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Nature Inspired Computational Approach to Solve the Model for HIV Infection of CD4$^+$T Cells

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Abstract

In this paper, a stochastic heuristic technique is investigated to obtain the approximate solution of the HIV infection model of CD4$^+$T cells. The proposed technique represents the approximate solution as a linear combination of some polynomial basis functions with unknown adaptable coefficients. The trial solution of the problem is formulated using a fitness function, which contains unknown adaptable coefficients. The minimization of the fitness function is performed using the hybrid heuristic computational approach. The stochastic global search technique such as genetic algorithm (GA) is hybridized with two local search optimizers such as interior point algorithm (IPA) and active set algorithm (ASA), for obtaining the unknown coefficients. The effectiveness of the proposed technique is illustrated in contrast with fourth-order Runge Kutta method (RK-4) and some well known deterministic standard methods. The results validate the accuracy and viability of the proposed technique for the approximate solution of the HIV infection model of CD4$^+$ T cells.

Keywords*:* HIV infection model of CD4$^+$T cells, evolutionary computation (EC), genetic algorithm (GA), interior point algorithm (IPA), active set algorithm (ASA)

Introduction

Many scientific phenomena arising in real life problems are mathematically modeled by nonlinear ordinary differential equations (ODEs). In view of the fact that most nonlinear ODEs either do not have the exact solution or attaining the same analytically is intricate, an incredibly huge number of approximate analytical and numerical standard techniques such as adomian decomposition method[1] (ADM), variational iteration method[2] (VIM), homotopy perturbation method[3] (HPM), homotopy analysis method[4] (HAM) etc. have been utilized to tackle these problems.

In this study our main goal is to present a nature inspired computational method to the numerical solution of the HIV infection model of CD4$^+$T cells[5], which is governed by the following system of nonlinear ODEs[6-11].

$$\frac{dT}{dt} = p - \alpha T + rT\left(1 - \frac{T+I}{T_{max}}\right) - kVT$$

$$\frac{dI}{dt} = kvT - \beta I$$

$$\frac{dV}{dt} = N\beta I - \gamma V \qquad (1)$$

Subject to the initial conditions

$$T(0) = T_0, \quad I(0) = I_0, \quad \text{and} \quad V(0) = V_0 \qquad (2)$$

In the model of HIV (1), the dependent variables T(t), I(t), and V(t) denote the concentration of susceptible CD4$^+$T cells, the concentration of CD4$^+$T cells infected by HIV viruses and free HIV virus particles in the blood respectively. The parameters α, β, and γ represent the natural turnover rates of uninfected T cells, infected T cells, and virus particles respectively. The logistic growth of the healthy CD4$^+$T cells is represented by $(1-(T+I)/T_{max})$ and the propagation of the infected CD4$^+$T cells is neglected. The term kVT describes the incidence of HIV infection of healthy CD4$^+$T cells, where $k>0$ is the infection rate. Each infected CD4$^+$T cell is assumed to produce N virus particles during its lifetime, including any of its daughter cells. The body is believed to produce CD4$^+$T cells from precursors in the bone marrow and thymus at a constant rate p. T cells multiply through mitosis with a rate r when they are stimulated by antigen or mitogen. T_{max} denotes the maximum level of CD4$^+$T cell concentration in the body[12-15].

Recently, many standard methods for solving numerically the HIV infection model of CD4$^+$T cells appeared in open literature. Among these methods, Ongun employed the Laplace adomian decomposition method[6] (LADM), for the numerical solution of (1). Merdan et al. applied multi-stage variational iteration method[7] (MSVIM). Yüzbaş proposed Bessel collocation method[8] for the numerical solution of (1). Doğan used multi-step laplace adomian decomposition method[9] (MSLADM) for solving (1). Homotopy perturbation method[10] (HPM) was used by Merdan. Recently Merdan et al. apllied modified variational iteration method[11] (MVIM) to obtain the numerical solution of

(1). Goreishi et al. solved the variant of (1) using homotopy analysis method[16] (HAM).

Although a number of powerful standard deterministic methods have been utilized for solving HIV model (1) in particular and other various different nonlinear ordinary differential equations (ODE's) in general, an incredibly great attention is still directed to seek for some new and alternate methods. In recent years many authors have used nature and biologically inspired based stochastic computation techniques, such as genetic algorithm (GA), particle swarm optimization (PSO), ant colony etc. for solving nonlinear ODEs arising in diverse fields of engineering and science. A large number of nonlinear ODEs have been solved numerically using these evolutionary computation based techniques but only a few are narrated here. Caetano et al.[17] used genetic algorithm (GA) based neural network (NN) for the solution of nonlinear ODEs arising in atomic and molecular physics. Arqub et al.[18] employed continuous genetic algorithm (CGA) based technique to solve the numerically linear and nonlinear singular two-point boundary value problems (BVPs). Khan et al.[19] used hybrid genetic algorithm (GA) based NN approach for the numerical treatment of van der pol oscillator equation. Malik et al.[20,21] used a GA based hybrid heuristic computing technique for numerically solving the Bratu problem and the Troesch's problem. Behrang et al.[22] employed particle swarm optimization (PSO) based neural network for solving the nonlinear ODE of Darcian fluid of vertical cone implanted in porous media. Recently Malik et al.[23] employed hybrid genetic algorithm (HGA) based approach for the numerical solution of nonlinear singular boundary value problems arising in physiology.

The key objective of this work is to investigate the numerical solution of HIV infection model of $CD4^+T$ cells given by (1) using a novel technique based on nature inspired computation. The proposed technique employs the hybridization approach of genetic algorithm (GA) with interior point algorithm (IPA) and active set algorithm (ASA). The two hybrid schemes used in this study are called as GA-IPA (GA hybridized with IPA) and GA-ASA (GA hybridized with ASA) in the rest of the paper. The main scientific contribution of this work is that a novel stochastic technique based on the hybrid polynomial basis heuristic computing is introduced for solving nonlinear coupled ODE system of HIV model (1). To the best of our knowledge no body yet has solved the HIV infection model (1) using the approach presented in this study. To prove the efficiency and the viability of the presented technique comparisons of our numerical results are made with fourth-order Runge Kutta method (RK-4) and some well known deterministic standard techniques including LADM[6], LADM-Padé[6], Bessel collocation method[8], HPM[10], VIM[11] and MVIM[11].

Material and Methods

A brief description of the proposed methodology and an introduction of heuristic search algorithms such as Genetic algorithm (GA), Pattern Search (PS), and Interior Point algorithm (IPA) are presented.

Proposed Methodology for HIV Model: To obtain the numerical solution of HIV infection model of $CD4^+T$ cells (1), we may assume the approximate solution of T(t), I(t), and V(t), and their first derivates dT/dt, dI/dt, and dV/dt are a linear combinations of some polynomial basis functions t^i, t^j, and t^k which can be expressed as follows (3) – (8).

$$T(t)=\sum_{i=0}^{m} a_i t^i \tag{3}$$

$$I(t)=\sum_{j=0}^{m} b_j t^j \tag{4}$$

$$V(t)=\sum_{k=0}^{m} c_k t^k \tag{5}$$

$$\frac{dT}{dt}=\sum_{i=0}^{m} a_i\, i.t^{i-1} \tag{6}$$

$$\frac{dI}{dt}=\sum_{j=0}^{m} b_j\, j.t^{j-1} \tag{7}$$

$$\frac{dV}{dt}=\sum_{k=0}^{m} c_k\, k.t^{k-1} \tag{8}$$

where a_i, b_j, and c_k are real valued unknown adaptable coefficients, m is the number of basis functions.

The approximate numerical solutions T(t), I(t), and V(t) of the HIV model (1) are obtained from (3) – (5) once the optimal values of the unknown adaptable coefficients are acquired. The optimal values of these unknown adaptable coefficients are determined by developing a fitness function ε_j of the HIV model (1). The fitness function ε_j consists of the sum of three parts as follows.

$$\varepsilon_j=\varepsilon_1+\varepsilon_2+\varepsilon_3 \tag{9}$$

where ε_1 , ε_2 , and ε_3 are given by (10) – (12), which represent the mean square errors associated with the HIV model for T(t), I(t), and V(t) respectively, while j is the cycle index.

$$\varepsilon_1=\frac{1}{m+1}\sum_{i=0}^{m}\left(\frac{dT(t_i)}{dt}-p+\alpha T(t_i)-rT(t_i)\left(1-\frac{T(t_i)+I(t_i)}{T_{max}}\right)+kV(t_i)T(t_i)\right)^2 \tag{10}$$

$$\varepsilon_2=\frac{1}{m+1}\sum_{i=0}^{m}\left(\frac{dI(t_i)}{dt}-kV(t_i)T(t_i)+\beta I(t_i)\right)^2 \tag{11}$$

$$\varepsilon_3=\frac{1}{m+1}\sum_{i=0}^{m}\left(\frac{dV(t_i)}{dt}-N\beta I(t_i)+\gamma V(t_i)\right)^2 \tag{12}$$

The fitness function given by (9) contains the unknown adaptable coefficients (a_i, b_j, and c_k). The minimization of (9) is carried out by employing the heuristic optimization algorithms for acquiring the unknown parameters. The optimal values of the unknown adaptable coefficients corresponding to the minimum fitness function are achieved. Consequently the approximate numerical solutions T(t), I(t), and V(t) of the HIV infection model of $CD4^+T$ cells are obtained using (3) - (5).

An overview of heuristic search algorithms: Genetic Algorithm (GA) proposed by Holland in 1975 is one of the most renowned stochastic global search methods in evolutionary algorithms. GA finds the optimal solution of a problem based on the evolutionary ideas of natural selection and genetics. GA starts from a randomly generated population of individuals called chromosome. Each individual within a population is regarded as a possible solution to the problem. The individuals within a population are evaluated using an exclusive fitness function of the problem at hand. The algorithm evolves population iteratively by means of three primary operations: selection, crossover, and mutation to reach the optimal solution[24].

Interior point algorithm (IPA) is a popular local search method which is widely used in varied optimization problems including linear and nonlinear, convex and non-convex. The IPA preserves an approximate solution of a sequence of barrier sub problems that lie inside a trust region. The algorithm navigates through the interior feasible region following a central path until it reaches an optimal solution. At each iteration the algorithm applies a direct step also called Newton step or a conjugate gradient step to solve a system of Karush-Kuhn-Tucker (KKT) equations[25-26].

Active set methods are iterative algorithms that solve a sequence of subproblems. The algorithm usually predicts and preserves a set of active and inactive constraints at an optimal solution. Generally these methods work in two separate phases such as feasibility phase and optimality phase. In the feasibility phase the method attempts to find a feasible point for the constraints while the objective function is ignored. In the optimality phase the method preserves the feasibility while it attempts to find an optimal point[27].

The hybridization of GA with local search methods can provide enhanced performance in many optimization problems[28]. In this study we have used the hybridization of GA with two local search methods such as interior point algorithm (IPA) and active set algorithm (ASA). The GA has been used as global optimizer which provides the global optimal solution which is subsequently fed into IPA and ASA for local search refinement to achieve the results.

The procedural steps of the hybridization of GA with IPA and ASA are given in Pseudocode 1 while the values and settings of different parameters for the implementation of these algorithms are given in table-1 for GA and table-2 for IPA and ASA respectively.

Pseudocode 1: Hybridization of GA with IPA and ASA: Step 1: (Population Initialization): A population of N individuals or chromosomes is generated using random number generator. The length of the chromosome represents the number of unknown adaptable coefficients to be optimized.

Step 2: (Fitness Evaluation): The fitness of each individual in the current population is computed.

Step 3: (Stoppage Criteria): The algorithm terminates if a certain level of fitness has reached or the maximum number of cycles (generations) has exceeded. If the stopping criterion is satisfied then go to step 6 for local search refinement, else continue and repeat steps 2 to 5.

Step 4: (Selection and Reproduction): The chromosomes from the current population are chosen on the basis of their fitness which acts as parents for new generation. These parents produce children (offsprings) with a probability to their fitness through crossover operation.

Step 5: Mutation: Mutation operation introduces random alterations in the genes to maintain the genetic diversity to find a good solution.

Step 6: (Local Search Refinement): The optimal chromosome achieved by the GA is subsequently provided to IPA and ASA for fine tuning.

Table-1
Parameter values and settings of GA

Parameter	Value/Setting
Population size	[240 240]
Chromosome size	15
Fitness scaling function	Proportional
Selection function	Stochastic uniform
Crossover function	Heuristic
Mutation function	Adaptive feasible
Reproduction crossover fraction	0.8
Generations	2000
Function tolerance	1E-18
Nonlinear constraint tolerance	1E-18

Results and Discussion

In this section we apply the proposed methodology to the HIV infection model of $CD4^+$ T cells (1) and obtain its numerical solution in the interval $0 \leq t \leq 1$with the initial conditions, $T(0) = a_0 = 0.1$, $I(0) = b_0 = 0.0$, $V(0) = c_0 = 0.1$, and $p = 0.1$, $\alpha = 0.02$, $\beta = 0.3$, $r = 3$, $\gamma = 2.4$, $k = 0.0027$, $T_{max} = 1500$, and $N = 10$.

Table-2
Parameter values and settings of IPA and ASA

Parameter	Value/Setting	
	IPA	**ASA**
Start point	Random/optimal chromosome from GA	Random/optimal chromosome from GA
Maximum iterations	200	200
Maximum function evaluations	60000	60000
Maximum perturbation	0.1	0.1
Function tolerance	1E-18	1E-18
Nonlinear constraint tolerance	1E-18	1E-18
Derivative type	Central differences	-
Hessian	BFGS	-
Subproblem algorithm	Ldl factorization	-

The approximate numerical solution of (1) using the proposed method is obtained by formulating its fitness function ε_j as follows.

$$\varepsilon_1 = \frac{1}{6}\sum_{i=1}^{6}\left(\frac{dT(t_i)}{dt} - 0.1 + 0.02T(t_i) - 3T(t_i)\left(1 - \frac{T(t_i)+I(t_i)}{1500}\right) + 0.0027V(t_i)T(t_i)\right)^2 \quad (13)$$

$$\varepsilon_2 = \frac{1}{6}\sum_{i=1}^{6}\left(\frac{dI(t_i)}{dt} - 0.0027V(t_i)T(t_i) + 0.3I(t_i)\right)^2 \quad (14)$$

$$\varepsilon_3 = \frac{1}{6}\sum_{i=1}^{6}\left(\frac{dV(t_i)}{dt} - 10*0.3I(t_i) + 2.4V(t_i)\right)^2 \quad (15)$$

$$\varepsilon_j = \varepsilon_1 + \varepsilon_2 + \varepsilon_3 \quad (16)$$

Where T(t), I(t), and V(t), and their first derivates dT/dt, dI/dt, and dV/dt are given by (3) – (8), and the number of basis functions m = 5. Therefore the length of chromosome which determines the number of unknown adaptable coefficients is chosen equal to 15 (a_1,…., a_5; b_1,....,b_5; c_1,….,c_5).

The fitness function given by (16) is subject to minimization by using heuristic optimization algorithms (GA, PS, IPA, GA-IPA, and GA-ASA) for acquiring the unknown adaptable coefficients (a_i, b_j, c_k). For simulations Matlab has been utilized.

The algorithms are executed according to the prescribed settings and values given in table-1 and table-2, to achieve the optimal values of the unknown adaptable coefficients. The optimal values of the unknown adaptable coefficients achieved by GA and two hybrid heuristic schemes GA-IPA, and GA-ASA are provided in table -3.

The approximate numerical solutions T(t), I(t), and V(t) of the HIV infection model (1) are obtained by substituting the optimal values of unknown adaptable coefficients in (3) - (5). The approximate numerical results obtained by the proposed method are presented in table- 4, table-5, and table- 6, for T(t), I(t), and V(t) respectively.

Table-3
Optimal values of unknown adaptable coefficients achieved by GA and hybrid schemes GA-IPA and GA-ASA

index	**GA**			**GA-IPA**			**GA-ASA**		
(i)	a_i	b_i	c_i	a_i	b_i	c_i	a_i	b_i	c_i
1	0.4014	0.0001	-0.2399	0.4016	0.0000	-0.2399	0.4016	0.0000	-0.2399
2	0.4355	-0.0008	0.2846	0.4353	0.0003	0.2853	0.4354	0.0003	0.2851
3	1.3520	0.0020	-0.2123	1.3571	-0.0008	-0.2143	1.3569	-0.0009	-0.2133
4	-0.9844	-0.0020	0.0977	-0.9905	0.0009	0.0995	-0.9902	0.0010	0.0984
5	1.2734	0.0007	-0.0209	1.2791	-0.0004	-0.0216	1.2790	-0.0004	-0.0211

Table-4
Numerical Results of T(t) by the proposed method

t	**GA**	**IPA**	**ASA**	**GA-IPA**	**GA-ASA**
0	0.1000000000	0.1000000000	0.1000000000	0.1000000000	0.1000000000
0.1	0.1457584044	0.1457825030	0.1457826361	0.1457825001	0.1457825798
0.2	0.2073422431	0.2074105042	0.2074114374	0.2074104817	0.2074111526
0.3	0.2912300144	0.2913795726	0.2913811695	0.2913795335	0.2913807032
0.4	0.4045938486	0.4048778868	0.4048797626	0.4048778405	0.4048792244
0.5	0.5568276069	0.5573211603	0.5573230637	0.5573211129	0.5573225192
0.6	0.7610749817	0.7618875655	0.7618895893	0.7618875149	0.7618890022
0.7	1.0357575959	1.0370526587	1.0370552779	1.0370525933	1.0370545028
0.8	1.4061031024	1.4081243044	1.4081282422	1.4081242065	1.4081270663
0.9	1.9056732838	1.9087776003	1.9087835217	1.9087774533	1.9087817565
1.0	2.5778921524	2.5825898013	2.5825978353	2.5825896014	2.5825954577

The comparison of our results is made with the fourth-order Runge Kutta (RK-4) method and some classical methods including Laplace adomian decomposition method[6] (LADM), LADM-padé[6], Bessel collocation method[8], homotopy perturbation method[10] (HPM), variational iteration method[11] (VIM) and modified variational method[11] (MVIM). In tables 7-9 we provide the comparison of numerical results between the proposed method, classical methods and also RK-4, and in figures 1-3 comparison of the results achieved by proposed scheme GA-IPA are made with the fourth-order Runge Kutta (RK-4) method graphically. It is evident from the comparison that the proposed method provides the results in a fairly good agreement with the fourth-order Runge Kutta (RK-4) method and some classical methods including LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], and MVIM[11].

Table-5
Numerical Results of I(t) by the proposed method

t	GA	IPA	ASA	GA-IPA	GA-ASA
0	0.0000000000E+00	0.0000000000E+00	0.0000000000E+00	0.0000000000E+00	0.0000000000E+00
0.1	4.2247217149E-06	3.0007580133E-06	2.6081890316E-06	2.9975707438E-06	2.8253143433E-06
0.2	2.8356194192E-06	7.6675275916E-06	7.2513797715E-06	7.6939016021E-06	7.7601392715E-06
0.3	1.7185289594E-06	1.2065044075E-05	1.1876592886E-05	1.2114148223E-05	1.2455531353E-05
0.4	3.5927679934E-06	1.5563886348E-05	1.5702938634E-05	1.5614544346E-05	1.6089543830E-05
0.5	8.8488408808E-06	1.8423288863E-05	1.8837490321E-05	1.8457437555E-05	1.8891177538E-05
0.6	1.6386143572E-05	2.1373953650E-05	2.1891157760E-05	2.1386325039E-05	2.1664331818E-05
0.7	2.4450668501E-05	2.5200862343E-05	2.5594560722E-05	2.5200889347E-05	2.5311755433E-05
0.8	3.1472709469E-05	3.0326088194E-05	3.0413902398E-05	3.0332034144E-05	3.0358997482E-05
0.9	3.6904566542E-05	3.6391608094E-05	3.6166842852E-05	3.6416919969E-05	3.6478358321E-05
1.0	4.2058250935E-05	4.1842114586E-05	4.1638372479E-05	4.1873999991E-05	4.2012840471E-05

Table-6
Numerical Results of V(t) by the proposed method

t	GA	IPA	ASA	GA-IPA	GA-ASA
0	0.1000000000	0.1000000000	0.1000000000	0.1000000000	0.1000000000
0.1	0.0786569813	0.0786562683	0.0786564093	0.0786562715	0.0786563685
0.2	0.0618619447	0.0618666712	0.0618649088	0.0618666565	0.0618652111
0.3	0.0486610371	0.0486715372	0.0486685740	0.0486715153	0.0486691647
0.4	0.0382845550	0.0382983109	0.0382957364	0.0382983011	0.0382963843
0.5	0.0301218290	0.0301356597	0.0301346870	0.0301356746	0.0301351714
0.6	0.0236961083	0.0237075809	0.0237083794	0.0237076190	0.0237086009
0.7	0.0186394449	0.0186475083	0.0186491339	0.0186475542	0.0186491494
0.8	0.0146675785	0.0146724192	0.0146733410	0.0146724517	0.0146733229
0.9	0.0115548203	0.0115569415	0.0115561643	0.0115569492	0.0115562839
1.0	0.0091089381	0.0091074600	0.0091062452	0.0091074649	0.0091064801

Table -7
Comparison of numerical results for T(t) between the proposed method, classical methods LADM[26] LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], MVIM[11], and RK-4

		t					
		0	**0.2**	**0.4**	**0.6**	**0.8**	**1.0**
Proposed Method	GA	0.1	0.2073422431	0.4045938486	0.7610749817	1.4061031024	2.5778921524
	IPA	0.1	0.2074105042	0.4048778868	0.7618875655	1.4081243044	2.5825898013
	ASA	0.1	0.2074114374	0.4048797626	0.7618895893	1.4081282422	2.5825978353
	GA-IPA	0.1	0.2074104817	0.2074104817	0.2074104817	0.2074104817	0.2074104817
	GA-ASA	0.1	0.2074111526	0.4048792244	0.7618890022	1.4081270663	2.5825954577
Classical Methods	LADM[6]	0.1	0.2088073298	0.4061358315	0.762476222	1.398082863	2.507874151
	LADM-Padé[6]	0.1	0.2088072731	0.4061052625	0.7611467713	1.377319859	2.329169761
	VIM[11]	0.1	0.2088073214	0.4061346587	0.762453035	1.397880588	2.506746669
	MVIM[11]	0.1	0.2088080868	0.4062407949	0.7644287245	1.414094173	2.591921076
	HPM[10]	0.1	0.2088073294	0.4061358277	0.7624762056	1.39808281	2.50787401
	Bessel[8]	0.1	0.2038616561	0.3803309335	0.6954623767	1.2759624442	2.3832277428
	RK-4	0.1	0.2087295621	0.2087295621	0.2087295621	0.2087295621	0.2087295621

Table-8
Comparison of numerical results for T(t) between the proposed method, classical methods LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], MVIM[11], and RK-4

		t					
		0	**0.2**	**0.4**	**0.6**	**0.8**	**1.0**
Proposed Method	GA	0.0	2.835619E-06	3.592768E-06	1.638614E-05	3.147271E-05	4.205825E-05
	IPA	0.0	7.667528E-06	1.556389E-05	2.137395E-05	3.032609E-05	4.184211E-05
	ASA	0.0	7.251380E-06	1.570294E-05	2.189116E-05	3.041390E-05	4.163837E-05
	GA-IPA	0.0	7.693902E-06	1.561454E-05	2.138633E-05	3.033203E-05	4.187400E-05
	GA-ASA	0.0	7.760139E-06	1.608954E-05	2.166433E-05	3.035900E-05	4.201284E-05
Classical Methods	LADM[6]	0.0	6.032706E-06	1.315891E-05	2.123298E-05	3.024270E-05	4.033321E-05
	LADM-Padé[6]	0.0	6.032707E-06	1.315916E-05	2.126836E-05	3.006918E-05	3.987365E-05
	VIM[11]	0.0	6.032634E-06	1.314878E-05	2.101417E-05	2.795130E-05	2.431562E-05
	MVIM[11]	1E-13	6.032701E-06	1.315830E-05	2.122331E-05	3.017450E-05	4.002540E-05
	HPM[10]	0.0	6.032706E-06	1.315890E-05	2.123298E-05	3.024270E-05	4.033321E-05
	Bessel[8]	0.0	6.247872E-06	1.293552E-05	2.035267E-05	2.837302E-05	3.690842E-05
	RK-4	0.0	6.031510E-06	1.315302E-05	2.121060E-05	3.015178E-05	3.999421E-05

Table-9
Comparison of numerical results for T(t) between the proposed method, classical methods LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], MVIM[11], and RK-4.

		t					
		0	**0.2**	**0.4**	**0.6**	**0.8**	**1.0**
Proposed Method	GA	0.1	0.0618619447	0.0382845550	0.0236961083	0.0146675785	0.0091089381
	IPA	0.1	0.0618666712	0.0382983109	0.0237075809	0.0146724192	0.0091074600
	ASA	0.1	0.0618649088	0.0382957364	0.0237083794	0.0146733410	0.0091062452
	GA-IPA	0.1	0.0618666565	0.0382983011	0.0237076190	0.0146724517	0.0091074649
	GA-ASA	0.1	0.0618652111	0.0382963843	0.0237086009	0.0146733229	0.0091064801
Classical Methods	LADM[6]	0.1	0.0618799531	0.0383081805	0.0239198161	0.0162123434	0.0160550224
	LADM-Padé[6]	0.1	0.0618799603	0.0383132488	0.0243917435	0.0099672189	0.0033050764
	VIM[11]	0.1	0.0618799531	0.0383082013	0.0239202926	0.0162170455	0.0160841871
	MVIM[11]	0.1	0.0618799088	0.0382959577	0.0237102948	0.0147004190	0.0091572387
	HPM[10]	0.1	0.0618799531	0.0383081805	0.0239198161	0.0162123434	0.0160550224
	Bessel[8]	0.1	0.0618799186	0.0382949349	0.0237043186	0.0146795698	0.0237043186
	RK-4	0.1	0.0618798527	0.0382948970	0.0237045492	0.0146803570	0.0091008245

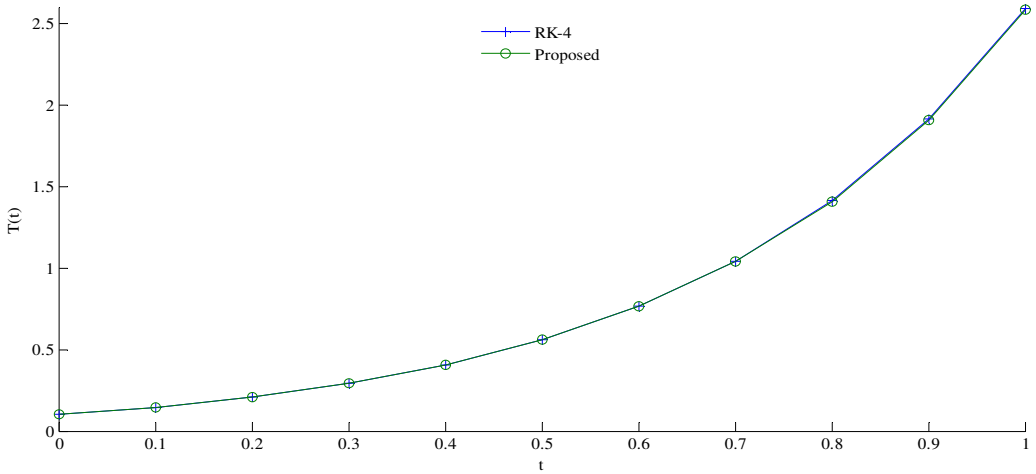

Figure-1
Comparison between proposed method and RK-4 for T(t)

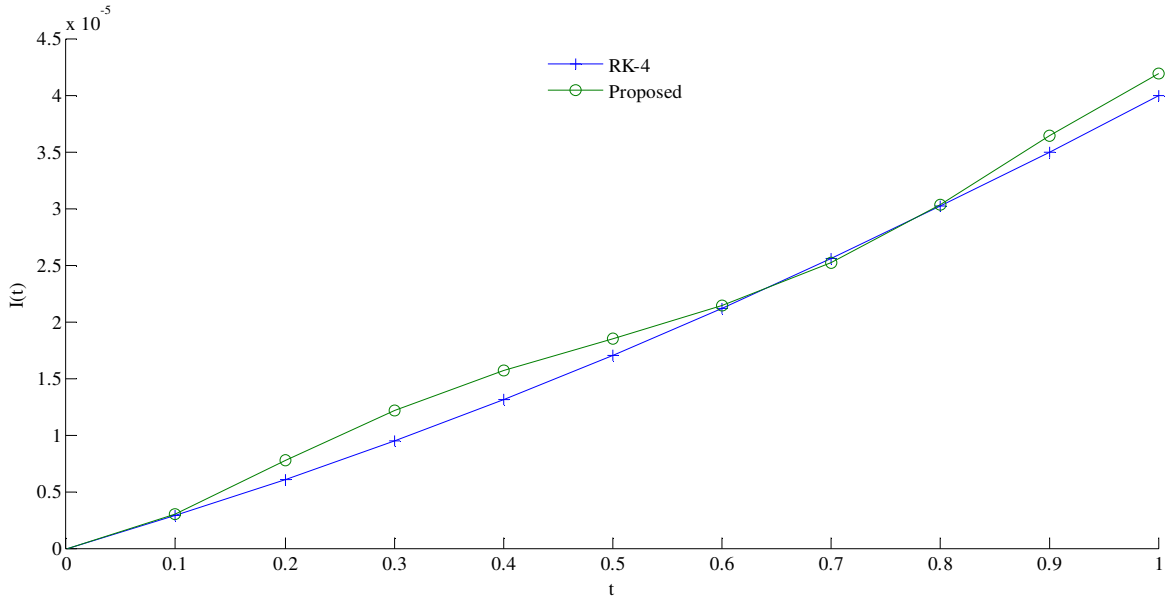

Figure-2
Comparison between proposed method and RK-4 for I(t)

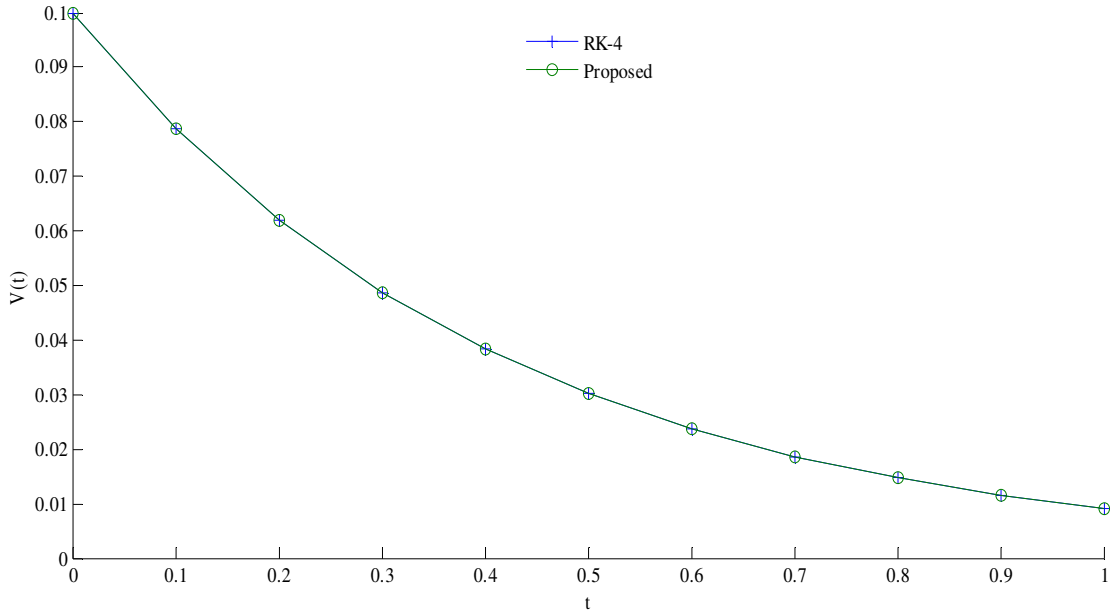

Figure-3
Comparison between proposed method and RK-4 for V(t)

To prove the accuracy and validity of the proposed method absolute errors relative to the fourth-order Runge Kutta method (RK-4) have been calculated and presented in tables 10-12. The comparison of the absolute errors from table-10 clearly reveals that the proposed technique yields the results of the HIV infection model of $CD4^{+}T$ cells (1) with fairly good accuracy. Furthermore from the comparison of table-10 it is observed that the absolute errors of T(t) by the proposed method are fairly smaller than Bessel collocation method[4], while the absolute errors of V(t) yielded by proposed method are much smaller than LADM-padé[6], LADM[6], HPM[10], and VIM[11]. However for I(t) our method gives relatively greater absolute errors as compared to other methods including LADM[6], LADM-padé[6], HPM[10], and VIM[11] but fairly comparable with Bessel collocation method[8]. Nonetheless the overall performance of the proposed method is fairly comparable with the standard methods LADM, LADM-padé, HPM, Bessel collocation, and VIM used in[6,8,10,11] in comparison with the RK-4.

Table-10
Comparison of absolute errors for T(t) between the proposed method and classical methods LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], and MVIM[11].

		t					
		0	0.2	0.4	0.6	0.8	1.0
Proposed Method	GA	0	1.39E-03	1.35E-03	2.50E-03	5.85E-03	8.88E-03
	IPA	0	1.32E-03	1.06E-03	1.69E-03	3.83E-03	4.19E-03
	ASA	0	1.32E-03	1.06E-03	1.69E-03	3.83E-03	4.18E-03
	GA-IPA	0	1.32E-03	1.06E-03	1.69E-03	3.83E-03	4.19E-03
	GA-ASA	0	1.32E-03	1.06E-03	1.69E-03	3.83E-03	4.18E-03
Classical Methods	LADM[6]	0	7.78E-05	1.95E-04	1.10E-03	1.39E-02	7.89E-02
	LADM-Padé[6]	0	7.77E-05	1.65E-04	2.43E-03	3.46E-02	2.58E-01
	VIM[11]	0	7.78E-05	1.94E-04	1.13E-03	1.41E-02	8.00E-02
	MVIM[11]	0	7.85E-05	3.00E-04	8.49E-04	2.14E-03	5.14E-03
	HPM[10]	0	7.78E-05	1.95E-04	1.10E-03	1.39E-02	7.89E-02
	Bessel[8]	0	4.87E-03	2.56E-02	6.81E-02	1.36E-01	2.04E-01

Table-11
Comparison of absolute errors for I(t) between the proposed method and classical methods LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], and MVIM[11].

		t					
		0	0.2	0.4	0.6	0.8	1.0
Proposed Method	GA	0	3.20E-06	9.56E-06	4.82E-06	1.32E-06	2.06E-06
	IPA	0	1.64E-06	2.41E-06	1.63E-07	1.74E-07	1.85E-06
	ASA	0	1.22E-06	2.55E-06	6.81E-07	2.62E-07	1.64E-06
	GA-IPA	0	1.66E-06	2.46E-06	1.76E-07	1.80E-07	1.88E-06
	GA-ASA	0	1.73E-06	2.94E-06	4.54E-07	2.07E-07	2.02E-06
Classical Methods	LADM[6]	0	1.20E-09	5.89E-09	2.24E-08	9.09E-08	3.39E-07
	LADM-Padé[6]	0	1.20E-09	6.15E-09	5.78E-08	8.26E-08	1.21E-07
	VIM[11]	0	1.12E-09	4.23E-09	1.96E-07	2.20E-06	1.57E-05
	MVIM[11]	0	1.19E-09	5.29E-09	1.27E-08	2.27E-08	3.12E-08
	HPM[10]	0	1.20E-09	5.89E-09	2.24E-08	9.09E-08	3.39E-07
	Bessel[8]	0	2.16E-07	2.17E-07	8.58E-07	1.78E-06	3.09E-06

Table-12
Comparison of absolute errors for V(t) between the proposed method and classical methods LADM[6], LADM-padé[6], Bessel collocation[8], HPM[10], VIM[11], and MVIM[11].

		t					
		0	0.2	0.4	0.6	0.8	1.0
Proposed Method	GA	0	1.79E-05	1.03E-05	8.44E-06	1.28E-05	8.11E-06
	IPA	0	1.32E-05	3.41E-06	3.03E-06	7.94E-06	6.64E-06
	ASA	0	1.49E-05	8.39E-07	3.83E-06	7.02E-06	5.42E-06
	GA-IPA	0	1.32E-05	3.40E-06	3.07E-06	7.91E-06	6.64E-06
	GA-ASA	0	1.46E-05	1.49E-06	4.05E-06	7.03E-06	5.66E-06
Classical Methods	LADM[6]	0	1.00E-07	1.33E-05	2.15E-04	1.53E-03	6.95E-03
	LADM-Padé[6]	0	1.08E-07	1.84E-05	6.87E-04	4.71E-03	5.80E-03
	VIM[11]	0	1.00E-07	1.33E-05	2.16E-04	1.54E-03	6.98E-03
	MVIM[11]	0	5.61E-08	1.06E-06	5.75E-06	2.01E-05	5.64E-05
	HPM[10]	0	1.00E-07	1.33E-05	2.15E-04	1.53E-03	6.95E-03
	Bessel[8]	0	6.59E-08	3.79E-08	2.31E-07	7.87E-07	1.46E-02

Conclusion

A stochastic technique based on hybrid heuristic computing has been presented for numerically solving a system of nonlinear ordinary coupled differential equations. The accuracy and the validity of the proposed technique have been demonstrated by numerically solving the HIV infection model of $CD4^+T$ cells. On the basis of the numerical results and comparisons made with the fourth-order Runge Kutta method (RK-4) and some classical approximate numerical methods, it can be concluded that the proposed method is efficient and viable for solving the HIV infection model. The proposed method gives fairly accurate results of the HIV infection model which are in a quite good agreement with RK-4. Moreover the proposed method gives approximate solutions that are fairly comparable with some of the classical methods including LADM, LADM-padé, VIM, MVIM, HPM, and Bessel collocation method. Furthermore our method can provide the approximate numerical solution of the problem conveniently and on the continuous grid of time once the optimal values of the unknown adaptable coefficients have been achieved.

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