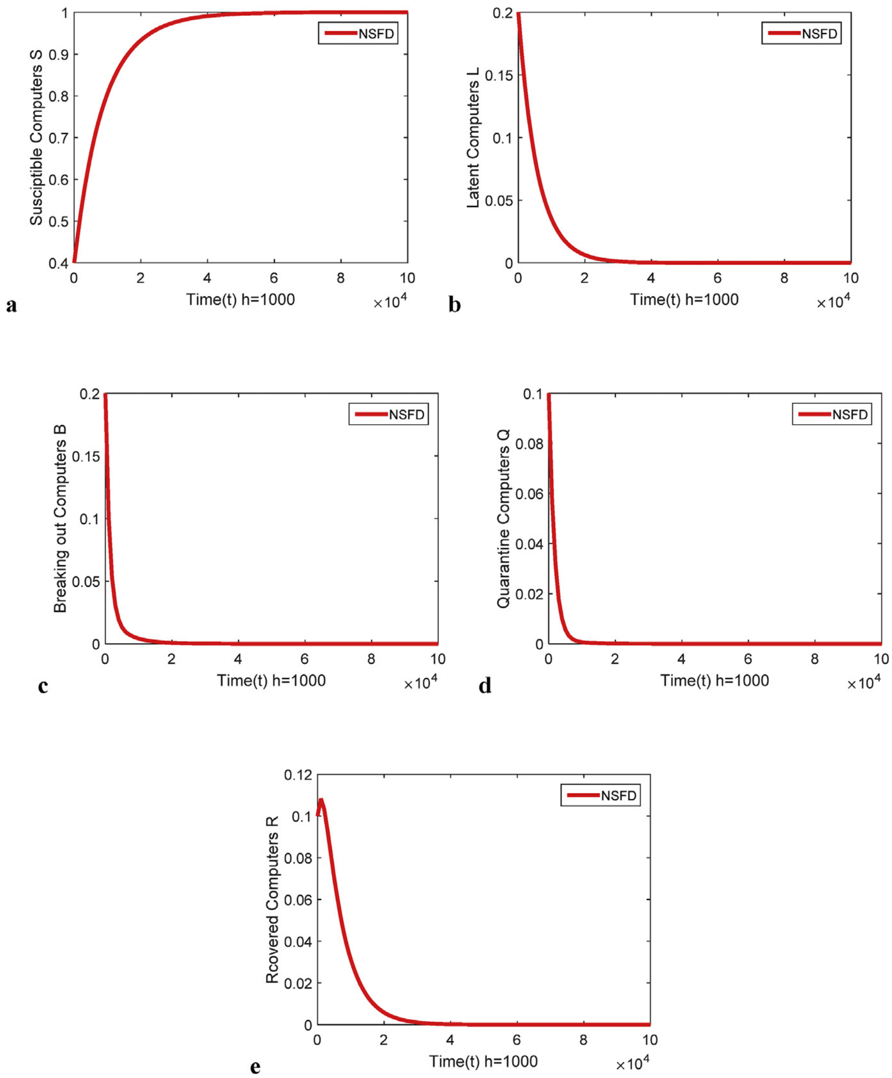

Fig. 7. Graphs (a)−(e) represent the susceptible, latent, breaking-out, quarantine and recovered computers respectively for virus free equilibrium using NSFD method at $h = 1000$.

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3.5. NSFD method at viral equilibrium point

Now, the graphs for NSFD scheme at VE are presented below.

Graphs (a)-(e) in Fig. 8 describe the viral equilibrium state using proposed finite difference method at $h = 1000$. It can be observed that proposed NSFD method converges to viral equilibrium point $\varepsilon_2(S_*, L_*, B_*, Q_*, R_*)$ for every time step and also preserves positivity property.

3.6. Effect of quarantine strategy

Fig. 9 reveals the effect of quarantine strategy by taking different values of γ. The values of γ influence the number of latent computers. Fig. 9 also depicts that both the quantities γ and latent computers L are inversely proportional to each other.

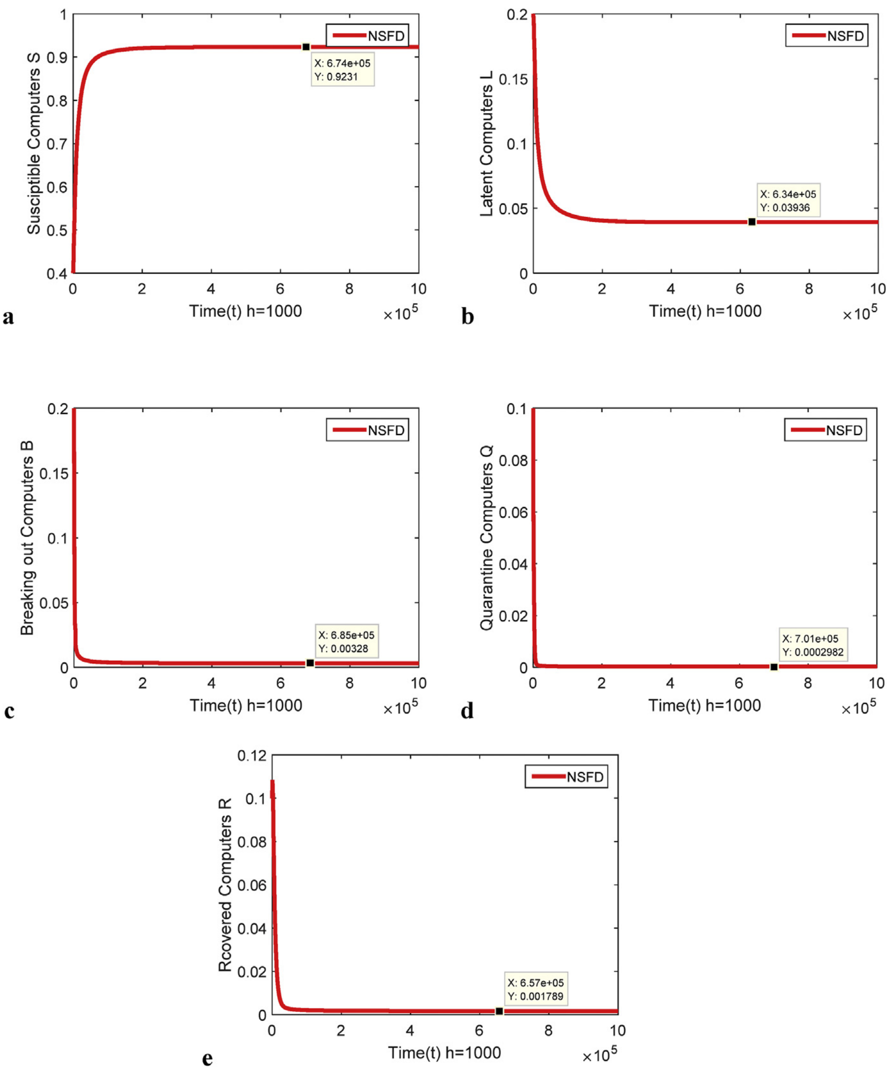

Fig. 8. Graphs (a)−(e) represent the susceptible, latent, breaking-out, quarantine and recovered computers respectively for viral equilibrium using NSFD method at $h = 1000$.

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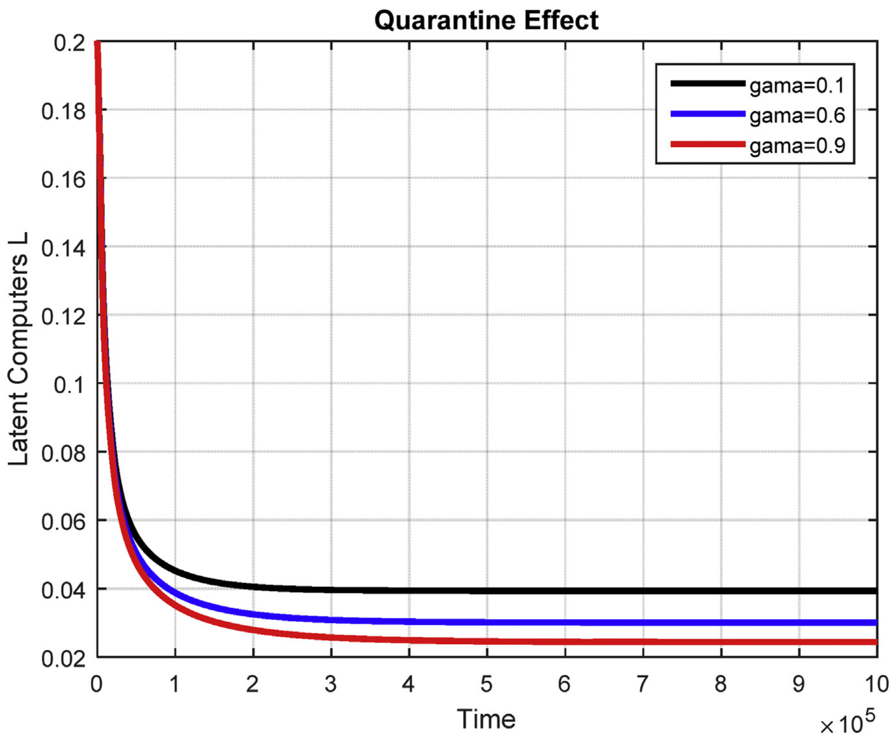

Fig. 9. Effect of quarantine strategy by taking different values of γ.

By enhancing the quarantine technique, the number of latent computers can be decreased. In this way, the virus transmission can be controlled.

4. Discussion

The selection of appropriate numerical method is very necessary to solve the dynamical systems. The numerical method must preserve all the essential properties demonstrate by the continuous system. In epidemic systems, positivity is necessary condition. NSFD method is positivity preserving method. By construction, Euler and RK-4 FD method have negative terms. This drawback of Euler and RK-4 FD methods is also verified via simulations. In NSFD scheme, positivity is maintained in its mathematical form and this attribute is verified by simulations. Also Euler and RK-4 FD schemes depends on time step and do not converge at different time steps to steady states of continuous system. While NSFD scheme is independent of time step and unconditionally converges to the true steady states of the system. The virus transmission can efficiently be controlled by quarantine strategy and this claim is verified by the simulations (Fig. 9).

5. Conclusions

This article is about the numerical study of SLBQR computer virus epidemic dynamics. In this paper, we used three numerical methods for SLBQR computer virus

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epidemic model and observes that classical numerical methods fail to preserve positivity property and do not converge to both equilibrium states of the model at each time step. While proposed NSFD scheme is positivity preserving and unconditionally convergent to both steady states of the model. Convergence of the proposed NSFD scheme is discussed with the help of Jacobian matrix at both equilibrium points of the model. Stability of the SLBQR system is also verified with the help of Routh-Hurwitz conditions. Moreover, the bifurcation value of infection coefficient in SLBQR system is evaluated with the help of Routh-Hurwitz criteria.

Declarations

Author contribution statement

Umbreen Fatima: Conceived and designed the experiments; Performed the experiments; Analyzed and interpreted the data; Wrote the paper.

Mubasher Ali: Performed the experiments.

Nauman Ahmed: Conceived and designed the experiments; Analyzed and interpreted the data; Wrote the paper.

Muhammad Rafiq: Analyzed and interpreted the data.

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Competing interest statement

The authors declare no conflict of interest.

Additional information

No additional information is available for this paper.

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