Dynamic model of worm propagation in computer network

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ABSTRACT

In this paper, an attempt has been made to mathematically formulate a compartmental susceptible – exposed – infectious – susceptible with vaccination (that is, anti-virus treatment) (SEIS-V) epidemic transmission model of worms in a computer network with natural death rate (which depends on the total number of nodes). The stability of the result is stated in terms of modified reproductive number R_v. We have derived an explicit formula for the modified reproductive number R_v, and have shown that the worm-free equilibrium, whose component of infective is zero, is globally asymptotically stable if $R_v < 1$, and unstable if $R_v > 1$. The contribution of vertical transmission to the modified reproductive number is also analyzed. Numerical methods are employed to solve and simulate the system of equations developed and interpretation of the model yields interesting revelations. Analysis of efficient antivirus software is also performed.

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1. Introduction

These are days of networked computers. Lot of effort has been devoted to the development of virtual vaccines but each time a new worm appears. All systems connected to the internet are potential targets to the attack of worms because the openness of internet makes them accessible to attack. It is well known that software can only offer a temporary immunity to the nodes. Thus once a software wanes from the node of the computer network, the node becomes susceptible to the attack again. Therefore, it is of vital importance to determine the optimal software needed to eradicate a computer worm from the network. Also the mathematical models give the clear view to identify and solve the many complex problems. Thus, we develop e-epidemic models for different classes of computer nodes and analyze the effect of antivirus software in the computer network.

In past several decades, many authors have studied different mathematical models which illustrate the dynamical behavior of the transmission of biological disease and/or computer viruses. Based on SIR classical epidemic models [1–3] and due to the lots of similarities between biological viruses and computer viruses, several extended research articles are proposed to study the spreading and attacking behavior of computer viruses in different phenomenon, e.g. virus propagation [4–13], quarantine [14–17], virus immunization [18–24], time delay [25], fuzziness [26], effect of antivirus software [27,28], vaccination [29,30], etc. May et al. [31] studied the dynamical behavior of viruses on scale free networks. Transmission of viruses in computer network in P2P network and its time relevance is well studied [32]. Wang et al. studied the robustness of filtering on nonlinearities in packet losses, sensors, etc. [33–38]. In the computer network, worms may transmit from main server to any of the end nodes using vertical transmission. In this condition, the anti-virus software is taken only to the new infected nodes. It can be easily observed that, the network cannot be recovered permanently from the worms till a single computer node is attached to the network, still we run the anti-virus software. Then, we propose an SEIS-V epidemic

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model with vertical transmission using vaccination (that is, run of anti-virus software time and again with full efficacy) such that we can get temporary recovery from the infection of worms.

The rest parts of this paper is structured as follows: In Section 2, we formulate the e-epidemic SEIS-V worm model and develop the system of differential equations, in Section 3, we introduce modified reproductive number and discuss the local stability conditions for worm free equilibrium, in Section 4, we establish that the worm free equilibrium is globally asymptotically stable if modified reproductive number is less than one, in Section 5, we discuss the stability of the system developed using numerical methods and MATLAB and finally, in Section 6, we conclude this paper.

2. The e-epidemic SEIS-V worm model

In any computer network, to derive the model equation, the total number of nodes (N) is divided into four classes: fully Susceptible nodes (S), Exposed nodes (E), Susceptible nodes with anti-virus software (V), Infected nodes (I), that is,

$$S + E + I + V = N. \tag{1}$$

In this model, the flow of worms is from class S to class E, class S to class V, class E to class I, class V to class I and class V to class S (due to lack of latest version of anti-virus software) which can be seen in Fig. 1. The transmission between model classes can be expressed by the following system of differential equations:

$$\begin{aligned}
\frac{dS}{dt} &= bN - \frac{\beta SI}{N} - f(N)S - pS + \gamma I + \varepsilon V, \\
\frac{dE}{dt} &= \frac{\beta SI}{N} - f(N)E - \eta E, \\
\frac{dI}{dt} &= \eta E - f(N)I - \alpha I - \gamma I + \frac{\sigma \beta VI}{N} + \theta b, \\
\frac{dV}{dt} &= pS - \frac{\sigma \beta VI}{N} - \varepsilon V - f(N)V.
\end{aligned} \tag{2}$$

In this model, we assume that the anti-virus software have full efficacy, but in reality, the efficacy of such software is usually not 100%. Hence, we need to take this into account when we formulate epidemic models with anti-virus software (shown by flow chart in Fig. 1) where we suppose that the birth rate coefficient is b, the natural death rate coefficient depends on the population size N, denoted by $f(N)$, the anti-virus software is given to both attached nodes and susceptible nodes, standard incidence is chosen. The software is not completely efficacious and σ ($0 \leqslant \sigma \leqslant 1$) describes the inefficaciousness of the software such that the infection incidence from the inefficaciously vaccinated nodes is $\sigma \beta VI/N$; p is the anti-virus software rate coefficient, β is the rate of contact, η is the rate coefficient of exposed class, α is the death rate coefficient due to the attack of worms, γ is the rate coefficient from class I to class S, ε is rate coefficient from class V to class S. The model also assumes that the flow of worms between the model classes can be spread through vertical transmission. In this case, the attack of worms through vertical transmission increases at the rate θ and introduced at the class I.

3. Worm free equilibrium & modified reproductive number

The modified reproductive number or simply the reproductive number (R_v) is the average number of secondary infections produced by one infected computer nodes. This can be obtained through the local analysis of the stability of the trivial equilibrium point. If $R_v < 1$, which implies that the worms fade out from the network eventually. If $R_v > 1$, which means the worms persists at a constant endemic level in the computer network.

We now get the modified reproductive number for the worm control or eradication and analyze the worm-free equilibrium. Our analysis will be restricted to the dynamics of the three equations of the system (2). By the Eq. (1) and the system (2), we get, $\frac{dN}{dt} = (b - f(N))N - \alpha I + \theta b$ which is also called as equation for the total population (i.e. total nodes) [30,19]. Thus, $b \to f(N)$ as $t \to \infty$.

This shows that, the feasible region,

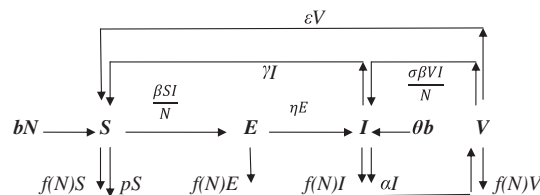$$U = \{(S, E, I, V) : S, E, I, V \geqslant 0, \quad S + E + I + V = N\}$$

Fig. 1. Schematic diagram for the flow of worms in computer network.