A Hybrid Method with RDTM for Solving the Biological Population Model

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Abstract

In this paper, we establish an analytical solution to the non-linear biological population model using a hybrid method that combines a reduced differential transform method with a resummation method based on Yang transform and a Padé approximant. The proposed method significantly improves the approximate solution series and broadens the convergence field, It is also dependent on a few straightforward steps, and does not depend on a perturbation parameter or produce secular terms. Three examples are given to test the effectiveness, accuracy, and performance of the suggested method. The results and graph demonstrate that the suggested method is successful and more accurate than other methods. In addition, PYRDTM is a useful tool with great potential for solving nonlinear BPM.

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1-Introduction

A biological population model (BPM) is a degenerate non-linear partial differential equation, which represents the distribution of population density in an area and it Written in the following form:

 $u(x, y, 0) = f(x, y),$ (2)

where $t > 0$, $x, y \in R$ (set of real numbers) and $u(x, y, t)$ denotes the population density and $f(u)$ represents the population supply due to births and deaths. Also, $f(u) = pu^a(1 - ru^b)$ with h, a, r, b are real numbers. If we take special value of numbers then

(i) For $f(u) = c u$, c (constant), we get Malthusian Law.

(ii) For $f(u) = c_1 u - c_2 u^2$ where c_1, c_2 are positive constants, we get Verhulst Law.

(iii) For $f(u) = -cu^n$, $(c \ge 0, 0 < n < 1)$ we get Parous Media.

There is a substantial body of work on biological population models which are resolved utilizing various numerical and analytical methodologies, such as: Liu et al. [1] employed the homotopy perturbation method for solve fractional biological population equation. Arafa, et. al. [2] utilized the homotopy analysis method (HAM). Shakeri, and Dehghan, [3] employed He's variational iteration method. Srivastava et al.[4] applied the fractional reduced transform method to study analytical solutions for time-fractional order population problems . The BPM model's numerical computation is performed by Cheng et al.[5]used element-free KP-Ritz method. Zhang et. al. [6] used the improved element-free Galerkin method (IEFGM). Brajesh Kumar [7] proposed the modified cubic B-spline differential quadrature method (MCB-DQM) to solve the two-dimensional BPM. The methods researchers use to solve the present problem, which we mentioned earlier, have many benefits. Still, there are also some disadvantages, such as the large number of iterations required to find an exact solution to the current problem. These methods also take a lot of time and effort to complete solution to the issues. There are several analytical approaches for example, the RDTM is a useful tool because it doesn't need a perturbation parameter. In 2009, the Turkish mathematician Keskin [8] proposed RDTM for the first time. It has drawn a lot of attention because several authors [9–16] have utilized it to find solutions to a variety of issues.Also the Yang transformation is suggested by Xiao-Jun Yang in 2016, which is applied to solve the steady heat transfer problem [17]. Henri Padé (1863- 1953) presented an approximation technique in his doctoral thesis in 1892 which is called Padé approximation. It has received much attention since it has been applied to solve a wide variety of problems by many authors[18-20]. In this paper, we will present a hybrid method that combines (Reduced differential transform method ,Yang transform, and Padé approximate to find analytic approximate solutions of nonlinear BPM. The solution to BPM is obtained in convergent series forms using YRDTM. After that, we create its Pad'e approximant of an order $[N/M]$ to convert the power series solution obtained by YRDTM into a meromorphic function. The values for N and M are selected at random. In this stage, the Pad's approximant improves the accuracy and convergence of the truncated series solution by expanding the domain of that solution. This is an method that we name PYRDTM. One of the advantages of the suggested method is that it reduces the number of iterations required to find approximate analytical solutions,and the time and effort required to solve the non-linear issue. The most

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important aspect of this study is that the suggested method significantly enhances the convergence rate of RDTM's truncated series solutions. This study aims to use the PYRDTM to solve a non-linear BPM and compare its efficiency and accuracy to other methods (ADM, VIM, and MCB-DQM). The numerical results demonstrated PYRDTM efficiency, activity, and accuracy in solving the non-linear biological population model.

2. Reduced differential transform method:

In 2009, the Turkish mathematician Keskin[8], suggested the reduced differential transform method (RDTM), to stdiy the analytical solutions of linear and non-linear wave equation. The following are the basic definitions and operations of the two-dimensional reduced differential transform method [11][12][21]:

Definition 2.1

"If function $u(x, y, t)$ is analytic and differentiated continuously with respect to time and space in the domain of interest, then let .

$$
U_k(x,y) = \frac{1}{k!} \left[\frac{\partial^k}{\partial t^k} u(x,y,t) \right]_{t=0},
$$
\n(3)

where the t-dimensional spectrum function $U_k(x, y)$ is the transformed function in this work, the lower case $u(x, y, t)$ represents the original function while the upper case $U_k(x, y)$ represents the transformed function". Definition 2.2

when the tail function $R_m(x, y, t)$ is insignificant. As a result, the exact solution to the problem is $u(x, y, t) = \lim_{m \to \infty} u_m(x, y, t)^n$. (7)

Table I: The fundamental operations of RDTM

3. Yang Transform

The integral transforms play a significant role in a variety of scientific disciplines and works of literature; they are used extensively in mathematical physics, optics, mathematical engineering, and other disciplines to solve differential equations such as those of Laplace, Fourier, Mellin, Hankel, and Sumudu. Recently, Xiao-Jun Yang[17] suggested a novel integral transform named the Yang Transform, It was initially used for the equation for steady-state heat transfer. Yang transform of function $u(t)$ is denoted by $Y\{u(t)\}$ or $T(s)$ and is defined as $Y[u(t)] = T(s) = \int_0^\infty$ $\int_{0}^{\infty} e^{-\frac{t}{s}} u(t) dt, t > 0.$ (8) Provided the integral exists for some *s*, where $s \in (-t_1, t_2)$.

If we substitute $\frac{-t}{s} = x$ then equation (8) becomes, $Y[u(t)] = T(s) = s \int_0^\infty$ $\int_{0}^{\infty} e^{-x} u(s \, x) dx, x > 0.$ (9)

3.1 Yang Transform of Derivatives : Theorem (1): Yang Transform of Derivatives [17] If $Y[u(t)] = T(u)$ then

1)
$$
Y\left[\frac{\partial u(x,t)}{\partial t}\right] = \frac{T(x,s)}{u} - u(x,0),
$$

\n2) $Y\left[\frac{\partial^2 u(x,t)}{\partial t^2}\right] = \frac{T(x,s)}{s^2} - \frac{u(x,0)}{s} - \frac{\partial u(x,0)}{\partial t},$
\n3) $Y\left[\frac{\partial^n u(x,t)}{\partial t^n}\right] = \frac{T(x,s)}{s^n} - \sum_{k=0}^{n-1} s^{-n+k+1} \frac{\partial^{(k)} u(x,0)}{\partial t^k} \quad \forall n = 1,2,3,4,...$

3.2. Yang Transform of some functions [17]:

Yang transform of some useful functions is given below.

1) $Y{1} = s$ 2) $Y(t) = s^2$ $3) Y(t^n) = n! \cdot s^{n+1}$ 4) $Y\{e^{at}\} = \frac{s}{1}$ 5) Y {sin αt } = $\frac{\alpha s^2}{1 + \alpha^2 s^2}$ 6) $Y\{\cos \alpha t\} = \frac{1+\frac{1}{s}}{1+\alpha^2 s^2}$ 7) $Y\{\sin \alpha t\} = \frac{\alpha s^2}{1 - \alpha^2 s^2}$
8) $Y\{\cos \alpha t\} = \frac{1 - \alpha^2 s^2}{1 - \alpha^2 s^2}$

4. The Padé approximants

Assume we are given a power series $\sum_{r=0}^{\infty} c_r x^r$, representing a function $f(x)$, so that $f(x) = \sum_{r=0}^{\infty} c_r x^r$, (10) The Padé approximant is a rational fraction, it is denoted by the formula [18] $[L/M] = \frac{A_L(\chi)}{B_M(\chi)}$, (11)

where $A_L(x)$ is a polynomial of degree at most Land $B_M(x)$ is a polynomial of degree at most M.We have $f(x) = c_0 + c_1 x + c_2 x^2 + c_3 x^3 + c_4 x^4 + \cdots,$ $A_L(x) = a_0 + a_1 x + a_2 x^2 + a_3 x^3 + \dots + a_L x^L,$ (12)

 $B_M(x) = b_0 + b_1 x + b_2 x^2 + b_3 x^3 + \dots + b_M x^M$, there are $L + 1$ numerator coefficients and $M + 1$ denominator coefficients in Eq. (11). We impose the normalizing condition because we container obviously multiply the numerator and denominator by a constant while leaving $[L, M]$ unaltered

$$
B_M(0) = 1.\tag{13}
$$

As a result, there are $L + 1$ independent numerator coefficients and M independent denominator coefficients, for a total of $L + M + 1$ unknown coefficients. This number implies that the [L, M] should generally fit the power series (10) through the orders $1, x, x^2, ..., x^{(L+M)}$. Using the conclusion from [18]. We already known that the $[L, M]$ approximation is unique.

$$
\sum_{r=0}^{\infty} c_r x^r = \frac{a_0 + a_1 x + a_2 x^2 + \dots + a_L x^L}{b_0 + b_1 x + b_2 x^2 + \dots + b_M x^M} + O(x^{L+M+1}).
$$
\n(14)

Using cross-multiplying Eq. (14), we found that

 $(a_0 + a_1x + a_2x^2 + \cdots + a_1x^1)(c_0 + c_1x + c_2x^2 + c_3x^3 + c_4x^4 + \cdots) = b_0 + b_1x + b_2x^2 + \cdots + b_Mx^M$ $O(x^{L+M+1})$. $\binom{L+M+1}{2}$. (15)

From Eq. (15), the set of equations can be found.

$$
\begin{cases}\nc_0 = a_0, \\
c_1 + c_0 b_1 = a_1, \\
c_2 + c_1 b_1 + c_0 b_2 = a_2, \\
\vdots \\
c_L + a_{L-1} b_1 + \dots + c_0 b_L = a_L,\n\end{cases}
$$
\n(16)

൞ $c_{L+1} + c_L b_1 + \dots + c_{L-M+1} b_M = 0,$ $c_{L+2} + c_{L+1}b_1 + \cdots + c_{L-M+2}b_M = 0,$ ⋮ $c_{L+M} + c_{L+M-1}b_1 + \cdots + c_L b_M = 0,$ (17) where $c_n = 0$ for $n < 0$ and $b_i = 0$ for $j > M$. If Eqs.(16),and(17) are nonsingular, then we can solve them directly
 a_{L-m+1} a_{L-m+2} a_{L+1} a_{L-m+2}

$$
[L/M] = \frac{\left|\sum_{j=M}^{L} a_{j-M} \chi^{j} \sum_{j=M-1}^{L} a_{j-M+1} \chi^{j} \cdots \sum_{j=0}^{L} a_{j} \chi^{j}\right|}{\left|\begin{array}{c} a_{L-m+1} & a_{L-m+2} & \cdots & a_{L+1} \\ \vdots & \vdots & \ddots & \vdots \\ a_{L+1} & a_{L+1} & \cdots & a_{L+M} \\ \chi^{M} & \chi^{M-1} & \cdots & 1 \end{array}\right|}.
$$

If the lower index of a sum is greater than the higher index, the sum is replaced by zero. Alternative forms include $I - M$ $l+n$

$$
[L/M] = \sum_{j=0} c_j x^j + x^{L-M+1} w_{L/M}^T W_{L/M}^{-1} w_{L/M} = \sum_{j=0} c_j x^j + x^{L+n+1} w_{(L+M)/M}^T W_{L/M}^{-1} w_{(L+n)/M}
$$
 for

$$
W_{L/M} = \begin{bmatrix} c_{L-M+1} - \chi c_{L-M+2} & \cdots & c_{L} - \chi c_{L+1} \\ \vdots & \ddots & \vdots \\ c_{L} - \chi c_{L+1} & \cdots & c_{L+M+1} - \chi c_{L+M} \end{bmatrix},
$$

\n
$$
W_{L/M} = \begin{bmatrix} c_{L-M+1} \\ c_{L-M+2} \\ \vdots \\ c_{L} \end{bmatrix}.
$$

The construction [L/M] of approximants can be made only by algebraic operations [18]. Each choice of L degree numerator and M degree denominator results in approximation. How to steer the choice to produce the best approximation is the technique's main point of difficulty. This necessitates the application of a selection criterion that is based on the solution's shape. The choice of $[L/M]$ approximants has proven to be a useful criterion in this situation.

5. The hybrid method algorithm.

Consider a typical nonlinear nonhomogeneous partial differential equation with initial conditions of the form: $Lu(x, y, t) + Ru(x, y, t) + Nu(x, y, t) = g(x, y, t),$ (20) with initial condition $u(x, y, 0) = h(x, y)$, (21)

where, L and R are a linear differential operators, N is a non-linear operator and $g(x, y, t)$ is an inhomogeneous term. Taking Yang transform on both sides of equation(20), to get:

 $Y[Lu(x, y, t)] + Y[Ru(x, y, t)] + Y[Nu(x, y, t)] = Y[g(x, y, t)].$ (22)

Using the differentiation property of Yang transforms(2.3) and above initial conditions, we have:

 $Y[u(x, y, t)] = sY[g(x, y, t)] + sh(x, y) - sY[Ru(x, y, t) + Nu(x, y, t)]$, (23) applying the inverse Yang transform on both sides of equation (23), to find:

 $u(x, y, t) = G(x, y, t) - Y^{-1}\{sY[Ru(x, y, t) + Nu(x, y, t)]\},\$

where $G(x, y, t)$ denotes for the term derived from the source term and the required initial conditions. Now, we apply reduced differential transform method:

 $U(x, y, 0) = G(x, y, t),$ (24)

$$
U(x, y, k+1) = -Y^{-1}\{sY[RU(x, y, k) + NU(x, y, k)]\},
$$
\n(25)

where $RU(x, y, k)$, $NU(x, y, k)$ are reduced transformation of functions $Ru(x, y, t)$, $Nu(x, y, t)$, respectively. This is coupling of Yang transform and reduced differential transform method. Then by YRDTM we have the solution of Eq. (20), with initial condition (21) in the form of infinite series which converge to the exact solution as follows:

$$
u(x, y, t) = \sum_{k=0}^{\infty} U(x, y, k). \tag{26}
$$

After that, we applied its Pad'e approximant of an order $[N/M]$ on the power series solution obtained by using YRDTM. The values N and M are arbitrarily selected. In this stage, we get the final solution.

6.Application:

In this section, we examine three test example that illustrate PYRDTM performance, accuracy, and efficiency in solving nonlinear biological population models.

Example 1:

If we take
$$
p = \frac{1}{5}
$$
, $\alpha = 1$ and $r = 0$, in Eq.(1), this equation becomes
\n
$$
u(x, y, t) = (u^2)_{xx} + (u^2)_{yy} + \frac{1}{5}u,
$$
\n(27)

with initial condition $u(x, y, 0) = \omega^{\frac{1}{2}}$ \overline{z} . (28) where $\omega = xy$. By taking Yang transform on both side of Eq.(27), subject to initial condition (28),we obtain $Y[u(x, y, t)] = Su(0) + SY\left[(u^2)_{xx} + (u^2)_{yy} + \frac{1}{5} \right]$ By applying inverse Yang transform for Eq. (29), we obtain u . (29) $u(x, y, t) = u(0) + Y^{-1} \left(S Y \left[(u^2)_{xx} + (u^2)_{yy} + \frac{1}{5} \right] \right)$ $\frac{1}{5}u\rfloor$).

(30)

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Applying reduce differential transform method, we obtain

$$
U(x, y, k+1) = Y^{-1} \Big(SY \Big[\frac{\partial^2}{\partial x^2} \big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \big] + \frac{\partial^2}{\partial y^2} \big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \big] + \frac{1}{5} U(x, y, k) \Big],
$$
\n
$$
(31)
$$
\nwith $U(x, y, 0) = \omega^{\frac{1}{2}}$. (32)

$$
J(x, y, 0) = \omega^{\frac{1}{2}}.
$$
\n(32)

\nrelationing (31) (32) we obtain

From relationship(31), (32), we obtain $U(x, y, 0)$ = $\frac{1}{2}$

$$
U(x, y, 0) = \omega^2
$$

\n
$$
U(x, y, 1) = \frac{1}{5} \omega^{\frac{1}{2}} t
$$

\n
$$
U(x, y, 2) = \frac{1}{50} \omega^{\frac{1}{2}} t^2
$$

\n
$$
U(x, y, 3) = \frac{1}{750} \omega^{\frac{1}{2}} t^3
$$

$$
\mathcal{L} \subset \mathcal{L}
$$

the solutions series obtained by YRDTM is

$$
u(x, y, t) = \sum_{k=0}^{\infty} U_k(x, y, k) = \omega^{\frac{1}{2}} (1 + \frac{1}{5}t + \frac{1}{50}t^2 + \frac{1}{750}t^3 + \ldots) = \omega^{\frac{1}{2}} e^{\frac{1}{5}t} = \sqrt{xy} e^{\frac{1}{5}t}.
$$
\n(33)
\nNow, the $[L/M]t$ -Padé approximation of Eq. (33), with $L = 1, M = 6$,

$$
\left[\frac{L}{M}\right]_{u}(x,y,t) = \frac{2250000(\omega^{\frac{1}{2}}t + 35\omega^{\frac{1}{2}})}{t^6 - 60t^5 + 2250^4 - 60000t^3 + 1125000t^2 - 13500000t + 78}.
$$
\n(34)

Example 2

If we take $p = -1$, $\alpha = 1$, $r = -\frac{8}{9}$ $\frac{8}{9}$, and $b = 1$, in Eq.(1), this equation becomes $u(x, y, t) = (u^2)_{xx} + (u^2)_{yy} - u - \frac{8}{9}$ $\frac{8}{9}u^2$ $, \, (35)$ with initial condition $u(x, y, 0) = \omega$, (36)

where $\omega = e^{\frac{1}{3}(x+y)}$

. By taking Yang transform on both side of Eq.(35),subject to initial condition (36),we obtain $Y[u(x, y, t)] = Su(0) + SY\left[(u^2)_{xx} + (u^2)_{yy} - u - \frac{8}{9}\right]$ $\frac{8}{9}u^2$ $\vert . \vert$ (37)

By applying inverse Yang transform for Eq. (37), we obtain
\n
$$
u(x, y, t) = u(0) + Y^{-1} \left(S Y \left[(u^2)_{xx} + (u^2)_{yy} - u - \frac{8}{9} u^2 \right] \right).
$$
\n(38)

Applying reduce differential transform method on Eq.(38), we obtain

$$
U(x, y, k+1) = Y^{-1} \Big(SY \Big[\frac{\partial^2}{\partial x^2} \Big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \Big] + \frac{\partial^2}{\partial y^2} \Big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \Big] - U(x, y, k) - \frac{8}{9} \sum_{r=0}^k U(x, y, r) U(x, y, k-r) \Big],
$$
\n
$$
(39)
$$
\nwith $U(x, y, 0) = \omega$. (40)

From relationship(39), (40), we obtain $U(x, y, 0) = \omega,$ $U(x, y, 1) = -\omega t,$ $U(x, y, 2) = \frac{1}{2}$ $\frac{1}{2}\omega t^2$, $U(x, y, 3) = \frac{-1}{6} \omega t^3$,

The solutions series obtained by YRDTM is

$$
u(x, y, t) = \sum_{k=0}^{\infty} U(x, y, k) = \omega \left(1 - t + \frac{1}{2} t^2 - \frac{1}{6} t^3 \dots \right) = \omega e^{-t} = e^{\frac{1}{3}(x+y)-t}.
$$

Now, the $[L/M]t$ -Padé approximation of (41), with $L = 1, M = 6$, is

$$
\left[\frac{L}{M}\right]_{u}(x, y, t) = \frac{720(-\omega t + 7\omega)}{t^{6} + 12t^{5} + 90t^{4} + 480t^{3} + 1800^{2} + 4320t + 5040} \tag{42}
$$

Example 3

If we take $p = \frac{1}{\gamma}$ $\frac{1}{96}$, $\alpha = -1$, $r = 48$, and $b = 1$, in Eq.(1), we have the following biological population equation $u(x, y, t) = (u^2)_{xx} + (u^2)_{yy} + \frac{1}{96}$ $rac{1}{96}u^{-1} - \frac{1}{2}$ 2^{3} (43)

with initial condition
$$
u(x, y, 0) = \frac{1}{4} \omega^{\frac{1}{2}}
$$
,
where $\omega = 2x^2 + y(2y + 1) + 5$. (44)

By taking Yang transform on both side of Eq.(43) subject to initial condition (44),we obtain $Y[u(x, y, t)] = Su(0) + SY\left[(u^2)_{xx} + (u^2)_{yy} + \frac{1}{96}\right]$ $rac{1}{96}u^{-1} - \frac{1}{2}$ 2. $\left| . \right|$. (45)

By applying inverse Yang transform for Eq. (45), we obtain
\n
$$
u(x, y, t) = u(0) + Y^{-1} \left(S Y \left[(u^2)_{xx} + (u^2)_{yy} + \frac{1}{96} u^{-1} - \frac{1}{2} \right] \right).
$$
\n(46)

Applying reduce differential transform method, we have

$$
U(x, y, k+1) = Y^{-1} \Big(SY \Big[\frac{\partial^2}{\partial x^2} \Big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \Big] + \frac{\partial^2}{\partial y^2} \Big[\sum_{r=0}^k U(x, y, r) U(x, y, k-r) \Big] +
$$

\n
$$
\frac{1}{96} A_k - \frac{1}{2} \delta(k) \Big] \Big),
$$

\nwhere A_k is transformation of the nonlinear term u^{-1} are as follow; (47)

where A_k is transformation of the nonlinear term u $A_0 = (U(x, y, 0))^{-1}$,

$$
A_1 = -(U(x, y, 0))^{-2}U(x, y, 1),
$$

\n
$$
\vdots
$$

\nwith $U(x, y, 0) = \frac{1}{4}\omega^{\frac{1}{2}}.$
\nFrom relationships (47), (48), we have
\n
$$
U(x, y, 0) = \frac{1}{4}\omega^{\frac{1}{2}}.
$$

\n
$$
U(x, y, 1) = \frac{1}{24}\omega^{\frac{-1}{2}}t,
$$
\n(48)

The solutions series obtained by YRDTM is $u(x, y, t) = \sum_{k=0}^{\infty} U_k(x, y, k) = \frac{1}{4}$ $\frac{1}{4} \omega^{\frac{1}{2}} + \frac{1}{24}$ $\frac{1}{24}\omega^{\frac{-1}{2}}t + \frac{-1}{288}\omega^{\frac{-3}{2}}t^2 + \cdots$ (49) Now, the $[L/M]t$ -Padé approximant of (49), with $L = 2, M = 1$, is $\frac{L}{M}$ $\frac{L}{M}\bigg]_u(x, y, t) = \frac{1}{48}$ ସ଼ $72\omega^2+24\omega t+t^2$ $6\omega^{\frac{3}{2}} + \omega^{\frac{1}{2}}t$. (50)

6. Discussions

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 $U(x, y, 2) = \frac{-1}{288} \omega^{\frac{-3}{2}} t^2,$

In this section, by solving three examples, we introduced the PYRDTM is a useful tool with a lot of potential for solving nonlinear BPM problems .We show the three-dimensional figures obtained by PYRDTM, we provide information for the errors between the numerical and analytical solutions of the non-linear BPM in tables and figures. Figs.(1-5) demonstrations the meticulous resolution, PYRDTM solve plus abselute errors at $(t = 0.1, 0.5)$ ", $(t = 0.1, 1)$, and $(t = 10, 20)$, respectively for examples 1,2 and 3. It should be note that all figures calculated at $[1/6]$ for examples1,2 implies at seven iteration and $[2/1]$ for example 3 implies at three iteration .Tables (1,2) illustrate a comparison of error and CPU time between RDTM, PYRDTM, and MCBS-DQM, the results shows that the L_2, L_∞ , and CPU time for PYRDTM are smaller than MCBS-DQM[23] with $\Delta t = 0.0001$ and $h_x = h_y = \frac{1}{15}$ $\frac{1}{12}$, and RDTM . Table 3 shows that L_2, L_∞ and CPU time for PYRDTM [2/1] at three iteration is better than MCBS-DQM[23] with $\Delta t = 0.0001$ and $h_x = h_y = 0.03,0.04$ at time 0.1,0.2 and 0.5 and RDTM. Table (4) shows that the PYRDTM $[2/1]$ at three iteration has absolute errors smaller than RDTM , ADM [3] ,and VTM [3] at time 10 and 20 .We note that L_2, L_{∞} for the series approximation solutions of the three examination examples computed by

$$
\| E \|_{L_2} = \sqrt{h^2 \sum_{i=0}^{M} \sum_{l=0}^{M} |\rho_{\text{exact}}(x, y) - \rho_{\text{approx}}(x, y)|^2},
$$

$$
\| E \|_{L_{\infty}} = \max_{u=0,1,M} (|\rho_{\text{exact}}(x, y) - \rho_{\text{approx}}(x, y)|).
$$

According to the calculations shown in the tables and figures, The PYRDTM procedures are very effective in resolving nonlinear BPM; the PYRDTM is the most efficient; it also provides high-precision solutions since it produces good results with few iterations of solutions and smaller errors with little CPU time.

8. Conclusion

In this research, the nonlinear BPM was successfully solved using the PYRDTM. This method, which we refer to as PYRDTM, significantly improves the convergence rate of RDTM truncated series solutions. The suggested method's key advantage is that it is dependent on a few simple stages and does not produce secular terms, and does not rely on a perturbation parameter.As a result, it is appropriate for engineers, especially those in mechanics, electronics, and electrical engineering. Three test examples demonstrate the method's efficiency and accuracy. The results show that PYRDTM is more efficient, accurate, and reliable than the methods (ADM, VIM, and MCB-DQM) [24][3][23]. Fur thermore, the plots of the novel solutions demonstrate the validity, utility, and necessity of the proposed approach.

Fig.1. (A) exact solution, (B) PYRDTM solution[1/6], (C) absolute error, at $t = 0.5$, $h = 0.05$, Example l.

Fig.2 (A) exact solution, (B) PYRDTM solution $[1/6]$, (C) absolute error, at $t = 0.1$, $h = 0.05$ Example l.

Fig.3. (A) exact solution, (B) PYRDTM solution[1/6], (C) absolute error, at $t = 0.1$, $h = 0.04$, Example 2.

Fig.4. (A) exact solution, (B) PYRDTM solution[1/6], (C) absolute error, at $t = 1$, $h = 0.04$, Example 2.

Fig.5. (A) exact solution, (B) PYRDTM solution $[2/1]$, (C) absolute error, at $t = 20$. Example 3.

Fig.6. (A) exact solution, (B) PYRDTM solution $[2/1]$, (C) absolute error, at $t = 10$. Example 3.

Table 1. Comparisun of error, and CPU time between MCBS-DQM ,and PYRDTM [1/6] ,with $h =$ $\mathbf 1$ $\frac{1}{12}$. Example 1.

	12							
	Method	Error	$t = 0.1$	$t=0.2$	$t = 0.3$	$t=0.4$	$t = 0.5$	$t=5$
		L ₂	$5.24E - 12$	$4.52E - 12$	$4.65E - 12$	$4.21 - 12$	$1.53E - 12$	$7.23E - 11$
	PYRDTM	L_{∞}	$1.00E - 11$	$1.00E-11$	$1.00 - 11$	$1.00E - 11$	$3.00E - 12$	$9.13E - 11$
		CPU(s)	0.016	0.016	0.016	0.016	0.016	0.016
		L ₂	$1.63E - 9$	$4.87E - 10$	$7.10E - 10$	$1.89E - 10$	$1.17E - 9$	$4.88E - 5$
	RDTM	L_{∞}	$2.00E - 9$	$6.16E - 5$				
		CPU(s)	0.61	0.61	0.781	0.657	0.641	0.641
	MCBS- DQM[23]	L ₂	$2.69 - 5$	$2.39E - 5$	$2.14E - 5$	$1.93E - 5$	$1.75E - 5$	$2.33E - 7$
		L_{∞}	$1.05E - 4$	$8.60E - 5$	$7.04E - 5$	$5.76E - 5$	$4.71E - 5$	$3.40E - 7$
		CPU(s)	0.33	0.64	0.96	1.29	1.58	15.17

Table2. Comparison of error and CPU time between MCBS-DQM and PYRDTM[1/19] ,with $h = \frac{1}{12}$. Example2.

Method	Error	$t=2$	$t=5$	$t=8$	$t=10$	
	L ₂	$2.43E - 9$	$1.00E - 5$	$1.18E - 3$	$1.38E - 2$	
PYRDTM	\mathbf{L}^{∞}	$4.48E - 9$	$1.85E - 5$	$2.17E - 3$	$2.54E - 2$	
	CPU	0.031	0.063	0.063	0.078	
RDTM	L ₂	$1.85E - 7$	$1.23E - 4$	$3.58E - 3$	$1.81E - 2$	
	∞	$3.42E - 7$	$2.26E - 4$	$6.62E - 3$	$3.35E - 2$	
	CPU	0.265	0.297	0.313	0.328	
	L ₂	$7.94E - 3$	$1.50E - 2$	$3.06E - 2$	$2.07E - 2$	
$MCBS-DOM[23]$	\mathbf{L}^{∞}	$2.31E - 3$	$4.10E - 3$	$1.13E - 2$	$9.34E - 2$	
	CPU	5.87	14.87	23.79	29.60	

Table 3. Comparison of error and CPU time between MCBS-DQM, and PYRDTM [2/1], Example 3.

		$t=10$	$t=20$					
(x, y)	ADM[3]	PYRDTM	<i>VIM[3]</i>	RDTM	ADM[3]	PYRDTM	VIM[3]	RDTM
$(-450, -450)$	2.57E	$5.05 - 22$	7.27E	2.53E	1.03E	8.08E	7.27E	4.04E
	-06		-12	-21	-05	-21	-12	-20
$(-400, -400)$	3.26E	1.15E	1.11E	5.76E	2.32E	1.84E	1.11E	9.22E
	-06	-21	-11	-21	-05	-20	-11	-20
$(-300, -300)$	5.79E	8.64E	3.58E	4.32E	2.32E	1.38E	3.58E	6.91E
	-06	-21	-11	-20	-05	-19	-11	-19
$(-250, -250)$	8.34E	3.10E	7.43E	1.55E	3.34E	4.96E	7.43E	2.48E
	-06	-20	-11	-19	-05	-19	-11	-18
(0,0)	8.09E	3.76E	1.78E	2.96E	3.254777	3.25E	1.78E	3.64E
	-01	-04	-01	-03		-03	-01	-02
(50, 50)	2.07E	2.36E	4.57E	1.18E	8.26E	3.78E	3.66E	1.89E
	-04	-15	-08	-14	-04	-14	-07	-13
(100, 100)	5.19E	1.87E	2.88E	9.33E	2.08E	5.48E	2.30E	1.49E
	-05	-17	-09	-17	-04	-17	-08	-15
(200, 200)	1.30E	1.47E	1.80E	7.33E	1.30E	2.34E	1.44E	1.17E
	-05	-19	-10	-19	-05	-18	-09	-17
(350, 350)	4.25E	2.92E	1.91E	1.46E	1.69E	4.67E	1.54E	2.34E
	-06	-21	-11	-20	-05	-20	-10	-19
(500, 500)	2.08E	2.41E	4.56E	1.20E	8.33E	3.85E	3.68E	1.93E
	-06	-22	-12	-21	-06	-21	-11	-20

Table4. Comparison of absolute error obtained by ADM, VIM, and PYRDTM[2/1], Example3.

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