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Transmission Dynamics Of Malicious Attacks In Network With Quarantine And Vertical Transmission

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Abstract: In this paper, we propose and analyze a susceptible- exposed-infectious-quarantine –vaccinated and susceptible (SEIQVS) epidemic model for malicious codes that spreads in the host node through vertical transmission. The basic reproduction number is found; under certain conditions on the incidence rate and treatment function. The model exhibits two equilibriums, namely, the disease-free equilibrium and the endemic equilibrium. The equilibrium analysis is presented and it is found that in each case the equilibrium points are locally asymptotically stable under certain conditions. Effect of quarantine and vaccination is critically analyzed under different parametric value. Numerical Simulation is performed to establish the analytical results.
Keywords: Epidemic model, Quarantine, Vaccination, Vertical transmission, local Stability.

1. INTRODUCTION:

A mathematical model which describes the dynamics of infectious disease have recently played a crucial role in the disease control in epidemiological aspect. Many authors have proposed various kinds of epidemic models to understand the mechanism of disease transmission [1,2,3,4], Biological epidemic disease are analogous to computer epidemic disease which are due to the attack of malicious objects in the network. Several computer epidemic models are developed in the recent years [5-13]. Actually, an infected host which is in latency can infect other hosts by means of some methods, e.g., vulnerability seeking. All the previous models do not take this passive infectivity into consideration. Recently, Yang et al. proposed some models [14,15,16], by considering the fact that a host immediately possesses infectivity once it is infected. These models, however, assume that exposed hosts and infected hosts have the same infectivity [17].

We propose susceptible- exposed-infectious-quarantine –vaccinated and susceptible computer epidemic model with vertical transmission in this paper.

2. BASIC DEFINITIONS:

i. ***Vertical Transmission:***When the main server of the computer network gets infected by the malicious objects, it may transmit the infection to the nodes which are communicating with the main server, said to be vertical transmission of the infection.
ii. ***Natural Death:***System in the computer network may crash due to hardware or software failure or physical damage said to be the natural death of the nodes.
iii. ***Death Due To Disease:***If a system crashes due to attack of malicious objects it is termed as death due to disease.
iv. ***Vaccination:***For the recovery of nodes in the network due to attack of malicious objects antivirus software is run in the system to makes the system immune, termed to be Vaccination.

3. THE MATHEMATICAL MODEL AND FORMULATION:

The schematic description of our model is depicted figure1

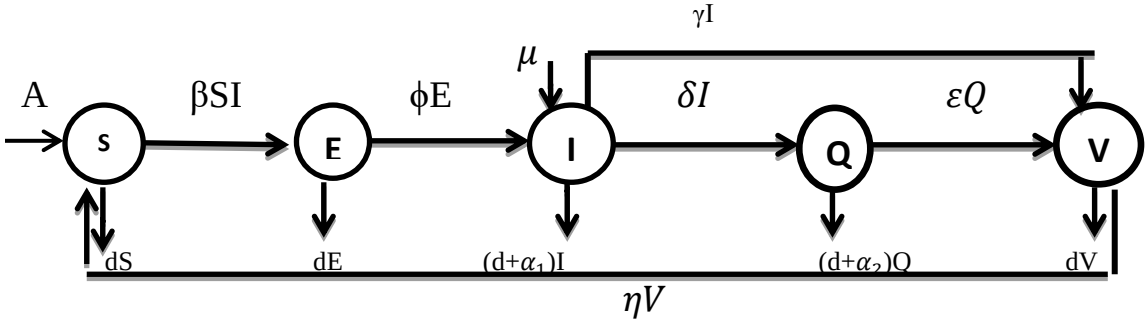

Figure 1: Schematic representation of transmission dynamics of malicious attacks in network with Quarantine and Vertical transmission

Assumptions:

(1) We assume that all the nodes attached in the network are susceptible towards the attack of malicious objects.

(2) β is the infectivity rate through which proportion of susceptible nodes become exposed. i.e. these node are infected but not infectious.

(3) μ is vertical transmission rate through which, the malicious objects transmit through main server to end user.

The transfer diagram leads to the following system of differential equations from figure1:

$$\left.\begin{aligned}
\frac{dS}{dt} &= A - \beta SI - dS + \eta V \\
\frac{dE}{dt} &= \beta SI - (d+\phi)E \\
\frac{dI}{dt} &= \phi E - (d + \alpha_1 + \gamma + \delta - \mu)I \\
\frac{dQ}{dt} &= \delta I - (d + \alpha_2 + \varepsilon)Q \\
\frac{dV}{dt} &= \varepsilon Q + \gamma I - (d+\eta)V
\end{aligned}\right\} \quad (1)$$

N(t)= S(t)+E(t)+I(t)+Q(t)+V(t)

Table 1: Nomenclature

Symbol	Description
A	Recruitment rate of susceptible class
S	Nodes in the susceptible class at any time t
E	Nodes in the exposed class at any time t
I	Nodes in the infectious class at any time t.
Q	Node in quarantine class at any time t.
V	Node in vaccination class at any time t.
$\boldsymbol{\beta}$	Infectivity contact rate
$\boldsymbol{\alpha}$	Natural death rate
$\boldsymbol{\gamma}$	Rate of infectious to vaccination class
$\boldsymbol{\delta}$	Rate of infectious class to quarantine class
$\boldsymbol{\varepsilon}$	Rate of quarantine class to vaccinated class
$\boldsymbol{\eta}$	Susceptible after vaccination
$\boldsymbol{\phi}$	Rate of exposed class to infectious class
$\boldsymbol{\mu}$	Vertical transmission rate
d	Natural death rate which is constant.
α_i	Disease death rate; i=1,

4. STABILITY ANALYSIS:

For the equilibrium points

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dV}{dt} = 0$$

We have five equilibrium points given by $P_0 = (A, 0,0,0,0)$ the disease-free equilibrium points of the system (1) and the unique endemic equilibrium points $P^* = (S^*, E^*, I^*, Q^*, V^*), where$

$$S^* = \frac{(d + \alpha_1 + \gamma + \delta - \mu)}{\beta}$$

$$E^* = \frac{(d + \alpha_1 + \gamma + \delta - \mu)(d+\phi)}{\delta\phi(\phi - 1)}$$

$$I^* = \frac{(d+\phi)}{\delta\phi(\phi-1)}$$

$$Q^* = \frac{(d+\phi)}{(d + \alpha_2 + \varepsilon)(d+\phi)}$$

$$V^* = \frac{\frac{(d+\phi)}{(\phi-1)}\left\{\frac{\varepsilon}{(d+\alpha_2+\varepsilon)} + \frac{\gamma}{\delta}\right\}}{(d+\eta)}$$

Reproduction Number:
The basic reproduction number,R_0 is defined as the expected number of secondary infections produced by an index case in a completely susceptible node.

R_0 is obtained by using R_0=FV^{-1}

$$F=\begin{bmatrix}\phi & 0 & 0\\ 0 & 0 & 0\\ 0 & 0 & 0\end{bmatrix},$$

V=
$$\begin{bmatrix}-(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & -(d+\phi) & 0\\ \delta & 0 & -(d+\alpha_2+\varepsilon)\end{bmatrix}$$

Thus,

$$R_0=\frac{\phi}{(d+\alpha_1+\gamma+\delta-\mu)}$$

3.1 Theorem. The disease-free equilibrium of the system is locally stable if $R_0<1$ and unstable if $R_0>1$.

Proof: We consider the following equations

$$\begin{aligned}F_1&=A-\beta SI-dS+\eta V\\ F_2&=\beta SI-(d+\phi)E\\ F_3&=\phi E-(d+\alpha_1+\gamma+\delta-\mu\ )I\\ F_4&=\delta I-(d+\alpha_2+\varepsilon)Q\\ F_5&=\varepsilon Q+\gamma I-(d+\eta)V\end{aligned}$$

The variation matrix of the system (1) is given by

$$J=\begin{bmatrix}-\beta I-d & 0 & \beta S & 0 & \eta\\ \beta I & -(d+\phi) & \beta S & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)\end{bmatrix}$$

At the equilibrium point $P_0=(A,0,0,0,0)$ the Jacobian matrix becomes

$$J=\begin{bmatrix}-d & 0 & \beta A & 0 & \eta\\ 0 & -(d+\phi) & \beta A & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)\end{bmatrix}$$

The characteristic equation $|J-\lambda I|=0$,can be written as

$$J=\begin{vmatrix}-d-\lambda & 0 & \beta A & 0 & \eta\\ 0 & -(d+\phi)-\lambda & \beta A & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu)-\lambda & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon)-\lambda & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)-\lambda\end{vmatrix}=0$$

$$J=\begin{vmatrix}-(\lambda+d) & 0 & \beta A & 0 & \eta\\ 0 & -(\lambda+d+\phi) & \beta A & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu)-\lambda & 0 & 0\\ 0 & 0 & \delta & -(\lambda+d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(\lambda+d+\eta)\end{vmatrix}=0$$

$$(\lambda+d)\ (\lambda+d+\phi)(\lambda+d+\alpha_2+\varepsilon)(\lambda+d+\eta)=0$$

It is evident that four Eigen values are negative and one Eigen value is negative if
$-(d+a_1+\gamma+\delta-\mu)<1$ or $\frac{\phi}{(d+\alpha_1+\gamma+\delta-\mu)}<1$
i.e.$R_0<1$
Therefore, all the Eigen value of the characteristic equation is negative. Hence the equilibrium point P_0 is locally asymptotically stable if $R_0<1$ and unstable if $R_0>1$.

3.2 Theorem. If $R_0>1$, the endemic equilibrium P^* is locally asymptotically stable.
Proof: we consider the following equations

$$\begin{aligned}F_1&=A-\beta SI-dS+\eta V\\ F_2&=\beta SI-(d+\phi)E\\ F_3&=\phi E-(d+\alpha_1+\gamma+\delta-\mu)I\\ F_4&=\delta I-(d+\alpha_2+\varepsilon)Q\\ F_5&=\varepsilon Q+\gamma I-(d+\eta)V\end{aligned}$$

The variation matrix of the system (1) is given by

$$J=\begin{bmatrix}-\beta I-d & 0 & \beta S & 0 & \eta\\ \beta I & -(d+\phi) & \beta S & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)\end{bmatrix}$$

At the endemic equilibrium point $P^*=S^*,E^*,I^*,Q^*,V^*$

$$J^*=\begin{bmatrix}-\beta I^*-d & 0 & \beta S^* & 0 & \eta\\ \beta I^* & -(d+\phi) & \beta S^* & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)\end{bmatrix}$$

Let $J_1=\beta I^*$
$J_2=\beta S^*$
Then,

$$J^*=\begin{bmatrix}-J_1-d & 0 & J_2 & 0 & \eta\\ J_1 & -(d+\phi) & J_2 & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu) & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta)\end{bmatrix}$$

The characteristic equation $|J^*-\lambda I|=0$ can be written as

$$\begin{vmatrix}-(J_1+d+\lambda) & 0 & J_2 & 0 & \eta\\ J_1 & -(d+\phi+\lambda) & J_2 & 0 & 0\\ 0 & \phi & -(d+\alpha_1+\gamma+\delta-\mu)-\lambda & 0 & 0\\ 0 & 0 & \delta & -(d+\alpha_2+\varepsilon+\lambda) & 0\\ 0 & 0 & \gamma & \varepsilon & -(d+\eta+\lambda)\end{vmatrix}=0$$

$(J_1 + d + \lambda)\ (d + \phi + \lambda)(d + \alpha_2 + \varepsilon + \lambda)(d + \eta + \lambda)$

$(J_1 + d + \lambda)(d + \phi + \lambda)\{-(d + \alpha_1 + \gamma + \delta - \mu + \lambda)(d + \alpha_2 + \varepsilon + \lambda)(d + \eta + \lambda)\}=0$

$\lambda = -(d + a_1 + \delta + \gamma - \mu)$
Or
$\lambda = \mu - (d + a_1 + \delta + \gamma)$

Where $\mu < 0$
$\mu < d + a_1 + \delta + \gamma$

Hence all five Eigen values are negative.
So $R_0 < 1$, Hence the equilibrium point P^* is locally asymptotically stable and if$R_0 > 1$, system is unstable.

5. NUMERICAL SIMULATIONS:

In order to verify the analytical results of the model, the numerical simulations of the model (1) are carried out using the following set of estimated parametric values:

Example1:

To understand the impact of Vaccination on infection node ,we assume that the following data set:

A=3,d=0.1, β=0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \delta = 0.5, \varepsilon = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \gamma = 0.40$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \delta = 0.5, \varepsilon = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \gamma = 0.60$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \delta = 0.5, \varepsilon = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \gamma = 0.80$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \delta = 0.5, \varepsilon = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \gamma = 0.99$;

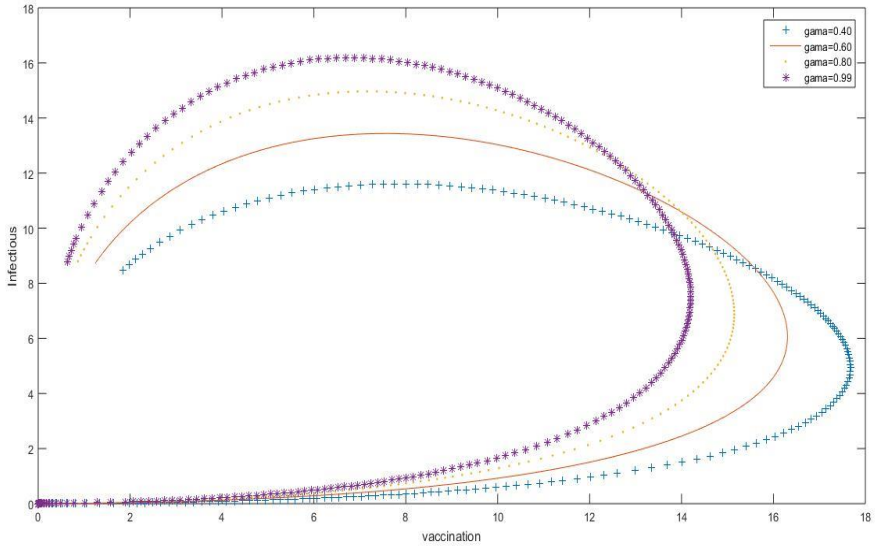

Figure 2: Impact of vaccination on infectious motes

We observe from figure 2 that is the rate of infections (γ) increases, the vaccination propagation also increases**.**

Example2:

To understand the impact of Vaccination on quarantine node, we assume that the following data set:

A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \varepsilon = 0.40$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \varepsilon = 0.60$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \varepsilon = 0.80$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1,\alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \eta = 0.5, \phi = 0.5, \mu = 0.5, \varepsilon = 0.99$;

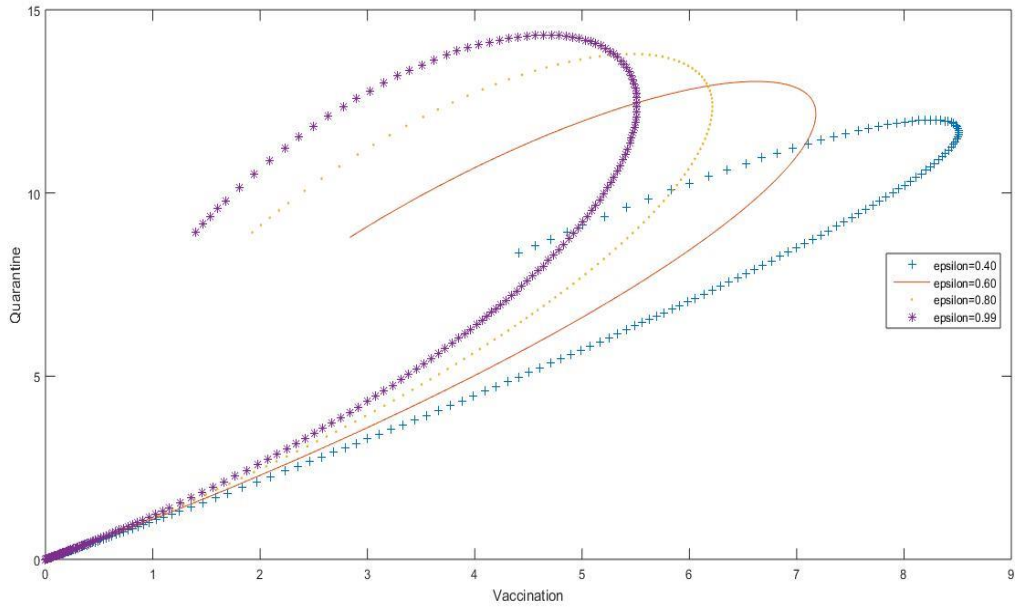

Figure 3: Time –series analysis of quarantine and Vaccination

From the figure 3 is clear that quarantine plays a vital role on making strategies for vaccination leading to the early recovery of the nodes, the more be quarantine the highly infectious node, the more is the possibility of the giving vaccination to the node leading towards the high recovery of system.

A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1, \alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \varepsilon = 0.5\eta = 0.5, \phi = 0.5, \mu = 0.10$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1, \alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \varepsilon = 0.5\eta = 0.5, \phi = 0.5, \mu = 0.20$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1, \alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \varepsilon = 0.5\eta = 0.5, \phi = 0.5, \mu = 0.40$;
A=3,d=0.1, β =0.5 ,$\alpha_1 = 0.1, \alpha_2 = 0.1, \gamma = 0.5, \delta = 0.5, \varepsilon = 0.5\eta = 0.5, \phi = 0.5, \mu = 0.60$;

Example3:
To understand the impact of vertical transmission on infectious node with respect to time, we assume that the following data set:

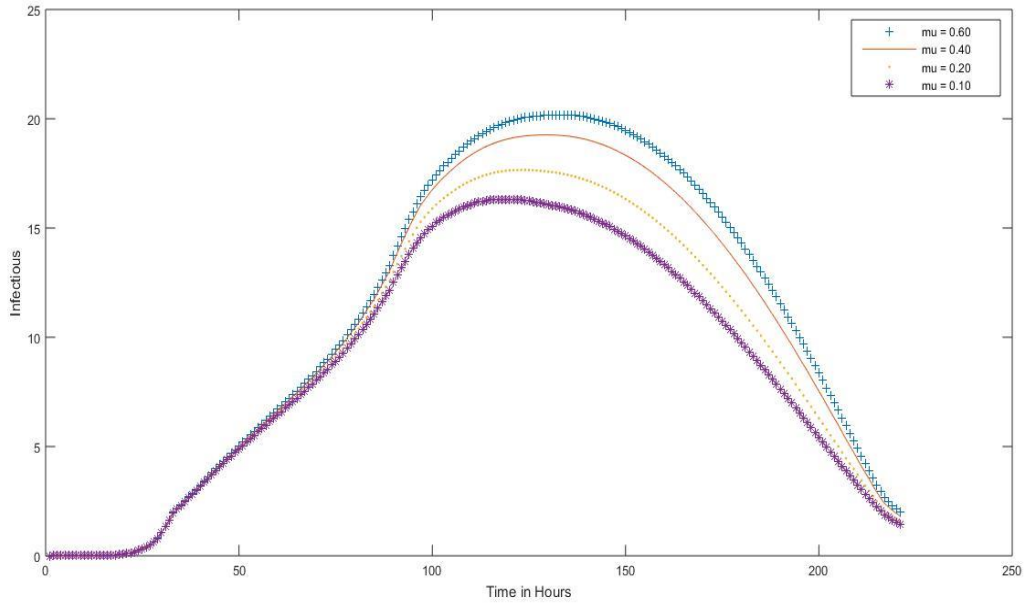

Figure 4 : Impact of vertical transmission on infectious class

We observe from figure 4 that is the rate of vertical transmission increases, the infections propagation also increases**.**

6. CONCLUSION:

In this paper, we have analyzed susceptible- exposed-infectious-quarantine –vaccinated and susceptible (SEIQVS) model with natural incidence rate and we observe that vaccination plays an important role to control the disease, when $R_0 < 1$, disease free equilibrium of the system is locally stable and if $R_0 > 1$, the endemic equilibrium is locally asymptotically stable.

By constructing a suitable linearization analysis. It is found that in each case the equilibrium points are locally asymptotically stable. Numerical simulations are also presented to illustrate our main results.

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