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Effect of Anti-Virus in Computer Network: A Mathematical Model in Deterministic and Stochastic Approach

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ABSTRACT

A mathematical model of computer network is designed and determined both deterministic and stochastic point of view. The model exhibits two equilibria which are virus free equilibrium and endemic equilibrium. Basic reproduction number R_0 is found and is used to study and predict the nature of the equilibrium points of the model. Numerical simulation is carried to show the validity of our analytical findings both in deterministic and stochastic. The results are also compared between deterministic and stochastic. Most of the parameters used in our model shows a significant change in the behaviour of the network, particularly anti-virus effect parameter exhibits better effect as we increase the vale of the parameter, the infected nodes gets decreases. In this manner it is good to consider our model to predict the nature of the computer networks under the assumptions of our model.

Keywords
Computer Virus, Simulation, Differential Equations, Stochastic Differential Equations, Virus breeding.

1. Introduction

efficiendi. The relationship between the computer virus and anti-virus with the poverty people handling capacity depends upon the software(program) selling Price based on the product/demand but not in people Economic level. Now a days computer programmers are becoming more and more realistic based social problems [1].

Virtual virus is a handheld malicious application that contains malware, Trojan horses, parasite, and logic blast.It is a machine capable of modifying itself and targeting other machines. And they reside by deleting records, destroying information, or altering regular operations. Since machine virus and biological virus are extremely similar [3]. This dynamic modeling of the computer virus spread process is a decisive method to identifying the behavior of computer virus. Because, some factual estimation could be put in place to avert infection on this basis [2]. Now a days computer virus are responsible for huge economic loss. It remove data, cause system failure, etc. The PC virus started in 1980s. When real computers came in the market and then computer virus also came along with these Computer virus were small code pieces which attached to large files and systems. If we running the affected files then the virus used to get loaded into memory [6]. A broad description of the development of computer virus concealment strategies and protection mechanisms associated in anti-virus devices. To remain hidden from the anti-virus scanners, machine viruses are increasingly refining their codes to render them invisible. Anti-virus techniques, on the other side, constantly pursue the techniques and methods of viruses to defeat their risks [7]. The integration of new machines into the network and the withdrawal of outdated machines from the network shall be taken into consideration. While the machines on the wireless network are loaded with antivirus applications [8]. Metamorphic strategies are

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widely used by computer virus developers to create viruses that alter their internal configuration during each infection. First, analyze four virus creation kits to determine the degree of metamorphism each provides, and to be able to quantify precisely the degree of metamorphism produced by these virus generators [11]. The above referred articles they are not used the external virus spreading devices. In this model newly we are introduces a parameter to affect the network through the external devices for example pendrive, memory card, memory stick and etc. It is a type of malicious software program that replicates itself or affecting other programs by moderate them. There are three main types of PC virus: File infectors: This type of virus affects applications contained in files. It spread once the user runs the affected file. This virus copies itself to locations on the computer where it can be accomplished and will affect files. Boot-sector virus: It is a malicious virus that affects the computer storage sector where startup files are accomplished when a computer starts. Macro virus: It affects a Microsoft Word and create a sequence of actions to be performed automatically when started. A typical virus is a introduction of some comic at certain points while writing. Macro virus also spreads as an e-mail virus. This is seem that the dynamic behavior of the purposed model is developed by a beginning R0.This paper is systematized as follows. Section 1 Introduction about the computer virus. Section 2 frame the computer virus based deterministic model Section 3 and 4 Analysis proves the local and global stability of the virus-free equilibrium and talked about the stability of the viral equilibrium are respectively. In section 5, Stochastic model. In Section 6, the numerical simulations are given to present the factualness of the theoretical results. Finally, Section 7 summarizing this work.

2. The Model Formulation and Analysis

We have planned and analyzed a non-linear model for computer virus at every time, a computer is divided as internal and external based on weather it is connected to website or not. On the time, all of the internet computers are further distinguished into three states. Based on this we considered the peoples in the age group involved in Poverty . Let N(t), I(t) and R(t) indicate their corresponding numbers on time t. N(t) is the total population of computers , I(t) is the computers are affected by the viruses and R(t) computers are made virus free and return to normal state. The SIR model is framed as follows

$$\begin{aligned} dS/dt &= \Lambda - \alpha S\, NI + \sigma R - \mu S \\ dI/dt &= \alpha S\, NI - \xi\delta I - (\theta + \mu)I \\ dR/dt &= \xi\delta I - \sigma R - \mu R + \theta I \end{aligned} \qquad (2.1)$$

where $N = S + I + R$ The model (2.1) can be simplified as follows:

$$\begin{aligned} dS/dt &= \Lambda - \mu N \\ dI/dt &= \alpha S - \xi\delta I - (\theta + \mu)I \\ dR/dt &= \xi\delta I - \sigma R - \mu R + \theta I \end{aligned} \qquad (2.2)$$

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Table 1. Description of parameters

Parameters	Description
Λ	**Recruitment value**
μ	**Ordinary removal**
σ	**Computer Networks can be susceptible again after the recovery**
α	**Rate of Computer virus transmission (Through External devices connecting susceptible and infected)**
ξ	**Anti-virus Inclusion and its effects**
δ	**Recovery rate due to Anti-Virus**
θ	**Normal Recovery rate of Computer Network**

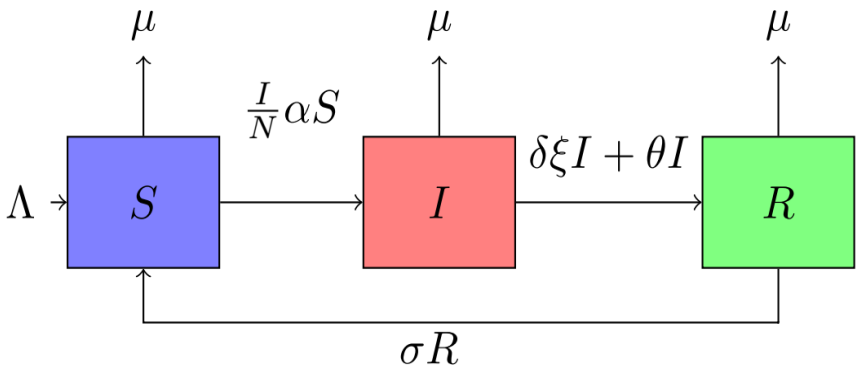

Figure 1. Model Transition Diagram

a. Existence of Equilibria

The equilibrium point for this NIR model (3) has been found at,

$$\Lambda - \mu N = 0$$
$$\alpha S(I/N) - \xi\delta I - (\theta + \mu)I = 0 \qquad (2.3)$$
$$\xi\delta I - \sigma R - \mu R + \theta I = 0$$

The system (2.3) has following equilibria namely

(i)Virus free equilibrium(VFE) $E_0(N^0; 0; 0) = (\Lambda/\mu , 0, 0)$

(ii)Endemic Equilibrium (EE) $E_1 (N^*,I^*,R^*) = (\Lambda/\mu, \frac{\Lambda(\sigma-\xi\delta-(\mu+\theta))}{\alpha\mu(1+\frac{\xi\delta+\theta}{\sigma+\mu})}, I(\frac{\xi\delta+\theta}{\sigma+\mu}))$

3. Stability Analysis

The variational matrix for the system (2.1) is given by

$$J_0 = \begin{pmatrix} S_{11} & 0 & 0 \\ S_{21} & S_{22} & S_{23} \\ 0 & S_{32} & S_{33} \end{pmatrix}$$

Where, $S_{11} = -\mu$, $S_{21} = \frac{\alpha I(I+R)}{N^2}$, $S22 = (\frac{\alpha N-2\alpha I-\alpha R}{N}) - (\xi\delta + \mu + \theta)$, $s_{23} = \frac{-\alpha I}{N}$,

$S_{32} = \xi\delta + \theta$, $S_{33} = -(\mu+\sigma)$

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3.1 Stability analysis of Virus free equilibrium

Theorem 3.1 The Virus Free Equilibrium E_0 is locally asymptotically stable provided $R_0 < 1$.

Proof To study the stability of virus free equilibrium the variational matrix M of the system corresponding to virus free equilibrium E0 is obtained as

$$M_1 = \begin{pmatrix} -\boldsymbol{\mu} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \left(\frac{\boldsymbol{\alpha N - \alpha R}}{\boldsymbol{N}}\right) - (\boldsymbol{\xi\delta} + \mu + \boldsymbol{\theta}) & \mathbf{0} \\ \mathbf{0} & \boldsymbol{\xi\delta} + \boldsymbol{\theta} & -(\boldsymbol{\mu} + \boldsymbol{\sigma}) \end{pmatrix}$$

The eigenvalues of this variational matrix are given by the roots of the following characteristic equation in λ.

$\lambda_1 = -\mu$, $\lambda_2 = -(\mu + \sigma)$, $\lambda_3 = \alpha - (\xi\delta + \mu + \theta)$.

Hence the equilibrium point E_0 is locally asymptotically stable provide $R_0 < 1$.

3.2 Stability analysis of endemic equilibrium

Theorem 3.2 The endemic equilibrium E_1 is locally asymptotically stable provided the parameters of the model satisfy Routh-Hurwitz criteria for $R_0 > 1$.

Proof The variational matrix , M_2 corresponding to $E_1$is given by

$$M_2 = \begin{pmatrix} S_{11} & 0 & 0 \\ S_{21} & S_{22} & S_{23} \\ 0 & S_{32} & S_{33} \end{pmatrix}$$

Where, $S_{11} = -\mu$, $S_{21} = \frac{\alpha I(I+R)}{N^2}$, $S22 = \left(\frac{\alpha N - 2\alpha I - \alpha R}{N}\right) - (\xi\delta + \mu + \theta)$, $s_{23} = \frac{-\alpha I}{N}$,

$S_{32} = \xi\delta + \theta$, $S_{33} = -(\mu + \sigma)$

The eigenvalues of this variational matrix are given by the roots of the following characteristic equation in $\lambda_1 = -\mu$, and $\begin{pmatrix} S_{22} & S_{23} \\ S_{32} & S_{33} \end{pmatrix}$ we get the quadratic equation .

$$b_1\lambda^2 + b_2\lambda + b_3 = 0 \ ,$$

where, $b_2 = -S_{22} - S_{33}$, $b_3 = S_{22}S_{33} - S_{32}S_{23}$ by Routh Hurwitz criteria, roots of the quadratic equation provided $R_0 > 1$.

Hence the equilibrium point E_1 is locally asymptotically stable provided $R_0 > 1$.

4. Global Stability

4.1 Global Stability of Virus Free Equilibrium

Theorem 4.1 The virus-free equilibrium E_0 of model (2.3) is globally asymptotically stable when $R_0 \leq 1$.

Proof We prove using comparison theorem described in,

$$\begin{pmatrix} \boldsymbol{I'} \\ \boldsymbol{R'} \end{pmatrix} = (\boldsymbol{F} - \boldsymbol{V})\begin{pmatrix} \boldsymbol{I} \\ \boldsymbol{R} \end{pmatrix} - \begin{pmatrix} \boldsymbol{\lambda_H(S - S^0)} \\ \mathbf{0} \end{pmatrix}$$

$$\text{i.e., } \begin{pmatrix} \boldsymbol{I'} \\ \boldsymbol{R'} \end{pmatrix} \leq (\boldsymbol{F} - \boldsymbol{V})\begin{pmatrix} \boldsymbol{I} \\ \boldsymbol{R} \end{pmatrix}$$

Since, the eigenvalues of the matrix *F-V* all have negative real parts, then system (2.3) is stable whenever $R_0 < 1$. So $(I,R) \to (0,0)$ as $t \to \infty$. By comparison theorem, it follows that $(I,R) \to (0,0)$

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and S→ $\frac{\Lambda}{\mu}$ at t→ ∞. Then (S, I, R)→ $\boldsymbol{E_1}$ **as t** → ∞. So, E_1 is globally asymptotically stable for $R_0<1$.

4.2 Global Stability of Virus Free Equilibrium

In order to investigate the global stability of the endemic equilibrium E_1, we adopt the approach developed by [3]. Assume that $R_0 > 1$, the E_1 exists for all N, I, R >∈, for some ∈> 0. Let $\boldsymbol{\lambda_H} N =$ g(N, I, R) be positive and monotonic function in $\mathbb{R}^3_+$.

$$V(N, I, R) = N - \int_{\in}^{N} \frac{g(N^*,I^*,R^*)}{g(\tau,I^*,R^*)} d\tau + I - \int_{\in}^{I} \frac{g(N^*,I^*,R^*)}{g(N^*,\tau,R^*)} d\tau + R - \int_{\in}^{R} \frac{g(N^*,I^*,R^*)}{g(N^*,I^*,\tau)} d\tau \quad (4.1)$$

If g(N, I, R) is monotonic with respect to its variables, then the state E_1 is the extremum and the global minimum of this function. So obviously

$$\frac{\partial V}{\partial N} = 1 - \frac{g(N^*,I^*,R^*)}{g(N\ \ ,I^*,R^*)}, \frac{\partial V}{\partial I} = 1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I\ \ ,R^*)}, \frac{\partial V}{\partial R} = 1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I^*,R\ \ )} \quad (4.2)$$

Grow monotonically, then the function g(N, I, R) and h(N, I, R) have only one stationary point. Further, since

$$\begin{aligned} \frac{\partial V^2}{\partial N^2} &= \frac{g(N^*,I^*,R^*)}{[g(N\ \ ,I^*,R^*)]^2} \cdot \frac{g(N,I^*,R^*)}{\partial N}, \\ \frac{\partial V^2}{\partial I^2} &= \frac{g(N^*,I^*,R^*)}{[g(N^*,I\ \ ,R^*)]^2} \cdot \frac{g(N^*,I\ \ ,R^*)}{\partial I}, \\ \frac{\partial V^2}{\partial R^2} &= \frac{g(N^*,I^*,R^*)}{[g(N^*,I^*,R\ \ )]^2} \cdot \frac{g(N^*,I^*,R\ \ )}{\partial R}, \end{aligned} \quad (4.3)$$

are non-negative, then g(N, I, R) have minimum. That is, V(N, I, R) ≥ V(N^*, I^*, R^*) and hence, V is a Lyapunov function, and its time derivative is given by

$$\begin{aligned} \frac{dV}{dt} &= N' - N' \frac{g(N^*,I^*,R^*)}{g(N\ \ ,I^*,R^*)} + I' - I' \frac{g(N^*,I^*,R^*)}{g(N^*,I\ \ ,R^*)} + R' - R' \frac{g(N^*,I^*,R^*)}{g(N^*,I^*,R\ \ )} \\ &= \mu N^* \left(1 - \frac{N}{N^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N\ \ ,I^*,R^*)}\right) + (\mu+\theta) I^* \left(1 - \frac{I}{I^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I\ \ ,R^*)}\right) \\ &\quad + (\mu+\sigma) R^* \left(1 - \frac{R}{R^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I^*,R\ \ )}\right) \end{aligned}$$

Since $E_1 > 0$, the functions g(N, I, R) is concave with respect to I & R and

$$\frac{\partial^2 g(N,\ I,\ R)}{\partial I^2} \leq 0, \frac{\partial^2 g(N,\ I,\ R)}{\partial R^2} \leq 0$$

Then $\frac{dV}{dt} \leq 0$ for all N, I, R > 0. The monotonicity of g(N, I, R) with respect to N, I & R ensure that

$$\begin{aligned} \left(1 - \frac{N}{N^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N\ \ ,I^*,R^*)}\right) &\leq 0, \\ \left(1 - \frac{I}{I^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I\ \ ,R^*)}\right) &\leq 0, \\ \left(1 - \frac{R}{R^*}\right)\left(1 - \frac{g(N^*,I^*,R^*)}{g(N^*,I^*,R\ \ )}\right) &\leq 0, \end{aligned}$$

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holds for all N, I, R > 0.Thus, we estabilish the following result.

Theorem 4.2 Tne endemic equilibrium E_1 0f the model(2) is globally asymptotically stable whenever conditions outlined in Eq.(4.3) are satisfied.

5. Stochastic Model

Here we are expanding our deterministic model to stochastic model, because stochastic model are more capable of detecting natural variations in the problem of computer viruses. Derivation of SDE model is based on Yuvan's approach[4]. Let $X(t) = (X_1(t), X_2(t), X_3(t))^T$ be a continuous random variable for $(N(t), I(t), R(t))^T$ and T denotes the transpose of a matrix. Let $\Delta X = X(t+\Delta t) - X(t) = (\Delta X_1, \Delta X_2, \Delta X_3)^T$ denotes the random vector for the change in random variables during time interval Δt. Here, we will write the transition maps which define all possible changes between states in the SDE model. Based on our ODE model system (2), here we see that there exist 11 possible changes between states in a small time interval Δt. State changes and their probabilities are discussed in Table 2. Let us consider the case the recruitment of one computer network becomes susceptible / infected network. In this case, the state change ΔX is denoted by $\Delta X = (1, 0, 0)$ its probability of the change is given by $\text{prob}(\Delta X_1, \Delta X_2, \Delta X_3) = (1, 0, 0) \mid (X_1, X_2, X_3) = P_1 = \Lambda\Delta t + o(\Delta t)$

One will quickly work out the expectation change $E(\Delta X)$ and its covariance matrix $V(\Delta X)$ associated with ΔX by neglecting the terms higher than $o(\Delta X)$. The expectation of ΔX is given by

$$E(\Delta X) = \sum_{i=1}^{11} P_i(\Delta X)_i \Delta t = \begin{pmatrix} \Lambda - \mu X_1 \\ \frac{\alpha X_2(X_1 - X_2 - X_3)}{X_1} - \xi\delta X_2 - (\theta + \mu)X_2 \\ \xi\delta X_2 - (\sigma + \mu)X_3 + \theta X_2 \end{pmatrix} \Delta t$$
$$= f(X_1, X_2, X_3)\ \Delta t$$

Here, it can be noted that the expectation vector and the function f are in the same form as those in ODE system (2.3). Since, $V(\Delta X) = E((\Delta X)(\Delta X)^T) - E(\Delta X)(E(\Delta X)^T)$ and $E((\Delta X)(\Delta X)^T) = f(X)f((X)^T)\Delta t$, it can be approximately diffusion matrix V times Δt by neglecting the term of $(\Delta t)^2$ such that $V(\Delta X) \approx E((\Delta X)(\Delta X)^T)$. Hence,

$$E((\Delta X)(\Delta X)^T) = \sum_{i=1}^{10} P_i((\Delta X)_i(\Delta X)_i^T)\Delta t = \begin{pmatrix} V_{11} & 0 & 0 \\ 0 & V_{22} & V_{23} \\ 0 & V_{32} & V_{33} \end{pmatrix} . \Delta t = \Omega . \Delta t$$

Table 2. Possible changes of states and their probabilities.

Possible State Change		Probability of state change
$(\Delta X)_1 = (1, 0, 0)^T$	Changed into the affected computer network	$P_1 = \Lambda\Delta t + o(\Delta t)$
$(\Delta X)_2 = (-1, 0, 0)^T$	Change into the Naturally Removed computer network	$P_2 = \mu X_1\Delta t + o(\Delta t)$
$(\Delta X)_3 = (0, 1, 0)^T$	Changed into susceptible network	$P_3 = \alpha X_2\Delta t + o(\Delta t)$
$(\Delta X)_4 = (0, -1, 1)^T$	Changed into susceptible and infected computer network	$P_4 = \alpha\frac{X_2^2}{X_1}\Delta t + o(\Delta t)$
$(\Delta X)_5 = (0, -1, 1)^T$	Change into infected and recovery network to the total network	$P_5 = \alpha X_2 X_3\Delta t + o(\Delta t)$

Annals of R.S.C.B., ISSN:1583-6258, Vol. 25, Issue 2, 2021, Pages. 3501 - 3512
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$(\Delta X)_6 = (0, -1, 1)^T$	Change into infected network to the recovery network	$P_6 = \xi\delta X_2\Delta t+o(\Delta t)$
$(\Delta X)_7 = (0, -1, 1)^T$	Change into infected network and the growth of recovery	$P_7 = \theta X_2\Delta t+o(\Delta t)$
$(\Delta X)_8 = (0, -1, 0)^T$	Changed into the network removed depend on the infection network down rate	$P_8 = \mu X_2\Delta t+o(\Delta t)$
$(\Delta X)_9 = (0, 0, -1)^T$	Changed into removed computer to susceptible by external device	$P_9 = \sigma X_3\Delta t+o(\Delta t)$
$(\Delta X)_{10} = (0, 0, -1)^T$	Changed into Natural Removed Computer Network	$P_{10} = \mu X_3\Delta t+o(\Delta t)$
$(\Delta X)_{11} = (0, 0, 0)^T$	No Change	$P_{11} = 1 - \sum_{i=1}^{10} Pi +o(\Delta t)$

where the above diffusion matrix is symmetric, positive-definite and each component of this 3x3 diffusion matrix can be obtained as follows:

$V_{11} = P_1+P_2$, $V_{22} = P_3+P_4+P_5+P_6+P_7+P_8$, $V_{33} = P_6+P_7+P_9+P_{10}$,

$V_{23} = V_{32} = P_6+P_7$, $V_{12} = V_{21} = 0$, $V_{13} = V_{31} = 0$.

We follow the approach discussed in [4, 7] and construct a matrix $V = MM^T$, where S is a 3x6 matrix. M =

$$\begin{pmatrix} \sqrt{\Lambda} & -\sqrt{\mu X_1} & 0 & 0 & 0 & 0 \\ 0 & 0 & \sqrt{\frac{\alpha X_2(X_1-X_2-X_3)}{X_1} - \mu X_2} & -\sqrt{\xi\delta X_2} & -\sqrt{\theta X_2} & 0 \\ 0 & 0 & 0 & \sqrt{\xi\delta X_2} & \sqrt{\theta X_2} & -\sqrt{(\sigma+\mu)X_2} \end{pmatrix}$$

Then, the Ito stochastic differential model has the following from:

$d(X(t)) = f(X_1,X_2,X_3)dt + M.dW(t)$

with initial condition $X(0) = (X_1(0), X_2(0), X_3(0))^T$ and a Wiener Process,

$W(t) = (W_1(t), W_2(t), W_3(t), W_4(t), W_5(t), W_6(t))^T$. Keeping in view of the above facts, we get the stochastic differential equation model as follows:

$dN = (\Lambda-\mu N)dt + \sqrt{\Lambda}dW_1 - \sqrt{\mu N}dW_2$

$dI = (\frac{\alpha I(N-I-R)}{N} - \xi\delta I - (\theta+\mu)I)dt + \sqrt{\frac{\alpha I(N-I-R)}{N} - \mu I}dW_3 - \sqrt{\xi\delta I}dW_4 - \sqrt{\theta I}dW_5$

$dR = (\xi\delta I - \sigma R - \mu R + \theta I)dt + \sqrt{\xi\delta I}dW_4 + \sqrt{\theta I}dW_5 - \sqrt{\sigma+\mu I}dW_6$

6. Numerical Simulation

In this section, we verified our analytical results using numerical simulation. Experimentally verified results are shown here with justification. The system (2.3) is simulated for various set of parameters satisfying the condition of local asymptotic stability of equilibria E_0 and E_1. To see the dynamic behaviour of the model for virus free equilibria. We consider the parameter set $S_1 = \{\Lambda = 10; \mu = 0.05; \delta = 0.4; \sigma = 0.006; \xi = 0.21; \alpha = 0.0008; \theta = 0.006\}$, For the parameter set S_1 the system (2.3) has only the virus free equilibrium and it is locally asymptotically stable (see Fig. 2).

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Again for a different set of parameters $S_2 = \{\Lambda = 1000; \mu = 0.0145; \delta = 0.000961; \sigma = 0.00612; \xi = 0.0051; \alpha = 0.9912; \theta = 0.0621\ \}$ For S_2 the system (2.3) has feasible equilibria is the endemic equilibrium is locally asymptotically stable (see Fig. 3). To verify the stability of equilibrium with respect to the initial conditions we plotted Figs.4,5 ,6 and 7. Fig. 4 depicts the stability of endemic equilibrium point for different initial values on both total computer 14 network and computer virus affected networks. Fig. 5 depicts the stability of endemic equilibrium point for different initial values on both virus removed computer networks again goes to affected network if we change the numeric values when it is stable at different position. Fig. 6 and 7 depicts the stability of endemic equilibrium point for different initial values on both δ and ξ parameters effects are respectively. Also for a different set of parameters at 3- Dimension $S_3 = \{\Lambda = 0.2; \mu = 0.001; \delta = 0.03; \sigma = 0.03; \xi = 0.03; \alpha = 0.01; \theta = 0.31\}$ For the system (2.3) has been feasible equilibria of 3-dimensional flow is stable at different position of each parameter in S_3 the endemic equilibrium is locally asymptotically stable (see Fig. 8). Here, we simulate both deterministic and stochastic models for the following set of parameters: $\Lambda = 01000$, $\mu = 0.0145$, $\delta = 0.000961$, $\alpha = 0.9912$, $\theta = 0.0621$, $\sigma = 0.051$, ξ 0.00612. The simulation results for both deterministic and stochastic models are shown in Figures 9. The stochastic model (SDE model) is simulated by Euler- Maruyama method. Here, the results of stochastic model seem better than the deterministic model as the curve corresponding to computer infected network lies below the one that corresponds to the deterministic model

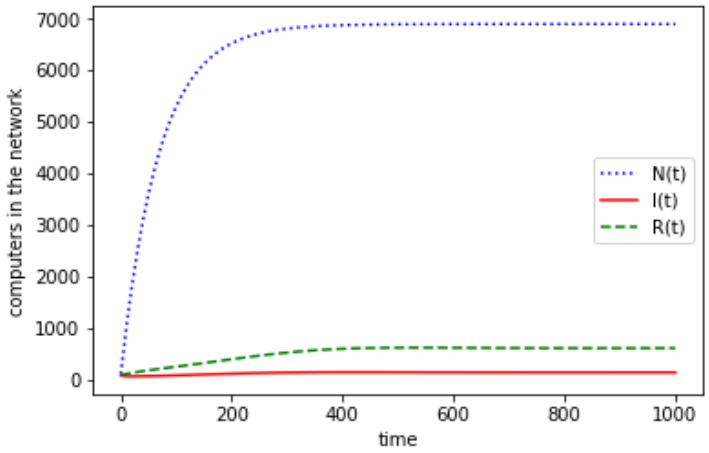

Figure 2. Variation of network population under the equilibrium E_0

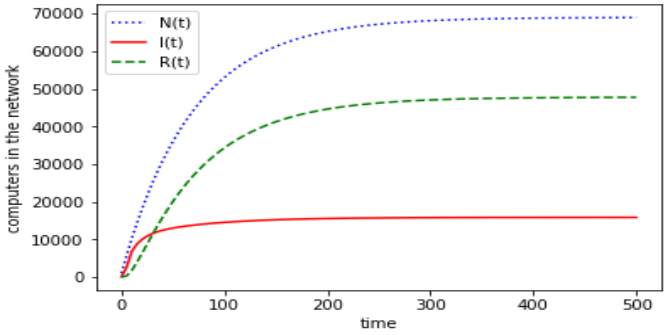

Figure 3. Variation of network population under the endemic equilibrium E_1

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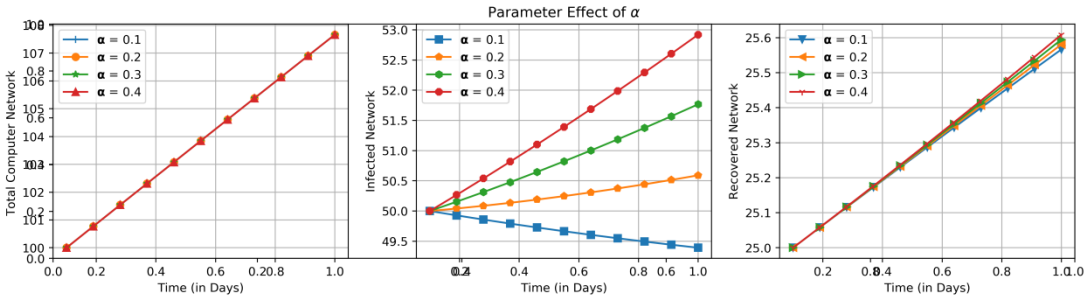

Figure 4. Plot of Parameter effects in α

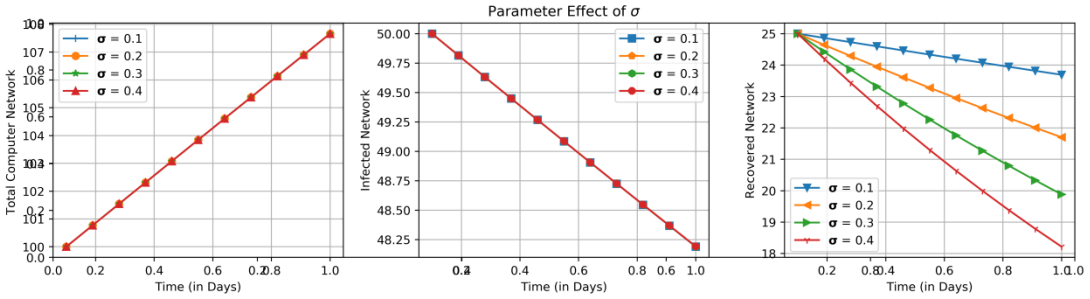

Figure 5. Plot of Parameter effect in σ

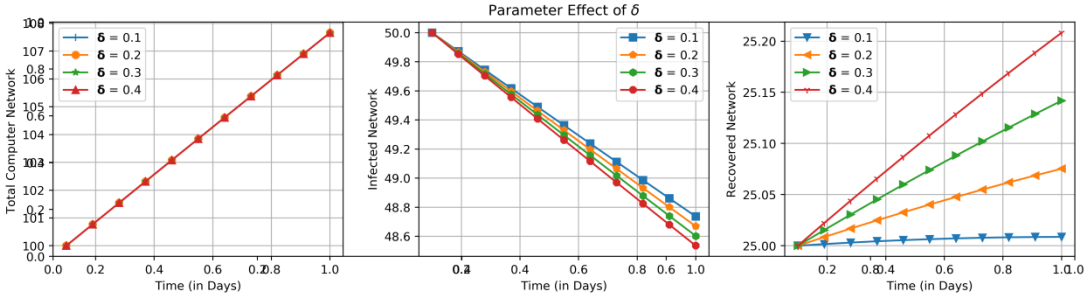

Figure 6. Plot of Parameter Effect in δ

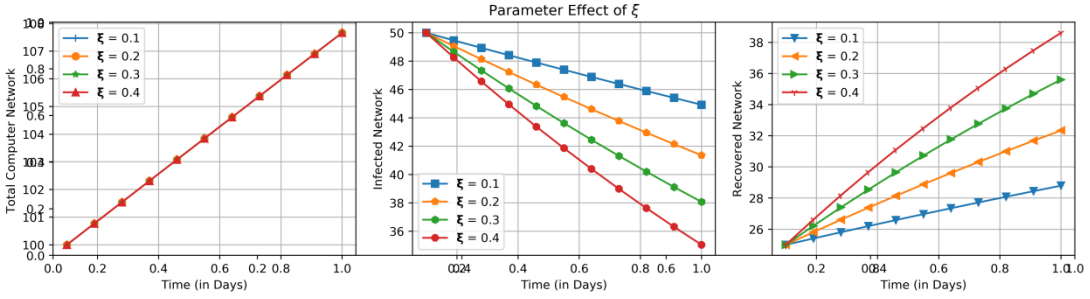

Figure 7. Plot of Parameter Effect in ξ

Annals of R.S.C.B., ISSN:1583-6258, Vol. 25, Issue 2, 2021, Pages. 3501 - 3512
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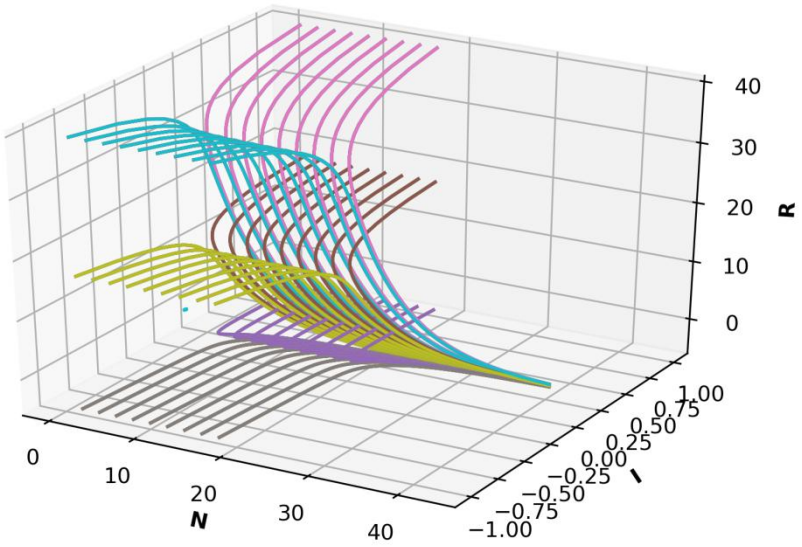

Figure 8. 3D-Plot of Computer virus network

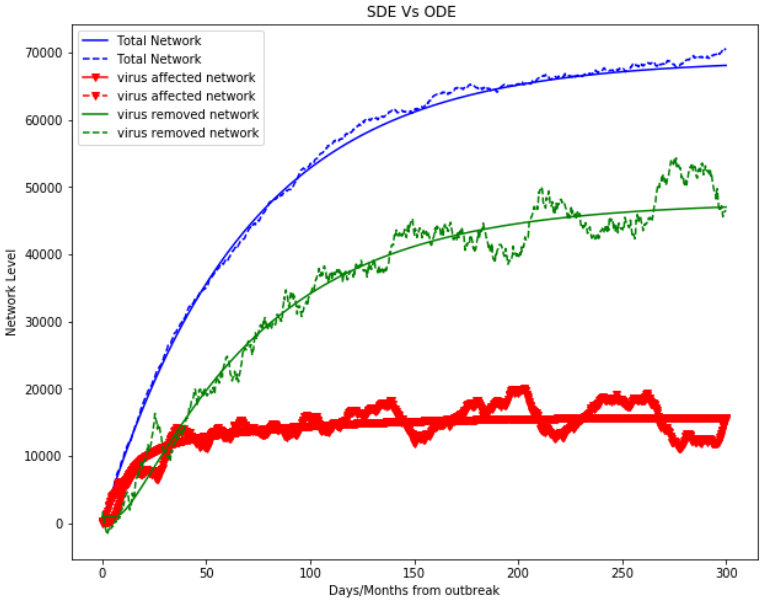

Figure 9. SDE Vs ODE-Plot of Computer virus Network

7. Results Discussion and Conclusion

We have found the equilibrium of the model and analyzed their stabilities for the deterministic model. The deterministic model has been extended to a stochastic model to see the effect of our model as realistic one since the stochastic models were exhibiting the real world scenario. Both the deterministic and stochastic models were simulated numerically to support our analytical findings. There are figures to show the stability of our model and there are figures to

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show the effectiveness of our parameters. Through our model, we found that the effect of virus transmission from outer/external sources (this parameter is known from our model as α). There are other parameters which are affecting network which makes our system susceptible after recovery, recovery due to anti-virus (as σ and ξ). We also found that anti-virus effect is to be followed on the computer network is a better advice and it is lowering down the infections on the network through computer viruses(as δ). The stability of equilibrium points of our model are plotted deterministic and as stochastically. We found that the stochastic effect also make our equilibrium points circulating very much nearer to our deterministic stable points. This confirms the convergence of our equilibrium point in deterministic and stochastic. These points were suggesting that the convergence of our model's equilibrium points are good and one may follow our findings for their future perspectives.

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