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A propagation model of computer virus with nonlinear vaccination probability

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ABSTRACT

This paper is intended to examine the effect of vaccination on the spread of computer viruses. For that purpose, a novel computer virus propagation model, which incorporates a nonlinear vaccination probability, is proposed. A qualitative analysis of this model reveals that, depending on the value of the basic reproduction number, either the virus-free equilibrium or the viral equilibrium is globally asymptotically stable. The results of simulation experiments not only demonstrate the validity of our model, but also show the effectiveness of nonlinear vaccination strategies. Through parameter analysis, some effective strategies for eradicating viruses are suggested.

1. Introduction

With the constant progress of software/hardware technologies and wide-spread popularization of computer networks, computer viruses have also been advancing; their structures are becoming increasingly complex, and their infecting capabilities are becoming increasingly strong. As a consequence, computer viruses have brought about huge financial losses and social panic [1].

There are two main approaches to struggling against computer virus: the *microscopic* approach and the *macroscopic* approach [2]. The microscopic approach is devoted to the development of more powerful antivirus programs by analyzing the structures and behaviors of new viruses. Due to the unpredictability of new viruses, there is a significant lag from the emergence of a new virus to the release of a software against the virus [3]. As a result, the virus can spread at a high speed across the Internet before its natural enemy appears. What is more serious, existing antivirus software cannot provide insight into the laws governing the propagation of computer virus across the network and, hence, cannot contain the spread of viruses. To remedy this shortage of the microscopic approach and inspired by the biologically epidemic models [4,5], Kephart [6] proposed a macroscopic model featuring the spread of computer viruses, showing that its propagating behavior can be predicted. Since then, multifarious computer virus propagation models have been presented by modifying their biological counterparts [7–36].

Vaccination is widely regarded as one of the most effective measures of repressing computer viruses, by which some susceptible computers inside or outside the Internet can acquire temporary immunity. Indeed, the awareness that there exist a large number of infected computers would enhance the probability that the user of a susceptible computer has his computer vaccinated. To our knowledge, however, the majority of previous models neglect the influence of vaccination strategy on the

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prevalence of viruses. Very recently, Gan et al. [37] suggested a computer virus propagation model with linear vaccination probability, i.e., the probability that a susceptible computer gets vaccinated is linear in the number of currently infected computers. In reality, however, a variety of nonlinear vaccination probabilities may appear. Consequently, it is worthwhile to study computer virus propagation models with nonlinear vaccination probability.

This paper aims to investigate the effect of nonlinear vaccination strategies on the spread of computer viruses. For that purpose, a new computer virus propagation model, which incorporates a nonlinear vaccination probability, is proposed. A systematic study shows that (a) the virus-free equilibrium is globally asymptotically stable when the basic reproduction number $R_0 \leqslant 1$, and (b) the viral equilibrium is globally asymptotically stable if $R_0 > 1$. Both theoretical predictions and simulation results show that vaccination can inhibit virus prevalence effectively. On this basis, some effective strategies for eradicating computer virus are advised.

The subsequent materials of this paper are organized as follows. Section 2 formulates the model and determines its basic reproduction number. Section 3 calculates the equilibria. The global stabilities of the virus-free equilibrium and the viral equilibrium are examined in Sections 4 and 5, respectively. Section 6 gives some simulation examples. In Section 7, some policies are posed for controlling the spread of computer virus. Finally, Section 8 summarizes this work.

2. Hypotheses and model formulation

For convenience, computers are called as *nodes*. For our purposes, all nodes worldwide are assumed to be in one of three possible states: *susceptible* (i.e., uninfected but not immune), *infected*, and *recovered* (i.e., uninfected and immune). Let $S(t)$, $I(t)$, and $R(t)$ denote the numbers of susceptible, infected, and recovered nodes in the Internet at time t, respectively. Let $N(t)$ denote the total number of internal nodes at time t. Then, $N(t) = S(t) + I(t) + R(t)$. Without ambiguity, $S(t), I(t), R(t)$, and $N(t)$ shall be abbreviated as S, I, R, and N, respectively.

For the modeling purpose, the following hypotheses are imposed (see Fig. 1):

- ($H1$) Nodes outside the Internet enters the Internet at rate $b > 0$, of which $(1-p)b$ nodes are susceptible, and pb nodes are recovered, $0 \leqslant p \leqslant 1$.
- ($H2$) Every node in the Internet leaves the Internet with probability $\mu > 0$.
- ($H3$) Every susceptible node in the Internet is infected by infected nodes in the Internet with probability $\beta I, \beta > 0$.
- ($H4$) Due to the effect of treatment, every infected node in the Internet becomes recovered with probability $\gamma_1 > 0$, or becomes susceptible with probability $\gamma_2 > 0$.
- ($H5$) Every recovered node in the Internet loses immunity with probability $\alpha_2 > 0$.
- ($H6$) Due to the appearance of new vaccine, every susceptible node in the Internet acquires temporary immunity with probability $\alpha_1 f(I)$, where $\alpha_1 > 0$, function f is continuously differentiable with $f(0) = 1$ and $f' \geqslant 0$.

This collection of hypotheses can be presented as the transfer diagram shown in Fig. 1, from which the dynamical model is established as

$$\begin{cases} \dot{S} = (1-p)b - \alpha_1 f(I)S - \mu S + \gamma_2 I - \beta SI + \alpha_2 R, \\ \dot{I} = \beta SI - \gamma_2 I - \mu I - \gamma_1 I, \\ \dot{R} = pb + \gamma_1 I + \alpha_1 f(I)S - \mu R - \alpha_2 R, \end{cases} \tag{1}$$

with initial condition $(S(0), I(0), R(0)) \in \mathbb{R}^3_+$.

The basic reproduction number of an infected computer, denoted R_0, is defined as the average number of computers that are infected by this computer during its infected period. For our purpose, let us introduce a standard method for calculating R_0 (see Ref. [38]).

Consider a compartment model for the spread of computer viruses, where all infected nodes are classified as m compartments, which are numbered as compartment 1 through m, and all uninfected nodes are classified as $n-m$ compartments, which are numbered as compartment $m+1$ through n. Let x_i denote the number (or proportion) of nodes in the i-th com-

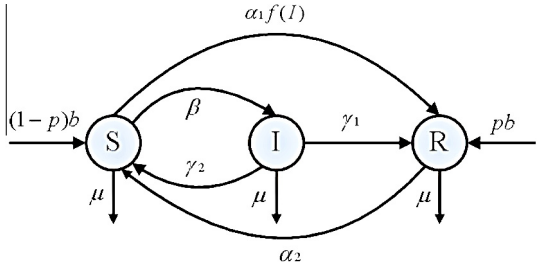

Fig. 1. The transfer diagram of the model.