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Effect of Quarantine & Vaccination on Infectious Nodes in Computer Network

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Abstract – A compartmental epidemic model of viruses in a computer network with vaccination and natural death is formulated. A strong impact of vaccination in the computer network reduces rapidly the spreading behavior of worms and Quarantine plays an important role in the recovery of the infectious nodes. The stability of the result is stated in terms of the Jacobian of the system and the basic reproduction number is also well - defined. The effect of vaccination in the system is also analyzed. Numerical methods and MATLAB are employed to solve and simulate the system of equations developed and analysis of the model gives remarkable exposure.

Index Terms – Epidemic Model, Basic Reproduction Number, Vaccination, Stability, Computer Network.

1. INTRODUCTION

With rapid development of the internet and information technology, the popularity of the Internet and its applications, such as email, Facebook and Twitter, has significantly increased in recent years. The Internet has become an important platform for people sharing news, ideas and opinions, etc. Its openness also enables malicious information, such as malicious objects and other forms of misinformation to spread all around the world [1].There are different kinds of malicious objects such as: Worm, Virus, Trojan horse etc., which differ according to the way they attack computer systems and the malicious actions they perform. Viruses behave like infectious diseases and are epidemic in nature. The mathematical models generalize to represent the behavior of numerous viruses. It makes us necessary to study and understand the different type of malicious objects and develop mathematical models to represent their behavior.

Inspired by the intriguing analogies between computer viruses and their biological counterparts, Cohen [2] and Murray [3] inventively suggested that the techniques developed in the epidemic dynamics of infectious diseases should be exploited to study the spread of computer viruses. Later, Kephart and White [4] borrowed a biological epidemic model (the SIS model) to investigate the way that computer viruses spread on the Internet. The spreading behavior of malicious objects in networks can be studied by using different epidemiological models. Based on Kermack and McKendrick [5-7], SIR classical epidemic model, different epidemic models are used to study the spread of malware in network [8-12]. The authors [13] proposed the model SEIR, which assumes that recovery hosts have a permanent immunization period with a certain probability is not consistent with real situation. An SEIRS model with latent and temporary immune periods presented by Mishra and Saini [14] can reveal common worm propagation. Now a day, to study the prevalence of virus, e.g., virus immunization [15-21] and quarantine [22-25], the more research attention has been paid to the combination of virus propagation model and antivirus countermeasures. Mishra et al developed an SEIQRS model taking quarantine as one of the compartment in the epidemic models [26].

In this paper, we discuss SEIQRS-V model (susceptible-exposed-infectious-quarantine- recovered-susceptible) with vaccination to describe the dynamics of worm propagation.

The organization of the paper is as follows: Section 1 deals with introduction of the paper. Section 2 formulates the SEIQRS-V model. Section 3 gives its basic reproduction number R_0. Section 4 gives its solutions and stability. Section 5 presents Numerical Methods and simulation. Section 6 gives its conclusion.

Nomenclature:
S: Uninfected computers having no immunity.
E: Exposed computers that are susceptible to infection.

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I: Infected computers that have to be cure.

Q: Infected computers that are quarantined.

R: Uninfected computers having temporary immunity.

V: Vaccinated computers having susceptibility to infection.

R_0: Basic reproduction number.

The following assumptions are made to characterize the model:

- All newly connected computers are all virus free and susceptible.
- Each virus-free computer gets contact with an infected computer at a bilinear incidence rate βSI, where β is positive constant.
- Death rate other than the attack of malicious objects is constant μ.
- Exposed computers become infectious at nonnegative constant rate γ.
- Infectious computers are quarantined at nonnegative constant rate δ.
- Infectious computers are cured at nonnegative constant rate η.
- Quarantined computers are cured at nonnegative constant rate ε.
- Recovered computers become susceptibly virus-free again at nonnegative constant rate θ.
- Vaccinated computers become susceptibly virus-free again at nonnegative constant rate χ due to lack of updated anti-virus.

2. FORMULATION OF SEIQRS-V MODEL

In the computer network, to derive the model equation, the total number of computer nodes (N) is divided into six classes: Susceptible (S), Exposed (E), Infectious (I), Quarantined (Q), Recovered (R), Vaccinated (V) , that is,

$$S + E + I + Q + R + V = N. \qquad (1)$$

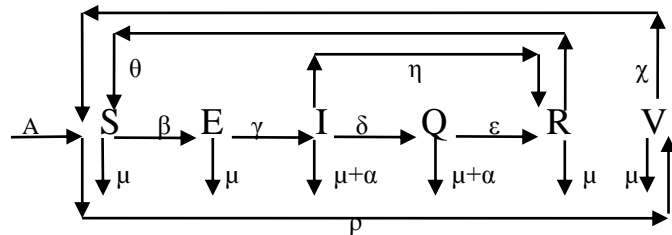Our assumptions on the transmission of viruses in computer nodes are depicted in figure 1.

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 E, class S to class V, class E to class I, class I to class Q, class I to class R, class Q to class R, class R to class S and class V to class S. The vaccinated nodes again enter into the susceptible

class due to the lack of updated anti – virus. The transmission between model classes can be expressed by the following system of differential equations:

$$\frac{dS}{dt} = A - \beta SI - \mu S - \rho S + \theta R + \chi V$$

$$\frac{dE}{dt} = \beta SI - \mu E - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \mu I - \alpha I - \delta I - \eta I$$

$$\frac{dQ}{dt} = \delta I - \mu Q - \alpha Q - \varepsilon Q$$

$$\frac{dR}{dt} = \varepsilon Q - \mu R - \theta R + \eta I$$

$$\frac{dV}{dt} = \rho S - \mu V - \chi V \qquad (2)$$

Where, *A* 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), *α* is the rate of crashing of the nodes due to the attack of viruses. Now, *ρ* is the rate coefficient of susceptible class (for S to V), *β* is the rate of contact (for S to E), *γ* is the rate coefficient of exposed class (for E to I), *δ* and *η* are the rate coefficients of infectious class (for I to Q) and (for I to R), *ε* is the rate coefficient of quarantined class (for Q to R), *θ* is the rate coefficient of recovery class (for R to S) and *χ* is the rate coefficient of vaccinated class (for V to S).

3. BASIC REPRODUCTION NUMBER (R_0)

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

$$\frac{dE}{dt} = \beta SI - \mu E - \gamma E$$

$$\frac{dI}{dt} = \gamma E - \mu I - \alpha I - \delta I - \eta I$$

$$\frac{dQ}{dt} = \delta I - \mu Q - \alpha Q - \varepsilon Q$$

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We now linearize these equations, we get,

$$\begin{bmatrix} \dfrac{dE}{dt} \\ \dfrac{dI}{dt} \\ \dfrac{dQ}{dt} \end{bmatrix} = (F - V) \begin{bmatrix} E \\ I \\ Q \end{bmatrix}, \text{ where, F, a matrix of rates of}$$

infection and V, a matrix of rates of transmission, are defined by,

$$F = \begin{bmatrix} 0 & \beta & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad \text{and}$$

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

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

$$R_0 = \frac{\beta\gamma}{(\mu+\gamma)(\mu+\alpha+\delta+\eta)} \qquad (3)$$

4. SOLUTION AND STABILITY

The system (2) is defined on the closed, positive invariant set $D = \{(S, E, I, Q, R, V); S, E, I, Q, R, V \geq 0 : S + E + I + Q + R + V = N\}$ which has two possible equilibriums, first, the virus free equilibrium, $D_0 = (N, 0, 0, 0, 0, 0)$ and second, the endemic equilibrium $D^* = (S^*, E^*, I^*, Q^*, R^*, V^*)$ which is the interior of D and can be obtained by taking all the equations of system (2) equal to zero. That is,

$$S^* = \frac{(\mu+\gamma)(\mu+\alpha+\delta+\eta)}{\beta\gamma} = \frac{1}{R_0},$$

$$E^* = \frac{\mu+\alpha+\delta+\eta}{\gamma} I^*, \qquad Q^* = \frac{\delta}{\mu+\alpha+\varepsilon} I^*,$$

$$R^* = \frac{\varepsilon\delta+\eta(\mu+\alpha+\varepsilon)}{(\mu+\theta)(\mu+\alpha+\varepsilon)} I^*, \quad V^* = \frac{\rho}{(\mu+\chi)R_0} \quad \text{and}$$

$$I^* = \frac{(\mu+\theta)(\mu+\alpha+\varepsilon)[\mu^2+(\rho+\chi)\mu-AR_0(\mu+\chi)]}{(\mu+\chi)[R_0\theta\varepsilon\delta+(\mu+\alpha+\varepsilon)(R_0\theta\eta-\beta\mu-\beta\theta)]}.$$

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,

$$J = \begin{bmatrix} -(\mu+\rho) & 0 & 0 & 0 & \theta & \chi \\ 0 & -(\mu+\gamma) & 0 & 0 & 0 & 0 \\ 0 & \gamma & -(\mu+\alpha+\delta+\eta) & 0 & 0 & 0 \\ 0 & 0 & \delta & -(\mu+\alpha+\varepsilon) & 0 & 0 \\ 0 & 0 & \eta & \varepsilon & -(\mu+\theta) & 0 \\ \rho & 0 & 0 & 0 & 0 & -(\mu+\chi) \end{bmatrix}$$

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

5. NUMERICAL METHODS AND SIMULATION

Runge-Kutta method of order 4 and MATLAB are employed to solve and simulate the system (2). The behavior of susceptible, exposed, infectious, recovered, quarantine and vaccination class with respect to time are shown in figure 2. The network is assumed to have initial values: S=30; E=5; I=2; Q=0; R=0; V=0. The effect of Quarantine class and vaccination class are observed on different classes as depicted in figure 3 and figure 4. Quarantine plays an important role in the recovery of the nodes.
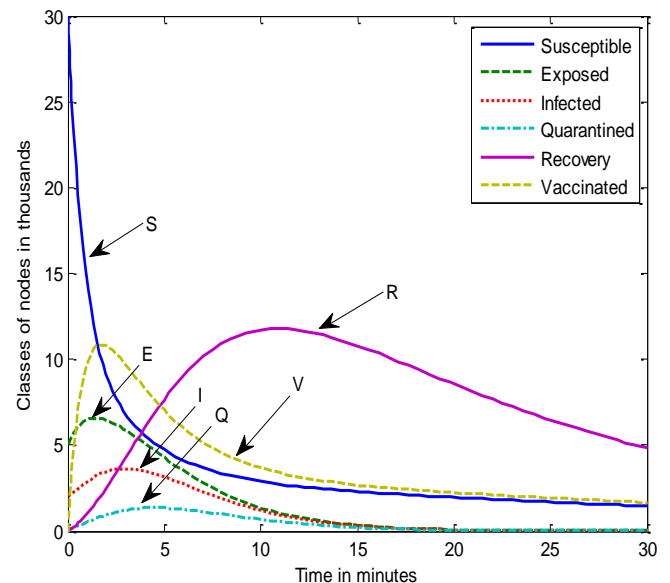

Figure 2 Dynamical behavior of the system (2) with the real parameters A=0.01; $\varepsilon = 0.65$; $\mu = 0.05$; $\gamma = 0.45$; $\alpha = 0.035$; $\eta = 0.35$; $\delta = 0.3$; $\beta = 0.09$; $\theta = 0.01$; $\chi = 0.55$; $\rho = 0.65$.
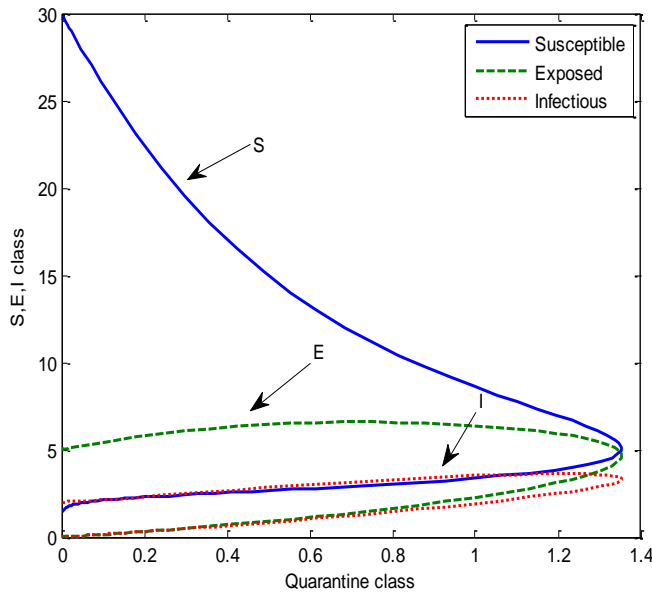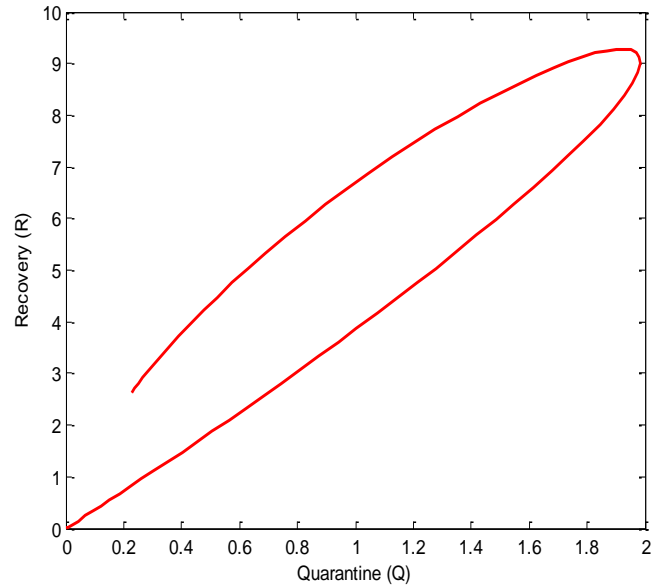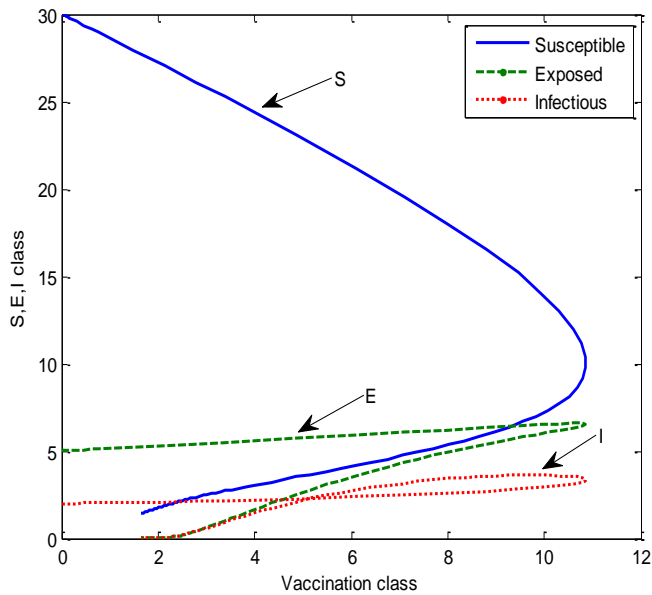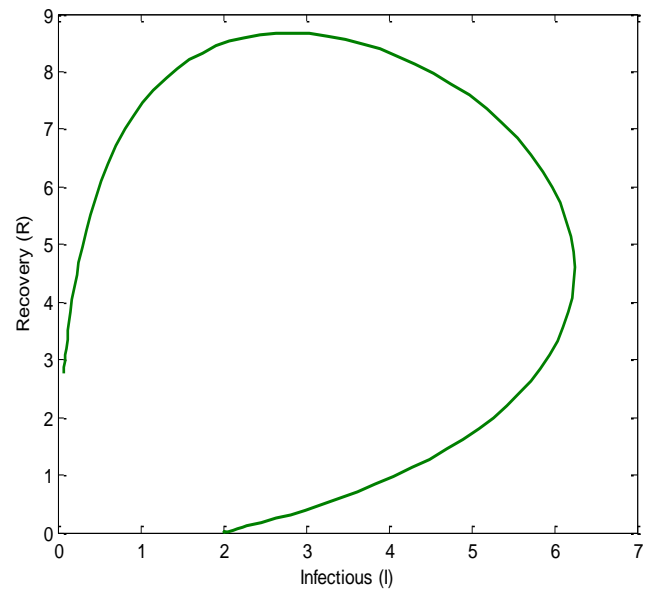
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Figure 3 Effect of quarantine class on different classes when A=0.01; ε = 0.65; μ = 0.05; γ = 0.45; α = 0.035; η = 0.35; δ = 0.3; β = 0.09; θ = 0.01; χ = 0.55; ρ = 0.65.

Figure 5 Dynamical behavior of the classes Q and R with A=0.01; ε = 0.07; μ = 0.05; γ = 0.45; α = 0.035; η = 0.35; δ = 0.1; β = 0.09; θ = 0.05; χ = 0.55; ρ = 0.65.

Figure 4 Effect of vaccination class on different classes when A=0.01; ε = 0.65; μ = 0.05; γ = 0.45; α = 0.035; η = 0.35; δ = 0.3; β = 0.09; θ = 0.01; χ = 0.55; ρ = 0.65.

Figure 6 Dynamical behavior of the classes I and R with A=0.01; ε = 0.07; μ = 0.05; γ = 0.45; α = 0.035; η = 0.25; δ = 0.1; β = 0.09; θ = 0.05; χ = 0.55; ρ = 0.65.

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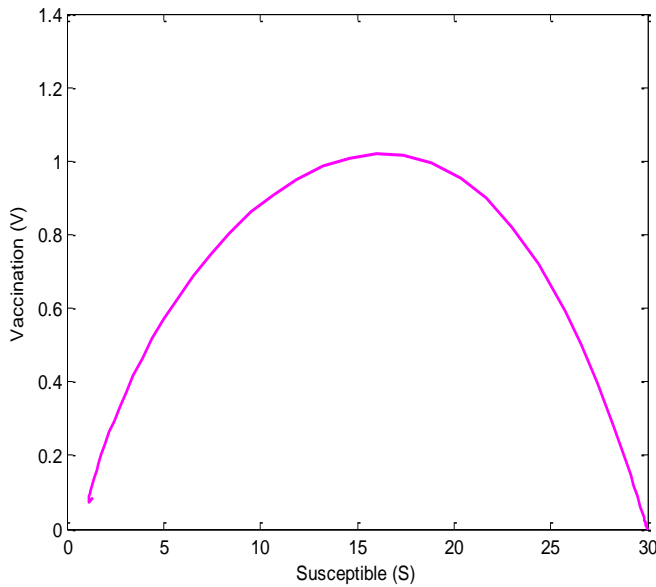

Figure 7 Dynamical behavior of the classes S and V with A=0.01; ε = 0.65; μ = 0.05; γ = 0.45; α = 0.035; η = 0.35; δ = 0.3; β = 0.09; θ = 0.01; χ = 0.75; ρ = 0.05.
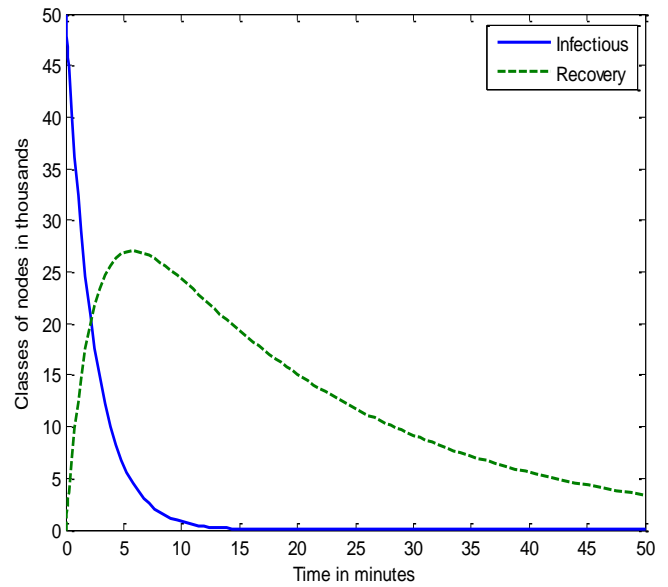

Figure 9 Dynamical behavior of the classes I and R with μ = 0.03; α = 0.035; η = 0.35; δ = 0.05; θ = 0.02.
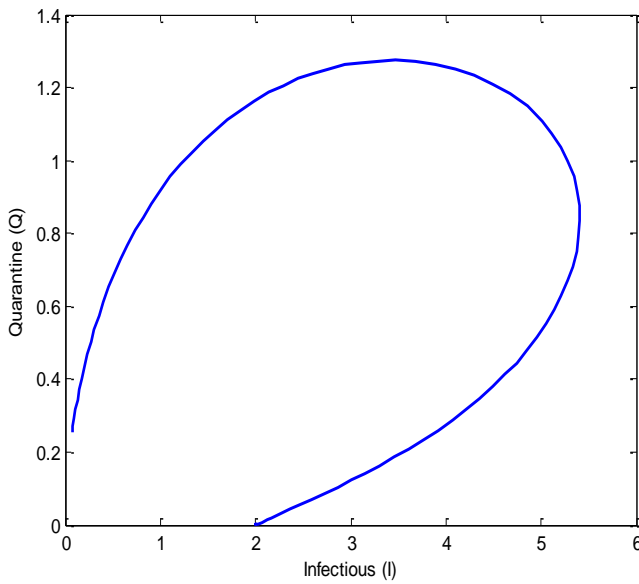

Figure 8 Dynamical behavior of the classes I and Q with A=0.01; ε = 0.05; μ = 0.05; γ = 0.30; α = 0.035; η = 0.25; δ = 0.05; β = 0.09; θ = 0.01; χ = 0.55; ρ = 0.65.

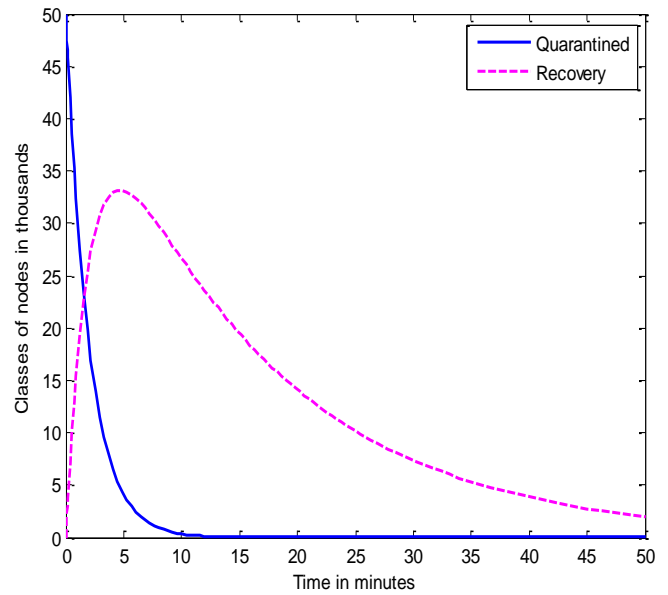Figure 10 Dynamical behavior of the classes Q and R with ε = 0.45; μ = 0.015; α = 0.035; θ = 0.05.
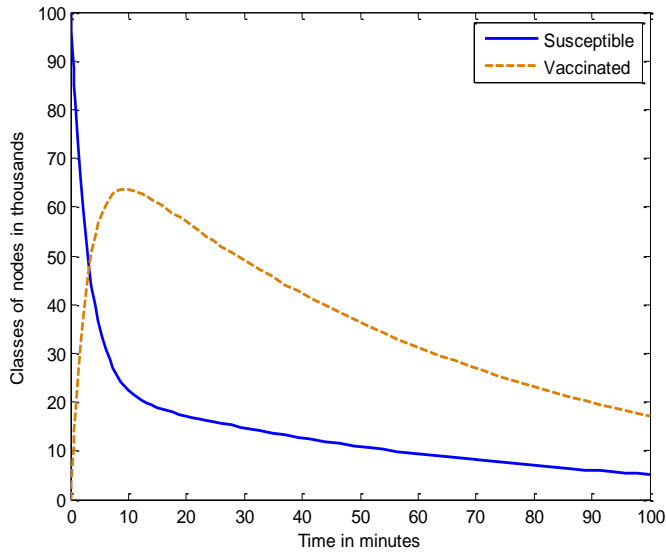
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Figure 11 Dynamical behavior of the classes S and V with μ = 0.015; χ = 0.075; ρ = 0.25.

6. CONCLUSION

A dynamical e-epidemic SEIQRS - V model for the transmission of viruses in computer network is formulated. We have assumed that the viruses possess a non-negligible latent period & infected nodes will stay in the latent period before they become infectious. By the help of basic reproduction number and the equilibrium, we have investigated that the more the system is susceptible towards the attack of worm, lesser the secondary infection will be there and vice – versa. The behavior of the different classes of nodes with respect to time are observed which is depicted in figures 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 and we also observed that the system is asymptotically stable. The effect of Q on R is also observed and is depicted in figure 5 & 10. 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 medications. The quarantined nodes are then treated with updated anti - virus software and are kept under constant observation. The more we quarantine the most infected nodes, the more is the recovery; the lesser we quarantine, the lesser is the recovery. As the quarantine rate increases recovery rate increases quickly and at a very short interval of time, the recovery of the nodes is constant when the quarantine rate decreases. Simulation result agrees with the real life situation. We have also analyzed the impact of vaccination in the system depicted in figure 7 & 11 which shows that the vaccinated nodes may become susceptible due to the lack of anti – virus with latest signature. It means that, to get the system virus – free, we have to update the anti – virus time and again.

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