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A Modified Iterative Algorithm for Numerical Investigation of HIV Infection Dynamics

Indranil Ghosh ^{1,*}, Muhammad Mahbubur Rashid ², Shukranul Mawa ³, Rupal Roy ², Md Manjurul Ahsan ⁴, Muhammad Ramiz Uddin ⁵, Kishor Datta Gupta ⁶ and Pallabi Ghosh ⁷

- ¹ Department of Science in Engineering, Faculty of Engineering, International Islamic University Malaysia, Jalan Gombak, Kuala Lumpur 53100, Malaysia
- ² Department of Mechatronics Engineering, Faculty of Engineering, International Islamic University Malaysia, Jalan Gombak, Kuala Lumpur 53100, Malaysia; mahbub96@gmail.com (M.M.R.); rupal.roy@live.iium.edu.my (R.R.)
- ³ Faculty of Pharmacy, Universiti Kebangsaan Malaysia, Jalan Raja Muda Abdul Aziz, Kuala Lumpur 50300, Malaysia; shukranulmawa@gmail.com
- ⁴ School of Industrial & Systems Engineering, University of Oklahoma, Norman, OK 73019, USA; ahsan@ou.edu
- ⁵ Department of Chemistry and Biochemistry, University of Oklahoma, Norman, OK 73019, USA; muhammadramizuddin@gmail.com
- ⁶ Department of Computer Science, Clark Atlanta University, Atlanta, GA 30314, USA; kgupta@cau.edu
- ⁷ Department of Teaching English as Second Language, Faculty of Education, International Islamic University Malaysia, Jalan Gombak, Kuala Lumpur 53100, Malaysia; pallabighosh368@gmail.com
- * Correspondence: indranilghosh343@gmail.com



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Abstract: The human immunodeficiency virus (HIV) mainly attacks CD4⁺ T cells in the host. Chronic HIV infection gradually depletes the CD4⁺ T cell pool, compromising the host's immunological reaction to invasive infections and ultimately leading to acquired immunodeficiency syndrome (AIDS). The goal of this study is not to provide a qualitative description of the rich dynamic characteristics of the HIV infection model of CD4⁺ T cells, but to produce accurate analytical solutions to the model using the modified iterative approach. In this research, a new efficient method using the new iterative method (NIM), the coupling of the standard NIM and Laplace transform, called the modified new iterative method (MNIM), has been introduced to resolve the HIV infection model as a class of system of ordinary differential equations (ODEs). A nonlinear HIV infection dynamics model is adopted as an instance to elucidate the identification process and the solution process of MNIM, only two iterations lead to ideal results. In addition, the model has also been solved using NIM and the fourth order Runge–Kutta (RK4) method. The results indicate that the solutions by MNIM match with those of RK4 method to a minimum of eight decimal places, whereas NIM solutions are not accurate enough. Numerical comparisons between the MNIM, NIM, the classical RK4 and other methods reveal that the modified technique has potential as a tool for the nonlinear systems of ODEs.

Keywords: new iterative method; Laplace transform; HIV infection model; ordinary differential equation; modified iterative algorithm; Runge–Kutta method

1. Introduction

Differential equations are the foundation of many scientific and engineering problems [1]. Differential equations are equations that express a relationship between certain variables and their derivatives. Variables are changing entities in mathematics, and the rate of change of one variable with respect to another is called a derivative [2].

In addition, an ordinary differential equation (ODE) is an equation that involves some ordinary derivatives of a function. In general, physical systems in nature consist of complicated phenomena for which accurate solutions can be difficult to compute. Numerical or semi-analytical methods may be preferable in such instances. In this context, there are

numerous standard books [3–7] on the solution of ordinary differential equations (ODEs). A first attempt at classifying ODE systems is with respect to the initial or boundary conditions connected with them, both mathematically and computationally [8]. It should be mentioned that the numerical solution of ordinary differential equations is a very active and ongoing topic of research [9].

Infectious diseases frequently affect a huge number of people spread across vast geographical regions. Mathematical models of ordinary differential equations have significance in studying the dynamic behavior of infectious diseases. In recent times, many mathematical models including mumps virus [10], ebola virus disease [11], dengue fever disease [12], rubella disease [13], influenza transmission [14], zika virus transmission [15], COVID-19 pandemic [16–18] and many others have been formulated using differential equations.

In the present study, the HIV infection model of CD4⁺ T cells has been investigated mathematically. HIV infection targets CD4⁺ T cells, the immune system's biggest white blood cells. HIV infection has a severe devastating impact on CD4⁺ T cells, killing them and weakening the immune system. When the number of CD4⁺ T cells falls below a particular threshold, the cell-mediated immune system vanishes, the immune system weakens, and the body is more likely to be infected [19]. The HIV infection model is represented by the standard three-compartmental system [20], such as susceptible CD4⁺ T cell concentration, CD4⁺ T cell infection and free HIV viral substance in the blood. They are denoted by time dependent variables such as $X(t)$, $Y(t)$ and $Z(t)$. A system of nonlinear differential equations characterizes this model as follows:

$$\frac{d}{dt} X(t) = p - \alpha X(t) + rX(t) \left(1 - \frac{X(t) + Y(t)}{T_{max}} \right) - kZ(t)X(t) \quad (1)$$

$$\frac{d}{dt} Y(t) = kZ(t)X(t) - \beta Y(t) \quad (2)$$

$$\frac{d}{dt} Z(t) = N\beta Y(t) - qZ(t) \quad (3)$$

Let us assume the initial conditions are as follows:

$$X(0) = x_0, Y(0) = y_0, Z(0) = z_0 \quad (4)$$

Several typical approaches to numerically address the HIV infection of the CD4⁺ T cells model have recently been introduced in the literature. For instance, Ongun [21] used the Laplace–Adomian decomposition method (LADM) to solve the HIV infection model. Merdan et al. [22] had developed the multi-stage variational iteration approach (MSVIM). In order to solve the HIV infection model, Yüzbaş [23] introduced the Bessel collocation approach. Doğan [24] solved the model using the multi-step Laplace–Adomian decomposition method (MSLADM). Merdan [25] employed the homotopy perturbation method (HPM) on the determined system. Merdan et al. [26] recently used the modified variational iteration technique (MVIM) to get the approximate solutions of (1)–(3). Goreishi et al. [27] used the homotopy analysis method (HAM) to resolve the variation of the noted model. To acquire the numeric solution of the HIV model, the stochastic global search approach known as genetic algorithm (GA) is combined with two local search optimizers known as interior point algorithm (IPA) and active set algorithm (ASA) in [28]. Very recently, Attaullah and Sohaib [29] used continuous Galerkin–Petrov (cGP) and the Legendre wavelet collocation method (LWCM) for the approximate solution to the selected mathematical model.

For the general nonlinear problem, the new iterative method (NIM) has received a lot of attention since it requires no multiplier or polynomials for nonlinear terms of the problems. The NIM algorithm was developed by Daftardar-Gejji and Jafari [30] to solve stochastic and deterministic problems. Recently, Adwan et al. [31] used NIM to identify analytical and numerical solutions for linear and nonlinear multidimensional problems. The approximate solutions for second order nonlinear ordinary differential equations (ODEs) have been

provided by Al-Jawary et al. [32] using NIM. By using semi analytic NIM, the nonlinear problem of Jeffery–Hamel flow has been solved analytically and numerically by AL-Jawary et al. [33]. Alderremy et al. [34] have extended the applications of NIM to find the solutions of Klein–Gordon equations (KGEs), which have been applied in the modeling of spin wave, quantum field theory, kink dynamics, astrophysics, cosmology and classical mechanics. First, they reduced the level of calculation by using the Elzaki transform method and then solved the corresponding equations with the help of NIM. Recently, the technique has been applied widely to several dynamical systems (see [35–39]).

The design of semi-analytical methods such as the Adomian decomposition, homotopy perturbation, variational iteration approaches and new iterative method (NIM) differ from each other. Although these methods provide some helpful solutions that are frequently represented in terms of polynomials and the region of convergences (ROCs) is relatively small in certain nonlinear problems such as the HIV infection model. Both perturbation techniques and non-perturbative approaches cannot provide a straightforward procedure for adjusting or controlling the convergence region and rate of a given approximation series [27]. So it is occasionally essential to improve them. Also, the recent results provided in the literature of Attaullah and Sohaib [21], used continuous Galerkin–Petrov (cGP) and the Legendre wavelet collocation method (LWCM) to match at least four decimal places with RK4, which is considered to be more accurate than all previous results published, so there could be the scope for further investigation to attain more accuracy.

The goal of this research is to modify the new iterative method (NIM) by implementing the modified new iterative method (MNIM), i.e., the combination of Laplace transformation and NIM to solve the class of nonlinear HIV infection model and achieve higher accuracy than previous methods.

The rest of the present study is presented as: the solution procedure of NIM and modified NIM are interpreted in Section 2. The applications of both NIM and MNIM for the considered HIV infection model are introduced in Section 3. The results and discussion of the present methods are illustrated in Section 4, and then the concluding remarks of the research has been given in Section 5.

2. Solution Procedure

2.1. Basic Idea of NIM

In this section we have discussed the new iterative method (NIM) as follows. Consider a general equation:

$$u = L(u) + N(u) + f \quad (5)$$

where L is a linear operator and N is a nonlinear operator from a Banach space $\mathcal{B} \rightarrow \mathcal{B}$ and f is a given analytic function. The solution of u for Equation (5) having in the series form,

$$u(t) = u_0(t) + u_1(t) + u_2(t) + \cdots = \sum_{i=0}^{\infty} u_i(t) \quad (6)$$

Since L is linear,

$$L\left(\sum_{i=0}^{\infty} u_i\right) = \sum_{i=0}^{\infty} L(u_i) \quad (7)$$

The nonlinear operator N can be decomposed as follows:

$$H_0 = N(u_0) \text{ and } H_m = N\left(\sum_{j=0}^m u_j\right) - N\left(\sum_{j=0}^{m-1} u_j\right) \quad (8)$$

Thus, according to NIM,

$$H_0 = N(u_0) \quad (9)$$

$$H_1 = N(u_0 + u_1) - N(u_0) \quad (10)$$

$$H_m = N(u_0 + \dots + u_m) - N(u_0 + \dots + u_{m-1}), \quad m \geq 1 \quad (11)$$

Therefore,

$$\begin{aligned} N\left(\sum_{i=0}^{\infty} u_i\right) &= H_0 + H_1 + H_2 + \dots \\ &= N(u_0) + (N(u_0 + u_1) - N(u_0)) \\ &\quad + (N(u_0 + u_1 + u_2) - N(u_0 + u_1)) + \dots \end{aligned} \quad (12)$$

$$\Rightarrow N\left(\sum_{i=0}^{\infty} u_i\right) = N(u_0) + \sum_{i=1}^{\infty} \left\{ N\left(\sum_{j=0}^i u_j\right) - N\left(\sum_{j=0}^{i-1} u_j\right) \right\} \quad (13)$$

Therefore, we define the recursive relation:

$$u_0 = f \quad (14)$$

$$u_1 = L(u_0) + N(u_0) \quad (15)$$

$$u_2 = L(u_1) + \{N(u_0 + u_1) - N(u_0)\} \quad (16)$$

$$u_3 = L(u_2) + \{N(u_0 + u_1 + u_2) - N(u_0 + u_1)\} \quad (17)$$

$$u_{m+1} = L(u_m) + \{N(u_0 + \dots + u_m) - N(u_0 + \dots + u_{m-1})\}, \quad m \geq 1 \quad (18)$$

Then series solution becomes

$$\begin{aligned} u_1 + u_2 + \dots + u_{m+1} &= \{L(u_0) + L(u_1) + L(u_2) + \dots + L(u_m)\} \\ &\quad + \{N(u_0)\} + \{N(u_0 + u_1) - N(u_0)\} + \dots + \{N(u_0 + \dots + u_m) - N(u_0 + \dots + u_{m-1})\} \end{aligned} \quad (19)$$

$$\Rightarrow u(t) = \sum_{i=0}^{\infty} u_i = f + L\left\{\sum_{i=0}^{\infty} u_i\right\} + \left[N(u_0) + \sum_{i=1}^{\infty} \left\{N\left(\sum_{j=0}^i u_j\right) - N\left(\sum_{j=0}^{i-1} u_j\right)\right\}\right] \quad (20)$$

Therefore,

$$u = f + \sum_{i=1}^{\infty} u_i \quad (21)$$

2.2. The Modified New Iterative Method (MNIM)

In this section we have proposed a modification of NIM using the combination of Laplace transform with the new iterative method to solve system of differential equations. Let us consider a system of differential equations in the operator form:

$$D(\mu_1) + R_1(\mu_1) + N_1(\mu_1, \mu_2, \dots, \mu_n) = g_1(t) \quad (22)$$

$$D(\mu_2) + R_2(\mu_2) + N_2(\mu_1, \mu_2, \dots, \mu_n) = g_2(t) \quad (23)$$

⋮

$$D(\mu_n) + R_n(\mu_n) + N_n(\mu_1, \mu_2, \dots, \mu_n) = g_n(t) \quad (24)$$

subjected to the initial conditions

$$\mu_1(0) = a_1, \mu_2(0) = a_2, \dots, \mu_n(0) = a_n \quad (25)$$

where D is an invertible linear differential operator, and $R_1, R_2, \dots, R_n$ are remaining linear operators order less than D and $N_1, N_2, \dots, N_n$ are nonlinear operators and $g_1, g_2, \dots, g_n$ are inhomogeneous terms. For the first order $D \equiv \frac{d}{dt}$, second order $D \equiv \frac{d^2}{dt^2}$ and so on.

The technique consists first of applying Laplace transformation (which is denoted by $\mathfrak{S}$) to both sides of systems (22)–(24), hence,

$$\mathfrak{S}\{D(\mu_1)\} + \mathfrak{S}\{R_1(\mu_1)\} + \mathfrak{S}\{N_1(\mu_1, \mu_2, \dots, \mu_n)\} = \mathfrak{S}\{g_1(t)\} \quad (26)$$

$$\Im\{D(\mu_2)\} + \Im\{R_2(\mu_2)\} + \Im\{N_2(\mu_1, \mu_2, \dots, \mu_n)\} = \Im\{g_2(t)\} \quad (27)$$

$$\vdots$$

$$\Im\{D(\mu_n)\} + \Im\{R_n(\mu_n)\} + \Im\{N_n(\mu_1, \mu_2, \dots, \mu_n)\} = \Im\{g_n(t)\} \quad (28)$$

Applying the formulas for Laplace transforms, we obtain

$$s\Im(\mu_1) - \mu_1(0) = \Im\{g_1(t)\} - \Im\{R_1(\mu_1)\} - \Im\{N_1(\mu_1, \mu_2, \dots, \mu_n)\} \quad (29)$$

$$s\Im(\mu_2) - \mu_2(0) = \Im\{g_2(t)\} - \Im\{R_2(\mu_2)\} - \Im\{N_2(\mu_1, \mu_2, \dots, \mu_n)\} \quad (30)$$

$$\vdots$$

$$s\Im(\mu_n) - \mu_n(0) = \Im\{g_n(t)\} - \Im\{R_n(\mu_n)\} - \Im\{N_n(\mu_1, \mu_2, \dots, \mu_n)\} \quad (31)$$

where ‘s’ is called a Laplace domain function.

Using the initial conditions (25), we have,

$$\Im(\mu_1) = \frac{a_1}{s} + \frac{\Im\{g_1(t)\}}{s} - \frac{1}{s}\Im\{R_1(\mu_1)\} - \frac{1}{s}\Im\{N_1(\mu_1, \mu_2, \dots, \mu_n)\} \quad (32)$$

$$\Im(\mu_2) = \frac{a_2}{s} + \frac{\Im\{g_2(t)\}}{s} - \frac{1}{s}\Im\{R_2(\mu_2)\} - \frac{1}{s}\Im\{N_2(\mu_1, \mu_2, \dots, \mu_n)\} \quad (33)$$

$$\vdots$$

$$\Im(\mu_n) = \frac{a_n}{s} + \frac{\Im\{g_n(t)\}}{s} - \frac{1}{s}\Im\{R_n(\mu_n)\} - \frac{1}{s}\Im\{N_n(\mu_1, \mu_2, \dots, \mu_n)\} \quad (34)$$

applying the inverse Laplace transform to the equations in (32)–(34), we get

$$\mu_1 = \Im^{-1}\left[\frac{a_1}{s} + \frac{\Im\{g_1(t)\}}{s}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{R_1(\mu_1)\}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{N_1(\mu_1, \mu_2, \dots, \mu_n)\}\right] \quad (35)$$

$$\mu_2 = \Im^{-1}\left[\frac{a_2}{s} + \frac{\Im\{g_2(t)\}}{s}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{R_2(\mu_2)\}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{N_2(\mu_1, \mu_2, \dots, \mu_n)\}\right] \quad (36)$$

$$\vdots$$

$$\mu_n = \Im^{-1}\left[\frac{a_n}{s} + \frac{\Im\{g_n(t)\}}{s}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{R_n(\mu_n)\}\right] - \Im^{-1}\left[\frac{1}{s}\Im\{N_n(\mu_1, \mu_2, \dots, \mu_n)\}\right] \quad (37)$$

Let the approximate solutions $\mu_1, \mu_2, \dots, \mu_n$ of system be expressed as

$$\mu_1 = \mu_{1,0} + \mu_{1,1} + \dots = \sum_{i=0}^{\infty} \mu_{1,i} \quad (38)$$

$$\mu_2 = \mu_{2,0} + \mu_{2,1} + \dots = \sum_{i=0}^{\infty} \mu_{2,i} \quad (39)$$

$$\vdots$$

$$\mu_n = \mu_{n,0} + \mu_{n,1} + \dots = \sum_{i=0}^{\infty} \mu_{n,i} \quad (40)$$

For the NIM, the nonlinear operators can be decomposed by,

$$G_0 = N_1(\mu_{1,0}) \text{ and } G_m = N_1\left(\sum_{i=0}^m \mu_{1,i}\right) - N_1\left(\sum_{i=0}^{m-1} \mu_{1,i}\right), m \geq 1 \quad (41)$$

$$H_0 = N_2(\mu_{2,0}) \text{ and } H_m = N_2\left(\sum_{i=0}^m \mu_{2,i}\right) - N_2\left(\sum_{i=0}^{m-1} \mu_{2,i}\right), m \geq 1 \quad (42)$$

$$\vdots$$

$$I_0 = N_n(\mu_{n,0}) \text{ and } I_m = N_n\left(\sum_{i=0}^m \mu_{n,i}\right) - N_n\left(\sum_{i=0}^{m-1} \mu_{n,i}\right), m \geq 1 \quad (43)$$

Since $R_1, R_2, \dots, R_n$ are linear,

$$\sum_{i=0}^{\infty} R_1(\mu_{1,i}) = R_1\left(\sum_{i=0}^{\infty} \mu_{1,i}\right) \quad (44)$$

$$\sum_{i=0}^{\infty} R_2(\mu_{2,i}) = R_2\left(\sum_{i=0}^{\infty} \mu_{2,i}\right) \quad (45)$$

$$\vdots$$

$$\sum_{i=0}^{\infty} R_n(\mu_{n,i}) = R_n\left(\sum_{i=0}^{\infty} \mu_{n,i}\right) \quad (46)$$

The NIM admits the use of the recursive relations in the following way:

$$\mu_{1,0} = \Im^{-1}\left[\frac{\Im\{g_1(t)\}}{s}\right] + a_1 = f_1(t) + a_1, \quad (47)$$

where $f_1(t)$ is the term arising after inverse Laplace transformation of the source term $\frac{\Im\{g_1(t)\}}{s}$, all of which are assumed to be prescribed.

$$\mu_{1,1} = -\Im^{-1}\left[\frac{1}{s}\Im\{R_1(\mu_{1,0})\}\right] - \frac{1}{s}\Im^{-1}[\Im(G_0)] \quad (48)$$

$$\vdots$$

$$\mu_{1,m+1} = -\Im^{-1}\left[\frac{1}{s}\Im\{R_1(\mu_{1,m})\}\right] - \Im^{-1}\left[\frac{1}{s}\Im(G_m)\right], m = 1, 2, \dots \quad (49)$$

Thus,

$$\therefore \mu_1 = \sum_{i=0}^{\infty} \mu_{1,i} = f_1 + \sum_{i=1}^{\infty} \mu_{1,i} = f_1 - \Im^{-1}\left[\frac{1}{s}\Im\left\{R_1\left(\sum_{i=0}^{\infty} \mu_{1,i}\right)\right\}\right] - \Im^{-1}\left[\frac{1}{s}\Im\left\{N_1\left(\sum_{i=0}^{\infty} \mu_{1,i}\right)\right\}\right] \quad (50)$$

By a similar manner, we have

$$\mu_{2,0} = \Im^{-1}\left[\frac{\Im\{g_2(t)\}}{s}\right] + a_2 = f_2(t) + a_2 \quad (51)$$

$$\mu_{2,1} = -\Im^{-1}\left[\frac{1}{s}\Im\{R_2(\mu_{2,0})\}\right] - \Im^{-1}\left[\frac{1}{s}\Im(H_0)\right] \quad (52)$$

$$\vdots$$

$$\mu_{2,m+1} = -\Im^{-1}\left[\frac{1}{s}\Im\{R_2(\mu_{2,m})\}\right] - \Im^{-1}\left[\frac{1}{s}\Im(H_m)\right], m = 1, 2, \dots \quad (53)$$

$$\therefore \mu_2 = \sum_{i=0}^{\infty} \mu_{2,i} = f_2 + \sum_{i=1}^{\infty} \mu_{2,i} = f_2 - \Im^{-1}\left[\frac{1}{s}\Im\left\{R_2\left(\sum_{i=0}^{\infty} \mu_{2,i}\right)\right\}\right] - \Im^{-1}\left[\frac{1}{s}\Im\left\{N_2\left(\sum_{i=0}^{\infty} \mu_{2,i}\right)\right\}\right] \quad (54)$$

and

$$\mu_{n,0} = \Im^{-1} \left[\frac{\Im\{g_n(t)\}}{s} \right] + a_n = f_n(t) + a_n \quad (55)$$

$$\mu_{n,1} = -\Im^{-1} \left[\frac{1}{s} \Im\{R_n(\mu_{n,0})\} \right] - \Im^{-1} \left[\frac{1}{s} \Im\{I_0\} \right] \quad (56)$$

$\vdots$

$$\mu_{n,m+1} = -\Im^{-1} \left[\frac{1}{s} \Im\{R_n(\mu_{n,m})\} \right] - \Im^{-1} \left[\frac{1}{s} \Im\{I_m\} \right], m = 1, 2, \dots \quad (57)$$

$$\therefore \mu_n = \sum_{i=0}^{\infty} \mu_{n,i} = f_n + \sum_{i=1}^{\infty} \mu_{n,i} = f_n - \Im^{-1} \left[\frac{1}{s} \Im \left\{ R_n \left(\sum_{i=0}^{\infty} \mu_{n,i} \right) \right\} \right] - \Im^{-1} \left[\frac{1}{s} \Im \left\{ N_n \left(\sum_{i=0}^{\infty} \mu_{n,i} \right) \right\} \right] \quad (58)$$

2.3. Convergence Analysis of MNIM

Let, χ, γ and μ_{ij} be the elements in a Banach space B , and N_i is nonlinear contraction from $B \rightarrow B$ such that $\|\mu_{ij}\| = \|N(\chi) - N(\gamma)\| \leq k\|\chi - \gamma\|$. Then according to the principle of Banach fixed-point theorem, $\sum \mu_{ij}$ converges if $\|\mu_{i,r+1}\| \leq k^{r+1}\|\mu_{i,0}\|$, where $0 < k < 1$, $i = 1, 2, \dots$ and $j = 0, 1, \dots, r + 1, \dots$

Proof. In general, let us take

$$\mu_{i,0} = f_i(t) + a_i \quad (59)$$

where $\mu_{i,0}$ is the initial approximation, $f_i(t)$ is a known function in Banach space B , a_i is an arbitrary constant and $i \in \mathbb{N}$. We can write

$$\|\mu_{i,1}\| = \|N_i(\mu_{i,0})\| \leq k\|\mu_{i,0}\| \quad (60)$$

$$\|\mu_{i,2}\| = \|N_i(\mu_{i,0} + \mu_{i,1}) - N_i(\mu_{i,0})\| \leq k\|\mu_{i,1}\| \leq k^2\|\mu_{i,0}\| \quad (61)$$

$$\|\mu_{i,3}\| = \|N_i(\mu_{i,0} + \mu_{i,1} + \mu_{i,2}) - N_i(\mu_{i,0} + \mu_{i,1})\| \leq k\|\mu_{i,2}\| \leq k^3\|\mu_{i,0}\| \quad (62)$$

$\vdots$

$$\|\mu_{i,r+1}\| = \|N_i(\sum_{j=0}^r \mu_{i,j}) - N_i(\sum_{j=0}^{r-1} \mu_{i,j})\| \leq k\|\mu_{i,r}\| \leq k^{r+1}\|\mu_{i,0}\|, r = 0, 1, 2, \dots \quad (63)$$

Hence, the series $\sum \mu_{i,j}$, (where $i \in \mathbb{N}$ and $j \in \mathbb{W}$) absolutely and uniformly converges, which is unique in view of the Banach contraction principle. $\square$

3. Application

3.1. NIM for HIV Infection Model

Here we introduce numerical outline of NIM for the approximate solution of the HIV infection model. Let the integration on the system (1)–(3), using initial conditions (4) and parameters of Table 1.

$$X(t) = x_0 + pt - \left(\int_0^t \alpha X(t) dt \right) + \int_0^t rX(t) \left(1 - \frac{X(t) + Y(t)}{T_{max}} \right) dt - \left(\int_0^t kZ(t)X(t) dt \right) \quad (64)$$

$$Y(t) = y_0 + \int_0^t kZ(t)X(t) dt - \left(\int_0^t \beta Y(t) dt \right) \quad (65)$$

$$Z(t) = z_0 + \int_0^t N\beta Y(t)dt - \left(\int_0^t \gamma Z(t) dt \right) \quad (66)$$

Table 1. List of parameters used in the HIV infection model.

Parameters	Remark
p	Production rate of healthy T cells from bone marrow and thymus
α	Uninfected T cell natural turn-over rate
r	Healthy T-cell growth rate through mitosis
T_{max}	CD4 ⁺ T cells maximum concentration level in the body
k	The rate of infection
β	Natural turn-over rates of infected T cells
N	Number of virus particles assumed to be produced by infected T cells
q	Virus particle natural turnover rate

In view of (14)–(18) and according to the solution procedure of NIM for system of differential equations, we find the approximations as follows:

$$X_0(t) = pt + x_0 \quad (67)$$

$$Y_0(t) = y_0 \quad (68)$$

$$Z_0(t) = z_0 \quad (69)$$

$$X_1(t) = -\frac{\alpha pt^2}{2} - \alpha x_0 t + \frac{rpt^2}{2} + rx_0 t - \frac{rp^2 t^3}{3T_{max}} - \frac{rx_0 pt^2}{T_{max}} - \frac{rx_0^2 t}{T_{max}} - \frac{rpy_0 t^2}{2T_{max}} - \frac{rx_0 y_0 t}{T_{max}} - \frac{kz_0 pt^2}{2} - kz_0 x_0 t \quad (70)$$

$$Y_1(t) = \frac{1}{2}kz_0 pt^2 + kz_0 x_0 t - \beta y_0 t \quad (71)$$

$$Z_1(t) = N\beta y_0 t - \gamma z_0 t \quad (72)$$

The next successive iterations can be obtained in a similar manner. Therefore,

$$X(t) = \sum_{i=0}^5 X_i(t) \quad (73)$$

$$Y(t) = \sum_{i=0}^5 Y_i(t) \quad (74)$$

$$Z(t) = \sum_{i=0}^5 Z_i(t) \quad (75)$$

For the computation purpose we have taken the 5-iterations of NIM solutions.

3.2. MNIM for the HIV Infection Model

Let us first apply the Laplace transform on both sides of Equations (1)–(3) and using the initial conditions (4) and model parameters discussed in Table 1.

$$\mathfrak{L}(X(t)) = \frac{1}{s+\alpha-r} \left[\left\{ \frac{p}{s} + x_0 - \frac{r}{T_{max}} \mathfrak{L}(X^2(t)) \right\} - \left\{ \frac{r}{T_{max}} \mathfrak{L}(Y(t)X(t)) + k \mathfrak{L}(Z(t)X(t)) \right\} \right] \quad (76)$$

$$\mathfrak{L}(Y(t)) = \frac{1}{s+\beta} \{ y_0 + k \mathfrak{L}(Z(t)X(t)) \} \quad (77)$$

$$\Im(Z(t)) = \frac{1}{s+q} \{z_0 + N\beta \Im(Y(t))\} \quad (78)$$

Again, applying the inverse Laplace transform on both sides of Equations (76)–(78), we get

$$X(t) = \Im^{-1} \left[\frac{1}{s+\alpha-r} \left\{ \frac{p}{s} + x_0 - \frac{r}{T_{\max}} \Im(X^2(t)) - \frac{r}{T_{\max}} \Im(Y(t)X(t)) - k\Im(Z(t)X(t)) \right\} \right] \quad (79)$$

$$Y(t) = \Im^{-1} \left\{ \frac{1}{s+\beta} (y_0 + k\Im(Z(t)X(t))) \right\} \quad (80)$$

$$Z(t) = \Im^{-1} \left\{ \frac{1}{s+q} (z_0 + N\beta \Im(Y(t))) \right\} \quad (81)$$

In view of (47)–(58), solutions are obtained by using MNIM, as follows

$$X_0(t) = \Im^{-1} \left\{ \frac{1}{s+\alpha-r} \left(\frac{p}{s} + x_0 \right) \right\} \quad (82)$$

$$Y_0(t) = \Im^{-1} \left\{ \frac{y_0}{s+\beta} \right\} \quad (83)$$

$$Z_0(t) = \Im^{-1} \left\{ \frac{z_0}{s+q} \right\} \quad (84)$$

$$X_1(t) = -\Im^{-1} \left[\frac{1}{s+\alpha-r} \left[\frac{r}{T_{\max}} \{ \Im(X_0^2(t)) + \Im(Y_0(t)X_0(t)) + k\Im(Z_0(t)X_0(t)) \} \right] \right] \quad (85)$$

$$Y_1(t) = \Im^{-1} \left[\frac{k}{s+\beta} \{ \Im(Z_0(t)X_0(t)) \} \right] \quad (86)$$

$$Z_1(t) = \Im^{-1} \left[\frac{N\beta}{s+q} \{ \Im(Y_0(t)) \} \right] \quad (87)$$

$$\begin{aligned} X_2(t) &= -\Im^{-1} \left[\frac{1}{s+\alpha-r} \left[\frac{r}{T_{\max}} \left\{ \Im(X_1(t) + X_0(t))^2 \right. \right. \right. \\ &\quad \left. \left. - \Im((Y_0(t) + Y_1(t))(X_1(t) + X_0(t))) - k\Im((Z_0(t) \right. \right. \\ &\quad \left. \left. + Z_1(t))(X_1(t) + X_0(t))) \right\} \right] \\ &\quad \left. + \Im^{-1} \left[\frac{1}{s+\alpha-r} \left[\frac{r}{T_{\max}} \{ \Im(X_0^2(t)) + \Im(Y_0(t)X_0(t)) \right. \right. \right. \right. \\ &\quad \left. \left. \left. + k\Im(Z_0(t)X_0(t)) \} \right] \right] \right] \end{aligned} \quad (88)$$

$$\begin{aligned} Y_2(t) &= \Im^{-1} \left[\frac{k}{s+\beta} \{ \Im((Z_0(t) + Z_1(t))(X_1(t) + X_0(t))) \} \right] \\ &\quad - \Im^{-1} \left[\frac{k}{s+\beta} \{ \Im(Z_0(t)X_0(t)) \} \right] \end{aligned} \quad (89)$$

$$Z_2(t) = \Im^{-1} \left[\frac{N\beta}{s+q} \{ \Im(Y_1(t)) \} \right] \quad (90)$$

The next successive iterations can be obtained in a similar manner. Therefore,

$$X(t) = \sum_{i=0}^2 X_i(t) \quad (91)$$

$$Y(t) = \sum_{i=0}^2 Y_i(t) \quad (92)$$

$$Z(t) = \sum_{i=0}^2 Z_i(t) \quad (93)$$

For the computation purpose we have taken the 2-iterations of MNIM solutions.

4. Results and Discussions

We take a scenario of Attaullah et al. [29], where the initial conditions are $x_0 = 0.1$, $y_0 = 0$, $z_0 = 0.1$, with parameter values $p = 0.1$, $\alpha = 0.02$, $\beta = 0.3$, $r = 3$, $q = 2.4$, $k = 1500$, $k = 0.0027$, $N = 10$. All our calculations as well as our graphs are carried out by Maple 2020. The Maple built-in programme has been used for RK4 solutions with step size $\Delta t = 0.001$. The new iterative method (NIM) and modified new iterative method's (MNIM) simulation results are illustrated graphically and numerically. We displayed the graphical outcomes of both NIM and MNIM strategies related to the RK4 method in Figure 1. The figure depicts that the 5-iterations of NIM solutions fail to provide suitable accuracy as time increases and solutions are only valid till $t \leq 1$, whereas the 2-iterations of modified NIM precisions agree well with those of RK4 precisions. Additionally, we contrasted the absolute errors of the proposed MNIM scheme to those of other conventional methods, such as cGP(2) and LWCM [29], GA-IPA and GA-ASA [28], LADM-Padé [21], MVIM [26], HPM [25], Bessel collocation [23] and NIM relative to RK4 method, as shown in Tables 2–4 for $X(t)$, $Y(t)$, $Z(t)$, respectively. The recent results via cGP(2) and LWCM [29] match to at least four decimal places with RK4. Further, the numeric solutions via NIM matched at least one decimal place with RK4. In contrast, the results show that the solutions by 2-iterations of MNIM match with those of RK4 at least eight decimal places. The comparisons with other methods used for the model clearly indicate that the MNIM scheme outperformed all the pre-existing solutions. Therefore, it suggests the high accuracy and validity of the proposed MNIM scheme with fewer iterative steps.

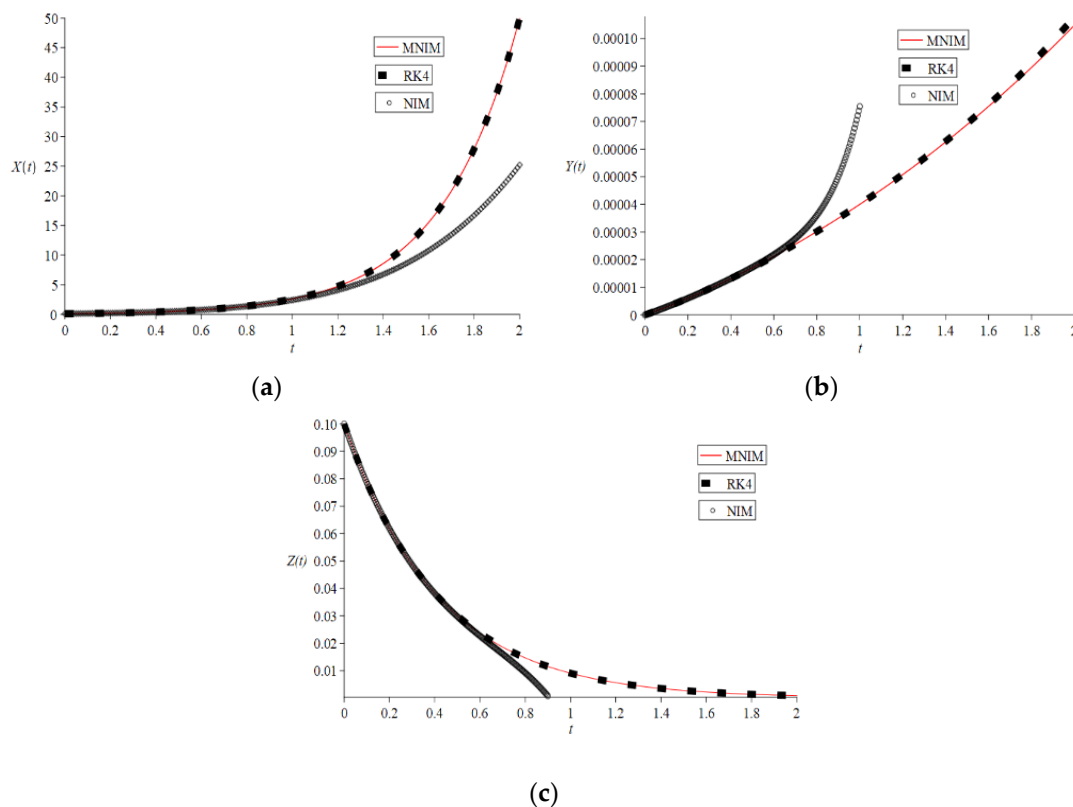


Figure 1. Graphical Comparison between the results of 2-Iterations MNIM, 5-Iterations NIM and RK4 method for (a) $X(t)$, (b) $Y(t)$, (c) $Z(t)$ of HIV Infection Model.

Table 2. Comparison of Absolute Errors for $X(t)$ of MNIM Scheme and LWCM, cGP(2), GA-IPA, GA-ASA, LADM-Padé, MVIM, HPM, Bessel collocation, NIM relative to RK4 Method for HIV Infection Model.

t	LWCM [29]	cGP(2) [29]	GA-IPA [28]	GA-ASA [28]	LADM-Padé [21]	MVIM [26]	HPM [25]	Bessel Collocation [23]	NIM (Present Method)	MNIM (Present Method)
0.2	7.50×10^{-6}	5.81×10^{-6}	1.32×10^{-3}	1.32×10^{-3}	7.77×10^{-5}	7.85×10^{-5}	7.78×10^{-5}	4.87×10^{-3}	6.979×10^{-6}	1×10^{-10}
0.4	2.70×10^{-5}	2.11×10^{-5}	1.06×10^{-3}	1.06×10^{-3}	1.65×10^{-4}	3.00×10^{-4}	1.95×10^{-4}	2.56×10^{-2}	0.0005035	7×10^{-10}
0.6	7.34×10^{-5}	5.74×10^{-5}	1.69×10^{-3}	1.69×10^{-3}	2.43×10^{-3}	8.49×10^{-4}	1.10×10^{-3}	6.81×10^{-2}	0.006497	5.0×10^{-9}
0.8	1.77×10^{-4}	1.38×10^{-4}	3.83×10^{-3}	3.83×10^{-3}	3.46×10^{-2}	2.14×10^{-3}	1.39×10^{-2}	1.36×10^{-1}	0.04157	2.14×10^{-8}
1	3.98×10^{-4}	3.98×10^{-4}	4.19×10^{-3}	4.18×10^{-3}	2.58×10^{-1}	5.14×10^{-3}	7.89×10^{-2}	2.04×10^{-1}	0.1816	7.92×10^{-8}

Table 3. Comparison of Absolute Errors for $Y(t)$ of MNIM Scheme and LWCM, cGP(2), GA-IPA, GA-ASA, LADM-Padé, MVIM, HPM, Bessel collocation, NIM relative to RK4 Method for HIV Infection Model.

t	LWCM [29]	cGP(2) [29]	GA-IPA [28]	GA-ASA [28]	LADM-Padé [21]	MVIM [26]	HPM [25]	Bessel Collocation [23]	NIM (Present Method)	MNIM (Present Method)
0.2	8.36×10^{-10}	6.67×10^{-10}	1.66×10^{-6}	1.73×10^{-6}	1.20×10^{-9}	1.19×10^{-9}	1.20×10^{-9}	2.16×10^{-7}	3.255×10^{-12}	0
0.4	1.95×10^{-9}	1.49×10^{-9}	2.46×10^{-6}	2.94×10^{-6}	6.15×10^{-9}	5.29×10^{-9}	5.89×10^{-9}	2.17×10^{-7}	2.255×10^{-8}	6×10^{-10}
0.6	3.20×10^{-9}	2.48×10^{-9}	1.76×10^{-7}	4.54×10^{-7}	5.78×10^{-8}	1.27×10^{-8}	2.24×10^{-8}	8.58×10^{-7}	5.876×10^{-7}	3.2×10^{-9}
0.8	4.63×10^{-9}	3.65×10^{-9}	1.80×10^{-7}	2.07×10^{-7}	8.26×10^{-8}	2.27×10^{-8}	9.09×10^{-8}	1.78×10^{-6}	5.825×10^{-6}	1.19×10^{-8}
1	6.44×10^{-9}	5.04×10^{-9}	1.88×10^{-6}	2.02×10^{-6}	1.21×10^{-7}	3.12×10^{-8}	3.39×10^{-7}	3.09×10^{-6}	3.538×10^{-5}	3.66×10^{-8}

Table 4. Comparison of Absolute Errors for $Z(t)$ of MNIM Scheme and LWCM, cGP(2), GA-IPA, GA-ASA, LADM-Padé, MVIM, HPM, Bessel collocation, NIM relative to RK4 Method for HIV Infection Model.

t	LWCM [29]	cGP(2) [29]	GA-IPA [28]	GA-ASA [28]	LADM-Padé [21]	MVIM [26]	HPM [25]	Bessel Collocation [23]	NIM (Present Method)	MNIM (Present Method)
0.2	1.00×10^{-10}	8.66×10^{-7}	1.32×10^{-5}	1.46×10^{-5}	1.08×10^{-7}	5.61×10^{-8}	1.00×10^{-7}	6.59×10^{-8}	1.591×10^{-6}	1×10^{-10}
0.4	1.24×10^{-6}	1.07×10^{-6}	3.40×10^{-6}	1.49×10^{-6}	1.84×10^{-5}	1.06×10^{-6}	1.33×10^{-5}	3.79×10^{-8}	9.555×10^{-5}	3×10^{-10}
0.6	1.15×10^{-6}	9.95×10^{-7}	3.07×10^{-6}	4.05×10^{-6}	6.87×10^{-4}	5.75×10^{-6}	2.15×10^{-4}	2.31×10^{-7}	0.001025	8×10^{-10}
0.8	9.50×10^{-7}	8.21×10^{-7}	7.91×10^{-6}	7.03×10^{-6}	4.71×10^{-3}	2.01×10^{-5}	1.53×10^{-3}	7.87×10^{-7}	0.005438	6×10^{-10}
1	7.61×10^{-7}	6.34×10^{-7}	6.64×10^{-6}	5.66×10^{-6}	5.80×10^{-3}	5.64×10^{-5}	6.95×10^{-3}	1.46×10^{-2}	0.01965	2.4×10^{-9}

5. Conclusions

In this paper, we propose an improvement to the existing new iterative method and prove that the improved method is more accurate than the new iterative method for solving a system of nonlinear differential equations that describes HIV infection in CD4⁺ T cells. The MNIM helps us to reduce the number of terms as well as iterations steps. The modified NIM solutions are more accurate than other numeric solutions of the HIV infection model. The recent results provided in Ref. [29], matches to at least four decimal places with RK4, in contrast, MNIM matches to at least eight decimal places. Furthermore, based on our observations, the numerical solutions of 5-iterations of NIM for the HIV infection model were valid only in a short time span ($t \leq 1$) and the modified NIM is used to extend the validity domains for selected disease model, calculating only 2-iteration steps. The modified method provides the solution in a rapid convergent series with computable terms. Analytic-numeric solutions were used to ensure that the MNIM technique is straightforward, reliable, and efficient. We hope that the modified iterative algorithm will be able to solve many types of interesting nonlinear problems. The implementation of this method in HIV infection dynamics may pave the way for a new horizon in the future. Future work should reapply these methods in developing a dynamic model for other diseases such as heart disease [40–42] and combine the proposed approach with the machine learning model to develop optimal solutions for infectious diseases such as COVID-19 and pneumonia [43–45].

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