e- SEIR EPIDEMIC MODEL FOR SPREAD OF MALICIOUS OBJECTS IN COMPUTER NETWORK.

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Abstract : We developed an e-SEIRS (susceptible, exposed, infectious, recovered) epidemic model for the transmission of malicious objects in computer network. Basic reproduction number R_0 , Equilibrium, and Locally stability are found. Numerical methods are employed to solve and simulate the system of equations developed. The simulated results may help us to understand the spread and malicious objects in computer network.

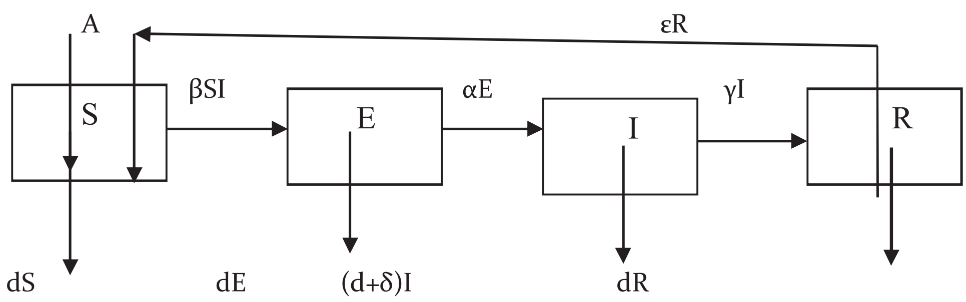
Keywords : computer network, basic reproduction number, epidemic model, locally stability.

Introduction : Developments of communication networks have made computers more and more important in our daily life. Different type of communication devices increased human dependence on computers. Thus the indefinitely number of existing malicious codes and their extreme destructivity appear as an important risk factor for large sectors and individuals. Since Transmission of malicious codes 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 [1.2, 3, 4,21,22, and 23]. Based on the classical work of Karmack and Mc Kendrick SIR model, [13,14,15]; dynamical models for malicious objects propagation were developed, providing estimations for temporal evolutions of infected nodes depending on network parameters considering topological aspects of the network[1,2,3,5,12,17.18] . The kind of approach was applied to e-mail propagation schemes [20] and modification of SIR models generated guides for infection prevention by using the concept of epidemiological threshold[1,2,3,6-8]. Richard W. T et al, 2005 propose an improved SEI (susceptible-exposed-infected) model to simulate virus propagation 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 [3,9,11,16,19,24-32] .

Mathematics Model And Assumptions

Consider the total computer nodes N (t) divided into four group, each of whom can either susceptible (S) or otherwise infected (I) with an infectious malicious object. Once the malicious objects enter into the network, the nodes become susceptible (S) and after a certain time delay the nodes become infected (E) and then it gets infectious (I). After it gets infectious, anti-malicious software is run which helps the nodes to recover (R) temporarily from the attack and provide temporary immunity to the node in the network.

The flow of malicious objects in the computer network is depicted in Figure. 1



(Figure. 1)

$$\begin{aligned} dS/dt &= A - \beta SI - dS + \varepsilon R \\ dE/dt &= \beta SI - dE - \alpha E \\ dI/dt &= \alpha E - (d+\delta) I - \gamma I \\ dR/dt &= \gamma I - dR - \varepsilon R \end{aligned} \qquad (1)$$

Where N (t) = S (t) + E (t) + I (t) + R (t) and

$dN/dt = dS/dt + dE/dt + dI/dt + dR/dt$ Consider a new set of equations which

Equlibrium And Stability Analysis

Disease free equilibrium is (A/d,0,0,0)

While endemic equilibrium is

$S^*=(d+\delta+\gamma)(d+\alpha)/\alpha\beta$

$E^* = (d+\delta+\gamma)/[\, d/\beta - A\alpha/(\, d+\alpha\ d+\delta+\gamma) + \alpha\varepsilon\gamma I/(\, d+\varepsilon\ d+\alpha\ d+\delta+\gamma)\,]$

$I^* =[\, d(\, d+\delta+\gamma)(\, d+\alpha)/\ \alpha\beta - A\,][\alpha\ (d+\varepsilon\ )/(d+\delta+\gamma\ )(d+\alpha\ )(d+\varepsilon\ )+\alpha\varepsilon\gamma]$

$R^* = \gamma I/\ (d+\varepsilon)$

Basic Reproduction Number

$$\begin{pmatrix} E' \\ I' \end{pmatrix}=\begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}\begin{pmatrix} E \\ I \end{pmatrix}-\begin{pmatrix} \alpha+d & 0 \\ -\alpha & (d+\delta+\gamma) \end{pmatrix}\begin{pmatrix} E \\ I \end{pmatrix}$$

$$F=\begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix} \text{ and } V=\begin{pmatrix} \alpha+d & 0 \\ -\alpha & (d+\delta+\gamma) \end{pmatrix}$$

$$V^{-1}=\begin{pmatrix} \dfrac{1}{(\alpha+d)} & 0 \\ \dfrac{\alpha}{(\alpha+d)(d+\delta+\gamma)} & \dfrac{1}{(d+\delta+\gamma)} \end{pmatrix}$$

$$\text{Therefore } FV^{-1}=\begin{pmatrix} \frac{\beta\alpha S_0}{(\alpha+d)(d+\delta+\gamma)} & \frac{\beta S_0}{(d+\delta+\gamma)} \\ 0 & 0 \end{pmatrix}$$

The spectral radius of above matrix is $\alpha\beta\ S_o/(\alpha+d)(d+\delta+\gamma)$

Therefore the Basic reproduction number is

$R_o = \alpha\beta\ S_o/\ (\alpha+d)(d+\delta+\gamma)$

5. Stability Analysis

Linearization of the model (1) is

$$E=\begin{pmatrix} -(\beta I+d) & 0 & -\beta S & \varepsilon \\ \beta I & -(d+\alpha) & \beta S & 0 \\ 0 & 0 & -(d+\delta+\gamma) & 0 \\ 0 & 0 & 0 & -(d+\varepsilon) \end{pmatrix}$$

Linearization of the model (1) at disease free equilibrium is

$$E_o=\begin{pmatrix} -d & 0 & -\beta\frac{A}{d} & \varepsilon \\ 0 & -(d+\alpha) & \beta\frac{A}{d} & 0 \\ 0 & 0 & -(d+\delta+\gamma) & 0 \\ 0 & 0 & 0 & -(d+\varepsilon) \end{pmatrix}$$

And the Eigen value of the above matrix is $-d$,$-(d+\alpha)$,$-(d+\delta+\gamma)$ and $-(d+\varepsilon)$

Therefore the model (1) at disease free equilibrium is Locally stable.

At endemic equilibrium the linearization of the model (1) is

$$E^*=\begin{pmatrix} -(\beta I^*+d) & 0 & -\beta S^* & \varepsilon \\ \beta I^* & -(d+\alpha) & \beta S^* & 0 \\ 0 & 0 & -(d+\delta+\gamma) & 0 \\ 0 & 0 & 0 & -(d+\varepsilon) \end{pmatrix}$$

And the Eigen value of the above matrix is $-(\beta I^* +d)$,$-(d+\alpha)$,$-(d+\delta+\gamma)$ and $-(d+\varepsilon)$

Science the all Eigen value of the matrix is negative the model (1) has Locally stable at endemic equilibrium

Model Parameters And Initial Values

Notation	Explanation	Initial value
N	Total number under consideration	10 000
S	Number of susceptible at time t	S(0)8,900
E	Total number in expose class	E(0) 1000
I	Number of infective at time t	I(0)100
A	Number of new born	70
R	Number of recovered people with immunity at time t	R(0)=0
α	Rate of node from E class to I class	0.6
β	Contact rate	0.0001
γ	Rate of node from I Class to R class	0.08
ε	Rate of node join to S class from R class	0.05
d	Natural death of the file	0.2
δ	Death of the node due to disease	0.2
R_o	Basic reproduction Number(endemic case)	1.390625
R_o	Basic reproduction Number(disease free case)	0.0546875

Numerical Discussions

Runge-Kutta Fehlberg fourth-fifth order method is employed to solve the system (1) and the behavior of the susceptible, exposed, infectious, and quarantined nodes with respect to time are observed which is depicted in Figure 2. From Figure 2 (plotted in MAPLE), we observe that the system is asymptotically stable.

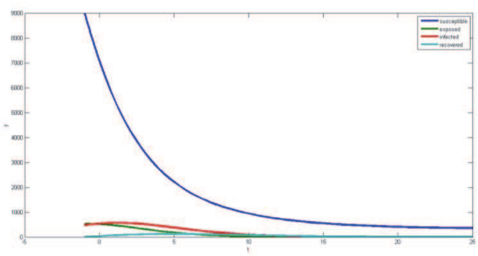


Figure 2

The basic reproduction number R_0 is obtained and has been identified as a threshold parameter. If $R_0 < 1$, the disease free equilibrium is locally stable in the feasible region E_o and the disease always dies out. If R_0 >1, a unique endemic equilibrium E* exists and is locally stable.

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