Evaluation of HIV infected Cells

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Abstract: In this paper, Human Immunodeficiency Virus (HIV) infected cells is found out using a Simulink model. The Simulink solution is equivalent or very close to the exact solution of the problem. Accuracy of the Simulink solution to this problem is better than the existing numerical methods. The main advantage of Simulink model is that solution of any problem can be obtained by anybody without writing any codes. An illustrative numerical example is presented for the proposed method.

Key words: $CD4^+T$ Cells, HIV, Immunotherapy, Ordinary differential equations and Simulink.

AMS (MOS) Subject Classifications: 49 K 30, 65 Y 15.

1. Introduction

AIDS-Acquired Immunity Deficiency Syndrome is the disease that has affected the whole world. It is caused by Human Immunodeficiency Virus (HIV). There is still much work to be completed in the search for an anti-HIV vaccine. The aim of chemotherapies are to kill or halt the pathogen, but treatment can boost the immune system, can serve to help the body fight infection on its own [6]. The new treatments are aimed to reducing viral population and improving the immune response. This brings new hope to the treatment of HIV infection.

Once HIV enters to a human body, the human immune system tries to get rid of it. The invasion is reported to $CD4^+T$ cells. The $CD4^+T$ is a protein marker in the surface of the *T* cells and the letter *T* refers to thymus, the organ responsible for maturing these cells after they migrate from the bone marrow. The surface of $CD4^+T$ possesses a protein that can bind to foreign substances such as HIV. The HIV needs a host in order to reproduce and the above mentioned protein provides shelter. The HIV virus is a retrovirus, the RNA of virus is converted into DNA inside the $CD4^+T$ cell. Thus, when infected $CD4^+T$ cells begin to multiply to fight this pathogen, they produce more virus [2, 4, 5, 6, 3].

Simulink is a MATLAB add-on package that many professional engineers use to model dynamical processes in control systems. Simulink allows to create a block diagram representation of a system and run simulations very easily. Simulink is really translating block diagram into a system of ordinary differential equations. Simulink is the tool of choice for control system design, digital signal processing (DSP) design, communication system design and other simulation applications [1]. This paper focuses upon the implementation of Simulink approach for finding HIV affected cells in a human body by solving differential equation.

This paper is organized as follows. In section 2, the Mathematical model of HIV immunology system is described. In section 3, simulink method is presented. In section 4, numerical example is given to evaluate HIV cells. The final conclusion section demonstrates the efficiency of the method.

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2. Mathematical model of HIV immunology system

The mathematical model of the HIV immunology system is described as a system of nonlinear differential equation:

$$\frac{dT(t)}{dt} = s_1 - \frac{s_2 V(t)}{B_1 + V(t)} - \mu T(t) - kV(t)T(t), \quad T(0) = T_0, \tag{1}$$

$$\frac{dV(t)}{dt} = \frac{gV(t)}{B_2 + V(t)} - cV(t)T(t), \quad V(0) = V_0,$$
(2)

where

- 1. T represents the concentration of $CD4^+T$ cells.
- 2. V is the concentration of HIV particles.
- 3. the term $s_1 \frac{s_2 V(t)}{B_1 + V(t)}$ is the source / proliferation of unaffected cells.
- 4. $\mu T(t)$ is the natural loss of uninfected T cells.
- 5. kV(t)T(t) is loss by infection.
- 6. cV(t)T(t) is the viral loss.
- 7. $\frac{gV(t)}{B_2+V(t)}$ is viral contribution to plasma.
- 8. μ is the death rate of T cells.
- 9. k is the infection rate of T cells.
- 10. g is the input rate of an external virus source.
- 11. c is the loss rate of virus and B_1, B_2 are half saturation constants.

3. Simulink method

Simulink is an interactive tool for modelling, simulating and analyzing dynamic systems. It enables engineers to build graphical block diagrams, evaluate system performance and refine their designs. Simulink integrates seamlessly with MATLAB and is tightly integrated with state flow for modelling event driven behavior. Simulink is built on top of MATLAB. A Simulink model for the given problem can be constructed using building blocks from the simulink library. The solution curves can be obtained from the model without writing any codes.

A simulink model is constructed for the following system of two differential equations as shown in the Figure 1.

$$\begin{aligned} x'(t) &= -x(t) + 1, \quad x(0) = -1\\ y'(t) &= -y(t) + 1, \quad y(0) = 1. \end{aligned}$$

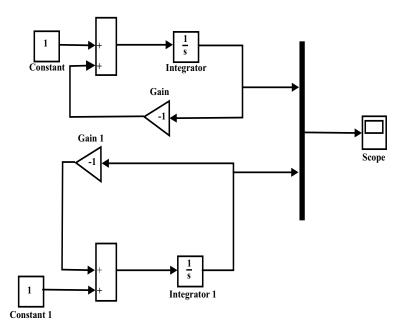


FIGURE 1. Simulink model

As soon as the model is constructed, the simulink parameters can be changed according to the problem. The solution of the system of differential equation can be obtained in the display block by running the model.

Procedure for simulink solution

Step 1. Select the required number of blocks from the simulink Library.

Step 2. Connect the appropriate blocks.

Step 3. Make the required changes in the simulation parameters.

Step 4. Run the simulink model to obtain the solution.

4. Evaluation of HIV cells

The variables and parameter values of the equations 1 and 2 are given in Table 1. Figure 2 is the Simulink model for the systems of differential equations 1 and 2. The Simulink curves for the systems are shown in Figure 2. The Simulink solution is displayed in Table 2.

Variables	Parameters
T(0)	$1000/mm^{3}$
V(0)	1000/ml
s_1	$2.0mm^{3}d^{-1}$
s_2	$1.5mm^{3}d^{-1}$
μ	$0.002d^{-1}$
k	$2.5 \times 10^4 mm^3 d^{-1}$
g	$30d^{-1}mm^{3}$
c	$0.007mm^3d^{-1}$
B_1	$14.0 mm^{3}$
B_2	$1.0mm^3$

TABLE 1. V	Variables	and	Parameters
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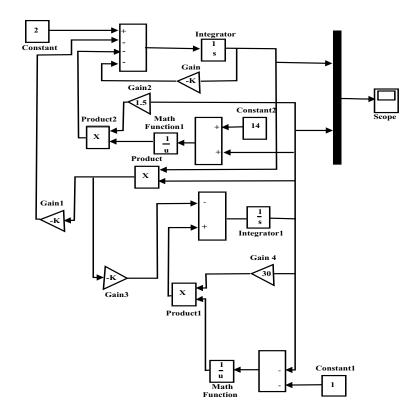


FIGURE 2. Simulink model for HIV Immunology System

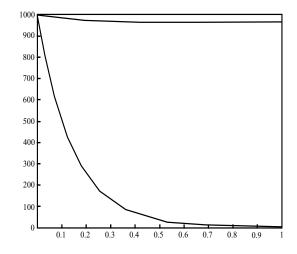


FIGURE 3. Simulink curve for HIV Immunology System

t	T(t)	V(t)
0	1000	1000
0.1	987.7	660.3
0.2	975.8	334.4
0.3	969.8	171.5
0.4	966.6	89.2
0.5	964.9	47.5
0.6	963.9	26.3
0.7	963.4	15.5
0.8	963.0	9.9
0.9	962.7	7.0
0.1	962.6	5.4

TABLE 2. Simulink Solution of HIV Immunology System

5. Conclusion

HIV affected cells can be found out by Simulink model. The simulink solution is equivalent or close to the exact solution of the problem. A numerical example is given to illustrate the derived results. In future, Simulink approach can be used to solve Mathematical model of any scientific and engineering problems without writing any codes.

References

- [1] Albagul, Othman O. Khalifa, Wahyudi, Matlab and Simulink in Mechatranics, Int. J. engng Ed., **21** (2005), 896–905.
- [2] K. R. Fister, S. Lenhart, J. S. Mc Nally, Optimizing Chemotherapy in an HIV Model, *Electron. J. Diff. Eqns.*, 32 (1998), 1–12.
- [3] M. Balter, New Hopes in HIV Disease, Science, 274 (1996), 1998–1991.
- [4] D. Kirschner, S. Lenhart, S. Sebin, Optimal control of the Chemotherapy of HIV, J. Math. Biol., 35 (1997), 775–792.
- [5] D. Kirschner, A. Perelson, R. Deboer, The Dynamics of HIV infection of CD4⁺T Cells, Mathematical Biosciences, 114 (1993), 81–125.
- [6] D. Kirschner, G. F. Webb, Immunotherapy of HIV-1 Infection, Journal of Biological Systems, 6 (1998), 71-83.