Mathematical Model For Cyber Attack In Computer Network

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Abstract- *Cyber Security plays an important role in the field of information technology .Securing the information have become one of the biggest challenges in the present day. Whenever we think about the cyber security the first thing that comes to our mind is 'cyber crimes' which are increasing immensely day by day. Various Governments and companies are taking many measures in order to prevent these cybercrimes. Besides various measures cyber security is still a very big concern to many. This paper mainly focuses on challenges faced by cyber security on the latest technologies .It also focuses on latest about the cyber security techniques, ethics and the trends changing the face of cyber security.*

Keywords- cyber security, cyber-crime, cyber ethics, SIRS Model, Malicious Object, e-epidemic model, statistical tool, Mean and ANOVA, Jacobian matrix.

I. INTRODUCTION

The advancement of society with the usage computer software and hard ware has created a new sort of crime in all domains known as cybercrime which is a new form of crime in the 21th century across the globe. So criminal investigation is a major topic for research in the present scenario to many academicians and practitioners. Improvements of correspondence systems have made computers more critical in our day-by-day life. Diverse kind of specialized gadgets expanded human reliance on computers. Unfortunately, with the advancement of internet and other communication network, some mischievous individuals who differ in their opportunity cost for the committing crime by various means of technological through computers involves in malicious activities. Links of computer networks and their communication channels spreads an infection and preventing the networks from doing its proper functionally which causes a huge loss of society. Thus the indefinite number of existing malicious codes and their appearances has vital risk factor for every individuals and large sectors. Computer viruses or malicious objects such as worms and Trojan horse travel through a process in the computer networks which resembles to the way towards spreading plagues through a populace. The diseases that can be transmitted by vectors when managing with public health are comparable to the virtual viruses that can propagate in the system of interacting computers. Therefore, concerning this similarity an epidemic model like SEIR has been adopted and used to study the action of malicious objects through networks. Substantial efforts have been made by many researchers to understand the effect of malicious behaviors on infection dynamics. However, such efforts have not always made its way into mathematical models. Therefore, by accepting the spread law of virus upon the network and the model analysis along with the characteristics of computer virus, we developed reasonable computer virus propagation model. Based on our model we would be able to obtain estimation from efficiency of different immunization method without assuming a set of initial infected agents and relying on a specific epidemiological model for spread of epidemics. It also provides a mean to human behaviors to infection dynamics by having informed individual try to buy the anti-malware software and reduce susceptibility of their system. This model reveals the equilibrium and stability condition both qualitatively and quantitatively.

II. METHODOLOGY

2.1 Mathematical Model and Assumptions:-

Consider the total computer nodes N (t) divided into four group, each of whom can either susceptible (S) or otherwise infected (I) with an infectious malicious object. Once the malicious objects enter into the network, the nodes become susceptible (S) and after a certain time delay the nodes become infected (E) and then it gets infectious (I). After it gets infectious, anti-malicious software is run which helps the nodes to recover (R) temporarily from the attack and provide temporary immunity to the node in the network.
The flow of malicious objects in the computer network is depicted in

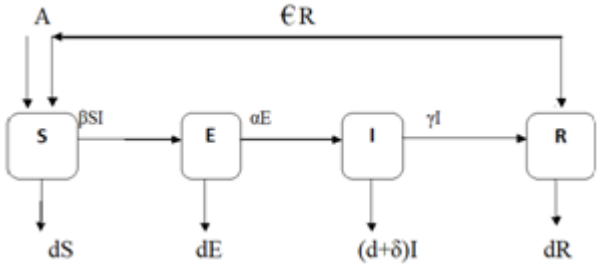

Fig. 2.1 Schematic diagram of the model

$$\frac{dS}{dt} = A - \beta SI - DS + \epsilon R$$
$$\frac{dE}{dt} = \beta SI - (D + \alpha)E$$
$$\frac{dI}{dt} = \alpha E - (d + \delta + \gamma)I$$
$$\frac{dR}{dt}\gamma I - (d + \varepsilon)R \quad (3.1)$$

Where N (t) = S (t) + E (t) + I (t) + R (t)

Adding all the equations from (2.1), we have Equation it can be seen that in the absence of the virus I=0 Thus D1

$$N \to \frac{A}{d}$$

D_1=((S, E, I):S≥0, E≥0S+E+1≤$\frac{A}{d}$)

Is a positively invariant region for the model?

$$(d+S * = (d + \delta + \gamma)(d + \alpha)/\alpha\beta$$

2.2Equilibrium and Stability Analysis

Virus free equilibrium is (A/d, 0, 0, 0). While endemic equilibrium is

S*= $(d+\delta+\gamma)(d+\alpha)/\alpha\beta$
E* = $(d+\delta+\gamma)/[d/\beta - A\alpha/(d+\alpha d+\delta+\gamma) + \alpha s\gamma I/(d+$s $d+\alpha d+\delta+\gamma)$]
I* =[$d(d+\delta+\gamma)(d+\alpha)/\alpha\beta - A][\alpha(d+$s $)/(d+\delta+\gamma)(d+\alpha)(d+$s $)+\alpha s\gamma]$
R* = $\gamma I/(d+$s)

2.3Calculation of Basic Reproduction Number

By using next generation matrix approach, let theR0 basic reproduction number defined as the average number of secondary infections that is a single viral computer can produce in a totally susceptible class during its life cycle.

$$\begin{pmatrix} \frac{dE}{dt} \\ d/_d \perp/_v \end{pmatrix} = \begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}\begin{pmatrix} E \\ I \end{pmatrix} - \begin{pmatrix} \alpha + d & 0 \\ -\alpha & d + \delta + y \end{pmatrix}\begin{pmatrix} E \\ I \end{pmatrix}$$

Where, F=$\begin{pmatrix} 0 & \beta S \\ 0 & 0 \end{pmatrix}$ and $V = \begin{pmatrix} \alpha + d & 0 \\ -\alpha & d + \delta + y \end{pmatrix}$

Inverse of V can calculate as

$$V^{-1} = \begin{pmatrix} \frac{1}{(\alpha + d)} & 0 \\ \frac{\alpha}{(\alpha + d)(d + \delta + \gamma)} & \frac{1}{(d + \delta + \gamma)} \end{pmatrix}$$

Therefore,

$$FV^{-1}\left(\frac{\beta\alpha S_0}{(\alpha + d)(d + \delta + \gamma)}\right)\left(\frac{\beta S_0}{(d + \delta + \gamma)}\right)$$

The spectral radius of above matrix is

$$\rho(FV^{-1}) = \left(\frac{\beta\alpha S_0}{(\alpha + d)(d + \delta + \gamma)}\right)$$

Hence the Basic reproduction number is

$$R_0 = \left(\frac{\beta\alpha S_0}{(\alpha + d)(d + \delta + \gamma)}\right)$$

Equilibrium points are the points where the variables do not change with time. In order to know about growth of infected nodes, i.e., the number of infected nodes increases indefinitely or not. So, it has been studied the stability of equilibrium points.

And there are two equilibrium point of the model given by Virus free equilibrium

$$D_0 = (\frac{A}{d}, 0,0,0)$$

Endemic equilibrium D* (S*, E*, I *, R*)

2.4 Stability Analysis for Virus free Equilibrium

For Steady state of the model is given by

$$\alpha E - dI - \delta I - \gamma I = 0$$
$$\gamma I - dR - \epsilon R = 0 \quad (2.2)$$

Proof: Linearization of the above model (2.2) about the virus free equilibrium points

$$D = \begin{matrix} -(\beta I + d) & 0 & -(\beta S) & \epsilon \\ \beta I & -(d + a) & \beta S & 0 \\ 0 & 0 & -(d + \gamma + \delta & 0 \\ 0 & 0 & 0 & -(d + \varepsilon) \end{matrix}$$

Linearization of the model (2.2) at virus free equilibrium in the absence of infection nodes is

$$D^* = \begin{matrix} -d & 0 & -\beta\frac{A}{d} & \varepsilon \\ 0 & -(d + a) & \beta\frac{A}{d} & 0 \\ 0 & 0 & -(d + \gamma + \delta) & 0 \\ 0 & 0 & 0 & -(d + \varepsilon) \end{matrix}$$

And the Eigen values of the above matrix are –d,-(d+α),-(d+δ+γ) and-(d+ε)

Therefore, the model (2.2) at virus free equilibrium. Hence D is asymptotically locally stable.

Stability Analysis for the Endemic equilibrium point

At endemic equilibrium the linearization of the model (2.2) is

$$D* = \begin{matrix} -(\beta I* +d) & 0 & -\beta S* & \in \\ \beta I* & -(d+a) & \beta S* & 0 \\ 0 & 0 & -(d+\gamma+\delta & 0 \\ 0 & 0 & 0 & -(d+\varepsilon) \end{matrix}$$

And the Eigen values of the above matrix are – (β$I*$ +d),-(d+α),-(d+δ+γ) and-(d+ε)

Since the all-Eigen value of the matrix is negative the model (2.2) has Asymptotically Locally stable at endemic equilibrium.

2.5Global Stability for Virus Free Equilibrium

In this section we represent the global stability of the equilibrium in the model Global stability of Virus free equilibrium

By the help of Lyapunov function we have to show that the global stability of virus free equilibrium.

Theorem If R0 ≤1, then the virus free equilibrium 'D' of the system is globally asymptotically stable in the region D1.

Proof Consider the Lyapunov function

$$M = E + 1$$

$$\frac{dM}{dt} = \frac{dE}{dt} + \frac{dI}{dt}$$

$$= \beta SI - dE - aE + aE - (d+\delta+y)I$$

$$\beta SI - (d+\delta+y)I$$

$$= [\beta S - (d+\delta+y)I - dE$$

$$= \frac{a+d}{a}\left(\frac{\beta S}{a+d} - \frac{a(d+\delta+\gamma}{(a+d)}\right)I - \frac{adE}{(a+d)}$$

$$= \frac{(\delta+d+\gamma)(a+d)}{a}\left[\frac{a\beta S}{(a+d)(d+\delta+y)} - \frac{a}{a+d}\right] - \frac{adE}{(a+d)(d+\delta+\gamma}$$

$$= \frac{(\delta+d+\gamma)(a+d)}{a}\left[R_o - \frac{a}{(a+d)}\right]I - \frac{adE}{(a+d)(d+\delta+\gamma}$$

When, hence by LaSalle's Invariance principle [22] D is globally stable in the region, R0 d1. This completes the proof.

2.6Global Stability for the Endemic Equilibrium

In this section, we will discuss the global stability of the virus –endemic equilibrium D* as R0 ≤ 1 by using the geometric approaches [23-24]. First, we can discuss the preliminaries of geometric approaches for the global stability of dynamic system.

Let us assume the autonomous system connected on Rn and f ≥ C '(D). X/ ∈ f (x), where f(x) be an open and simple.

Let the new Bendixson criteria [25] using the Lozinkskii measure by taking Z (x) to be an $\binom{n}{2} \times \binom{n}{2}$ be the matrix valued function for which C' on D and defining the $Q = \limsup \sup \frac{1}{t} n \to \infty \; x0 \; e \; k \; t \int_0^1 \mu(B(s, xo))) \, ds)$ B= $\check{Z}_f Z^{-1}$ + $\check{Z}_f J^{(2)}$ Z and Z These values can substitute in g1 and g2 we get Now from the system of equation (2.2) we know Consider can be calculated by substituting the elements of Z

By its derivatives in the direction of the function f. The Lozinskii measure of the matrix B with respect to vector norm is defined as

$$\mu(B) = \lim_{h \to 0} \frac{\|I + h_3\|^{-1}}{h}$$

The second additive compound matrix of the Jacobian matrix for n=3 is defined

$$J^{[2]} == \begin{pmatrix} j11 + j22 & j23 & -j13 \\ j & j + j33 & j12 \\ -j & j21 & j + j \\ 31 & 21 & 33 & 22 \end{pmatrix}$$

Based on this definition we follow the theorem the unique endemic equilibrium D* is globally asymptotically stable in the region D1, if R0>1.

Proof For the general solution of the system of differential equation (2.2), the Jacobian matrix is,

$$J = \begin{pmatrix} -(\beta I + d) & 0 & -\beta S \\ \beta I & -(d+a) & \beta S \\ 0 & 0 & -(d+\gamma+\delta \end{pmatrix}$$

Using the second additive compound matrix J [2] is

$$J^{[2]} = \begin{pmatrix} -(\beta I + 2d + a) & \beta S \\ 0 & -(\beta I + 2d + \delta + \gamma) \\ 0 & \beta I \end{pmatrix}$$

Let Z = Z(S, E, I) be defined as

$$Z = Z(S, E, I = \begin{pmatrix} 1 & 0 & 0 \\ 0 & E & 0 \\ & I & \\ 0 & 0 & E \\ & I & \end{pmatrix} = diag \left\{1 \frac{E}{I} \quad \frac{I}{I}\right\}$$

Then,

$$Z_f - Z^{-1} \begin{pmatrix} 1 & 0 & 0 \\ 0 & \frac{E'}{E} - \frac{I'}{I} & 0 \\ 0 & 0 & \frac{E'}{E} - \frac{I'}{I} \end{pmatrix}$$

And

$$Z_f J^{[2]} Z^{-1} \begin{pmatrix} -(\beta I + 2d + a) & \beta S & -\beta S \\ 0 & -(\beta I + 2d + \delta + \gamma) & 0 \\ 0 & \beta I & -(2d + a + \delta + \gamma) \end{pmatrix}$$

Let the block matrix defined as

$$B = Z_f Z + Z J^{[2]} Z^{-1} = \begin{pmatrix} B11 & B12 \\ B21 & B22 \end{pmatrix}$$

Where,

$$B11 = [-(\beta I + 2d + a)$$

$$[\frac{\beta SI}{E} \frac{\beta SI}{E}]$$

$$B_{21} = [\begin{matrix} 0 \\ 0 \end{matrix}]$$

$$B_{22} = \begin{bmatrix} (\beta I + 2d + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I} & 0 \\ \beta I & -(2d + a + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I} \end{bmatrix}$$

Next for a vector norm and

¦ (u, v, w) ¦= max {¦u¦, ¦v+w¦} the Lozinskii measure for the norm is followed by μ (B) ≤ sup {g1, g2}

$$g_1 = \mu_1(B_{11}) + B_{12}$$

Where g1 and g2 are defined as the $g_2 = B_{21} + \mu_1(B_{22})$

Here B12 and B21 are the matrix norm with respect to vector norms and μ1 is Lozinkskii measure norm, so we have

$$\mu_1(B_{11}) = -(\beta I + 2d + a)$$

$$|B_{12}| = \frac{\beta SI}{E}$$

$$|B_{21}| = 0$$

$$\mu_1(B_{22}) = \max\{-(2d + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I}, -(2d + a + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I}\}$$

$$= -(2d + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I}$$

Where μ1 (B22) can be calculated by taking the maximum of the two sums by adding the absolute values of non-diagonal in column with diagonal element in that column

These values can substitute in g1 and g2 we get

$$g_1 = (\beta I + 2d + a) + \frac{\beta SI}{E}$$

$$g_2 = (2d + \delta + \gamma) + \frac{E'}{E} - \frac{I'}{I}$$

$$\frac{E'}{E} + (d + a) \quad \frac{\beta SI}{E}$$

$$\frac{E'}{E} \quad a \frac{I'}{I} \quad (d + \delta + \gamma)$$

Putting the above value in g1 and g2

$$g_1 \quad (\beta I + 2d + a) + \frac{E'}{E} + (d + a) - \frac{E'}{E} \quad d$$

$$g_2 \quad (2d + \delta + \gamma) + \frac{E'}{E} \quad \frac{I'}{I} \quad -(d + \delta + \gamma) - \frac{E'}{E} - d$$

$$\mu_{(B)} \quad \frac{E'}{E} - d \quad \text{and so}$$

$$\int_0^t (\mu(B))ds \quad \ln \frac{E(t)}{E(0)} \quad d$$

Therefore − Q2 < 0 and Bendxison criteria [25] is fulfilled, so by global stability of the endemic equilibrium .The reproduction number is larger than one.

2.7 Model parameters and initial values (in thousands)

Parameter	Fig. 1.2
S(0)	8900
N	9000
E(0)	1000
I(0)	100

R(0)	**0**
A	**70**
B	**0.0001**
A	**0.06**
Γ	**0.08**
D	**0.2**
Δ	**0.2**
E	**0.05**

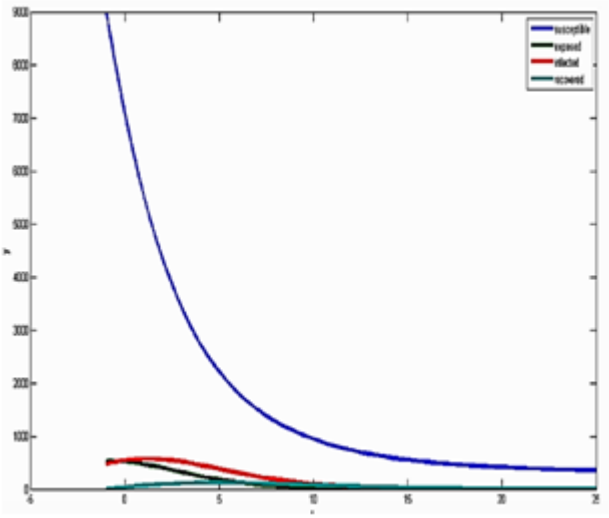

Fig. 2.2: Dynamical behavior of the model

III. RESULTS AND DISCUSSION

The proposed model includes Exposed class in addition to the susceptible, infected and recovered. We have applied a variable population malicious object transmission model in computer network with constant latent and immune periods. We have derived the equilibrium of the model and correspondingly, plotted the graphs for analysis of the stability. Runge-Kutta Fehlberg fourth-fifth order method is used to solve the system of equations (2.2) and the behavior of the susceptible, exposed, infectious, and recovery nodes with respect to time are observed as depicted in Fig.2.2. From Fig.2.2, we observe that the system is asymptotically stable.

The basic reproduction number R0 is obtained and has been identified as a threshold parameter. If R0 1, the virus free equilibrium is asymptotically stable in the feasible region D and the virus always dies out. This means that when such a condition holds, the introduction of a few infected computers into an infective-free population won't give rise to an epidemic out break and no endemic situation will developed i.e. the infection will vanish along the time. Our model showed that malicious codes were able to pervade if R0 > 1. If R0 >1, a unique endemic equilibrium D* exists and is locally asymptotically stable. It implies that longer the exposure period of the system, the less likely it is that it will become endemic in the long run. Important information of this model is that the most connected nodes are most vulnerable to an attack. From the model we calculate the reproduction number through the use of spectral radius of generation matrix resulting in the approximate threshold condition. Stability of the model is stated in terms of reproduction number.

IV. CONCLUSION

Based on the proposed model, we have presented a general methodology for network immunization. Our proposed strategy can effectively utilize the effect of locally spreading awareness to prevent an infection breaking out in the network. It hopes that this provides a more accurate model of the spread of malicious attack. We see that in formulation of the model we have not assumed the immunity after first infection of the machine and allowed for recovering machine to be once again susceptible to future infection. We discussed the computer virus can be closely modeled by biological virus. The interactions among the parameters are analyzed and plausibility of model is verified by examining their mathematical characteristics. Global stability of endemic equilibrium for the epidemic prototype has been identified. Therefore, this model is useful tool to control the multiply of computer virus and gives some insight in to the dynamics of computer virus. Simulation result shows that the proposed model describes the outbreak law of the virus and predictive capability of the follow up outbreak of the virus .Therefore for complex network of real society will be able to improve the entire network for immunization rates of virus propagation.

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