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REVIEW ARTICLE

THE ADOMIAN DECOMPOSITION METHOD FOR SOLVING HIV INFECTION MODEL OF LATENTLY INFECTED CELLS

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ABSTRACT

In this article, the Adomian decomposition method (ADM) is applied to find the solution of HIV infection model of latently infected CD4+T cells. This method investigates the solution of ordinary differential equation which is calculated in the form of the components of an infinite series. These components can be easily calculated. The efficiency and the reliability of proposed method is demonstrated in different time intervals by numerical example. The derived results indicate that the approximate solution by using the ADM can be obtained in a more efficient way. All computations have been carried out by computer code written in Mathematica.

KEYWORDS

Differential Equation, HIV-1 Infection model, Adomian Decomposition Method

1. INTRODUCTION

HIV is a virus which spreads through certain body fluids that attacks the body's immune system. It kills and destroys CD4 cells, often called T cells. Over time, HIV can destroy so many of these cells and the body fails to fight off infections and disease. These special cells help the immune system to fight off infections. Untreated, HIV reduces the number of CD4 cells (T cells) in the body. This damage to the immune system makes it harder and harder for the body to fight off infections and some other diseases. Opportunistic infections or cancers take advantage of a very weak immune system and signal that the person has AIDS. HIV/AIDS is a major global health problem all over the world. Millions of dollars have been spent every year in the treatment of the disease, but no cure is available yet [1]. Approximately 25 million HIV infected individuals live in sub-Saharan Africa [Center for Disease Control (CDC); http://www.cdc.gov/ HIV].

A number of mathematical models have been proposed to understand HIV dynamics, disease progression, anti-retroviral response etc. [2-4]. Recent studies have shown that a significant proportion of CD4+T-cells are infected by the virus, and that this specific population of T-cells might be preferentially infected [5,6]. In 1989, a model for the infection of HIV was developed by a researcher. This model of the spread of the virus has three variables: the population sizes of uninfected cells, infected cells, and free virus particles. Mathematical and computational models of the human immune response under viral infection combined with experimental measurements has yielded important insights into HIV-1 pathogenesis and has enhanced progress in the understanding of HIV-1 infection. Hence, it is a useful tool to formulate meaningful mathematical models. Mathematical modeling makes the prediction of disease outbreak. Also, it evaluates the prevention and drug therapy strategies used against HIV-1 infection.

In this work, the Adomian decomposition method (ADM) will be applied to the solution of HIV-1 infection model. For this, present work is divided in following section: In section (1.1), the formulation of the proposed model is discussed. Section (1.2) is application of ADM to the proposed model. Section 3 is the numerical section. Conclusion is drawn in section 4.

1.1 Model of HIV-1 Infection with Latently Infected Cells

In the rest of our work we will apply ADM to the solution of HIV-1 infection model. We suppose that infected CD4+ T-cells [7,8] are either active or latent. From the loss of healthy T-cells due to infection, one fraction of these cells becomes active, or productively infected, while the rest remains latent. Both classes of infected cells are assumed to die with exponentially distributed waiting time [9]. With the simple mass-action infection term, we first study the following system of differential equations:

$$\left.\begin{aligned} \tfrac{dx}{dt} &= \lambda - dx - \beta xv \\ \tfrac{dw}{dt} &= (1-q)\beta xv - ew - \delta w \\ \tfrac{dy}{dt} &= q\beta xv - ay + \delta w \\ \tfrac{dv}{dt} &= ky - uv \end{aligned}\right\} \qquad (1)$$

With the initial conditions

$$x_0 = N_1, w_0 = N_2, y_o = N_3, \qquad v_0 = N_4,$$

where uninfected susceptible $CD4^+T$ T-cells are created from sources within the body at a rate λ. Uninfected $CD4^+T$ -cells die at rate d and become infected at rate βxv where β is the rate constant describing the infection process infected cells and die at rate ay free virus are produced from infected cells at rate ky and are removed at rate uv. Free virus interact with the uninfected cells to produce actively infected cells at a rate $q\beta xv$ and latently infected cells at a rate $(1-q)\beta xv$ where the

parameter q , $0 < q < 1$. Latently infected cells containing pro-viral DNA die at a rate $e\omega$ and become activated at rate $\delta\omega$.

1.2 Solution of the system (3.1) by (ADM)

Consider the following series [10-12]:

$$x = \sum_{n=0}^{\infty} x_n \,,\; y = \sum_{n=0}^{\infty} y_n \,,\; w = \sum_{n=0}^{\infty} w_n \,,\; v = \sum_{n=0}^{\infty} v_n \,.$$

Applying inverse of the operator $\frac{d}{dt}(.)$ which is integration operator $\int_0^t (.)dt$ to each equation in the system (1.1), we get

$$\left.\begin{aligned} x(t) &= x(t=0) \int_0^t \lambda t dt - d\int_0^t x(t)dt - \beta \int_0^t x(t)v(t)dt \\ w(t) &= w(t=0) + (1-q)\beta \int_0^t x(t)v(t)dt - e\int_0^t w(t)dt \\ &\quad - \delta \int_0^t w(t)dt \\ y(t) &= y(t=0) + q\beta \int_0^t x(t)v(t)dt - a\int_0^t y(t)dt \\ &\quad + \delta \int_0^t w(t)dt \\ v(t) &= v(t=0) + k\int_0^t y(t)dt - u\int_0^t v(t)dt \end{aligned}\right\}$$

Using an alternate algorithm for computing Adomain polynomial and substitute initial conditions, we have the following scheme.

$$\left.\begin{aligned} x(t) &= N_1 + \lambda t - d\int_0^t \sum_{n=0}^{\infty} x_n dt - \beta \int_0^t \sum_{n=0}^{\infty} x_n v_n dt \\ w(t) &= N_2 + (1-q)\beta \int_0^t \sum_{n=0}^{\infty} x_n v_n dt - \int_0^t \sum_{n=0}^{\infty} w_n \\ &\quad - \delta \int_0^t \sum_{n=0}^{\infty} w_n dt \\ y(t) &= N_3 + q\beta \int_0^t \sum_{n=0}^{\infty} x_n v_n dt - a\int_0^t \sum_{n=0}^{\infty} y_n dt \\ &\quad + \delta \int_0^t \sum_{n=0}^{\infty} w(t)dt \\ v(t) &= N_4 + k\int_0^t \sum_{n=0}^{\infty} y_n dt - u\int_0^t \sum_{n=0}^{\infty} v(t)dt \end{aligned}\right\}$$

The first few first terms can be calculated as follows:

$$x_1 = -(N_1 + N_1 N_4 \beta)t - (\frac{\lambda}{2}d + \frac{\lambda\beta N_4}{2})t^2$$

$$x_2 = [-\frac{d}{2}(N_1 + N_1 N_2 \beta) + \beta(N_1 + N_1 N_4 \beta)(kN_3 - uN_4)]t^2 + [\frac{d}{3}(\frac{\lambda d}{2} + \frac{\lambda\beta N_4}{2}) + (\frac{\lambda d}{2} + \frac{\lambda\beta N_4}{2})(kN_3 - uN_4)]$$

$$y_1 = (q\beta N_1 N_4 - aN_3 + \delta N_3)t + (\frac{q\beta N_4 \lambda}{2})t^2$$

$$y_2 = [-q\beta(N_1 + N_1 N_4 \beta)(kN_3 - uN_4) - a(q\beta N_1 N_4 - aN_3 + \delta N_3)\frac{1}{2} + \delta(\beta N_1 N_4 - q\beta N_1 N_4 - eN_3 - \delta N_2)\frac{1}{2}]t^2 + [-q\beta(\frac{\lambda d}{2} + \frac{\lambda d N_4}{2})(kN_3 - uN_4) - \frac{q\beta N_4}{2}\frac{\lambda}{3} + \delta(\frac{N_4\beta\lambda}{2} - \frac{q\beta N_4 \lambda}{2})(\frac{1}{3})]t^3$$

$$w_1 = (\beta N_1 N_4 - q\beta N_1 N_4 - eN_2 - \delta N_2)t + (\frac{\beta N_4 \lambda}{2} - \frac{q\beta N_1 \lambda}{2})t^2$$

$$w_2 = -[(1-q)\beta(N_1 + N_1 N_4 \beta)(kN_3 - uN_3) + (e+\delta)(\beta N_1 N_4 - q\beta N_1 N_4 - eN_2 - \delta N_2)\frac{1}{2}]t^2 + [-(1-q)\beta(kN_3 - uN_3) - (\frac{e+\delta}{3})(\frac{\beta N_4 \lambda}{2} + \frac{q\beta N_4 \lambda}{2})]t^3$$

$$v_1 = (kN_3 - uN_4)t$$

$$v_2 = [k(q\beta N_1 N_4 - aN_3 + \delta N_3) - u(kN_3 - uN_4)]\frac{t^2}{2} + \frac{kq\beta N_4 \lambda}{2}\frac{t^3}{3}$$

Similarly, three terms approximations are given below:

$$\left.\begin{aligned} x_3(t) &= 8.316504t - 0.3055667t^2 \\ y_3(t) &= 9.06t - 0.7300668t^2 - 0.08621824t^3 \\ w_3(t) &= -22.08t - 0.081254t^2 - 0.0966512t^3 \\ v_3(t) &= 0.48t + 0.09936t^2 + 0.0512t^3 \end{aligned}\right\}$$

Parameters	Definitions	values with sources
N_1	constant	7
N_2	constant	2
N_3	constant	1
N_4	constant	4
β	infected cells	0.04
λ	uninfected $CD4^+T$	0.4
δ	constant	0.3
d	Death rate of host cell	0.01
e	infection rate by recombinant	0.1
a	Death rate of HIV-1infected cell	0.2
k	HIV-1 production rate by cell	0.6
u	pathogen removed rate	0.03
q	Removal rate of recombinant	0.8

Four terms approximations:

$$\left.\begin{aligned} x_4(t) &= 8.316504t - 0.3055667t^2 - 0.000656550t^3 \\ &\quad - 0.000246791t^4 + 0.0011804889^5 \\ &\quad - 0.0006447046t^6 - 0.0056144t^7 \\ y_4(t) &= 9.06t + 0.7300668t^2 - 0.44987584t^3 \\ &\quad + 0.0694761807t^4 + 0.00002515887t^5 \\ &\quad + 0.0194114t^6 + 0.01637533t^7 \\ w_4(t) &= -22.08t - 0.081254t^2 + 0.056839573t^3 \\ &\quad - 0.0000743659t^4 + 0.001180707018t^5 \\ &\quad + 0.0002588186t^6 + 0.00011228t^7 \\ v_4(t) &= 0.48t + 0.09936t^2 + 0.06596768t^3 \\ &\quad - 0.00368988t^4 \end{aligned}\right\}$$

Five terms approximations:

$$\left.\begin{aligned} x_5(t) &= -8.316504t - 0.3055667t^2 - 0.000656550t^3 \\ &\quad - 0.002451496t^4 + 0.0000256512t^5 \\ &\quad - 0.0010980136t^6 - 0.005606856t^7 \\ &\quad + 0.000007192t^8 - 0.0000013827t^9 \\ &\quad + 0.000311487t^{10} + 0.0000000075t^{11} \\ y_5(t) &= 9.06t + 0.7300668t^2 - 0.44987584t^3 \\ &\quad + 0.091762767t^4 - 0.0024385026t^5 \\ &\quad + 0.0195065472t^6 + 0.0163697032t^7 \\ &\quad + 0.0061406104t^8 + 0.0000000110t^9 \\ &\quad - 0.00003077984t^{10} - 0.00000006t^{11} \\ w_5(t) &= -22.08t - 0.081254t^2 + 0.056839573t^3 \\ &\quad - 0.2301617941t^4 + 0.0011896308t^5 \\ &\quad + 0.0001497696t^6 + 0.0000733375t^7 \\ &\quad - 0.0000084225t^8 + 0.000002765t^9 \\ v_5(t) &= 0.48t + 0.09936t^2 + 0.06596768t^3 \\ &\quad + 0.225508634t^4 + 0.0072593479t^5 \\ &\quad + 0.0001880702t^6 + 0.0016638348t^7 \\ &\quad + 0.00122815t^8 \end{aligned}\right\}$$

2. NUMERICAL RESULTS AND DISCUSSION

The results are plotted in Figure (3.1) to (3.4). Figure (3.1) describes that normal CD4+cells increase with the passage of time. Figure (3.2) shows that latently infected cells decrease after some time while Figure (3.3) confirms that infected cells decrease and Figure (3.4) show that free virus decrease with time. For numerical results the values given in Table 1 are considered [13-15].

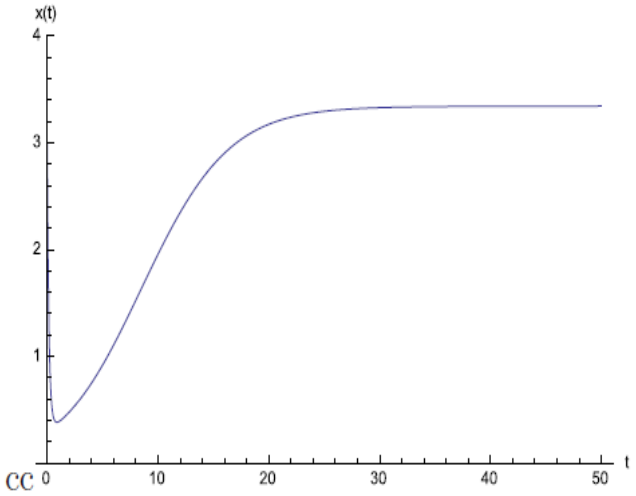

Figure 1: The plot shows the concentration of uninfected cells with respect to time t .

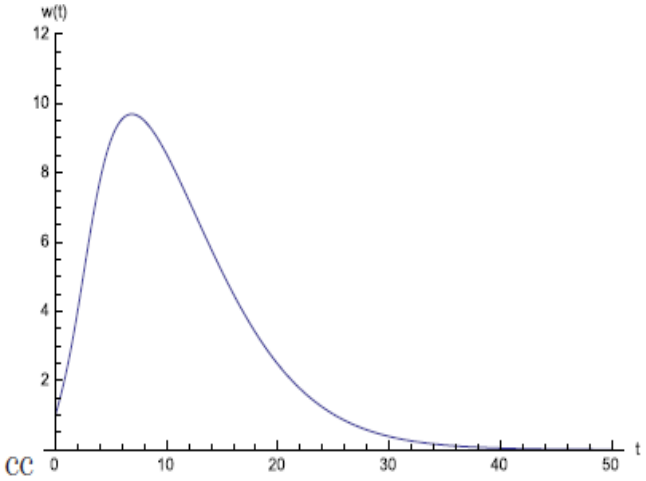

Figure 2: The plot shows the concentration of latently infected cells with respect to time t .

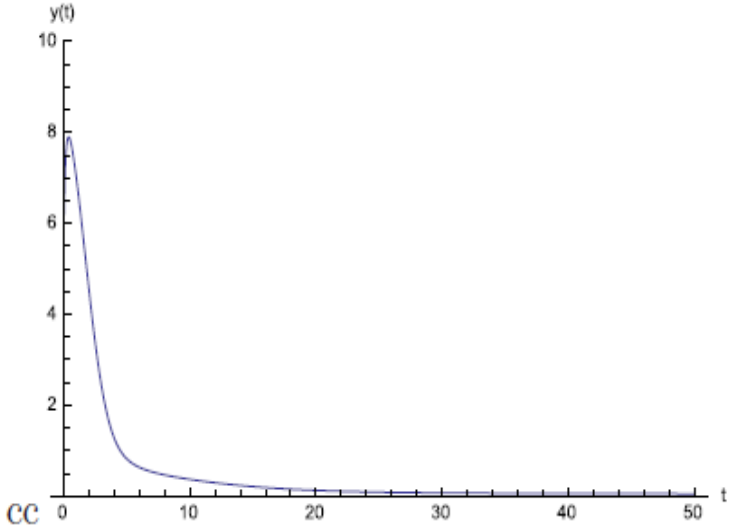

Figure 3: The plot shows the concentration of infected cells with respect to time t .

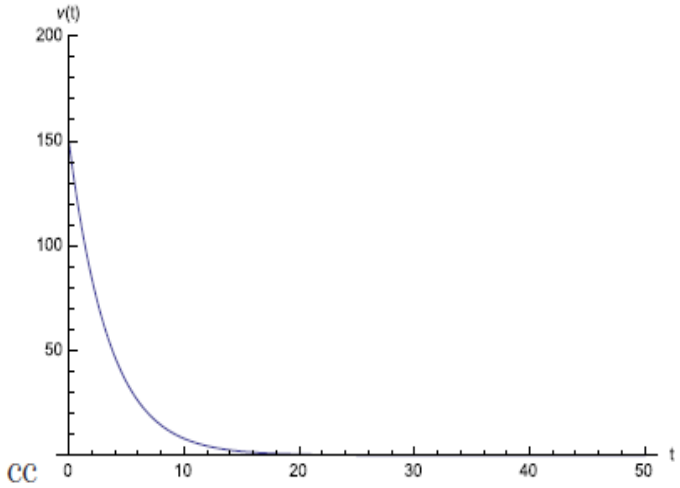

Figure 4: The plot shows the concentration of pathogen virus with respect to time t .

3.CONCLUSION

HIV infection model for the transmission dynamics of four-compartmental deterministic mathematical model was considered qualitatively and quantitatively. The ability and power of the Adomian decomposing method (ADM) confirm that there is no need of effort device for investigating the solution of a non-linear system of ordinary differential equations and reliable. A significant use of the proposed method is that the approximate solutions can be find out effortlessly with computer programs in lesser amount of time.

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