Southeast Asian Journal of Sciences: Vol. 6, No 2 (2018) pp. 134-146

MATHEMATICAL MODEL FOR MALICIOUS OBJECTS IN COMPUTER NETWORK WITH THE EFFECT OF EDUCATION CAMPAIGN

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Abstract

In this paper, a modified SI_1I_2R model for the transmission of malicious objects in a computer network with the effect of the education campaign and its applications were proposed and analyzed. The standard method is used to analyze the behaviors of the proposed model. The results show that there were two equilibrium points; virus disease free and virus endemic equilibrium point. The qualitative results are depended on a basic reproductive number(R_0). We obtained the basic reproductive number by using the next generation method and finding the spectral radius. Routh-Hurwitz criteria are used for determining the stabilities of the model. If $R_0<1$, then the virus disease-free equilibr ium point is local asymptotically stable, but if $R_0>1$, then the endemic equilibrium is local asymptotically stable. In order to get more good results the perturbation iteration method to be applied and derived the iteration scheme with the algorithm that includes a combination of perturbation expansion and Taylor series expansion. The result from the numerical solutions of the models be shown and compared for supporting the analytic results.

Key words: Malicious objects, stability, equilibrium point, basic reproductive number, perturbation iteration.
(2010) Mathematics Subject Classification: 00A71, 68U07, 81T80

1 Introduction

In many years ago, the internet technology has been continuously offering multiple functionalities, facilities and maybe the fifth factor for everyday life. The addition of cyber technology has helped in data and information exchange to take at high speed which transforms the world into a global village. It has made the life easier and world accessible with the touch of a button. But everything is not well in the cyber world; it is facing several challenges in the form of malicious objects. These malicious objects are worms and virus. Malicious objects have more and more influence on a computer network. Currently, e-mail has become one of the main factors for the transmission of malicious objects. Transmission of malicious objects in a computer network is epidemic in nature and is analogous to biological epidemic diseases. Controlling the malicious objects in a computer network has been an increasingly complex issue in recent years. In order to control the malicious object, Mishra *et al.* has introduced mathematical models for the transmission of malicious objects in the computer network and has given epidemic models on times delays, the fixed period of temporary immunity after the use of anti-malicious software, effect of quarantine, fuzziness of the system [3]-[10],[12]-[13],[17]. Richard and Mark proposed an improved SEI (Susceptible Exposed Infectious) model to simulate virus propagation [14]. Anderson and May [15]-[16] discussed the spreading nature of biological viruses, parasite *etc.* B. K. Mishra proposed $\mathrm{SI_1I_2R}$ epidemic model for the simple mass action incidence rate in which infected population is divided into two groups where first group consists of those nodes which are infected by the worms and second for the Population of Viruses Population of Recovered Nodes Worm Infected Nodes Recovered Nodes which infected by virus is developed [20].Then we propose a modified model from [20] with education campaign be taken into account for the model with two different kinds of malicious groups. This paper is organized as follows. In section 2, we present a modified $\mathrm{SI_1I_2R}$ model for the transmission dynamics of malicious objects in the computer network with the effect of the education campaign and its applications. The standard method is used to analyze the behaviors of the proposed model. The perturbation iteration scheme is presented in section 3. In section4, we give a numerical appropriate method and the simulation corresponding results. Finally, the conclusions are summarized in section 5.

2 Mathematical model

In this work, a modified $\mathrm{SI_1I_2R}$ model for the transmission of malicious objects in the computer network was proposed. The efficiency of education campaign; $(1-u)$ and $(1-v)$ are taken into account for the contract group between the susceptible computer(S) and the number of infected nodes with worms(I_1) and virus(I_2), the standard method is used to analyze the behaviors of the proposed model which was adopted from [20]. The total computer population is N . Computer population be divided into four disease-state compartments: susceptible computer(S) ; computer that risk to catch the disease ;worms or virus, the number of infected nodes with worm(I_1) ; infectious computer, nodes infected with worms and can transmit the disease, the number of nodes infected with virus(I_2) ; infectious computer, nodes infected with virus and can transmit the disease, (R) be the recover nodes after the run of anti-malicious software. In this study, we assumed that there are numbers of the computer in the populations that have already infected by the virus while others have not. It is also assumed that the transmission of the virus continues in the population but a number of computer population is constant. We obtained the transmission dynamics model as shown by a system of ordinary differential equations as the following.

$$\frac{dS}{dt} = \mu B - (1-u)q_1(\beta_1)I_1S - (1-v)q_2(\beta_2)I_2S - \mu S + \delta R \tag{1}$$

$$\frac{dI_1}{dt} = (1-u)q_1(\beta_1)I_1S - (\mu + \alpha_1 + \gamma_1)I_1 \tag{2}$$

$$\frac{dI_2}{dt} = (1-v)q_2(\beta_2)I_2S - (\mu + \alpha_2 + \gamma_2)I_2 \tag{3}$$

$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 - (\mu + \delta)R \tag{4}$$

Where; $$S + I_1 + I_2 + R = N$$

$$\frac{dN}{dt} = \mu(B - N) - (\alpha_1 I_1 + \alpha_2 I_2)$$

B is the recruitment rate of susceptible nodes of a computer network

μ is the per capita birth rate and death rate due to the reason other than the attack of the malicious objects

q_1 and q_2 are the probability of infected nodes which enter the group and from susceptible class

δ is the rate of transmission of nodes from recovered class to susceptible class

γ_1 and γ_2 are the rates of nodes leaving the infected class and to recovered class respectively

α_1 and α_2 are the crashing rate of the nodes due to the attack of malicious objects in the infectious class and respectively

$1-u$ and $1-v$ are the efficiency of an education campaign for people to protect the nodes due to the attack from worm and virus respectively

2.1 Basic properties of the model

2.1.1 Invariant Region

It is reasonable to assume that all its state variables and parameters are non-negative for all $t>0$,Furthermore, it can be shown as the region Ω;

$\Omega = \{(S, I_1, I_2, R) \in R_+^4 / S>0; I_1 \geq 0; I_2 \geq 0; S + I_1 + I_2 + R \leq B\}$ is positive invariant with respect to the system of equations (10), with the initial condition in Ω Hence the system (1)-(4) is considered mathematically and epidemiologically well posed. The existence, uniqueness and continuation results hold for the system.

2.1.2 Positivity of Solution

For the system of equations (1)-(4), it is necessary to prove that all state variables are nonnegative. First, we have to show that the state variables satisfied the condition $S(t)>0$, for $t>0$, consider;

$$
\begin{aligned}
\frac{dS}{dt} &= \mu B - \mu S - (1-u)\beta_1 I_1 S + \delta R - (1-v)\beta_2 I_2 S > - \\
&\quad \mu S - (1-u)\beta_1 I_1 S - (1-v)\beta_2 I_2 S; \\
\frac{dS}{S} &> -(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)dt; \\
\int \frac{dS}{S} &> -(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)dt; \\
In\ S &> -(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)t + c; \\
S(t) &> e^{-(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)t + c}; then \\
S(t) &> S(0)e^{-(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)t + c}; fort>0;
\end{aligned}
$$

For the state variables $I_1(t), I_2(t) and R(t)$, we can do at the same method then we get $I_1(t), I_2(t), R(t) \geq 0$ and $i(t) \geqslant 0$ for $t>0$
The equilibrium points for (S, I_1, I_2, R) are found by setting the right-hand side of each equation (1)-(4) equal to zero. We obtained two equilibrium points as follows;

$$S = \frac{\mu B + \delta R}{(\mu + (1-u)\beta_1 I_1 + (1-v)\beta_2 I_2)},$$
$$I_1 = \frac{(R_0 - 1)\gamma_1 \mu B(\mu + \delta)}{((\mu + \delta)(1-u)\beta_1 B - \delta\gamma_1 R_0)\gamma_1},$$
$$I_2 = \frac{(R_0 - 1)\gamma_2 \mu B(\mu + \delta)}{((\mu + \delta)(1-v)\beta_2 B - \delta\gamma_2 R_0)\gamma_2},$$

$$R = \frac{\gamma_1 I_1 + \gamma_2 I_2}{(\mu + \delta)},$$

2.1.3 Malicious Objects Disease Free Equilibrium Point(E_0) : In the absence of the disease in the community, there are $I_1 = 0$, $I_2 = 0$ and $R = 0$, we obtained $E_0(S, I_1, I_2, R)$where

$$S = B, I_1 = 0, I_2 = 0, R = 0,$$

2.1.4 Malicious Objects Endemic Equilibrium Point(E_0) : In case the disease is presented in the community, I_1>0 and I_2>0we obtained,
$E_1(S^*, I_1^*, I_2^*, R^*)$ where;

$$S^* = \frac{\mu B + \delta R^*}{(\mu + (1-u)\beta_1 I_1^* + (1-v)\beta_2 I_2^*)},$$
$$I_1^* = \frac{(R_0 - 1)\gamma_1 \mu B(\mu + \delta)}{((\mu + \delta)(1-u)\beta_1 B - \delta\gamma_1 R_0)\gamma_1},$$
$$I_2^* = \frac{(R_0 - 1)\gamma_2 \mu B(\mu + \delta)}{((\mu + \delta)(1-v)\beta_2 B - \delta\gamma_2 R_0)\gamma_2},$$
$$R^* = \frac{\gamma_1 I_1^* + \gamma_2 I_2^*}{(\mu + \delta)},$$

Where $R_0 = B(\frac{(1-u)\beta_1}{\mu+\alpha_1+\gamma_1} + \frac{(1-v)\beta_2}{\mu+\alpha_2+\gamma_2})$

2.2 Basic Reproductive Number (R_0)
We obtained a basic reproductive number by using the next generation method [1],[2],[11]. Next rewriting the system equations (1) - (4) in the matrix form;

$$\frac{dX}{dt} = F(X) - V(X) \tag{5}$$

Where, is the non-negative matrix of new infection terms and is the non-singular matrix of remaining transfer terms.

And setting;

$$F = [\frac{\partial F_i(E_0)}{\partial}]X_i \text{ and } V = [\frac{\partial V_i(E_0)}{\partial}]X_i, \tag{6}$$

for all $i, j = 1, 2, 3, 4$, be the Jacobean matrix of $F(X)$ and $V(X)$ at E_0 .The basic reproductive number (R_0) is the number of secondary case generated by a primary infectious case [11], or basic reproductive number is a measure of the power of an infectious disease to spread in a susceptible population. It can be evaluated through the formula;

$$\rho(FV^{-1}). \tag{7}$$

Where FV^{-1} is called the next generation matrix and $\rho(FV^{-1})$ is the spectral radius (largest eigenvalues) of FV^{-1}. Then we get the reproduction number R_0 where,

$$R_0 = B(\tfrac{(1-u)\beta_1}{\mu+\alpha_1+\gamma_1} + \tfrac{(1-v)\beta_2}{\mu+\alpha_2+\gamma_2}) \tag{8}$$

Finally, Routh-Hurwitz criteria are used for determining the stabilities of the model. If $R_0<1$, then malicious objects disease-free equilibrium point is local asymptotically stable: that is the disease will die out, but if $R_0>1$, then malicious objects endemic equilibrium is local asymptotically stable.

3 Perturbation Iteration Methods

In this section, we applied the perturbation iteration method that had been derived by [18], [19] to the model. This method uses a combination of perturbation expansions and Taylor series expansions to derive an iteration scheme. Lets consider the following system of first-order differential equations.

$$V_k(x'_k, x_j, \varepsilon, t) = 0; k = 1, 2, ..., K; j = 1, 2, ..., K;$$

Where; k is representing the number of differential equations in the system and the number of dependent variables, $k = 1$ for a single equation. In general, the system of equations is given as the following;

$$\begin{aligned}
&V_1 = V_1(x'_1, x_1, x_2, x_3, ..., x_K, \varepsilon, t) = 0;\\
&V_2 = V_2(x'_2, x_1, x_2, x_3, ..., x_K, \varepsilon, t) = 0;\\
&V_3 = V_3(x'_3, x_1, x_2, x_3, ..., x_K, \varepsilon, t) = 0;\\
&.\\
&.\\
&V_K = V_K(x'_K, x_1, x_2, x_3, ..., x_K, \varepsilon, t) = 0;
\end{aligned} \tag{9}$$

Next, we assume an approximate solution of (9) is;

$$x_{k,n+1} = x_{k,n} + \varepsilon x^c_{k,n} \tag{10}$$

With one correction term in the perturbation expansion, where the subscript n represents the n^{th} iteration on this approximate solution. We can be approximated this system by Taylor series expansion in the neighborhood of ε as;

$$V_k = \sum_{m=0}^{D} \frac{1}{m!}[(\frac{d}{d\varepsilon})^m V_k]_{\varepsilon=0} \times \varepsilon^m; k = 1, 2, ..., K; \tag{11}$$

Where; the $(n+1)^{th}$ iteration equations be given by;

$$\frac{d}{d\varepsilon} = \frac{\partial x'^{c}_{k,n+1}}{\partial \varepsilon} \frac{\partial}{\partial x'_{k,n+1}} + \sum_{j=0}^{K} (\frac{\partial x^{c}_{j,n+1}}{\partial \varepsilon} \frac{\partial}{\partial x_{j,n+1}}) + \frac{\partial}{\partial \varepsilon} \tag{12}$$

And; $V_k(x'_{k,n+1}, x_{j,n+1}, \varepsilon, t) = 0$ (13)

By substituting equation (12) into equation (11) then we get an iteration equation for the first-order differential equation and can be solved for the correction terms $X^c_{k,n}$;

$$V_k = \sum_{m=0}^{D} \frac{1}{m!}[(\frac{\partial x'^{c}_{k,n+1}}{\partial \varepsilon} \frac{\partial}{\partial x'_{k,n+1}} + \sum_{j=0}^{K} (\frac{\partial x^{c}_{j,n+1}}{\partial \varepsilon} \frac{\partial}{\partial x_{j,n+1}}) + \frac{\partial}{\partial \varepsilon})^m (V_k)]_{\varepsilon=0} \times \varepsilon^m = 0; \tag{14}$$

Where $k = 1, 2, ..., K$. Next, we can use equation (14) to find the $(n+1)^{th}$ iteration solution.

4 Numerical simulations

In this section, the Perturbation Iteration Algorithm is derived for solving the transmission dynamics of SI_1I_2R a model as the following system:

$$\frac{dS}{dt} = \mu B - (1-u)q_1(\beta_1)I_1S - (1-v)q_2(\beta_2)I_2S - \mu S + \delta R \tag{1}$$
$$\frac{dI_1}{dt} = (1-u)q_1(\beta_1)I_1S - (\mu + \alpha_1 + \gamma_1) \tag{2}$$
$$\frac{dI_2}{dt} = (1-v)q_2(\beta_2)I_2S - (\mu + \alpha_2 + \gamma_2) \tag{3}$$
$$\frac{dR}{dt} = \gamma_1 I_1 + \gamma_2 I_2 - (\mu + \delta)R \tag{4}$$

We assume an approximate solution of the system as;

$$x_{k,n+1} = x_{k,n} + \varepsilon x^c_{k,n}; \tag{15}$$

Where$\varepsilon$is the perturbation iteration parameter. The system is resolved by giving;

$$
\begin{aligned}
&V_1 = S\prime - \mu(B - S) + (1-u)(q_1(\beta_1)I_1S\varepsilon + (1-v)q_2(\beta_2)I_2S)\varepsilon - \delta R\\
&V_2 = I\prime_1 - (1-u)(q_1(\beta_1)I_1S)\varepsilon + (\mu + \alpha_1 + \gamma_1)I_1\\
&V_3 = I\prime_2 - (1-v)(q_2(\beta_2)I_2S)\varepsilon - (\mu + \alpha_2 + \gamma_2)I_2\\
&V_4 = R\prime - \gamma_1 I_1\varepsilon + \gamma_2 I_2\varepsilon - (\mu + \delta)R
\end{aligned} \tag{16}
$$

The result from (15)-(16) and lets $V_z = 0$ for $z = 1, 2, 3, 4$. Then we get

$$
\begin{aligned}
S\prime_{1,n} &= \mu B - \mu S\prime^c_{1,n}\mu\varepsilon - S^c_{1,n}\mu\varepsilon - q_1(1-u)\beta_1(I_1)_{1,n}\varepsilon - q_2(1-v)\beta_2(I_2)_{1,n}\varepsilon +\\
&\quad \delta R_{1,n};\\
(I_1)\prime_{1,n} &= q_1(1-u)\beta_1(I_1)_{1,n}S_{1,n}\varepsilon - (\mu + \alpha_1 + \gamma_1)(I_1)_{1,n} - (I_1)'^c_{1,n}\varepsilon -\\
&\quad (\mu + \alpha_1 + \gamma_1)(I_1)^c_{1,n};\\
(I_2)\prime_{1,n} &= q_2(1-u)\beta_2(I_2)_{1,n}S_{1,n}\varepsilon - (\mu + \alpha_2 + \gamma_2)(I_2)_{1,n} - (I_2)'^c_{1,n}\varepsilon -\\
&\quad (\mu + \alpha_2 + \gamma_2)(I_2)^c_{1,n};\\
R\prime &= \gamma_1(I_1)_{1,n}\varepsilon + \gamma_2(I_2)_{1,n}\varepsilon - (\mu_v + \delta_v)e_{1,n+1} - (\mu + \alpha_1 + \gamma_1)R^c_{1,n}\varepsilon -\\
&\quad R^c_{1,n}\prime_\varepsilon - (\mu + \delta)R_{1,n};
\end{aligned}
$$

By using the above technique, t he simulations at endemic state were carried out. The parameter values are given in Table1, with the following initial condition: $S(0) = 10000, I_1(0) = 1000, I_2(0) = 2000, R(0) = 0$ and results show below.

Table1. Parameters values used in numerical simulation at endemic state.

Parameters	**Description**	**Value**
B	The recruitment rate of infective nodes	0.009
μ	The per capita birth rate and death rate due to the reason other than the attack of the malicious objects	0.05
q_1, q_2	The probability of infected nodes which enter the group I_1 and I_2 from susceptible class respectively	0.26,0.27
β_1, β_2	The sufficient rate of correlation from susceptible nodes to infected nodes I_1 and I_2 respectively	0.0015,0.0028
δ	the rate of transmission of nodes from recovered class to susceptible class	0.005
γ_1, γ_2	the rates of nodes leaving the infected class I_1 and I_2 to recovered class respectively	0.008,0.007
N	Number of nodes populations	18000
α_1, α_2	the crashing rate of the nodes due to the attack of malicious objects in the infectious class I_1 and I_2 respectively	0.992,0.889
u, v	The efficiency of an education campaign for people to protect the nodes due to the attack from worm and virus respectively	$0 < u < 1, 0 < v < 1$
ε	The perturbation parameter	$0 < \varepsilon < 1$

4.1 Numerical results for the modified SI_1I_2R model at endemic state with the different values of u and v.

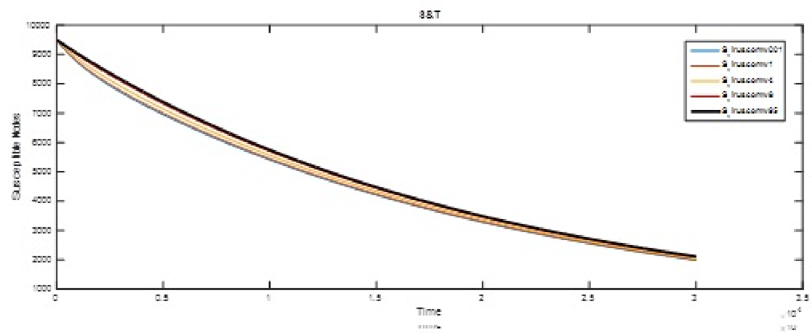

Fig.1 Represent time series of susceptible nodes of computer network population (S) with different values of u. It shows the number of susceptible nodes population (S) is increased when the values of u are increased.

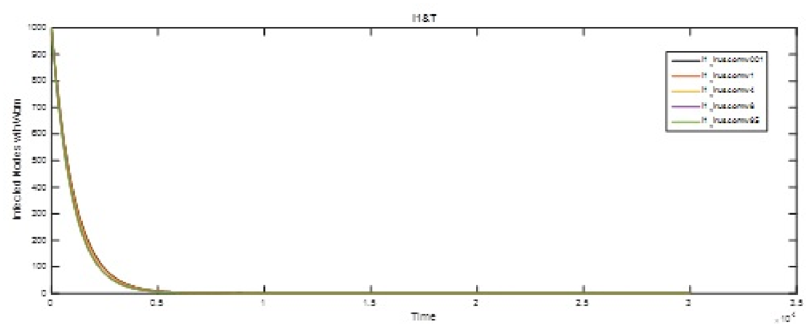

Fig.2 Represent time series of the worm infected nodes I_1 with the different value of u. It shows the number of the worm infected nodes I_1 is decreased when the values of u are increased.

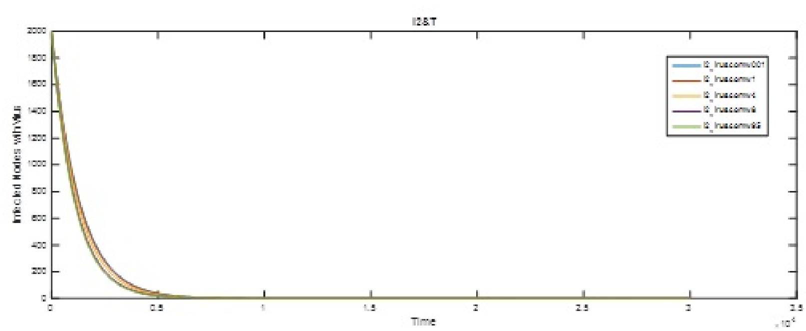

Fig.3 Represent time series of the worm infected nodes I_2 with the different value of u. It shows the number of the worm infected nodes I_2 is decreased when the values of u are increased.

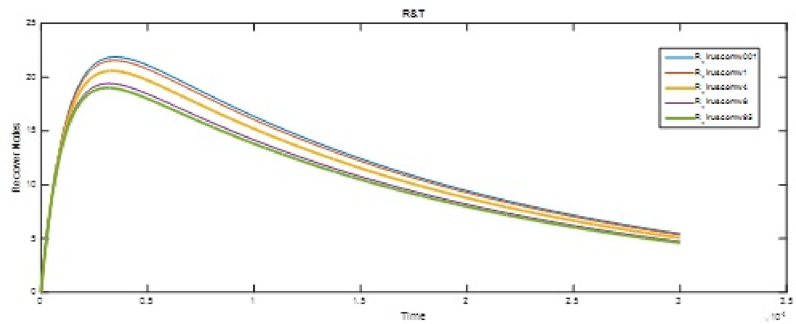

Fig. 4 Represent time series of recover nodes (R) after the run anti-malicious software with different values of u. It shows that the number of recover nodes (R) is increased when the values of u are decreased

4.2 Numerical results for the SI_1I_2R model be applied perturbation iteration technique with different values of the perturbation parameter ε.

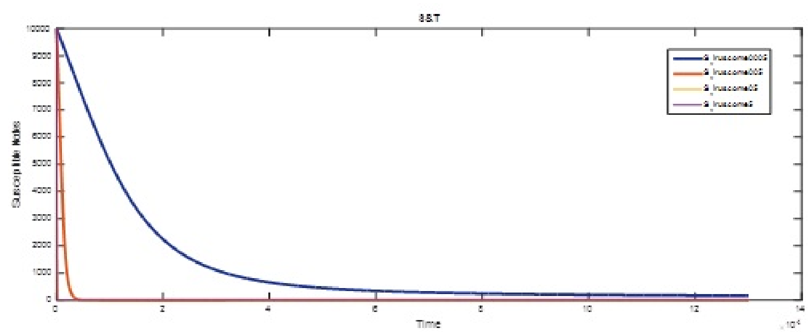

Fig.5 Represent time series of susceptible nodes of the computer network population (S) with different values of ε . It shows the number of susceptible nodes population (S) be increased when the values of ε be decreased.

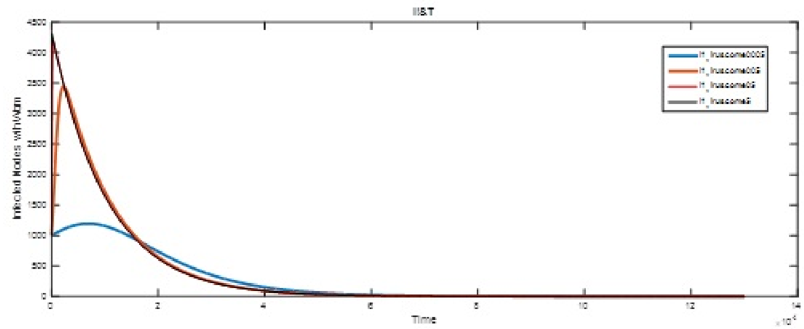

Fig.6 Represent time series of the worm infected nodes I_1 with a d ifferent value of ε. It shows the number of the worm infected nodes I_1 is decreased when the values ε are decreased .

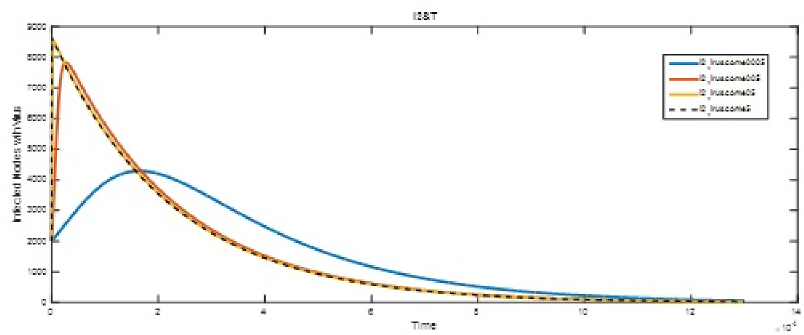

Fig.7 Represent time series of the worm infected nodes I_2 with the different value of ε. It shows the number of the worm infected nodes I_1 is decreased when the values of ε is decreased.

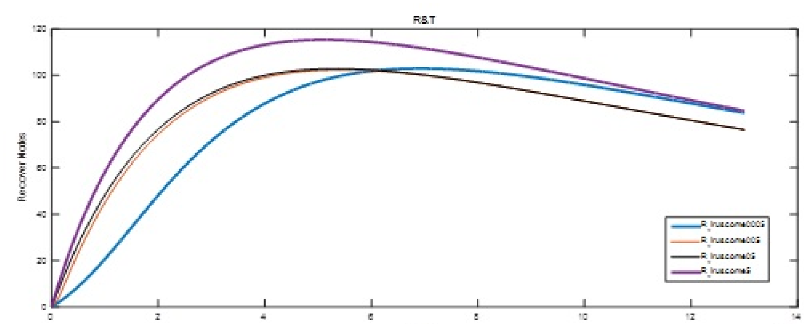

Fig.8 Represent time series of recover nodes (R) after the run anti-malicious software with different values of ε. It show that the number of recover nodes(R) is increased when the values of ε is increased.

5 Conclusion

In this paper, the modified SI_1I_2R model for the transmission of a malicious object on the computer network with the efficiency of the education campaign, to protect the nodes due to the attack from worm and virus are $(1-u)$ and $(1-v)$ respectively, were proposed and analyzed. The standard method is used to analyze the behaviors of the proposed model. The results have shown that there were two equilibrium points; disease free and endemic equilibrium point. The qualitative results are depended on a basic reproductive number(R_0). We obtained the basic reproductive number by using the next generation method and finding the spectral radius. Routh-Hurwitz criteria are used for determining the stabilities of the model. If $R_0 < 1$, then the disease-free equilibrium point is local asymptotically stable: that is the disease will die out, but if $R_0 > 1$, then the endemic equilibrium is local asymptotically stable. We used the control $(1-u)$ and $(1-v)$ to reduce the contract between the susceptible nodes and the infected nodes with worm and virus. The other, minimizing the population of the infected nodes, the result shows that if the values of $(1-u)$ and $(1-v)$ is increased, then the number of infected nodes is decreased but the number of susceptible humans is increased. The system is resolved for supporting the analytical result by using t he perturbation iteration technique. The results show that when the perturbation parameter;(ε) decrease, then the number of infected nodes decrease.

Acknowledgment The authors are grateful to the Department of Mathematics, Faculty of Science and Technology and Phuket Rajabhat University, Thailand for providing the facilities to carry out the research.

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