

DISCRETIZATION FRACTIONAL-ORDER SEIR WORM PROPAGATION MODEL IN COMPUTER NETWORKS

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ABSTRACT. This model focuses on the investigation of potential worm-attacking behaviour in networked computers. Using epidemic theory, a discrete fractional order SEIR (Susceptible-Exposed-Infectious-Recovered) model is developed to represent the dynamics of worms in computer networks. Following parameter analysis, some successful worm-removal tactics are recommended. The discretized fractional order SEIR model considers the fractional order $0 < \phi < 1$ and step denoted by h . The nodes $S(\ell), E(\ell), I(\ell), R(\ell)$ represent the fraction of susceptible, exposed, infectious and recovered populations with time ℓ with non negative parameters $A, \sigma, \mu, \epsilon, \alpha, \rho, \beta$. Theoretical research shows that the Reproduction Number (RN) threshold RN_0 determines the dynamics of the propagation of worms. When $RN_0 \leq 1$ the worm-free equilibrium is globally asymptotically stable, while $RN_0 > 1$, the worm-endemic equilibrium is globally asymptotically stable. The analytical findings are backed by a numerical investigation.

Keywords: Epidemic Model, fractional difference equation, computer networks, basic reproduction number, global stability, neimark-sacker bifurcation

AMS Subject Classification: 39A13, 39A28, 39A30, 39A33, 92D30

1. INTRODUCTION

Worm threats pose the greatest threat to the assets, functionality and security of computer networks. One of the most significant and dangerous security risks currently facing the business, political, military and research groups is externally launched computer worms that maliciously spread within networks. By gaining unauthorized access to computer resources, malware, also known as harmful software, such as viruses, worms, trojan horses, or rootkits worm poses a serious threat to the community of computer users. Because they

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may infect millions of machines quickly and do hundreds of millions of dollars' worth of harm. Worms are among the types of malware that computer security researchers are most interested in studying. Computer worms have recently grown to represent a significant threat to the security of computer networks, requiring significant resources and recovery time from vicious attacks. [3, 17] The epidemiological component of computer virus/worm propagation in networks is greatly aided by mathematical modelling. Understanding the pattern of worm transmission from one node to another and controlling transmission can both benefit from a mathematical model of propagation. One of the most crucial areas of research is epidemiology. Many academics have thought about studying infectious illness modelling and analysis.

In the real world, the discovery of an outbreak is a prerequisite for the later creation of a treatment for the undiagnosed illness. To evaluate the malicious traffic and then create an appropriate fix, one must first be aware that a worm epidemic is occurring from the perspective of network security. The worst form of worm is one that is never discovered since it can cause significant harm without the user ever realizing it. However, despite the fact that such a worm will leave no trace of its presence on the target hosts, it will still increase network traffic in the target port in order to spread.

Both biological and computer viruses exhibit remarkably similar behavioural traits. As a result, by introducing factors important to worm/virus propagation, mathematical models of computer worm/virus propagation in computer networks will be built based on the epidemic models. The creation of mathematical models in epidemiology was greatly influenced by historical studies on epidemic models. A variety of epidemic models, including SIRS model [4], SEIR model [15], SIR-A model [1], SIQR model [10, 14], SEIQR model [21], SEIRS-V model [19], VEISV model [20], VEIQS model [6] and SLBS model [18], have been used to analyze and describe the internet's role in the transmission of computer worms. This researches the pattern of worm/malicious code transmission and spread in computer networks based on a review of the literature. The structure of this article is as follows: The discretization procedure was applied to the SEIR worm propagation epidemic model in Section 2 to produce the discrete fractional order SEIR model. The equilibrium points of the model (2) were determined and the fundamental reproduction number was evaluated in section 3. The free and endemic equilibrium points of the model (2) were then examined for local and global stability. Numerical simulations that support the established requirements are presented in Section 4. The discussion in the final section brings the article to a close.

2. SEIR WORM PROPAGATION EPIDEMIC MODEL

For each host, there are only two possible states in the traditional simple epidemic model: susceptible (vulnerable) and infectious. The non-vulnerable hosts are not taken into account in this model because infection efforts have no effect on them. Kermack-Mckendrick expanded the straightforward epidemic model by taking the process of removing infectious hosts into account [5]. In this expanded model, it is assumed that some infectious hosts either recover or pass away during an epidemic; however, once a host recovers from the illness, it develops a lifelong immunity to the illness. The diseased hosts who heal or pass away are placed in the removed condition. Exposed class was created in the SIR compartmental epidemic model to study the spread of harmful code. Generalization of classical calculus to include derivatives and integrals of any order is known as fractional calculus. Additionally, fractional calculus is challenging in several ways. In recent decades, it has become increasingly clear that this mathematical theory provides

benefits both to pure mathematics and applications. The stability of the system for different fractional orders are discussed by including fractional order in the SEIR model. Consider about the SEIR model with fractional order as follows:

$$\begin{aligned} D^\phi S(\ell) &= A - \sigma S(\ell)E(\ell) - (\mu + \epsilon)S(\ell) \\ D^\phi E(\ell) &= \sigma S(\ell)E(\ell) - (\alpha + \mu + \rho)E(\ell) \\ D^\phi I(\ell) &= \alpha E(\ell) - (\mu + \beta)I(\ell) \\ D^\phi R(\ell) &= \epsilon S(\ell) + \rho E(\ell) + \beta I(\ell) - \mu R(\ell) \end{aligned} \quad (1)$$

where $A, \sigma, \mu, \epsilon, \alpha, \rho, \beta$ are all positive and $0 < \phi < 1$. Researchers have started to endorse fractional order difference equations [7, 8, 9, 11, 12]. Following parameter analysis, some successful worm-removal tactics are recommended. It has been demonstrated that, compared to their continuous counterparts, discretized systems produce substantially richer complicated dynamics. The discrete fractional order SEIR model is of the following form after discretizing the fractional-order system utilizing piecewise constant arguments approaches to (1).

$$\begin{aligned} S(\ell + 1) &= S(\ell) + \frac{h^\phi}{\Gamma(1 + \phi)} [A - \sigma S(\ell)E(\ell) - (\mu + \epsilon)S(\ell)] \\ E(\ell + 1) &= E(\ell) + \frac{h^\phi}{\Gamma(1 + \phi)} [\sigma S(\ell)E(\ell) - (\alpha + \mu + \rho)E(\ell)] \\ I(\ell + 1) &= I(\ell) + \frac{h^\phi}{\Gamma(1 + \phi)} [\alpha E(\ell) - (\mu + \beta)I(\ell)] \\ R(\ell + 1) &= R(\ell) + \frac{h^\phi}{\Gamma(1 + \phi)} [\epsilon S(\ell) + \rho E(\ell) + \beta I(\ell) - \mu R(\ell)] \end{aligned} \quad (2)$$

where h is the step size and ℓ is time. $S(\ell)$ is the number of susceptible nodes, devices that are not infected by the computer worm. $E(\ell)$ is the number of exposed nodes, devices reached by the computer worm such that it is not activated (it is not able to propagate to another host and to perform its malicious payload). $I(\ell)$ is the number of infected nodes, exposed devices such that the computer worm is activated. $R(\ell)$ is the number of recovered nodes, infected devices where the computer worm have been successfully detected and removed. Here, A, σ, μ represents the replacement of the computer networks, contact rate of the computer networks and rate of removable from the computer networks. Also $\epsilon, \alpha, \rho, \beta$ are transition rate from S to R , E to I , E to R and I to R respectively. Figure 1 represents the state transition diagram for worm propagation model of (2).

3. ANALYSIS OF THE SEIR MODEL (2)

In this section the basic reproduction number has been evaluated and the equilibrium positions for the model (2) have been obtained. The free and endemic equilibrium points of the model (2) also were explored for local and global stability.

3.1. Equilibria. Consider the algebraic equation as

$$\begin{aligned} A - \sigma S(\ell)E(\ell) - (\mu + \epsilon)S(\ell) &= 0 \\ \sigma S(\ell)E(\ell) - (\alpha + \mu + \rho)E(\ell) &= 0 \\ \alpha E(\ell) - (\mu + \beta)I(\ell) &= 0 \\ \epsilon S(\ell) + \rho E(\ell) + \beta I(\ell) - \mu R(\ell) &= 0 \end{aligned} \quad (3)$$

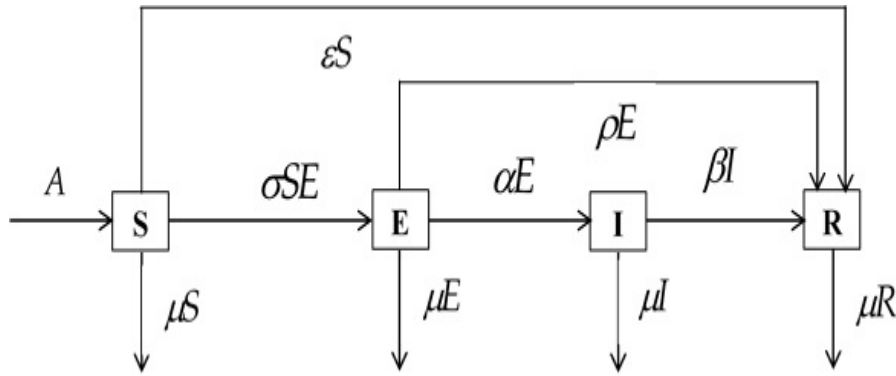


FIGURE 1. Transition diagram of the model (2)

Solving (3), If $I_* = 0$, the unique positive worm-free equilibrium point is

$$W_0 = \left(S_*, 0, 0, \frac{\epsilon}{\mu} S_* \right),$$

where $S_* = \frac{A}{\mu + \epsilon}$ otherwise, the unique positive worm-endemic equilibrium point is

$$W_1 = (S^*, E^*, I^*, R^*),$$

where $S^* = \frac{\mu + \rho + \alpha}{\sigma}$,

$$E^* = \frac{A}{\mu + \rho + \alpha} - \frac{\mu + \epsilon}{\sigma},$$

$$I^* = \frac{A\alpha}{(\mu + \beta)(\mu + \rho + \alpha)} - \frac{\alpha(\mu + \epsilon)}{\sigma(\mu + \beta)} \text{ and}$$

$$R^* = \frac{(A\sigma - \mu(\mu + \rho + \alpha))(\alpha\beta + \beta\rho + \mu\rho)}{\sigma\mu(\mu + \beta)(\mu + \rho + \alpha)} + \frac{\epsilon(\mu + \beta + \alpha)}{\sigma(\mu + \beta)} \text{ when } A > \frac{(\mu + \epsilon)(\mu + \rho + \alpha)}{\sigma}.$$

The following theorems were exhibited from the above analysis.

Theorem 3.1. *If $I_* = 0$, then the unique positive worm-free equilibrium point is $W_0 = \left(S_*, 0, 0, \frac{\epsilon}{\mu} S_* \right)$, where $S_* = \frac{A}{\mu + \epsilon}$.*

Theorem 3.2. *If $A > \frac{(\mu + \epsilon)(\mu + \rho + \alpha)}{\sigma}$, then the unique positive worm-endemic equilibrium point is $W_1 = (S^*, E^*, I^*, R^*)$, where $S^* = \frac{\mu + \rho + \alpha}{\sigma}$, $E^* = \frac{A}{\mu + \rho + \alpha} - \frac{\mu + \epsilon}{\sigma}$, $I^* = \frac{A\alpha}{(\mu + \beta)(\mu + \rho + \alpha)} - \frac{\alpha(\mu + \epsilon)}{\sigma(\mu + \beta)}$ and $R^* = \frac{(A\sigma - \mu(\mu + \rho + \alpha))(\alpha\beta + \beta\rho + \mu\rho)}{\sigma\mu(\mu + \beta)(\mu + \rho + \alpha)} + \frac{\epsilon(\mu + \beta + \alpha)}{\sigma(\mu + \beta)}$.*

3.2. Basic reproduction number (RN_0). The basic reproduction number, R_0 , is defined as the expected number of secondary cases produced by a single infection in a completely susceptible node. In epidemiological theory, RN_0 has a threshold centered on 1. However, RN_0 is not related to the intensity of transmission. When $RN_0 \leq 1$ the worm-free equilibrium is globally asymptotically stable, while $RN_0 > 1$, the worm-endemic equilibrium is globally asymptotically stable. Now, the basic reproduction number is derived from the model (2) by applying next generation method [2]. The basic reproduction

number is found from

$$\frac{dx}{dt} = F(x) - V(x),$$

where $F(x) = \begin{bmatrix} \sigma SE \\ 0 \\ 0 \\ 0 \end{bmatrix}$ and $V(x) = \begin{bmatrix} (\mu + \rho + \epsilon)E \\ -\alpha E + (\mu + \beta)I \\ -A + \sigma SE + (\mu + \epsilon)S \\ -\epsilon S - \rho E - \beta I + \mu R \end{bmatrix}$.

Now

$$T = \begin{bmatrix} \frac{\partial T_1}{\partial E} & \frac{\partial T_1}{\partial I} \\ \frac{\partial T_2}{\partial E} & \frac{\partial T_2}{\partial I} \end{bmatrix} = \begin{bmatrix} \sigma S & 0 \\ 0 & 0 \end{bmatrix} = \begin{bmatrix} \frac{\sigma A}{\mu + \epsilon} & 0 \\ 0 & 0 \end{bmatrix},$$

$$Z = \begin{bmatrix} \frac{\partial Z_1}{\partial E} & \frac{\partial Z_1}{\partial I} \\ \frac{\partial Z_2}{\partial E} & \frac{\partial Z_2}{\partial I} \end{bmatrix} = \begin{bmatrix} \alpha + \rho + \mu & 0 \\ -\alpha & \mu + \beta \end{bmatrix}.$$

Also,

$$Z^{-1} = \begin{bmatrix} \frac{1}{\alpha + \rho + \mu} & 0 \\ \frac{\alpha}{(\mu + \beta)(\alpha + \rho + \mu)} & \frac{1}{\mu + \beta} \end{bmatrix}.$$

The generation matrix of the system is

$$TZ^{-1} = \begin{bmatrix} \frac{\sigma A}{(\mu + \epsilon)(\alpha + \rho + \mu)} & 0 \\ 0 & 0 \end{bmatrix}.$$

The spectral radius of matrix TZ^{-1} is $\Omega(TZ^{-1}) = \frac{\sigma A}{(\mu + \epsilon)(\alpha + \rho + \mu)}$. Hence the basic reproduction number is

$$RN_0 = \frac{\sigma A}{(\mu + \epsilon)(\alpha + \rho + \mu)}.$$

3.3. Local stability of the worm-free equilibrium. The Jacobian matrix of the model (2) is

$$J = \begin{bmatrix} 1 - \Theta[\sigma E + (\mu + \epsilon)] & -\Theta\sigma S & 0 & 0 \\ \Theta\sigma E & 1 + \Theta[\sigma S - (\alpha + \rho + \mu)] & 0 & 0 \\ 0 & \Theta\alpha & 1 - \Theta[\mu + \beta] & 0 \\ \Theta\epsilon & \Theta\rho & \Theta\beta & 1 - \Theta\mu \end{bmatrix}$$

The characteristic equation is $|J - \lambda I| = 0$, that implies

$$\begin{aligned} & [1 - \Theta[\sigma E + (\mu + \epsilon)] - \lambda] [1 + \Theta[\sigma S - (\alpha + \rho + \mu)] - \lambda] \\ & [1 - \Theta[\mu + \beta] - \lambda] [1 - \Theta\mu - \lambda] + \Theta^2\sigma^2SE [1 - \Theta[\mu + \beta] - \lambda] [1 - \Theta\mu - \lambda] = 0 \end{aligned} \tag{4}$$

For the worm free equilibrium point W_0 , the characteristic equation (4) is modified by

$$[1 - \Theta(\mu + \epsilon) - \lambda] \left[1 + \frac{\Theta\sigma A}{\mu + \epsilon} - \Theta(\alpha + \rho + \mu) - \lambda \right] [1 - \Theta[\mu + \beta] - \lambda] [1 - \Theta\mu - \lambda] = 0.$$

Here the eigenvalues $\lambda_1, \lambda_3, \lambda_4$ are negative. If $RN_0 < 1$, then $\lambda_2 > 0$, that implies that W_0 is locally asymptotically stable. While, W_0 is unstable if $RN_0 > 1$. Hence, the following theorem holds good from the above discussion.

Theorem 3.3. *The worm-free equilibrium point W_0 of the model (2) is locally asymptotically stable if $RN_0 < 1$ while, W_0 is unstable if $RN_0 > 1$.*

3.4. Global stability of the worm-free equilibrium. Define the Lyapunov function

$$\begin{aligned} L(\ell) &= \alpha E(\ell) + (\mu + \alpha + \rho)I(\ell) \\ \frac{dL}{d\ell} &= \alpha \frac{dE}{d\ell} + (\mu + \alpha + \rho) \frac{dI}{d\ell} \\ &= \alpha [\sigma S(\ell)E(\ell) - (\alpha + \mu + \rho)E(\ell)] + (\mu + \alpha + \rho) [\alpha E(\ell) - (\mu + \beta)I(\ell)] \\ &= \alpha \sigma S(\ell)E(\ell) - (\mu + \alpha + \rho)(\mu + \beta)I(\ell) \\ &= (\mu + \beta)\sigma S(\ell)I(\ell) - (\mu + \alpha + \rho)(\mu + \beta)I(\ell) \end{aligned}$$

Since $S(\ell) \leq \frac{A}{(\mu + \epsilon)} + \left[S(0) - \frac{A}{(\mu + \epsilon)} \right] e^{-(\mu + \epsilon)\ell}$ from $S'(\ell) \leq A - (\mu + \epsilon)S(\ell)$.

Therefore,

$$\begin{aligned} \frac{dL}{d\ell} &\leq \left[\frac{(\mu + \beta)\sigma A}{(\mu + \epsilon)} - (\mu + \alpha + \rho)(\mu + \beta) \right] I(\ell) \\ &\leq (\mu + \alpha + \rho)(\mu + \beta) \left[\frac{\sigma A}{(\mu + \epsilon)(\mu + \alpha + \rho)} - 1 \right] I(\ell) \\ &\leq (\mu + \alpha + \rho)(\mu + \beta) [RN_0 - 1] I(\ell) \end{aligned}$$

Since $RN_0 < 1$, which concludes that $L'(\ell) < 0$. From the LaSalle invariance principle [16], the worm-free equilibrium point W_0 is globally stable. Hence, the following theorem holds good from the above discussion.

Theorem 3.4. *The worm-free equilibrium point W_0 of the model (2) is globally asymptotically stable if $RN_0 < 1$.*

3.5. Local stability of the worm-endemic equilibrium. The characteristic equation of worm-endemic equilibrium of the model (2) is

$$\lambda^4 + c_1\lambda^3 + c_2\lambda^2 + c_3\lambda + c_4 = 0,$$

where $c_1 = a_1 + a_2 + a_3 - 4$, $c_2 = (a_2 - 1)(a_1 - 3) + (a_1 + a_2 - 3)(a_3 - 1)$, $c_3 = (a_1 - 2)(a_2 - 2)(a_3 - 1) - (1 - a_1 - a_2 + a_1a_2)$ and $c_4 = (1 - a_3)(1 - a_1 - a_2 + a_1a_2)$.

Also,

$$a_1 = \frac{\Theta\sigma A}{\mu + \rho + \alpha}, a_2 = \Theta(\mu + \beta) \quad \text{and} \quad a_3 = \Theta\mu.$$

From the Routh-Hurwitz criterion [13], the worm-endemic equilibrium point is locally stable when

$$c_4 > 0, c_3 > 0, c_1 > 0 \quad \text{and} \quad c_1c_2c_3 - c_3^2 - c_4c_1^2 > 0.$$

Also, satisfied $RN_0 > 1$. Hence, the following theorem holds good from the above discussion.

Theorem 3.5. *The worm-endemic equilibrium point W_1 of the model is locally asymptotically stable for $RN_0 > 1$.*

4. NUMERICAL SIMULATIONS

This section presents numerical simulations for the SEIR transmission model over a time ℓ via fractional order ϕ by taking into account some special model conditions (2). These simulations are designed to highlight the most important findings from theoretical research and graphical displays like time plots and bifurcation diagrams. Simulations using numbers show very interesting, complex dynamical features.

Example 4.1. Consider the parameter value $h = 0.95, A = 0.95, \phi = 0.75, \sigma = 1.9, \mu = 0.76, \epsilon = 0.94, \alpha = 0.24, \rho = 0.25$ and $\beta = 0.03$ with the initial condition $S = 0.85, E = 0.10, I = 0.05, R = 0$. Computation yields $(S_*, E_*, I_*, R_*) = (0.5588, 0, 0, 0.6912)$ and the basic reproduction value $RN_0 = \frac{1.805}{2.125} = 0.8494 < 1$. The criteria for the stability are satisfied from Theorem 3.3 and hence the model (2) is locally stable for worm-free equilibrium point, see Figure 2.

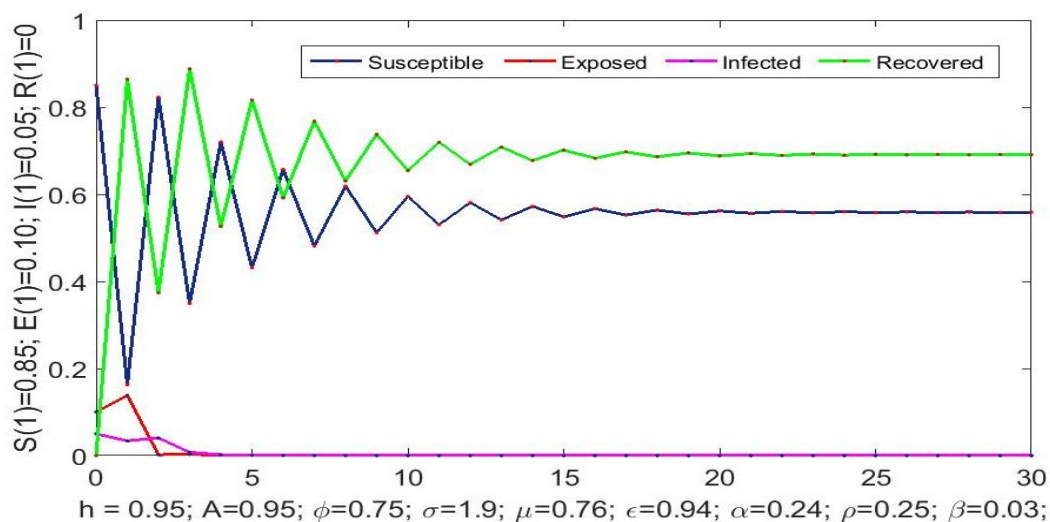


FIGURE 2. Local stability of the worm-free equilibrium of the model (2)

Example 4.2. Consider the parameter value $h = 1.45, A = 0.9, \phi = 0.95, \sigma = 1.5, \mu = 0.6, \epsilon = 0.25, \alpha = 0.14, \rho = 0.01$ and $\beta = 0.01$ with the initial condition $S = 0.85, E = 0.10, I = 0.05, R = 0$. Computation yields $(S_*, E_*, I_*, R_*) = (0.5588, 0, 0, 0.6912)$, the condition $0.97 > 0.4250$ and the basic reproduction value $RN_0 = \frac{1.35}{0.6375} = 2.1176 > 1$. The criteria for the stability are satisfied from Theorem 3.4 and hence the model (2) is locally stable for worm-endemic equilibrium point as seen in Figure 3. Taking another set of appropriate value as $h = 1.45, A = 1.3, \phi = 0.95, \sigma = 1.5, \mu = 0.6, \epsilon = 0.25, \alpha = 0.14, \rho = 0.01$ and $\beta = 0.01$ and for these value the model (2) is unstable for worm-endemic equilibrium point, see Figure 4.

In order to discuss a discrete Hopf bifurcation for the system (2) at the worm-endemic equilibrium point W_1 , we choose the fractional order ϕ as bifurcation parameter. Taking $h = 1.45, A = 1.25, \sigma = 1.5, \mu = 0.6, \epsilon = 0.25, \alpha = 0.14, \rho = 0.01, \beta = 0.01$ and $\phi \in (0, 2)$ with the initial condition $S = 0.85, E = 0.10, I = 0.05, R = 0$, then the SEIR model (2) undergoes a discrete Hopf bifurcation emerges from the worm-endemic equilibrium

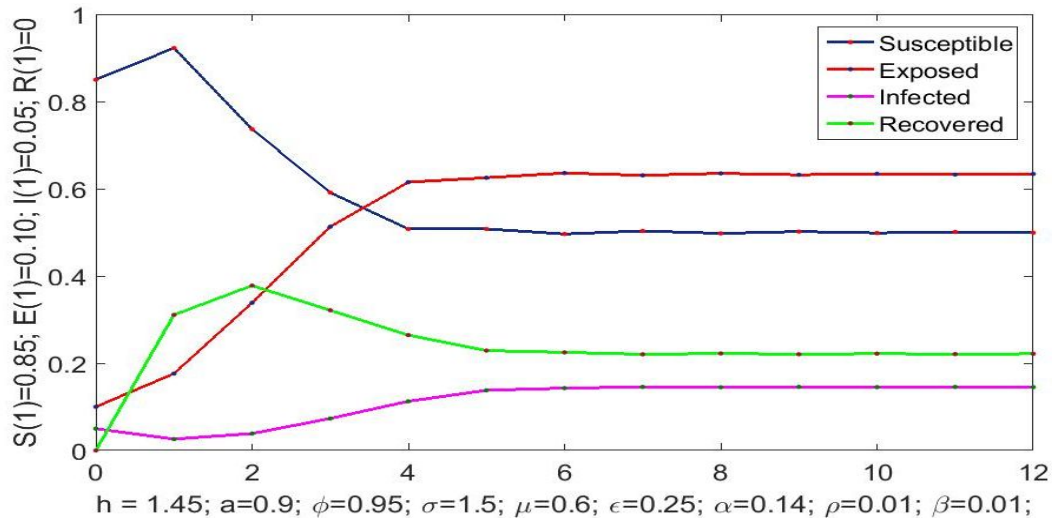


FIGURE 3. Local stability of the worm-endemic equilibrium of the model (2)

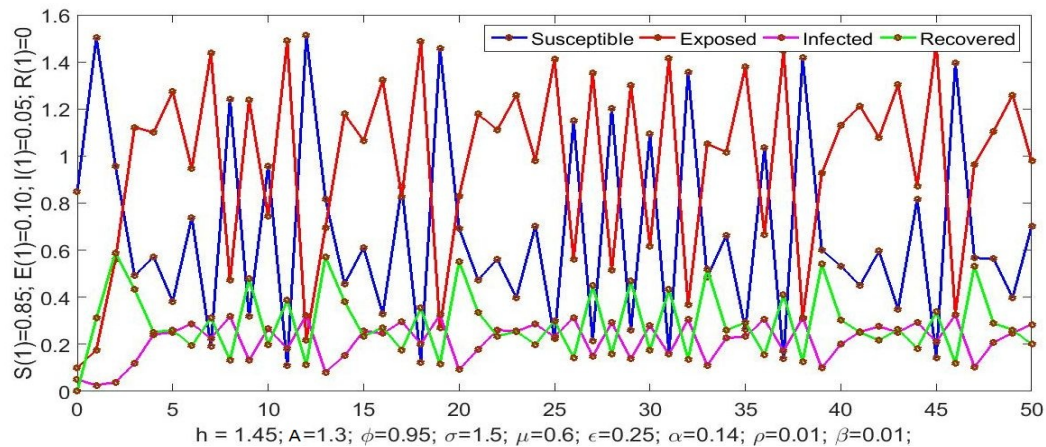


FIGURE 4. Unstable nature of the worm-endemic equilibrium of the model (2)

point W_1 at bifurcate value $\phi = 0.175$, see Figure 5. From Figure 5, the worm-endemic equilibrium point of the model (2) stable for $\phi < 0.175$ and it loses its stability through a discrete hopf bifurcation for $\phi = 0.175$ and an invariant circle appears for $\phi > 0.175$.

In order to discuss a discrete Periodic-doubling bifurcation for the system (2) at the worm-endemic equilibrium point W_1 , we choose A as bifurcation parameter. Taking $h = 1.45, \phi = 0.95, \sigma = 1.5, \mu = 0.6, \epsilon = 0.25, \alpha = 0.14, \rho = 0.01, \beta = 0.01$ and $A \in (0.9, 1.37)$ with the initial condition $S = 0.85, E = 0.10, I = 0.05$ and $R = 0$, then the SEIR model (2) undergoes a discrete Periodic-doubling bifurcation and this bifurcation emerges from the worm-endemic equilibrium point W_1 at bifurcate value $A = 1.015$, see Figure 6. From Figure 6, the worm-endemic equilibrium point of the model (2) is stable for $A < 1.015$ and it loses its stability through a discrete Periodic-doubling bifurcation for $A = 1.015$. Periodic doubling cascade in orbits of periods - 2, 4, 8, 16, 32 and non-periodic oscillations appear, that is usually referred to as chaos for $A > 1.015$.

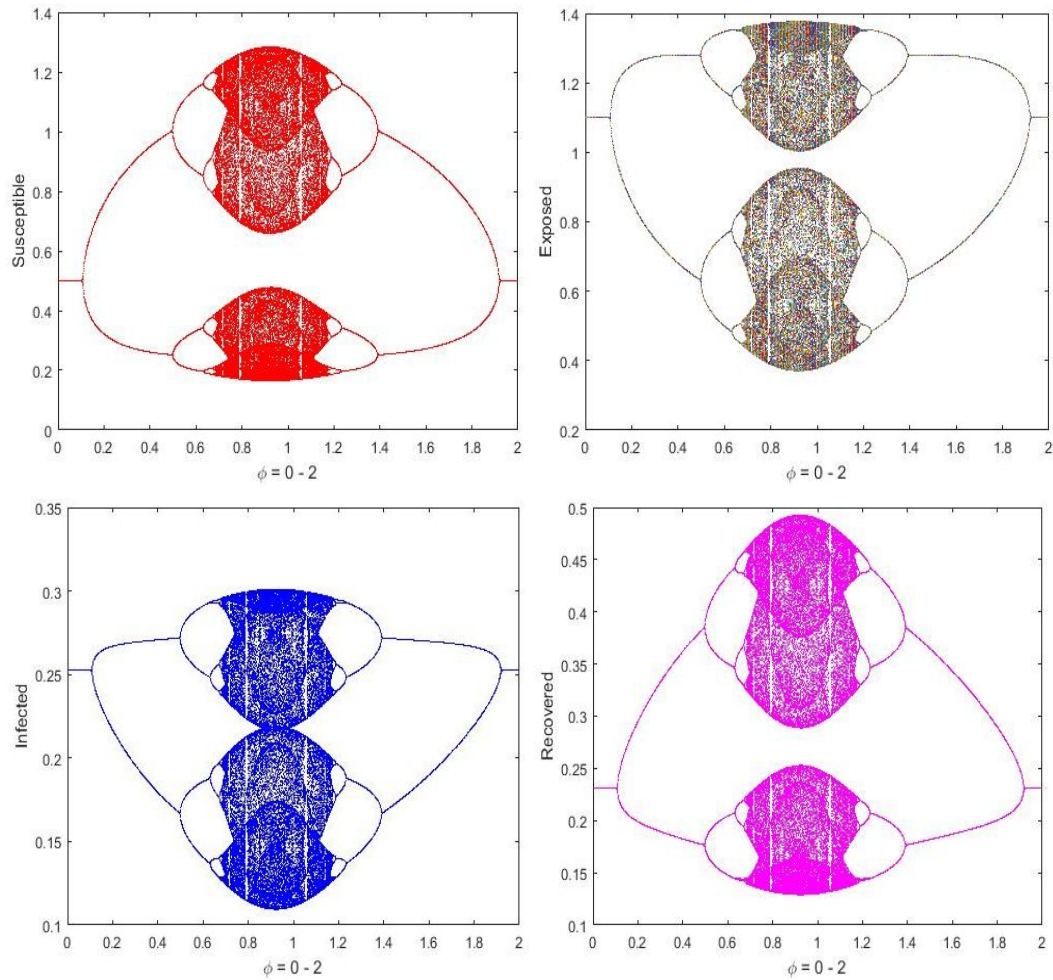


FIGURE 5. Bifurcation diagrams of the model (2) for the bifurcate value ϕ

5. DISCUSSION

In this paper, the discrete fractional order model is explored by using the discretization method after a brief proposal of a new SEIR worm propagation epidemic model. The model's (2) equilibrium points were acquired, and the basic reproduction number was also computed. The free and endemic equilibrium points of the model (2) were then examined for local and global stability. The theoretical criteria were validated by numerical simulations. The simulation findings showed that the worm's ability to spread can be managed by choosing the right settings. The figures show that, in the case of worm free equilibrium, the number of susceptible and recovered nodes increases and the number of infected and exposed nodes decreases. In the case of worm endemic equilibrium, the susceptible node decreased as the exposed node increased, and the infected node decreased as the recovered node increased. Future analysis of the dynamical behavior of the discrete fractional **SEIAR** model can include Asymptomatic (A) node.

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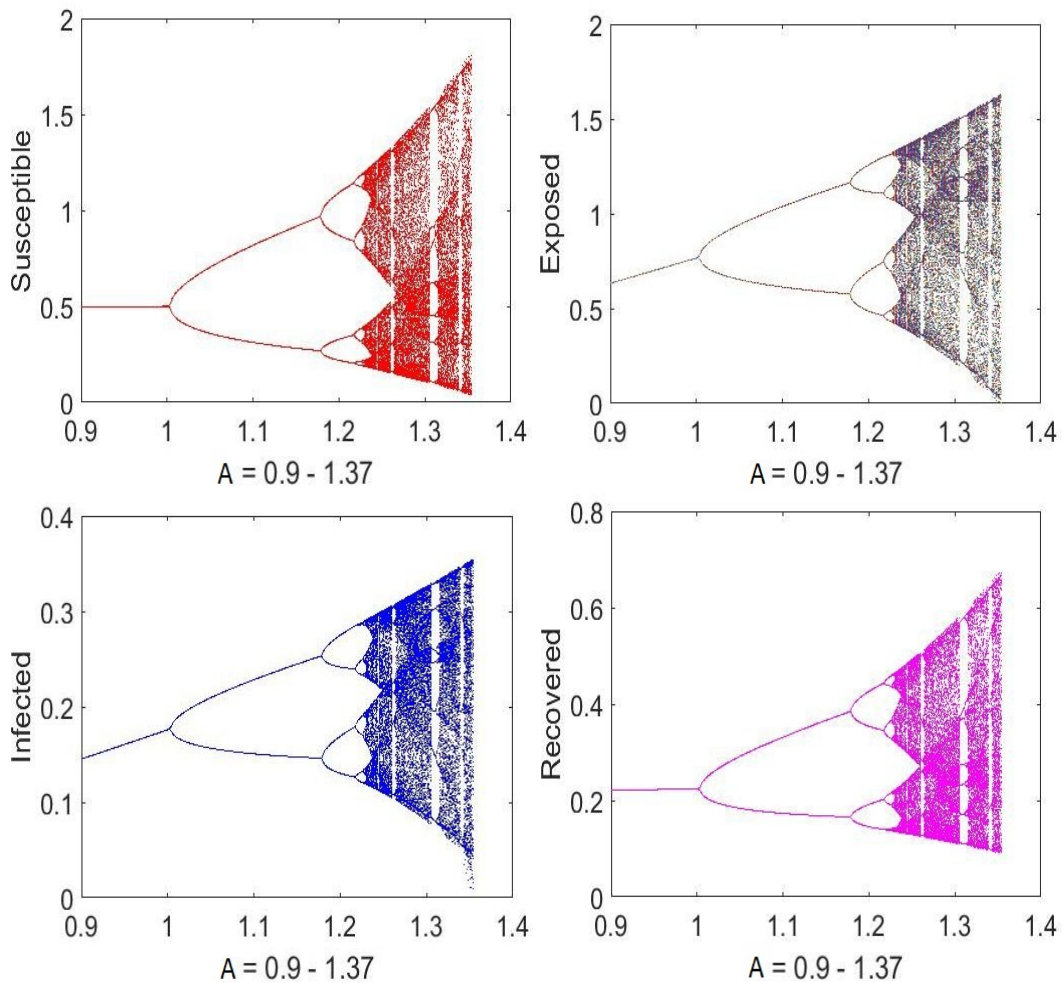


FIGURE 6. Bifurcation diagrams of the model (2) for the bifurcate value A

REFERENCES

- [1] Batistela, C. M. and Piqueira, J. R. C., (2018), Sira computer viruses propagation model: Mortality and robustness, *Int. J. Appl. Comput. Math.*, 50 (13), pp. 1–13.
- [2] Driessche, V. D. and Watmough, J., (2002), The reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, *Mathematical Biology Science*, 180 (1-2), pp. 29-48.
- [3] Edelstein-Keshet, L., (2005), *Mathematical Models in Biology*, SIAM, Random House, New York, USA.
- [4] Feng, L., Song, L., Zhao, Q. and Wang, H., (2015), Modeling and stability analysis of worm propagation in wireless sensor network, *Math. Probl. Eng.*, 2015, pp. 1-8.
- [5] Frauenthal, J. C., (1980), *Mathematical Modeling in Epidemiology*, Springer-Verlag, New York, USA .
- [6] Gao, Q. and Zhuang, J., (2020), Stability analysis and control strategies for worm attack in mobile networks via a veiqs propagation model, *Applied Mathematics and Computation*, 368, pp. 1-25.
- [7] George Maria Selvam, A., Godfrey Winster, S., Janagaraj, R. and Maria Jones, G., (2020), Modeling worm proliferation in wireless sensor networks with discrete fractional order system, *International Journal of Recent Technology and Engineering*, 8 (5), pp. 1815-1820.
- [8] George Maria Selvam, A. and Janagaraj, R., (2018), Numerical analysis of a fractional order discrete prey-predator system with functional response, *International Journal of Engineering & Technology*, 7 (4.10), pp. 681-684.

- [9] George Maria Selvam, A., Janagaraj, R. and Jacintha, M., (2020), Dynamical analysis of a discrete fractional order prey-predator system incorporating a prey refuge with holling type II response, *J. Phys. Conf. Ser.* 1597, pp. 1–11.
- [10] George Maria Selvam, A., Janagaraj, R. and Maria Jones, G., (2018), Dynamics in a fractional order siqr model of worm propagation, *International Journal of Pure and Applied Mathematics*, 119 (3), pp. 549–558.
- [11] George Maria Selvam, A., Janagaraj, R. and Vignesh, D., (2021), Discretization and chaos control in a fractional order predator-prey harvesting model, *Commun. Fac. Sci. Univ. Ank. Ser. A1 Math. Stat.*, 70 (2), pp. 950-964.
- [12] Higazy, M., George Maria Selvam, A. and Janagaraj, R., (2021), Chaotic dynamics of a novel 2d discrete fractional order ushiki map, *Fractals*, 29 (8), pp. 1-11.
- [13] Hurwitz, A., (1985), On the conditions under which an equation has only roots with negative real parts, *Mathematische Annalen*, 46, pp. 273-284.
- [14] HuuKhanh, N., (2016), Dynamics of a worm propagation model with quarantine in wireless sensor networks, *Appl. Math. Inf. Sci.*, 10 (5), pp. 1739–1746.
- [15] Keshri, N. and Mishra, B. K., (2014), Two time-delay dynamic model on the transmission of malicious signals in wireless sensor network, *Chaos Solitons Fractals*, 68, pp. 151-158.
- [16] LaSalle, J. P., (1976), *The stability of Dynamical Systems*, SIAM, Philadelphia, USA.
- [17] Murray, J. D., (2002), *Mathematical Biology I: An Introduction*, Springer-Verlag, New York, USA.
- [18] Ren, J. and Xu, Y., (2014), Stability and bifurcation of a computer virus propagation model with delay and incomplete antivirus ability, *Mathematical Problems in Engineering*, 2014, pp. 1-9.
- [19] Singh, A., Awasthi, A., Singh, K. and Srivastava, P., (2018), Modeling and analysis of worm propagation in wireless sensor networks, *Wirel. Pers. Commun.*, 98 (3), pp. 2535-2551.
- [20] Toutonji, O. A., Yoo, S. M. and Park, M., (2012), Stability analysis of veisv propagation modeling for network worm attack, *Applied Mathematical Modelling*, 36 (6), pp. 2751-2761.
- [21] Xiao, X., Fu, P., Dou, C. S., Li, Q., Hu, G. W. and Xia, S. T., (2017), Design and analysis of seiqr worm propagation model in mobile internet, *Commun. Nonlinear Sci. Numer. Simul.*, 43, pp. 341-350.



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