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Research Article

Numerical Treatment of the Model for HIV Infection of CD4$^+$T Cells by Using Multistep Laplace Adomian Decomposition Method

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A new method for approximate analytic series solution called multistep Laplace Adomian Decomposition Method (MLADM) has been proposed for solving the model for HIV infection of CD4$^+$T cells. The proposed method is modification of the classical Laplace Adomian Decomposition Method (LADM) with multistep approach. Fourth-order Runge-Kutta method (RK4) is used to evaluate the effectiveness of the proposed algorithm. When we do not know the exact solution of a given problem, generally we use the RK4 method for comparison since it is widely used and accepted. Comparison of the results with RK4 method is confirmed that MLADM performs with very high accuracy. Results show that MLADM is a very promising method for obtaining approximate solutions to the model for HIV infection of CD4$^+$T cells. Some plots and tables are presented to show the reliability and simplicity of the methods. All computations have been made with the aid of a computer code written in Mathematica 7.

1. Introduction

In this study, we consider that the HIV infection model of CD4$^+$T cells is examined [1]. This model is characterized by a system of the nonlinear differential equations

$$\begin{aligned} \frac{dT}{dt} &= q - \alpha T + rT\left(1 - \frac{T+I}{T_{\max}}\right) - kVT \\ \frac{dI}{dt} &= kVT - \beta I \\ \frac{dV}{dt} &= \mu\beta I - \gamma V. \end{aligned} \qquad , T(0) = r_1,\ I(0) = r_2,\ V(0) = r_3,\ 0 \le t \le R < \infty \qquad (1.1)$$

Here, R is any positive constant, $T(t)$, $I(t)$ and $V(t)$ show the concentration of susceptible CD4$^+$T cells, CD4$^+$T cells infected by the HIV viruses and free HIV virus particles in the blood, respectively, α, β, and γ denote natural turnover rates of uninfected Tcells, infected Tcells and virus particles, respectively, $(1-((T+I)/T_{\max}))$ describes the logistic growth of the healthy CD4$^+$T cells, and proliferation of infected CD4$^+$T cells is neglected. For $k > 0$ is the infection rate, the term kVT describes the incidence of HIV infection of healthy CD4$^+$T cells. Each infected CD4$^+$T cell is assumed to produce μ virus particles during its lifetime, including any of its daughter cells. The body is believed to produce CD4$^+$T cells from precursors in the bone marrow and thymus at a constant rate q. Tcells multiply through mitosis with a rate r when Tcells are stimulated by antigen or mitogen. $T_{\max}$ denotes the maximum CD4$^+$T-cell concentration in the body [2–5]. Throughout this paper, we set $q = 0.1$, $\alpha = 0.02$, $\beta = 0.3$, $r = 3$, $\gamma = 2.4$, $k = 0.0027$, $T_{\max} = 1500$, $\mu = 10$,$r_1 = 0.1$, $r_2 = 0$, $r_3 = 0.1$.

Recently, several methods have been utilized to solve numerically the HIV infection model of CD4$^+$T cells in literature. For example, Ghoreishi et al. [6] introduced and applied homotopy analysis method for solving a variant of (1.1). Ongun [7] introduced and applied the Laplace Adomian decomposition method (LADM) for solving of (1.1). The HPM was used by Merdan in [8] for finding the approximate solution of the model. Yüzbaşı has considered the Bessel collocation method in his valuable study [9]. Merdan at al. have considered the variational iteration method (VIM) [10]. Merdan at al. have considered the multistage variational iteration method (MSVIM) [11]. Although it was reported that the all mentioned methods were accurate and effective, the convergence regions are narrow in these works. But the new MLADM method increases convergence region for the series solution.

In the last decade, LADM method attracted many scientists attention [7, 12–19]. The main advantage of LADM is its capability of combining the two powerful methods for obtaining exact solutions for nonlinear equations. Although LADM gives sufficient results for small regions like VIM, MVIM, and MDTM, it does not give a satisfactory approximation to solution of some differential equation for larger t. For this reason, a multistep approach is used for obtaining the solution of the HIV infection model of CD4$^+$T cells by using the LADM method in this paper. Conceptually, a numerical method starts from an initial point and then takes a short step forward in time to find the next solution point. The process continues with subsequent steps to map out the solution in multistep methods. The newly proposed method is called multistep Laplace Adomian decomposition method (MLADM).

The results obtained with MLADM are compared with numerical solutions of the fourth-order Runge-Kutta method (RK4) since it is widely accepted and used. It is observed that the MLADM is useful to obtain exact and approximate solutions of linear and nonlinear differential equation systems.

This paper is organized as follows: Section 2 gives the LADM solution, Section 3 deals with the MLADM, and, lastly, Section 4 presents conclusions on the new MLADM method used.

2. Laplace Adomian Decomposition Method

Application of the LADM to the HIV infection model of CD4$^+$T cells is introduced in this section. In this model initial conditions were given as $T(0) = 0.1$, $I(0) = 0$, $V(0) = 0.1$. To solve this model by using the LADM, the Laplace transform is recalled. As known, the Laplace transform of $x'(t)$ is defined as

$$L\{x'(t)\} = s \cdot L\{x(t)\} - x(0). \tag{2.1}$$

We consider the following HIV infection model of CD4$^+$T cells:

$$\begin{aligned}\frac{dT}{dt} &= q - \alpha T + rT\left(1 - \frac{T+I}{T_{\max}}\right) - kVT,\\ \frac{dI}{dt} &= kVT - \beta I,\\ \frac{dV}{dt} &= \mu\beta I - \gamma V.\end{aligned} \tag{2.2}$$

If we apply the Laplace transform to both sides of (2.2) we obtain the following equations:

$$\begin{aligned}L\{T(t)\} &= \frac{T(0)}{s} + \frac{q}{s^2} + \frac{(r-\alpha)}{s}L\{T(t)\} - \frac{r}{s\cdot T_{\max}}L\left\{T^2(t)\right\} - \frac{r}{s\cdot T_{\max}}L\{T(t).I(t)\}\\ &\quad - \frac{k}{s}L\{V(t)T(t)\},\\ L\{I(t)\} &= \frac{I(0)}{s} + \frac{k}{s}L\{V(t)T(t)\} - \frac{\beta}{s}L\{I(t)\},\\ L\{V(t)\} &= \frac{V(0)}{s} + \frac{\mu\beta}{s}L\{I(t)\} - \frac{\gamma}{s}L\{V(t)\}.\end{aligned} \tag{2.3}$$

To address the nonlinear terms, $F = T^2(t)$, $G = T(t)\cdot I(t)$, $H = V(t)T(t)$ in (2.3), the Adomian decomposition method and the Adomian polynomials can be used. Solutions in this method are represented by infinite series such as

$$T = \sum_{k=0}^{\infty} T_k, \qquad I = \sum_{k=0}^{\infty} I_k, \qquad V = \sum_{k=0}^{\infty} V_k, \tag{2.4}$$

where the components T_k, I_k, and V_k are recursively computed. However, the nonlinear terms $F = T^2(t)$, $G = T(t)\cdot I(t)$, and $H = V(t)T(t)$ at the right side of (2.3) will be represented by an infinite series of Adomian polynomials:

$$F(t,x) = \sum_{k=0}^{\infty} A_k, \quad G(t,x) = \sum_{k=0}^{\infty} B_k, \quad H(t,x) = \sum_{k=0}^{\infty} C_k, \tag{2.5}$$

where A_k, B_k, and C_k, $k \geq 0$ are defined by

$$\begin{aligned}A_k &= \frac{1}{k!}\frac{d^k}{d\lambda^k}\left[F\left(t, \sum_{j=0}^{k}\lambda^j T_j\right)\right], \quad k = 0,1,2,\ldots,\\ B_k &= \frac{1}{k!}\frac{d^k}{d\lambda^k}\left[G\left(t, \sum_{j=0}^{k}\lambda^j T_j, \sum_{j=0}^{k}\lambda^j I_j\right)\right], \quad k = 0,1,2,\ldots,\\ C_k &= \frac{1}{k!}\frac{d^k}{d\lambda^k}\left[H\left(t, \sum_{j=0}^{k}\lambda^j V_j, \sum_{j=0}^{k}\lambda^j T_j\right)\right], \quad k = 0,1,2,\ldots.\end{aligned} \tag{2.6}$$

Substitution of (2.4) and (2.5) into (2.3) leads to

$$
\begin{aligned}
L\left\{\sum_{k=0}^{\infty} T_k\right\} &= \frac{T(0)}{s} + \frac{q}{s^2} + \frac{(r-\alpha)}{s} L\left\{\sum_{k=0}^{\infty} T_k\right\} - \frac{r}{s\cdot T_{\max}} L\left\{\sum_{k=0}^{\infty} A_k\right\} - \frac{r}{s\cdot T_{\max}} L\left\{\sum_{k=0}^{\infty} B_k\right\} \\
&\quad - \frac{k}{s} L\left\{\sum_{k=0}^{\infty} C_k\right\}, \\
L\left\{\sum_{k=0}^{\infty} I_k\right\} &= \frac{I(0)}{s} + \frac{k}{s} L\left\{\sum_{k=0}^{\infty} C_k\right\} - \frac{\beta}{s} L\left\{\sum_{k=0}^{\infty} I_k\right\}, \\
L\left\{\sum_{k=0}^{\infty} V_k\right\} &= \frac{V(0)}{s} + \frac{\mu\beta}{s} L\left\{\sum_{k=0}^{\infty} I_k\right\} - \frac{\gamma}{s} L\left\{\sum_{k=0}^{\infty} V_k\right\}.
\end{aligned}
\tag{2.7}
$$

An iterative approximation algorithm by means of both sides of (2.7) could be obtained as follows:

$$
\begin{aligned}
L\{T_0\} &= \frac{T(0)}{s} + \frac{q}{s^2}, \\
L\{T_{k+1}\} &= \frac{(r-\alpha)}{s} L\{T_k\} - \frac{r}{s\cdot T_{\max}} L\{A_k\} - \frac{r}{s\cdot T_{\max}} L\{B_k\} - \frac{k}{s} L\{C_k\}, \\
L\{I_0\} &= \frac{I(0)}{s}, \qquad L\{I_{k+1}\} = \frac{k}{s} L\{C_k\} - \frac{\beta}{s} L\{I_k\}, \\
L\{V_0\} &= \frac{V(0)}{s}, \qquad L\{V_{k+1}\} = \frac{\mu\beta}{s} L\{I_k\} - \frac{\gamma}{s} L\{V_k\}.
\end{aligned}
\tag{2.8}
$$

The inverse Laplace transform of the first part of (2.8) gives the first terms of solutions T_0, I_0 and V_0 which will be used to calculate, A_0, B_0, and C_0. Consequently, the first term of Adomian polynomials, A_0, B_0, and C_0 is used to evaluate T_1, I_1, and V_1. Subsequently, the determination of T_1, I_1, and V_1 leads to the determination of A_1, B_1, and C_1, which are used to determine T_2, I_2, and V_2 and so on. Finally, the components of T_k, I_k, and V_k, $k \geq 0$, are determined by the second part of (2.8) and the series solutions of the (2.5) are obtained.

3. Multistep Laplace Adomian Decomposition Method

The multistep approach is used by many authors for different methods to find the solutions of various problems [11, 20–23]. The multistep approach for LADM proposed in this section is as a new idea for constructing the approximate solutions for the given HIV infection model of CD4$^+$T cells. Let $[0,T]$ be the interval over which we want to find the solution of the initial value problem (1.1). The solution interval, $[0,T]$, is divided into M subintervals $[t_{m-1}, t_m]$, $m = 1,2,\ldots,M$ of equal step size, $h = T/M$ by using the nodes, $t_m = mh$. The solution algorithm of the MLADM consists of the following steps. Initially, the LADM is applied to obtain the approximate solutions of T_1, I_1, and V_1 on the interval $[0,t_1]$ by using the initial conditions, $T(0) = 0.1$, $I(0) = 0$ and $V(0) = 0.1$, respectively. For obtaining the

Table 1: Numerical comparison for $T(t)$.

t	MLADM	Ref. [7]	RK4 method
0	0.1	0.1	0.1
0.2	0.2088080843	0.2088072731	0.2088080833
0.4	0.4062405429	0.4061052625	0.4062405393
0.6	0.7644239214	0.7611467713	0.7644238890
0.8	1.414047962	1.377319859	1.414046831
1	2.591621398	2.329169761	2.591594802

Table 2: Numerical comparison for $I(t)$.

t	MLADM	Ref [7]	RK4 method
0	0.0	0.0	0.0
0.2	$0.6032702241e-5$	$0.6032707289e-5$	$0.6032702150e-5$
0.4	$0.1315834094e-4$	$0.1315916175e-4$	$0.1315834073e-4$
0.6	$0.2122378571e-4$	$0.2126836882e-4$	$0.2122378506e-4$
0.8	$0.3017742928e-4$	$0.3006918678e-4$	$0.3017741955e-4$
1	$0.4003796451e-4$	$0.3987365427e-4$	$0.4003781468e-4$

Table 3: Numerical comparison for $V(t)$.

t	MLADM	Ref [7]	RK4 method
0	0.1	0.1	0.1
0.2	0.06187984322	0.06187996025	0.06187984331
0.4	0.03829488777	0.03831324883	0.03829488788
0.6	0.02370454989	0.02439174349	0.02370455014
0.8	0.01468036135	0.009967218934	0.01468036377
1	0.009100827185	0.003305076447	0.009100845043

approximate solutions of (1.1) over the interval $[t_{m-1}, t_m]$, the LADM for $m > 2$ is used with the initial conditions $T_1(t_{m-1})$, $I_1(t_{m-1})$, $V_1(t_{m-1})$. The similar process is repeated to generate a sequence of approximate solutions of $T_m(t)$, $I_m(t)$, $V_m(t)$, $m = 1, 2, \ldots, M$. Consequently, final approximate MLADM solutions are obtained as follows:

$$T(t) = \begin{cases} T_1(t), & [0, t_1] \\ T_2(t), & [t_1, t_2] \\ \vdots & \vdots \\ T_M(t), & [t_{M-1}, t_M], \end{cases} \qquad I(t) = \begin{cases} I_1(t), & [0, t_1] \\ I_2(t), & [t_1, t_2] \\ \vdots & \vdots \\ I_M(t), & [t_{M-1}, t_M], \end{cases}$$
$$V(t) = \begin{cases} V_1(t), & [0, t_1] \\ V_2(t), & [t_1, t_2] \\ \vdots & \vdots \\ V_M(t), & [t_{M-1}, t_M]. \end{cases} \tag{3.1}$$

3.1. Application

To demonstrate the effectiveness of the proposed algorithm, the MLADM and RK4 are applied to the HIV infection model of $CD4^+T$ cells. Firstly for comparison purpose we implement the present method on small interval ($t \in [0, 1]$) as given in [7]. Tables 1, 2, and 3

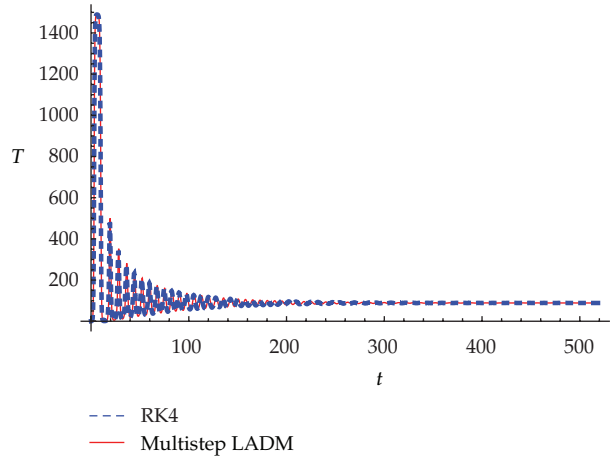

Figure 1: Graphical comparison of $T(t)$.

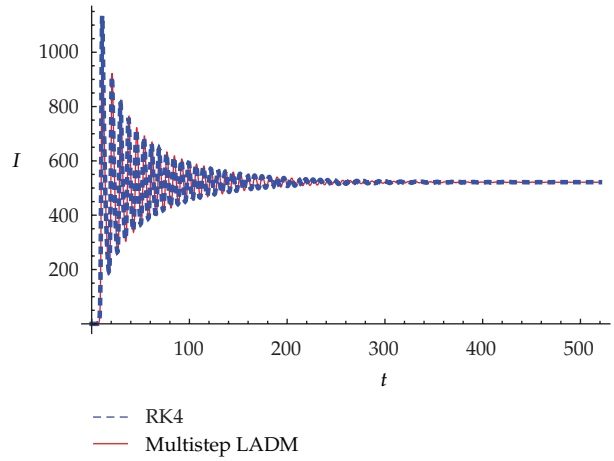

Figure 2: Graphical comparison of $I(t)$.

show the comparison between the results of MLADM solution and results of classical LADM solution.

As could be seen in Figures 1–3 we obtain better results than Classical LADM solutions given in [7] for the same interval ($t \in [0,1]$).

Now we implement the MLADM for larger time interval ($t \in [0,520]$). We obtain MLADM results for $M = 2000$, $T = 520$, and $n = 10$. These results, obtained by MLADM and the RK4 method for $T(t)$, $I(t)$ and $V(t)$ are presented as figures. Figures 1–3 show the graphical outputs for MLADM and RK4 for $t = 0$ to $t = 520$. Figures 1–3 show that the multistep LADM solutions are very close to the Runge-Kutta solutions. Additionally, Table 4 shows the absolute errors between MLADM solutions and RK4 solutions. According to the Table 4 the amount of the absolute errors is small according to the values of variables. Figures 1–3 and Table 4 show that there is a good agreement between MLADM and RK4 for given time interval. It is observed that the MLADM gives a much better performance in approximate solutions compared to other mentioned methods in the literature for larger time interval.

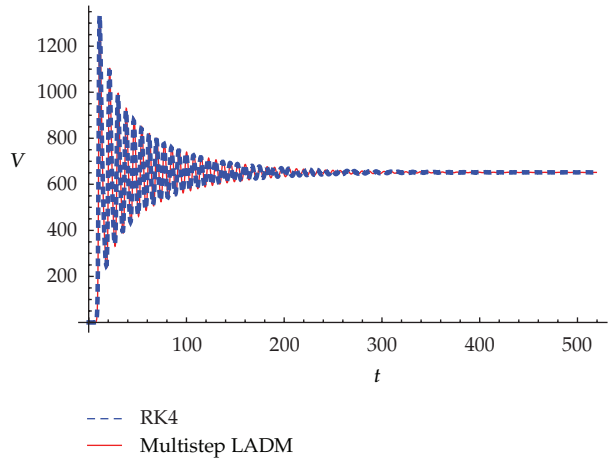

Figure 3: Graphical comparison of $V(t)$.

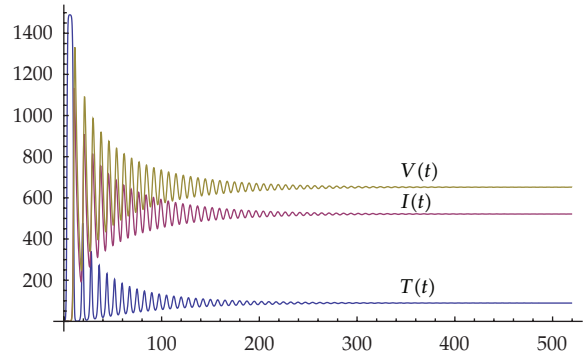

Figure 4: MLADM solutions.

Table 4: Absolute errors obtained by using Runge Kutta fourth-order method and MLADM for $M = 2000$, $T = 520$, $n = 10$.

t_i	$\lvert T(t_i) - \text{RK4}\rvert$	$\lvert I(t_i) - \text{RK4}\rvert$	$\lvert V(t_i) - \text{RK4}\rvert$
0	0	0	0
40	$6.722383180e-1$	46.86952484	61.52645903
80	12.36468885	17.63351026	30.34225709
120	2.065681397	24.99035749	25.92786405
160	5.554143394	7.508678561	3.918979165
200	3.574014571	2.126970283	5.025263611
240	$8.334624885e-1$	4.137182586	5.257455641
280	$5.685900002e-1$	1.874669218	1.657584783
320	$6.796667264e-1$	$5.102750400e-1$	$9.926127081e-2$
360	$3.137926428e-1$	$6.395250064e-1$	$9.774255721e-1$
400	$1.396180212e-2$	$1.990135677e-1$	$2.083582079e-1$
440	$8.809542889e-2$	$3.718439944e-1$	$3.793007988e-1$
480	$6.832579814e-2$	$2.195343654e-1$	$3.237937858e-1$
520	$2.190590978e-2$	$1.506888643e-1$	$1.794267434e-1$

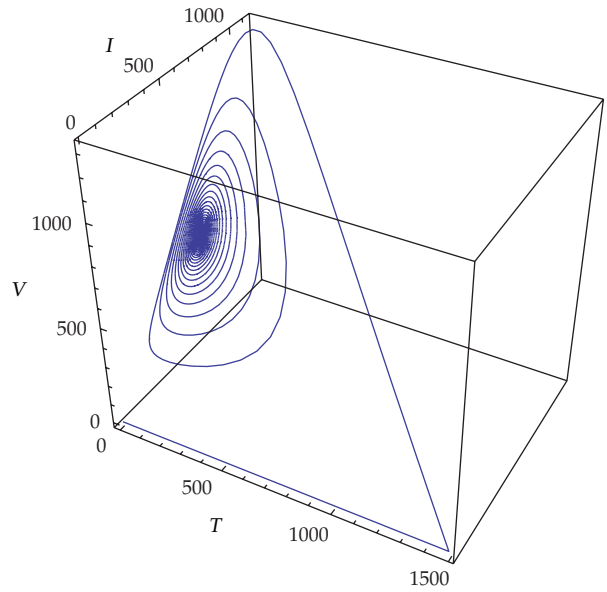

Figure 5: Phase portrait for HIV infection model of CD4$^+$T cells (1.1) by using MLADM.

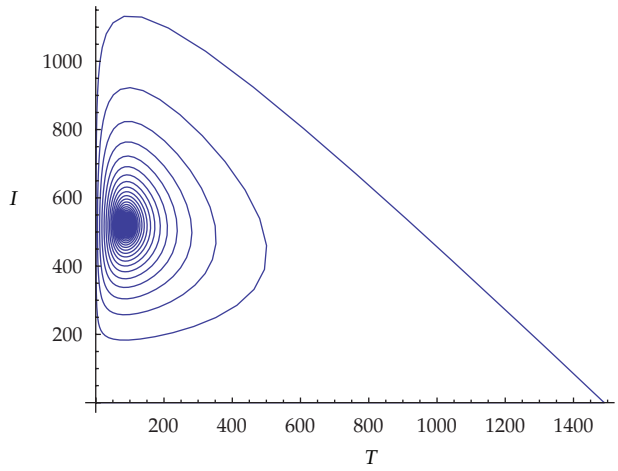

Figure 6: $T(t) - I(t)$: phase portrait for HIV infection model of CD4$^+$T cells (1.1) by using MLADM.

Table 4 shows the absolute errors between MALDM solutions and RK4 solutions. As could be seen from Figures 1–4, large oscillations have occurred between $t = 0$ and $t = 100$. Due to large oscillations big absolute errors have occurred from $t = 0$ to $t = 100$. But absolute errors become smaller after $t = 100$. Initial oscillations effectively disappear after $t = 200$. Damped oscillations are clearly visible after $t = 200$.

As could be seen in Figure 1, the concentration of susceptible CD4$^+$T cells approaches around 90 by oscillating with time while CD4$^+$T cells infected by the HIV viruses converges to around 520 by oscillating as shown in Figure 2 and free HIV virus particles in the blood converges to around 650 by oscillating as shown in Figure 3. The main aim of this study is to find mathematical solution to given model for HIV infection of CD4$^+$T cells. Besides Figures 5, 6, 7, and 8 indicate the phase diagram obtained from the MLADM solutions. As could be

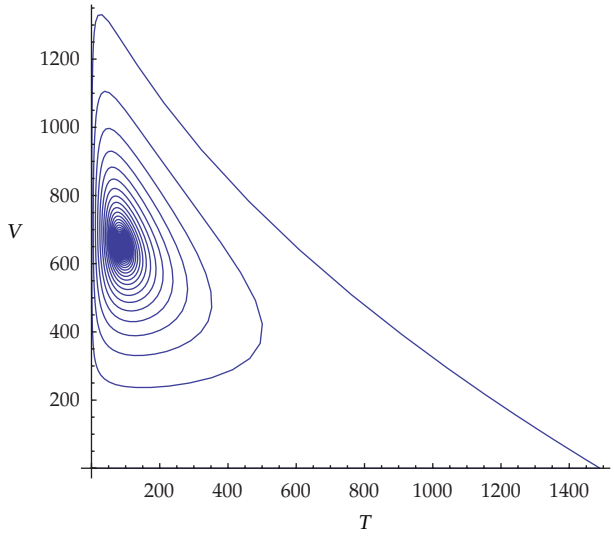

Figure 7: $T(t) - V(t)$: phase portrait for HIV infection model of CD4$^+$T cells (1.1) by using MLADM.

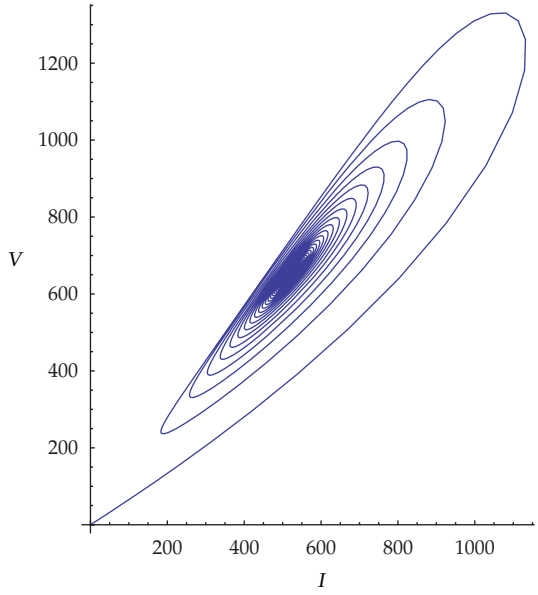

Figure 8: $I(t) - V(t)$: phase portrait for HIV infection model of CD4$^+$T cells (1.1) by using MLADM.

seen in Figures 5–8, solutions of HIV infection model of CD4$^+$T cells exhibit chaotic behavior. Although every point in the phase diagram has medically individual meaning, it was not focused on the detailed medical interpretation of figures related to solutions.

4. Conclusions

In this study, a new method called multistep LADM for solution of the HIV infection model of CD4$^+$T cells is introduced. Figures 1, 2, 3 and Table 4 shows that the MLADM approximate

solutions for the HIV infection model of CD4$^+$T cells are very close to the Runge-Kutta approximate solutions. As can be seen clearly from the graphics, MLADM gives considerably good results on a longer time interval of $t \in [0, 520]$. This confirms that this new algorithm of the LADM increases the interval of convergence for the series solution. We have shown that the proposed algorithm is a very accurate and efficient method compared with RK4 method for the HIV infection model of CD4$^+$T cells and it can be applied to other nonlinear systems.

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