# ANALYSIS OF OPTIMAL MINIMIZATION OF MALICIOUS CODES: PRE QUARANTINE APPROACH

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## Introduction

It is often found that sharing information over a computer network for a days is extremely detrimental due to a number of malicious codes surfacing in the network and the attacking conduct of malicious codes is often undetectable by the traditional antivirus. Therefore, in order to safely store data in a network and share unmodified information, some mechanism needs to be developed to avoid malicious codes. The attacking nature of malicious codes must be studied to develop the required mechanism.

Although the biological virus and computer virus are absolutely different from each other, some of their attacking behaviour and characteristics resemble. However, the spread of malicious codes in a computer network is infectious in nature just like a biological virus in the population. Therefore, the behaviour of malicious codes across a network can be analysed using epidemic model for estimating spread of disease [1,2,5,9,12]. Non -linear incidence rate is another comparable character between a computer network and a biological model. A significant progress has been made in the research on non linear incident attack of malicious codes in a computer network [11, 14, 17, 18]. Because modern programming environments and the use of external devices can lead to rapidly spreading viruses for which an up-to-date approach turns out to be more difficult. As of late more research has been taken up for the prevalence of virus e.g., virus immunization [10,11,13, 15] and quarantine [3,4, 6,16].

In this article, we consider the impact of pre-quarantine and isolation on infected nodes and recovery nodes during the attack of malicious codes, for which we form a mathematical model namely SQEIJR e- epidemic models which is an extension article of SEIR models [1,8].

## Assumptions And Notations

1. $N(t)$: ‘Total number of nodes attached to the computer network’
2. $S(t)$: ‘Number of susceptible nodes in the computer network interacting with each other continuously’
3. $Q(t)$: ‘Number of pre-quarantine nodes attached to the computer network’
4. $E(t)$: ‘Number of exposed nodes attached to the computer network’
5. $I(t)$: ‘Number of infected nodes in the computer network’
6. $J(t)$: ‘Number of isolated nodes in the computer network’
7. $R(t)$: ‘Number of recovery nodes in the computer network interacting with each other continuously’
8. $\Lambda$ : ‘Rate at which new nodes entered in the network’
9. $\delta$ : ‘Natural death rate’
10. $\nu$ : ‘Death rate due to attack’
11. $\beta$ : ‘Per capita contact rate’
12. $\xi$ : ‘Rate of transformation of susceptible nodes to quarantine nodes’
13. $\alpha$ : ‘Rate at which nodes abandon the exposed class’
14. $\eta$ : ‘Rate at which nodes abandon the infectious class and enters the isolated class’
15. $\rho$: ‘Rate at which nodes abandon the isolated class and enters the recovered class after successful treatment of anti-virus software’

## MATHEMATICAL MODEL AND FORMULATION

To maintain a strategic distance from the total crash of the computer network,we divide the size of the population into subclasses of nodes that are susceptible, quarantine, exposed, infected, isolated, recover with sizes denoted by S(t), Q(t), E(t), I(t), J(t), R(t) respectively. We assume that,

1. Individual nodes join the susceptible class at the rate Λ.
2. The local density of the total population size N = S + Q + E + I + J + R may vary with time.
3. Infected nodes are entered into an infection free population of susceptible nodes.
4. 'βSI' number of newly infectives leave the susceptible class at time t and 'βQI' leave the quarantine class.
5. Quarantine, Exposed, Infective and Isolation nodes die at a rate 'd' due to the attack of malicious objects.
6. A proportion of susceptible class ξS move to Quarantine class is assumed as pre quarantine class.

The nodes become susceptible, once the malicious codes enter into the network and then the nodes become exposed or pre quarantine after certain period of time and consequently it gets infective (I). Once it becomes infective, the infectious nodes may keep as Isolation. Then, with the help of anti-malicious software, the nodes go to recovery class (R). Anti-malicious software temporarily protects the nodes from malicious code attacks and provides temporary protection for the nodes in the network. Based on the above assumptions on the dynamical transmission of the malicious codes, we develop a model depicted in Fig.1.

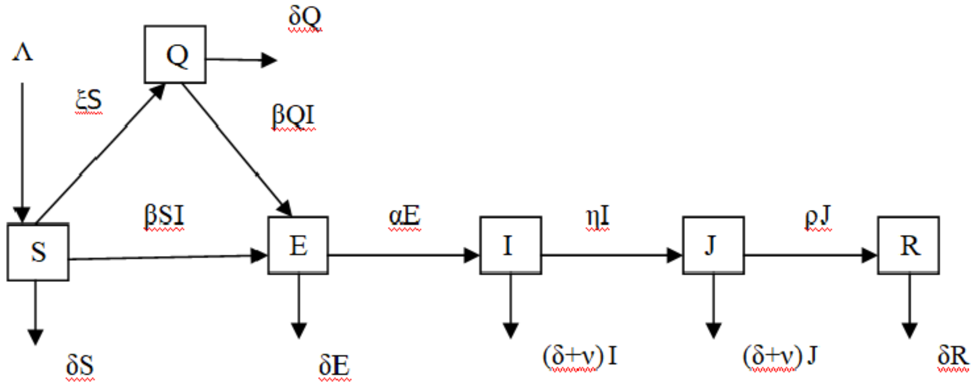

Figure 1.Dynamical Transfer Of Malicious Objects in Computer Network

The model equations are,

$$
\begin{aligned}
\frac{dS}{dt} &= \Lambda - \delta S - \xi S - \beta SI \\
\frac{dQ}{dt} &= \xi S - \delta Q - \beta QI \\
\frac{dE}{dt} &= \beta QI + \beta SI - (\delta + \alpha)E \\
\frac{dI}{dt} &= \alpha E - (\delta + \nu)I - \eta I \\
\frac{dJ}{dt} &= \eta I - (\delta + \nu)J - \rho J \\
\frac{dR}{dt} &= \rho J - \delta R
\end{aligned}
\qquad (1)
$$

Each parameters of the above model are positive constants.

Adding all the equations of the above system (1), We have,

$$\frac{dN}{dt} = \Lambda - \delta N - \nu\left(I + J\right)$$

We can say, from the above equation, in the absence of the malicious codes,

$$I = J = 0 \text{ and hence } N \to \frac{\Lambda}{\delta}$$

$$\text{So, } D = \left( S, Q, E, I, J, R;\ S \geq 0, Q \geq 0, E \geq 0, I \geq 0, J \geq 0, R \geq 0; S + Q + E + I + J + R \leq \frac{\Lambda}{\delta} \right)$$

is positively invariant region for the model.

**Basic Reprodection Number**

By using next generation matrix approach,

$$\begin{pmatrix} E' \\ I' \\ J' \end{pmatrix} = \begin{pmatrix} 0 & \beta(S+Q) & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} E \\ I \\ J \end{pmatrix} - \begin{pmatrix} \delta+\alpha & 0 & 0 \\ -\alpha & \delta+\nu+\eta & 0 \\ 0 & -\eta & \delta+\nu+\rho \end{pmatrix} \begin{pmatrix} E \\ I \\ J \end{pmatrix}$$

$$\text{Where, } F = \begin{pmatrix} 0 & \beta(S+Q) & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \quad and \quad V = \begin{pmatrix} \delta+\alpha & 0 & 0 \\ -\alpha & \delta+\nu+\eta & 0 \\ 0 & -\delta & \delta+\nu+\rho \end{pmatrix}$$

$$\text{So, } V^{-1} = \begin{pmatrix} \frac{1}{\delta+\alpha} & 0 & 0 \\ \frac{\alpha}{(\delta+\alpha)(\delta+\nu+\eta)} & \frac{1}{\delta+\nu+\eta} & 0 \\ \frac{\alpha\delta}{(\delta+\alpha)(\delta+\nu+\eta)(\delta+\nu+\rho)} & \frac{\delta}{(\delta+\nu+\eta)(\delta+\nu+\rho)} & \frac{1}{\delta+\nu+\rho} \end{pmatrix}$$

$$\text{Therefore, } FV^{-1} = \begin{pmatrix} \frac{\alpha\beta(S+Q)}{(\delta+\alpha)(\delta+\nu+\eta)} & \frac{\beta(S+Q)}{\delta+\nu+\eta} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

Hence the basic reproduction number is,

$$R_0 = \frac{\alpha\beta(S+Q)}{(\delta+\alpha)(\delta+\nu+\eta)} = \frac{\alpha\beta(S+Q)}{k_1 k_2}. \qquad (2)$$

Where, $k_1 = (\delta+\alpha)$ *and* $k_2 = (\delta+\nu+\eta)$.

**Equilibrium Point**

Virus free equilibrium point is,

$$V_0 = \left\{ \frac{\Lambda}{\delta+\xi}, \frac{\xi}{\delta}\frac{\Lambda}{\delta+\xi}, 0, 0, 0, 0 \right\} \qquad (3)$$

Endemic Equilibrium point is,
Steady state of the model is given as follows,

$$0 = \Lambda - \delta S - \xi S - \beta SI$$

$$0 = \xi S - \delta Q - \beta QI$$

$$0 = \beta QI + \beta SI - (\delta+\alpha)E \qquad (4)$$

$$0 = \alpha E - (\delta+\nu)I - \eta I$$

$$0 = \eta I - (\delta+\nu)J - \rho J$$

$$0 = \rho J - \delta R$$

The endemic equilibrium point is,

$$S* = \frac{\Lambda}{\delta+\xi+\beta I^*}$$

$$Q* = \frac{\xi}{\delta+\beta I^*}\frac{\Lambda}{\delta+\xi+\beta I^*}$$

$$E* = \frac{\delta+\nu+\eta}{\alpha} I^* \qquad (5)$$

$$J* = \frac{\eta}{\delta+\nu+\rho} I^*$$

$$R* = \frac{\rho}{\delta}\frac{\eta}{\delta+\nu+\rho} I^*$$

where $I^*$ is the positive root of the quadratic equation ,

$$aI^2 + bI + c = 0. \qquad (6)$$

where,

$$a = \beta^2(\delta+\alpha)(\delta+\nu+\eta)$$

$$b = \beta(\delta+\alpha)(\delta+\xi)(\delta+\nu+\eta) + \delta\beta(\delta+\alpha)(\delta+\nu+\eta) - \alpha\beta^2\Lambda$$

$$= \beta\left[(\delta+\alpha)(\delta+\xi)(\delta+\nu+\eta) + \delta(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)\right]$$

$$c = \delta(\delta+\alpha)(\delta+\xi)(\delta+\nu+\eta) - \alpha\beta\Lambda\xi - \alpha\delta\beta\Lambda$$

$$= (\delta+\xi)\left[\{\delta(\delta+\alpha)(\delta+\nu+\eta)\} - \alpha\beta\Lambda\right]$$

$$= (\delta+\xi)\left[\{\delta(\delta+\alpha)(\delta+\nu+\eta)\}(1-R_0)\right]$$

The endemic equilibrium for the model (1) can be obtained by solving for $I^*$ in (6) and then substituting the solutions in th expression (5). We can see that, in the quadratic equation (6), ‘a’ is always positive, the sign of ‘c’ depends on $R_0 > 1$ or $R_0 < 1$.

So, ‘c’ is positive, when $R_0 < 1$ and negative otherwise.

Now, the quadratic equation (6) will be analyzed for the possibility of two endemic equilibria, when $R_0 < 1$.

The following result is established.

**Theorem**

The model (1) has,

(i) a unique positive endemic equilibrium, if ($R_0 = 1$ and $b < 0$) or the discriminant $b^2 - 4ac = 0$.

(ii) a unique positive endemic equilibrium, if $c < 0$ if and only if $R_0 > 1$.

(iii) two endemic equilibrium if $c > 0$, $b < 0$ or, the discriminant $b^2 - 4ac > 0$

(iv) no positive endemic equilibria if $b > 0$ and $R_0 \leq 1$.

Hence, it is clear from the above that, case (ii) is applicable in the the model (1).

Therefore the model (1) has unique endemic equilibrium.

## Stability Analysis

**Theorem 1: The virus free equilibrium point is locally asymptotically stable in D, if $R_0 < 1$ and is unstable otherwise.**

Proof: The linearization of the model about the virus free equilibrium point gives,

$$J(S,Q,0,0,0,0) = \begin{bmatrix} -\delta-\xi & 0 & 0 & -\beta S & 0 & 0 \\ \xi & -\delta & 0 & -\beta Q & 0 & 0 \\ 0 & 0 & -\delta-\alpha & \beta(S+Q) & 0 & 0 \\ 0 & 0 & \alpha & -(\delta+\nu+\eta) & 0 & 0 \\ 0 & 0 & 0 & \eta & -(\delta+\nu+\rho) & 0 \\ 0 & 0 & 0 & 0 & \rho & -\delta \end{bmatrix}$$

The eigen values of the above matrix are, $\lambda_1 = -(\delta+\xi)$, $\lambda_2 = -\delta$.

and the other four eigen values can be obtained from the following two quadratic equations,

$$\lambda^2+(2\delta+\nu+\rho)\lambda+\delta(\delta+\nu+\rho)=0$$

$$\lambda^2+(2\delta+\alpha+\nu+\eta)\lambda+\{(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)\}=0$$

Hence, by applying Rowth-Hurwitz criteria $V_0$ is stable, if $R_0<1$ and if $R_0>1$, it is unstable.

**Theorem 2. The virus free equilibrium point, $V_0$ is globally asymptotically stable in D, if $R_0< 1$.**

Proof: Consider a Lyapnouv function,

$$L=\alpha E+(\delta+\alpha)I$$

$$\Rightarrow \frac{dL}{dt}=\{\alpha\beta(S+Q)-(\delta+\alpha)(\delta+\nu+\eta)\}I$$

$$=\left\{\frac{\alpha\beta(S+Q)}{(\delta+\alpha)(\delta+\nu+\eta)}-1\right\}(\delta+\alpha)(\delta+\nu+\eta)I$$

$$=(R_0-1)(\delta+\alpha)(\delta+\nu+\eta)I$$

Thus, if $R_0< 1$, then $\frac{dL}{dt}<0$.

**Theorem 3: If $R_0$ > 1, the unique endemic equilibrium is locally asymptotically stable.**

Proof: The jacobian matrix of the model (1) taking five compartment (S(t), Q(t), E(t), I(t), J(t)), as the R compartment does not spread the disease,

$$J^*=\begin{bmatrix} -(\delta+\xi+\beta I) & 0 & 0 & -\beta S & 0 \\ \xi & -(\delta+\beta I) & 0 & -\beta Q & 0 \\ \beta I & \beta I & -(\delta+\alpha) & \beta(S+Q) & 0 \\ 0 & 0 & \alpha & -(\delta+\nu+\eta) & 0 \\ 0 & 0 & 0 & & -(\delta+\nu+\rho) \end{bmatrix}$$

The characteristic equation of the above matrix is,

$$-(\delta+\nu+\rho+\lambda)\begin{bmatrix} \lambda^4+\{(3\delta+\beta I+\alpha+\nu+\eta)+(\delta+\xi+\beta I)\}\lambda^3+ \\ \left\{\begin{matrix}(\delta+\xi+\beta I)(3\delta+\beta I+\alpha+\nu+\eta)+ \\ ((\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+(\delta+\beta I)(2\delta+\alpha+\nu+\eta))\end{matrix}\right\}\lambda^2 \\ \left\{\begin{matrix}(\delta+\xi+\beta I)((\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+(\delta+\beta I)(2\delta+\alpha+\nu+\eta))+ \\ ((\delta+\beta I)(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+\alpha\beta^2 IQ+\alpha\beta SI)\end{matrix}\right\}\lambda+ \\ \{(\delta+\xi+\beta I)((\delta+\beta I)(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+\alpha\beta^2 IQ)+\alpha\beta SI(\delta+\xi+\beta I)\} \end{bmatrix}=0$$

Hence, from the above equation, one of the eigen value is $\lambda_1=-(\delta+\nu+\rho)$ and the other four eigen value can be obtained from the following equation,

$$\begin{bmatrix} \lambda^4 + \{(3\delta+\beta I+\alpha+\nu+\eta)+(\delta+\xi+\beta I)\}\lambda^3 + \\ \\ \left\{\begin{matrix}(\delta+\xi+\beta I)(3\delta+\beta I+\alpha+\nu+\eta)+ \\ ((\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+(\delta+\beta I)(2\delta+\alpha+\nu+\eta))\end{matrix}\right\}\lambda^2 + \\ \\ \left\{\begin{matrix}(\delta+\xi+\beta I)((\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+(\delta+\beta I)(2\delta+\alpha+\nu+\eta))+ \\ ((\delta+\beta I)(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+\alpha\beta^2 IQ+\alpha\beta SI)\end{matrix}\right\}\lambda + \\ \\ \{(\delta+\xi+\beta I)((\delta+\beta I)(\delta+\alpha)(\delta+\nu+\eta)(1-R_0)+\alpha\beta^2 IQ)+\alpha\beta SI(\delta+\xi+\beta I)\} \end{bmatrix} = 0$$

By applying the Rowth-Hurwitz criteria, all the eigen values of the above equations are negative, if the following conditions are satisfied,

$(\delta+\beta I)(2\delta+\alpha+\nu+\eta) > (\delta+\alpha)(\delta+\nu+\eta)(R_0-1)$

and,

$\alpha\beta^2 IQ > (\delta+\beta I)(\delta+\alpha)(\delta+\nu+\eta)(R_0-1)$

Therefore, the model (1) is locally asymptotically stable at endemic equilibrium point.

**Theorem 4: The unique EE of the model (1) is GAS in $D^0$, whenever $R_0$>1.**

**where** $(S(0),Q(0),E(0),I(0),J(0),R(0)) \in D^0$. **(the interior of the region D)**

Proof: Considering the model (1) and $R_0$>1, so that the associated unique endemic equilibrium of the model exists. We consider the following non-linear Lyapunov function of Goh-Volterra type:

$$Z = (S - S^* - S^*\log\frac{S}{S^*}) + (Q - Q^* - Q^*\log\frac{Q}{Q^*}) + (E - E^* - E^*\log\frac{E}{E^*}) + \frac{k_1}{\alpha}(I - I^* - I^*\log\frac{I}{I^*}) \quad (6)$$

$$\Rightarrow \dot{Z} = \left(\dot{S} - S^*\frac{\dot{S}}{S}\right) + \left(\dot{Q} - Q^*\frac{\dot{Q}}{Q}\right) + \left(\dot{E} - E^*\frac{\dot{E}}{E}\right) + \frac{k_1}{\alpha}\left(\dot{I} - I^*\frac{\dot{I}}{I}\right)$$

$$\begin{aligned} \Rightarrow \dot{Z} = & \left[\{\Lambda - (\delta+\xi)S - \beta SI\} - \frac{S^*}{S}\{\Lambda - (\delta+\xi)S - \beta SI\}\right] \\ & + \left[\{\xi S - (\delta+\beta I)Q\} - \frac{Q^*}{Q}\{\xi S - (\delta+\beta I)Q\}\right] \\ & + \left[\{\beta(S+Q)I - k_1 E\} - \frac{E^*}{E}\{\beta(S+Q)I - k_1 E\}\right] \qquad (7) \\ & + \frac{k_1}{\alpha}\left[\{\alpha E - k_2 I\} - \frac{I^*}{I}\{\alpha E - k_2 I\}\right] \end{aligned}$$

From the model (1) at the endemic steady state ,

$\Lambda = k_3 S^* + \beta S^* I^*.$

where, $k_1 = \dfrac{\beta(S^* + Q^*)I^*}{E^*}, k_2 = \dfrac{\alpha E^*}{I^*},\ k_3 = \delta + \xi$ .

From the above using the values of Λ, $k_1$ and $k_2$ and then adding and subtracting

$\dfrac{\beta Q^{*2} I^*}{Q}$ and $\beta Q^* I^*$,

we get,

$$\dot{Z} = k_3 S^*\left[2-\frac{S}{S^*}-\frac{S^*}{S}\right]+\beta S^* I^*\left[3-\frac{S^*}{S}-\frac{SE^*I}{S^*I^*E}-\frac{I^*E}{E^*I}\right]+\beta Q^* I^*\left[3-\frac{QE^*I}{Q^*I^*E}-\frac{I^*E}{E^*I}-\frac{Q^*}{Q}\right]$$
$$-\left[\frac{Q^*-Q}{Q}\right]\left[\xi S-\delta Q-\beta Q^* I^*\right] \qquad (8)$$

Finally since the arithmetic mean exceeds the geometric mean, the following inequality from (8) holds

$$\left[2-\frac{S}{S^*}-\frac{S^*}{S}\right]\leq 0,\ \left[3-\frac{S^*}{S}-\frac{SE^*I}{S^*I^*E}-\frac{I^*E}{E^*I}\right]\leq 0\ \ and\ \left[3-\frac{QE^*I}{Q^*I^*E}-\frac{I^*E}{E^*I}-\frac{Q^*}{Q}\right]\leq 0$$

Again as $\frac{dQ}{dt}=0$ in the endemic state, so the last term of the above equation (8) is zero.

Thus, we can say that $\dot{Z}\leq 0$

Hence, Z is a Lyapnov function in D and it follows by 'LaSalle's Invariance Principle' [19] that each solution of the equation with initial value $D^0$, gives rise to the unique endemic equilibrium (4) as $t\to\infty$ $for\ R_0>1$.

Therefore, the endemic equilibrium point is globally asymptotically stable.

## CONCLUSION AND FIGURE ANALYSIS

Here we build up a pre-quarantine e-SEIJR model for the attacking actions of malicious codes in a computer network by utilizing the Biological epidemic model. We consider the model's Basic reproduction number to grasp the attacking existence of malicious codes. At the equilibrium points, we analyze the model's asymptotic behaviours. MATLAB ODE 45 is employed for solving and simulating the system of equation; the simulated Fig.2 represents the dynamical behaviour of our developed model under different parametric values.

Fig.3 called attention to when we fix 0-4 unit of pre quarantine nodes there is no change on susceptible class for while implies the malicious codes won't move inside the network at that period while Fig.4 describes how susceptible class changes rapidly with few change in Isolation class.

Fig.5 and Fig.6 reflect the effect of quarantine and isolation on the exposed class. In Fig.5 if we vary 0-6 units of the quarantine class, the exposed class will increase to 25 units and then continue to decrease. This means that the outbreak will be the smaller duration, where as Fig.6 depicts the impact of isolation class on exposed class. In Fig.6, we can see, when we fix 0-6 units of isolation class the exposed class will increase up to 65 units then starts to decrease slowly , which means the longer period of an outbreak.

Fig.7 and Fig.8 show the impact of quarantine and isolation on the infected class, in Fig.7 in the event that we start to quarantining the nodes, the nodes in the infected class will diminish rapidly and when quarantine reach up to 30, the epidemic dies out while the impact of isolation on the infected class is depicted in Fig.8, which shows when the number of nodes in isolation class will increase, the nodes in infected class will also increase, this shows the epidemic present in the network for a longer period.

Fig.9 and Fig.10 reflect the effect of quarantine and isolation on the recovery class. In Fig.9, if we start quarantining the nodes, the nodes in recovery class will decrease quickly, whereas Fig.10 represent the impact of isolation on the recovery class, this indicates that if we increase the isolation class, the nodes in recovery class will also decrease gradually, which implies the epidemic will cease to exist subsequent to remaining in the system for some time spent.

From above discussion it is clear that pre quarantine approaches is a smart good idea of mitigating malicious code attack to the limit..The analysis will help the software organization in growing profoundly proficient antivirus programming to mitigate malicious code attacks.

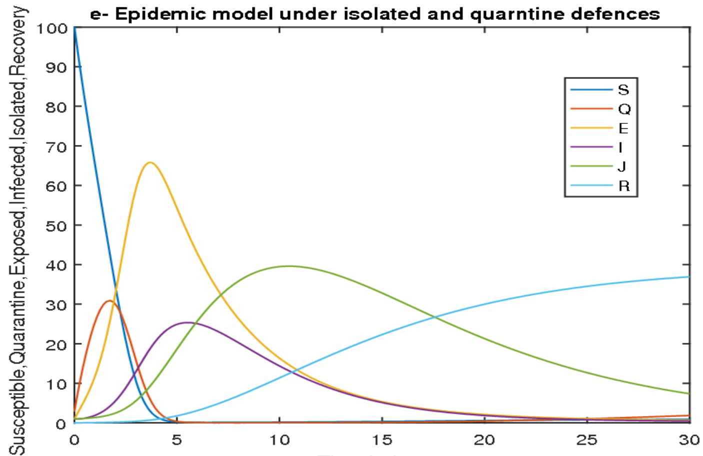

Figure 2

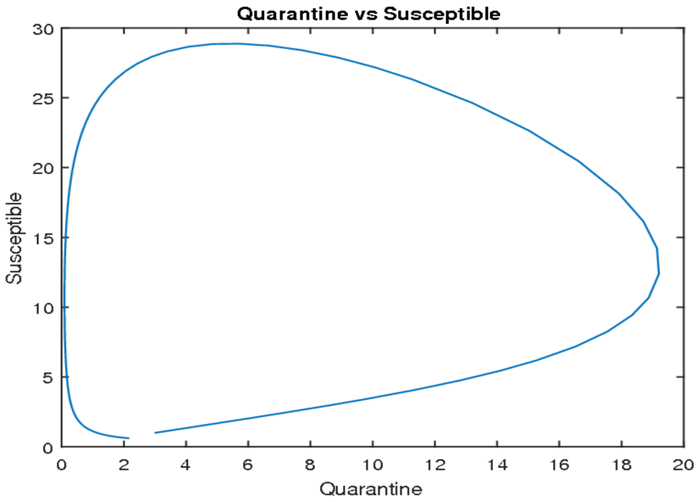

Figure 3

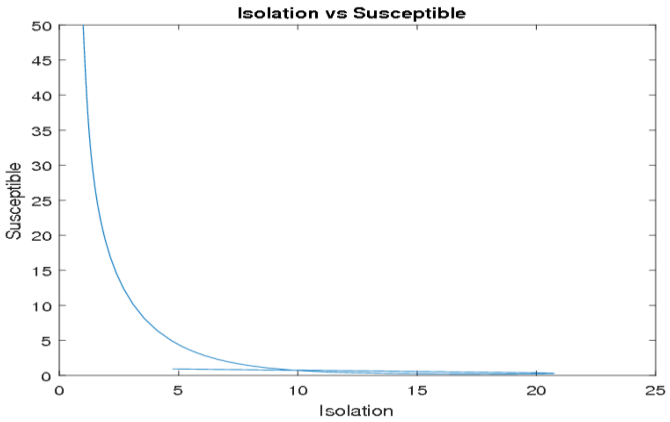

Figure 4

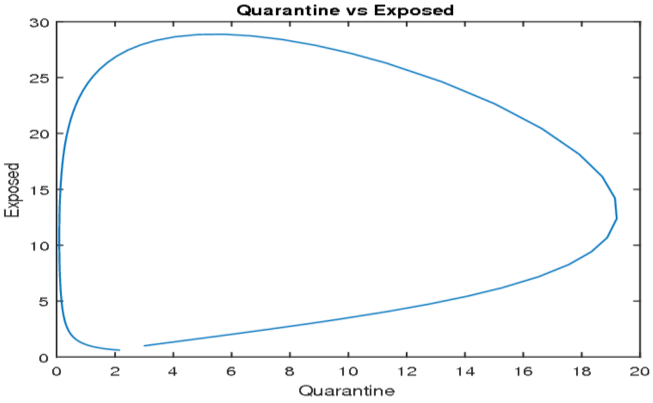

Figure 5

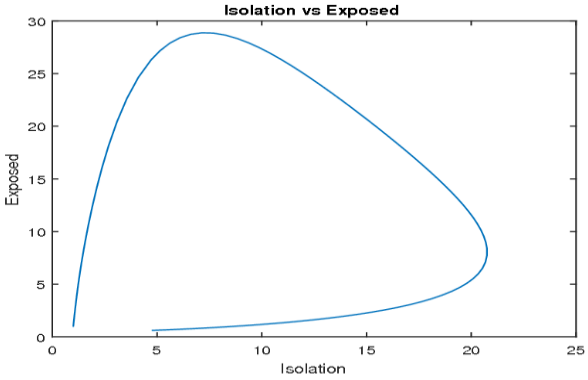

Figure 6

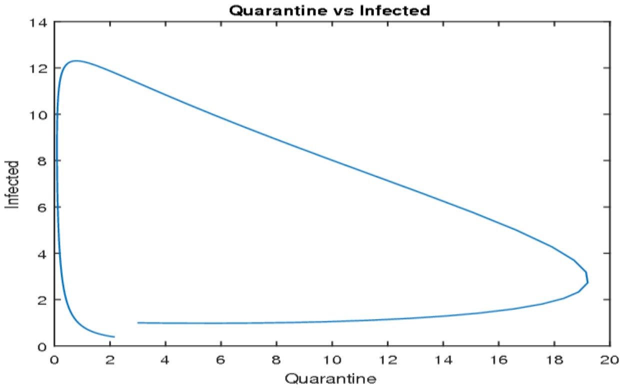

Figure 7

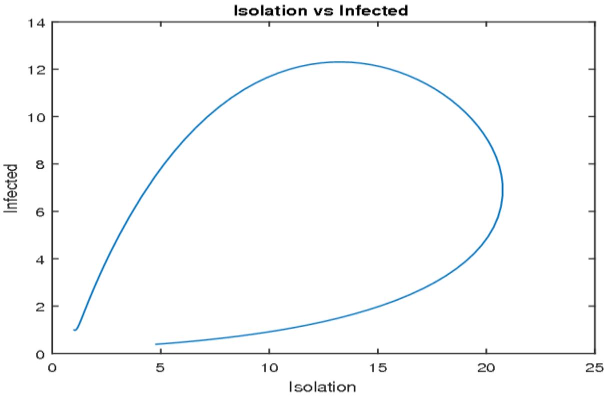

Figure 8

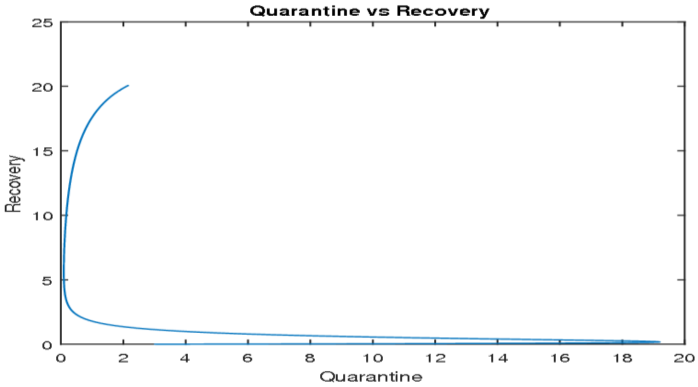

Figure 9

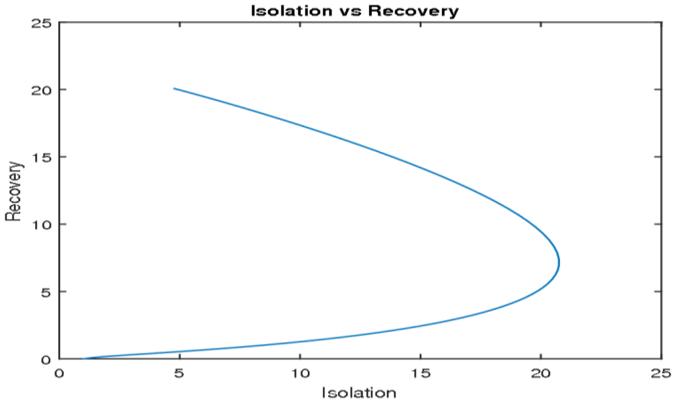

Figure 10