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A computer virus model with graded cure rates

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ABSTRACT

A dynamical model characterizing the spread of computer viruses over the Internet is established, in which two assumptions are imposed: (1) a computer possesses infectivity once it is infected, and (2) latent computers have a lower cure rate than seizing computers. The qualitative properties of this model are fully studied. First, the basic reproduction number, R_0, for this model is determined. Second, by introducing appropriate Lyapunov functions, it is proved that the virus-free equilibrium is globally asymptotically stable if $R_0 \leq 1$, whereas the viral equilibrium is globally asymptotically stable if $1 < R_0 \leq 4$. Next, the sensitivity analysis of R_0 to three system parameters is conducted, and the dependence of R_0 on the remaining system parameters is investigated. On this basis, a set of policies is recommended for eradicating viruses spreading across the Internet effectively.

1. Introduction

Computer viruses are malicious codes or programs which can replicate themselves and spread via wired or wireless networks. With the ever increasing number of Internet applications, computer viruses have come to be a great threat to our work and daily life. With the advent of the Internet of Things, this threat would become increasingly serious. Consequently, it is urgent to understand how computer viruses spread over the Internet and to propose effective measures to cope with this issue. To achieve this goal, and in view of the fact that the spread of virus among computers resembles that of biological virus among a population, it is suitable to establish dynamical models describing the propagation of computer viruses across the Internet by appropriately modifying epidemic models [1].

One common feature shared by a computer virus and a biological virus is infectivity [2]. Based on this fact, some classic epidemic models, such as the *SIRS* model [3–7], *SEIR* model [8,9], *SEIRS* model [10], *SEIQV* model [11] and *SEIQRS* model [12], were usually borrowed to depict the spread of a computer virus in such a way that (1) susceptible individuals correspond to uninfected computers, (2) latent patients correspond to infected computers in which all viruses are in latency, and (3) infecting patients correspond to infected computers in which at least one virus is breaking out. In biological background, it is well known that an infected individual who is in latency cannot infect other individuals. In computer background, however, an infected computer which is in latency can infect other computers through, say, file copying or file downloading. Unfortunately, all the previous computer virus models failed to consider this passive infectivity. Indeed, a reasonable computer virus model should assume that both seizing and latent computers have infectivity.

On one hand, a computer user will clear viruses within his computer by running antivirus software immediately when he clearly perceives the existence of viruses (he feels that his computer is suffering from significant performance degradation, say). On the other hand, a computer user might also try to clear viruses spontaneously even if he is not sure that viruses are staying in his computer possibly because

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(1) he is accustomed to running antivirus program regularly, or
(2) he is informed that viruses are spreading over the Internet.

As a consequence, latent computers would be cured at a lower (but positive) rate than seizing computers. When attempting to model a computer virus, this feature of graded cure rates should be taken into consideration.

In this paper, a new computer virus propagation model, which incorporates the two features mentioned above, is proposed. One major difficulty in studying the qualitative properties of this model lies in the construction of suitable Lyapunov functions. We choose to use linear combinations of quadratic functions in independent variables as the candidate Lyapunov functions. Equipped with this tool, it is proved that the dynamic behavior of the model is determined by a threshold R_0. Specifically, the virus-free equilibrium is globally asymptotically stable if $R_0 \leq 1$, whereas the viral equilibrium is locally asymptotically stable if $R_0 > 1$ and, furthermore, is globally asymptotically stable if $R_0 \leq 4$. Based on these results and further analysis, some effective strategies for eradicating computer viruses are recommended.

The subsequent materials of this paper is organized as follows: Section 2 formulates the new model and determines its basic reproduction number. Section 3 proves the global stability of the virus-free equilibrium. Section 4 examines the local and global stabilities of the viral equilibrium. In Section 5, the dependence of R_0 on the system parameters is analyzed, and some policies for controlling the spread of computer virus are posed. Finally, Section 6 summarizes this work.

2. Mathematical model

A computer is *internal* or *external* depending on whether it is currently connected to the Internet or not. For our purpose, only internal computers are concerned, and all internal computers are categorized into three classes: uninfected computers (i.e., virus-free computers), infected computers that are currently latent (latent computers, for short), and infected computers that are currently breaking out (seizing computers, for short). Due to the fact that in the future, the total amount of computers in the world would tend to saturation, it is reasonable to suppose that this total number is constant. Let $S(t)$, $L(t)$ and $B(t)$ denote, at time t, the percentages of uninfected, latent and seizing computers in all internal computers, respectively. Then $S(t) + L(t) + B(t) \equiv 1$. Unless otherwise stated, let S, L and B stand for $S(t)$, $L(t)$ and $B(t)$, respectively.

By carefully considering the features of a computer virus, the following hypotheses are made:

(H1) External computers are connected to the Internet at positive constant rate δ, and internal computers are disconnected from the Internet also at this rate.
(H2) All newly connected computers are virus-free.
(H3) The percentage of internal computers infected at time t increases by $\beta S(L + B)$, where β is a positive constant. This hypothesis says that both seizing and latent computers have infectivity. In contrast, all traditional models assumed that only seizing individuals have infectivity, i.e., at time t the force of infection can be described as $\beta S f(B)$ [13].
(H4) Latent computers break out at positive constant rate α.
(H5) Latent computers are cured at positive constant rate γ_1, while breaking-out computers are cured at positive constant rate γ_2. For the graded cure rates, we have $\gamma_2 > \gamma_1 > 0$.

Based on the previous assumptions, one can derive the following computer virus propagation model:

$$\begin{cases} \dot{S} = \delta - \beta S(L + B) + \gamma_1 L + \gamma_2 B - \delta S, \\ \dot{L} = \beta S(L + B) - \gamma_1 L - \alpha L - \delta L, \\ \dot{B} = \alpha L - \gamma_2 B - \delta B. \end{cases} \tag{1}$$

Usually, the *basic reproduction number* for a virus propagation model is defined as the average number of previously virus-free computers that are infected by a single viral computer during its life cycle. By the physical meanings of the system parameters in model (1), the following results are obtained:

(a) The average lifetime of a latent computer is $T_1 = \frac{1}{\alpha+\gamma_1+\delta}$.
(b) A latent computer converts an uninfected computer to a latent one at rate $\upsilon_1 = \beta$.
(c) The average lifetime of a seizing computer is $T_2 = \frac{1}{\gamma_2+\delta}$.
(d) A seizing computer converts an uninfected computer to a seizing one at rate $\upsilon_2 = \frac{\beta\alpha}{\alpha+\gamma_1+\delta}$.

Thus, the basic reproduction number is obtained as

$$R_0 = T_1\upsilon_1 + T_2\upsilon_2 = \frac{\beta(\alpha + \gamma_2 + \delta)}{(\alpha + \gamma_1 + \delta)(\gamma_2 + \delta)}. \tag{2}$$

Because $S(t) + L(t) + B(t) \equiv 1$, it is sufficient to consider the following two-dimensional subsystem:

$$\begin{cases} \dot{L} = \beta(1 - L - B)(L + B) - \gamma_1 L - \alpha L - \delta L, \\ \dot{B} = \alpha L - \gamma_2 B - \delta B \end{cases} \tag{3}$$

with initial conditions $L(0) \geq 0$ and $B(0) \geq 0$. The feasible region for system (3) is $\Omega = \{(L, B) : L \geq 0, B \geq 0, L + B \leq 1\}$, which is positively invariant.

An equilibrium of system (3) is *virus-free* or *viral* depending on whether $L + B = 0$ or not.