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Stability Analysis of a Computer Virus Epidemic Model at disease-free equilibrium

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In this study, we partitioned the population into Susceptible (Sc), Protected (Pc), Exposed (Ec), Infected (Ic), Quarantined (Qc) and recovered (Rc) individuals with their corresponding parameters. We analyzed a ScPcEcIcQcRcSc compartmental nonlinear deterministic mathematical model of Computer virus epidemic in a community with constant population. Analytical studies were carried out on the model to: investigate the existence and uniqueness of solution of the model equations and explore the basic properties of the model equations. The disease-free equilibrium points of the model is computed and proved to be locally and globally asymptotically stable if $R_0 < 0$ and unstable if $R_0 > 0$. Finally, we simulate the model system in MATLAB and obtained the graphical behavior of the infected compartmental variables in the model. From the simulation, we observed that the Computer virus infection was eradicated when $R_0 < 0$ while it persist in the environment when $R_0 > 0$.

Keywords: ScPcEcIcQcRcSc Model, transmission, Computer Virus, antivirus, local and global stability, treatment, basic reproduction number, simulation

1. Introduction

A computer virus is a program which can harm our device and files and infect them for no further use. When a virus program is executed, it replicates itself by modifying other computer programs and instead enters its own coding. This code infects a file or program and if it spreads massively, it may ultimately result in crashing of the device.

A computer virus [1] is a type of malware that, when executed, replicates itself by modifying other computer programs and inserting its own code into those programs [2][3][4]. If this replication succeeds, the affected areas are then said to be "infected" with a computer virus, a metaphor derived from biological viruses [5][6]. Computer viruses generally require a host program [3]. The virus writes its own code into the host program. When the program runs, the written virus program is executed first, causing infection and damage. By contrast, a computer worm does not need a host program, as it is an independent program or code chunk. Therefore, it is not restricted by the host program, but can run independently and actively carry out attacks [7][8]. Virus writersuse social engineering deceptions and exploit detailed knowledge of security vulnerabilities to initially infect systems and to spread the virus. Viruses use complex anti-detection /stealth strategies to evade antivirus software [6][9][10][11] . As of 2013, computer viruses caused billions of dollars' worth of economic damage each year [10]. Motives for creating viruses can include seeking profit (e.g., with ransom ware), desire to send a political message, personal amusement, to demonstrate that a vulnerability exists in software, for sabotage and denial of service, or simply because they wish to explore cyber security issues, artificial life and evolutionary algorithms [12]. For better understanding about spreading and to increase security in computer networks, the spreading dynamics of computer viruses is also an important matter [13]. In response, an industry of antivirus software has cropped up, selling or freely distributing virus protection to users of various operating systems [14]. Damage is due to causing system failure, corrupting data, wasting computer resources, increasing maintenance costs or stealing personal information. Even though no antivirus software can uncover all computer viruses (especially new ones), computer security researchers are actively searching for new ways to enable antivirus solutions to more effectively detect emerging viruses, before they become widely distributed [15]. "Malware" encompasses computer viruses along with many other forms of malicious

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software, such as computer "worms", ransomware, spyware, adware, trojan horses, keyloggers, rootkits, bootkits, malicious Browser Helper Object (BHOs), and other malicious software. The majority of active malware threats are trojan horse programs or computer worms rather than computer viruses. The term computer virus, coined by Fred Cohen in 1985, is a misnomer [11].

2. Related Literature Review

Here are some literatures on the model:

[13] considered the problem which computer malware cause to personal computers with its control by proposing a compartmental model SVEIRS (Susceptible Vaccinated Exposed-infected-Recovered-Susceptible) for malware transmission in computer network using nonlinear ordinary differential equation. Through the analysis of the model, the basic reproduction number were obtained, and the malware free equilibrium was proved to be locally asymptotical stable if is less than unity and globally asymptotically stable if is less than some threshold using a Lyapunov function. Also, the unique endemic equilibrium exists under certain conditions and the model underwent backward bifurcation phenomenon. Their results showed that vaccination and treatment is very essential for malware control. A large number of mathematical models have been developed to simulate, analyze and understand computer virus in a related work, none have considered vaccination and treatment in preventing program files damage. In this research, we proposed an optimal control model in computer network considering effective vaccination and treatment on the virus infection. The proposed model consists of five compartments of susceptible, exposed, infected, program files damaged and recovered computers.

[14] build a mathematical model to study the impact of external removable devices on a network with weakly and strongly protected computers. Their model, describes the dynamics between weak, strong, infected computers and susceptible, infected removable media. Analytical investigations of the model produce two equilibrium points: virus free and endemic equilibria. They also investigated the local and global stability conditions of the equilibrium points depending primarily on the basic reproduction of the model. Their observation was that user awareness plays an essential role in limiting the spread of viruses.

[15] formulated an SEIQR (Susceptible, Exposed, Infectious Quarantined, and Recovered) models for the transmission of malicious objects with simple mass action incidence and standard incidence rate in computer network. Threshold, equilibrium and their stability are discussed for the simple mass action incidence and standard incidence rate. They showed the global stability and asymptotic stability of endemic equilibrium for simple mass action incidence.

[16] motivated by the epidemic theory proposed the Q-SEIR and Q-SEIRV models to present the dynamics of the pre-quarantining of nodes in wireless sensor networks. They established that the disease free equilibrium is asymptotically stable. Runge Kutta –Fehlberg Method of order 4 and 5 was used to solve and simulate the proposed systems of equation. They showed that the impact of pre-quarantine compartment in the proposed model is very strong on the recovery nodes.

[17] considered the problem which computer malware cause to personal computers with its control by proposing a compartmental model SVEIRS (Susceptible Vaccinated Exposed-infected-Recovered-Susceptible) for malware transmission in computer network using nonlinear ordinary differential equation. Through the analysis of the model, the basic reproduction number were obtained, and the malware free equilibrium was proved to be locally asymptotical stable if is less than unity and globally asymptotically stable if is less than some threshold using a Lyapunov function. Also, the unique endemic equilibrium exists under certain conditions and the model underwent backward bifurcation phenomenon. Their results showed that vaccination and treatment is very essential for malware control. A large number of mathematical models have been developed to simulate, analyze and understand computer virus in a related work, none have considered vaccination and treatment in preventing program files damage. In this research, we proposed an optimal control model in computer network considering effective vaccination and treatment on the virus infection. The proposed model consists of five compartments of susceptible, exposed, infected, program files damaged and recovered computers.

3. Mathematical Formulations

In this section, we developed a compartmental mathematical model of ($S_cP_cE_cI_cQ_cR_cS_c$) to investigate the effectiveness of an antivirus and treatment computer system in a virus infected areas. The computer population is subdivided into six classes. These classes of computers are: Susceptible (S_c), Protected (P_c), exposed (E_c), Infected (I_c), Quarantined (Q_c) and recovered (R_c) population. The formulation of the model is based on the following assumptions:

3.1 Assumptions

i. All the Computers are newly connected.
ii. The newly connected Computers are virus-free and protected by a strong

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antivirus at a rate $(1-p)\Delta$.

iii. The newly connected Computers are virus-free and susceptible due to either the absence of a strong antivirus or the antivirus installed in the system has expired since the effectiveness of antivirus is time dependent at a rate at a rate $p\Delta$.

iv. The protected Computers moved to the susceptible Computer class due to the waning and not updating the antivirus software.

v. The susceptible Computers moved to the protected Computers class due to the installation of a strong antivirus software.

vi. The protected Computers moved to the exposed Computers class due to the fact that no antivirus offers the susceptible computers 100% protection.

vii. The recovered Computers moved to the susceptible Computer class at a rate θ_1 due to failure in installing strong antivirus to the recovered Computers.

viii. The recovered Computers also moved to the protected Computer class at a rate θ_2 due to the installation of strong antivirus to the recovered Computers.

3.2 Flow diagram of the model with constant control

We demonstrate the dynamical transfer of the population with the flow diagram in Figure 1 below

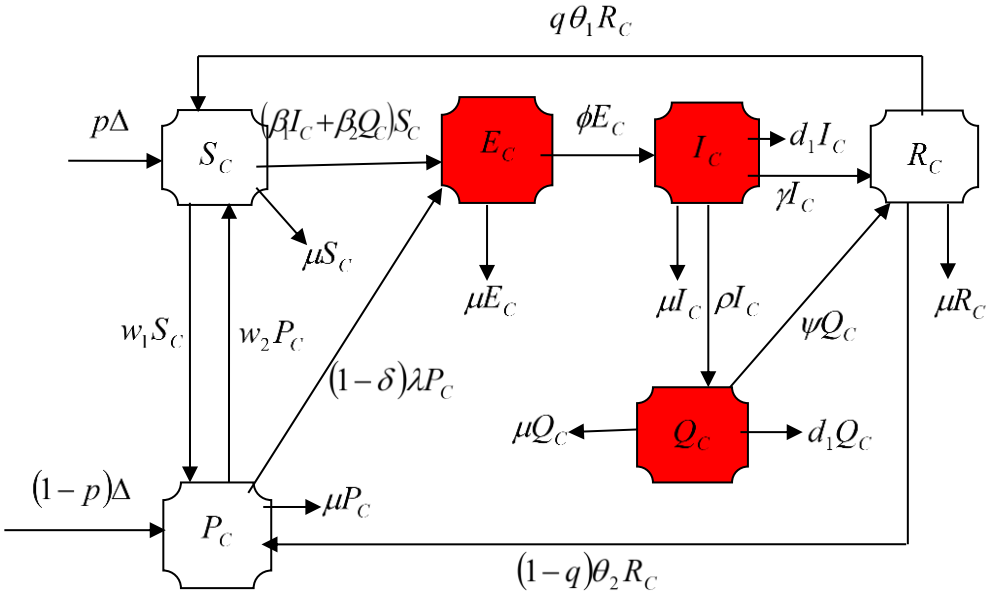

Figure 1: Flow diagram for the $S_cP_cE_cI_cQ_cR_cS_c$ Model

Table 1: Description of the variables of the models

Variables	Description	Values	Reference
$S_C(0)$	Number of susceptible computers at time (t).	65	[17]
$P_C(0)$	Number of protected computers at time (t).	20	[17]
$E_C(0)$	Number of exposed computers at time (t).	10	[17]
$I_C(0)$	Number of infected computers at time (t).	6	Assumed
$Q_C(0)$	Number of quarantined computers at time (t).	2	Assumed
$R_C(0)$	Number of Recovered individuals at time (t).	5	[17]

Table 2: Description of the parameters of the models

Parameters	Description	Values	Reference
Δ	The recruitment rate.	0.30	[10]
w_1	The rate at which the susceptible computers moved to the protected computer class.	0.65	[17]
w_2	The rate at which the protected computers moved to the susceptible	0.35	Assumed

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	computer class.		
μ	The death rate of computers due to other factors that are not connected to computer virus.	0.10	[10]
d_1	The death rate of computers due to computer virus.	0.65	[10]
ϕ	The rate at which the exposed computers moved to the infected computer class.	0.20	[17]
p	The proportion of the recruited computers that moved to the susceptible class due none installation of antivirus at a rate Δ.	0.90	Assumed
$(1-p)$	The proportion of the recruited computers that moved to the protected class due to the installation of a strong antivirus at a rate Δ.	0.10	Assumed
θ_1	The rate at which the recovered computers moved to the susceptible computer class.	0.01	[17]
θ_2	The rate at which the recovered computers moved to the protected computer class.	0.05	Assumed
q	The proportion of the recovered computers that moved to the susceptible class at a rate θ_1.	0.75	Assumed
$(1-q)$	The proportion of the recovered computers that moved to the protected class at a rate θ_2.	0.25	Assumed
ψ	The rate at which the quarantined computers moved to the recovered computer class.	0.03	Assumed
ρ	The rate at which the infected Computers moved to the quarantined class.	0.02	[10]
β_1	The transmission rate of computer virus to the infected computers due to the transfer of files from one computer to another using flash or other means.	0.09	[17]
β_2	The transmission rate of computer virus to the quarantined computers due to the transfer of files from one computer to another using flash or other means.	0.05	Assumed
$1-\delta$	The proportion of the protected computers that moved to the exposed class due to the fact that no antivirus offers computers 100% protection .	0.35	[17]
γ	The rate at which the infected computers moved to the recovered computer class.	0.45	[17]

(2)

3.3 Equations of the model

$$\frac{dS_C}{dt} = p\Delta - (\beta_1 I_C + \beta_2 Q_C)S_C - (w_1 + \mu)S_C + w_2 P_C + q\theta_1 R_C \qquad \frac{dE_C}{dt} = (\beta_1 I_C + \beta_2 Q_C)S_C + (1-\delta)(\beta_1 I_C + \beta_2 Q_C)P_C - (\phi + \mu)E_C$$

(1) (3)

$$\frac{dP_C}{dt} = (1-p)\Delta + w_1 S_C - (w_2 + \mu)P_C - (1-\delta)(\beta_1 I_C + \beta_2 Q_C)P_C + (1-q)\theta_2 R_C \qquad \frac{dI_C}{dt} = \phi E_C - (\gamma + \rho + d_1 + \mu)I_C$$

(4)

$$\frac{dQ_C}{dt} = \rho I_C - (\psi + d_1 + \mu)Q_C \quad (5)$$

$$\frac{dR_C}{dt} = \gamma I_C + \psi Q_C - q\theta_1 R_C - (1-q)\theta_2 R_C - \mu R_C \quad (6)$$

$$N_C = S_C + P_C + E_C + I_C + Q_C + R_C \quad (7)$$

where

$S_C(0) = S_{C0} > 0$, $P_C(0) = P_{C0} > 0$, $E_C(0) = E_{C0} > 0$,

$I_C(0) = I_{C0} > 0$, $Q_C(0) = Q_{C0} > 0$, $R_C(0) = R_{C0} > 0$,

$0 \le p \le 1$, $0 \le q \le 1$, $0 \le \delta \le 1$.

3.4 Model analysis

3.4.1 Existence and Uniqueness of Solution for the Model

Suppose that $f(t, y)$ satisfies the Lipchitz condition

$$\|f(t, y_n) - f(t, y_{n-1})\| \le L\|y_n - y_{n-1}\|, \quad n = 1,2,3,\ldots \quad (8)$$

whenever the pair (t, y_n) and (t, y_{n-1}) belong to R, where L is a Lipchitz positive constant, then

there exist a constant number $\delta > 0$ such that there exists a unique continuous vector solution $\bar{y}(t)$ of the system in the interval $|t - t_0| < \delta$.

It is important to note that condition (8) is satisfied by the requirement that $\frac{\partial f_i}{\partial y_j}$, $\forall i, j = 1,2,3,\ldots,n$ are continuous and bounded in the region R.

Lemma 1. If $f(t, y)$ has continuous partial derivative $\frac{\partial f_i}{\partial y_j}$ on a bounded closed convex domain R, then it satisfies a Lipchitz condition in R.

We are interested in the region

$$1 \le \varepsilon \le R. \quad (9)$$

We look for a bounded solution of the form

$$0 < R \le \infty. \quad (10)$$

We shall prove the following existence theorem.

Theorem 2. Let $D^{/}$ denote the region defined in (8) such that (9) and (10) hold.

Proof:

From (1)

$$\frac{dS_C}{dt} = p\Delta - (\beta_1 I_C + \beta_2 Q_C)S_C - (w_1 + \mu)S_C + w_2 P_C + q\theta_1 R_C \quad (5)$$

$$f_1(t, S_C) = p\Delta - (\beta_1 I_C + \beta_2 Q_C)S_C - (w_1 + \mu)S_C + w_2 P_C + q\theta_1 R_C \quad (6)$$

$$\left|\frac{\partial f_1}{\partial S_C}\right| = \left|-((\beta_1 I_C + \beta_2 Q_C) + (w_1 + \mu))\right| < \infty,$$

$$\left|\frac{\partial f_1}{\partial P_C}\right| = |w_2| < \infty, \left|\frac{\partial f_1}{\partial E_C}\right| = 0 < \infty \left|\frac{\partial f_1}{\partial I_C}\right| = |-\beta_1 S_C| < \infty,$$

$$\left|\frac{\partial f_1}{\partial Q_C}\right| = |-\beta_2 S_C| < \infty, \left|\frac{\partial f_1}{\partial R_C}\right| = |q\theta_1| < \infty$$

Similarly, we can also show that the remaining equations satisfy Lipchitz conditions.

This completes the proof.

Since all f_i and their partial derivatives of the model equations with respect to each dependent variables (i.e. S_c, P_c, E_c, I_c, Q_c, R_c and S_c) are continuous and bounded in the interval $0 < R < \infty$ by Lemma1, there exists a unique solution of (1) to (6) in the region R.

3.4.2 The positivity of solution of model

Theorem 3:

Let the initial values of the variables be

$$\left\{\begin{matrix} S_C(0) = S_{C0} > 0, P_C(0) = P_{C0} > 0, E_C(0) = E_{C0} > 0, \\ I_C(0) = I_{C0} > 0, Q_C(0) = Q_{C0} > 0, R_C(0) = R_{C0} > 0 \in R_6^+ \end{matrix}\right\}$$

$0 \le p \le 1$, $0 \le q \le 1$, $0 \le \delta \le 1$.

Then, the solution set $\{S_C(t), P_C(t), E_C(t), I_C(t), Q_C(t), R_C(t)\}$ of the system (1) to (6) is non-negative for all t > 0.

Proof

From (1)

$$\frac{dS_C}{dt} = p\Delta - (\beta_1 I_C + \beta_2 Q_C)S_C - (w_1 + \mu)S_C + w_2 P_C + q\theta_1 R_C$$

It follows by comparison theorem that

$$\frac{dS_C}{dt} \ge -(\beta_1 I_C + \beta_2 Q_C + w_1 + \mu)S_C \quad (11)$$

Integrating (11), we have

$$S_C(t) \ge S_C(0)e^{-(\beta_1 I_C + \beta_2 Q_C + w_1 + \mu)t} > 0$$

Similarly, we can show that $P_C(t) \ge 0$, $E_C(t) \ge 0$, $I_C(t) \ge 0$, $Q_C(t) \ge 0$ and $R_C(t) \ge 0$.

This completes the proof.

3.4.3 The boundedness of solutions of the model

Theorem 4:

The closed set

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$$\Theta=\left\{\begin{matrix}S_C, P_C, E_C, I_C, Q_C, R_C \in R_6^+ : S_C,+P_C,+E_C+I_C+Q_C+R_C<N \\ ;0<N(t)\leq \dfrac{\Delta}{\mu}\end{matrix}\right\}$$

(12)

is positively invariant.

Proof

From the model equations (1) to (6), the total population is given by

$$N=S_C,+P_C,+E_C+I_C+Q_C+R_C \quad (13)$$

Differentiating the total human population $N(t)$ in (13) with respect to time t, we have

$$\frac{dN}{dt}=\frac{dS_C}{dt}+\frac{dP_C}{dt}+\frac{dE_C}{dt}+\frac{dI_C}{dt}+\frac{dQ_C}{dt}+\frac{dR_C}{dt} \quad (14)$$

Substituting the differential equations (1) to (6) in (14), we have

$$\frac{dN}{dt}=\Delta-\mu S_C-\mu P_C-\mu E_C-\mu I_C-\mu Q_C-\mu R_C-d_1(I_C+Q_C) \quad (15)$$

In the absence of Computer virus, (i.e. $I_C=Q_C=0$) then (15) becomes

$$\lim_{t\to\infty} N(t)=\frac{\Delta}{\mu} \quad (16)$$

This result implies that if there is no disease, $N=\dfrac{\Delta}{\mu}$. It also means that we have a steady state population.

$$\Theta=\left\{\begin{matrix}S_C, P_C, E_C, I_C, Q_C, R_C \in R_6^+ : S_C,+P_C,+E_C+I_C+Q_C+R_C<N \\ ;0<N(t)\leq \dfrac{\Delta}{\mu}\end{matrix}\right\}$$

This is a positive invariant set of the model which shows that the model is both biologically and mathematically meaningful in the domain Θ.

3.4.4 Disease-free equilibrium points of the model

The equilibrium points of the system of non-linear ordinary differential equation are obtained by setting the derivatives of the model equation to zero (0).

$$\Theta^\circ=\left\{\frac{\Delta[w_2+p\mu]}{\mu(w_1+w_2+\mu)},\frac{\Delta[w_1+\mu(1-p)]}{\mu(w_1+w_2+\mu)},0,0,0,0\right\} \quad (17)$$

3.4.5 Computation of the Basic Reproduction Number R_0

The basic reproduction number R_0 is the average number of new infections that one infected case will generate during their entire infectious lifetime [14][15].

$$\frac{dy_i}{dt}=f_i(y)=F_i(y)-V_i(y),\ i=1,2,3,\ldots,n \quad (18)$$

where $V_i(y)=V_i^-(y)-V_i^+(y)$. (19)

$$\frac{d}{dt}=F-V=\begin{pmatrix}(\beta_1 I_C+\beta_2 Q_C)S_C+(1-\delta)(\beta_1 I_C+\beta_2 Q_C)P_C\\0\\0\end{pmatrix}-\begin{pmatrix}(\phi+\mu)E_C\\(\gamma+\rho+d_1+\mu)I_C-\phi E_C\\(\psi+d_1+\mu)Q_C-\rho I_C\end{pmatrix}$$

$$R_0=\rho(FV^{-1})=\rho\left(\left(\frac{\partial F_i}{\partial y_j}\Big|_{E^0}\right)\left(\frac{\partial V_i}{\partial y_j}\Big|_{E^0}\right)^{-1}\right)$$

where F are the new infection transfer terms and V is the non-singular matrix of the remaining transfer terms. The basic reproduction number R_0 of the model (1) – (6) is calculated using the next generation matrix [15]. In using their approach [15], we have:

$$F=\left(\frac{\partial F_i}{\partial y_j}\Big|_{E^\circ}\right)=\begin{pmatrix}0 & \beta_1 S_C+(1-\delta)\beta_1 P_C & \beta_2 S_C+(1-\delta)\beta_2 P_C\\0 & 0 & 0\\0 & 0 & 0\end{pmatrix}$$

Similarly,

$$V=\left(\frac{\partial V_i}{\partial y_j}\Big|_{E^\circ}\right)=\begin{pmatrix}(\phi+\mu) & 0 & 0\\-\phi & (\gamma+\rho+d_1+\mu) & 0\\0 & -\rho & (\psi+d_1+\mu)\end{pmatrix}$$

$$|V|=\begin{vmatrix}(\phi+\mu) & 0 & 0\\-\phi & (\gamma+\rho+d_1+\mu) & 0\\0 & -\rho & (\psi+d_1+\mu)\end{vmatrix}$$

$$\left|FV^{-1}-\lambda I\right|=\left|\begin{pmatrix}m-\lambda & n & b\\0 & -\lambda & 0\\0 & 0 & -\lambda\end{pmatrix}\right|=0$$

$$\Rightarrow (m-\lambda)\lambda^2=0$$

$$\lambda=m=R_e$$

$$R_e=\frac{\phi\Delta[(1-\delta)w_1+\mu(1-\delta+\delta p)][(\psi+d_1+\mu)\beta_1+\beta_2\rho]}{\mu(w_1+w_2+\mu)(\phi+\mu)(\psi+d_1+\mu)(\gamma+\rho+d_1+\mu)} \quad (20)$$

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3.4.6 The local stability analysis of the disease-free equilibrium of the model

To examine the local stability of the disease-free E° equilibrium, we obtain the Jacobian matrix by differentiating the functions $(f_i : i = 1,2,3,4,5)$ partially with respect to the variables in the system of the equations. The Jacobian matrix from the partial derivatives of (1) to (6) at disease-free $|J_{E^{\circ}} - \lambda I|$ is given

Let $k_1 = (w_1 + \mu), k_2 = (w_2 + \mu),\ k_3 = -(1-\delta)\beta_1 P_C^{\circ},$

$k_4 = -(1-\delta)\beta_2 P_C^{\circ},\ k_5 = (1-q)\theta_2,\ k_6 = (\phi + \mu),$

$k_7 = \beta_1\left(S_C^{\circ} + (1-\delta)P_C^{\circ}\right),\ k_8 = \beta_2\left(S_C^{\circ} + (1-\delta)P_C^{\circ}\right),$

$k_9 = (\gamma + \rho + d_1 + \mu),\ k_{10} = (\psi + d_1 + \mu),$

$k_{11} = (q\theta_1 + (1-q)\theta_2 + \mu), -\beta_1 S_C^{\circ}, -\beta_2 S_C^{\circ}$

$$\left|J_{E^{\circ}} - \lambda I\right| = \begin{vmatrix} -k_1 - \lambda & w_2 & 0 & a & b & q\theta_1 \\ w_1 & -k_2 - \lambda & 0 & -k_3 & -k_4 & k_5 \\ 0 & 0 & -k_6 - \lambda & k_7 & k_8 & 0 \\ 0 & 0 & \phi & -k_9 - \lambda & 0 & 0 \\ 0 & 0 & 0 & \rho & -k_{10} - \lambda & 0 \\ 0 & 0 & 0 & \gamma & \psi & -k_{11} - \lambda \end{vmatrix} = 0$$

Therefore, the eigenvalues of the Jacobian matrix are:

$$[-k_{11} - \lambda] = 0 \Rightarrow \lambda_1 = -k_{11} = (q\theta_1 + (1-q)\theta_2 + \mu)$$

Similarly $[(k_1 + \lambda)(k_2 + \lambda) - w_1 w_2] = 0$

$$\lambda^2 + (k_1 + k_2)\lambda + (k_1 k_2 - w_1 w_2) = 0 \quad (21)$$

From quadratic equation: $a = 1$,

$b = k_1 + k_2,\ c = k_1 k_2 - w_1 w_2$

$$\lambda_{2,3} = \frac{-b \pm \sqrt{b^2 - 4ac}}{2a} =$$

$$= \frac{-(k_1 + k_2) \pm \sqrt{(k_1 + k_2)^2 - 4(k_1 k_2 - w_1 w_2)}}{2}$$

Moreso,

$$\begin{vmatrix} -k_6 - \lambda & k_7 & k_8 \\ \phi & -k_9 - \lambda & 0 \\ 0 & \rho & -k_{10} - \lambda \end{vmatrix} = 0 \quad (22)$$

We applied Routh-Hurwitz criterion for stability to investigate the stability of (22)

$a_0 = 1,\ a_1 = k_6 + k_9 + k_{10},$

$a_2 = k_9 k_{10} + k_6(k_9 + k_{10}) - \phi k_7,$

$a_3 = k_6 k_9 k_{10} - \phi k_7 k_{10} - \phi\rho k_8$

For order one

$$\Delta_1 = |a_1| = k_6 + k_9 + k_{10} > 0$$

For order two

$$\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} \Rightarrow a_1 a_2 - a_0 a_3$$

For order three

$$\Delta_3 = \begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{vmatrix} = \begin{vmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{vmatrix} = a_3 \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} \Rightarrow \Delta_3 = a_3 \Delta_2$$

3.4.7 The global stability analysis of the disease-free equilibrium of the model

We investigated the global asymptotic stability of the disease- free equilibrium of computer virus using Castillo-Chavez theorem [18]. We write the model equations (1) – (6) in the form:

$$\frac{dX}{dt} = F(X, Z) \quad (23)$$

$$\frac{dY}{dt} = G(X, Z),\ \ G(X,0) = 0 \quad (24)$$

Where $X = (S_C, P_C, R_C) \in R_+^3$ represents the uninfected individuals and $Z = (E_C, I_C, Q_C) \in R_+^3$ represents the infected individuals. Let $E^{\circ} = (X^{\circ}, 0)$ represents the disease-free equilibrium point of the system.

The disease-free equilibrium E° to be globally asymptotically stable equilibrium for the model, the conditions $(H1)$ and $(H2)$ shown below should be satisfied:

Condition $(H1)$:

$$\frac{dX}{dt} = F(X,0) = \begin{pmatrix} \left.\frac{dS_C}{dt}\right|_{E^{\circ}} = p\Delta - (w_1 + \mu)S_C + w_2 P_C \\ \left.\frac{dP_C}{dt}\right|_{E^{\circ}} = (1-p)\Delta + w_1 S_C - (w_2 + \mu)P_C \\ \left.\frac{dR_C}{dt}\right|_{E^{\circ}} = 0 \end{pmatrix} \quad (25)$$

Therefore, the convergence of the solutions of the reduced system equation (25) is globally asymptotically stable in Ω.

More so,

$$G(X, Z) = AZ - \hat{G}(X, Z) \quad \Rightarrow$$

$$\hat{G}(X, Z) = AZ - G(X, Z)$$

Where

$$A = \frac{\partial G}{\partial Z}(X^{\circ}, 0) = D_Z(X^{\circ}, 0) \text{ is a metzler}$$

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The Jacobian matrix from the partial derivatives of (3), (4) and (5) with respect to the infected variables at disease-free $\left(A = J_{E^\circ}\right)$ is given by:

$$A = J_{E^\circ} = \begin{pmatrix} -(\phi+\mu) & \beta_1\left(S_C^\circ + (1-\delta)P_C^\circ\right) & \beta_2\left(S_C^\circ + (1-\delta)P_C^\circ\right) \\ \phi & -(\gamma+\rho+d_1+\mu) & 0 \\ 0 & \rho & -(\psi+d_1+\mu) \end{pmatrix}$$

$$\hat{G}(X,Z) = AZ - G(X,Z)$$

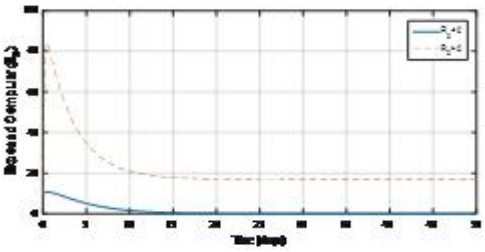
$$\hat{G}(X,Z) = \begin{pmatrix} \hat{G}_1(X,Z) \\ \hat{G}_2(X,Z) \\ \hat{G}_3(X,Z) \end{pmatrix} =$$

$$\hat{G}(X,Z) = \begin{pmatrix} \left(\beta_1 I_C + \beta_2 Q_C\right)\left[\left(S_C^\circ - S_C\right) + (1-\delta)\left(P_C^\circ - P_C\right)\right] \\ 0 \\ 0 \end{pmatrix} > 0$$

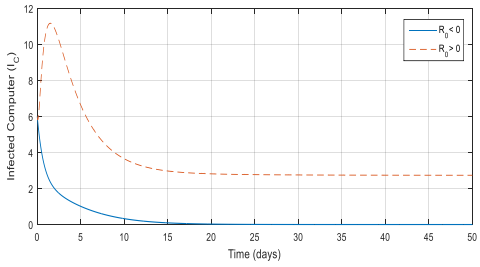
$\hat{G}(X,Z) \geq 0 \; \forall \; (X,Z) \in \Omega$, provided that $S_C^\circ \geq S_C$ and $P_C^\circ \geq P_C$

4. Numerical Results

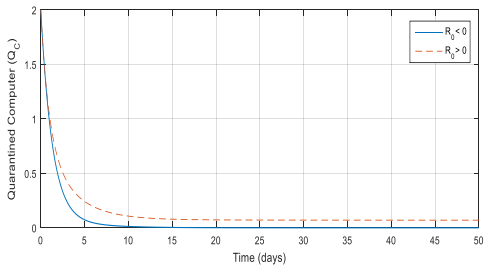
In this section, the numerical solution of the system (1) – (6) was carried out using the



(2a)



(2b)



(2c)

Figure2: shows the graphical behaviour of the exposed, infected and quarantined computers with given initial conditions and parameter values. When $R_e = 0.2327 < 1$, the disease-free equilibrium point is locally asymptotically stable and when $R_e = 3.8779 > 1$, the disease-free equilibrium point is unstable. Where $R_e = 0.2327 < 1$ when $\Delta = 0.3$, $\mu = 0.1$, $\beta_1 = 0.09$, $\beta_2 = 0.05$, $w_1 = 0.65$, $w_2 = 0.35$, $\phi = 0.2$, $d_1 = 0.065$, $\delta = 0.065$, $\theta_1 = 0.01$, $\theta_2 = 0.05$, $p = 0.9$, $q = 0.75$, $\psi = 0.03$, $\gamma = 0.45$, $\rho = 0.02$ and $R_e = 3.8779 > 1$ when $\Delta = 5$, $\mu = 0.1$, $\beta_1 = 0.09$, $\beta_2 = 0.05$, $w_1 = 0.65$, $w_2 = 0.35$, $d_1 = 0.65$, $p = 0.9$, $\delta = 0.065$, $\phi = 0.2$, $\theta_1 = 0.01$, $\theta_2 = 0.05$ $q = 0.75$, $\psi = 0.03$, $\gamma = 0.45$, $\rho = 0.02$.

4.1 Interpretation of the results of the Computer virus-Model

In figure 2(a), the exposed computers when the basic reproduction number $R_e = 0.2327 < 1$ increases from its initial number to 12 after t = 2days and then drops gradually to zero after 12days while the exposed computers when the basic reproduction number $R_e = 3.8779 > 1$ increases rapidly from its initial number to 85 after t = 1day and then drops gradually to 18 after 15days and remains constant throught the remaining time.

In figure 2(b), when the basic reproduction number $R_e = 0.2327 < 1$, the number of infected computers drop gradually to zero after 15days and when the basic reproduction number $R_e = 3.8779 > 1$,the number of infected computers increased rapidly from its initial number to 11 after t = 2days and then drops gradually to 3 after 16days and remains constant throught the remaining time.

In figure 2(c), when the basic reproduction number $R_e = 0.2327 < 1$, the number of quarantined computers dropped gradually to zero from its initial number after 14days and when the basic reproduction number $R_e = 3.8779 > 1$,the number of quarantined computers also dropped gradually to zero from its initial number after t = 12days and remains constant throught the remaining time.

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5. Conclusion

In this Paper, we formulated mathematical model equations of computer virus epidemic with the aid of the system of ordinary differential equations to study the dynamics of computer virus infection with six compartments; susceptible class (S_C), protected class (P_C), exposed class (E_C), infected class (I_C), quarantined class (Q_C) and Recovered class (R_C) with their corresponding parameters. We investigated the existence and uniqueness of solution for the dynamic system using the Lipchitz condition to ascertain the effectiveness of the model as well as the positively invariant region of the system. The disease free equilibrium (DFE) was obtained to be

$$\Theta^{\circ} = \left\{ \frac{\Delta\left[w_2 + p\mu\right]}{\mu\left(w_1 + w_2 + \mu\right)}, \frac{\Delta\left[w_1 + \mu\left(1-p\right)\right]}{\mu\left(w_1 + w_2 + \mu\right)}, 0, 0, 0, 0 \right\}.$$

The next generation matrix approach was used to determine the basic reproduction number

$$R_e = \frac{\phi\Delta\left[\left(1-\delta\right)w_1 + \mu\left(1-\delta+\delta p\right)\right]\left[\left(\psi + d_1 + \mu\right)\beta_1 + \beta_2\rho\right]}{\mu\left(w_1 + w_2 + \mu\right)\left(\phi + \mu\right)\left(\psi + d_1 + \mu\right)\left(\gamma + \rho + d_1 + \mu\right)}$$

Conflict of interest

The authors declare no conflict of interest.

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