



ANALYTICAL EXPRESSION OF HIV INFECTION MODEL USING TAYLOR SERIES METHOD (TSM)

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Abstract: This paper focuses on the analysis of a first-order non-linear differential equation model for HIV infection in CD4+ T cells. The objective is to solve this model analytically using the Taylor series method (TSM). The TSM offers a straightforward way to determine the components of the series. As the order of approximation increases, the accuracy of the method also improves. By comparing the analytical expression with numerical simulations, we establish the superior accuracy and reliability of the Taylor series method's approximate solution. Additionally, we leverage Python's graphical capabilities to visually represent the HIV infection model.

Keywords: HIV infection of CD4+ T-cells, Taylor series method (TSM), First order non-linear differential equation, Mathematical modelling, Numerical simulation, Python-jupyter.

Introduction:

The primary target of the HIV virus within the human body is healthy T-cells. Upon entering the body, HIV infects a substantial number of these healthy T-cells, leading to a gradual depletion in their count. This progressive reduction in healthy T-cells disrupts the body's immune system, thereby compromising the host's ability to mount effective immune responses against opportunistic infections. Eventually, this cascade of events culminates in the development of acquired immunodeficiency syndrome (AIDS).

The mathematical framework describing the infection of CD4+ T-cells by the HIV virus was initially introduced by [1], and subsequent studies rapidly expanded upon this foundation [2]-[3]. Over time, various analytical and numerical techniques have been employed to address the solution to this HIV infection model. Notable contributions include Mehmet Merdan's utilization of the variational iteration method for obtaining an analytical solution [4], Abdon Atangana's application of the homotopy decomposition method [5], M. Khalid's implementation of the perturbation iterative algorithm [6], R. Senthurai's use of the homotopy perturbation method [7], and Fang Chen's innovative combination of the Adomian decomposition method with Padé Approximation and Laplace Transformation [8].

This current study presents a novel analytical approach to the HIV infection model [10] by employing the Taylor series method (TSM). The resulting analytical outcomes are rigorously compared against numerical simulations to gain comprehensive insights into the system's behavior. Additionally, the investigation extends to employing a Jupyter notebook to implement Python-based graphical representations of the HIV infection model.

Problem Description:

A naturalistic approach to addressing the HIV infection of CD4+ T-cells model was originally introduced by [9]. Subsequently, [10] delved into the realm of numerical simulations for this particular model of HIV infection.

Consider the first order differential equation of the form [10]

$$T'(t) = f_1(T(t), I(t), V(t)) = s_0 - \mu_T T(t) + \alpha T(t) \left(1 - \frac{T(t)+I(t)}{T_{max}}\right) - \beta V(t)T(t) \quad (1)$$

$$I'(t) = f_2(T(t), I(t), V(t)) = \beta V(t)T(t) - \mu_I I(t) \quad (2)$$

$$V'(t) = f_3(T(t), I(t), V(t)) = \gamma \mu_I I(t) - \mu_V V(t) \quad (3)$$

With initial conditions:

$$T(0) = 0.1, I(0) = 0, V(0) = 0.1 \quad (4)$$

Where T, I and V are the dependent variables of this model. Representation and values of the given parameters $s_0, \alpha, \mu_T, \mu_I, \mu_V, \beta, T_{max}, \gamma$ are shown in Table 1.

Table 1: List of parameters used in this model.

| Parameters | Description | Values |
|------------|--|--|
| T | Population of healthy T-cells | 0.1 mm^{-3} |
| I | Population of infected T-cells | 0.0 mm^{-3} |
| V | Free HIV virus particles in the blood of HIV infected individual | $0.1 \text{ day}^{-1} \text{ mm}^{-3}$ |
| s_0 | The new supply rate of healthy T-cells from thymus | $0.1 \text{ day}^{-1} \text{ mm}^{-3}$ |
| α | Growth rate of healthy T-cells population | 3 day^{-1} |
| μ_T | Turnover rate of healthy T-cells | 0.02 day^{-1} |
| μ_I | Turnover rate of infected T-cells | 0.3 day^{-1} |
| μ_V | Turnover rate of free virus | 2.4 day^{-1} |
| β | The infection rate | 0.0027 day^{-1} |
| T_{max} | Maximum population level of healthy T-cells | 1500 mm^{-3} |
| γ | Number of virus produced by infected T-cells | 10 day^{-1} |

Analytical expressing using TSM:

In 1715, Brooke Taylor developed Taylor series method (TSM). Many differential problems have been solved in the past using this technique. Using Taylor series method to solve the Lane-Emden equation [11], For a class of second kind integral equations [12], Fractal Bratu type equations [13]. Many academics have discovered analytical solutions for nonlinear equations using Taylor series method in a variety of fields since it is one of the more accurate methods [14]-[16].

In this paper, The first order differential equation of the HIV model (1-3) is solved using the Taylor series approach with the given initial conditions (4). The detailed expansion of this method for the given model is shown in Appendix 1.

To gain more accuracy we derived 9th order Taylor series as follows:

$$T(t) = \sum_{n=0}^9 \frac{d^n T}{dt^n} \Big|_{t=0} \frac{t^n}{n!} = T(0) + \frac{T'(0)}{1!} t + \frac{T''(0)}{2!} t^2 + \dots + \frac{T^{ix}(0)}{9!} t^9 \quad (5)$$

$$I(t) = \sum_{n=0}^9 \frac{d^n I}{dt^n} \Big|_{t=0} \frac{t^n}{n!} = I(0) + \frac{I'(0)}{1!} t + \frac{I''(0)}{2!} t^2 + \dots + \frac{I^{ix}(0)}{9!} t^9 \quad (6)$$

$$V(t) = \sum_{n=0}^9 \frac{d^n V}{dt^n} \Big|_{t=0} \frac{t^n}{n!} = V(0) + \frac{V'(0)}{1!} t + \frac{V''(0)}{2!} t^2 + \dots + \frac{V^{ix}(0)}{9!} t^9 \quad (7)$$

Upon substituting the derivative values of each order (11, 15, 16-22) and the initial conditions (4) from Appendix 1 into the equation above, we derive the analytical expression for the HIV infection model.

$$T(t) = 0.1 + 0.397953t + 0.5928490530t^2 + 0.5887187713t^3 + 0.4382951580t^4 \\ + 0.2608632930t^5 + 0.1291947319t^6 + 0.05468617024t^7 + 0.02013540082t^8 \\ + 0.006511629543t^9 \quad (8)$$

$$I(t) = 0.000027t + 0.000017273655t^2 - 8.405153733 \cdot 10^{-6}t^3 + 6.147278220 \cdot 10^{-6}t^4 \\ - 2.835861908 \cdot 10^{-6}t^5 + 1.153299823 \cdot 10^{-6}t^6 + 3.907515083 \cdot 10^{-7}t^7 + 4.269757468 \cdot 10^{-7}t^8 \\ + 4.140705624 \cdot 10^{-6}t^9 \quad (9)$$

$$V(t) = 0.1 - 0.24t + 0.2880405000t^2 - 0.2304151263t^3 + 0.1382427719t^4 \\ - 0.06635284216t^5 + 0.02653971893t^6 - 0.009098837933t^7 + 0.002729504846t^8 \\ - 0.0007277256334t^9 \quad (10)$$

Numerical Simulation:

In this paper, the first order nonlinear differential equations of the HIV infection model [9] were solved using the Taylor series method (TSM). With the given parameter values, TSM and numerical simulation (Runge Kutta 4th order method-Appendix 2) have been compared. The maximum average error between TSM and numerical simulation for T(t), I(t) and V(t) are 0.0999, 0.1426 and 0.1384 respectively. Using pertinent figures 1-4 and table 2, we demonstrated TSM effectiveness and accuracy for non-linear equations.

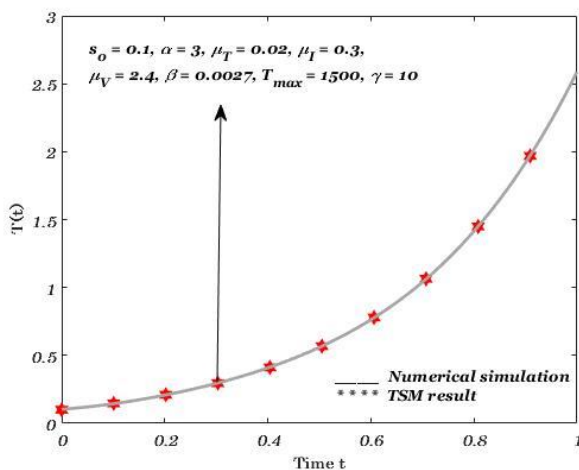


Figure 1: Comparison of analytical expression obtained by TSM eqn.(8) and numerical simulation for the concentration T(t). Solid line represents numerical simulation and *** represents eqn.(8).

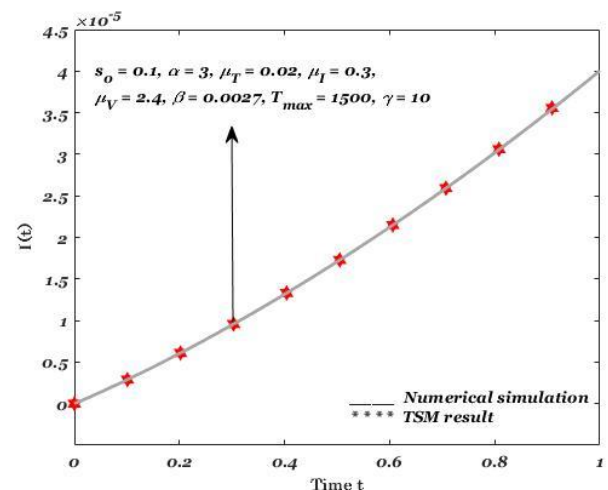


Figure 2: Comparison of analytical expression obtained by TSM eqn.(9) and numerical simulation for the concentration I(t). Solid line represents numerical simulation and *** represents eqn.(9).

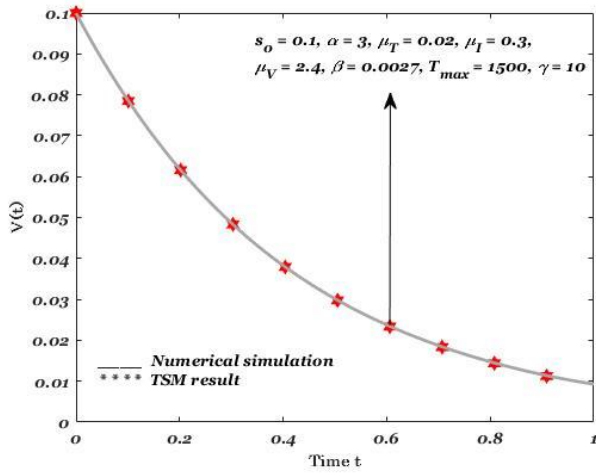


Figure 3: Comparison of analytical expression obtained by TSM eqn.(10) and numerical simulation for the concentration $V(t)$. Solid line represents numerical simulation and *** represents eqn.(10).

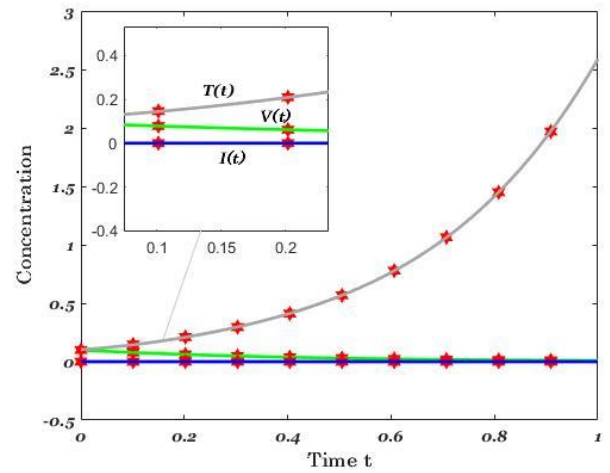


Figure 4: Comparison of analytical expression obtained by TSM eqn.(8-10) and numerical simulation for the concentration $T(t)$, $I(t)$ and $V(t)$. Solid line represents numerical simulation and *** represents eqn.(8-10).

Python based Graphical approach:

Algebraic problems are solved in Python using the Scipy module and the function odeint, we plot HIV infection model with python simulations using jupyter notebook. Fitting the given parameters ref (Table 1). We implemented the HIV infection model for various time ranges given in figures 5-7 using the Python-jupyter code. The python coding to obtain graphical representation for the HIV infection model is shown in Appendix 3.

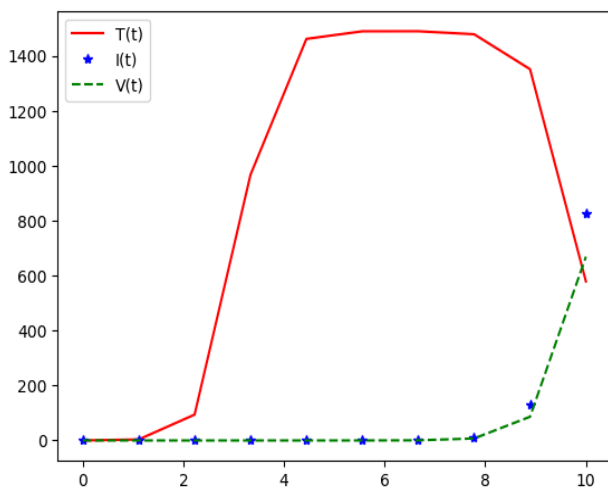


Figure 5: Using python-jupyter notebook, the HIV infection model eqn. (1-3) with initial conditions (4) has been analysed for the time range (Setting up the time range start = 0, stop = 10)

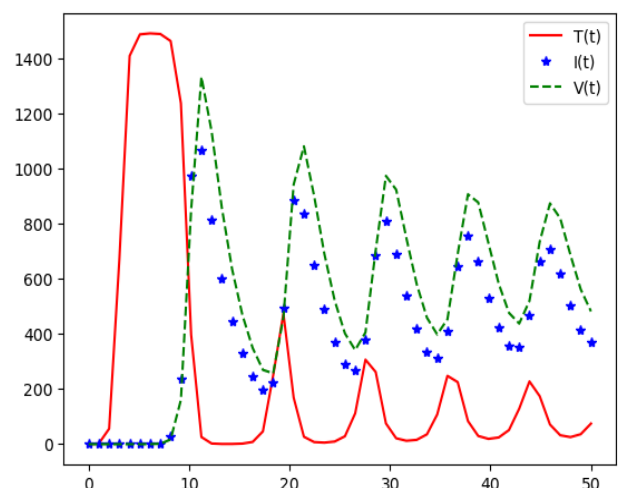


Figure 6: Using python-jupyter notebook, the HIV infection model eqn. (1-3) with initial conditions (4) has been analysed for the time range (Setting up the time range start = 0, stop = 50)

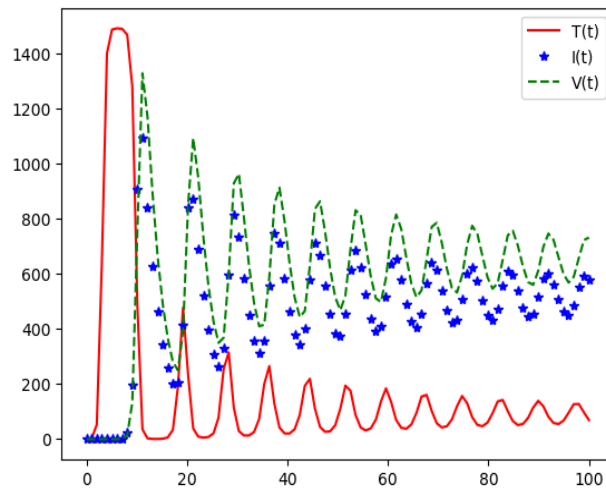


Figure 7: Using python-jupyter notebook, the HIV infection model eqn. (1-3) with initial conditions (4) has been analysed for the time range (Setting up the time range start = 0, stop = 100)

Table 2: Comparison of analytical and numerical simulation for the HIV infection model. $s_0 = 0.1, \alpha = 3, \mu_T = 0.02, \mu_I = 0.3, \mu_V = 2.4, \beta = 0.0027, T_{max} = 1500, \gamma = 10, T(0) = 0.1, I(0) = 0, V(0) = 0.1$.

| t | T(t) | | | I(t) | | | V(t) | | | | |
|-----------------|--------|--------|---------|-----------------|-----------|---------|--------|-----------------|---------|--|--------|
| | Num. | TSM | Error % | Num. | TSM | Error % | Num. | TSM | Error % | | |
| 0 | 0.1000 | 0.1000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.1000 | 0.1000 | 0.0000 | | |
| 0.1 | 0.1467 | 0.1464 | 0.2044 | 2.8649 e-6 | 2.8649e-6 | 0.0000 | 0.0786 | 0.0786 | 0.0000 | | |
| 0.2 | 0.2088 | 0.2088 | 0.0000 | 6.0327e-6 | 6.0327e-6 | 0.0000 | 0.0618 | 0.0618 | 0.0000 | | |
| 0.3 | 0.2937 | 0.2929 | 0.2723 | 9.4713e-6 | 9.4713e-6 | 0.0000 | 0.0486 | 0.0486 | 0.0000 | | |
| 0.4 | 0.4068 | 0.4064 | 0.0983 | 1.3166e-5 | 1.3158e-5 | 0.0607 | 0.0382 | 0.0382 | 0.0000 | | |
| 0.5 | 0.5591 | 0.5589 | 0.0357 | 1.1743e-5 | 1.1707e-5 | 0.3065 | 0.0301 | 0.0301 | 0.0000 | | |
| 0.6 | 0.7648 | 0.7644 | 0.0523 | 2.1240e-5 | 2.1228e-5 | 0.0564 | 0.0236 | 0.0237 | 0.4237 | | |
| 0.7 | 1.0417 | 1.0411 | 0.0575 | 2.5622e-5 | 2.5606e-5 | 0.0624 | 0.0186 | 0.0186 | 0.0000 | | |
| 0.8 | 1.4143 | 1.4138 | 0.2190 | 3.0199e-5 | 3.0226e-5 | 0.0894 | 0.0146 | 0.0146 | 0.0000 | | |
| 0.9 | 1.9164 | 1.9151 | 0.0678 | 3.5026e-5 | 3.5116e-5 | 0.2569 | 0.0115 | 0.0115 | 0.0000 | | |
| 1 | 2.5916 | 2.5892 | 0.0926 | 4.0033e-5 | 4.0328e-5 | 0.7368 | 0.0091 | 0.0090 | 1.0989 | | |
| Average error % | | | 0.0999 | Average error % | | | 0.1426 | Average error % | | | 0.1384 |

Discussion:

The numerical simulation was utilised to compare with the analytical solution obtained by Taylor series method. For the given parameters $s_0 = 0.1, \alpha = 3, \mu_T = 0.02, \mu_I = 0.3, \mu_V = 2.4, \beta = 0.0027, T_{max} = 1500, \gamma = 10$ the comparison of these two results shown in figures 1-4. Figure 1 represents numerical and analytical results of the population of healthy T-cells $T(t)$ and there is no deviation between these two results. Similarly, Figures 2-3 shows numerical and analytical findings for the dynamics of the free virus $V(t)$ and the population of infected T-cells $I(t)$, respectively. The resulting plotted data is combined in figure 4. Table 2 shows the error estimation between the Taylor series approach and the numerical simulation. We achieve good agreements between Taylor series method and numerical simulation.

In figures 5-7, Using Python-Jupyter, we illustrate the HIV infection model over several time scales. These graphs show the system's behaviour for the populations of healthy T-cells $T(t)$, infected T-cells $I(t)$, and free HIV virus particles in the blood of an HIV-infected individual $V(t)$. According to these graphs, $T(t)$ has a wider range than $I(t)$ and $V(t)$.

Conclusion:

This paper focuses on obtaining the analytical solution of the HIV infection model through the application of the Taylor series method. A comparison between the obtained analytical solution and a numerical simulation is performed. The results indicate a favorable level of agreement for the provided parameter values. The efficacy of the Taylor series method in handling nonlinear equations is highlighted through tables and graphs. Furthermore, a Python-based graphical approach using Jupyter notebooks is explored to visualize the model's behavior across different time intervals.

Appendix 1: Taylor series method is used for solving eqn.(1-3). We assume that $t = 0$ in eqn.(1-3) and using initial conditions (4) we get,

$$T'(0) = 0.397953, I'(0) = 0.000027, V'(0) = -0.24 \quad (11)$$

Now differentiate eqn.(1-3) with respect to t we get,

$$T'' = (\alpha - \mu_T)T' - \frac{\alpha(2TT' + T'I' + T'I)}{T_{max}} - \beta(VT' + V'T) \quad (12)$$

$$I'' = \beta(VT' + V'T - \mu_I I') \quad (13)$$

$$V'' = \gamma\mu_I I' - \mu_V V' \quad (14)$$

Setting up $t = 0$ in eqn.(12-14) and substituting necessary values we get,

$$T''(0) = 1.185698106, I''(0) = 0.00003454731, V''(0) = 0.5760810 \quad (15)$$

Proceeding like this, one can obtain the 9th order Taylor series derivatives as follows:

$$T'''(0) = 3.0532312627, I'''(0) = -0.0000504309224, V'''(0) = -1.382490758 \quad (16)$$

$$T^{iv}(0) = 10.51908379, I^{iv}(0) = 0.0001475346773, V^{iv}(0) = 30317826526 \quad (17)$$

$$T^v(0) = 31.30359531, I^v(0) = -0.0003403034290, V^v(0) = -7.962341058 \quad (18)$$

$$T^{vi}(0) = 93.02020695, I^{vi}(0) = 0.000830375873, V^{vi}(0) = 19.10859763 \quad (19)$$

$$T^{vii}(0) = 275.6182979, I^{vii}(0) = -0.001969387602, V^{vii}(0) = -45.85814318 \quad (20)$$

$$T^{viii}(0) = 3811.8717428, I^{viii}(0) = 0.017215662110, V^{viii}(0) = 110.0536354 \quad (21)$$

$$T^{xi}(0) = 2362.940128, I^{xi}(0) = -0.0150259257, V^{xi}(0) = -264.0770780 \quad (22)$$

Appendix 2: MATLAB program for Numerical simulation eqn.(1-3) with initial condition (4)

```

function HIV
options= odeset ('RelTol',1e-6,'Stats','on');
%initial conditions
Xo= [0.1; 0; 0.1];
tspan = [0,1];
tic
[t,X] = ode45(@TestFunction,tspan,Xo,options);
%-----
figure
hold on
%plot(t, X(:,1),'-')
plot(t, X(:,2),'-')
%plot(t, X(:,3),'-')
legend('x1','x2','x3')
ylabel('x')
xlabel('t')
return
%-----
function [dx_dt]= TestFunction(t,x)
s=0.1; a=3; r=10; b=0.0027; u1 = 0.3; mu=0.02; Tmax=1500; uv=2.4;
dx_dt(1)=s-mu*x(1)+a*x(1)*(1-((x(1)+x(2))/Tmax))-b*x(3)*x(1);
dx_dt(2)=b*x(3)*x(1)-u1*x(2);
dx_dt(3)=r*u1*x(2)-uv*x(3);
dx_dt = dx_dt';
return

```

Appendix 3: Python coding for eqn.(1-3) with initial conditions (4)

```

# FROM SCIPY INTEGRATE IMPORT ODEINT
import numpy as np
import matplotlib.pyplot as plt
from scipy.integrate import odeint
# DEFINE CONSTANTS
a = 3
b = 0.0027
r = 10
m = 0.3
p = 1500
n = 2.4
s = 0.1
d = 0.02
# FUNCTION TO RETURN DERIVATIVES AT “t”
def f(y,t):
    T, I, V = y
    d0 = s - d*T + a*T*(1-(T+I)/p) - b*V*T
    d1 = b*V*T - m*I
    d2 = r*m*I - n*V
    return [d0, d1, d2]
# INITIAL VALUES OF EACH FUNCTION
T_0 = 0.1
I_0 = 0
V_0 = 0.1
y_0 = [T_0,I_0,V_0]
t = np.linspace(start=0,stop=100,num=100)
y = odeint(f,y_0,t)

```

```

T = y[:,0]
I = y[:,1]
V = y[:,2]
plt.figure()
plt.plot(t,T,'r',label="T(t)")
plt.plot(t,I,'b',label="I(t)")
plt.plot(t,V,'g',label="V(t)")
plt.legend()
plt.show()

```

References:

- [1] Wang, L., & Li, M. Y: Mathematical analysis of the global dynamics of a model for HIV infection of CD4+ T cells, *Mathematical Biosciences*, (2006, March), 200(1), 44–57. <https://doi.org/10.1016/j.mbs.2005.12.026>
- [2] Sutimin, Sunarsih, & Thahjana, H: Analysis of mathematical model of HIV-1 infection of CD4+ T cells with CTL response and antiretroviral treatment, *Journal of Physics: Conference Series*, (2019, May 1), 1217(1), 012074. <https://doi.org/10.1088/1742-6596/1217/1/012074>
- [3] Mohyud-Din, S. T., Nazir, A., Almohsin, B., Ahmed, N., Khan, U., Waheed, A., & Hussain, T.: On mathematical model of HIV CD4+T-cells, *Alexandria Engineering Journal*, (2021, February), 60(1), 995–1000. <https://doi.org/10.1016/j.aej.2020.10.026>
- [4] Merdan, M., Gokdogan, A. & Yildirim, A: On the numerical solution of the model for HIV infection of CD4+ T cells, *Computers & Mathematics With Applications*, (2011, July), 62(1), 118–123. <https://doi.org/10.1016/j.camwa.2011.04.058>
- [5] Atangana, A., & Dounomo Goufo, E. F: Computational Analysis of the Model Describing HIV Infection of CD4+T Cells, *BioMed Research International*, (2014), 2014, 1–7. <https://doi.org/10.1155/2014/618404>
- [6] M. Khalid, Mariam Sultana, Faheem Zaidi and Fareeha Sami Khan: A numerical solution of a model for HIV infection CD4+ T-Cell, *International Journal of Innovation and Scientific Research* . Vol. 16 No. 1 Jun. 2015, pp. 79-85
- [7] R.Senthamarai , Keshiya Shamen Anthony 2 and V. Ananthaswamy: Approximate analytical solution of a differential equation model in HIV infection of CD4+ T- cells using HPM, *NONLINEAR STUDIES*, Vol. 25, No. 2, pp. 395-402, 2018
- [8] Chen, F., & Liu, Q. Q: Adomian Decomposition Method Combined with Padé Approximation and Laplace Transform for Solving a Model of HIV Infection of CD4+T Cells, *Discrete Dynamics in Nature and Society*, (2015), 2015, 1–7. <https://doi.org/10.1155/2015/584787>
- [9] Malik S.A, Qureshi I.M, Amir M and Malik A.N: Nature Inspired Computational Approach to Solve the Model for HIV Infection of CD4+T Cells, *Research Journal of Recent Sciences* . Vol. 3(6), 67-76, June (2014).
- [10] Attaullah, & Sohaib, M.: Mathematical modeling and numerical simulation of HIV infection model, *Results in Applied Mathematics*. (2020 August), 7, 100118. <https://doi.org/10.1016/j.rinam.2020.100118>
- [11] He, J. H., & Ji, F. Y: Taylor series solution for Lane–Emden equation, *Journal of Mathematical Chemistry*, (2019, July 2), 57(8), 1932–1934. <https://doi.org/10.1007/s10910-019-01048-7>
- [12] Ren, Y., Zhang, B., & Qiao, H: A simple Taylor-series expansion method for a class of second kind integral equations, *Journal of Computational and Applied Mathematics*, (1999, October), 110(1), 15–24. [https://doi.org/10.1016/s0377-0427\(99\)00192-2](https://doi.org/10.1016/s0377-0427(99)00192-2)
- [13] He, C. H., Shen, Y., Ji, F. Y., & He, J. H: Taylor series solution for fractal Bratu-type equation arising in electrospinning process, *fractals*, 28(01), 2050011, (2020, February), 147(1), 290–297. <https://doi.org/10.1142/s0218348x20500115>
- [14] Vinolyn Sylvia, S., Joy Salomi, R., Rajendran, L., & Abukhaled, M: Solving nonlinear reaction–diffusion problem in electrostatic interaction with reaction-generated pH change on the kinetics of immobilized enzyme systems using Taylor series method, *Journal of Mathematical Chemistry*, (2021, March 22), 59(5), 1332–1347. <https://doi.org/10.1007/s10910-021-01241-7>
- [15] Dharmalingam K.M. and Valli K: Solving necrotizing enterocolitis model by the Taylor series method, *Journal of Mathematical and Computational Science*, (2021). <https://doi.org/10.28919/jmcs/6634>

[16] Visuvasam, J., Meena, A., & Rajendran, L: New analytical method for solving nonlinear equation in rotating disk electrodes for second-order ECE reactions, Journal of Electroanalytical Chemistry, (2020, July), 869, 114106. <https://doi.org/10.1007/s10910-021-01241-7>

