Attack of malicious objects in computer network under antivirus and quarantine defence

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Abstract

Here we develop an epidemic model in a computer network under quarantine and antivirus treatment. Effect of antivirus in the computer network prevents rapidly the spreading behaviour of malicious objects and the role of Quarantine treatment in a computer network increases recovery rate of the infectious computers. The stability of the model and basic

reproduction number (R_0^V) of the model is also derived. Moreover, the effect of antivirus and quarantine in the system

is analyzed. MATLAB is employed to solve and simulate the $dV = \gamma - \theta + \mu - \sigma\beta$

system of equations. S The(simulated)V resultsVI help us to dt

understand the spread and control of malicious objects in a computer networkdI $dt = \cdot\ \beta SI + \sigma\beta VI$

$-(\mu + \alpha)I - \eta I$

Keywords: Basic reproduction number, e-Epidemic model, $dQ = \eta I - (\mu + \alpha + \varepsilon)Q$

Local stability, Quarantine. dt

$$dR = \varepsilon Q - (\mu + \omega)R$$

dt

Introduction

Now a day most of the people do skype, whatsApp, Webchat, facebook and other top chat App over internet therefore internet is a big dais for the people who share new ideas, news and views etc. Due to its openness many malicious objects enable to spread misinformation throughout the world [16]. There are different kinds of malicious objects such as: Worm, Virus, Trojan-horse etc., which differ according to the way they attack computer systems and the malicious actions they perform. Attacking nature of the malicious objects are generally like infectious diseases and are epidemic in nature. Therefore the action of malicious objects throughout a network can be studied by using epidemiological models for disease propagation [1-10, 22, 23, 26 and 27]. Based on Kermack and McKendrick [24 and 25], SIR classical epidemic model, different epidemic models are used to study the spread of malicious objects in network [11-14, 18 and 26-27]. Now a day, researchers focus on the prevalence of malicious objects, e. g., virus immunization [15, 17, 19, 20 and 21] and quarantine [1, 4 and 23]. The more attention is paid to the research involving combination of virus propagation model and antivirus countermeasures.

In this paper, we discuss SIR dynamic epidemic model under Quarantine and antivirus defences.

Mathematical model and assumptions

A population size N (t) is partitioned into subclasses of nodes which are susceptible, antivirus treatment, infected;

quarantine; recover with sizes denoted by $S(t), V(t), I(t), Q(t), R(t)$ respectively. Our assumptions

on the dynamical transfer of the population are depicted in the Figure1.

In this model, the flow of viruses is from class S to class V, class S to class I, class V to class I, class I to class Q, class Q to class R. The antivirus nodes again enter into the susceptible class due to the lack of updated anti-virus. The transmission between model classes can be expressed by the following system of differential equations:

$$\frac{ds}{dt} = \wedge + \theta V - \beta SI - (\gamma + \mu)S + \omega R$$

$$\begin{aligned} \frac{dV}{dt} &= \gamma S - (\theta + \mu)V - \sigma\beta VI \\ \frac{dI}{dt} &= \beta SI + \sigma\beta VI - (\mu + \alpha) I - \eta I \\ \frac{dQ}{dt} &= \eta I - (\mu + \alpha + \varepsilon)Q \qquad (1) \\ \frac{dR}{dt} &= \varepsilon Q - (\mu + \omega)R \end{aligned}$$

Equilibrium point

The system (1) is defined on the closed, positive invariant set E = {(S, V, I, Q, R); S, V, I, Q, R ≥ 0 : S + V+ I +Q+ R = N} which has two possible equilibriums, first, the virus free equilibrium, E_0= (S, V, 0, 0, 0) and second, the endemic equilibrium E*=(S*, V*, I*, Q^*, R*) which is the interior of E and can be obtained by taking all the equations of system (1) equal to zero.

Disease free equilibrium

E_0 =(S, V, 0, 0, 0)=

$$\left(\frac{\wedge(\theta + \mu)}{\theta\mu + \mu\gamma + \mu^2}, \frac{\wedge\gamma}{\theta\mu + \mu\gamma + \mu^2}, 0,0,0 \right) \qquad (2)$$

Endemic equilibrium

$$0 = \wedge + \theta V + \omega R - \beta SI - (\gamma + \mu)S \qquad (3)$$

$$\begin{aligned} 0 &= \gamma S - (\theta + \mu)V - \sigma\beta VI \\ 0 &= \beta SI + \sigma\beta VI - (\mu + \alpha)I - \eta I \\ 0 &= \eta I - (\mu + \alpha + \varepsilon)Q \\ 0 &= \varepsilon Q - (\mu + \omega)R \end{aligned}$$

$$V^* = \frac{\gamma(\wedge + \omega R)}{(\beta I + \gamma + \mu)(\theta + \mu + \sigma\beta I) - \gamma\theta}$$

$$S^* = \frac{(\theta + \mu + \sigma\beta I)(\wedge + \omega R)}{(\theta + \mu + \sigma\beta I)(\theta + \mu + \sigma\beta I) - \gamma\theta}$$

From last two equations (3) we have

$$Q^* = \frac{\eta I}{(\mu + \alpha + \varepsilon)}$$

$$\left[\begin{matrix} -(\gamma + \mu) & \theta & -\beta S \\ \gamma & -(\theta + \mu) & -\sigma\beta V \\ 0 & 0 & \beta S + \sigma\beta V - (\mu + \alpha + \eta) \\ 0 & 0 & \eta \\ 0 & 0 & 0 \end{matrix} \right. \qquad (4)$$

The Eigen value of above matrix is

$$\begin{aligned} \lambda_2 &= \beta S + \sigma\beta V - (\mu + \alpha + \eta) \\ &= (R_0{}^V - 1) \end{aligned}$$

If $R_0^V < 1$, λ_2 is negative

$$\begin{array}{cc} 0 & \omega \\ 0 & 0 \\ 0 & 0 \\ -(\mu+\alpha+\varepsilon) & 0 \\ \square & -(\omega+\mu) \end{array}$$

$_1 = -(\mu+\omega)$

$$R^* = \frac{\varepsilon Q}{(\mu+\omega)} = \frac{\varepsilon\eta I}{(\mu+\omega)(\mu+\alpha+\varepsilon)}$$

$\lambda_3=-(\mu+\alpha+\varepsilon)$

And other two Eigen value having negative real part can be finding from the quadratic equation
Put V, S in third equation of (3) we have a quadratic equation further more I^* is the positive root of the quadratic equation

$$aI^2 + bI + c = 0$$

Where

$$a = (\mu+\alpha+\eta)\sigma\beta^2$$

$$b = \beta(\theta+\mu+\lambda\sigma+\mu\sigma)(\mu+\alpha+\eta) - \beta^2\sigma\eta - \sigma\beta^2\omega R^*$$

$$c = (\gamma\mu+\mu\theta+\mu^2)(\mu+\alpha+\eta) - \sigma\gamma(\wedge+\omega R^*) - \beta\theta\wedge - \beta\theta\omega R^* - \beta\mu\wedge - \beta\mu\omega R^*$$

Basic reproductive number

By using Next Generation matrix approach, let us take F=

$$\begin{bmatrix} \beta S+\sigma V & 0 \\ 0 & 0 \end{bmatrix} \qquad V = \begin{bmatrix} (\mu+\alpha+\eta) & 0 \\ -\eta & (\mu+\alpha+\varepsilon) \end{bmatrix}$$

$$\Rightarrow FV^{-1} = \frac{1}{(\mu+\alpha+\eta)(\mu+\alpha+\varepsilon)} \begin{bmatrix} (\beta S+\sigma V)(\mu+\alpha+\varepsilon) & 0 \\ 0 & 0 \end{bmatrix}$$

The largest Eigen value of FV^{-1} is the Basic reproduction number

Therefore the Basic reproduction of our model is

$$R_0^V = \frac{\beta S+\sigma V}{(\mu+\alpha+\eta)}$$

(5) In the absence of antivirus treatment nodes the Basic reproduction number is

$$R_0 = \frac{\beta S}{(\mu+\alpha+\eta)}$$

Stability analysis

Theorem 1 (local stability) The disease free equilibrium point of system (1) is locally asymptotically stable, If

$R_0^V < 1$; and unstable $R_0^V > 1$.

Proof: Linearizing system (1) at disease free equilibrium points we will get

$$\lambda^2 + A\lambda + B = 0$$

Where $A=(\gamma+\theta+2\mu)$, $B=(\gamma+\mu)(\theta+\mu)-\gamma\theta$ where A and B>0 by Hurwitz condition it is stable, Therefore all the Eigen value are negative if $R_0^V < 1$

Therefore the system is locally asymptotic stable at disease free equilibrium

Model parameters and Notation:

Notation	Explanation
N	Total number nodes under consideration
S	Number of susceptible nodes at time t
V	Number of antivirus treatment nodes individuals at time t
I	Number of infective nodes at time t
Q	Number of quarantine nodes at time t
R	Number of recovered nodes with immunity at time t
Λ	Number of new born
β	Contact rate
ε	Recovery rate
γ	antivirus treatment rate
θ	Rate at which the antivirus treatment wears off
µ	Natural death rate that is not related to the malicious objects
α	Disease-related death rate
σ	Factor by which the antivirus treatment nodes has the effect of reducing the infection
η	Rate of infected fraction from I class to Q class.
ω	Rate of susceptible from R class to S class
R 0	Basic reproductive number without antivirus treatment nodes
R_0^V	antivirus treatment reproductive number with antivirus treatment nodes

Numerical methods and discussion

SVIQRS e-epidemic model have been developed for the transmission of malicious objects in computer network. Locally stability of the unique endemic equilibrium for the epidemic model has been established. MATLAB are employed to solve and simulate the system (1) and the behaviour of the susceptible, antivirus treatment nodes, infected, And recovered nodes with respect to time during epidemic are observed which is depicted in Fig. 2.

of Quarantine class is observed on recovery classes as depicted in figure 3. Quarantine plays an important role in the recovery of the nodes.

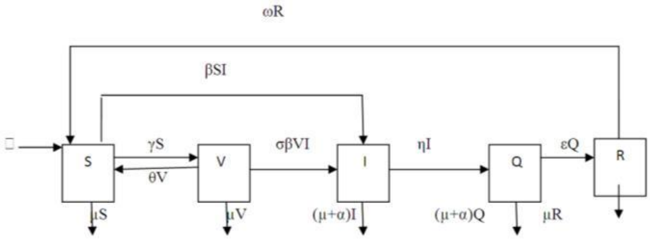

Figure 1: Figure 1 Schematic diagram for the flow of viruses in computer network

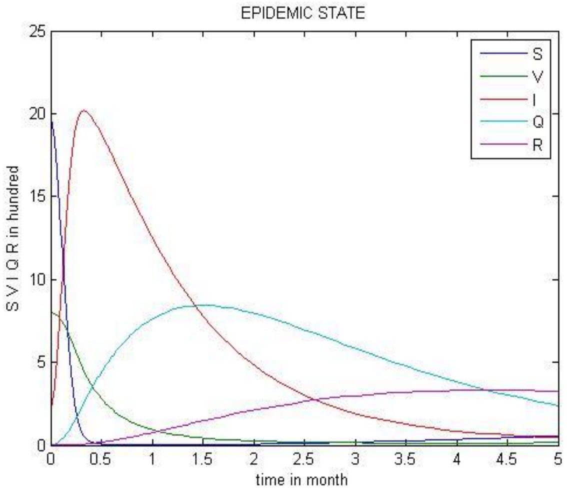

Figure 2: epidemic state of the given model under "not updated antivirus software" and "low quarantine rate"

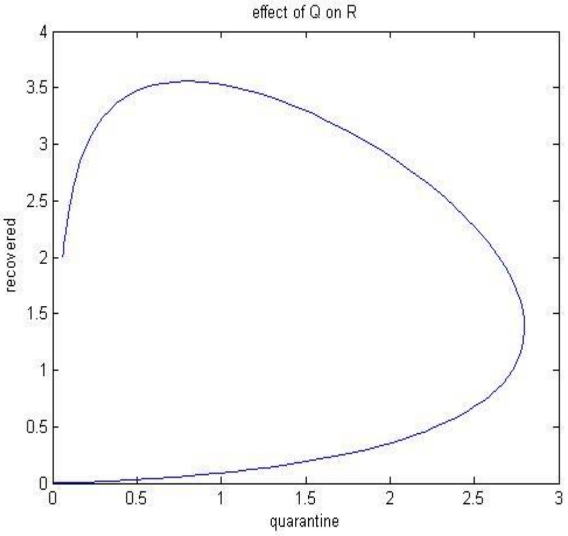

Figure 3: Dynamical behaviour of the system (1) with the real parameters ∧ =0. 01;β=0. 85;μ=0. 05;γ=0. 15;θ=0. 20;α=0. 35;η=0. 65; σ=0. 15; ω=0. 15;ε=0. 2;

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