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STABILITY ANALYSIS OF GENERALIZED MODEL OF HUMAN T-CELL LYMPHOTROPIC VIRUS I (HTLV-I) INFECTION OF $CD4^+$ T-CELLS

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Abstract. In this paper, we present the fractional-order model of (HTLV-I) infection of $CD4^+$ T-cells. We show that this model possesses non-negative solutions as desired in any population dynamics. The stability of different equilibria of this model are discussed in detail. Natural-Adomian Decomposition method (N-ADM) is used to compute an analytical solution of the system of nonlinear fractional differential equations governing the problem. The results are compared with the results obtained by the classical Runge-Kutta method in the case of integer-order derivatives.

1. Introduction

Human T cell lymphotropic virus I (HTLV-I) is the first human retrovirus to be discovered and has continued to be an important transfusion transmissible infection (TTI) especially in highly endemic regions such as the subSaharan Africa [1]. The virus has been associated with several diseases including adult T cell leukemia (ATL), tropical spastic paraparesis, HTLV-I uveitis and HTLV-I associated infective dermatitis [2, 3].

Infection with HTLV-I is now a global epidemic, affecting 10 million to 20 million people. HTLV-1 is spread by blood transfusions, sexual contact and sharing needles. It can also be spread from mother to child during birth or breast-feeding. There is no cure or treatment for HTLV-1 and it is considered a lifelong condition; however, most (95%) infected people remain asymptomatic (show no symptoms) throughout life [4, 5]. HTLV-I infection is achieved primarily through cell-to-cell contact [6]. HTLV-I is a single-stranded RNA retrovirus, the activity of which produces a DNA copy of the viral genome that is integrated into the DNA of the host genome [7]. After this takes place, the latency period can persist for a long period of time. Latently infected cells contain the virus, but do not produce DNA and are incapable of contagion. When such cells are stimulated by antigen, they can become active and infect healthy cells. Taking these factors into consideration, the first classical of HTLV-I model proposed by Stilianakis and Seydel [6] and Patricia Katri et al

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[7] modified the classic model for the system of non-linear differential equations as follow:

$$\begin{cases} \frac{dT(t)}{dt} = \lambda - \mu_T\ T(t) - \kappa\ V(t)T(t), \\ \frac{dI(t)}{dt} = \kappa_1 V(t)T(t) - (\mu_L + \varepsilon)I(t), \\ \frac{dV(t)}{dt} = \varepsilon I(t) - (\mu_A + \rho)V(t), \\ \frac{dL(t)}{dt} = \rho V(t) + \beta L(1 - \frac{L}{L_{max}}) - \mu_M L. \end{cases} \tag{1.1}$$

That model describes the T-cell dynamics of human T-cell lymphotropic virus I (HTLV-I) infection and the development of adult T-cell leukemia (ATL), where $T(t)$ represents the concentration of healthy $CD4^+$ T-cells at time t, $I(t)$ represents the concentration of latently infected $CD4^+$ T-cells, $V(t)$ the concentration of actively infected $CD4^+$ T-cells, and $L(t)$ the concentration of leukemic cells at time t. To explain the parameters, we note that λ is the source of $CD4^+$ T-cells from precursors μ_T is the natural death rate of $CD4^+$ T-cells, κ is the rate at which uninfected cells are contacted by actively infected cells. The parameter κ_1 represents the rate of infection of T-cells with virus from actively infected cells. μ_L, μ_A, and μ_M are blanket death terms for latently infected, actively infected and leukemic cells, to reflect the assumption that we do not initially know whether the cells die naturally or by bursting. In addition, ε and ρ represent the rates at which latently infected and actively infected cells become actively infected and leukemic, respectively. The ATL cells grow at a rate β of a classical logistic growth function. L_{max} is the maximal population level of leukemic $CD4^+$ T-cells.

The fractional order extension of the classical model (1.1) have been first studied in [8]. The reason of using fractional differential equations (FDEs) is that FDEs are naturally related to systems with memory which exists in most biological system. Also they show the realistic biphasic decline behavior of infection of diseases but at a slower rate. In our work, we consider fractional-order for the system (1.1), where $D^\alpha T, D^\alpha I, D^\alpha V$ and $D^\alpha L$ are the derivatives of $T(t), I(t), V(t)$ and $L(t)$ respectively, of arbitrary order α (where $0 < \alpha \leq 1$) in the sense of Caputo (see e.g. [9]), then our system is described by the following set of fractional order differential equations

$$\begin{cases} D^\alpha T(t) = \lambda - \mu_T\ T(t) - \kappa\ V(t)T(t), \\ D^\alpha I(t) = \kappa_1 V(t)T(t) - (\mu_L + \varepsilon)I(t), \\ D^\alpha V(t) = \varepsilon I(t) - (\mu_A + \rho)V(t), \\ D^\alpha L(t) = \rho V(t) + \beta L(1 - \frac{L}{L_{max}}) - \mu_M L. \end{cases} \tag{1.2}$$

Subject to the following initial conditions, all parameters are assumed to be positive as in Table 1.

$$T(0) = 1000,\ I(0) = 250,\ V(0) = 1.5,\ L(0) = 0. \tag{1.3}$$

The Adomian Decomposition method (ADM) was frist ntroduced by Adomian in the 1980's [10, 11]. Since then the ADM has emerged as efficient procedure for finding the solution of large and general class of problems. The Natural transform was defined by Khan [12]. Applications of Natural transform in the solution of

differential and integeral equations can be found in [13, 14]. The N-ADM basically demonstrates how the Natural transform maybe combined with ADM to obtain analytic approximate solution of nonlinear differential equations such as [15, 16]. The motivation of this paper is to find analytical solution for the generalized model of (HTLV-I) infection in the sense of Caputo by using the N-ADM .

The rest of the paper is organized as follow. In Section 2, a brief review of the fractional calculus and definitions of Natural, Laplace transform and Mittag-Leffler function is presented. In Section 3, we show that the model (1.2) possesses a unique solution which is non-negative. Section 4 is devoted to study the equilibrium points and the stability analysis of our model (1.2). In Section 5, we apply the Natural-Adomian Decomposition method for obtaining the solution of the fractional order model of Human T-cell Lymphotropic virus I (HTLV-I) infection of $CD4^+$ T-Cells. Numerical simulations are represented graphically and discussed in Section 6. Finally, we conclude the paper in Section 7

2. Preliminary

Here, we present some necessary definitions and notations related to fractional calculus (see e.g. [9]) and the Natural transform [15, 16, 17]. The most commonly used definitions are Riemann-Liouville and Caputo.

Definition 2.1. The Riemann-Liouville fractional integeration of order α is defined as:

$$\begin{aligned}(J^{\alpha}_{t_0}f)(t) &= \frac{1}{\Gamma(\alpha)}\int_{t_0}^{t}(t-s)^{\alpha-1}f(s)ds,\ \alpha>0,\ t>t_0,\\ (J^{0}_{t_0}f)(t) &= f(t).\end{aligned}$$

The Riemann-Liouville derivative has certain disadvantages such that the fractional derivative of a constant is not zero. Therefore, we will make use of Caputo's definition owing to its convenience for initial conditions of the fractional differential equations.

Definition 2.2. Riemann-Liouville and Caputo fractional derivatives of order α can be defined respectively as:

$$\begin{aligned}D^{\alpha}_{*}f(t) &= D^{n}(J^{n-\alpha}f(t)),\\ D^{\alpha}f(t) &= J^{n-\alpha}(D^{n}f(t)),\end{aligned}$$

where $n-1<\alpha\leq n,\ n\in\mathbb{N}$, f is a given function, and $\Gamma(\cdot)$ denotes the gamma function. It is known that $(D^{\alpha}_{t_0}f)(t)\to f'(t)$ as $\alpha\to 1$.

Now, we recall the definitions of Natural transform, Laplace transform of Caputo's derivative and Mittag-Leffler function in two arguments.

Definition 2.3. Over the set of functions

$$A=\{f(t):\exists M,\tau_1,\tau_2>0,|f(t)|<Me^{|t|/\tau_j},\ \text{if } t\in(-1)^{j}\mathrm{x}[0,\infty)\}.$$

The Natural transform of $f(t)$ is defined by

$$\mathcal{N}\{f(t)\}=R(s,u)=\int_0^{\infty}f(ut)\ e^{-st}dt,\ u>0,\ s>0,$$

where $R(s,u)$ is the Natural transform of the time function $f(t)$.

Theorem 2.1. *If $\mathcal{N}\{f(t)\}$ is the natural transform of the function $f(t)$, then the natural transform of the fractional derivative of order α is defined as:-*

$$\mathcal{N}\{D^{\alpha}(f(t))\} = \frac{s^{\alpha}}{u^{\alpha}}R(s,u) - \sum_{k=0}^{n-1}\frac{s^{\alpha-(k+1)}}{u^{\alpha-k}}f^{(k)}(0)$$

Definition 2.4.

$$\begin{aligned}\mathcal{L}\{D^{\alpha}f(t),s\} &= s^{\alpha}F(s) - \sum_{i=0}^{n-1}s^{\alpha-i-1}f^{(i)}(0),\ (n-1<\alpha\leq n);\ n\in\mathbb{N}.\\ E_{a,b}(x) &= \sum_{n=0}^{\infty}\frac{x^{n}}{\Gamma(an+b)},\ a>0,\ b>0.\end{aligned}$$

3. Non-negative solutions

Let $\mathbb{R}^4_+ = \{X\in\mathbb{R}^4 | X\geq 0\}$ and $X(t) = (T(t), I(t), V(t), L(t))^T$, we now prove the main theorem.

Theorem 3.1. *There is a unique solution $X(t) = (T(t), I(t), V(t), L(t))^T$ for model (1.2) at $t\geq 0$ (where, $t_0 = 0$) and the solution will remain in $\mathbb{R}^4_+$.*

Proof. From Theorem 3.1 and Remark 3.2 of [18], we know that the solution on $(0,\infty)$ is existent and unique. Now, we will show that the feasible region $\mathbb{R}^4_+$ is positively invariant (non-negative solutions). Rearranging the following equation

$$D^{\alpha}V(t) + (\mu_A+\rho)V(t) = \varepsilon I(t),$$

and we assume that $g(t) = \varepsilon I$ is a constant function of time. Then we get the fractional order differential equation representing the concentration of actively infected $CD4^+$T-cells as follows:

$$D^{\alpha}V(t) + (\mu_A+\rho)V(t) = g(t). \tag{3.1}$$

Solving equation (3.1) using Laplace transform (from Definition 2.4) method [9] and taking the initial condition to be zero (to simplify), we have the following solution

$$V(t) = \int_0^t (t-\tau)^{\alpha-1}E_{\alpha,\alpha}(-(\mu_A+\rho)\ (t-\tau)^{\alpha})g(\tau)d\tau\ \geq 0,$$

where $0<\alpha<1$, $\mu_A+\rho>0$ and $E_{l,m}(x)$ is the two-parameter Mittag-Leffler function (see Definition 2.4). For $T(t)$, $I(t)$ and $L(t)$ by the same way we have $T(t), I(t), L(t)\geq 0$, hence proved that the solution $X(t)$ is positive invariant. □

4. The stability of the equilibrium points

We frist evaluate the equilibrium points or steady states of the fractional system (1.2). To evaluate the equilibrium points, let

$$\begin{cases} D^{\alpha}T = 0,\\ D^{\alpha}I = 0,\\ D^{\alpha}V = 0,\\ D^{\alpha}L = 0,\end{cases} \tag{4.1}$$

then, the system (1.2) has two equilibrium points

(1) *At disease-free equilibrium:*

We now consider the equations below and solve it (where there is no infection).

$$\lambda - \mu_T\ T(t) - \kappa\ V(t)T(t) = 0, \tag{4.2}$$

$$\kappa_1 V(t)T(t) - (\mu_L + \varepsilon)I(t) = 0, \tag{4.3}$$

$$\varepsilon I(t) - (\mu_A + \rho)V(t) = 0, \tag{4.4}$$

$$\rho V(t) + \beta L(1 - \frac{L}{L_{max}}) - \mu_M L = 0. \tag{4.5}$$

From equation (4.4), we have $V = 0$ and by substituting in equation (4.2), then disease-free equilibrium (DFE) of the system (1.2) is

$$E^0 = (T_{eq}, I_{eq}, V_{eq}, L_{eq})_{I=0} = \left(\frac{\lambda}{\mu_T},\ 0,\ 0,\ 0\right).$$

(2) *At endemic equilibrium:*

We now consider the case where there is infection, thus we have

$$E^* = (T_{eq}, I_{eq}, V_{eq}, L_{eq})_{I\neq 0} = (T^*, I^*, V^*, L^*),$$

where

$$\begin{aligned} T^* &= \frac{(\mu_A + \rho)(\mu_L + \varepsilon)}{\varepsilon\kappa_1}, \\ I^* &= \frac{\varepsilon\lambda\kappa_1 - \mu_T(\mu_A + \rho)(\mu_L + \varepsilon)}{\kappa\varepsilon(\mu_L + \varepsilon)}, \\ V^* &= \frac{\varepsilon\lambda\kappa_1 - \mu_T(\mu_A + \rho)(\mu_L + \varepsilon)}{\kappa(\mu_L + \varepsilon)(\mu_A + \rho)}, \end{aligned}$$

and L^* is calculated by the following equation

$$L^{*2} + a_1 L^* + a_2 = 0, \tag{4.6}$$

where

$$\begin{aligned} a_1 &= -\tfrac{(\beta - \mu_M)L_{max}}{\beta}, \\ a_2 &= -\tfrac{\rho L_{max}\ V^*}{\beta};\ \text{is always negative.} \end{aligned} \tag{4.7}$$

We can note that the equilibrium points are the same for both integer and fractional system. But the stability region of the fractional-order system with order α, which is illustrated in Figure 1 (where σ, ω refer to the real and imaginary parts of the eigenvalues, respectively, and $j = \sqrt{-1}$), is greater than the stability region of the integer order case (see e.g.[19]). Therefore, we will now drive analytically the stability of different equilibria of the model (1.2). For E^0 , we have the following theorem:

Theorem 4.1. *If $\beta - \mu_M < 0$, then the disease free equilibria E^0 of the system (1.2) is Locally asymptotically stable if $\mathcal{R}_0 \leq 1$ (see equation 7.1) and if $\mathcal{R}_0 > 1$, E^0 unstable, thus E^* exists.*

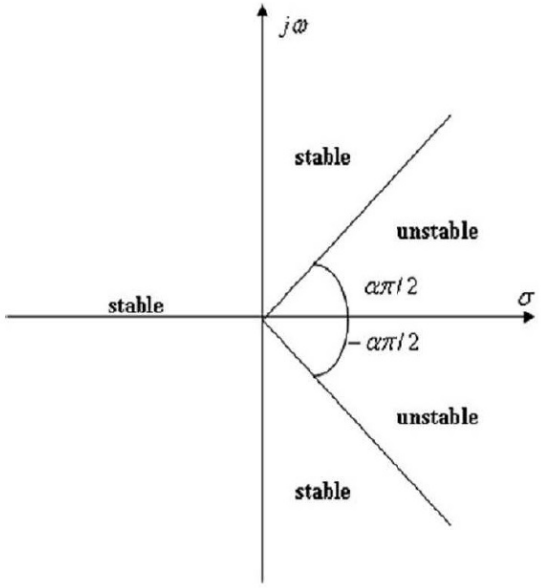

FIGURE 1. Stability region of the fractional-order system.

Proof. Determining the Jacobian matrix of the system (1.2) at E^0 we have:

$$J_{E^0} = \begin{bmatrix} -\mu_T & 0 & \frac{-\kappa\lambda}{\mu_T} & 0 \\ 0 & -(\mu_L+\varepsilon) & \frac{\kappa_1\lambda}{\mu_T} & 0 \\ 0 & \varepsilon & -(\mu_A+\rho) & 0 \\ 0 & 0 & \rho & \beta-\mu_M \end{bmatrix}$$

Calculate the eigenvalues of J_{E^0},

$$\chi_1 = -\mu_T < 0,\ \chi_2 = \beta - \mu_M < 0,$$

and the last two eigenvalue are given by the quadratic equation

$$\chi^2 + B\ \chi + C = 0, \tag{4.8}$$

where

$$B = (\mu_L + \varepsilon + \mu_A + \rho),$$

$$C = (\mu_L+\varepsilon)(\mu_A+\rho) - \tfrac{\kappa\lambda\varepsilon}{\mu_T} = (\mu_L+\varepsilon)(\mu_A+\rho)(1-\mathcal{R}_0).$$

This shows that if $\mathcal{R}_0 \le 1$, then $\chi_{3,4} = \frac{-(\mu_L+\varepsilon+\mu_A+\rho)\pm\sqrt{(\mu_L+\varepsilon+\mu_A+\rho)^2-4(\mu_L+\varepsilon)(\mu_A+\rho)(1-\mathcal{R}_0)}}{2} < 0$, hence it becomes stable. □

For E^*, we have the following theorem:

Theorem 4.2. *Whenever $\mathcal{R}_0 > 1$, the positive infected steady states E^* of the fractional-order system (1.2) is asymptotically stable.*

Proof. We consider the linearized system of (1.2) at E^*. The Jacobian matrix evaluated at the endemic equilibrium is given by

$$J_{E^*} = \begin{bmatrix} -(\mu_T + \kappa V^*) & 0 & -\kappa T^* & 0 \\ \kappa_1 V^* & -(\mu_L + \varepsilon) & \kappa_1 T^* & 0 \\ 0 & \varepsilon & -(\mu_A + \rho) & 0 \\ 0 & 0 & \rho & \beta(1 - \frac{2L^*}{L_{max}}) - \mu_M \end{bmatrix},$$

then, one of its eigenvalues be $\beta(1 - \frac{2L^*}{L_{max}}) - \mu_M$ (always negative, since L^* is higher than the carrying capacity $L_{max} = \frac{\beta - \mu_M}{\beta}$, when infection is chronic) and the remaining eigenvalues are given by solving the following characteristic polynomials:

$$\sigma^3 + F_1\sigma^2 + F_2\sigma + F_3 = 0 \tag{4.9}$$

with $F_1,\ F_2$ and F_3 being

$$F_1 = kV^* + \mu_L + \rho + \mu_T + \varepsilon + \mu_A,$$

$$F_2 = (kV^* + \mu_T)(\mu_L + \varepsilon)(\mu_A + \rho),$$

$$F_3 = kV^*(\mu_L + \varepsilon)(\mu_A + \rho).$$

Obviously, all the eigenvalues of equation (4.9) have negative real parts if and only if the coefficients $F_1,\ F_2$ are positive, and $F_1\ F_2 - F_3 > 0$ (Routh's criterion, see, e.g. [20, 21]), when $\mathcal{R}_0 > 1$. Thus it follows from Routh-Hurtwiz criteria that the system (1.2) at the endemic equilibrium E^* is asymptotically stable, whenever $\mathcal{R}_0 > 1$ and this inequalities $F_1 > 0,\ F_2 > 0,\ F_1\ F_2 > F_3$ are satisfied. □

5. The Natural-Adomian Decomposition Method (N-ADM)

Consider the fractional-order model (1.2) subject to the initial condition (1.3). The nonlinear terms in this model Eqs. (1.2) are VT and L^2. For $\alpha = 1$ the fractional order model converts to the classical model (see e.g.[7]). Applying the Natural transform on both sides of Eqs. (1.2)

$$\begin{cases} \mathcal{N}\{D^\alpha(T)\} = \lambda\,\mathcal{N}\{1\} - \mu_T\,\mathcal{N}\{T(t)\} - \kappa\,\mathcal{N}\{V(t)T(t)\}, \\ \mathcal{N}\{D^\alpha(I)\} = \kappa_1\,\mathcal{N}\{V(t)T(t)\} - (\mu_L + \varepsilon)\,\mathcal{N}\{I(t)\}, \\ \mathcal{N}\{D^\alpha(V)\} = \varepsilon\,\mathcal{N}\{I(t)\} - (\mu_A + \rho)\,\mathcal{N}\{V(t)\}, \\ \mathcal{N}\{D^\alpha(L)\} = \rho\,\mathcal{N}\{V(t)\} + \beta\mathcal{N}\{L(1 - \frac{L}{L_{max}})\} - \mu_M\mathcal{N}\{L\}, \end{cases} \tag{5.1}$$

using property of the Natural transform, we get

$$\begin{cases} \frac{s^\alpha}{u^\alpha}\mathcal{N}\{T\} - \frac{s^{\alpha-1}}{u^\alpha}T(0) = \lambda\,\mathcal{N}\{1\} - \mu_T\,\mathcal{N}\{T(t)\} - \kappa\,\mathcal{N}\{V(t)T(t)\}, \\ \frac{s^\alpha}{u^\alpha}\mathcal{N}\{I\} - \frac{s^{\alpha-1}}{u^\alpha}I(0) = \kappa_1\,\mathcal{N}\{V(t)T(t)\} - (\mu_L+\varepsilon)\,\mathcal{N}\{I(t)\}, \\ \frac{s^\alpha}{u^\alpha}\mathcal{N}\{V\} - \frac{s^{\alpha-1}}{u^\alpha}V(0) = \varepsilon\,\mathcal{N}\{I(t)\} - (\mu_A+\rho)\,\mathcal{N}\{V(t)\}, \\ \frac{s^\alpha}{u^\alpha}\mathcal{N}\{L\} - \frac{s^{\alpha-1}}{u^\alpha}L(0) = \rho\,\mathcal{N}\{V(t)\} + \beta\mathcal{N}\{L(1-\frac{L(t)}{L_{max}})\} - \mu_M\mathcal{N}\{L(t)\}, \end{cases} \tag{5.2}$$

using initial conditions (1.3)

$$\begin{cases} \mathcal{N}\{T\} = \frac{T(0)}{s} + \lambda\,\frac{u^\alpha}{s^{\alpha+1}}\,\mathcal{N}\{1\} - \mu_T\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{T(t)\} - \kappa\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{V(t)T(t)\}, \\ \mathcal{N}\{I\} = \frac{I(0)}{s} + \kappa_1\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{V(t)T(t)\} - (\mu_L+\varepsilon)\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{I(t)\}, \\ \mathcal{N}\{V\} = \frac{V(0)}{s} + \varepsilon\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{I(t)\} - (\mu_A+\rho)\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{V(t)\}, \\ \mathcal{N}\{L\} = \frac{L(0)}{s} + \rho\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{V(t)\} + \beta\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{L(t)\} - \frac{u^\alpha}{s^\alpha}\,\frac{\beta}{L_{max}}\,\mathcal{N}\{L^2(t)\} - \mu_M\,\frac{u^\alpha}{s^\alpha}\,\mathcal{N}\{L(t)\}. \end{cases} \tag{5.3}$$

The method assumes the solution as an infinite series:

$$T = \sum_{k=0}^{\infty} T_k, \quad I = \sum_{k=0}^{\infty} I_k, \quad V = \sum_{k=0}^{\infty} V_k, \quad L = \sum_{k=0}^{\infty} L_k. \tag{5.4}$$

The nonlinearity VT and L^2 are decomposed as

$$VT = \sum_{k=0}^{\infty} A_k,\ L^2 = \sum_{k=0}^{\infty} A_k^*,$$

where $A_k,\ A_k^*$ so-called Adomian Polynomials given as

$$A_k = \frac{1}{k!}\frac{d^k}{d\lambda^k}\left[\sum_{j=0}^{k}\lambda^j V_j \sum_{j=0}^{k}\lambda^j T_j\right]\Bigg|_{\lambda=0},\ A_k^* = \frac{1}{k!}\frac{d^k}{d\lambda^k}\left[\sum_{j=0}^{k}\lambda^j L_j\right]^2\Bigg|_{\lambda=0}. \tag{5.5}$$

Substituting from Eqs. (5.4), (5.5) into (5.3) the result is

$$\begin{cases} \mathcal{N}\{T_0\} = \frac{T(0)}{s} + \frac{\lambda u^\alpha}{s^{\alpha+1}}, \\ \mathcal{N}\{I_0\} = \frac{I(0)}{s}, \\ \mathcal{N}\{V_0\} = \frac{V(0)}{s}, \\ \mathcal{N}\{L_0\} = \frac{L(0)}{s}, \end{cases} \tag{5.6}$$

$$\begin{cases} \mathcal{N}\{T_1\} = -\mu_T \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{T_0\} - \kappa \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{A_0\}, \\ \mathcal{N}\{I_1\} = \kappa_1 \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{A_0\} - (\mu_L + \varepsilon) \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{I_0\} \\ \mathcal{N}\{V_1\} = \varepsilon \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{I_0\} - (\mu_A + \rho) \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{V_0\}, \\ \mathcal{N}\{L_1\} = \rho \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{V_0\} + \beta \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{L_0\} - \frac{u^\alpha}{s^\alpha} \ \frac{\beta}{L_{max}} \ \mathcal{N}\{A_0^*\} - \mu_M \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{L_0\}, \end{cases} \tag{5.7}$$

$$\vdots$$

$$\begin{cases} \mathcal{N}\{T_{k+1}\} = -\mu_T \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{T_k\} - \kappa \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{A_k\}, \\ \mathcal{N}\{I_{k+1}\} = \kappa_1 \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{A_k\} - (\mu_L + \varepsilon) \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{I_k\} \\ \mathcal{N}\{V_{k+1}\} = \varepsilon \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{I_k\} - (\mu_A + \rho) \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{V_k\}, \\ \mathcal{N}\{L_{k+1}\} = \rho \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{V_k\} + \beta \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{L_k\} - \frac{u^\alpha}{s^\alpha} \ \frac{\beta}{L_{max}} \ \mathcal{N}\{A_k^*\} - \mu_M \ \frac{u^\alpha}{s^\alpha} \ \mathcal{N}\{L_k\}. \end{cases}$$

The aim is to study the mathematical behavior of the solution $T(t)$, $I(t)$, $V(t)$, $L(t)$ for the different values of α. By Applying the inverse Natural transform to both sides of Eqs.(5.6) the values of T_0, I_0, V_0, L_0 are obtained. Substituting these values of A_0, A_0^*, T_0, I_0, V_0, L_0 into Eqs.(5.7), the first component T_1, I_1, V_1, L_1 are obtained. The other terms of $T_2, T_3, ...$, $I_2, I_3, ...$ $V_2, V_3, ...$ and $L_2, L_3, ...$ can be calculated recursively in a similar way and we can write the solution

$$T(t) = T_0 + T_1 + ... \, , I(t) = I_0 + I_1 + ... \, , V(t) = V_0 + V_1 + ... \, , L(t) = L_0 + L_1 + ... \, . \tag{5.8}$$

6. Numerical results and discussion

The N-ADM provides an analytical approximate solution in terms of an infinite power series. For numerical results, the following values, for parameters, are considered [7]. The first few components of N-ADM solution $T(t)$, $I(t)$, $V(t)$ and $L(t)$

Parameter	μ_T	μ_L	μ_A	μ_M	κ	κ_1	β	ε	ρ	L_{max}	λ
Values (mm^3/ day)	0.6	0.006	0.05	0.0005	varies	varies	0.0003	0.0004	0.00004	2200	6

Table 1. Parameters values.

are calculated. We computed the first three terms of the N-ADM series solution for the system (1.2). We present two of them as follows:

$$T_0 = 1000 + \frac{\lambda}{\Gamma(\alpha+1)} t^\alpha, \ I_0 = 250, \ V_0 = 1.5, \ L_0 = 0,$$

$$T_1 = \frac{-(1000\mu_T + 1500\kappa)}{\Gamma(\alpha+1)} t^\alpha - \frac{(\lambda\mu_T + 1.5\lambda\kappa)}{\Gamma(2\alpha+1)} t^{2\alpha}, \ I_1 = \frac{(1500\kappa_1 - 250(\mu_L+\varepsilon))}{\Gamma(\alpha+1)} t^\alpha + \frac{1.5\kappa_1}{\Gamma(2\alpha+1)} t^{2\alpha},$$

$$V_1 = \frac{(250\varepsilon - 1.5(\mu_A+\rho))}{\Gamma(\alpha+1)} t^\alpha, \ L_1 = \frac{1.5\rho}{\Gamma(\alpha+1)} t^\alpha,$$

thus, the N-ADM series solution of the system (1.2) can be given by Eqs.5.8, with the values of initial conditions and parameters in Table 1. The approximate solutions displayed in Figures 2-4 with different value of fractional order $0 < \alpha \leq 1$ and it is clear that varying the values of κ and κ_1 will alter the number of uninfected $CD4^+$ T-cells, infected cells, and leukemic cells.

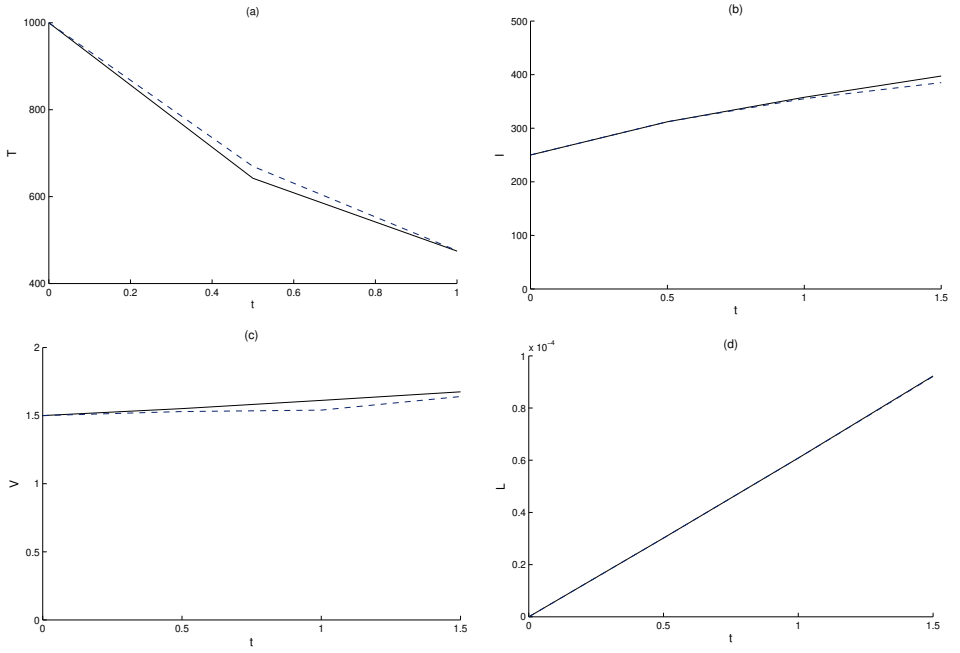

FIGURE 2. The solutions by N-ADM (Solid line) (a) $T(t)$, (b) $I(t)$, (c) $V(t)$ and (d) $L(t)$ at $\alpha = 1$ compared with RK4 (Dashed line).

7. Conclusion

In this work we have introduced a generalized of HTLV-I model in Caputo sense. We obtained the non-negative solutions of the fractional model by Laplace transform. The basic reproduction number "represents the average number of secondary infections caused by a single primary actively infected T cell introduced into a pool of susceptible T cells during its entire infection period" is given by (see e.g.[7])

$$\mathcal{R}_0 = \frac{\varepsilon\lambda\kappa}{\mu_T(\mu_L + \varepsilon)(\mu_A + \rho)}. \tag{7.1}$$

We carried out numerical solutions to demonstrate the theoretical analysis by applying the Natural-Adomian Decomposition method. For example, if $\kappa = \kappa_1 = 0.1$, then $\mathcal{R}_0 = 1.2 > 1$, from Figure 3 the disease will persist and in Figures 3-4 the results show that increasing the value of κ and κ_1 makes the number of healthy $CD4^+$ T-cells decreases dramatically, while the numbers of latently infected cells and leukemic cells increase substantially. The comparison for some different values of α has been obtained and the results show that the solution continuously depends on the time-fractional derivative.

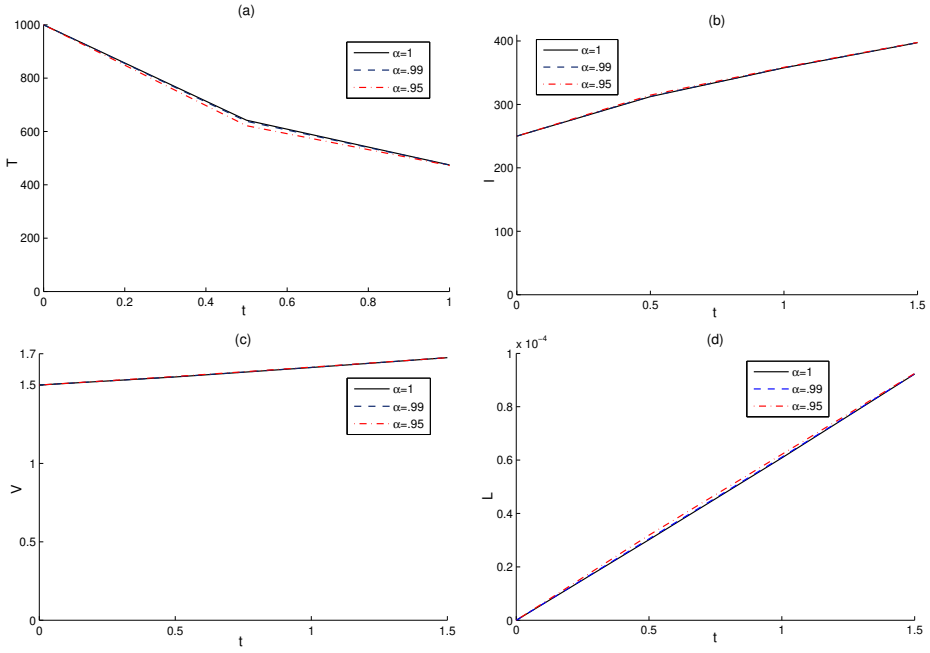

FIGURE 3. The numerical results (a) $T(t)$, (b) $I(t)$, (c) $V(t)$, and (d) $L(t)$ at $\kappa = \kappa_1 = 0.1$ different values of α.

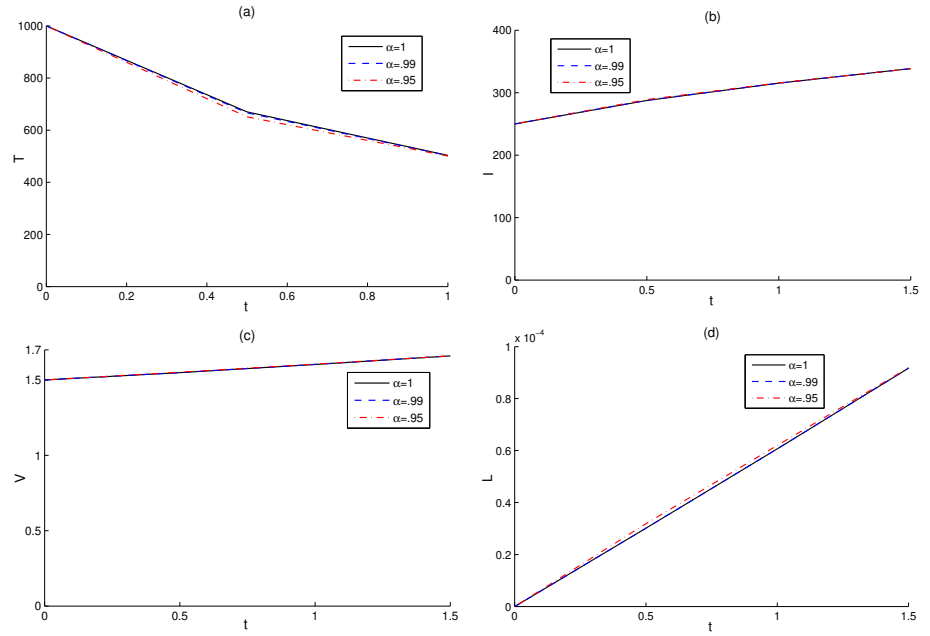

FIGURE 4. The numerical results (a) $T(t)$, (b) $I(t)$, (c) $V(t)$, and (d) $L(t)$ at $\kappa = \kappa_1 = 0.06$ different values of α.

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