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## Nonlinear Analysis: Real World Applications

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# Global exponential stability of nonresident computer virus models<sup>☆</sup>

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## ABSTRACT

This paper is concerned with nonresident computer virus models which are defined on the nonnegative real vector space. By using differential inequality technique, we employ a novel argument to show that the virus-free equilibrium is globally exponentially stable, and the exponential convergent rate can be unveiled. Moreover, a numerical simulation is given to demonstrate our theoretical results.

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## 1. Introduction

Network is an indispensable part of everyday life, it develops so fast and offers us more and more functionalities and facilities. At the same time, there is a rapid increase in computer viruses. In recent years, many dynamical models characterizing the spread of computer viruses over the internet were investigated, for example [1–9] and the cited references there in. Therefore, it is extremely important to analyze and protect computers against virus, particularly nonresident computer virus that does not store or execute itself from the computer memory.

Let  $S(t)$ ,  $L(t)$  and  $A(t)$  respectively denote percentage of susceptible computers, infected computers in which viruses have not been loaded in their memory, and infected computers in which viruses have been located in memory in the computers at time  $t$ . In various recent literature [5,6,10], the following system of differential equations is used to describe the dynamics of nonresident computer virus

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$$\begin{cases} \frac{dS(t)}{dt} = b - \mu_1 S(t) - \beta_1 S(t)L(t) - \beta_2 S(t)A(t) + \gamma_1 L(t) + \gamma_2 A(t) \\ \frac{dL(t)}{dt} = \beta_1 S(t)L(t) + \beta_2 S(t)A(t) + \alpha_2 A(t) - (\mu_2 + \alpha_1 + \gamma_1)L(t) \\ \frac{dA(t)}{dt} = \alpha_1 L(t) - (\mu_3 + \alpha_2 + \gamma_2)A(t). \end{cases} \quad (1.1)$$

It is assumed in the above model that all newly accessed computers are free of virus, and all viruses in the computers are nonresident. It is also assumed that the external computers are accessed to the internet at a constant rate  $b$  at each time  $t$ , the uninfected and latent computers as well as the infectious computers of the internal computers are disconnected from the internet respectively at the rates of  $\mu_1, \mu_2$ , and  $\mu_3$ . The percentage of internal computers infected at time  $t$  increases by  $\beta_1 SL + \beta_2 SA$ , where  $\beta_1$  and  $\beta_2$  are positive constants.  $\alpha_1$  denotes the rate at which nonresident viruses within latent computers are loaded into memory, and  $\alpha_2$  is the rate at which nonresident viruses within infectious computers transfer control to the application program.  $\gamma_1$  and  $\gamma_2$  are the cure rates of latent and infectious computers. By the biological meanings, all parameters in model (1.1) are positive.

Under the following initial condition:

$$S(0) > 0, \quad L(0) > 0 \quad \text{and} \quad A(0) > 0, \quad (1.2)$$

the authors in [10] proved the following results on the global asymptote stability of system (1.1) with initial value (1.2).

**Theorem A** (See [10, Theorem 1.1]). *Let the basic reproduction number be*

$$R_0 = \frac{b\{\beta_1 + \beta_2\alpha_1/(\mu_3 + \alpha_2 + \gamma_2)\}}{\mu_1\{(\mu_2 + \alpha_1 + \gamma_1) - \alpha_1\alpha_2/(\mu_3 + \alpha_2 + \gamma_2)\}} < 1$$

and  $\mu_1 \leq \min(\mu_2, \mu_3)$ . Then, the virus-free equilibrium  $E^0 = (S^0, 0, 0) = (\frac{b}{\mu_1}, 0, 0)$  is globally asymptotically stable, and every solution  $(S(t), L(t), A(t))$  of (1.1) with initial value (1.2) satisfies

$$\lim_{t \rightarrow +\infty} (S(t), L(t), A(t)) = (S^0, 0, 0).$$

But in fact, as a model of biological system, the initial condition:

$$S(0) \geq 0, L(0) \geq 0 \quad \text{and} \quad A(0) \geq 0, \quad (1.3)$$

is more realistic than (1.2) in practical application of model (1.1). Set

$$IV_1 = \{(S(0), L(0), A(0)) | S(0) \geq 0, L(0) \geq 0 \text{ and } A(0) \geq 0\},$$

$$IV_2 = \{(S(0), L(0), A(0)) | S(0) \geq 0, \text{ and } L(0) = A(0) = 0\},$$

and

$$IV_3 = \{(S(0), L(0), A(0)) | S(0) \geq 0, L(0) \geq 0, A(0) \geq 0 \text{ and } L(0) + A(0) > 0\}.$$

It is obvious that

$$IV_3 = IV_1 \setminus IV_2,$$

and

$$(S(t), L(t), A(t)) \Big|_{IV_2} = \left( \left[ S(0) - \frac{b}{\mu_1} \right] e^{-\mu_1 t} + \frac{b}{\mu_1}, 0, 0 \right), \quad (1.4)$$

exponentially converges to the virus-free equilibrium  $E^0 = (S^0, 0, 0) = (\frac{b}{\mu_1}, 0, 0)$ . Thus, to reveal the global dynamics of system (1.1) with initial value (1.3), we only need to study all solutions of system (1.1) with the

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