ISSN 1 746-7233, England, UK
World Journal of Modelling and Simulation
Vol. 9 (2013) No. 1, pp. 38-46

On the numerical solutions to nonlinear biochemical reaction model using Picard-Padé technique

Mohamed Meabed Khader*

Department of Mathematics, Faculty of Science, Benha University, Benha 13111, Egypt

(*Received March 5 2012, Accepted November 27 2012*)

Abstract. In this paper, we introduce a modification of the Picard iteration method (PIM) using Padé approximation and so called Picard-Padé technique. Special attention is given to study the convergence analysis of the proposed method. Convergence analysis is reliable enough to estimate the maximum absolute error of the solution given by PIM. A basic enzyme kinetics is used to test the effectiveness of the proposed method. This enzyme-substrate reaction is formed by a system of nonlinear ordinary differential equations. We compare our numerical results against the conventional numerical method, fourth-order Runge-Kutta method (RK4). Numerical results were obtained for these two methods and we found that Picard-Padé technique and RK4 are in excellent conformance. The results obtained ensure that the presented procedure needs less work in comparison with the traditional methods and decreases considerable volume of calculation and a powerful tool for solving large amount of other problems in physics and engineering.

Keywords: Picard iteration method, nonlinear biochemical reaction model, Padé approximation, Fourth-order Runge-Kutta method

1 Introduction

In 1913, Michaelis and Menten proposed a simple yet powerful framework to describe enzyme processes, and the basic enzymatic reaction model is given by the scheme [18]

$$E + A \rightleftharpoons Y \rightarrow E + X, \tag{1}$$

where E is the enzyme, A the substrate, Y the enzyme-substrate intermediate complex and X the product. By applying the law of mass action, which states that reaction rates are proportional to the concentrations of the reactants, the time evolution of the scheme Eq. (1) can be determined from the solution of the system of coupled nonlinear ordinary differential equations [19]

$$\frac{\mathrm{d}A}{\mathrm{d}t} = -k_1 EA + k_{-1}\, Y, \tag{2}$$

$$\frac{\mathrm{d}E}{\mathrm{d}t} = -k_1 EA + (k_{-1} + k_2)\, Y, \tag{3}$$

$$\frac{\mathrm{d}Y}{\mathrm{d}t} = k_1 EA - (k_{-1} + k_2)\, Y, \tag{4}$$

$$\frac{\mathrm{d}X}{\mathrm{d}t} = k_2\, Y, \tag{5}$$

subject to the initial conditions

$$A(0) = A_0, \qquad E(0) = E_0, \qquad Y(0) = 0, \qquad X(0) = 0, \tag{6}$$

* Corresponding author. Tel.: +20-0100-7782748, *E-mail address*: mohamedmbd@yahoo.com.

here the parameters k_1, k_{-1} and k_2 are positive rate constants for each reaction. Systems Eqs. (2) $\sim$ (5) can be reduced to only two equations for A and Y and in dimensionless form of concentrations of substrate, u, and intermediate complex between enzyme and substrate, v, are given by [19]

$$\frac{\mathrm{d}u}{\mathrm{d}t} = -u + (\beta - \alpha)v + uv, \tag{7}$$

$$\frac{\mathrm{d}v}{\mathrm{d}t} = \frac{1}{\gamma}(u - \beta v - uv), \tag{8}$$

subject to the initial conditions

$$u(0) = 1, \qquad v(0) = 0, \tag{9}$$

here α, β and γ are dimensionless parameters. For more details on mathematical formulation of Eqs. (7) $\sim$ (8) and an intrinsic knowledge of its analysis, see [19].

Our motivation for this work is to provide an alternative analytical method to find the solution for the transient phase of the enzyme-catalyzed reaction apart. As explained in [19], the transient phase of such a reaction typically consists of the first few milliseconds after the start of the reaction, and is often observed by biochemists with meticulous techniques. The knowledge of this transient phase is crucial for the determination of the various system parameters such as the rate constants and for distinguishing among the different mechanisms of enzyme catalysis.

Many different methods have recently introduced to solve nonlinear differential equations, such as, variational iteration method[2, 5, 7, 9, 20, 23], Adomian decomposition method[1, 24, 25] and homotopy perturbation method[6, 8, 10, 13, 21, 22]. The Adomian decomposition method provides solutions as a series by employing the so-called Adomian's polynomials which are related to the derivatives of the nonlinearities; therefore, these nonlinearities must be analytical functions of the dependent variables and this has often been ignored in the literature, for the existence and uniqueness of solutions to, for example, initial-value problems in ordinary differential equations is ensured under much milder conditions[11, 15]. However, the decomposition method may be formulated in a manner that does not require that the nonlinearities be differentiable with respect to the dependent variables and their derivatives[16]. Other techniques that also require that the nonlinearities be analytical functions of the dependent variable and provide either convergent series or asymptotic expansions to the solution include perturbation methods[14], the homotopy perturbation technique and the homotopy analysis procedure[13].

By way of contrast, iterative techniques for solving a large class of linear or nonlinear differential equations without the tangible restriction of sensitivity to the degree of the nonlinear term and also it reduces the size of calculations besides, its interactions are direct and straightforward. These techniques include the well-known Picard fixed-point iterative procedure[3, 12].

Some highlights of new developments of PIM include work by Ramos, who solved the nonlinear second-order differential equations[15], nonlinear ordinary differential equations[16], and the nonlinear advection-reaction-diffusion equations[17]. Further discussions on latest innovations in the PIM can be found in Section 2. Goha, et al. used the variational iteration method to solve the biochemical reaction model[7]. Also, Hashim, et al. implemented the multistage homotopy perturbation method applied to nonlinear biochemical reaction model[8].

In this paper we present a modification of PIM, this modification depends on the Padé approximation [4]. Special attention is given to study the convergence analysis of the proposed method. Convergence analysis is reliable enough to estimate the maximum absolute error of the solution given by PIM. To guarantee this study, effectively employ this modification to solve nonlinear biochemical reaction model. Therefore, this modification of PIM has been widely used for solving nonlinear problems to overcome the shortcoming of other methods.

The rest of this paper is organized as follows: In Section 2, we introduce the Picard iteration method. In Section 3, we study the convergence analysis of the proposed method. In Section 4, we present the Padé approximation on the series solution. In Section 5, we give the modified algorithm of PIM. In Section 6, we implement the Picard-Padé-technique to nonlinear biochemical reaction model. In Section 7, we end the paper with the concluding remarks and discussion.

2 Picard iteration method

To illustrate the analysis of PIM, we limit ourselves to consider the following system of nonlinear ordinary differential equations (NODEs) in the type

$$Lu = R_1\, u + N_1(u) + F_1(u, v), \tag{10}$$
$$Lv = R_2\, v + N_2(v) + F_2(u, v), \tag{11}$$

with specified initial conditions, where $L = \frac{\partial}{\partial t}$, R_1 and R_2 are linear bounded operators i.e., it is possible to find numbers $m_i > 0,\ (i = 1, 2)$ such that $||R_i\, u|| \leq m_i||u||$. The nonlinear terms $N_1(u)$ and $N_2(v)$ are Lipschitz continuous with $|N_1(u)-N_1(\theta)| \leq r_1\,|u-\theta|$, and $|N_2(v)-N_2(\theta)| \leq r_2\,|v-\theta|,\ \forall\ t\ \in J = [0, T]$, also, the coupled nonlinear terms $F_1(u, v)$ and $F_2(u, v)$ are Lipschitz continuous with

$$|F_1(u, v) - F_1(\theta, v)| \leq s_1|u - \theta|, \qquad \text{and} \qquad F_2(u, v) - F_2(u, \theta)| \leq s_2|v - \theta|,$$

for some constants $r_i > 0,\ s_i > 0,\ (i = 1, 2)$.
The PIM gives the possibility to write the solution of the system Eqs. (10) $\sim$ (11) in the following iteration formula

$$u_n(t) = u(0) + \int_0^t [R_1\, u_{n-1} + N_1(u_{n-1}) + F_1(u_{n-1}, v_{n-1})\,]d\tau, \qquad n \geq 1, \tag{12}$$
$$v_n(t) = v(0) + \int_0^t [R_2\, v_{n-1} + N_2(v_{n-1}) + F_2(u_{n-1}, v_{n-1})\,]d\tau, \qquad n \geq 1. \tag{13}$$

The successive approximations $u_n,\ v_n,\ n \geq 0$, of the solutions will be readily obtained upon using any selective functions u_0 and v_0. The initial values of the solution are usually used for selecting the zeroth approximation u_0 and v_0. Consequently, the exact solutions may be obtained by using

$$u = \lim_{n\to\infty} u_n, \qquad v = \lim_{n\to\infty} v_n. \tag{14}$$

3 Study of convergence analysis

In this section, the sufficient conditions are presented to guarantee the convergence of PIM, when applied to solve NODEs, where the main point is that we prove the convergence of the recurrence sequence[3, 12], which is generated by using PIM.

Lemma 1. *Let $A : U \to V$ be a bounded linear operator and let $\{u_p\}$ be a convergent sequence in U with limit u, then $u_p \to u$ in U implies that $A(u_p) \to A(u)$ in V.*

Proof. Since

$$\|Au_p - Au\|_V = \|A(u_p - u)\|_V \leq \|A\|\,\|u_p - u\|_U,$$

hence

$$\lim_{p\to\infty} \|Au_p - Au\|_V \leq \|A\| \lim_{p\to\infty} \|u_p - u\|_U = 0,$$

implies that $A(u_p) \to A(u)$.

Theorem 1. *(Uniqueness theorem) The nonlinear problem Eqs. (10) $\sim$ (11) has a unique solution, whenever $0 < \alpha_i < 1,\ (i = 1, 2)$, where, $\alpha_i = (m_i + r_i + s_i)T$, where the constants m_i, r_i and s_i are defined above.*

Proof. Since the solution of Eqs. (10) $\sim$ (11) can be written in the following form

$$u(t) = u(0) + L^{-1}[R_1\, u + N_1(u) + F_1(u, v)],$$

$$v(t) = v(0) + L^{-1}[R_2\, v + N_2(v) + F_2(u, v)],$$

where the inverse operator L^{-1} defined by $L^{-1}(.) = \int_0^t (.)dt$.
Now let, (u, v) and (u^*, v^*) be two different solutions to Eqs. (10) $\sim$ (11), then by using the above equations, we get

$$\begin{aligned}
|u - u^*| &= \Big| \int_0^t [\ R_1\,(u - u^*) + N_1(u) - N_1(u^*) + F_1(u, v) - F_1(u^*, v)\ ]\,dt \Big| \\
&\le \int_0^t \Big[\, |R_1\,(u - u^*)| + |N_1(u) - N_1(u^*)| + |F_1(u, v) - F_1(u^*, v)| \,\Big] dt \\
&\le (\, m_1 |u - u^*| + r_1\,|u - u^*| + s_1\,|u - u^*|\,)T \\
&\le \alpha_1\,|u - u^*|, \\
|v - v^*| &= \Big| \int_0^t [\ R_2\,(v - v^*) + N_2(v) - N_2(v^*) + F_2(u, v) - F_2(u, v^*)\ ]\,dt \Big| \\
&\le \int_0^t \Big[\, |R_2\,(v - v^*)| + |N_2(v) - N_2(v^*)| + |F_2(u, v) - F_2(u, v^*)| \,\Big] dt \\
&\le (\, m_2 |v - v^*| + r_2\,|v - v^*| + s_2\,|v - v^*|\,)T \\
&\le \alpha_2\,|v - v^*|,
\end{aligned}$$

from which we get $(1 - \alpha_1)\,|u - u^*| \le 0$ and $(1 - \alpha_2)\,|v - v^*| \le 0$. Since $0 < \alpha_i < 1,\ i = 1, 2$, then $|u - u^*| = 0$ and $|v - v^*| = 0$ implies, $u = u^*$, $v = v^*$ and this completes the proof.

Now, to prove the convergence of the Picard iteration method, we will rewrite the equations Eqs. (12) $\sim$ (13) in the operator form as follows

$$u_n = A_1[u_{n-1}], \qquad v_n = A_2[v_{n-1}], \tag{15}$$

where the operators A_1 and A_2 take the following forms

$$A_1\,[u] = \int_0^t [R_1\,u + N_1(u) + F_1(u, v)\,]\,d\tau, \tag{16}$$

$$A_2\,[v] = \int_0^t [R_2\,v + N_2(v) + F_2(u, v)\,]\,d\tau. \tag{17}$$

Theorem 2. *(Convergence theorem) Assume that X be a Banach space and $A_i : X \to X$, $(i = 1, 2)$ are nonlinear mappings, and suppose that*

$$||\,A_i[u] - A_i[v]\,|| \le \alpha_i\,||u - v||, \quad \forall\ u, v \in X. \tag{18}$$

Then A_i, $(i = 1, 2)$ have unique fixed point. Furthermore, the sequences Eqs. (16) $\sim$ (17) using PIM with an arbitrary choice of u_0, $v_0 \in X$, converge to the fixed point of A_i and

$$||u_n - u_m|| \le \frac{\alpha_1^m}{1 - \alpha_1}\,||u_1 - u_0||, \tag{19}$$

$$||v_n - v_m|| \le \frac{\alpha_2^m}{1 - \alpha_2}\,||v_1 - v_0||. \tag{20}$$

Proof. Denoting $(C[J], ||.||)$ Banach space of all continuous functions on J with the norm defined by

$$||f(t)|| = \max_{t \in J} |f(t)|.$$

We are going to prove that the sequence $\{u_n\}$ is a Cauchy sequence in this Banach space

$$\begin{aligned}\|u_n - u_m\| &= \max_{t\in J} \mid u_n - u_m \mid \\ &= \max_{t\in J} \Big| \int_0^t [\, R_1\,(u_{n-1} - u_{m-1}) + N_1(u_{n-1}) - N_1(u_{m-1}) + F_1(u_{n-1}, v) - F_1(u_{m-1}, v)\,]\, d\tau \Big| \\ &\le \max_{t\in J} \int_0^t [\, |R_1\,(u_{n-1} - u_{m-1})| + |N_1(u_{n-1}) - N_1(u_{m-1})| + |F_1(u_{n-1}, v) - F_1(u_{m-1}, v)|\,]\, d\tau \\ &\le \max_{t\in J} \int_0^t [\, (m_1 + r_1 + s_1)(u_{n-1} - u_{m-1})\,]\, d\tau \\ &\le \alpha_1 ||u_{n-1} - u_{m-1}||.\end{aligned}$$

Let, $n = m + 1$ then

$$\|u_{m+1} - u_m\| \le \alpha_1 \|u_m - u_{m-1}\| \le \alpha_1^2 \|u_{m-1} - u_{m-2}\| \le \cdots \le \alpha_1^m \|u_1 - u_0\|.$$

From the triangle inequality we have

$$\begin{aligned}||u_n - u_m|| &\le ||u_{m+1} - u_m|| + ||u_{m+2} - u_{m+1}|| + ... + ||u_n - u_{n-1}|| \\ &\le [\, \alpha_1^m + \alpha_1^{m+1} + ... + \alpha_1^{n-1}\,]\, ||u_1 - u_0|| \\ &\le \alpha_1^m [\, 1 + \alpha_1 + \alpha_1^2 + ... + \alpha_1^{n-m-1}\,]\, ||u_1 - u_0|| \\ &\le \alpha_1^m [\, \frac{1 - \alpha_1^{n-m-1}}{1 - \alpha_1}\,]\, ||u_1 - u_0||.\end{aligned}$$

Since $0 < \alpha_1 < 1$ so, $(1 - \alpha_1^{n-m-1}) < 1$ then

$$||u_n - u_m|| \le \frac{\alpha_1^m}{1 - \alpha_1} ||u_1 - u_0||.$$

But $||u_1 - u_0|| < \infty$ so, as $m \to \infty$ then $||u_n - u_m|| \to 0$. We conclude that $\{u_n\}$ is a Cauchy sequence in $C[J]$ so, the sequence converges. Also, by the same way, we can prove the convergence of the sequence in equation Eq. (15) and obtain the relation Eq. (20) and this ends the proof of the theorem.

Theorem 3. *(Error estimate theorem)*

The maximum absolute errors of the approximate solutions u_n and v_n to Eqs. (10) and (11) is estimated to be

$$\max_{t\in J} |u_{exact} - u_n| \le \beta_1, \tag{21}$$

$$\max_{t\in J} |v_{exact} - v_n| \le \beta_2, \tag{22}$$

where $\beta_1 = \frac{\alpha_1^m T[m_1||u_0|| + h_1 + k_1]}{1-\alpha_1}$ *and* $\beta_2 = \frac{\alpha_2^m T[m_2||v_0|| + h_2 + k_2]}{1-\alpha_2}$,
$h_1 = \max_{t\in J} |N_1(u_0)$, $h_2 = \max_{t\in J} |N_2(v_0)|$, *and* $k_i = \max_{t\in J} |F_i(u_0, v_0)|, \quad (i = 1, 2)$.

Proof. From Theorem 2 and inequality Eq. (19), we have

$$||u_n - u_m|| \le \frac{\alpha_1^m}{1 - \alpha_1} ||u_1 - u_0||,$$

as $n \to \infty$ then $u_n \to u_{\text{exact}}$ and

$$\begin{aligned}||u_1 - u_0|| &= \max_{t\in J} \Big| \int_0^t [\, R_1\, u_0 + N_1(u_0) + F_1(u_0, v_0)\,]\, d\tau \Big| \\ &\le \max_{t\in J} \int_0^t [\, |R_1\, u_0| + |N_1(u_0)| + |F_1(u_0, v_0)|\,]\, d\tau\end{aligned}$$

$$\leq T\,[\,m_1\,||u_0||+h_1+k_1\,],$$

$$||v_1-v_0||=\max_{t\in J}\Big|\int_0^t[\,R_2\,v_0+N_2(v_0)+F_2(u_0,v_0)\,]\,d\tau\Big|$$

$$\leq \max_{t\in J}\int_0^t[\,|R_2\,v_0|+|N_2(v_0)|+|F_2(u_0,v_0)|\,]\,d\tau$$

$$\leq T\,[\,m_2\,||v_0||+h_2+k_2\,],$$

so, the maximum absolute errors in the interval J are

$$||u_{\text{exact}}-u_n||=\max_{t\in J}|u_{\text{exact}}-u_n|\leq\beta_1,\quad ||v_{\text{exact}}-v_n||=\max_{t\in J}|v_{\text{exact}}-v_n|\leq\beta_2.$$

This completes the proof.

Now, we present some basic definition of the Padé approximation (PA), which needed in the next sections of the paper.

4 The padé approximation on the series solution

The general setup in approximation theory is that a function f is given and that one wants to approximate it with a simpler function g but in such a way that the difference between f and g is small. The advantage is that the simpler function g can be handled without too many difficulties, but the disadvantage is that one loses some information since f and g are different.

Definition 1. *When we obtain the truncated series solution of order at least $L+M$ in t by PIM, we will use it to obtain Padé approximation $PA[L/M](t)$ for the solution $u(t)$. The Padé approximation [?] is a particular type of rational fraction approximation to the value of the function. The idea is to match the Taylor series expansion as far as possible. We denote the $PA[L/M]$ to $R(t)=\sum_{i=0}^{\infty}a_i\,t^i$ by*

$$PA[L/M](t)=\frac{P_L(t)}{Q_M(t)},\tag{23}$$

where $P_L(t)$ is a polynomial of degree at most L and $Q_M(t)$ is a polynomial of degree at most M,

$$P_L(t)=p_0+p_1\,t+p_2\,t^2+...+p_L\,t^L,\qquad Q_M(t)=1+q_1\,t+q_2\,t^2+...+q_M\,t^M.\tag{24}$$

Each choice of L, degree of the numerator and M, degree of the denominator, leads to an approximation. The major difficulty in applying the technique is how to direct the choice in order to obtain the best approximation. This needs the use of a criterion for the choice depending on the shape of the solution. A criterion which has worked well here is the choice of $[L/M]$ approximation such that $L=M$. We construct the approximation by built-in utilities of Mathematica in the following sections. If PIM truncated Taylor series of the exact solution with enough terms and the solution can be written as the ratio of two polynomials with no common factors, then the Padé approximation for the truncated series provides the exact solution. Even when the exact solution cannot be expressed as the ratio of two polynomials, the Padé approximation for the PIM truncated series usually greatly improve the accuracy and enlarge the convergence domain of the solutions.

5 The modified algorithm of pim

In spite of the advantages of PIM, it has some drawbacks. By using PIM, we get a series, in practice a truncated sequence solution. The series often coincides with the Taylor expansion of the true solution at point $t=0$, in the initial value case. Although the series can be rapidly convergent in a very small region, it has very slow convergence rate in the wider region we examine and the truncated series solution is an inaccurate

solution in that region, which will greatly restrict the application area of the method. All the truncated series solutions have the same problem. Many examples given can be used to support this assertion[24].

In this section, we present a modification of PIM by using the Padé approximation and then apply this modification to some systems of NODEs such as, nonlinear system of biochemical reaction model. The suggested modification of PIM can be done by using the following algorithm.

Algorithm

Step 1. Solve the differential equation using standard PIM;

Step 2. Truncate the obtained sequence solution by using PIM;

Step 3. Find the Padé approximation of the previous step.

This modification often gets the solution with excellent agreement with the exact solution of the differential equation and enlarge the convergence domain of the truncated Taylor series and can improve greatly the convergence rate of the truncated Taylor series.

6 Picard-padé-technique to nonlinear biochemical reaction model

In this section, we implement the Picard-Padé-technique for solving nonlinear biochemical reaction model Eqs. (7) $\sim$ (9).

Step 1. Solve the system Eqs. (7) $\sim$ (8) by using PIM;

According to PIM, we construct the following recurrence formula

$$u_{n+1}(t) = u(0) + \int_0^t [-u_n + (\beta - \alpha)v_n + u_n v_n]d\tau, \tag{25}$$

$$v_{n+1}(t) = v(0) + \int_0^t [\frac{1}{\gamma}(u_n - \beta\, v_n - u_n v_n)]d\tau. \tag{26}$$

Using the above formula, we can obtain the components of the solution of Eqs. (7) $\sim$ (8) at $\alpha = 0.375,\ \beta = 1,$ and $\gamma = 0.1$:

$u_0(t) = 1, \quad u_1(t) = 1 - t, \quad u_2(t) = 1 - t + 8.625\, t^2 - 3.33333\, t^3,$

$u_3(t) = 1 - t + 8.625\, t^2 - 63.0833\, t^3 + 62.1875\, t^4 - 194.458\, t^5 + 106.25\, t^6 - 15.873\, t^7, ...$

$v_0(t) = 0, \quad v_1(t) = 10\, t, \quad v_2(t) = 10\, t - 105\, t^2 + 33.3333\, t^3,$

$v_3(t) = 10\, t - 105\, t^2 + 762.083\, t^3 - 653.125\, t^4 + 1944.58\, t^5 - 1062.5\, t^6 + 158.73\, t^7, ...$ Therefore, the complete approximate solution can be readily obtained by the same iterative process.

Step 2. Truncate the series solution obtained by PIM;

We have applied the method by using ten-iterations only, i.e. the approximate solutions are:

$$u(t) \cong u_{10}(t) = 1 - t + 8.625t^2 - 63.0833t^3 + 373.18t^4 - 1979.38t^5 + 10156.3t^6 - \ldots - 1.04289 \times 10^{94} t^{1023}, \tag{27}$$

$$v(t) \cong v_{10}(t) = 10t - 105t^2 + 762.083t^3 - 4446.25t^4 + 23128.4t^5 - 116018t^6 + \ldots + 1.04289 \times 10^{95} t^{1023} \tag{28}$$

Step 3. Find the Padé approximation of the previous step;

The $PA[5/5]$ of $u_{10}(t)$ and $v_{10}(t)$ respectively are

$$PA[5/5](u_{10}(t)) = \frac{1 + 8.94633\, t + 36.5182\, t^2 + 66.6104\, t^3 + 54.4863\, t^4 - 27.6561\, t^5}{1 + 9.94633\, t + 37.8395\, t^2 + 81.7462\, t^3 + 64.1346\, t^4 - 13.9321\, t^5},$$

$$PA[5/5](v_{10}(t)) = \frac{10\, t + 16.744\, t^2 + 114.282\, t^3 + 154.241\, t^4 + 118.571\, t^5}{1 + 12.1744\, t + 63.0511\, t^2 + 194.294\, t^3 + 347.13\, t^4 + 316.443\, t^5}.$$

The results of the above example show that our method was capable for solving the problems and generates improves the convergence rate of the PIM, and that it often is in excellent agreement to their solutions.

Fig. 1 presents the approximate solutions of $u(t)$ (Top) and $v(t)$ (Bottom) using the standard PIM with 10-iterations. From this figure, we can conclude that the standard method is failed for solving the proposed model. But, the Fig. 2 presents the approximate solutions of $u(t)$ (Top) and $v(t)$ (Bottom) using our method, where we computed $PA[5/5]$ of $u(t)$ and $v(t)$. Also, a comparison with the numerical method, fourth-order Runge-Kutta is done. From these figures, we can see that the two methods are in excellent agreement.

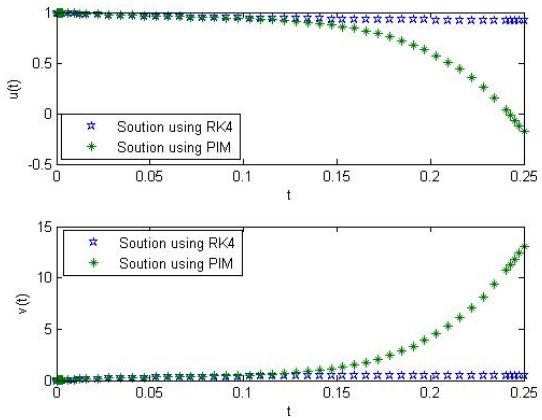

Fig. 1. The solutions $u(t)$ (Top) and $v(t)$ (Bottom) using 10-terms of PIM

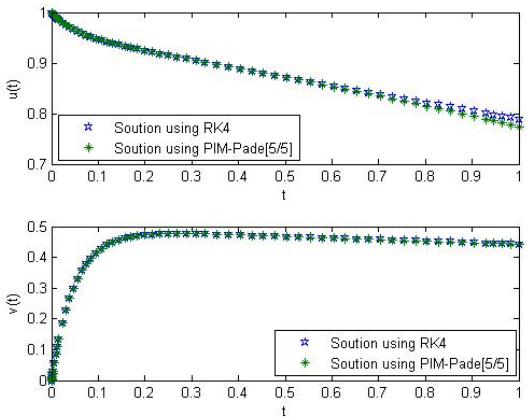

Fig. 2. The solutions $u(t)$(Top) and $v(t)$(Bottom) using [5/5] Padé-PIM and RK4 ($\Delta t = 0.001$)

7 Concluding remarks and discussion

This paper centralized on a newly modified version of PIM, which is generally called the Picard-Padé technique and we presented comparative solutions with PIM and the numerical method, fourth-order Runge-Kutta method. We chose the conventional RK4 as our benchmark, as it is widely accepted and used. The proposed possesses a time marching algorithm which speeds the convergence of the solutions rapidly. This analysis shows that Picard-Padé technique has much impact on the accuracy and efficiency of the solution on this basic enzyme kinetics scheme. We found that the traditional PIM was not efficient and sufficient to solve the problem. On the other hand, the numeric-analytic Picard-Padé showed good parity against PIM, but with results conforming only for a short period of time $t \in [0, 1]$. Its long term efficacy is unknown for this system. We conclude that Picard-Padé technique is a very reliable method for solving a broad array of applications in science and engineering due to its consistency used in a longer time frame. The analytical approximation to the solutions is reliable, and confirms the power and ability of the Picard-Padé technique as an easy device for computing the solution of ordinary differential equations. Special attention is given to study the convergence analysis of the proposed method. In the future, we will modified and treatment this modification to implement it to solve the nonlinear fractional system of biochemical reaction. All computations in this paper are done using Matlab 8.

References

[1] S. Abbasbandy. A numerical solution of Blasius equation by Adomian's decomposition method and comparison with HPM. *Chaos, Solitons and Fractals*, 2007, **31**: 257-260.

[2] T. Abassy, M. El-Tawil, H. El Zoheiry. Solving nonlinear partial differential equations using the modified variational iteration Padé technique. *Journal of Computational and Applied Mathematics* 2007, **207**:73-91.

[3] R. Agarwal, M. Meehan, D. O'Regan. Fixed Point Theory and Applications. Cambridge University Press, New York, 2001.

[4] G. Jr. Baker. *Essentials of Padé Approximants.* in Academic Press, 1975.

[5] J. Biazar, H. Ghazvini. He's variational iteration method for solving hyperbolic differential equations. *International Journal of Nonlinear Sciences and Numerical Simulation* 2007, **8**(3):311-314.

[6] D. Ganji. The application of He's homotopy perturbation method to nonlinear equations arising in heat transfer. *Physics Letters A*, 2006, **355**:337-341.

[7] S. Goha, M. Noorani, I. Hashim. Introducing variational iteration method to a biochemical reaction model. *Nonlinear Analysis: Real World Applications.* 2010, **11**:2264-2272.

[8] I. Hashim, M. Chowdhurly, S. Mawa. On multistage homotopy perturbation method applied to nonlinear biochemical reaction model. *Chaos, Solitons and Fractals,* 2008, **36**:823-827.

[9] J. He. Variational iteration method for autonomous ordinary differential systems. *Applied Mathematics and Computation*, 2000, **114**(2-3):115-123.

[10] J. He. Homotopy perturbation technique. *Comput. Methods Appl. Mech. Engng.,* 1999, **178**(3-4):257-262.

[11] W. Kelley, A. Petterson. *The Theory of Differential Equations: Classical and Qualitative.* Pearson Education Inc., Upper Saddle River, NJ, 2004.
[12] E. Kreyszig. *Introductory Functional Analysis with Applications,* John Wiley & Sons, New York, 1989.
[13] S. Liao. Comparison between the homotopy analysis method and homotopy perturbation method. *Applied Mathematics and Computation.*, 2005, **169**:1186-1194.
[14] A. Nayfeh. *Perturbation Methods*. John Wiley & Sons, New York, 1973.
[15] J. Ramos. On the Picard-Lindelof method for nonlinear second-order differential equations. *Applied Mathematics and Computation*, 2008. **203**:238-242.
[16] J. Ramos. A non-iterative derivative-free method for nonlinear ordinary differential equations. *Applied Mathematics and Computation,* 2008, **203**:672-678.
[17] J. Ramos. Picard's iterative method for nonlinear advection-reaction-diffusion equations. *Applied Mathematics and Computation*, 2009, **215**:1526-1536.
[18] S. Schnell, C. Mendoza. Closed form solution for time-dependent enzyme kinetics. *Journal of Theoret. Biol.*, 1997, **187**:207-212.
[19] A. Sen. An application of the Adomian decomposition method to the transient behavior of a model biochemical reaction. *Journal of Math. Anal. Appl.*, 1998, **131**:232-245.
[20] N. Sweilam, M. Khader. Variational iteration method for one dimensional nonlinear thermoelasticity. *Chaos, Solitons and Fractals,* 2007, **32**:145-149.
[21] N. Sweilam, M. Khader. Exact solutions of some coupled nonlinear partial differential equations using the homotopy perturbation method. *Computers and Mathematics with Applications,* 2009, **58**:2134-2141.
[22] N. Sweilam, M. Khader, R. Al-Bar. Homotopy perturbation method for multi-dimensional nonlinear coupled system of parabolic and hyperbolic equations. *Topological Methods in Nonlinear Analysis,* 2008, **31**:295-304.
[23] N. Sweilam, M. Khader. On the convergence of VIM for nonlinear coupled system of partial differential equations. *Int. Journal of Computer Maths.,* 2010, **87**(5): 1120-1130.
[24] A. Wazwaz. A comparison between Adomian decomposition method and Taylor series method in the series solution. *Applied Mathematics and Computation.* 1998, **97**:37-44.
[25] P. Yang, Y. Chen, Z. Li. ADM-Padé technique for the nonlinear lattice equations. *Applied Mathematics and Computation,* 2009, **210**:362-375.