

Research Article

Modified Step Variational Iteration Method for Solving Fractional Biochemical Reaction Model

**R. Yulita Molliq,¹ M. S. M. Noorani,²
R. R. Ahmad,² and A. K. Alomari³**

¹ Department of Mathematics, Faculty of Mathematics and Natural Sciences,
State University of Medan (UNIMED), Medan, Sumatera Utara 20221, Indonesia

² School of Mathematical Sciences, Faculty of Science and Technology,
National University of Malaysia (UKM), Bangi, 43600 Selangor, Malaysia

³ Department of Sciences, Faculty of Nursing and Science, Jerash Private University, Jerash 26150, Jordan

Correspondence should be addressed to R. Yulita Molliq, yulitamolliq@yahoo.com

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A new method called the modification of step variational iteration method (MoSVIM) is introduced and used to solve the fractional biochemical reaction model. The MoSVIM uses general Lagrange multipliers for construction of the correction functional for the problems, and it runs by step approach, which is to divide the interval into subintervals with time step, and the solutions are obtained at each subinterval as well adopting a nonzero auxiliary parameter h to control the convergence region of series' solutions. The MoSVIM yields an analytical solution of a rapidly convergent infinite power series with easily computable terms and produces a good approximate solution on enlarged intervals for solving the fractional biochemical reaction model. The accuracy of the results obtained is in an excellent agreement with the Adam Bashforth Moulton method (ABMM).

1. Introduction

The mathematical modelling of numerous phenomena in various areas of science and engineering using fractional derivatives naturally leads, in most cases, to what is called fractional differential equations (FDEs). Although the fractional calculus has a long history and has been applied in various fields in real life, the interest in the study of FDEs and their applications has attracted the attention of many researchers and scientific societies beginning only in the last three decades [1, 2]. Since the exact solutions of most of the FDEs cannot be found easily, thus analytical and numerical methods must be used. For example,

the ABMM is one of the most used methods to solve fractional differential equations [3–5]. Several of the other numerical analytical methods for solving fractional problems are the Adomian decomposition method (ADM), the homotopy perturbation method (HPM) and the homotopy analysis method (HAM). For example, Ray [6] and Abdulaziz et al. [7] used ADM to solve fractional diffusion equations and solve linear and nonlinear fractional differential equations, respectively. Hosseinnia et al. [8] presented an enhanced HPM to obtain an approximate solution of FDEs, and Abdulaziz et al. [9] extended the application of HPM to systems of FDEs. The HAM was applied to fractional KDV-Burgers-Kuramoto equations [10], systems of nonlinear FDEs [11], and fractional Lorenz system [12].

Another powerful method which can also give explicit form for the solution is the variational iteration method (VIM). It was proposed by He [13, 14], and other researchers have applied VIM to solve various problems [15–17]. For example, Song et al. [18] used VIM to obtain approximate solution of the fractional Sharma-Tasso-Oleiver equations. Yulita Molliq et al. [19, 20] solved fractional Zhakanov-Kuznetsov and fractional heat-and wave-like equations using VIM to obtain the approximate solution have shown the accuracy and efficiently of VIM. Nevertheless, VIM is only valid for short-time interval for solving the fractional system.

In this paper, we propose a modification of VIM to overcome this weakness of VIM. In particular, motivated by the work of [12] the procedure of dividing the time interval of solution in VIM to subintervals with the same step size Δt and the solution at each subinterval must necessary to satisfy the initial condition at each of the subinterval has been considered. Unfortunately, this idea does not give a good approximate solution when compared to the ABMM. Therefore, to obtain a good approximate solution which has a good agreement with ABMM, another idea is used: motivated by HAM, a nonzero auxiliary parameter \hbar is considered into the correction functional in VIM. This parameter \hbar was inserted to adjust and control the convergence region of the series solutions. In general, it is straightforward to choose a proper value of \hbar from the so-called \hbar -curve. We call this modification involving time step and auxiliary parameter \hbar the MoSVIM. Strictly speaking MoSVIM is a modification of our earlier proposed method—step variational iteration method—which is still under review [21].

As an application, this paper investigates for the first time the applicability and effectiveness of MoSVIM to obtain the approximate solutions of the fractional version of the biochemical reaction model as studied in [22] for interval $[0, T]$. The fractional biochemical reaction model (shortly called FBRM) is considered in the following form:

$$\begin{aligned}\frac{d^\theta u}{dt} &= -u + (\beta - \alpha) v + uv, \\ \frac{d^\theta v}{dt} &= \frac{1}{\mu}(u - \beta v - uv),\end{aligned}\tag{1.1}$$

subject to initial conditions

$$u(0) = 1, \quad v(0) = 0,\tag{1.2}$$

where θ is a parameter describing the order of the fractional derivative ($0 < \theta \leq 1$), α , β , and μ are dimensionless parameters.

Our objective is to provide an alternative analytical method to achieve the solution and also highlight the limitations of solutions using VIM, MoVIM, and SVIM for solving the fractional biochemical reaction model when compared to ABMM.

2. Basic Definitions

Fractional calculus unifies and generalizes the notions of integer-order differentiation and n -fold integration [1, 2]. We give some basic definitions and properties of fractional calculus theory which will be used in this paper.

Definition 2.1. A real function $f(x)$, $x > 0$, is said to be in the space C_μ , $\mu \in \mathbb{R}$ if there exists a real number $p > \mu$, such that $f(x) = x^p f_1(x)$, where $f_1(x) \in C[0, \infty)$, and it is said to be in the space C_μ^q if and only if $f^{(q)} \in C_\mu$, $q \in \mathbb{N}$.

The Riemann-Liouville fractional integral operator is defined as follows.

Definition 2.2. The Riemann-Liouville fractional integral operator of order $\theta \geq 0$, of a function $f \in C_\mu$, $\mu \geq -1$, is defined as

$$J^\theta f(x) = \frac{1}{\Gamma(\theta)} \int_0^x (x-t)^{\theta-1} f(t) dt, \quad \theta > 0, x > 0, \quad (2.1)$$

$$J^0 f(x) = f(x).$$

In this paper only real and positive values of θ will be considered.

Properties of the operator J^θ can be found in [2], and we mention only the following: For $f \in C_\mu$, $\mu \geq -1$, $\theta, \eta \geq 0$, and $\gamma \geq -1$,

- (1) $J^\theta J^\eta f(x) = J^{\theta+\eta} f(x)$,
- (2) $J^\theta J^\eta f(x) = J^\eta J^\theta f(x)$,
- (3) $J^\theta x^\gamma = (\Gamma(\gamma+1)/\Gamma(\theta+\gamma+1))x^{\theta+\gamma}$.

The Reimann-Liouville derivative has certain disadvantages when trying to model real-world phenomena with FDEs. Therefore, we will introduce a modified fractional differential operator D_*^θ proposed by Caputo in his work on the theory of viscoelasticity [23].

Definition 2.3. The fractional derivative of $f(x)$ in Caputo sense is defined as

$$D_*^\theta f(x) = J^{q-\theta} D^q f(x)$$

$$= \frac{1}{\Gamma(q-\theta)} \int_0^x (x-\xi)^{q-\theta-1} f^{(q)}(\xi) d\xi, \quad (2.2)$$

for $q-1 < \theta \leq q$, $q \in \mathbb{N}$, $x > 0$, $f \in C_{-1}^q$.

In addition, we also need the following property.

Lemma 2.4. *If $q - 1 < \theta \leq q$, $q \in \mathbb{N}$, and $f \in C_\mu^q$, $\mu \geq -1$, then*

$$D_*^\theta J^\theta f(x) = f(x),$$

$$J^\theta D_*^\theta f(x) = f(x) - \sum_{i=0}^{q-1} f^{(i)}(0^+) \frac{x^i}{i!}, \quad x > 0. \quad (2.3)$$

The Caputo differential derivative is considered here because the initial and boundary conditions can be included in the formulation of the problems [1]. The fractional derivative is taken in the Caputo sense as follows.

Definition 2.5. For m to be the smallest integer that exceeds θ , the Caputo fractional derivative operator of order $\theta > 0$ is defined as

$$D_t^\theta u(t) = \begin{cases} \frac{1}{\Gamma(q-\theta)} \int_0^t (t-\xi)^{q-\theta-1} \frac{\partial^q u(\xi)}{\partial \xi^q} d\xi, & \text{for } q-1 < \theta < q, \\ \frac{\partial^q u(t)}{\partial t^q}, & \text{for } \theta = q \in \mathbb{N}. \end{cases} \quad (2.4)$$

For more information on the mathematical properties of fractional derivatives and integrals, one can consult [1, 2].

3. Step Variational Iteration Method

The approximate solutions of fractional biochemical reaction model will be obtained in this paper. A simple way of ensuring validity of the approximations is solving under arbitrary initial conditions. In this case, $[0, T]$ is regarded as interval. From idea of Alomari et al. [12], the $[0, T]$ interval is divided to subintervals with time step Δt , and the solution at each subinterval was obtained. So it is necessary to satisfy the initial condition at each of the subinterval. Thus the step technique can describe as the following formula:

$$u_{i,n+1}(t) = u_{i,n}(t) + \int_0^{t-t^*} \lambda_i(\xi) [Lu_{i,n}(\xi) + N\tilde{u}_{i,n}(\xi) - g_i(\xi)] d\xi, \quad (3.1)$$

where λ_i , for $i = 1, \dots, m$, is a general Lagrange multiplier, L is linear operator, N is nonlinear operator, and g is inhomogeneous term. As knowledge, the optimal general Lagrange multiplier is obtained by constructing the correction functional as in VIM which is $\tilde{u}_{i,n}$ is considered as restricted variations, that is, $\delta \tilde{u}_{i,n} = 0$.

Accordingly, the initial values $u_{1,0}, u_{2,0}, \dots, u_{m,0}$ will be changed for each subinterval, that is, $u_1(t^*) = c_1^* = u_{1,0}$, $u_2(t^*) = c_2^* = u_{2,0}, \dots, u_m(t^*) = c_m^* = u_{m,0}$, and it should be satisfied through the initial conditions $u_{i,n}(t^*) = 0$ for all $n \geq 1$, so

$$u_i(t) \simeq u_{i,n}(t - t^*), \quad i = 0, 1, \dots, m, \quad (3.2)$$

where t^* starting from $t_0 = 0$ until $t_j = T$, J is number of subinterval. To carry out the solution on every subinterval of equal length Δt , the values of the following initial conditions are shown below:

$$c_i^* = u_i(t^*), \quad i = 0, 1, \dots, m. \quad (3.3)$$

In general, we do not have this information at our clearance except at the initial point $t^* = t_0 = 0$, but these values can be obtained by assuming that the new initial condition is the solution in previous interval (i.e., if the solution in interval $[t_j, t_{j+1}]$ is necessary, then the initial conditions of this interval will be as follows:

$$c_i = u_i(t) \simeq u_{i,n}(t_j - t_{j-1}), \quad (3.4)$$

where $c_i, i = 0, 1, \dots, m$ are the initial conditions in the interval $[t_j, t_{j+1}]$.

4. Modified Step Variational Iteration Method

Furthermore, to implement the modification of SVIM, we consider $\hbar \neq 0$, a nonzero auxiliary parameter. Multiply \hbar by correction functional in (3.1), yield

$$u_{i,n+1}(t) = u_{i,n}(t) + \hbar \int_0^{t-t^*} \lambda_i(\xi) [Lu_{i,n}(\xi) + N\tilde{u}_{i,n}(\xi) - g_i(\xi)] d\xi, \quad (4.1)$$

where $i = 0, 1, 2, \dots, m$, $m \in \mathbb{N}$ and \hbar is the convergence-control parameter which ensures that this assumption can be satisfied. The subscript n denotes the n th iteration.

Accordingly, the successive approximations $u_n(t)$, $n \geq 0$ of the solution $u(t)$ will be readily obtained by selecting initial approximation u_0 that at least satisfies the initial conditions. The computations and plotting of figures for the algorithm, has been done using Maple package.

5. Application

In this section, we demonstrate the efficiency of MoSVIM of fractional biochemical reaction model in (1.1). The correction functionals for the system (1.1) can be approximately constructed as used by VIM and (2.4) to find the general Lagrange multiplier in the following forms:

$$u_{n+1}(t) = u_n(t) + \int_0^t \lambda_1(\xi) \left[\frac{d^q u_n}{d\xi^q} + u_n - (\beta - \alpha) \tilde{v}_n - \widetilde{u_n v_n} \right] d\xi, \quad (5.1)$$

$$v_{n+1}(t) = v_n(t) + \int_0^t \lambda_2(\xi) \left[\frac{d^q v_n}{d\xi^q} - \frac{1}{\mu} (\tilde{u}_n - \beta v_n - \widetilde{u_n v_n}) \right] d\xi,$$

where λ_1 and λ_2 are general Lagrange multipliers which can be identified optimally via variational theory. n denotes the n th iteration. \tilde{u}_n , \tilde{v}_n , and $\widetilde{u_n v_n}$ denote restricted variations,

that is, $\delta\widetilde{u}_n = 0$, $\delta\widetilde{v}_n = 0$, and $\delta\widetilde{u}_n\widetilde{v}_n = 0$. In this case, the general Lagrange multiplier can be easily determined by choosing the number of order q , that is, $q = 1$. Thus, the following sets of stationary conditions was obtained as follows:

$$\begin{aligned} 1 + \lambda_1(t)|_{\xi=t} = 0, \quad \lambda_1(\xi) - \lambda_1'(\xi) = 0, \\ 1 + \lambda_2(t)|_{\xi=t} = 0, \quad \beta\lambda_2(\xi)\mu - \lambda_2'(\xi) = 0. \end{aligned} \quad (5.2)$$

Therefore, the general Lagrange multipliers can be easily identified as

$$\begin{aligned} \lambda_1(\xi) &= -e^{(\xi-t)}, \\ \lambda_2(\xi) &= -e^{\beta(\xi-t)/\mu}. \end{aligned} \quad (5.3)$$

Here, the general Lagrange multiplier in (5.3) is expanded by Taylor series and is chosen only one term in order to calculate, the general Lagrange multiplier can write as follows

$$\begin{aligned} \lambda_1(\xi) &= -1, \\ \lambda_2(\xi) &= -\frac{\beta}{\mu}. \end{aligned} \quad (5.4)$$

Substituting the general Lagrange multipliers in (5.4) into the correction functional in (5.1) results in the following iteration formula:

$$\begin{aligned} u_{n+1}(t) &= u_n(t) - \int_0^{t-t^*} \left[\frac{d^\theta u_n}{d\xi} + u_n - (\beta - \alpha)v_n - u_n v_n \right] d\xi, \\ v_{n+1}(t) &= v_n(t) - \int_0^{t-t^*} \frac{\beta}{\mu} \left[\frac{d^\theta v_n}{d\xi} - \frac{1}{\mu}(u_n - \beta v_n - u_n v_n) \right] d\xi. \end{aligned} \quad (5.5)$$

Furthermore, we multiply the nonzero auxiliary parameter \hbar by (5.5) which yields:

$$\begin{aligned} u_{n+1}(t) &= u_n(t) - \hbar \int_0^{t-t^*} \left[\frac{d^\theta u_n}{d\xi} + u_n - (\beta - \alpha)v_n - u_n v_n \right] d\xi, \\ v_{n+1}(t) &= v_n(t) - \hbar \int_0^{t-t^*} \frac{\beta}{\mu} \left[\frac{d^\theta v_n}{d\xi} - \frac{1}{\mu}(u_n - \beta v_n - u_n v_n) \right] d\xi. \end{aligned} \quad (5.6)$$

Then, the interval $[0, 2]$ is divided into subintervals with time step Δt , and we get the solution at each subinterval. In this case, the initial condition is regarded as initial approximation,

which is necessary satisfied at each of the subinterval, that is, $u(t^*) = c_1^* = u_0$, $v(t^*) = c_2^* = v_0$, and the initial conditions should be satisfied $u_n(t^*) = 0$, $v_n(t^*) = 0$ for all $n \geq 1$, so

$$\begin{aligned}
 u_1 &= c_1 - \hbar \left[c_1 - \frac{5}{8} c_2 - c_1 c_2 \right] (t - t^*), \\
 v_1 &= c_2 - 100\hbar [-c_1 + c_2 + c_1 c_2] (t - t^*), \\
 u_2 &= c_1 - \hbar \left[c_1(t - t^*) - \frac{5}{8} c_2(t - t^*) - c_1 c_2(t - t^*) \right] \\
 &\quad - \hbar \left[-\frac{30553}{37952} \hbar c_1(t - t^*)^{7/5} + \frac{9897}{19670} \hbar c_2(t - t^*)^{7/5} + c_1(t - t^*) \right. \\
 &\quad \left. - \frac{127}{4} \hbar c_1(t - t^*)^2 + \frac{505}{16} \hbar c_2(t - t^*)^2 + \frac{329}{4} \hbar c_1(t - t^*)^2 c_2 \right. \\
 &\quad \left. + \frac{30553}{37952} \hbar c_1 c_2(t - t^*)^{7/5} - \frac{5}{8} c_2(t - t^*) + \frac{100}{3} \hbar^2(t - t^*)^3 c_1^2 \right. \\
 &\quad \left. - \frac{200}{3} \hbar^2(t - t^*)^3 c_1^2 c_2 + \frac{125}{6} \hbar^2(t - t^*)^3 c_2^2 + \frac{325}{6} \hbar^2(t - t^*)^3 c_1 c_2^2 \right. \\
 &\quad \left. + \frac{100}{3} \hbar^2(t - t^*)^3 c_1^2 c_2^2 - 50(t - t^*)^2 \hbar c_1^2 + 50(t - t^*)^2 \hbar c_1^2 c_2 \right. \\
 &\quad \left. - \frac{1}{2}(t - t^*)^2 \hbar c_1 c_2^2 - c_1 c_2(t - t^*) \right], \\
 v_2 &= c_2 - \hbar [-100c_1(t - t^*) + 100c_2(t - t^*) + 100c_1 c_2(t - t^*)] \\
 &\quad - \hbar \left[\frac{1583520}{1967} \hbar c_1(t - t^*)^{7/5} - \frac{1583520}{1967} \hbar c_2(t - t^*)^{7/5} - 100c_1(t - t^*) \right. \\
 &\quad \left. - \frac{1583520}{1967} \hbar c_1 c_2(t - t^*)^{7/5} + 5050 \hbar c_1(t - t^*)^2 - \frac{20125}{4} \hbar c_2(t - t^*)^2 \right. \\
 &\quad \left. - 10100 \hbar c_1(t - t^*)^2 c_2 - \frac{10000}{3} \hbar^2(t - t^*)^3 c_1^2 + \frac{16250}{3} \hbar^2(t - t^*)^3 c_1 c_2 \right. \\
 &\quad \left. + \frac{20000}{3} \hbar^2(t - t^*)^3 c_1^2 c_2 - \frac{6250}{3} \hbar^2(t - t^*)^3 c_2^2 - \frac{16250}{3} \hbar^2(t - t^*)^3 c_1 c_2^2 \right. \\
 &\quad \left. - \frac{10000}{3} \hbar^2(t - t^*)^3 c_1^2 c_2^2 + 5000(t - t^*)^2 \hbar c_2^2 - 5000(t - t^*)^2 \hbar c_1^2 c_2 \right. \\
 &\quad \left. + \frac{125}{4}(t - t^*)^2 \hbar c_2^2 + 50(t - t^*)^2 \hbar c_1 c_2^2 + 100c_1 c_2(t - t^*) \right. \\
 &\quad \left. + 100c_2(t - t^*) \right].
 \end{aligned}$$

(5.7)

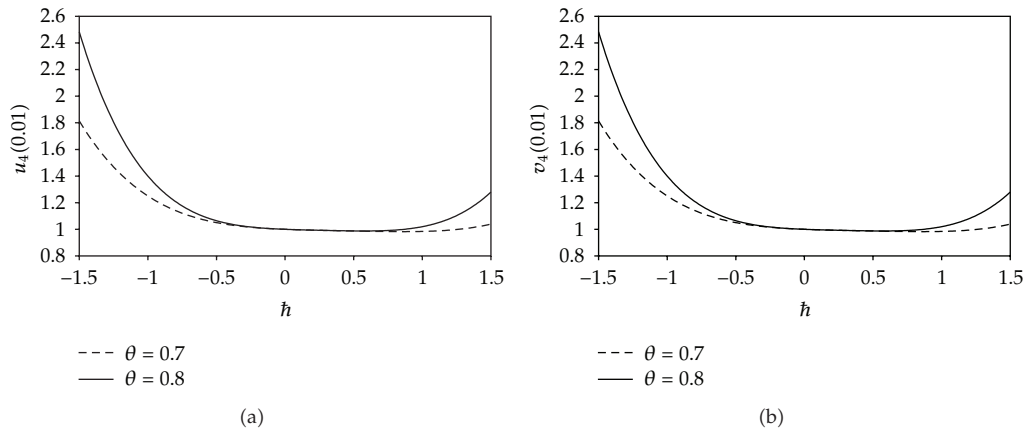


Figure 1: h -curve for fractional biochemical reaction model using the third iteration MoSVIM with different value of θ , that is, (0.7,0.8).

Here, the iteration was chosen from previously research by Goh et al. [24]. Thus, the solution will be as follows:

$$\begin{aligned}
 u(t) &\simeq u_5(t - t^*), \\
 v(t) &\simeq v_5(t - t^*),
 \end{aligned}
 \tag{5.8}$$

where t^* start from $t_0 = 0$ until $t_j = T = 2$. To carry out the solution on every subinterval of equal length Δt , the values of the following initial conditions is presented below:

$$c_1 = u(t^*), \quad c_2 = v(t^*). \tag{5.9}$$

In general, we do not have this information at our clearance except at the initial point $t^* = t_0 = 0$, but we can obtain these values by assuming that the new initial condition is the solution in the previous interval (i.e., If we need the solution in interval $[t_j, t_{j+1}]$ then the initial conditions of this interval will be as

$$\begin{aligned}
 c_1 &= u(t) \simeq u_5(t_j - t_{j-1}), \\
 c_2 &= v(t) \simeq v_5(t_j - t_{j-1}),
 \end{aligned}
 \tag{5.10}$$

where c_1, c_2 are the initial conditions in the interval $[t_j, t_{j+1}]$.

6. Result and Discussion

To investigate the influence of h on convergence of the solution series, we plot the h -curves of $u_4(0.01)$ and $v_4(0.01)$ using the fifth iteration of MoSVIM when $\theta = 0.7$, and $\theta = 0.8$ as shown in Figure 1. We found that the range of values for h is between 0.1 and 0.7. Because the accuracy and efficiency, $\Delta t = 0.001$ was chosen as the benchmark for comparison between MoSVIM and ABMM. The constants $\mu = 0.1$, $\beta = 1$, $\tau = 0.375$ were fixed, as was chosen

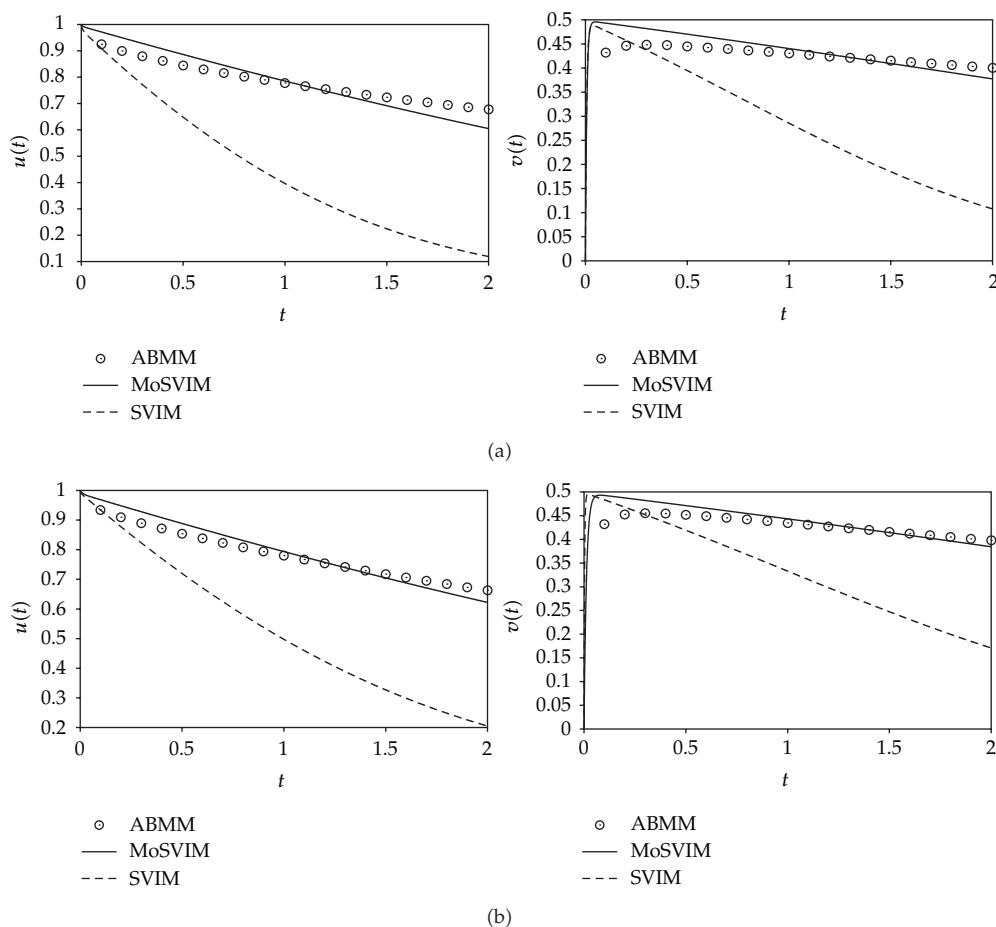


Figure 2: Approximate solution of fractional biochemical reaction model via the fifth iterate MoSVIM, SVIM and ABMM with different value of $\bar{h} = 0.25$; (a) $\theta = 0.7$, (b) $\theta = 0.8$.

by Hashim et al. [25]. In this case, the computational algorithms for the system in (1.1) are written using the Maple software. A good solutions of fractional biochemical reaction model when $\bar{h} = 0.25$ and $\theta = 0.7$ and $\theta = 0.8$ was presented in Tables 1 and 2, respectively. From the tables, MoSVIM is more accurate than SVIM in different value of θ , that is, $\theta = 0.7$ and $\theta = 0.8$. Figure 2 shows comparison of MoSVIM and SVIM. From the figure, MoSVIM solution is more closer to ABMM solution if it compare to SVIM solution. The comparison of MoSVIM, VIM and MoVIM is shown to exhibit the accuracy of MoSVIM, see Figure 3. From the figure, MoSVIM solutions is more accurate than the VIM and MoVIM solutions, and also is in good agreement with that of ABMM with $\Delta t = 0.001$.

7. Conclusions

In this paper, an algorithm of fractional biochemical reaction model (FBRM) using step modified variational iteration method (MoSVIM) was developed. For computations and plots, the Maple package were used. We found that MoSVIM is a suitable technique to

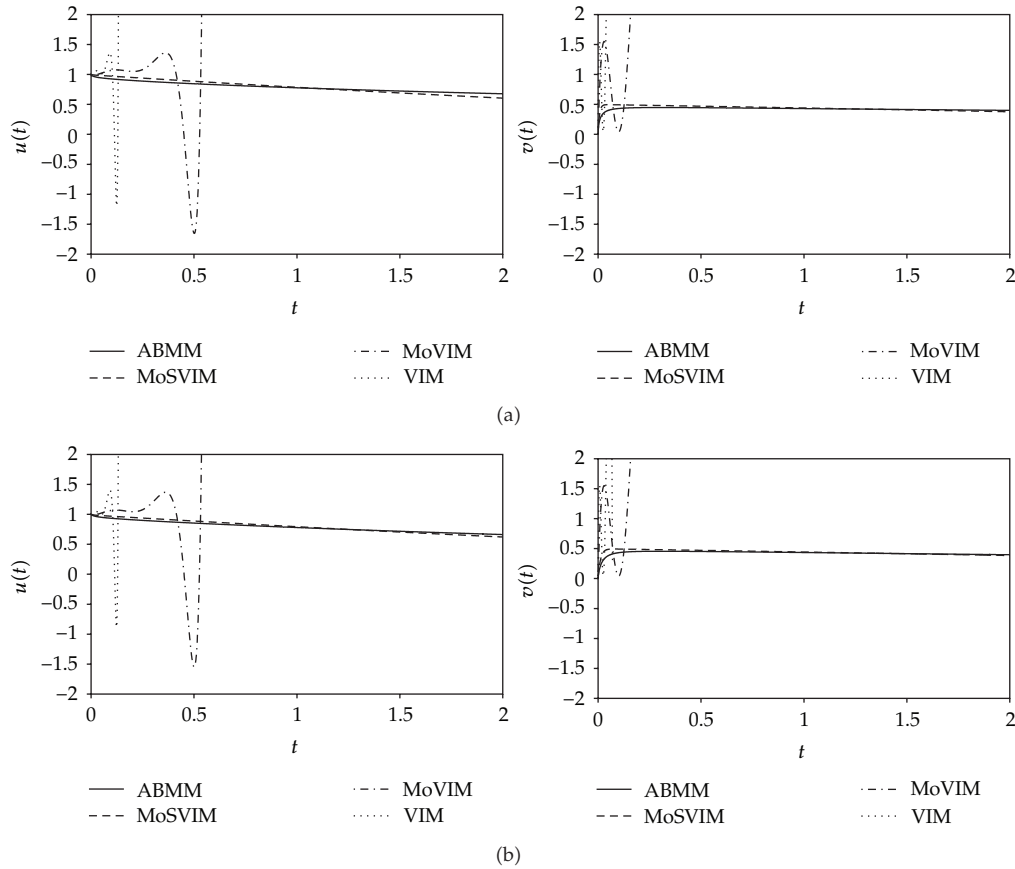


Figure 3: Approximate solution of fractional biochemical reaction model via the fifth iterate MoSVIM, VIM, MOVIM and ABMM with different value $\bar{h} = 0.25$; (a) $\theta = 0.7$, (b) $\theta = 0.8$.

Table 1: Approximate solution of fractional biochemical reaction model for $\theta = 0.7$, $\bar{h} = 0.25$ using fifth iterate of SVIM and MoSVIM, respectively, and ABMM in comparison with $\Delta t = 0.001$.

t	$u(t)$			$v(t)$		
	SVIM	MoSVIM $\bar{h} = 0.25$	ABMM	SVIM	MoSVIM $\bar{h} = 0.25$	ABMM
0.2	0.8386059622	0.94971579713	0.8997902940	0.4573898218	0.4875079322	0.4460892838
0.4	0.7085282553	0.90710678781	0.8613048034	0.4161477755	0.4760660497	0.4472272725
0.6	0.5912666037	0.86552788930	0.8298424157	0.3731707422	0.4643967818	0.4425233401
0.8	0.4871830355	0.82499870384	0.8023145667	0.3293135117	0.4525101582	0.4366487301
1.0	0.3963375974	0.78553782917	0.7774913063	0.28564459059	0.4404180963	0.4304899916
1.2	0.3184413078	0.74716268585	0.7547144581	0.2433500553	0.4281344807	0.4243110704
1.4	0.2528478376	0.70988933887	0.7335763272	0.2035911835	0.4156752212	0.4182067957
1.6	0.1985917817	0.67373231562	0.7138006533	0.1673493331	0.4030582851	0.4122134576
1.8	0.1544686371	0.63870442274	0.6951883968	0.1353025692	0.3903036993	0.4063440765
2.0	0.1191395751	0.60481656498	0.6775895839	0.1077686026	0.3774335172	0.4006016629

Table 2: Approximate solution of fractional biochemical reaction model for $\theta = 0.8$, $\hbar = 0.25$ using fifth iterate of SVIM and MoSVIM, respectively, and ABMM in comparison with $\Delta t = 0.001$.

t	$u(t)$			$v(t)$		
	SVIM	MoSVIM $\hbar = 0.25$	ABMM	SVIM	MoSVIM $\hbar = 0.25$	ABMM
0.2	0.8774940768	0.9483122837	0.9097501570	0.4679040865	0.4873856458	0.4527160444
0.4	0.7705371139	0.9082752827	0.8712461769	0.4357928339	0.4766431773	0.4544461158
0.6	0.6714218302	0.8691504634	0.83806131857	0.4023638935	0.4657006445	0.4488806205
0.8	0.5804145345	0.8309540052	0.80798209220	0.3679711022	0.4545663318	0.4419163408
1.0	0.4976827145	0.7937012985	0.78014908465	0.3330695561	0.4432499550	0.4345614413
1.2	0.4232727663	0.7574068186	0.75409601514	0.2982002140	0.4317049001	0.4271103147
1.4	0.3570935610	0.7220839956	0.72952829585	0.2639592227	0.4201174892	0.4196723265
1.6	0.2989092929	0.6877450824	0.70624217621	0.2309539383	0.4083285633	0.4122937832
1.8	0.2483439988	0.6544010212	0.68408785674	0.1997517207	0.3964119332	0.4049957868
2.0	0.2048982187	0.6220613114	0.66295019827	0.1708306193	0.3843851419	0.3977883047

solve the fractional problem. This modified method yields an analytical solution in iterations of a rapid convergent infinite power series with enlarged intervals. Comparison between MoSVIM, MoVIM and ABMM were made; the MoSVIM was found to be more accurate than the MoVIM. MoSVIM is easier in calculation yet powerful method and also is readily applicable to the more complex cases of fractional problems which arise in various fields of pure and applied sciences.

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