International Journal of Academic and Applied Research (IJAAR)
ISSN: 2643-9603
Vol. 5 Issue 10, October - 2021, Pages: 131-138

A Fractional Order Mathematical Modeling the Spread of Computer Viruses on Networks

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Abstract: *A computer virus is a program that can replicate, multiply and infect from one program to another, user to user, computer to computer, and network to network. The mathematical model approach can be used to predict the dynamics of spread of computer viruses on a network. The model of spread of computer viruses on network is based on the fact that computer will be infected by infected computers and exposed computers and some computers that are in a vulnerable and exposed status can obtain immunity with antivirus capabilities. In this paper, we present a fractional mathematical model of the spread of computer viruses on networks with fractional order. The dynamic behavior of this model is investigated. First, we determine the stability of the equilibrium point for the fractional model. Based on the model analysis, we gained two points of equilibrium, the equilibrium point is virus-free computer and equilibrium point endemic virus computer . We also obtain basic reproduction rate, which determine the existence and stability os the equilibrium point. The equilibrium point is virus-free computer is stable asymptotic locally if basic reproduction number less than one and equilibrium endemic virus computer point stable asymptotic locally if basic reproduction number more than one. Next, we analyze the sensitivity of the parameters that most influence the spread of computer viruses. Finally, we carry out numerical simulations with variations α to illustrate analytical result.*

Keywords— *computer viruses, fractional mathematical model, stability, equilibrium, sensitivity, numerical simulations.*

1. INTRODUCTION

A computer virus is a computer program that can reproduce and infect a program, user, computer, or network [1]. Computer viruses work by deleting data, corrupting files, or modifying normal operations [2]. Computer viruses have similarities with viruses in the case of biology, especially in the way they are spread. A computer virus rides on a program or document which if the program or document is executed, the virus is like being given permission to infect other programs or documents. This is similar to a virus in the case of biology that hitches a ride on the cells of other living things for their survival. The living thing that is carried by this biological virus is called the host. The virus also causes the host to become sick. A comparison between biological viruses and computer viruses is presented in Table 1 [3].

Table 1. Comparison between biological viruses and computer viruses

Characteristic	Biological viruses	Computer Viruses
• Size • Composition • Infection • Life Cycle	• 100 – 300 nm • contains protein • living cells • 20 – 45 minutes	• 124 bytes – 5 kb • contains malicious code • files, programs • almost the same as the application software
• Deployment • Main enemy • Consequence • Reproduction • Antidetect	• The intervention of other living things is required • antibodies • cause disease and cell damage • by creating the genetic code • evolution of forms and abilities	installation process • human intervention is required • antivirus • manipulating the system and potensially damaging it • by replicating the program code • polymorphic, encryption, anti debugging, stealth

The high similarity between computer viruses and biological viruses has led to the emergence of various papers on computer virus transmission models [4].

Computer viruses have a latency period, the computer can be exposed to the virus but cannot transmit it. An infected computer that is in latency, is called an exposed computer and will not directly infect other computers. Based on these characteristics, the delay in the spread of computer viruses is used in several computer virus models

to illustrate that although the exposed computer does not infect other computers, it still has infectivity [5]. Yang et al [6] developed SLB and SLBS models to study the dynamics of computer viruses. In the model, Yang et al. assumed that computer viruses have latency, and computers also have infectivity in the latency period. However, Yang et al. did not show the length of latency and took into account the impact of artificial immunization methods such as installing antivirus software. Computers that have just been connected to the internet are vulnerable. While Mei Peng et al [2] developed a SEIR model for computer viruses by dividing the population into four compartments, namely the susceptible computer population S, the computer population exposed to E, the computer population infected with I and the computer population recovered from infection with R. Mei Peng et al [2] developed mathematical models of computer viruses and their dynamics using a system of ordinary differential equations.

System of ordinary differential equations (ODE) which consists of a first-order differential equation can be generalized to system of fractional differential equations (FDE) which consists of a fractional order differential equation α, with $0 < \alpha \leq 1$. [7]. In most biologic cases, FDEs are naturally connected to systems with memory [8]. In addition, memory effects have an important role in the spread of disease. The presence of memory effects on past events will influence the spread of disease in the future. The distance from the memory effect indicates the history of the spread of the disease. Thus, the effect of memory on the spread of infectious diseases could be investigated using fractional derivatives [9, 10, 11, 12, 13, 14].

Based on the explanation above, in this paper, a review of the ODE model from Mei Peng et al [2] is carried out but using the FDE model approach. This paper also determines the equilibrium point, stability of the equilibrium point and analysis of the sensitivity of the model made. Furthermore, numerical simulations were carried out to support the interpretation of the mathematical model created.

This paper is structured as follows: part 2 formulating a computer virus model, part 3 testing the stability of the equilibrium point, part 4 determining the sensitivity of the model and part 5 performing numerical simulations to show the correctness of the analytical results. Finally, in section 6, conclusions and suggestions from this paper are given.

2. MATHEMATICAL MODEL FORMULATION

In this section, a mathematical model of the fractional order of the spread of computer viruses in the network is formulated based on the model developed by Mei Peng et al [2]. The model consists of four compartments, namely:

- Susceptible computers, which are computers that have just been connected to the internet network and are not infected, are denoted by $S(t)$.
- Exposed computer, a computer that is infected with a virus but has not been able to transmit the virus, is denoted by $E(t)$.
- The computer is infected, denoted by $I(t)$.
- Recovered computer, a virus-free computer that has immunity, is denoted by $R(t)$.

Furthermore, without having a double meaning, $S(t), E(t), I(t)$ and $R(t)$ will be abbreviated as S, E, I, R.

The model transmission diagram is shown in Figure 1.

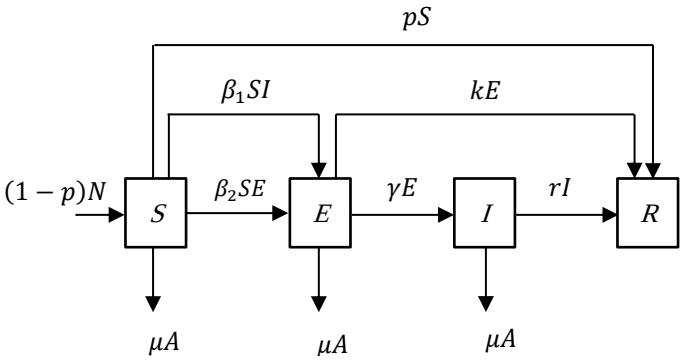


Fig. 1 Transmission diagram of a mathematical model of the spread of a computer virus on a network

The basic model for the spread of computer viruses in the form of ODE developed by Mei Peng et al [2] is given by equations (1) – (4) below:

$$\frac{dS}{dt} = (1-p)N - \beta_1 SI - \beta_2 SE - pS - \mu S \quad (1)$$

$$\frac{dE}{dt} = \beta_1 SI + \beta_2 SE - kE - \gamma E - \mu E \quad (2)$$

$$\frac{dI}{dt} = \gamma E - rI - \mu I \quad (3)$$

$$\frac{dR}{dt} = pS + kE + rI \quad (4)$$

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

With all parameters $p, \mu, k, \gamma, r, \beta_1, \beta_2 > 0$ and $S(t), E(t), I(t), R(t), N(t) \geq 0$.

We can see that equations (1), (2) and (3) are independent of equation (4). Therefore, equation (4) can be omitted, so the above model can be written as follows:

$$\frac{dS}{dt} = A - \beta_1 SI - \beta_2 SE - aS \quad (5)$$

$$\frac{dE}{dt} = \beta_1 SI + \beta_2 SE - bE \quad (6)$$

$$\frac{dI}{dt} = \gamma E - cI \quad (7)$$

with $a = p + \mu,\ b = k + \gamma + \mu,$

$$c = r + \mu,\ A = (1 - p)N$$

Furthermore, a mathematical model of the fractional order of the spread of computer viruses on a network in the form of an SPDF can be built according to equations (5) – (7) as follows:

$$\frac{d^\alpha S}{dt^\alpha} = A - \beta_1 SI - \beta_2 SE - aS$$
$$\frac{d^\alpha E}{dt^\alpha} = \beta_1 SI + \beta_2 SE - bE \qquad (8)$$
$$\frac{d^\alpha I}{dt^\alpha} = \gamma E - cI$$

with fractional order $0 < \alpha \leq 1$.

The parameters used in the mathematical model of the fractional order of the spread of computer viruses on the network are presented in Table 2.

Table 2. Description of the parameters in the model

Parameters	Description
p	Computer recovery rate is vulnerable due to network antivirus capabilities
μ	The rate at which a computer is disconnected from the network
k	Computer recovery rate exposed due to network antivirus capabilities
γ	The speed of the exposed computer cannot be recovered with antivirus and is corrupted
r	Infected computer recovery rate
β_1	The rate when a vulnerable computer has a connection to an infected computer, then a vulnerable computer can be infected but cannot infect
β_2	The rate at which a vulnerable computer has a connection to a computer is exposed, then a vulnerable computer can be exposed
N	Number of external computers connected to the network

The fractional derivative of model (8) is adopted from Caputo's fractional derivative. Caputo's fractional derivative has advantages, namely the initial value of the fractional-order differential equation is in the form of an integer order, which means it has the same shape as the integer-order differential equation [15]. Caputo's fractional derivative is defined as follows:

Definition 1 [15]. Given $\alpha > 0,\ t > 0$ and $n \in \mathbb{N}$. Caputo fractional derivative $D^\alpha := \frac{d^\alpha}{dt^\alpha}$, with fractional order α, from function $f(t)$ defined by:

$$D^\alpha f(t) = I^{n-\alpha} D^n f(t) = \begin{cases} \frac{1}{\Gamma(n-\alpha)} \int_0^t \frac{f^{(n)}(s)}{(t-s)^{\alpha-n+1}} ds, n-1 < \alpha < n \\ f^{(n)}(t), \alpha = n \end{cases} \qquad (9)$$

with $\Gamma(\cdot)$ is gamma function.

3. Equilibrium Point Stability Analysis

Equilibrium point is a condition when the rate of change of a particular subpopulation over time is zero. In this section, we study the equilibrium point stability of the model (8). The stability theorem for a system of fractional order is given by the following theorem.

Theorem 1 [16]. Consider a nonlinear fractional system

$$D^\alpha \boldsymbol{x}(\boldsymbol{t}) = \boldsymbol{f}(\boldsymbol{t})$$

with $0 < \alpha \leq 1,\ \boldsymbol{x} \in \mathbb{R}^n$ and $\boldsymbol{f} \in \mathbb{R}^n$. Equilibrium point $\boldsymbol{x}^*$ from system (10) calculated by solving the equation $\boldsymbol{f}(\boldsymbol{x}) = \boldsymbol{0}$. Equilibrium point $\boldsymbol{x}^*$ is said to be locally asymptotically stable if all the eigenvalues $\lambda_j (j = 1, 2, \ldots, n)$ from Jacobian matrix $A = \frac{\partial f}{\partial x}$ evaluated at equilibrium points $\boldsymbol{x}^*$ following conditions:

$$\left|\arg \lambda_j\right| > \frac{\alpha\pi}{2} \qquad (11)$$

The equilibrium point of the model (8) satisfies the following equations:

$$A - \beta_1 SI - \beta_2 SE - aS = 0 \qquad (12)$$
$$\beta_1 SI + \beta_2 SE - bE = 0 \qquad (13)$$
$$\gamma E - cI = 0 \qquad (14)$$

Model (8) has two equilibrium points, namely the computer virus-free equilibrium point $P_0 = (S_0, E_0, I_0)$ and the equilibrium point of endemic computer viruses $P^* = (S^*, E^*, I^*)$.

3.1 Computer Virus Free Equilibrium Point

Computer virus free equilibrium point $P_0 = (S_0, E_0, I_0)$ is a condition when no computer is infected with a virus, which means $E_0 = 0$ and $I_0 = 0$. Meanwhile for vulnerable computers $S_0 \neq 0$, This means that there are uninfected computers among the computers that have just connected to the internet network. The virus-free equilibrium point of model (8) is given by $P_0 = \left(\frac{A}{a}, 0, 0\right)$.

The basic reproduction number (R_0) will be calculated from model (8). The basic reproduction number (R_0) is an important parameter in epidemiological cases. The basic reproduction number (R_0) defined as the rate of secondary infection caused by one primary infection in a susceptible population [17]. Basic reproduction number (R_0) can be used to measure the potential spread of disease in a population. If $R_0 < 1$, then there is no endemic, meaning that the population is free from disease infection. Whereas if $R_0 > 1$, disease

infection occurs in that population and results in endemic [18]. In this paper, the method used to determine R_0 is *Next Generation Matrix* (NGM) method developed by Driessche and Watmough [19]. By using the NGM method, we get $R_0 = \frac{A(\beta_1\gamma+\beta_2 c)}{abc}$.

The stability of the computer virus-free equilibrium point is presented in Theorem 2.

Theorem 2. The virus-free equilibrium point P_0 of model (8) is locally asymptotically stable if and only if $R_0 < 1$.

Proof: Model (8) can be presented as follows:

$$\frac{d^\alpha S}{dt^\alpha} = A - \beta_1 SI - \beta_2 SE - aS = f_1(S,E,I)$$
$$\frac{d^\alpha E}{dt^\alpha} = \beta_1 SI + \beta_2 SE - bE = f_2(S,E,I) \qquad (15)$$
$$\frac{d^\alpha I}{dt^\alpha} = \gamma E - cI = f_3(S,E,I)$$

with fractional order $0 < \alpha \leq 1$.

The mathematical model in the system (15) above is in the form of a non-linear FDE. Therefore, it is necessary to linearize around the equilibrium point using the Jacobian matrix. The Jacobian matrix of the system (15) above is obtained by partially deriving each of the three equations f_1 to f_3 for the variables S, E and I respectively as follows [20]:

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial I} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial I} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial I} \end{bmatrix}$$

The Jacobian matrix is obtained for the mathematical model of the fractional order of the spread of computer viruses as follows:

$$J = \begin{bmatrix} -\beta_1 I - \beta_2 E - a & -\beta_2 S & -\beta_1 S \\ \beta_1 I + \beta_2 E & \beta_2 S - b & \beta_1 S \\ 0 & \gamma & -c \end{bmatrix} \qquad (16)$$

Furthermore, stability analysis was carried out against the computer virus-free equilibrium point, $P_0 = \left(\frac{A}{a}, 0,0\right)$, by using the eigenvalue approach so that the stability properties obtained are local stability.

Analysis of local asymptotic stability at the computer virus-free equilibrium point begins by substituting the equilibrium point $P_0 = \left(\frac{A}{a}, 0,0\right)$ to Jacobian matrix (16), we get:

$$J(P_0) = \begin{bmatrix} -a & -\beta_2 \frac{A}{a} & -\beta_1 \frac{A}{a} \\ 0 & \beta_2 \frac{A}{a} - b & \beta_1 \frac{A}{a} \\ 0 & \gamma & -c \end{bmatrix}$$

From matrix $J(P_0)$ characteristic equation can be formed through $\det(\lambda I - J(P_0)) = 0$, and got:

$$(\lambda + a)[\lambda^2 - (\beta_2 S_0 - b - c)\lambda - bc(R_0 - 1)] = 0 \qquad (17)$$

Equation (17) has a characteristic root $\lambda_1 = -a$ and $\lambda_i, i = 2,3$ is the root of the equation of:

$$\lambda^2 - (\beta_2 S_0 - b - c)\lambda - bc(R_0 - 1) = 0 \qquad (18)$$

Based on Proposition 1 (vi) [21], necessary conditions so that $\arg|\lambda_i| > \frac{\alpha\pi}{2}, i = 2,3$ that is $-bc(R_0 - 1) > 0$, that is $R_0 < 1$. Whereas if $R_0 < 1$, than $-(\beta_2 S_0 - b - c) > 0$. Therefore, based on the Routh-Hurwitz criteria [21] t is found that the roots of equation (18) are negative real numbers or negative real parts. Based on the description above, $\arg|\lambda_i| > \frac{\alpha\pi}{2}, i = 1,2,3$ for every $0 < \alpha \leq 1$ if and only if $R_0 < 1$. So, virus-free equilibrium point $P_0 = \left(\frac{A}{a}, 0,0\right)$ from model (8) is a locally asymptotically stable equilibrium point if and only if $R_0 < 1$.

3.2 Equilibrium Point of Endemic Computer Virus

Equilibrium point of endemic computer virus $P^* = (S^*, E^*, I^*)$ is a condition when a computer virus spreads, meaning that a computer is infected with a virus. The computer virus endemic equilibrium point is found if $S^*, E^*, I^* \neq 0$. The computer virus endemic equilibrium point of model (8) is given by $P^* = \left(\frac{A}{aR_0}, \frac{A(R_0-1)}{bR_0}, \frac{A\gamma(R_0-1)}{bcR_0}\right)$, with $R_0 = \frac{A(\beta_1\gamma+\beta_2 c)}{abc}$. This non-virus-free equilibrium point exists if $R_0 > 1$.

Theorem 3. Suppose $R_0 > 1$. Computer virus endemic equilibrium point $P^* = \left(\frac{A}{aR_0}, \frac{A(R_0-1)}{bR_0}, \frac{A\gamma(R_0-1)}{bcR_0}\right)$ locally asymptotically stable

(1) For every $\alpha \in (0,1]$ if and only if $a_1\, a_2 > a_3$
(2) For a $\alpha \in (0,1]$ if and only if $a_1\, a_2 \leq a_3$.

Proof. Analysis of local asymptotic stability at the computer virus endemic equilibrium point begins by substituting the equilibrium point $P^* = (S^*, E^*, I^*) = \left(\frac{A}{aR_0}, \frac{A(R_0-1)}{bR_0}, \frac{A\gamma(R_0-1)}{bcR_0}\right)$, with $R_0 = \frac{A(\beta_1\gamma+\beta_2 c)}{abc}$ to Jacobian matrix (16), so we get:

$$J(P^*) = \begin{bmatrix} -aR_0 & -\beta_2 S^* & -\beta_1 S^* \\ a(R_0 - 1) & \beta_2 S^* - b & \beta_1 S^* \\ 0 & \gamma & -c \end{bmatrix}$$

International Journal of Academic and Applied Research (IJAAR)
ISSN: 2643-9603
Vol. 5 Issue 10, October - 2021, Pages: 131-138

From matrix $J(P^*)$, characteristic equation can be formed through $\det(\lambda I - J(P^*)) = 0$, and got

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0, \qquad (19)$$

with

$$a_1 = aR_0 - (\beta_2 S^* - b - c),$$
$$a_2 = abR_0 + acR_0 - a\beta_2 S^*, \text{ and}$$
$$a_3 = abc(R_0 - 1).$$

Based on Proposition 1 (vi) [21], necessary conditions $\arg|\lambda_i| > \frac{\alpha\pi}{2}, i = 1,2,3$ that is $a_3 > 0$, that is $abc(R_0 - 1) > 0$, than obtained $R_0 > 1$.

Previously obtained that $\beta_2 S^* - b - c < 0$, than $-a\beta_2 S^* > -a(b + c)$. So that $a_2 = abR_0 + acR_0 - a\beta_2 S^* > abR_0 + acR_0 - a(b + c) = a(b + c)(R_0 - 1)$. Because $R_0 > 1$, than $a(b + c)(R_0 - 1) > 0$, so that it is obtained $a_2 > 0$. Because $R_0 > 1$ and $\beta_2 S^* - b - c < 0$, than $a_1 = aR_0 - (\beta_2 S^* - b - c) > 0$.

Since all coefficients of equation (19) are positive, then based on Descartes' sign test, equation (19) has no positive roots. So the roots are negative or complex roots whose real parts are negative. Based on the Routh-Hurwitz criteria [21], the root of equation (19) is negative or the real part is negative if and only if $a_1\, a_2 > a_3$. Therefore, equation (19) has roots with positive real parts if and only if $a_1\, a_2 \leq a_3$.

4. Sensitivity Analysis

In this section, we will analyze the sensitivity of the parameters in model (8) above. Parameter sensitivity analysis is used to determine which parameters in the model have a major influence on the rate of change of the model. Parameter sensitivity analysis was performed by calculating the sensitivity index value of each parameter.

The amount $\frac{\partial R_0}{\partial k}\frac{k}{R_0}$ is the sensitivity index of parameter k, where k is the parameter of R_0 to be analyzed [22]. The parameter values used for the calculation of the sensitivity index refer to [2]. In Basic Reproductive Numbers $R_0 = \frac{A(\beta_1\gamma + \beta_2 c)}{abc}$ with $a = p + \mu,\ b = k + \gamma + \mu,\quad c = r + \mu$ and $A = (1 - p)N$ there are seven parameters for which the sensitivity index will be searched, namely $p, \mu, k, \gamma, r, \beta_1$ and β_2. The results of the parameter sensitivity index analysis of R_0 in model (8) are shown in Table 3 with the following calculations:

$\frac{\partial R_0}{\partial p}\frac{p}{R_0}, \frac{\partial R_0}{\partial \gamma}\frac{\gamma}{R_0}, \frac{\partial R_0}{\partial r}\frac{r}{R_0}, \frac{\partial R_0}{\partial \mu}\frac{\mu}{R_0}, \frac{\partial R_0}{\partial k}\frac{k}{R_0}, \frac{\partial R_0}{\partial \beta_1}\frac{\beta_1}{R_0}$ and $\frac{\partial R_0}{\partial \beta_2}\frac{\beta_2}{R_0}$.

Table 3 Parameter sensitivity index

Parameters	Parameters Value	Sensitivity Index
p	0.5	–1.539
μ	0.02	0.125
k	0.4	–0.001
γ	0.6	0.703
r	0.6	0.803
β_1	0.7	0.705
β_2	0.8	0.832

Based on Table 3 above, it can be explained as follows:

- The sensitivity index for p is -1.539, meaning that if the recovery rate of the computer is vulnerable because the network antivirus capability is increased (decreased) by 10%, it will result in R_0 decreasing (increasing) by 15.39%.
- The sensitivity index for μ is 0.125, meaning that if the speed of computers disconnected from the network increases (decreases) by 10%, it will cause R_0 to increase (decrease) by 1.25%.
- The sensitivity index for k is -0.001, meaning that if the recovery rate of the computer is exposed because the network antivirus capability is increased (decreased) by 10%, it will cause R_0 to decrease (increase) by 0.01%.
- The sensitivity index for γ is 0.703, meaning that if the rate at which the computer is exposed cannot be recovered with antivirus and is damaged increases (decreases) by 10%, it will cause R_0 to increase (decrease) by 7.03%.
- The sensitivity index for r is 0.803, meaning that if the recovery rate of the infected computer increases (decreases) by 10%, it will cause R_0 to increase (decrease) by 8.03%.
- The sensitivity index for β_1 is 0.705, meaning that when a computer is connected to an infected computer, if the rate at which a vulnerable computer can become exposed increases (decreases) by 10%, it will cause R_0 to increase (decrease) by 7.05%.
- The sensitivity index for β_2 is 0.832, meaning that when a computer connected to a computer is exposed, then if the rate at which vulnerable computers can become exposed increases (decreases) by 10%, it will result in R_0 increasing (decreasing) by 8.32%.

Based on the explanation above, it can be concluded that the most influential parameter on the rate of change of the computer virus distribution model is p.

5. Numerical Simulation

Numerical simulation of the mathematical model of the spread of computer viruses on the network for computer virus-free equilibrium points and computer virus endemic equilibrium points was carried out using MATLAB R2013a software. The parameter values used for this numerical simulation can be seen in Table 4. The simulation was carried out by taking four different fractional order values, $\alpha \in (0, 1]$, namely $\alpha = 0.3$, $\alpha = 0.5$, $\alpha = 0.9$ and $\alpha = 1$. Simulations are carried out for $t = 0$ to $t = 200$ time units.

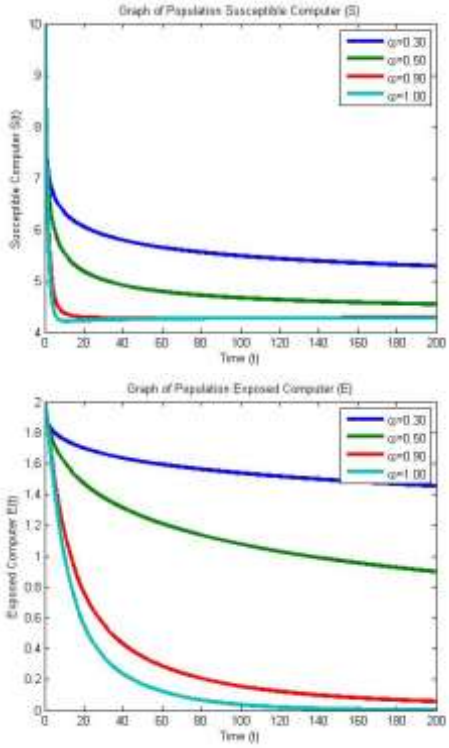
International Journal of Academic and Applied Research (IJAAR)
ISSN: 2643-9603
Vol. 5 Issue 10, October - 2021, Pages: 131-138

Table 4 Parameter values for the mathematical model of the spread of computer viruses on the network

Parameters	Parameter Value		Source
	$R_0 < 1$	$R_0 > 1$	
p	0.7	0.5	Mei Peng et al (2013)
μ	0.001	0.02	
k	0.02	0.4	
γ	0.09	0.6	
r	0.04	0.6	
β_1	0.002	0.7	
β_2	0.003	0.8	
N	10	100	

5.1 Numerical Simulation in Non-Endemic Conditions (Computer Virus Free)

In the simulation of the virus-free condition, the initial value used is $P(0) = (S(0), E(0), I(0)) = (10, 2, 4)$ [2]. Based on the parameter values listed in Table 4, the value of $R_0 = \frac{A(\beta_1\gamma+\beta_2 c)}{abc} = 0.284931 < 1$ which indicates non-endemic conditions or no spread of computer viruses. The results of the numerical simulation in non-endemic conditions can be seen in Figure 2.



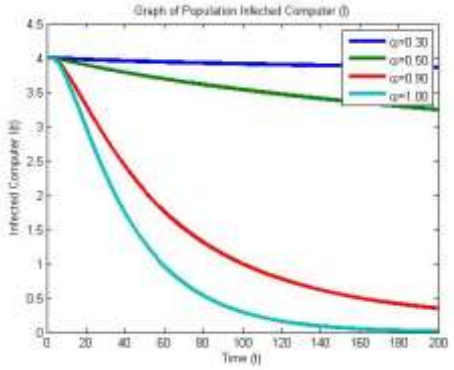
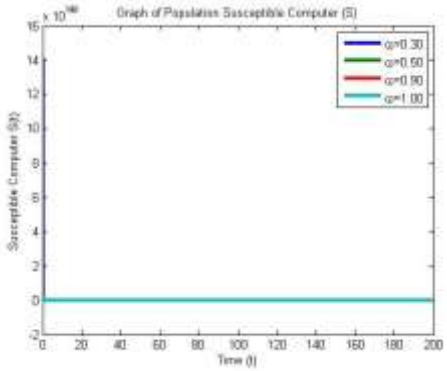


Fig. 2 Model of computer virus spread for non-endemic conditions

In Figure 2, it can be seen that the greater the value of used, the faster the model will reach the equilibrium point $P_0 = \left(\frac{A}{a}, 0, 0\right) = (4.2796, 0, 0)$. In Figure 2 it can also be seen that the greater the value of α used, the population of vulnerable computers tends to increase, while the population of exposed computers and infected computers decreases. This is because there is no transmission of computer viruses on computer networks.

5.2 Numerical Simulation in Virus Endemic Conditions (Computer Virus Spread)

Furthermore, numerical simulations will be carried out during endemic conditions. The initial value used is $P(0) = \left(S(0), E(0), I(0)\right) = (50, 50, 10)$ [2]. Based on the parameter values listed in Table 4, the value of $R_0 = \frac{A(\beta_1\gamma+\beta_2 c)}{abc} = 139.2741 > 1$ indicating endemic conditions or the spread of computer viruses. The results of numerical simulations in endemic conditions can be seen in Figure 3.



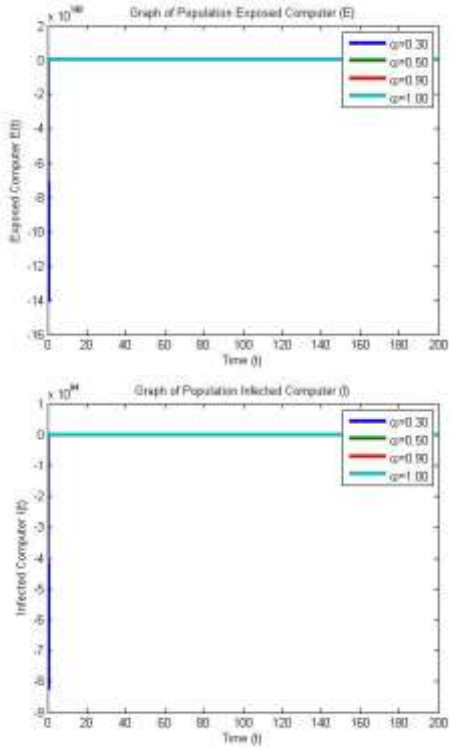


Fig. 3 Computer virus spread model for endemic conditions

In Figure 3, it can be seen that the greater the value of used, the faster the model will reach the equilibrium point $P^* = \left(\frac{A}{aR_0}, \frac{A(R_0-1)}{bR_0}, \frac{A\gamma(R_0-1)}{bcR_0}\right) = (0.6904, 48.6676, 47.0977)$. In Figure 3 it can also be seen that the greater the value of α used, the population of vulnerable computers tends to decrease, while the population of exposed computers and infected computers increases. This is due to the transmission of computer viruses on computer networks.

6. CONCLUSION

We assume that the computer virus process has a latency period and currently the infected computer also has infectivity. In this paper, a fractional order mathematical model has been formulated for the spread of computer viruses on a network and its dynamics have been studied.

The result shows that we should try to make effort so that $R_0 < 1$. The most effective way is to increase the parameter p, k and decrease the parameter $\beta_1, \beta_2, \mu, , \gamma, r$. Thus, computer viruses can be predicted and controlled.

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