GLOBAL DYNAMICS OF A COMPUTER VIRUS PROPAGATION MODEL WITH FEEDBACK CONTROLS

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Abstract. A computer virus propagation model with feedback controls is first proposed and investigated. We show that the control variables do not influence on the global stability of the original differential model, they only alter the position of the unique viral equilibrium. The mathematical analyses and numerical simulations show that this equilibrium can be completely eliminated, namely, moved to the origin of coordinates if suitable values of the control variables are chosen. In the other words, the control variables are effective in the prevention of viruses in computer systems. Some numerical simulations are presented to demonstrate the validity of the obtained theoretical results.

Keywords. Global stability; Computer virus model; Lyapunov functions; Feedback controls; Numerical simulations.

1. INTRODUCTION

The models describing the computer virus propagation play especially important role in both theory and practice. In recent two decades, many authors make mathematical modeling of computer virus propagation based on differential equations, for examples, [10, 14, 15, 16, 17]. The construction and study of these models help us to understand the mechanism of propagation of computer viruses across the Internet. On this base we can make policies and decisions to prevent and control the spread of computer viruses effectively.

In this paper, we start with a computer virus model with graded cure rates proposed by Yang (see [16]), and described by the following system of nonlinear ordinary differential equations

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

where $S(t), L(t)$ and $B(t)$ denote, at time t, the percentages of uninfected, latent and seizing computers in all internal computers, respectively. For more detail of this model we refer the readers to [16].

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

$$
\begin{aligned}
\dot{L} &= \beta(1 - L - B)(L + B) - \gamma_1 L - \alpha L - \delta L, \\
\dot{B} &= \alpha L - \gamma_2 B - \delta B,
\end{aligned}
\tag{2}
$$

with initial conditions $L(0) \geq 0$ and $B(0) \geq 0$. The feasible region for system (2) is $\Omega = \{(L, B) : L \geq 0, B \geq 0, L + B \leq 1\}$, which is positively invariant. The mathematical analysis in [16] shows that the model (2) has two equilibrium points. They are the virus-free equilibrium E_0 and the viral equilibrium E_*, where

$$
E_0 = (0, 0), \quad E_* = (L_*, B_*) = \left(\frac{(\gamma_2 + \delta)(1 - \frac{1}{\mathcal{R}_0})}{\alpha + \delta + \gamma_2}, \quad \frac{\alpha(1 - \frac{1}{\mathcal{R}_0})}{\alpha + \delta + \gamma_2} \right).
$$

In the above formula $\mathcal{R}_0 = \dfrac{\beta(\alpha + \gamma_2 + \delta)}{(\alpha + \gamma_1 + \delta)(\gamma_2 + \delta)}$ is the basic reproduction number of model (2). The property of global stability of model (2) was established by using quadratic Lyapunov's functions (see [16]). The obtained results are:

(i) The virus-free equilibrium E_0 is globally asymptotically stable with respect to Ω if $\mathcal{R}_0 \leq 1$;

(ii) The viral equilibrium E_* is globally asymptotically stable with respect to $\Omega' = \Omega \setminus E_0$ if $1 < \mathcal{R}_0 \leq 4$.

In the case $\mathcal{R}_0 > 4$ Lyapunov's stability theorem cannot ensure the global stability of E_*. However, the numerical simulations in [16] show that E_* is also globally asymptotically stable if $\mathcal{R}_0 > 4$. Very recently, in [9] the property of global stability of (2) was reestablished on the basis of the classical method of Lyapunov functions combined with the Volterra-Lyapunov matrix properties.

Based on the analysis of global stability of the model it is seen that a good strategy for protecting computer systems from viruses is the tuning of parameters so that $\mathcal{R}_0 \leq 1$ (see [16]). However, if this is not possible, i.e., if $\mathcal{R}_0 > 1$ then we have to accept the fact that the system is always attacked by viruses. In this situation one of the effective approaches is to consider the model with feedback control variables. For models with feedback controls see [3, 4, 6, 7, 11, 12] and the references therein. If it is possible to prove that the feedback control variables do not affect the global stability of the original differential model but only change the position of the viral equilibrium, then the feedback control variables can be used to limit the number of computers infected with viruses in the system. Concerning the model (2), to the best of our knowledge, until now no feedback controls have been considered with it.

Motivated by this, in this paper we will study the model with feedback control variables. Theoretical analyzes show that feedback control variables do not affect the global stability of the original differential model but only change the position of the unique equilibrium point. Especially, the position of the viral equilibrium can be changed by changing the values of the control variables. In particular, this equilibrium may be eliminated if suitable

control variables are chosen. This result plays an important role in constructing strategies for protection of computer systems.

To analyze the global stability of the proposed model, we use an appropriate Lyapunov for investigating the global stability of the virus-free equilibrium. Meanwhile, in the context that the proposed model consists of many equations and contains many parameters, the analysis of stability of the positive equilibrium point is very difficult because the expressions of this equilibrium point as well as the associated Jacobian matrix are very complicated. Therefore, we investigate the global stability of the equilibrium point via numerical simulations. The numerical simulations agree that if the equilibrium point exists then it is indeed global stable. This fact completely agrees with the related results of ordinary differential models in ecology and epidemiology, namely, for the majority of models in these fields, if the positive equilibrium points exist then they are globally asymptotically stable, i.e,. the models achieve the robust development (see [1, 2]).

The paper is organized as follows. In Section 2, a model with feedback controls is proposed. The global stability of the model is investigated in Section 3. Numerical simulations are presented in Section 4. Finally, some conclusions are given in Section 5.

2.   THE MODEL WITH FEEDBACK CONTROLS

We first consider the following computer virus propagation model with feedback controls

$$
\begin{aligned}
\dot{L} &= \beta(1 - L - B)(L + B) - \gamma_1 L - \alpha L - \delta L - c_1 L u_1 := f_1(L, B, u_1, u_2), \\
\dot{B} &= \alpha L - \gamma_2 B - \delta B - c_2 B u_2 := f_2(L, B, u_1, u_2), \\
\dot{u_1} &= d_1 L - e_1 u_1 := f_3(L, u_1), \\
\dot{u_2} &= d_2 B - e_2 u_2 := f_4(B, u_2),
\end{aligned}
\tag{3}
$$

where $u_1(t)$ and $u_2(t)$ are feedback control variables and the parameters c_i, d_i, e_i $(i = 1, 2)$ are positive constants.

Lemma 1. *The set $\Omega^* := \{(L, B, u_1, u_2) \in \mathbb{R}_+^4 : L + B \leq 1\}$ is a positive invariant set of* (3). *Furthermore, we have* $\limsup_{t \to \infty} u_i(t) \leq d_i/e_i$ $(i = 1, 2)$.

Proof. Set $\xi(t) := 1 - L(t) - B(t)$. Then $\dot{\xi} = \beta\xi(\xi - 1) + (\gamma_1 + \delta)L + (\gamma_2 + \delta)B + c_1 L u_1 + c_2 B u_2$. Combining this with (3) we obtain the system

$$
\begin{aligned}
\dot{\xi} &= \beta\xi(\xi - 1) + (\gamma_1 + \delta)L + (\gamma_2 + \delta)B + c_1 L u_1 + c_2 B u_2, \\
\dot{L} &= \beta\xi(L + B) - (\gamma_1 + \alpha + \delta)L - c_1 u_1 L, \\
\dot{B} &= f_2(L, B, u_1, u_2), \qquad \dot{u_1} = f_3(L, u_1), \qquad \dot{u_2} = f_4(B, u_2).
\end{aligned}
$$

It is easy to verify that $\mathbb{R}_+^5$ is a positive invariant set of the above system. This implies that Ω^* is a positive invariant set of (3). On the other side, from (3) we have $u_i(t) \leq d_i - e_i u_i(t)$ $(i = 1, 2)$. By a standard comparison argument and basic ODE theory, it follows the remaining assertion of the lemma. ∎

Analogously as in our previous work [5], it is easy to calculate the basic reproduction number of the model (3) by the next generation matrix method [13]. Therefore, we have the following.

Lemma 2. *The number*

$$\mathcal{R}_0^* = \frac{\beta(\alpha + \gamma_2 + \delta)}{(\alpha + \gamma_1 + \delta)(\gamma_2 + \delta)}$$

is the basic reproduction number of model (3).

Theorem 1. *The model* (3) *always possesses the free virus equilibrium* $E^0 = (0,0,0,0)$ *for all values of the parameters. Meanwhile, the necessary and sufficient condition for the existence of the viral equilibrium* $E^* = (L^*, B^*, u_1^*, u_2^*)$ *is* $\mathcal{R}_0^* > 1$, *where* E^* *is defined by*

$$u_2^* = \frac{d_2}{e_2}B^*, \quad u_1^* = \frac{d_1}{e_1}L^*, \quad L^* = \frac{\gamma_2 + \delta}{\alpha}B^* + \frac{c_2 d_2}{\alpha e_2}B^{*2}, \tag{4}$$

B^* *being the unique root of the equation* $P_3(X) := \tau_3 X^3 + \tau_2 X^2 + \tau_1 X + \tau_0 = 0$ *with the coefficients*

$$\tau_3 = -\frac{c_1 d_1}{e_1}\left(\frac{c_2 d_2}{\alpha e_2}\right)^2 - \beta\left(\frac{c_2 d_2}{\alpha e_2}\right)^2, \quad \tau_2 = -2\beta\frac{\gamma_2 + \alpha + \delta}{\alpha^2}\frac{c_2 d_2}{e_2} - 2\frac{c_1 d_1}{e_1}\frac{\gamma_2 + \delta}{\alpha^2}\frac{c_2 d_2}{e_2},$$

$$\tau_1 = \beta\frac{c_2 d_2}{\alpha e_2} - \frac{\gamma_1 + \alpha + \delta}{\alpha}\frac{c_2 d_2}{e_2} - \frac{c_1 d_1}{e_1}\left(\frac{\gamma_2 + \delta}{\alpha}\right)^2 - \beta\left(\frac{\gamma_2 + \alpha + \delta}{\alpha}\right)^2, \tag{5}$$

$$\tau_0 = \frac{(\alpha + \gamma_1 + \delta)(\gamma_2 + \delta)}{\alpha}(\mathcal{R}_0^* - 1).$$

Moreover, if $\mathcal{R}_0^* > 1$ *then we have the estimate*

$$L^* + B^* \leq (1 - \mathcal{R}_0^{*-1})(1+K)^{-1}, \quad K := \min\left\{\frac{1}{2}\frac{1}{\beta}\frac{c_1 d_1}{e_1}, \quad \frac{1}{2}\frac{\gamma_1 + \alpha + \delta}{\beta(\gamma_2 + \alpha + \delta)}\frac{c_2 d_2}{e_2}\right\}. \tag{6}$$

Proof.

Indeed, the equilibrium points of (3) are the solutions of the system

$$f_1(L, B, u_1, u_2) = 0, \quad f_2(L, B, u_1, u_2) = 0, \quad f_3(L, u_1) = 0, \quad f_4(B, u_2) = 0. \tag{7}$$

It is easy to see that from the 4th, 3rd and 2nd equations of (7) we obtain (4). Next, substituting (4) into the first equation of (7) we obtain $BP_3(B) = 0$. From here it follows that $B = 0$ or $P_3(B) = 0$.

Notice that $\tau_3 < 0$ and $\tau_2 < 0$. Besides, if $\mathcal{R}_0^* > 1$ then $\tau_0 > 0$ and vice versa. Moreover, if $\mathcal{R}_0^* \leq 1$ then $\dfrac{\beta}{\alpha + \gamma_1 + \delta} \leq \dfrac{\gamma_2 + \delta}{\alpha + \gamma_2 + \delta} < 1$. Therefore, $\beta < \alpha + \gamma_1 + \delta$. It follows that $\tau_1 < 0$.

Consider three cases of $\mathcal{R}_0^*$:

Case 1. If $\mathcal{R}_0^* = 1$ then the equation $P_3(B) = 0$ has a trivial root $B_1 = 0$ and has no positive roots.

Case 2. If $\mathcal{R}_0^* < 1$ then by standard techniques of mathematical analysis it is easy to prove that the equation $P_3(B) = 0$ has no positive roots.

Case 3. If $\mathcal{R}_0^* > 1$ then it is easy to prove that the equation $P_3(B) = 0$ has a unique positive root.

Thus, the existence of the viral equilibrium is proved.

Next, consecutively multiplying the first and the second equations of (7) by $\gamma_2 + \alpha + \delta$ and $\gamma_1 + \alpha + \delta$ respectively, and adding side-by-side of the resulting equations we obtain

$$
\begin{aligned}
&- \beta(\gamma_2 + \alpha + \delta)(L^* + B^*)^2 + (\gamma_2 + \delta)(\gamma_1 + \alpha + \delta)(\mathcal{R}_0^* - 1)(L^* + B^*) \\
&- (\gamma_2 + \alpha + \delta)c_1 u_1^* L^* - (\gamma_1 + \alpha + \delta)c_2 u_2^* B^* = 0.
\end{aligned}
$$

It follows that

$$
L^* + B^* = (1 - \mathcal{R}_0^{*-1}) - \left[\frac{1}{\beta} c_1 u_1^* L^* + \frac{\gamma_1 + \alpha + \delta}{\beta(\gamma_2 + \alpha + \delta)} c_2 u_2^* B^* \right] \frac{1}{L^* + B^*}.
$$

Taking into account $u_1^* = \dfrac{d_1 L^*}{e_1}$, $u_2^* = \dfrac{d_2 B^*}{e_2}$ and using the simple inequality $2(L^2 + B^2) \geq (L + B)^2$ we obtain

$$
\frac{1}{\beta} c_1 u_1^* L^* + \frac{\gamma_1 + \alpha + \delta}{\beta(\gamma_2 + \alpha + \delta)} c_2 u_2^* B^* = \frac{1}{\beta} \frac{c_1 d_1}{e_1} L^{*2} + \frac{\gamma_1 + \alpha + \delta}{\beta(\gamma_2 + \alpha + \delta)} \frac{c_2 d_2}{e_2} B^{*2} \geq K(L^* + B^*)^2.
$$

Therefore,

$$
L^* + B^* \leq (1 - \mathcal{R}_0^{*-1}) - K(L^* + B^*).
$$

From here it follows the inequality (6) to be proved.   ∎

Remark.

Suppose it is proved that if the viral equilibrium exists ($\mathcal{R}_0^* > 1$) then it is globally stable (this result will be established in the next section). Then, we desire $L^* + B^*$ to be as small as possible. The estimate (6) shows that it is possible to make $L^* + B^*$ arbitrarily small by making K sufficiently large. This may be achieved because K depends on the control variables (see Table 1 in Section 4.) Particularly, when $K \to \infty$ then E^* moves to the origin, i.e., the viral equilibrium vanishes. In that time, for the model (2) we always have $L_* + B_* = 1 - \mathcal{R}_0^{-1}$ (see [16]). This fact indirectly confirms the important role of the control variables.

3.   GLOBAL STABILITY OF THE MODEL WITH FEEDBACK CONTROLS

In this section, we will establish the global stability property of the model (3).

3.1.   Global stability of the equilibrium E^0

The following theorem is of the global stability of E^0 established with the use of a linear Lyapunov function.

Theorem 2.   *The equilibrium point E^0 is globally asymptotically stable of (3) in Ω^* if $\mathcal{R}_0^* \leq 1$.*

Proof.

We define the Lyapunov function $V : \Omega^* \to \mathbb{R}_+$ by

$$V(L, B) = (\alpha + \gamma_2 + \delta)L + (\alpha + \gamma_1 + \delta)B + \frac{1}{2}\frac{\alpha + \gamma_2 + \delta}{d_1}c_1 u_1^2 + \frac{1}{2}\frac{\alpha + \gamma_1 + \delta}{d_2}c_2 u_2^2.$$

The time derivative of the function $V(L, B)$ along the trajectories of system (3) is

$$\begin{aligned}
\frac{dV}{dt} &= [\beta(\alpha + \gamma_2 + \delta) - (\gamma_2 + \delta)(\alpha + \gamma_1 + \delta)]B + [\beta(\alpha + \gamma_2 + \delta) - (\gamma_2 + \delta)(\alpha + \gamma_1 + \delta)]L \\
&\quad - \beta(\alpha + \gamma_2 + \delta)(L + B)^2 - \frac{\alpha + \gamma_2 + \delta}{d_1}e_1 c_1 u_1^2 - \frac{\alpha + \gamma_1 + \delta}{d_2}e_2 c_2 u_2^2 \\
&\leq [\beta(\alpha + \gamma_2 + \delta) - (\gamma_2 + \delta)(\alpha + \gamma_1 + \delta)]B + [\beta(\alpha + \gamma_2 + \delta) - (\gamma_2 + \delta)(\alpha + \gamma_1 + \delta)]L \\
&= (\gamma_2 + \delta)(\alpha + \gamma_1 + \delta)(\mathcal{R}_0^* - 1)(L + B).
\end{aligned}$$

Obviously, $dV/dt < 0$ strictly for all $(L, B) \in \Omega^*$ except for the equilibrium E^0, where $dV/dt = 0$. Hence, the function V satisfies Lyapunov's asymptotic stability theorem [8], and the equilibrium point E^0 of system (3) is globally stable. ∎

3.2. Numerical simulations for investigating global stability of the positive equilibrium point

In this subsection, some numerical simulations are performed to investigate the global stability of the positive equilibrium point E^*. For this purpose, we consider model (3) with the parameters

$$\alpha = 0.1, \quad \beta = 0.8, \quad \delta = 0.2, \quad \gamma_1 = 0.1, \quad \gamma_2 = 0.2.$$

In this case, we have $\mathcal{R}_0^* = 2.5 > 1$. We select the control variables as follows

$$c_1 = 1, \quad c_2 = 2, \quad d_1 = 1, \quad d_2 = 1.25, \quad e_1 = 2, \quad e_2 = 5.$$

Consequently, the unique positive equilibrium point is given by

$$E^* = (0.3413, 0.0778, 0.1707, 0.0194).$$

The solution of the model (3) with several initial values are depicted in Figure 1. From this figure it is seen that E^* is globally stable. It should be emphasized that all other numerical simulations, including those in Section 4, give similar results. This means the global stability of E^* is observed.
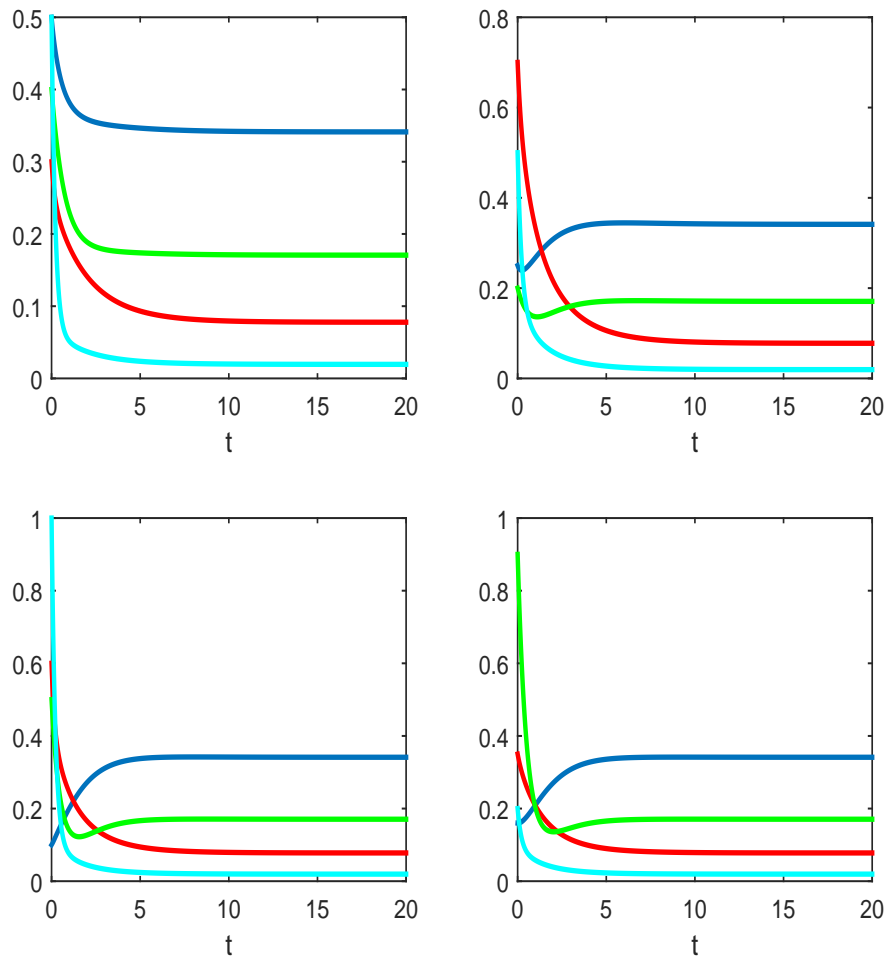
Figure 1. Solution of model (3) by the classical fourth order Runge-Kutta method (L-blue, $B-$red, u_1-green, u_2-cyan)

4. NUMERICAL SIMULATIONS

In this Section, we perform some numerical simulations to show the influence of control variables.

Consider model (3) with the parameters (see [16])

$$\alpha = 0.05, \qquad \beta = 0.8, \qquad \delta = 0.1, \qquad \gamma_1 = 0.05, \qquad \gamma_2 = 0.1.$$

In this case $\mathcal{R}_0^* = 5 > 4$. Select two sets of control variables:

Set 1. $c_1 = 1$, $\quad c_2 = 2$, $\quad d_1 = 1$, $\quad d_2 = 0.8$, $\quad e_1 = 0.5$, $\quad e_2 = 0.4$.

Set 2. $c_1 = 1.6$, $\quad c_2 = 2$, $\quad d_1 = 1$, $\quad d_2 = 0.8$, $\quad e_1 = 0.5$, $\quad e_2 = 0.5$.

The solution of the model (3) is depicted in Figures 2 and 3. From these figures it is seen that E^* is globally stable and the position of E^* depends on the values of the control variables.
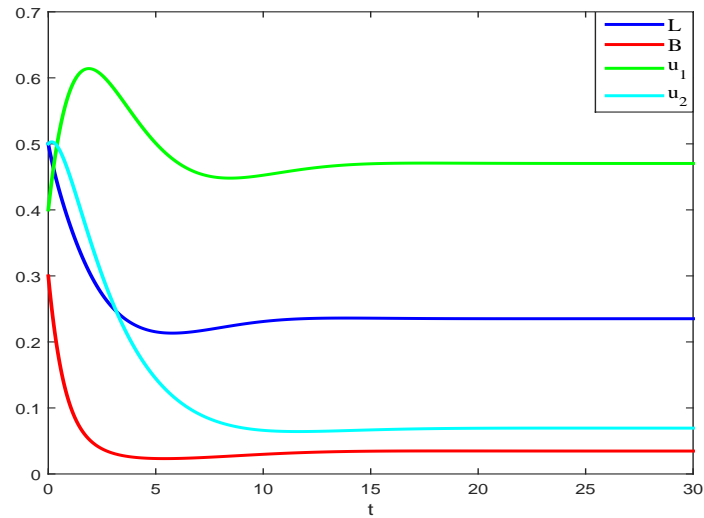
Figure 2. The solutions of model (3) for Set 1: $K = 1.25$, $E^* = (0.2352, 0.0347, 0.4703, 0.0694)$
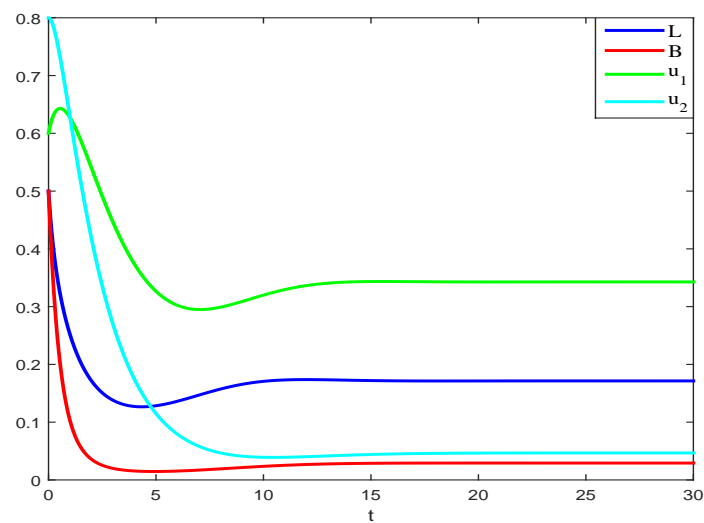

Figure 3. The solutions of model (3) for Set 2: $K = 1.6$, $E^* = (0.1714, 0.0292, 0.3428, 0.0465)$

We draw a special attention to the fact that the model (2) has $E_* = (0.64, 0.16)$, meanwhile the values of E^* of the model (3) for Set 1 and Set 2 are $(0.2352, 0.0347, 0.4703, 0.0694)$ $(K = 1.25)$ and $E^* = (0.1714, 0.0292, 0.3428, 0.0465)$ $(K = 1.6)$, respectively. From that we see that the control variables have active influence on the position of equilibrium points. Table 1 gives the position of the equilibrium E^* for different sets of the control variables. Obviously, we can make the value of $L^* + B^*$ arbitrarily small if choosing K sufficiently large. In particular case, E^* can be eliminated when K is sufficiently large. This result prompts a good strategy for preventing computer systems from viruses when $\mathcal{R}_0^* > 1$.

Table 1. The values of L^*, B^* and $L^* + B^*$

c_1	c_2	d_1	d_2	e_1	e_2	K	L^*	B^*	$L^* + B^*$
2	2	1	2	0.5	0.5	2.5	0.1412	0.0197	0.1609
16	8	10	5	1	1	20	0.0048	0.0010	0.0058
50	8	16	16	1	1	64	0.0010	0.0002	0.0012
100	80	160	125	4	4	1250	0.00018	0.00003	0.00021

5. CONCLUSIONS

In this paper, a computer virus propagation model with feedback controls is first proposed and investigated. The global stability of the model is established based on the Lyapunov stability theorem and numerical simulations. The results of the numerical simulations show that the control variables do not influence on the global stability of the original model but only change the position of the viral equilibrium. Especially, this equilibrium may be completely eliminated if the control variables are chosen suitably. Therefore, the control variables are very effective tool in prevention of viruses in computer systems.

In the future we shall develop the results of the present paper to other applied models including models of virus propagation.

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