e-Epidemic Model On Highly Infectious Nodes in the Computer Network

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Abstract

In this paper, we have developed a compartmental e-Epidemic SIJR (Susceptible-Infectious-Highly Infectious-Recovered) model of viruses in a computer network with natural death (that is, crashing of nodes due to the reason other than the attack of viruses). The local asymptotically stability of the system has been discussed using the Jacobian and the explicit formula for basic reproduction number has been derived. Numerical methods and MATLAB are employed to solve and simulate the system of equations developed and analysis of the model gives remarkable exposure.

Key-words

e-Epidemic Model; Basic Reproduction Number; Asymptotically Stability; Virus

1. Introduction

The developments in cyber world With the increasing technology of Internet, the usage has drastically increased, offering functionalities and facilities. It has also thrown several challenges in the form of increasing attacks on cyber world leading to increasing concerns over cyber defense to safeguard the valuable information from certain malicious agents over the Internet. Towards this goal it makes us necessary to study and understand the different type of viruses and develop mathematical models to represent their behavior. Viruses behave like infectious diseases and are epidemic in nature. The mathematical models generalize to represent the behavior of numerous viruses. The generalized model will be incorporated into a cyber defense system to proactively safeguard the information and information interchange.

The action of worms throughout a network can be studied by using epidemiological models for disease propagation [1-10]. Based on the Kermack and McKendrick SIR classical epidemic model [11-13], dynamical models for malicious objects propagation were proposed, providing estimations for temporal evolutions of nodes depending on network parameters considering topological aspects of the network[1-3, 14-17]. The kind of approach was applied to e-mail propagation schemes [18] and modification of SIR models generated guides for infection prevention by using the concept of epidemiological threshold [1-3, 19]. Richard and Mark [20] propose an improved SEI (susceptible-exposed-infected) model to simulate virus propagation. However, they do not show the length of latency and take into account the impact of anti-virus software. The model SEIR proposed by the authors [21] assumes that recovery hosts have a permanent immunization period with a certain probability, which is not consistent with real situation. In order to overcome limitation, Mishra and Saini [1] present an SEIRS model with latent and temporary immune periods, which can reveal common worm propagation. Recently, more research attention has been paid to the combination of virus propagation model and antivirus countermeasures to study the prevalence of virus, e.g., virus immunization [3, 22-26, 27]

2. Formulation of SIJR Model

In the computer network, to derive the model equation, the total number of computer nodes (N) is divided into four classes: Susceptible (S), Infectious (I), Highly Infectious (J), Recovered (R), that is,

$$S + I + J + R = N. \tag{1}$$

Our assumptions on the transmission of viruses in computer nodes are depicted in figure 1.

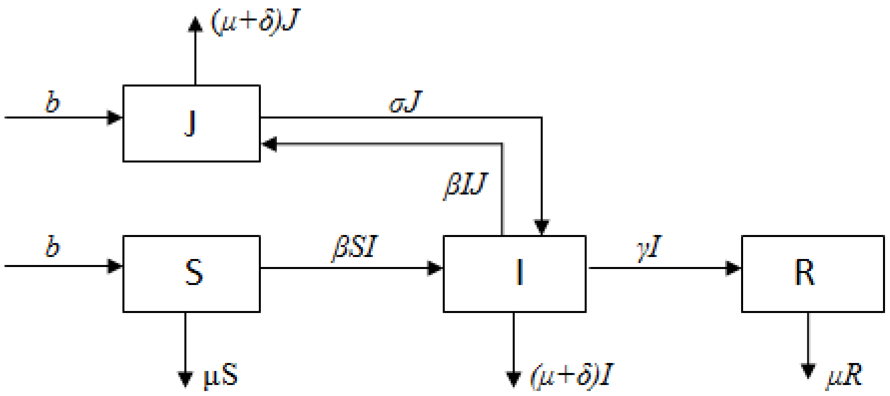

Figure 1: Schematic diagram for the flow of viruses in computer network

In this model, the flow of viruses is from class S to class I, class I to class J, class J to class I, class I to class R . The addition of new nodes is considered in classes S and J while the removal of nodes due to infection is only from classes I and J.The transmission between model classes can be expressed by the following system of differential equations:

$$\frac{dS}{dt} = b - \mu S - \beta SI$$

$$\frac{dI}{dt} = \beta SI + \sigma J - \beta IJ - \gamma I - (\mu+\delta)I$$

$$\frac{dJ}{dt} = \beta IJ - (\mu+\delta)J - \sigma J + b$$

$$\frac{dR}{dt} = \gamma I - \mu R \qquad (2)$$

Where, b is the birth rate (new nodes attached to the network), μ is the natural death rate (that is, crashing of the nodes due to the reason other than the attack of viruses), δ is the rate of crashing of the nodes due to the attack of viruses. Now, β is the rate coefficient of Susceptible class (for S to I), β is the rate coefficient of infectious class (for I to J), σ is the rate coefficient of highly infectious class (for J to I), γ is the rate coefficient of infectious class (for I to R).

3. Basic Reproduction Number (R_0)

Since the model has two infected classes (I & J), so, to get R_0, we take only two equations from the system (2) corresponding to these classes. That is,

$$\frac{dI}{dt} = \beta SI + \sigma J - \beta IJ - \gamma I - (\mu+\delta)I$$

$$\frac{dJ}{dt} = \beta IJ - (\mu+\delta)J - \sigma J + b$$

We now linearize these equations, we get, $\begin{bmatrix} \frac{dI}{dt} \\ \frac{dJ}{dt} \end{bmatrix}$ = (F – V)$\begin{bmatrix} I \\ J \end{bmatrix}$, where, F, a matrix of rates of new infection and V, a matrix of rates of transmission, are defined by, F = $\begin{bmatrix} \beta & 0 \\ 0 & 0 \end{bmatrix}$ and

V = $\begin{bmatrix} \mu+\delta+\gamma & -\sigma \\ 0 & \mu+\delta+\sigma \end{bmatrix}$.

Then the basic reproductive number R_0 is defined as the dominant eigen value of F V^{-1} .That is

$$R_0 = \frac{\beta}{(\mu+\delta+\gamma)} \tag{3}$$

4. Solutions and Stability

The system (2) is defined on the closed, positive invariant set D = {(S, I, J, R); S, I, J, R ≥ 0 : $S + I + J + R = N$} which has two possible equilibriums, first, the virus free equilibrium,

D_0 = (N, 0, 0, 0) and second, the endemic equilibrium $D^* = (S^*, I^*, J^*, R^*)$ which is the interior of D and can be obtained by taking all the equations of system (2) equal to zero. That is, $S^* = \frac{b}{\mu+\beta I^*}$, $J^* = \frac{b}{\mu+\delta+\sigma-\beta I^*}$, $R^* = \frac{\gamma I^*}{\mu}$, and I^* can be obtained numerically by the given cubic equation together with the prescribed values of all parameters involved.

$$I^3\beta^2(\mu+\delta+\gamma) - I^2\beta[2b\beta+(\delta+\sigma)(\mu+\delta+\gamma)] + I[b\beta(\delta+2\sigma) - \mu(\mu+\delta+\sigma)(\mu+\delta+\gamma)] + b\mu\sigma = 0$$

Theorem 1: The system (2) is locally asymptotically stable if all its eigen values are negative.

Proof: By using system (2), the Jacobian can be taken as,

$$J = \begin{bmatrix} -\mu & 0 & 0 & 0 \\ 0 & -(\mu+\delta+\gamma) & \sigma & 0 \\ 0 & 0 & -(\mu+\delta+\sigma) & 0 \\ 0 & \gamma & 0 & -\mu \end{bmatrix}$$

Solving, we get the eigen values, $-\mu$, $-(\mu+\delta+\gamma)$, $-(\mu+\delta+\sigma)$, $-\mu$, which all are negative. So, the system (2) is locally asymptotically stable.

5. Conclusion

A compartmental e-Epidemic SIJR model for the transmission of viruses in computer network is formulated. We have assumed that the nodes have two levels of infection. On interaction with the infectious (I) nodes the infectious (J) nodes become highly infectious. By the help of basic reproduction number and the equilibrium points we have investigated that the more the system is susceptible, lesser the secondary infection will be there and vice – versa. Numerical methods and MATLAB are employed to solve and simulate the system (2) and the behavior of the different classes of nodes with respect to time are observed which is depicted in figures 2, 3, 4 and we observe that the system is asymptotically stable. The effect of I and R is also observed and is depicted in figure 3 & 5. Efforts to recover highly infectious nodes (J) make them less infectious while the infectious nodes (I) directly recover. The effect of J and R is also observed and is depicted in figure 4. Simulation result agrees with the real life situation.

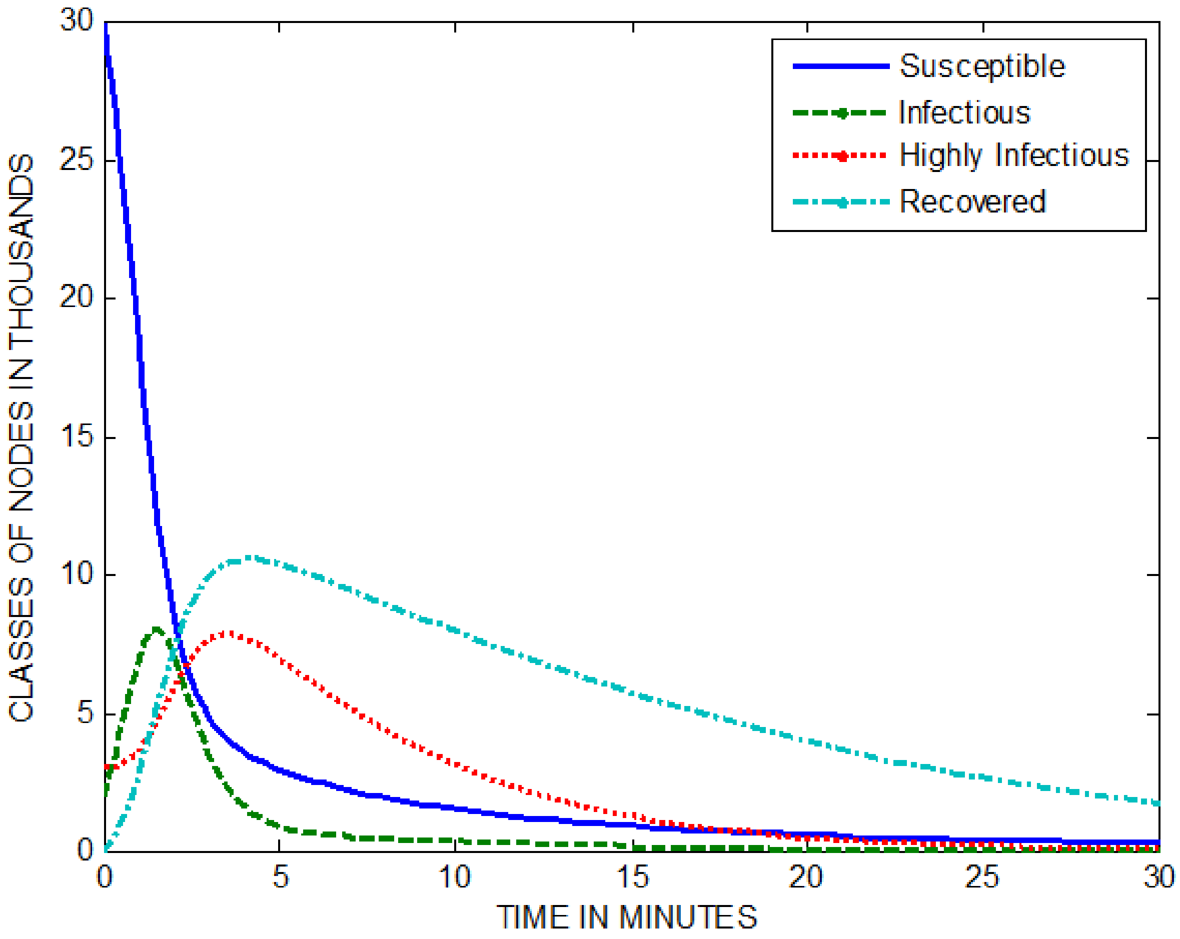

Figure 2: Dynamical behavior of the system (2) with the real parameters b = 0.01 ;μ = 0.09 ; β = 0.09 ; σ = 0.09 ; γ = 0.65 ; δ = 0.03.

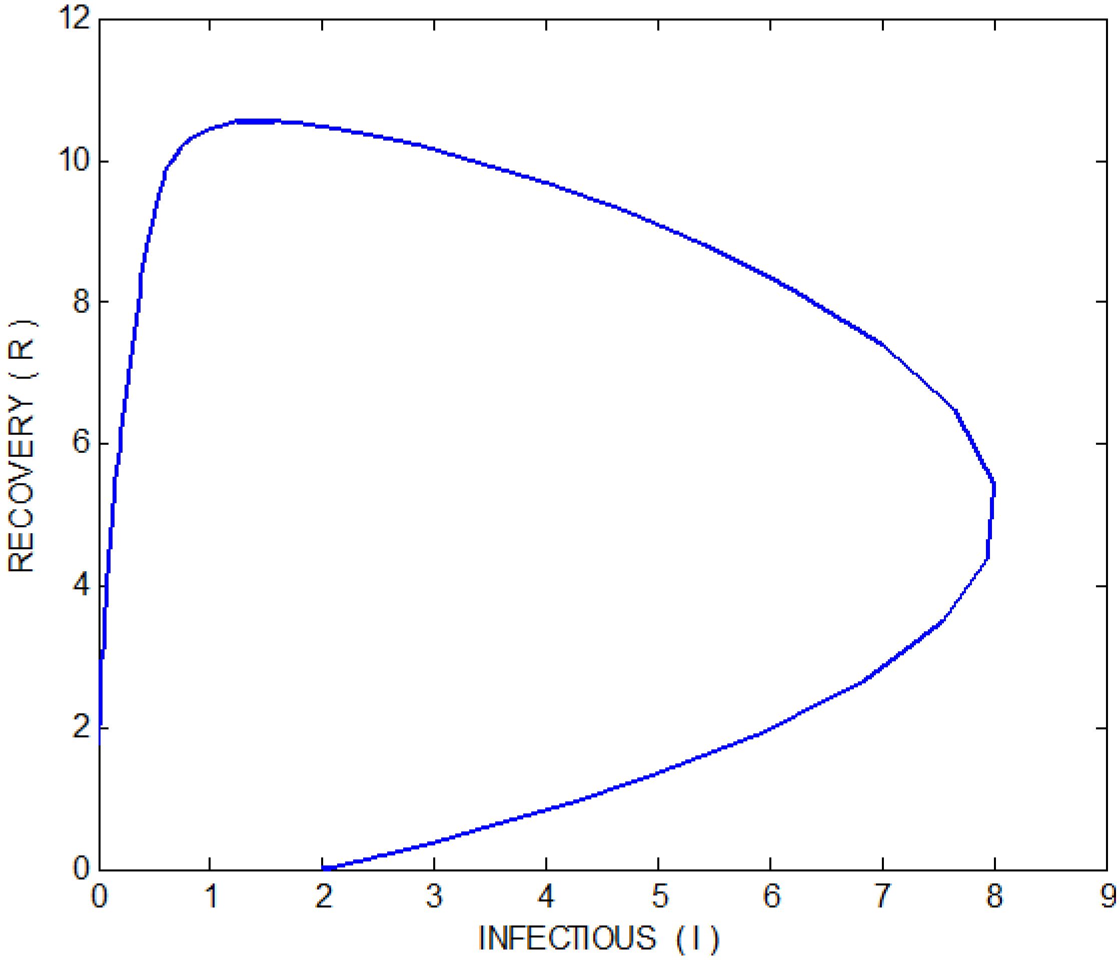

Figure 3: Dynamical behavior of the classes I and R with b = 0.01 ; $\mu = 0.09$; $\beta = 0.09$; $\sigma = 0.09$; $\gamma = 0.65$; $\delta = 0.03$

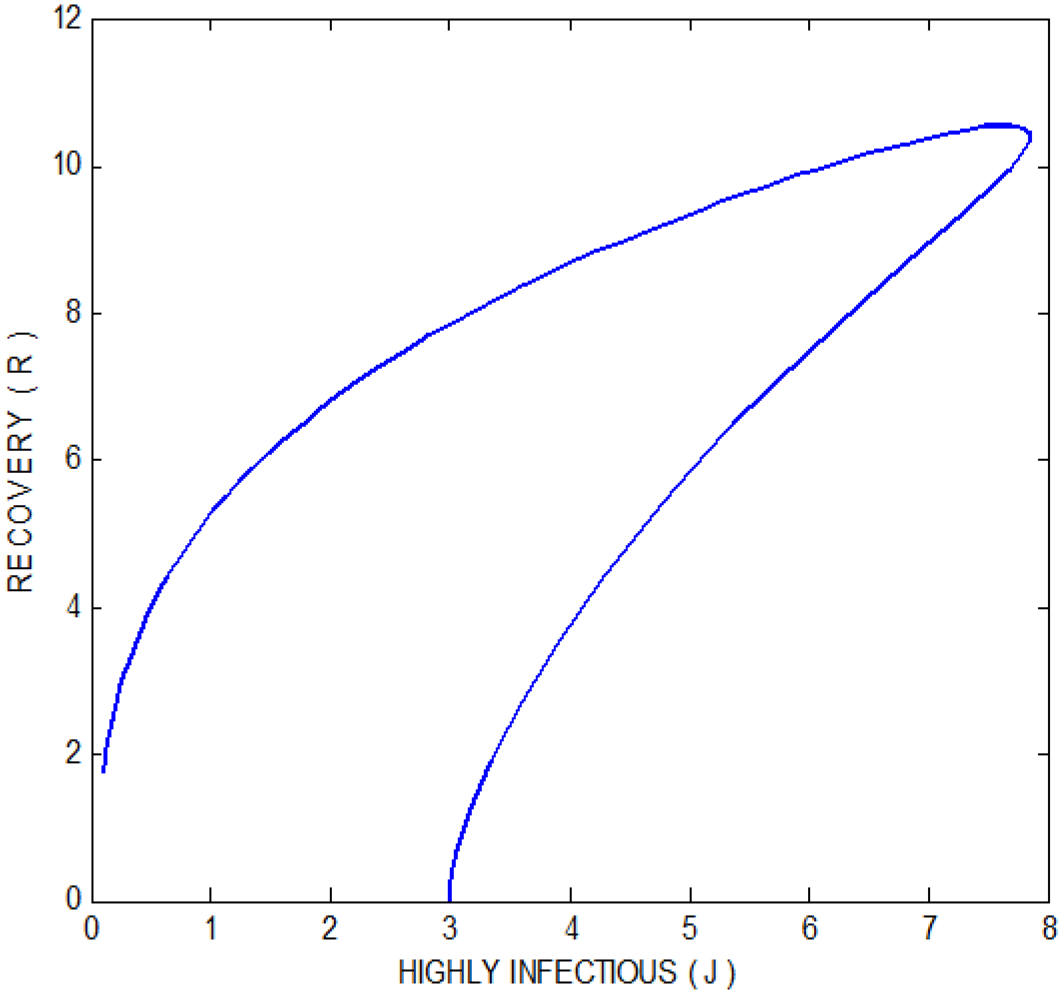

Figure 4: Dynamical behavior of the classes J and R with b = 0.01 ; μ = 0.09 ; β = 0.09 ; σ = 0.09 ; γ = 0.65 ; δ = 0.03.

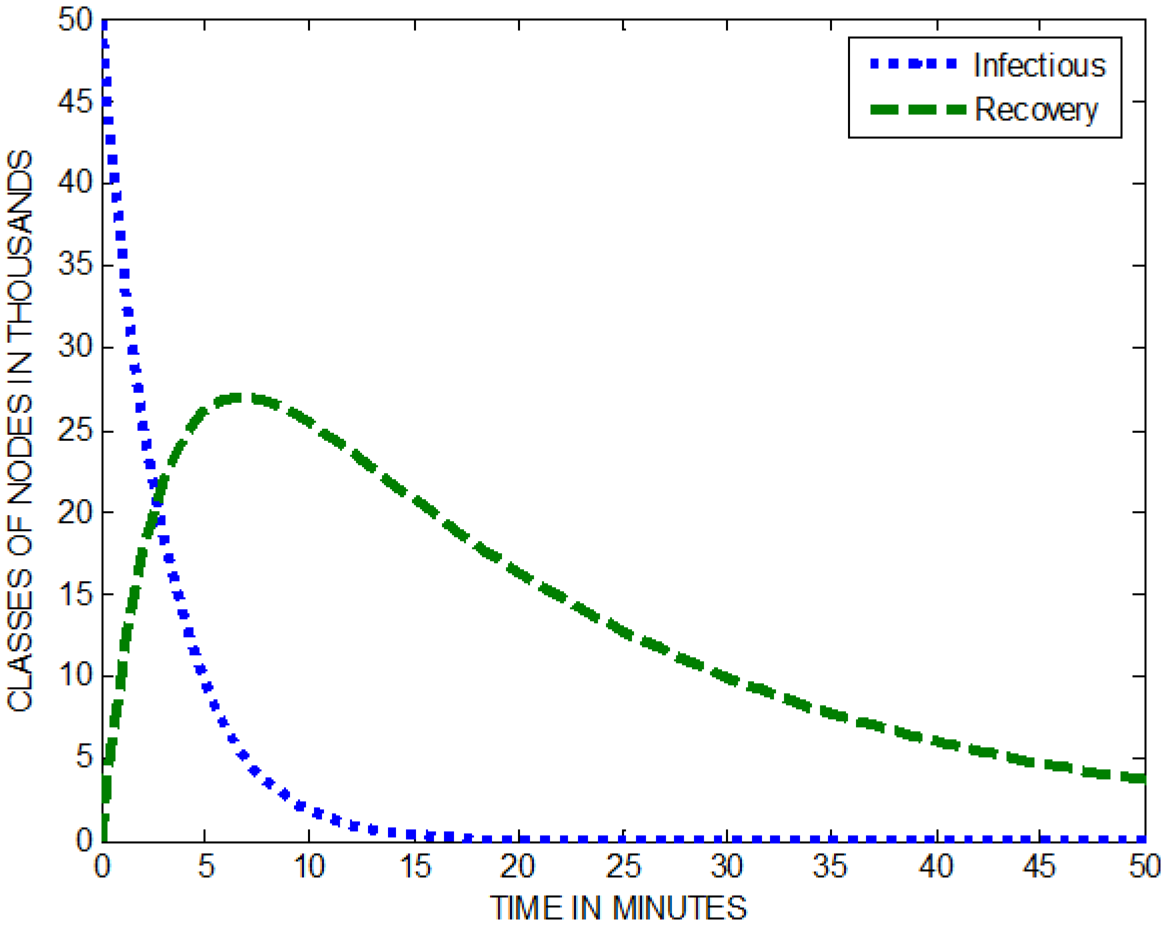

Figure 5: Dynamical behavior of the classes I and R with $\gamma = 0.25$; $\delta = 0.03$; $\mu = 0.05$;

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