

QUALITATIVE AND BIFURCATION ANALYSIS USING A COMPUTER VIRUS MODEL WITH A SATURATED RECOVERY FUNCTION

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Abstract In this paper, we introduce a saturated treatment function into the computer virus propagation model, where the treatment function is limited for increasing number of infected computers. By carrying out global qualitative and bifurcation analysis, it is shown that the system exhibits some new and complicated behaviors: if the basic reproduction number is larger than unity, the number of infected computers will show persistent behavior, either converging to some positive constant or oscillating; and if the basic reproduction number is below unity, the model may exhibit complicated behaviors including: (i) backward bifurcation; (ii) almost sure virus eradication where the number of infective computers tends to zero for all initial positions except the interior equilibria; (iii) oscillating backward bifurcation where either the number of infective computers oscillates persistently, if the initial position lies in a region covering the stable virus equilibrium, or virus eradication, if the initial position lies outside this region; (iv) virus eradication for all initial positions if the basic reproduction number is less than a turning point value.

Keywords Global stability, virus infection, ratio-dependent, basic reproduction number.

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1. Introduction

Mathematical modeling has been playing an ever more important role in the study of epidemiology. Various epidemic models have been proposed and explored extensively and great progress has been achieved in the studies of disease control and prevention [3, 4, 6, 7, 8, 11] and the references therein.

Due to the high similarity between computer viruses and biological viruses [2], the classical SIR (Susceptible-Infected- Recovered) computer virus propagation model was proposed [5, 9, 12], which is formulated as the following system of differential equations:

$$\begin{cases} \frac{dS}{dt} = b - \lambda S(t)I(t) - dS(t), \\ \frac{dI}{dt} = \lambda S(t)I(t) - \varepsilon I(t) - dI(t), \\ \frac{dR}{dt} = \varepsilon I(t) - dR(t), \end{cases} \quad (1.1)$$

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Here it is assumed that all the computers connected to the network in concern are classified into three categories: susceptible, infected and recovered computers. Let $S(t)$, $I(t)$ and $R(t)$ denote their corresponding numbers at time t , respectively. This model involves four positive parameters: b denotes the rate at which external computers are connected to the network, ε denotes the recovery rate of infected computers due to the anti-virus ability of the network, d denotes the rate at which one computer is removed from the network, λ denotes the rate at which, when having a connection to one infected computer, one susceptible computer can become infected.

Recently, Jianguo Ren et. all in [10] introduced a new recovery function

$$T(I) = \begin{cases} \varepsilon I, & \text{if } 0 \leq I \leq I_0, \\ m, & \text{if } I > I_0, \end{cases}$$

where ε is the recovery rate when the anti-virus ability is not fully utilized, $m = \varepsilon I_0$ to characterize the saturation phenomenon of the limited anti-virus ability of a network and carefully investigated the dynamics of the following computer virus propagation model

$$\begin{cases} \frac{dS}{dt} = rS\left(1 - \frac{S}{k}\right) - \lambda SI - dS, \\ \frac{dI}{dt} = \lambda SI - T(I) - dI, \\ \frac{dR}{dt} = T(I) - dR. \end{cases} \quad (1.2)$$

Similar to the argument in [13], we take the saturated recovery function as

$$T(I) = \frac{\mu I}{1 + \alpha I},$$

where μ is positive and α is nonnegative, to show that the network condition is limited for increasing number of infected computers. Then the model to be studied takes the following form:

$$\begin{cases} \frac{dS}{dt} = rS\left(1 - \frac{S}{k}\right) - \lambda SI - dS, \\ \frac{dI}{dt} = \lambda SI - \frac{\mu I}{1 + \alpha I} - dI, \\ \frac{dR}{dt} = \frac{\mu I}{1 + \alpha I} - dR. \end{cases} \quad (1.3)$$

Before going into any detail, we simplify the model. Since the first two equations of (1.3) are independent of the third one and its dynamic behavior is trivial when $I(t_0) = 0$ for some $t_0 > 0$, it suffices to consider the first two equations with $I > 0$. Thus, we restrict our attention to the following reduced model:

$$\begin{cases} \frac{dS}{dt} = rS\left(1 - \frac{S}{k}\right) - \lambda SI - dS, \\ \frac{dI}{dt} = \lambda SI - \frac{\mu I}{1 + \alpha I} - dI. \end{cases} \quad (1.4)$$

To our knowledge, this is the first time the effect of anti-virus ability is taken into account this way. First, we give the threshold value determining whether the virus dies out completely. Second, we study the existence of equilibria, and investigate their local asymptotic stability. Next, we find that, depending on the anti-virus ability, the system may undergo a backward bifurcation, which is instructive for us when choosing an appropriate virus-controlling strategy. Finally, we prove that,

under appropriate conditions, the system may admit bistable states: a stable virus-free equilibrium and a stable virus equilibrium, or two stable virus equilibria.

The organization of this paper is as follows. In the next section, we present preliminary results for our model including the boundedness and existence of equilibria and backward bifurcation. In Section 3, we present a stability on virus-free equilibrium.

2. Backward bifurcation

In this section, we will give some preliminary results from (1.4), including the boundedness and existence of equilibria and backward bifurcation.

One of the key concepts in dealing with computer virus models is the basic reproduction number, usually denote it by R_0 , which plays an important role in computer virus propagation. One often observes the threshold property that the virus removed out if $R_0 \leq 1$ and invade the susceptible host if $R_0 > 1$. In this case, the bifurcation leading from a virus-free equilibrium to an virus equilibrium is called forward bifurcation.

However, more and more studies reveal that, under appropriate conditions, many computer virus and epidemic models admit backward bifurcation, i.e., both the virus-free equilibrium and the virus equilibrium coexist when $R_0 \leq 1$ and the basic reproduction number cannot be the necessary threshold for the virus eradication. It is very important to identify the backward bifurcations to obtain some necessary thresholds for the control of virus.

We can define the basic reproduction number as

$$R_0 = \frac{k\lambda(r-d)}{r(d+\mu)}.$$

It is obvious that (1.4) always has a trivial equilibrium $E = (0, 0)$ and unique virus-free equilibrium $E_0 = (\frac{k(r-d)}{r}, 0)$. The virus equilibria of (1.4) can be obtained by solving the following algebraic equations

$$rS\left(1 - \frac{S}{k}\right) - \lambda SI - dS = 0, \quad \lambda SI - \frac{\mu I}{1 + \alpha I} - dI = 0. \quad (2.1)$$

First, from the first equation of (2.1), we obtaining $I = \frac{k(r-d)-rS}{k\lambda}$. We substitute this into the second equation, which yields

$$S^2 - \left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} + \frac{d}{\lambda}\right]S + \frac{k\mu}{\alpha r} + \frac{d}{\lambda}\left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r}\right] = 0. \quad (2.2)$$

Let the discriminant of (2.2) be $\Delta = \left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} - \frac{d}{\lambda}\right]^2 - 4\frac{k\mu}{\alpha r}$. Then it is easy to see that

$$\Delta = \left[\frac{k\lambda}{\alpha r} + R_0\left(\frac{d}{\lambda} + \frac{\mu}{\lambda}\right) - \frac{d}{\lambda}\right]^2 - 4\frac{k\mu}{\alpha r}. \quad (2.3)$$

Therefore, we have the following simple statements which describe the number and location of equilibria of system (1.4).

Now, we know that $\Delta \geq 0$ is equivalent to

$$R_0 \geq 1 - \frac{k\lambda^2 + \mu\alpha r}{\alpha r(d+\mu)} + \frac{2\lambda}{d+\mu}\sqrt{\frac{k\mu}{\alpha r}} := \varrho_0, \quad (2.4)$$

$$R_0 \leq 1 - \frac{k\lambda^2 + \mu\alpha r}{\alpha r(d + \mu)} - \frac{2\lambda}{d + \mu} \sqrt{\frac{k\mu}{\alpha r}}, \quad (2.5)$$

Note that $\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} + \frac{d}{\lambda} > 0$ is equivalent to

$$R_0 > -1 - \frac{k\lambda^2 - \mu\alpha r}{\alpha r(d + \mu)}.$$

It follows that $\Delta \geq 0$ if and only if (2.4) holds. Let us suppose that (2.4) holds. Then (2.2) has two positive solutions S_1 and S_2 , where

$$S_1 = \frac{\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} + \frac{d}{\lambda} + \sqrt{\Delta}}{2}, \quad \text{and} \quad S_2 = \frac{\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} + \frac{d}{\lambda} - \sqrt{\Delta}}{2},$$

where $S_2 < S_1$. So one can get

$$I_1 = \frac{k(r-d) - rS_1}{k\lambda}, \quad \text{and} \quad I_2 = \frac{k(r-d) - rS_2}{k\lambda},$$

then $E_1 = (S_1, I_1)$ and $E_2 = (S_2, I_2)$ are the candidates of the virus equilibria of (1.4). Then E_i ($i = 1, 2$) is an virus equilibrium of (1.4) if $S_i < \frac{k(r-d)}{r}$.

To facilitate the discussion below, define

$$\varrho_1 := 1 + \frac{k\lambda^2 - \mu\alpha r}{\alpha r(d + \mu)}.$$

Theorem 2.1. *Assume that $R_0 \geq \varrho_0$.*

- (i) *If $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$, then both $E_1 = (S_1, I_1)$ and $E_2 = (S_2, I_2)$ exist when $\varrho_1 < R_0 < 1$.*
- (ii) *If $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$, then E_1 does not exist but E_2 exists if $R_0 > 1$.*
- (iii) *If $\lambda \geq \sqrt{\frac{\mu\alpha r}{k}}$, then E_1 does not exist. Furthermore, E_2 exists when $R_0 > 1$, and E_2 does not exist when $R_0 \leq 1$.*

Proof. We know that E_i ($i = 1, 2$) is an virus equilibrium of (1.4) if $S_i < \frac{k(r-d)}{r}$. Let us consider the conditions under which $S_1 < \frac{k(r-d)}{r}$. By the definitions, we see that this is equivalent to

$$-\sqrt{\Delta} > \frac{k\lambda}{\alpha r} + \frac{d}{\lambda} - \frac{k(r-d)}{r}. \quad (2.6)$$

This implies that

$$\frac{k\lambda}{\alpha r} + \frac{d}{\lambda} - R_0 \left(\frac{d + \mu}{\lambda} \right) < 0. \quad (2.7)$$

It follows that

$$R_0 > 1 + \frac{k\lambda^2 - \mu\alpha r}{\alpha r(d + \mu)} = \varrho_1. \quad (2.8)$$

On the other hand, by (2.6), we have

$$\left[\frac{k(r-d)}{r} - \frac{k\lambda}{\alpha r} - \frac{d}{\lambda} \right]^2 > \Delta. \quad (2.9)$$

It follows that (2.9) is equivalent to

$$R_0 < 1. \tag{2.10}$$

Hence, $S_1 < \frac{k(r-d)}{r}$ holds if and only if (2.8) and (2.10) are valid. Moreover, if $R_0 \leq \varrho_1$ or $R_0 \geq 1$, we have $S_1 \geq \frac{k(r-d)}{r}$.

By arguments similar to those above, we see that $S_2 < \frac{k(r-d)}{r}$ if (2.8) holds or $1 < R_0 < \varrho_1$.

Note that $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$ is equivalent to $\varrho_1 < 1$. The proof is complete. \square

Note that $\varrho_0 < 1$. If $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$, then $\varrho_1 < 1$. Then, from (i) of Theorem 2.1, we have the following corollary for giving conditions for such a backward bifurcation to occur.

Corollary 2.1. *System (1.4) has a backward bifurcation with virus equilibria when $R_0 < 1$ and $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$.*

Note that a backward bifurcation with virus equilibria when $R_0 < 1$ is very interesting in applications. The basic reproduction number does not provide a description of the necessary elimination effort; rather the description of the effort is provided through the value of the critical parameter at the turning point. Thus, it is important to identify backward bifurcation to obtain thresholds for the control of virus.

3. Stability of equilibria

In this section, we deal with the global dynamics of (1.4). First, we examine the local stability of the equilibria by analyzing the eigenvalues of the Jacobian matrices of (1.4) at the equilibria.

The Jacobian matrix of (1.4) at the virus-free equilibrium E is

$$J_E = \begin{pmatrix} r - d & 0 \\ 0 & -(d + \mu) \end{pmatrix},$$

which implies that E is always a saddle.

The Jacobian matrix evaluated at E_0 is

$$J_{E_0} = \begin{pmatrix} -(r - d) & -\frac{k\lambda(r-d)}{r} \\ 0 & \frac{k\lambda(r-d)}{r} - \mu - d \end{pmatrix},$$

which has negative eigenvalues, implying asymptotic stability of the disease-free equilibrium if and only if

$$\frac{k\lambda(r - d) - r(\mu + d)}{r} < 0,$$

which is equivalent to $R_0 < 1$. So the virus-free equilibrium E_0 is locally asymptotically stable if $R_0 < 1$, and is unstable when $R_0 > 1$.

Then, from the above discussions, we get

Theorem 3.1. *Consider model (1.4). The following assertions hold.*

- (i) E is a saddle.

(ii) If $0 < R_0 < 1$, then the virus-free equilibrium E_0 is locally asymptotically stable while it is unstable if $R_0 > 1$.

Let J_i be the Jacobian matrix of (1.4) at $E_i = (S_i, I_i)$, $i = 1, 2$; then we get

$$J_i = \begin{pmatrix} -\frac{r}{k}S_i & -\lambda S_i \\ \lambda S_i & \frac{\mu\alpha I_i}{(1+\alpha I_i)^2} \end{pmatrix}.$$

Thus, one can get

$$\det(J_1) = S_1 I_1 \left(\lambda^2 - \frac{\mu\alpha r}{k(1+\alpha I_1)^2} \right).$$

Note that $R_0 > \varrho_0$ and

$$I_1 = \frac{k(r-d) - \frac{k\lambda}{\alpha} - \frac{dr}{\lambda} - r\sqrt{\left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} - \frac{d}{\lambda}\right]^2 - 4\frac{k\mu}{\alpha r}}}{2k\lambda}.$$

It follows from the above two conditions that

$$\begin{aligned} (1 + \alpha I_1)^2 &= \left[\frac{\alpha r}{\lambda} \cdot \frac{\frac{k(r-d)}{r} + \frac{k\lambda}{\alpha r} - \frac{d}{\lambda} - \sqrt{\left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} - \frac{d}{\lambda}\right]^2 - 4\frac{k\mu}{\alpha r}}}{2k} \right]^2 \\ &< \frac{\alpha^2 r^2 \left[\frac{k\lambda}{\alpha r} + \frac{k(r-d)}{r} - \frac{d}{\lambda}\right]^2}{4k^2 \lambda^2} \\ &< \frac{\mu\alpha r}{k\lambda^2}, \end{aligned}$$

then, $\det(J_1) < 0$. It follows that $E_1 = (S_1, I_1)$ is a saddle point.

By the same argument, we obtain $\det(J_2) > 0$. Thus, $E_2 = (S_2, I_2)$ is a focus, a node, or a center. Further, we have

$$\text{tr} J_2 = \frac{k\mu\alpha I_2 - rS_2(1 + \alpha I_2)^2}{k(1 + \alpha I_2)^2} \quad (3.1)$$

Since $\frac{\mu I_2}{1 + \alpha I_2} = \lambda S_2 I_2 - dI_2$, we see that the trace of J_2 is

$$\text{tr} J_2 = \frac{1}{(1 + \alpha I_2)} \left[\alpha \left(\lambda - \frac{r}{k} \right) S_2 I_2 - \alpha d I_2 - \frac{r}{k} S_2 \right]. \quad (3.2)$$

Thus, the $\text{tr} J_2$ is negative if $\lambda \leq \frac{r}{k}$. Suppose that $\lambda > \frac{r}{k}$. Let us find the conditions under which $\text{tr} J_2 = 0$. Since $S_2 = \frac{k(r-d)}{r} - \frac{\lambda k}{r} I_2$, it follows from (3.2) that $\text{tr} J_2 = 0$ is equivalent to

$$\frac{\alpha\lambda(r-k\lambda)}{r} I_2^2 + \left[\frac{\alpha(k\lambda-r)(r-d)}{r} - \alpha d + \lambda \right] I_2 - (r-d) = 0. \quad (3.3)$$

Thus, by (3.3), we can get that $\text{tr} J_2 \neq 0$ if

$$\frac{\alpha(k\lambda-r)(r-d)}{r} - \alpha d + \lambda \leq 0. \quad (3.4)$$

Suppose that

$$\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda > 0. \quad (3.5)$$

It follows from

$$\Delta_2 = \left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]^2 + 4(r - d) \frac{\alpha\lambda(r - k\lambda)}{r} > 0, \quad (3.6)$$

that we obtain

$$I_2 = \frac{\left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]}{2 \frac{\alpha\lambda(k\lambda - r)}{r}} \left[1 \pm \sqrt{1 + \frac{4(r - d) \frac{\alpha\lambda(r - k\lambda)}{r}}{\left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]^2}} \right].$$

In view of $I_2 < \frac{r-d}{\lambda}$, we have

$$I_2 = \frac{\left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]}{2 \frac{\alpha\lambda(k\lambda - r)}{r}} \left[1 - \sqrt{1 + \frac{4(r - d) \frac{\alpha\lambda(r - k\lambda)}{r}}{\left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]^2}} \right]. \quad (3.7)$$

Hence, after a long and tedious calculation and using (3.7) can be reduced to

$$\mu = \frac{\alpha r}{4k} \left[\left[\frac{k\lambda}{\alpha r} + \frac{k(r - d)}{r} - \frac{d}{\lambda} \right]^2 - H^2 \right], \quad (3.8)$$

where

$$H := \frac{\lambda^2 r}{\alpha(k\lambda - r)} - \frac{dr}{\lambda(k\lambda - r)} - \sqrt{\left[\frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda \right]^2 + 4(r - d) \frac{\alpha\lambda(r - k\lambda)}{r}}. \quad (3.9)$$

As a consequence, we see that (3.6), (3.5) and (3.8) are the necessary and sufficient conditions for $\text{tr}J_2 = 0$. The previous discussion show that the stability of E_2 does not change if (3.4) holds. It follows from the definition of $\text{tr}J_2 = 0$ that (3.4) implies that $\text{tr}J_2 < 0$. Therefore, E_2 is stable if (3.4) holds. It follows from (3.1) and (3.9) that $\text{tr}J_2 < 0$ if

$$\begin{aligned} & \frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda > 0, \\ \mu & < \frac{\alpha r}{4k} \left[\left[\frac{k\lambda}{\alpha r} + \frac{k(r - d)}{r} - \frac{d}{\lambda} \right]^2 - H^2 \right], \end{aligned} \quad (3.10)$$

and that $\text{tr}J_2 > 0$ if

$$\begin{aligned} & \frac{\alpha(k\lambda - r)(r - d)}{r} - \alpha d + \lambda > 0, \\ \mu & > \frac{\alpha r}{4k} \left[\left[\frac{k\lambda}{\alpha r} + \frac{k(r - d)}{r} - \frac{d}{\lambda} \right]^2 - H^2 \right]. \end{aligned} \quad (3.11)$$

From the above discussions, we get

Theorem 3.2. Let $\lambda < \sqrt{\frac{\mu\alpha r}{k}}$, $\varrho_1 < R_0 < 1$ and (3.6) hold. For system (1.4), we have

- (i) E_2 is stable if either (3.4) or (3.11) hold.
- (ii) E_2 is unstable if (3.11) hold.

3.1. Analysis at $R_0 = 1$

In this section, we consider the system (1.3), when $\alpha = 0$. To use the center manifold theory, as described in [1] (Theorem 4.1). To apply this method, the following simplification and change of variables are made first. Let $S = x_1$, $I = x_2$, $R = x_3$, the system (1.3) with $\alpha = 0$ becomes

$$\begin{cases} \frac{dx_1}{dt} = rx_1\left(1 - \frac{x_1}{k}\right) - \lambda x_1 I - dx_1 = f_1, \\ \frac{dx_2}{dt} = \lambda x_1 x_2 - \mu x_2 - dI = f_2, \\ \frac{dx_3}{dt} = \mu x_2 - dx_3 = f_3. \end{cases} \quad (3.12)$$

with $R_0 = 1$ corresponding to $\lambda = \lambda^* = \frac{r(d+\mu)}{k(r-d)}$. The virus-free equilibrium is $(x_1^* = \frac{k(r-d)}{r}, x_2^* = 0, x_3^* = 0)$. The linearization matrix of system (3.12) around the infection-free equilibrium when $\lambda = \lambda^*$ is

$$\begin{aligned} J_{xf} &= \begin{pmatrix} -(r-d) & -\frac{k\lambda^*(r-d)}{r} & 0 \\ 0 & \frac{k\lambda^*(r-d)}{r} - \mu - d & 0 \\ 0 & \mu & -d \end{pmatrix} \\ &= \begin{pmatrix} -(r-d) & -(d+\mu) & 0 \\ 0 & 0 & 0 \\ 0 & \mu & -d \end{pmatrix}. \end{aligned}$$

The matrix J_{xf} has eigenvalues $(0, -d, -(r-d))^T$, which meets the requirement of a simple zero eigenvalue and others having negative real part. A right eigenvector ω corresponding to the zero eigenvalue is $\omega = (-\frac{d+\mu}{r-d}, 1, \frac{\mu}{d})$ and the left eigenvector satisfying $\nu \cdot \omega = 1$ is $\nu = (0, 1, 0)$. For the system (3.12) we can get

$$a = \sum_{k,i,j=1}^3 \nu_k \omega_i \omega_j \frac{\partial^2 f_k}{\partial x_i \partial x_j} \left(\frac{k(r-d)}{r}, 0, 0 \right) = -\frac{2r}{k} \left(\frac{d+\mu}{r-d} \right)^2 < 0,$$

and

$$b = \sum_{k,i=1}^3 \nu_k \omega_i \frac{\partial^2 f_k}{\partial x_i \partial \lambda} \left(\frac{k(r-d)}{r}, 0, 0 \right) = \frac{k(r-d)}{r} > 0.$$

Thus, $a < 0$, $b > 0$, by item (iv) of Theorem 4.1 in [1], we can give the following result:

Theorem 3.3. The virus equilibrium point $E_1 = \left(x_1^* = \frac{k(r-d)}{r}, x_2^* = 0, x_3^* = 0 \right)$ for system (1.3) is locally asymptotically stable for R_0 near 1.

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