

# A Numerical Study on a Model for HIV Infection of CD4<sup>+</sup>T-cells by Shifted Chebyshev Polynomials

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**Abstract:** In this paper, we propose a new method to approximate the solution of a model for Human immunodeficiency virus (HIV) infection of CD4<sup>+</sup>T-cells. A collocation method based on shifted Chebyshev orthogonal polynomials is implemented for solving the model. Using the proposed method, the model is converted to a system of nonlinear algebraic equations. In addition, the accuracy of our method are investigated by comparing our results with the state-of-the-art methods, and the results indicate that our method improves the precision of the solution and has a uniform accuracy in comparison with previous methods in the same interval.

**Keywords:** Shifted-Chebyshev polynomials, HIV infection, CD4<sup>+</sup>T-cells, Collocation methods, Nonlinear differential equations.

## Introduction

Mathematical models are valuable in understanding natural problems. Scientists obtain important information about the problems by solving these models. A major problem for human health in the recent decades is Acquired Immune Deficiency Syndrome (AIDS) and one of the most famous models for dynamics of Human immunodeficiency virus (HIV) infection of CD4<sup>+</sup>T-cells was developed by Perelson et al. [24, 25] described by a system of nonlinear ordinary differential equations. Many other models have already been suggested, which have taken this model as their inspiration. The CD4<sup>+</sup>T-cells, also named as leukocytes or T helper cells, have a main role in protecting the body against diseases. Generally, the number of T helper cells in a healthy person is about 800-1200 mm<sup>3</sup> and the HIV viruses use these cells maliciously to pervade and weaken human immunity system. The model contains three components; the concentration of the susceptible CD4<sup>+</sup>T-cells, the CD4<sup>+</sup>T-cells infected by the HIV viruses and the free HIV virus particles in the blood which are denoted by  $T(t)$ ,  $I(t)$  and  $V(t)$ , respectively.

The model is represented below:

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

Also, the initial conditions are:  $T(0) = \gamma_1, I(0) = \gamma_2, V(0) = \gamma_3, 0 \leq t \leq l < \infty$ .

The explanation of these parameters and the terms of the equations are given in Table 1. In the last decade, many researchers have used different approaches to approximate the solution of the model [7, 13, 16, 19]. Ding and Ye [8] introduced a fractional order into a model of HIV CD4<sup>+</sup>T-cells infection and obtained some numerical results by Adams-type predictor-corrector method (APCM). In 2011, Gökdoğan et al. [10] used a multi-step differential transform method (MsDTM) to approximate the solution of the fractional order model. Moreover, in the same year, Merdan et al. [15] approximated the solution of the model by a modified variational iteration method (MVIM) based on the Padé approximation. One year later, Yüzbaşı [30] applied the Bessel collocation method (BCM) for solving this system of nonlinear ordinary differential equations (NODE). Srivastava et al. [26] employed a semi-numerical analytical method called differential transform method (DTM) that is an infinite power series for an appropriate initial condition. Zurigat and Ababneh [32] investigated a fractional order into Perelson and Nelson’s extended model which has four basic components: the concentration of the healthy CD4<sup>+</sup>T-cells at time  $t$ , the concentration of the latently infected CD4<sup>+</sup>T-cells, the concentration of the actively infected CD4<sup>+</sup>T-cells and the concentration of the leukemic cells at time  $t$  [27]. They implemented a multi-step differential transform (MsDT) to approximate the solution of the above model [32]. Khalid [12] presented a perturbation iteration algorithm (PIA). For this purpose, recently, Gandomani [11] provided an approximate solution using collocation method based on the Müntz-Legendre polynomials (MLP) for the fractional order model of HIV infection of CD4<sup>+</sup>T-cells. Yüzbaşı [31] solved this model by an exponential method which is based on exponential polynomials (EM-EP) and collocation points. The Legendre wavelet (LW) method was proposed by Venkatesh et al. in 2016 [28] for solving Eq. (1). The previous methods are summarized in Table 2.

Table 1. The definitions of the parameters and terms

| Parameters                | Definition  |
|---------------------------|---|
| $q$                       | Source term for uninfected CD4 <sup>+</sup> T-cells                         |
| $\alpha$                  | Natural death rate of uninfected CD4 <sup>+</sup> T-cells                   |
| $r$                       | Growth rate of CD4 <sup>+</sup> T cell concentration                        |
| $T_{max}$                 | Maximum concentration of CD4 <sup>+</sup> T-cells                           |
| $k$                       | Rate of CD4 <sup>+</sup> T-cells that become infected with virus            |
| $\beta$                   | Natural death rate of infected CD4 <sup>+</sup> T-cells                     |
| $\mu$                     | Number of virus particles produced by each infected CD4 <sup>+</sup> T-cell |
| $\gamma$                  | Natural death rate of virus particles                                       |
| Terms                     | Definition  |
| $1 - \frac{T+I}{T_{max}}$ | The logistic growth of healthy T helper cells                               |
| $\frac{KV}{T}$            | The occurrence of HIV infection of healthy CD4 <sup>+</sup> T-cells         |

It is worth noting that proliferation of infected CD4<sup>+</sup>T-cells is neglected. Furthermore, each infected leukocyte is assumed to produce  $\mu$  virus particles in its lifetime. The human’s body produces the CD4<sup>+</sup>T-cells from the precursors in the bone marrow and thymus at a constant rate  $q$ . T-cells multiply through the mitosis with a rate  $r$  when T-cells are stimulated by the antigen or mitogen [2, 25, 29].

Table 2. The traditional proposed methods

| Authors                                     | Proposed method  | Year |
|---|--|------|
| Ding, Ye [8]                                | Adams-type predictor-corrector method                            | 2009 |
| Gökdoğan et al. [10]                        | Multi-step differential transform method                         | 2011 |
| Merdan et al. [15]                          | Modified variational iteration method                            | 2011 |
| Yüzbaşı [30]                                | Bessel collocation method  | 2012 |
| Atangana, Goufo [3]                         | Homotopy decomposition method                                    | 2014 |
| Srivastava et al. [26]                      | Differential transform method                                    | 2014 |
| Chen et al. [7]                             | Adomian decomposition method<br>combined with Padé approximation | 2015 |
| Zurigat,<br>Ababneh et al. [32]             | Multistep differential transform                                 | 2015 |
| Khalid [12]                                 | Perturbation iteration algorithm                                 | 2015 |
| Rasouli Gandomani,<br>Tavassoli Kajani [11] | Using Müntz-Legendre polynomials                                 | 2016 |
| Yüzbaşı [31]                                | Exponential method which is based<br>on exponential polynomials  | 2016 |
| Venkatesh et al. [28]                       | Legendre wavelet   | 2016 |
| Parand et al. [19]                          | Shifted Lagrangian Jacobi collocation method                     | 2017 |

The orthogonal polynomials are widely used for solving various numerical problems. The Chebyshev polynomials are among the most useful orthogonal polynomials, which have four various types [6]. They are efficient in solving different problems in Physics, Astronomy, Biology, etc as they can approximate the solutions with high accuracy [4, 5, 9, 17, 23]. In this study, we intend to solve the model (1) by a spectral method based on the different kinds of shifted Chebyshev polynomials. The remainder of this paper are organized as follows: in Section 2, we describe the Chebyshev polynomials and the shifted Chebyshev polynomials. Section 3, contains numerical simulations and comparisons, and in the last section, the conclusion is presented.

## Methodology

### *Properties of the Chebyshev polynomials*

In this section, we explain some of the most useful properties of Chebyshev polynomials. The Chebyshev polynomials of the first, second, third, and fourth kinds of degree  $n$  in  $t$  are denoted by  $T_n(t)$ ,  $U_n(t)$ ,  $V_n(t)$ , and  $W_n(t)$ , respectively. Moreover, they are defined in [14] as:

$$T_n(t) = \cos n\theta, \quad (2)$$

$$U_n(t) = \frac{\sin(n+1)\theta}{\sin\theta}, \quad (3)$$

$$V_n(t) = \frac{\cos(n+\frac{1}{2})\theta}{\cos\frac{1}{2}\theta}, \quad (4)$$

$$W_n(t) = \frac{\sin(n+\frac{1}{2})\theta}{\sin\frac{1}{2}\theta}, \quad (5)$$

where  $t = \cos \theta$ . The range of the variable  $t$  is  $[-1,1]$  [14,20]. Additionally, the respected weight functions are explained in Table 3.

Table 3. Definition of  $w(t)$  for different kinds Chebyshev polynomials

| Polynomial | $w(t)$                   |
|------------|--------------------------|
| $T_n(t)$   | $\frac{1}{\sqrt{1-t^2}}$ |
| $U_n(t)$   | $\sqrt{1-t^2}$           |
| $V_n(t)$   | $\sqrt{\frac{1+t}{1-t}}$ |
| $W_n(t)$   | $\sqrt{\frac{1-t}{1+t}}$ |

In this article, the Chebyshev polynomials are represented by the following notation:

$$\phi_n^i(t) = \begin{cases} T_n(t) & i = 1, \\ U_n(t) & i = 2, \\ V_n(t) & i = 3, \\ W_n(t) & i = 4. \end{cases} \quad (6)$$

Based on the definition of the Chebyshev polynomials, the following recurrence relation is obtained:

$$\phi_{n+1}^i(t) = 2t\phi_n^i(t) - \phi_{n-1}^i(t) \quad n = 1, 2, \dots$$

$$\phi_0^i(t) = 1, \quad \phi_1^i(t) = \begin{cases} t & i = 1, \\ 2t & i = 2, \\ 2t - 1 & i = 3, \\ 2t + 1 & i = 4. \end{cases} \quad (7)$$

### Shifted Chebyshev polynomials

Some problems are defined on the interval  $[a, b]$  where  $a$  and  $b$  are integer numbers. Based on the conditions of Eq. (1), the defined interval for the aforementioned model is  $[0, l]$ . Accordingly, we map the variable  $t$  in  $[0, l]$  and define the shifted Chebyshev polynomials [14]. We define the shifted Chebyshev polynomials (SCP) suitable for any finite range  $[a, b]$  of  $t$ , denoted by  $S\phi_n^i(t)$ , by changing the  $\phi_n^i(t)$  input to a new variable  $s$  under the following linear transformation [14]:

$$s = \frac{2t - (a + b)}{b - a}. \quad (8)$$

As a result, the shifted Chebyshev polynomials in  $[a, b]$  are  $\phi_n^i(s)$ . In the specific case that  $[a, b] \equiv [0, l]$  the transformation becomes  $s = \frac{2t - l}{l}$  and the shifted Chebyshev polynomials related to the interval of (1) are obtained.

An inner product for functions  $u$  and  $v$  in  $L^2[a, b]$ , as the Hilbert space, is defined by:

$$\langle u, v \rangle_w = \int_a^b u(t)v(t)w(t)dt. \quad (9)$$

Clearly, the shifted Chebyshev polynomials are orthogonal with respect to the weight function  $sw(t) = \frac{2}{b-a}w(s)$ . It means that

$$\langle S\phi_m^i(t), S\phi_n^i(t) \rangle_{sw} = c_i \delta_{mn}, \quad (10)$$

where  $\delta_{mn}$  is the Kronecker function and  $c_i$  is a number which depends on  $i$

$$c_1 = \begin{cases} \pi & m, n = 0 \\ \frac{\pi}{2} & o.w. \end{cases}, c_2 = \frac{\pi}{2}, c_3 = \pi, c_4 = \pi. \quad (11)$$

### Numerical application

In this section, the numerical applications are considered and results are obtained. The values of the initial conditions and parameters are given as:

$$\begin{aligned} T(0) &= 0.1, I(0) = 0, V(0) = 0.1. \\ q &= 0.1, \alpha = 0.02, \beta = 0.3, r = 3, \gamma = 2.4. \\ k &= 0.0027, T_{max} = 1500, \mu = 10. \end{aligned}$$

The solutions have been obtained in the interval  $[0, 1]$  in most of the previous investigations. We have applied our method and have solved system (1). Then, the solutions of  $T(t)$ ,  $I(t)$ , and  $V(t)$  in the specific interval  $[0, 1]$  have been obtained and compared with some of the previous methods.

Table 4 contains the solutions of  $T(t)$ ,  $I(t)$  and  $V(t)$  for different values of  $t$  by four kinds of shifted Chebyshev polynomials and 25 collocation points.

All of the shifted Chebyshev polynomials approximate the solutions of  $T(t)$ ,  $I(t)$ , and  $V(t)$  with 23, 27, and 29 decimal digits, respectively. The solution of the proposed method for  $T(t)$ ,  $I(t)$ ,  $V(t)$  are compared with the previous methods and Runge-Kutta method (RK) in Tables 5, 6, and 7, respectively.

Fig. 1 shows  $T(t)$ ,  $I(t)$  and  $V(t)$  for  $N = 25$ . Fig. 1a illustrates that the number of susceptible  $CD4^+$ T-cells increases in interval  $[0, 1]$ . Fig. 1b shows the increasing of the number of the infected T-cells. Furthermore, Fig. 1c displays that the number of the free HIV virus in interval  $[0, 1]$  decreases.

Fig. 2 demonstrates the logarithm of the absolute values of  $Res_1(t)$ ,  $Res_2(t)$ , and  $Res_3(t)$  for  $N = 25$ . Since the residual functions are very close to zero in  $[0, 1]$ , the presented method shows a high accuracy.

Furthermore, Fig. 3 illustrates that the new method has an appropriate convergence rate by demonstrating the absolute values of the coefficients for  $N = 25$ .

Table 4. The values of  $T(t)$ ,  $I(t)$ ,  $V(t)$  for various kinds of shifted Chebyshev polynomials

| $t$ | $S\phi_{25}^1(t)$ | $S\phi_{25}^2(t)$ | $S\phi_{25}^3(t)$ | $S\phi_{25}^4(t)$ |
|-----|-------------------|-------------------|-------------------|-------------------|
| 0   | 0.100000000000    | 0.100000000000    | 0.100000000000    | 0.100000000000    |
| 0.4 | 0.406240542788    | 0.406240542788    | 0.406240542788    | 0.406240542788    |
| 0.8 | 1.414046851898    | 1.414046851898    | 1.414046851898    | 1.414046851898    |
| 1.0 | 2.591594851696    | 2.591594851696    | 2.591594851696    | 2.591594851696    |
| 0   | 0                 | 0                 | 0                 | 0                 |
| 0.4 | 0.1315834093e-4   | 0.1315834093e-4   | 0.1315834093e-4   | 0.1315834093e-4   |
| 0.8 | 0.3017742011e-4   | 0.3017742011e-4   | 0.3017742011e-4   | 0.3017742011e-4   |
| 1.0 | 0.4003781547e-4   | 0.4003781547e-4   | 0.4003781547e-4   | 0.4003781547e-4   |
| 0   | 0.100000000000    | 0.100000000000    | 0.100000000000    | 0.100000000000    |
| 0.4 | 0.038294887773    | 0.038294887773    | 0.038294887773    | 0.038294887773    |
| 0.8 | 0.014680363684    | 0.014680363684    | 0.014680363684    | 0.014680363684    |
| 1.0 | 0.009100844996    | 0.009100844996    | 0.009100844996    | 0.009100844996    |

Table 5. Numerical comparison for  $T(t)$

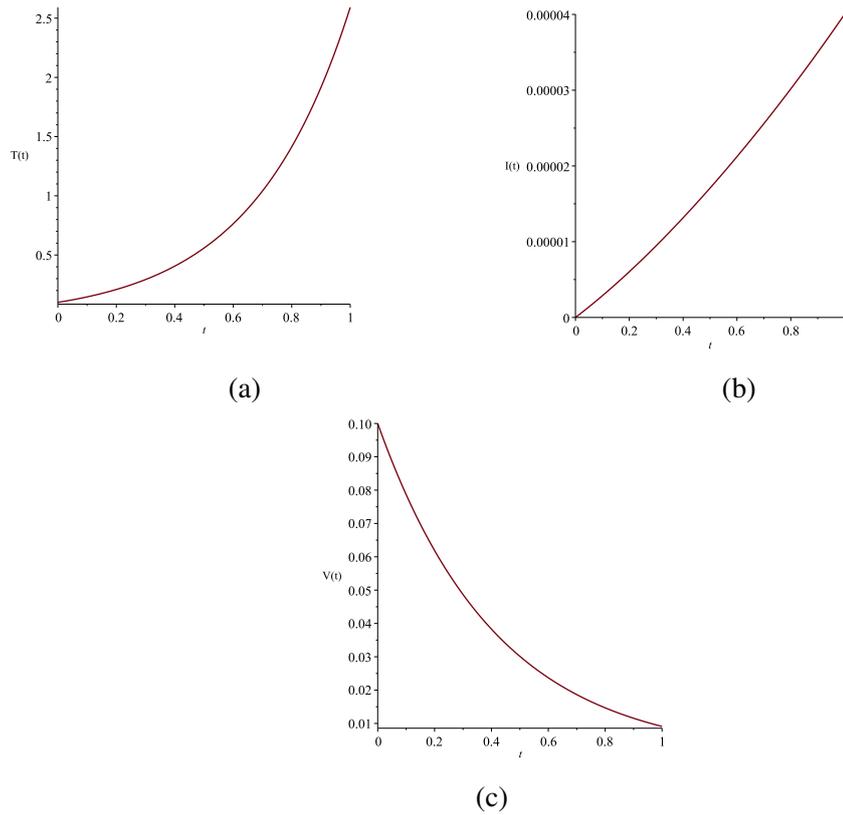
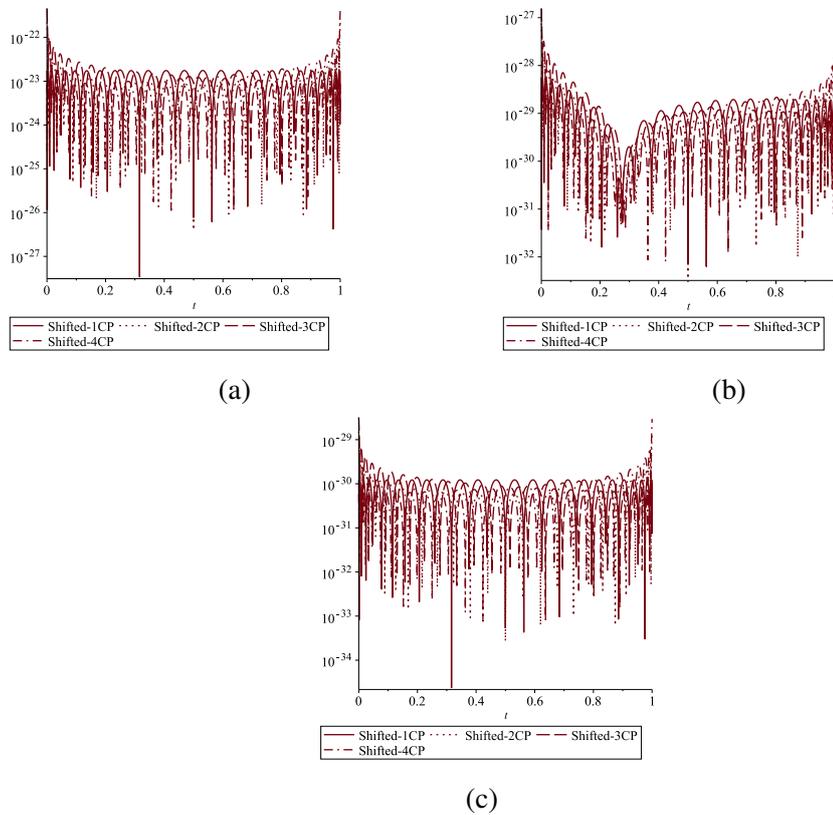
| $t$ | MVIM [15]    | RK           | MLP [11]    | LW [28]      | Present method |
|-----|--------------|--------------|-------------|--------------|----------------|
| 0   | 0.1          | 0.1          | 0.1         | 0.1          | 0.1            |
| 0.2 | 0.2088080868 | 0.2088080833 | 0.208808084 | 0.2088073215 | 0.208808084325 |
| 0.4 | 0.4062407949 | 0.4062405393 | 0.406240543 | 0.4061245634 | 0.406240542788 |
| 0.6 | 0.7644238890 | 0.7644238890 | 0.766442390 | 0.7641476415 | 0.764423898504 |
| 0.8 | 1.4140941730 | 1.4140468310 | 1.414046852 | 1.3977746217 | 1.414046851898 |
| 1.0 | 2.5919210760 | 2.5915948020 | 2.591559480 | 2.5571462314 | 2.591594851696 |

Table 6. Numerical comparison for  $I(t)$

| $t$ | MVIM [15]        | RK              | MLP [11]        | LW [28]          | Present method   |
|-----|------------------|-----------------|-----------------|------------------|------------------|
| 0   | 0.1e-13          | 0               | 0               | 0                | 0                |
| 0.2 | 0.60327016510e-5 | 0.6032702150e-5 | 0.6032702224e-5 | 0.60327046634e-5 | 0.60327022240e-5 |
| 0.4 | 0.13158301670e-4 | 0.1315834073e-4 | 0.131583409e-4  | 0.1316784536e-4  | 0.1315834093e-4  |
| 0.6 | 0.21223310013e-4 | 0.2122378506e-4 | 0.212237854e-4  | 0.2112628765e-4  | 0.2122378543e-4  |
| 0.8 | 0.30174509323e-4 | 0.3017741955e-4 | 0.301774201e-4  | 0.2998139732e-4  | 0.3017742011e-4  |
| 1.0 | 0.40025404050e-4 | 0.4003781468e-4 | 0.400378155e-4  | 0.328765432e-4   | 0.4003781547e-4  |

Table 7. Numerical comparison for  $V(t)$

| $t$ | MVIM [15]      | RK             | MLP [11]     | LW [28]       | Present method |
|-----|----------------|----------------|--------------|---------------|----------------|
| 0   | 0.1            | 0.1            | 0.1          | 0.1           | 0.1            |
| 0.2 | 0.06187990876  | 0.06187984331  | 0.061879843  | 0.06187990765 | 0.061879843223 |
| 0.4 | 0.03829595768  | 0.03829488788  | 0.038294888  | 0.03832341574 | 0.038294887773 |
| 0.6 | 0.02371029480  | 0.02370455014  | 0.023704550  | 0.02381098734 | 0.023704550044 |
| 0.8 | 0.01470041902  | 0.01468036377  | 0.014680364  | 0.01621389765 | 0.014680363684 |
| 1.0 | 0.009157238735 | 0.009100845043 | 0.0091008450 | 0.01605042314 | 0.009100844996 |

Fig. 1 (a)  $T(t)$ , (b)  $I(t)$ , (c)  $V(t)$  functions for  $N = 25$ Fig. 2 Logarithmic absolute residual errors by the various kinds of CPs  
(a)  $Res_1(t)$ , (b)  $Res_2(t)$  and (c)  $Res_3(t)$

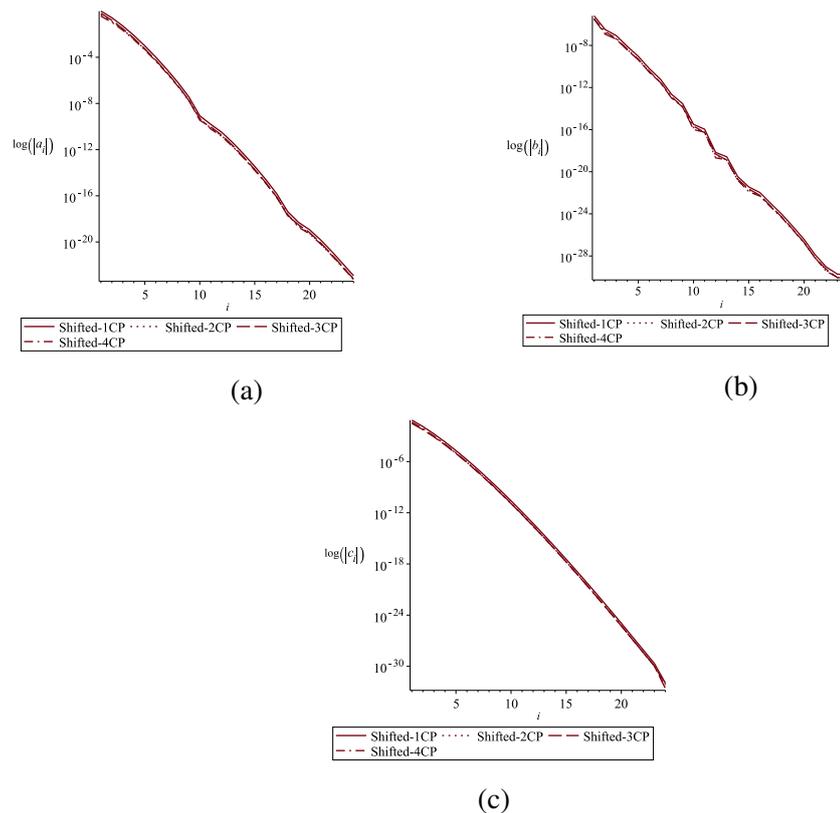


Fig. 3 The logarithmic graph of absolute coefficients (a)  $|a_i|$ , (b)  $|b_i|$ , and (c)  $|c_i|$  for  $N = 25$

## Conclusion

In this study, the collocation method based on the shifted Chebyshev polynomials has been proposed for solving the model of HIV infection of  $CD4^+$ T-cells. Firstly, the different kinds of Chebyshev polynomials and the shifted Chebyshev polynomials have been presented. Then, the model has been approximated using the collocation method. Moreover, the solutions of the proposed method have been compared with the well-known methods previously presented in the literature. The results and comparisons indicate that our method is more acceptable, accurate and efficient as compared to the previous methods. Furthermore, it seems that the proposed method can be used to solve other similar mathematical models.

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