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Calculation of Basic Reproduction Number by Graph Reduction Method and Stability Analysis in SEIQR e-Epidemic Model in Computer Network

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Abstract: In this study, we determine the basic reproduction number using a graph-theoretic form of Gaussian elimination using digraph reduction method and stability analysis in e-SEIQRS (e-Electronic, Susceptible, Exposed, Infectious, Quarantined, Recovered) Epidemic Model of a computer network.

Key words: Basic reproduction number, e-Epidemic Model, graph reduction method, stability analysis, computer network, e-Electronic

INTRODUCTION

Electronic mail and use of secondary devices are the major sources for the transmission of malicious objects in computer network these days. Malicious object is a code that infects computer systems. There are different kinds of malicious objects such as: Worm, Virus, Trojan etc. which differ according to the way they attack computer systems and the malicious actions they perform. Since, transmission of malicious objects in computer network is epidemic in nature. The action of malicious objects throughout a network can be studied by using epidemiological models for disease propagation (Mishra and Pandey, 2012; Mishra and Jha, 2009; Yuan and Chen, 2008). Based on the Kermack and McKendrick (1927, 1932, 1933) SIR Model, dynamical models for malicious objects propagation were proposed, providing estimations for temporal evolutions of infected nodes depending on network parameters considering topological aspects of the network (Draief *et al*., 2008; Kephart, 1994; Kephart *et al*., 1993; Keeling and Eames, 2005; Williamson and Leveille, 2003; Piqueira and Cesar, 2008; Piqueira *et al*., 2005; Datta and Wang, 2005). Modification of SIR models generated guides for infection prevention by using the concept of epidemiological threshold (Mishra and Pandey, 2012; Mishra and Jha, 2010; Draief *et al*., 2008). Recently, more research attention has been paid to the combination of virus propagation models and antivirus countermeasures to study the prevalence of virus, for example, virus immunization (Kephart, 1994; Kephart *et al*., 1993; Chen and Jamil, 2006) and quarantine (Mishra and Jha, 2010; Hethcote *et al*., 2002). Since, the malicious objects differ in their attacking behavior, a non-linear incidence rates can give a reasonable qualitative description of the disease dynamics. Many researchers have developed mathematical models with non-linear incidence rate (Keeling and Eames, 2005; Piqueira *et al*., 2005; Datta and Wang, 2005).

In a certain sense, the propagation of virtual malicious objects in a system of interacting computers could be compared with a disease transmitted by vectors when dealing with public health. Concerning diseases transmitted by vectors, one has to take into account that the parasites spend part of its lifetime inhabiting the vector, so that the infection switches back and forth between host and vector. May and Lloyd (2001), Anderson and May (1991) discussed the spreading nature of biological viruses, parasites, etc., leading to infectious diseases in human population through several epidemic models. Here, we do the following for a e-SEIQRS epidemic model:

- Determine R_0 by graph reduction method
- Stability analysis of model under quarantine defense

Basic terminologies: Malicious objects are computer programs that operate on behalf of a potential intruder to aid in attacking on network. Historically, an arsenal of such agents consisted of viruses, worms and trojanized programs. By combining key feature of these agents, attackers are now able to create software that poses a serious threat even to organization that fortify their network perimeter with firewalls.

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Quarantine a node: To move an undesired node form the computer network which is infected by any malicious objects and is not accessible by regular users. Anti-malicious software is a class of program that searches the hard drive and floppy disks for any known or potential malicious objects. As new malicious objects are discovered by the anti-malicious vendor, their binary patterns are added to a signature database that is downloaded periodically to the user's anti-malicious program via. the web.

MATERIALS AND METHODS

The e-SEIQRS Model formulation and assumtions: In the proposed SEIQRS Model for infections that don't confer immunity, susceptible nodes first goes through a latent period (and is said to become exposed) after infection before becoming infectious, thereafter, some infected nodes stay in the I class while they are infectious and then move to the recovery class after the run of anti malicious software. Other infected nodes are transferred into the quarantine class Q while they are infectious and then move to the R class. Since, in the cyber world the acquired immunity is not permanent, the recovered nodes return back to the susceptible class. The schematic diagram for the flow of malicious objects in the computer network is depicted in Fig. 1.

We assume the population has a homogeneous spatial distribution and the mixing of hosts follow the law of mass action. More specifically, we assume that the local density of the total population is a constant though the total population size N(t) = S(t)+E(t)+I(t)+Q(t)+R(t) may vary with time. Here, S(t), E(t), I(t), Q(t), R(t) denote the sizes of S, E, I, Q, R classes at any time t, respectively. The per capita contact rate σ which is the average number of effective contacts with other nodes per unit time is assumed to be a constant.

To avoid the total crash of the computer network, we divide the total node N(t) into subclasses of nodes which are susceptible, exposed, infectious, quarantined and recovered with sizes denoted by S(t), E(t), I(t),Q(t) R(t), respectively. We assume that the local density of the total population size, N = S+E+I+Q+R may vary with time and we let, A = S+E+I+R be the active nodes (that is the nodes which are not isolated). Based on our assumptions on the dynamical transfer of the population depicted in Fig. 1, we have the following system of Eq. 1:

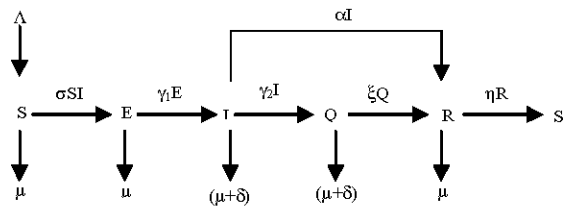

Fig. 1: Schematic diagram for the flow of worms in the computer network

$$\begin{aligned}
\frac{dS}{dt} &= \wedge -\mu S-\sigma SI+\eta R\\
\frac{dE}{dt} &= \sigma SI-(\mu+\gamma_1)E\\
\frac{dI}{dt} &= \gamma_1 E-(\mu+\delta+\gamma_2+\alpha)I\\
\frac{dQ}{dt} &= \gamma_2 I-(\mu+\delta+\xi)Q\\
\frac{dR}{dt} &= \xi Q+\alpha I-(\eta+\mu)R
\end{aligned} \tag{1}$$

Thus:

$$\frac{dN}{dt} = \wedge -\mu N-\delta(I+Q)$$

All the model parameters are positive constants. In this SEIQRS Model, the flow is from the S class to the E class, E class to the I class and then directly to the Am class or to the Q class and then to the Am class and as the recovery is not permanent in the cyber world, it again returns back to the S class.

The total population size N (t) is variable with $N'(t) = A-\mu N-\delta(I(t)+Q(t))$. In the absence of the attack of malicious objects, the population size of the node N approaches the carrying capacity A/μ. Therefore, the region:

$$D = \left\{(S, E, I, Q, Am) \in R_+^5 / S \geq 0, E \geq 0, I \geq 0, Q \geq 0, R \geq 0, S+E+I+Q+Am \leq A/\mu\right\}$$

is a positive invariant set for Eq. 1. To eliminate R form the Eq. 1, we use:

$$R = \frac{\wedge}{\mu}-S-E-I-Q$$

The reduced model is:

$$\begin{aligned}
\frac{dS}{dt} &= \wedge -\mu S-\sigma SI+\eta\left(\frac{\wedge}{\mu}-S-E-I-Q\right)\\
\frac{dE}{dt} &= \sigma SI-(\mu+\gamma_1)E\\
\frac{dI}{dt} &= \gamma_1 E-(\mu+\delta+\gamma_2+\alpha)I\\
\frac{dQ}{dt} &= \gamma_2 I-(\mu+\delta+\xi)Q
\end{aligned} \tag{2}$$

Let:

$$N_1 = S+E+I+Q$$

Thus, form the reduced model Eq. 2 we have:

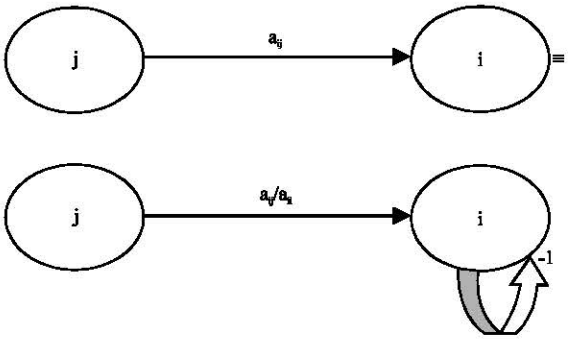

Fig. 2: Creating a trivial node

$$\frac{dN_1}{dt} = \wedge + \frac{\wedge\eta}{\mu} - N_1(\mu+\eta) - I(\delta+\alpha) - Q(\delta+\xi)$$

Form the Eq. 2, it can be seen that in the absence of the malicious objects I = 0 = Q, $N_1 \rightarrow \wedge/\mu$. Thus, $D_1 = ((S, E, I, Q): S \geq 0, E \geq 0, I \geq 0, Q \geq 0, S+E+I+Q \geq \wedge/\mu$ is a positively invariant region for model (Eq. 2) and it will is posed in D_1.

V Calculation basic reproduction number by di-graph reduction method: We use the notation as by De-Camino-Beck *et al.* (2009) Van Den Driessche and Watmough (2002) for an ODE disease transmission model which is assumed to have a Disease Free Equilibrium (DFE) in which all infected variables are zero and model without disease is assumed to be stable.

Consider the ODE system for the infected variables linearized about the DFE and write the coefficient matrix as F-V assumed to be irreducible where F contains new infection terms and V contains the terms representing transfer between compartments. From Van Den Driessche and Watmough (2002), F is (entry wise) non-negative, non zero and V is a non-singular M-matrix. Thus, the next generation matrix FV^{-1} is non negative and non zero. The basic reproduction number R_0 is defined as, $R_0 = \rho(FV^{-1})$ where ρ denotes the spectral radius.

Graph reduction rule associated with $F\lambda^{-1}$-V: Rule 1; (Creating a trivial node) to reduce the loop $-a_{ii}<0$ to -1 at node i, every arc entering i has weight divided by a_{ii}.

Rule 2; (Elimination of arcs through a trivial node) for a trivial node i on a path j→i→k,the two arcs are replaced by j→k with weight equal to the product of weights on arc j→i and i→k. Weights on multiple arcs j→k are added. If there are no more paths through the trivial node I, then it can be disregarded (Fig. 2 and 3).

Algorithm to compute R_0 from the digraph associated with $F\lambda^{-1}$-V: Consider the matrix $F\lambda^{-1}$ is irreducible, then

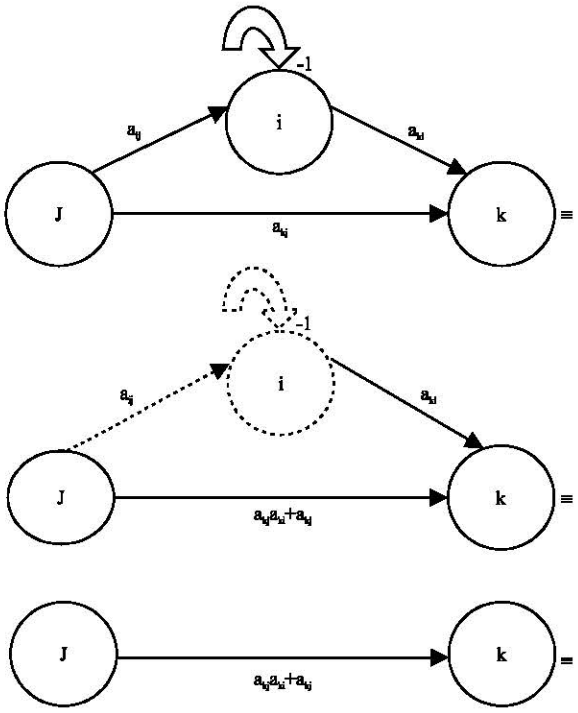

Fig. 3: Elimination of arcs through trivial node

draw the associated digraph with arc j→i if and only if the (i, j) entry of the matrix is nonzero. If j = i and (i, i) entry is -1, then i called a trivial node:

- Choose a node i with a loop
- Use rule 1 to make node i trivial
- Disregarded node i by rule 2
- Repeat steps 1-3 until only one node remains
- Set the weight of this loop to zero giving an equation for λ

Then, R_0 is the reciprocal of the smallest positive root x of the polynomial equation. Detail can be found by De-Camino-Bek *et al.* (2009) on a graph-theoretic method for the basis reproduction number in continuous time epidemiolological methods.

Calculation of basic reproduction number by graph reduction method in SEIQR e-Epidemic model: Consider the SEIQRS Model presented in Eq. 1 and:

$$F = \begin{bmatrix} 0 & \sigma S \\ 0 & 0 \end{bmatrix}, V = \begin{bmatrix} (\mu+\gamma_1) & 0 \\ -\gamma_1 & (\mu+\delta+\gamma_2+\alpha) \end{bmatrix}$$

With V non singular, Fig. 4 with nodes E, I shows the digraph representation of matrix $F\lambda^{-1}$-V and the detailed digraph reduction procedure to obtain R_0:

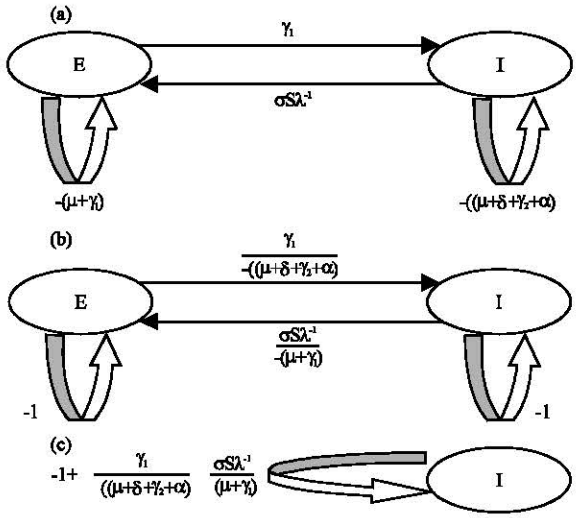

Fig. 4a-c): Graph reduction procedure applied to the SEIQRS Model

$$R_0 = \frac{\sigma\gamma_1 S}{(\mu+\gamma_1)(\delta+\alpha+\gamma_2+\mu)}$$

$$\equiv R_0 = \frac{\Lambda}{\mu}\frac{\sigma\gamma_1}{(\mu+\gamma_1)(\delta+\alpha+\gamma_2+\mu)}$$

Stability analysis of the disease-free equilibrium: Steady states of model (Eq. 2) are given as:

$$\begin{aligned} &\Lambda-\mu S-\frac{\sigma SI}{A}+\eta(\frac{\Lambda}{\mu}-S-E-I-Q)=0 \\ &\frac{\sigma SI}{A}-(\mu+\gamma_1)E=0 \\ &\gamma_1 E-(\mu+\delta+\gamma_2+\alpha)I=0 \\ &\gamma_2 I-(\mu+\delta+\xi)Q=0 \end{aligned} \quad (3)$$

System (Eq. 3) has always the malicious objects-free equilibrium $P_0 = (\Lambda/\mu, 0, 0, 0)$.

Lemma 1: If $R_0<1$, the malicious objects-free equilibrium P_0 is locally asymptotically stable.

Proof: The linearization of Model (Eq. 1):

$$\begin{bmatrix} -\mu & -\eta & -\sigma S & 0 & \eta \\ 0 & -(\mu+\gamma_1) & \sigma S & 0 & 0 \\ 0 & \gamma_1 & -(\mu+\delta+\gamma_2+\alpha) & 0 & 0 \\ 0 & 0 & \gamma_2 & -(\mu+\delta+\xi) & 0 \\ 0 & 0 & \alpha & \xi & -(\mu+\gamma_1) \end{bmatrix}$$

Gives negative eigen values:

$$\lambda = -(\mu+\eta),\ \lambda = -\mu,\ \lambda = -(\mu+\delta+\xi)$$

And other eigen values we will get from quadric polynomial:

$$\lambda^2+\lambda(2\mu+\gamma_1+\delta+\gamma_2+\alpha)+(\mu+\gamma_1)(\mu+\delta+\gamma_2+\alpha)-\sigma S\gamma_1 = 0$$

Rewrite equation:

$$\lambda^2+\lambda(2\mu+\gamma_1+\delta+\gamma_2+\alpha)+(\mu+\gamma_1)(\mu+\delta+\gamma_2+\alpha)(1-R_0) = 0$$

From this equation, we will get two eigen value having negative sign if $R_0<1$. Hence, by applying Routh-Herwitz criteria, P_0 is locally asymptotically stable.

Theorem 1: If $R_0<1$ then the malicious objects free equilibrium P_0 is globally asymptotically stable. Consider a Lyapunov function:

$$L = \gamma_1 E+(\mu+\gamma_1)I$$

$$L^1 = I(\mu+\gamma_1)(\mu+\delta+\gamma_2+\alpha)(R_0-1)$$

If $R_0<1$ then $L^1<0$ and $L^1 = 0$ only if $I = 0$ or $R^0 = 1$. The maximum invariant set in $\{(S, E, I, Q, R): L^1 = 0\}$ is singleton $\{P_0\}$. By Lasalle's invariance principle, P_0 is globally asymptotically stable in D_1 when $R_0 \le 1$.

Stability of the endemic equilibrium P*: Now, we try to investigate the local stability of the endemic equilibrium $P^*(S^*, E^*, I^*, Q^*, R^*)$. The unique endemic equilibrium is:

$$S^* = \frac{\Lambda}{\mu}\frac{1}{R_0}$$

$$E^* = \frac{\Lambda}{\mu+\gamma_1}[1-\frac{1}{R_0}]$$

$$I^* = \frac{\gamma_1 E^*}{(\mu+\delta+\gamma_2+\alpha)}$$

$$Q^* = \frac{\gamma_2}{\mu+\delta+\xi}I^*$$

$$R^* = \left[\frac{\xi\gamma_2}{(\mu+\mu)(\mu+\delta+\xi)}+\frac{\eta}{\mu}R_0\right]$$

For endemic analysis, we will take that compartment class who spread the disease that is $P^*(S^*, E^*, I^*, Q^*)$.

Theorem 2: If $R_0>1$, then the system Eq. 2 has a unique equilibrium $P^*(S^*, E^*, I^*, Q^*)$ which is locally asymptotically stable.

Proof: Linearizing system Eq. 2 at the equilibrium gives: $P^*(S^*, E^*, I^*, Q^*)$ gives:

$$E^* = \begin{bmatrix} -(\mu+\sigma I^*+\eta) & -\eta & -(\sigma S^*+\eta) & -\eta \\ \sigma I^* & -(\mu+\gamma_1) & \sigma S^* & 0 \\ 0 & \gamma_1 & -(\mu+\delta+\gamma_2+\alpha) & 0 \\ 0 & 0 & \gamma_2 & -(\mu+\delta+\xi) \end{bmatrix}$$

The characteristic equation of the E^* is:

$$F(\lambda) = \lambda^4+A\lambda^3+B\lambda^2+C\lambda+D = 0 \quad (4)$$

Where:

$$A = \mu I+\eta+3\mu+\gamma_1+2\delta+\gamma_2+\alpha+\xi)$$

$$B = -\sigma S\gamma_1+\eta\sigma I+(\mu I+\eta)(\mu+\gamma_1)+(\mu+\delta+\gamma_2+\alpha)$$
$$(\mu+\delta+\xi)+(\mu I+\eta+\mu+\gamma_1)(2\mu+2\delta+\gamma_2+\alpha+\xi)$$

$$C = \sigma S\gamma_1(\mu+\sigma I+\eta+\mu+\delta+\xi)+\eta\sigma I(2\mu+2\delta+\gamma_2+$$
$$\alpha+\xi)(\sigma S+\eta)(\sigma I)\gamma_1(\mu I+\eta+\mu+\gamma_1)(\mu+\delta+\gamma_2+\alpha)$$
$$(\mu+\delta+\xi)+(\mu I+\eta)(\mu+\gamma_1)(2\mu+2\delta+\gamma_2+\alpha+\xi)$$

$$D = -\sigma S\gamma_1(\mu+\sigma I+\eta)(\mu+\delta+\xi)+\eta\sigma I(2\mu+2\delta+\gamma_2+\alpha+\xi)$$
$$(\sigma S+\eta)(\sigma I\gamma_1)(\mu+\delta+\xi)+\eta\sigma I\gamma_1\gamma_2+(\mu+\delta+\gamma_2+\alpha)(\mu+\delta+\xi)$$

where, A-D positive constant. Now, Eq. 4 can be expressed as a product of two quadratic equations, i.e.,:

$$F(\lambda) = (\lambda^2+a\lambda+b)(\lambda^2+d\lambda+e)$$

Where:

$$\begin{aligned} a+d &= A \\ b+ad+e &= B \\ ae+bd &= C \\ be &= D \end{aligned} \quad (5)$$

Since, the coefficients C and D are generally much smaller than 'A' and 'B', the quantities d and e in Eq. 5 are much smaller than 'a' and 'b'. Hence, the first approximations of a, b, e and d, denoted by: a1 ,b1, e1, d1 and are written as:

$$\begin{aligned} a1 &\approx A>0 \\ b1 &\approx B>0 \end{aligned} \quad (6)$$

$$e1 \approx \frac{D}{b} \approx \frac{D}{B} > 0 \quad (7)$$

$$d1 \approx \frac{BC-AD}{B^2} > 0 \text{ if } R_0 > 1 \quad (8)$$

Hence, Eq. 8 can be written as:

$$(\lambda^2+A\lambda+B)(\lambda^2+\frac{BC-AD}{B^2}+\frac{D}{B})$$

Since, each product are stable therefore, Eq. 4 is stable if $R_0>1$ (Raymond, 2000).

Theorem: If $R_0>1$; then the infected equilibrium point E^* is globally asymptotically stable. The proof can be found by Wang *et al.* (2013) study on global stability in some SEIR Epidemic Models.

RESULTS AND DISCUSSION

Runge-Kutta Fehlberg fourth-fifth order method is employed to solve the system Eq. 1 and the behavior of the susceptible, exposed, infectious and quarantined nodes with respect to time are observed which is depicted in Fig. 5 (plotted in MATLAB) and we observe that the system is asymptotically stable.

The effect of Q on I and Q on R is also observed and is depicted in Fig. 6 and 7 (plotted in MATLAB). Quarantine of the nodes plays an important role for the recovery of the nodes. When the nodes are highly infected by different kinds of malicious objects, quarantine is one of the remedy. The quarantined nodes are then treated with anti-malicious software of latest signature and are kept under constant observation. The

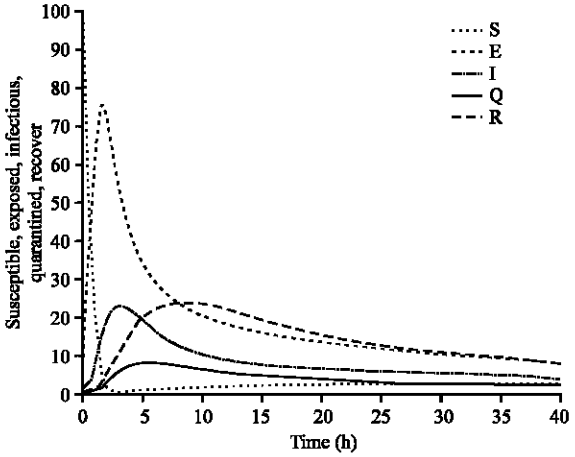

Fig. 5: Dynamical behavior of the system Eq. 1 with $\Lambda = 0.3$, $\mu = 0.1$, $\delta = 0.3$, $\eta = 0.2$, $\gamma_1 = 0.3$, $\delta = 0.2$, $\gamma_2 = 0.2$, $\alpha = 0.3$, $\xi = 0.2$, time series, S (t), E (t), I(t), Q(t) and R(t) (effect of quarantine Q on I) (SEIQR epidemic model)

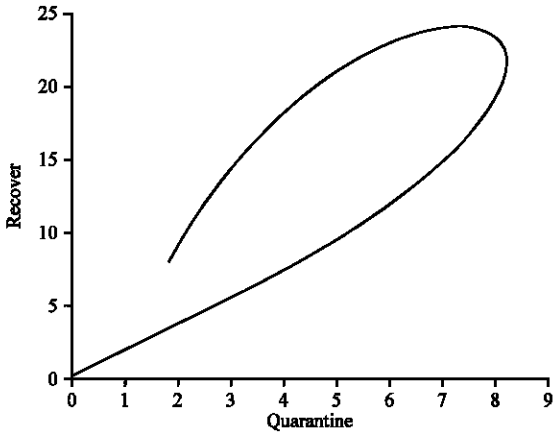

Fig. 6: Effect of quarantine nodes Q on recovered nodes R

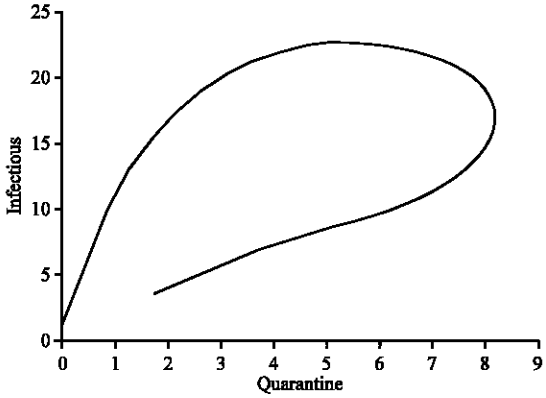

Fig. 7: Effect of Quarantine nodes Q on recovered nodes I

more, we quarantine the most infected nodes, more is the recovery; the lesser, we quarantine lesser is the recovery (which is very true in real situations). These can be observed in Fig. 6 and 7. Simulation result agrees with the real life situation.

The basic reproduction number R_0 is obtained and has been identified as a threshold parameter. If $R_0<1$, the malicious objects-free equilibrium P_0 is globally stable in the feasible region and the malicious objects always dies out. If $R_0>1$, a unique endemic equilibrium P* exists and is locally asymptotically stable.

CONCLUSION

Inspired by the biological epidemic compartment models, an e-SEIQRS Epidemic Model for the transmission and control of worms in computer network is developed. It has been shown that as the number of secondary infection which arises from primary infection is >1, that is, basic reproductive ratio $R_0>1$, then epidemic starts (that is, worms were able to pervade) and the worm endemic would die out when $R_0<1$. Numerical methods are employed to solve and simulate the system of equations developed. Time for the infection is simulated using real parametric values and its use might help in estimating the dynamic behavior of worms in nodes of real systems. Using real parametric values, we were able to show from the simulated results that the use of quarantine to control a worm not only decreases the endemic infective class size when R_0 remains above 1 but also, makes it easier to obtain R_0 leading to worm's extinction.

RECOMMENDATIONS

The future research will center on extending the model by taking certain time-delay parameters in different compartments.

NOMENCLATURE

$N(t)$ = Total number of nodes attached to a computer networks and interacting continuously with each other
$S(t)$ = Number of susceptible nodes in the computer networks and interacting continuously with each other
$E(t)$ = Number of exposed nodes in the computer networks and interacting continuously with each other
$I(t)$ = Number of infectious nodes in the computer networks and interacting continuously with each other
$Q(t)$ = Number of quarantine nodes in the computer networks and interacting continuously with each other
$R(t)$ = Number of recover nodes in the computer networks and interacting continuously with each other
Λ = Rate at which new nodes are attached to the computer network
μ = Natural death rate
δ = Death rate due to attack of malicious codes
σ = Per capita contact rate
γ_1 = Rates at which nodes leave the exposed class
γ_2 = The rates at which nodes leave infectious class
ξ = The rates at which nodes leave isolated classes
α = The rate at which the nodes leave the infectious class and directly enter the recovered class after treatment of antivirus software
η = The rate at which the nodes leave the recovered class and enter the susceptible class

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