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Research Article

Enhanced Multistage Differential Transform Method: Application to the Population Models

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We present an efficient computational algorithm, namely, the enhanced multistage differential transform method (E-MsDTM) for solving prey-predator systems. Since the differential transform method (DTM) is based on the Taylor series, it is difficult to obtain accurate approximate solutions in large domain. To overcome this difficulty, the multistage differential transform method (MsDTM) has been introduced and succeeded to have reliable approximate solutions for many problems. In MsDTM, it is the key to update an initial condition in each subdomain. The standard MsDTM utilizes the approximate solution directly to assign the new initial value. Because of local convergence of the Taylor series, the error is accumulated in a large domain. In E-MsDTM, we propose the new technique to update an initial condition by using integral operator. To demonstrate efficiency of the proposed method, several numerical tests are performed and compared with ones obtained by other numerical methods such as MsDTM, multistage variational iteration method (MVIM), and fourth-order Runge-Kutta method (RK4).

1. Introduction

The analytical approaches such as the differential transform method (DTM) and the homotopy perturbation method (HPM) have been succeeded to solve differential equations and integral equations in many fields [1–10]. The basic concept of the DTM is based on the Taylor series. Suppose the solution is represented by the Taylor series. DTM provides a recursive relations for the coefficients of the Taylor series which can be solved easily. However, it is different from the conventional high-order Taylor series method which requires a complex symbolic computation. Even if DTM provides a promising algorithm for solving many linear and nonlinear problems arising in various science and engineering fields, it also has some drawbacks. Since DTM is based on the Taylor series which gives a local convergences and it has only a truncated approximation, it does not exhibits a good approximation in a large domain. Recently, the multistage DTM (MsDTM) [11–16] is proposed to accelerate the convergence of the truncated approximation in a large domain as well as to improve the accuracy of the standard DTM. The MsDTM applies the standard DTM in each subdomain. In MsDTM, it is a key to improve accuracy as well as convergence how to assign a new initial condition at each subdomain. In this paper, we demonstrate that the conventional initial updating in MsDTM accumulates an error for the nonlinear systems. In order to overcome those difficulties, a modified version of MsDTM, which is called a enhanced MsDTM (E-MsDTM), is presented. We apply the E-MsDTM to the two prey-predator models. One is a simple prey-predator model [17] as follows:

$$\begin{aligned} \frac{d}{dt}x(t) &= x(t)\left(a - by(t)\right), \\ \frac{d}{dt}y(t) &= -y(t)(c - dx(t)), \end{aligned} \tag{1.1}$$

where $x(t)$ and $y(t)$ represent the populations of prey and predator such as rabbits and foxes, respectively, at time t and a, b, c, and d are known constants. Another model is a Gauss-type prey-predator model [18] which describes the population dynamics that incorporate functional responses. Specially, we study the following Holling-type II ($p = 1$) and Holling-type III ($p = 2$):

$$\begin{aligned} \frac{d}{dt}x(t) &= rx(t)\left(1 - \frac{x(t)}{k}\right) - \frac{mx^p(t)}{1 + x^p(t)}y(t), \\ \frac{d}{dt}y(t) &= y(t)\left(\mu\frac{mx^p(t)}{1 + x^p(t)} - D\right), \end{aligned} \tag{1.2}$$

where $x(t)$ and $y(t)$ are the population size for the prey and the predator, respectively; r, k, μ, and D are the positive constants representing prey intrinsic growth rate, carrying rate of prey to predator, and death rate of predator, respectively.

2. Description of Enhanced Multistage Differential Transform Method

Let us describe the basic definition and some properties of the standard DTM. Suppose a function $y(t)$ is the solution of the following equation:

$$\frac{d}{dt}y(t) = f\left(t, y(t)\right), \qquad x(0) = c. \tag{2.1}$$

Let us define the differential transform $Y(k)$ of $y(t)$ at $t = t_i$ as

$$Y(k) = \frac{1}{k!}\left[\frac{d^k y(t)}{dt^k}\right]_{t=t_i}. \tag{2.2}$$

The differential inverse transform of $Y(k)$ is defined by

$$y(t) = \sum_{k=0}^{\infty} Y(k)(t - t_i)^k. \tag{2.3}$$

Suppose that $y(t) = \sum_{k=0}^{\infty} Y(k)t^k$. Using some fundamental properties for the DTM, we have the following recursive relation:

$$(k + 1)Y(k + 1) = F(k), \qquad Y(0) = c, \tag{2.4}$$

where $F(k)$ is the differential transform of $f(t, y(t))$. One can obtain the $Y(k)$ by solving the recursive relation (2.4). Then $y(t)$ can be approximated by the finite-term Taylor series. In other words,

$$y(t) \approx \sum_{k=0}^{n} Y(k)(t - t_i)^k \equiv s_n(t). \tag{2.5}$$

It is well known that the approximated error is given by

$$\left|y(t) - s_n(t)\right| \leq \frac{M}{(n + 1)!}|t - t_i|^{n+1}, \tag{2.6}$$

where $|x^{(n+1)}(t)| \leq M$. Thus, it is easy to see that, for the fixed term n, the error is getting bigger if $|t - t_i|$ is increasing. To reduce the error, the more terms are added. But it requires cumbersome computational work. Moreover, it is possible that the error blows up even with many terms if the value t is outside of convergence radius of the function $y(t)$.

To overcome difficulties arising in the standard DTM, the multistage differential transform method is introduced. The basic idea of the MsDTM is to apply the standard DTM to each subdomain. To describe the MsDTM we consider the equally spaced nodal points t_l; $0 = t_0 < t_1 < \cdots < t_{N-1} < t_N = T$ and $t_{l+1} - t_l = T/N$. On lth subdomain $(t_l, t_{l+1}) \equiv D_l$, we define $y(t)|_{D_l} \equiv y_l(t)$. The differential transform $Y_l(k)$ of $y_l(t)$ at $t = t_l$ is defined by

$$Y_l(k) = \frac{1}{k!}\left[\frac{d^k y_l(t)}{dt^k}\right]_{t=t_l}. \tag{2.7}$$

The differential inverse transform of $Y_l(k)$ is defined by

$$y_l(t) = \sum_{k=0}^{\infty} Y_l(k)(t - t_l)^k. \tag{2.8}$$

Similarly, $y_l(t)$ can be approximated by solving the recursive relation (2.4) on D_l. Then we have

$$y_l(t) \approx \sum_{k=0}^{n} Y_l(k)(t - t_l)^k \equiv s_{l,n}(t). \tag{2.9}$$

It is an issue to give the initial condition $y_l(t_l)$ in each subdomain D_l. Since $y(0) = c$ in (2.1) is given by the initial condition, we have $Y(0) = c$. For $l > 0$, we approximate $y_l(t_l)$ by computing $s_{l-1,n}(t_l)$ and assign the approximate value as the initial condition in D_l. Then $Y_l(0) = s_{l-1,n}(t_l)$. This standard MsDTM has been successful to obtain accurate approximation for many problems in [11–13]. However, it is easy to see that the approximate solution obtained by the standard MsDTM may yield an increasing error due to the nonlinearity because the DTM employs only finite term Taylor series for the given problems. For instance, let us consider

$$y'(t) = y(t)^m. \tag{2.10}$$

Applying the DTM gives

$$\left(\sum_{k=0}^{\infty} Y(k)(t-t_i)^k\right)' = \left(\sum_{k=0}^{\infty} Y(k)(t-t_i)^k\right)^m \equiv \sum_{k=0}^{\infty} F(k)(t-t_i)^k. \tag{2.11}$$

The basic properties of DTM have the following recursive relation for $m = 3$:

$$(k+1)Y(k+1) = \sum_{s=0}^{k}\left[\sum_{r=0}^{s} Y(r)Y(s-r)\right]Y(k-\mathrm{s}) = F(k). \tag{2.12}$$

One can solve the above recursive relation easily to obtain the differential transforms $Y(k),\ k = 0,\ \dots, n$. Then we can approximate

$$y(t) \approx \sum_{k=0}^{n} Y(k)(t-t_i)^k. \tag{2.13}$$

Since the recursive relation (2.12) is derived by equating the coefficients for $(t-t_i)^k$ in (2.11), the differential transforms $Y(k)$ are determined by solving

$$(k+1)Y(k+1) = F(k), \qquad k = 0, 1, \dots, n. \tag{2.14}$$

However, the right-hand side of (2.11) has the coefficients of $(t-t_i)^k$, $k = 0, 1, \dots, 3n$ so that as many as $2n$ coefficients of $(t-t_i)^k$, $k = n+1, \dots, 3n$ are not considered to approximate $y(t)$. Thus, it could have a poor approximation $y(t)$. It is supposed to take care of all terms in obtaining the differential transform $Y(k)$ especially for the nonlinear problem.

In what follows we describe some modifications of MsDTM, which is called the Enhanced MsDTM. Suppose that $y_{l-1}(t)$ is approximated by the standard MsDTM, that is, $y_{l-1}(t) \approx s_{l-1,n}(t)$. Then, the solution $y_l(t)$ can be determined by solving the following problem:

$$\frac{d}{dt} y_l(t) = f(t, y_l(t)), \qquad y_l(t_l) = s_{l-1,n}(t_l). \tag{2.15}$$

Applying the DTM to (2.15) gives the differential transform $Y_l(k)$. Then $y_l(t)$ is approximated by

$$y_l(t) \approx \sum_{k=0}^{n} Y_l(k)(t-t_i)^k \equiv s_{l,n}(t). \tag{2.16}$$

In the standard MsDTM, $y_l(t_{l+1}) \approx s_{l,n}(t_{l+1})$ which gives $Y_{l+1}(0)$. As mentioned before, it could give inaccurate approximate solution $y_{l+1}(t)$. Here, taking the integral operator to (2.15), the solution $y_l(t)$ can be represented by

$$y_l(t) = y_l(t_l) + \int_{t_l}^{t} f(\tau, y_l(\tau))\,d\tau. \tag{2.17}$$

Thus, we have

$$y_l(t_{l+1}) = y_l(t_l) + \int_{t_l}^{t_{l+1}} f(\tau, y_l(\tau))\,d\tau. \tag{2.18}$$

Since $y_l(t) \approx s_{l,n}(t)$ in (2.16), we can approximate the value of $y_l(t_{l+1})$ by

$$y_l(t_{l+1}) = y_l(t_l) + \int_{t_l}^{t_{l+1}} f(\tau, s_{l,n}(\tau))\,d\tau. \tag{2.19}$$

Then, $y_l(t_{l+1}) = Y_{l+1}(0)$. For each subdomain D_l, repeat this process (2.19) to approximate $y_l(t)$. Thus, the solution $y(t)$ can be approximated by

$$y(t) \approx \sum_{l=0}^{N-1} s_{l,n}(t)\chi(t-t_l)\chi(t_{l+1}-t), \tag{2.20}$$

where

$$\chi(t-t_l) = \begin{cases} 1, & t \geq t_l, \\ 0, & \text{otherwise}. \end{cases} \tag{2.21}$$

3. Application

To apply the MsDTM, we consider a subdomain with uniform length $T/N = h$ stated in the previous section. For each subdomain $(t_l, t_{l+1}) \equiv D_l$, we apply the DTM to the model problem (1.1), then the following recursive relation is obtained:

$$\begin{aligned} (k+1)X_l(k+1) &= aX_l(k) - b\sum_{r=0}^{k} X_l(r)Y_l(k-r), \\ (k+1)Y_l(k+1) &= -cY_l(k) + d\sum_{r=0}^{k} Y_l(r)X_l(k-r). \end{aligned} \tag{3.1}$$

In order to compare the numerical performance for the enhanced MsDTM, we demonstrate comparative approximations with the standard MsDTM, the multistage variational iteration method (MVIM) [17, 19, 20], and the fourth-order Runge-Kutta method (RK4). In MVIM, for each subdomain D_l, the solutions $x_l(t)$ and $y_l(t)$ can be determined by

$$x_l(t) = \lim_{n\to\infty} x_{l,n}(t), \qquad y_l(t) = \lim_{n\to\infty} y_{l,n}(t), \tag{3.2}$$

where

$$\begin{aligned} x_{l,n+1}(t) &= x_{l,n}(t) + \int_{t_l}^{t} \lambda_1(\tau)\left(\frac{d}{dt}x_{l,n}(\tau) - ax_{l,n}(\tau) + bx_{l,n}(\tau)y_{l,n}(\tau)\right), \\ y_{l,n+1}(t) &= y_{l,n}(t) + \int_{t_l}^{t} \lambda_2(\tau)\left(\frac{d}{dt}y_{l,n}(\tau) - cy_{l,n}(\tau) + dx_{l,n}(\tau)y_{l,n}(\tau)\right). \end{aligned} \tag{3.3}$$

Here, λ_1, λ_2 are general Lagrange multiplier which are determined by solving the stationary problem. Here, the multipliers are given by [17]

$$\lambda_1(\tau) = -\exp[a(t-\tau)], \qquad \lambda_2(\tau) = -\exp[c(\tau - t)]. \tag{3.4}$$

In order to apply DTM to the Holling-type prey-predator model (1.2) we let $\phi(t)$ be the functional response of predator to prey as

$$\phi(t) = \frac{mx^p(t)}{1 + x^p(t)}. \tag{3.5}$$

For each subdomain D_l, using the basic properties of DTM to (1.2) gives the following recursive relation:

$$\begin{aligned} (k+1)X_l(k+1) &= rX_l(k) - \frac{r}{k}\sum_{i}^{k} X_l(i)X_l(k-i) - \sum_{i}^{k} \Phi_l(i)X_l(k-i), \\ (k+1)Y_l(k+1) &= \mu\sum_{i}^{k} Y_l(i)\Phi(k-i) - DY_l(k), \end{aligned} \tag{3.6}$$

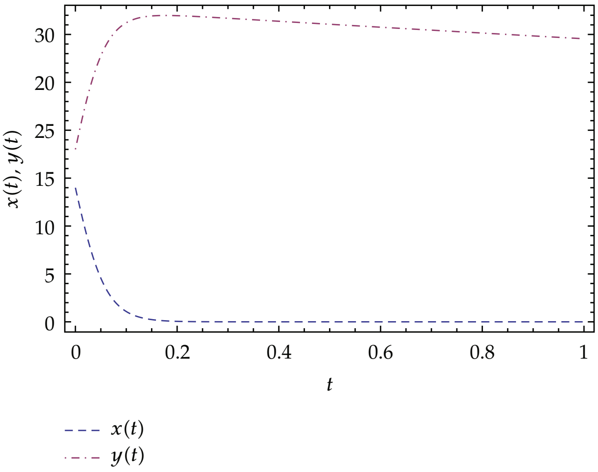


Figure 1: Population of $x(t)$ and $y(t)$ by RK4 ($h = 0.0001$) in case 1.

Table 1: Various parameters.

Case	a	b	c	d	$x(0)$	$y(0)$
1	1	1	0.1	1	14	18
2	0.1	1	1	1	16	10
3	2	0.1	1	1	0.1	0.2

where for $p = 1$,

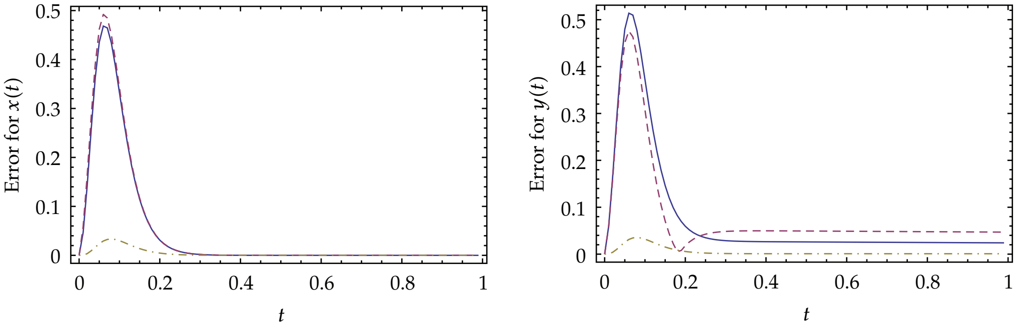
$$\Phi_l(k) = \begin{cases} \dfrac{1}{1 + X_l(k)}\left(mX_l(k)\right), & k = 0, \\ \dfrac{1}{1 + X_l(0)}\left(mX_l(k) - \displaystyle\sum_{i=1}^{k} X_l(i)\Phi_l(k-i)\right), & k > 0, \end{cases} \tag{3.7}$$

and for $p = 2$

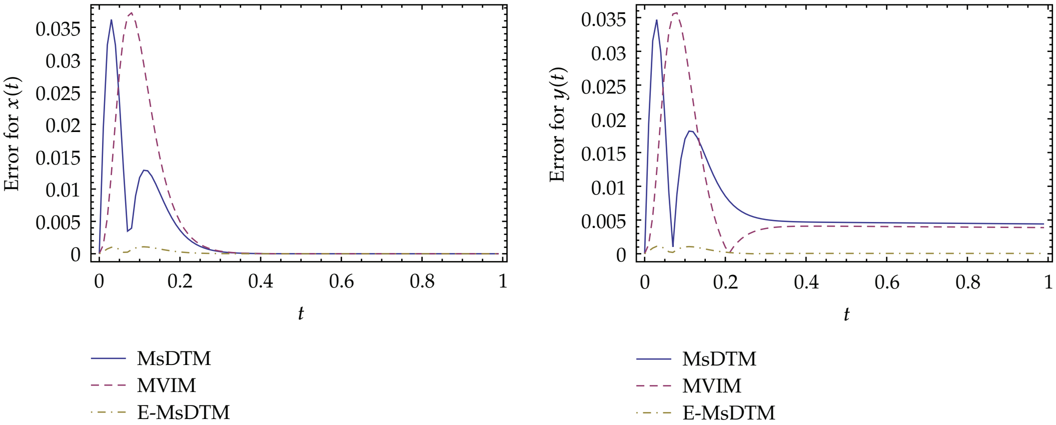
$$\Phi_l(k) = \begin{cases} \dfrac{1}{1 + X_l^2(k)}\left(mX_l^2(k)\right), & k = 0, \\ \dfrac{1}{1 + X_l^2(0)}\left(m\displaystyle\sum_{i=0}^{k} X_l(i)X_l(k-i) - \sum_{j=1}^{k}\sum_{i=0}^{j} X_l(j)X_l(j-i)\Phi_l(k-j)\right), & k > 0. \end{cases} \tag{3.8}$$

4. Numerical Experiment and Discussion

In this section, several numerical tests are demonstrated to show the effectiveness of the E-MsDTM. For the simple prey-predator model (1.1), the constants in three different cases are shown in Table 1. Figure 1 shows the population $x(t)$ and $y(t)$ for the case 1 by using RK4 with time step $h = 0.0001$ in $(0, 1)$. With a dense time step $h < 0.001$ all approximations are fitted well in graph. Thus it is difficult to show the effectiveness for the proposed method,



(a) Absolute error with one iteration: $x(t)$ (left), $y(t)$ (right)



(b) Absolute error with two iterations: $x(t)$ (left), $y(t)$ (right)

Figure 2: Comparison of absolute errors in case 1.

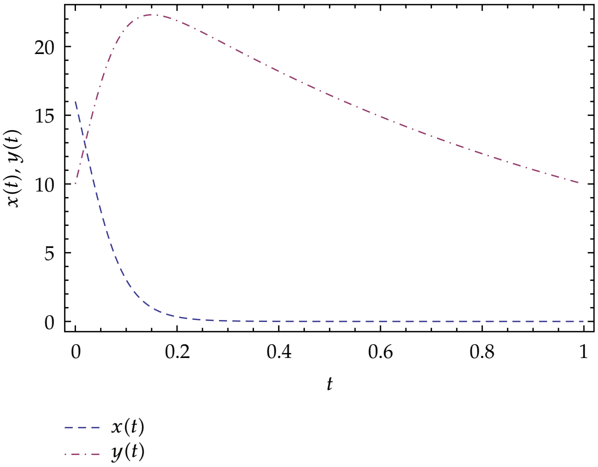
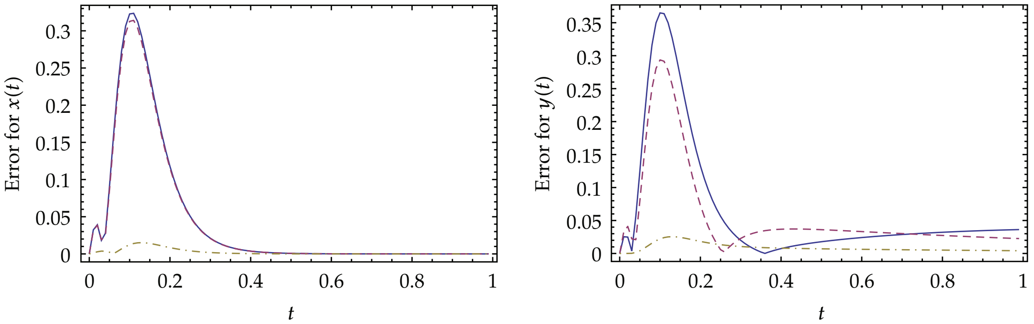
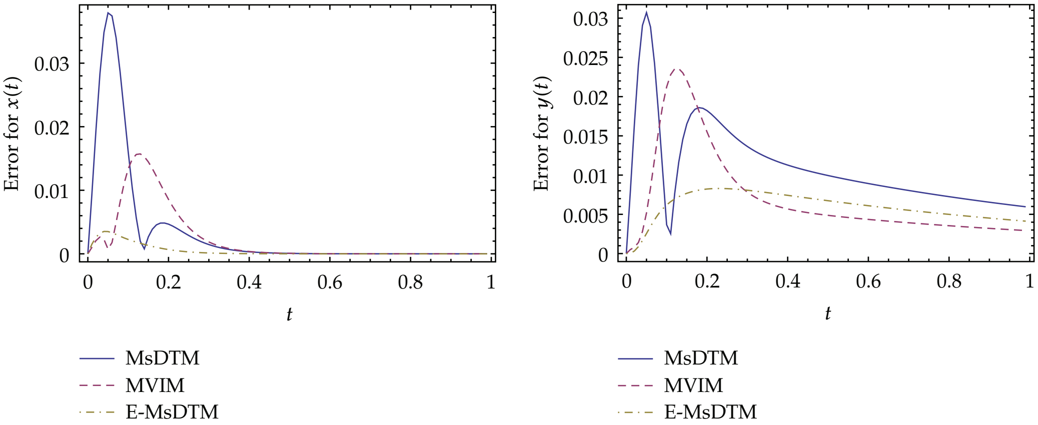


Figure 3: Population of $x(t)$ and $y(t)$ by RK4 ($h = 0.0001$) in case 2.



(a) Absolute error with one iteration: $x(t)$ (left), $y(t)$ right



(b) Absolute error with two iterations: $x(t)$ (left), $y(t)$ right

Figure 4: Comparison of absolute errors in case 2.

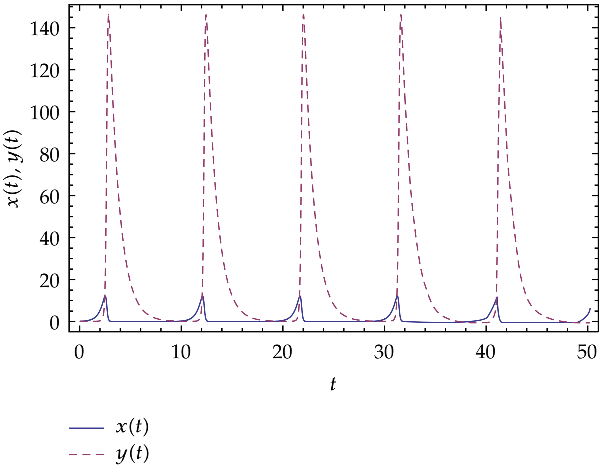
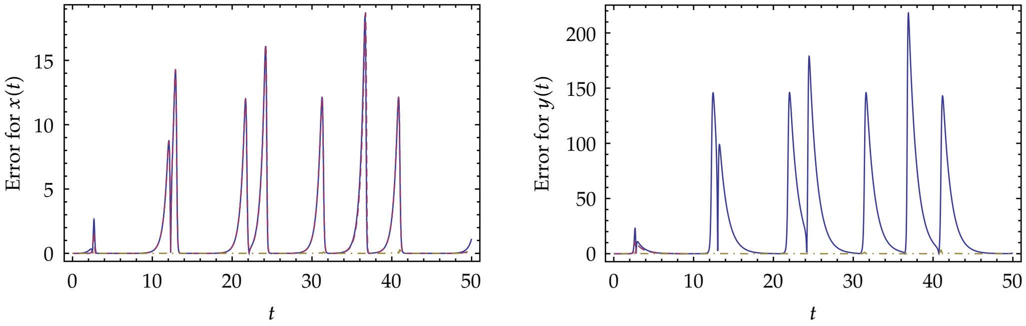
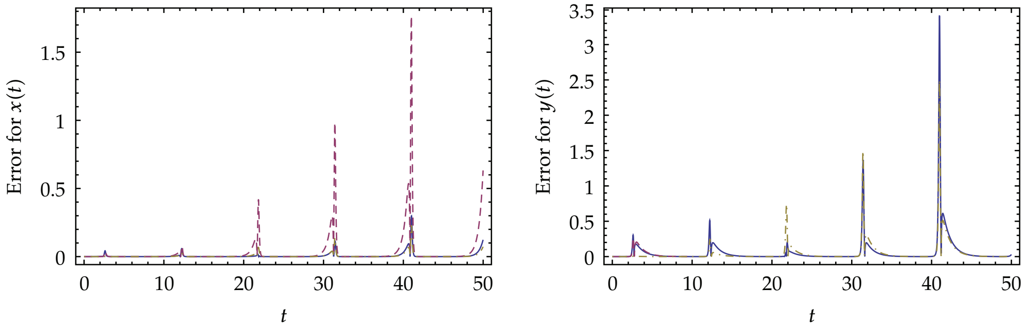


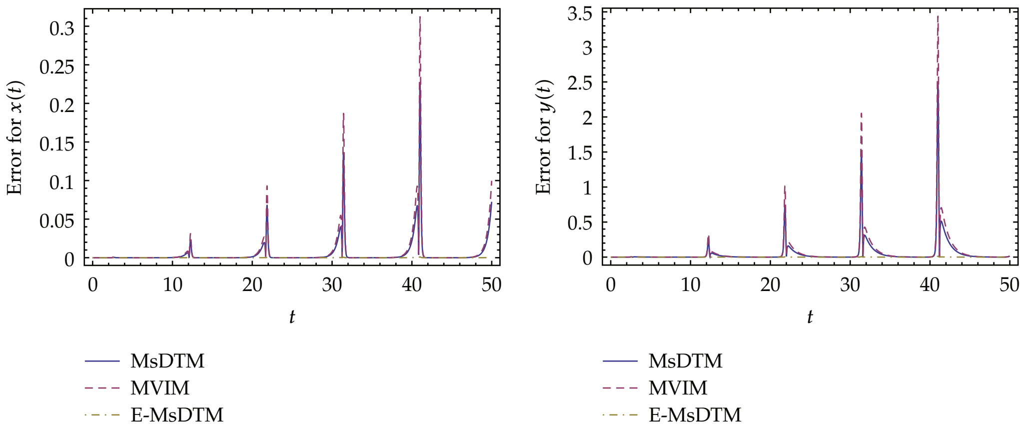
Figure 5: Population of $x(t)$ and $y(t)$ by RK4 ($h = 0.0001$) in case 3.



(a) Absolute error with one iteration: $x(t)$ (left), $y(t)$ right



(b) Absolute error with two iterations: $x(t)$ (left), $y(t)$ right



(c) Absolute error with three iterations: $x(t)$ (left), $y(t)$ right

Figure 6: Comparison of absolute errors in case 3.

E-MsDTM. In order to show the performance of each method clearly, we fix the time-step $h = 0.01$ at MsDTM, MVIM, and E-MsDTM. Figure 2 shows the absolute error of the approximations obtained by RK4 and other methods with one iteration (a) and two iterations (b). Since the solution is stable for $t > 0.2$ in Figure 1, all methods give reliable approximations for $t > 0.2$. However, MVIM and MsDTM give a large error compared with the result by E-MsDTM in $(0, 0.2)$. Moreover, E-MsDTM gives an accurate approximation in all domain $(0, 1)$. In case 2, all numerical results present the similar behavior shown in case 1. See Figures 3 and 4. In order to see the effectiveness of the E-MsDTM in a more complex population system,

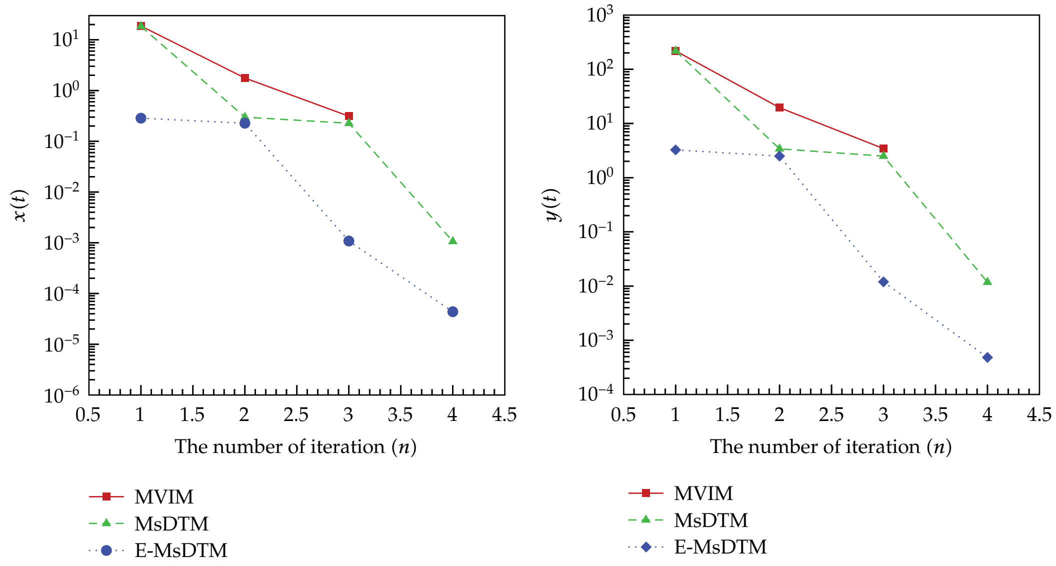


Figure 7: Maximum error with the number of iteration.

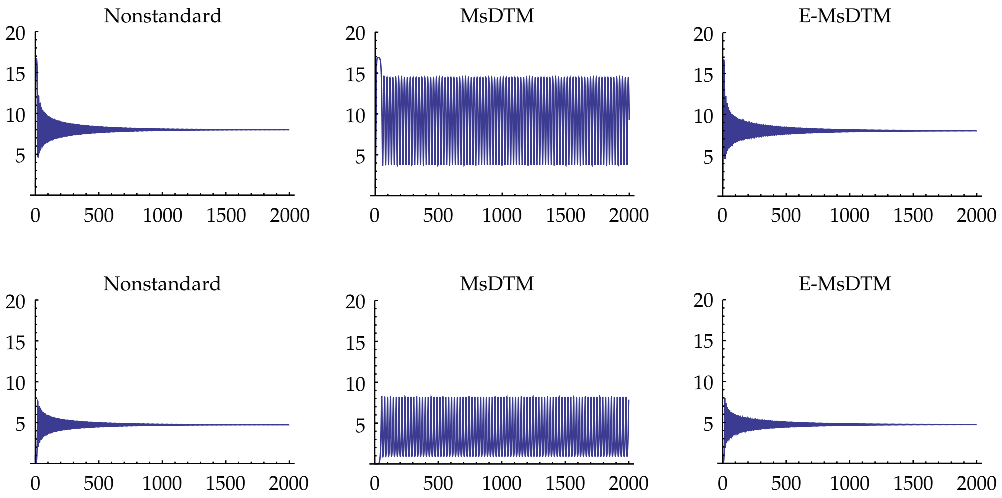


Figure 8: $x(t)$ (Top) and $y(t)$ (Bottom); nonstandard scheme (Left, $h = 0.01$), MsDTM (Middle, $h = 0.25$), E-MsDTM (Right, $h = 0.25$); $k = 16.9$.

we consider the population model in case 3 in a large domain $(0, 50)$. Here we used a RK4 at $h = 0.0001$ and all other methods at $h = 0.01$. As seen in Figure 5 this system exhibits a oscillatory dynamics as well as many peaks. In Figure 6 the absolute errors are demonstrated as the number of iteration is increasing. All approximations have large errors at peaks, but still the E-MsDTM yields a better performance than others. In order to see the performance associated to the number of iteration, the maximum absolute errors between RK4 and other methods are presented in Figure 7. As the number of iteration is increasing, it is shown that MVIM and MsDTM give similar performance. However, the accuracy of the E-MsDTM is dramatically increasing when the number of iteration is bigger than 2.

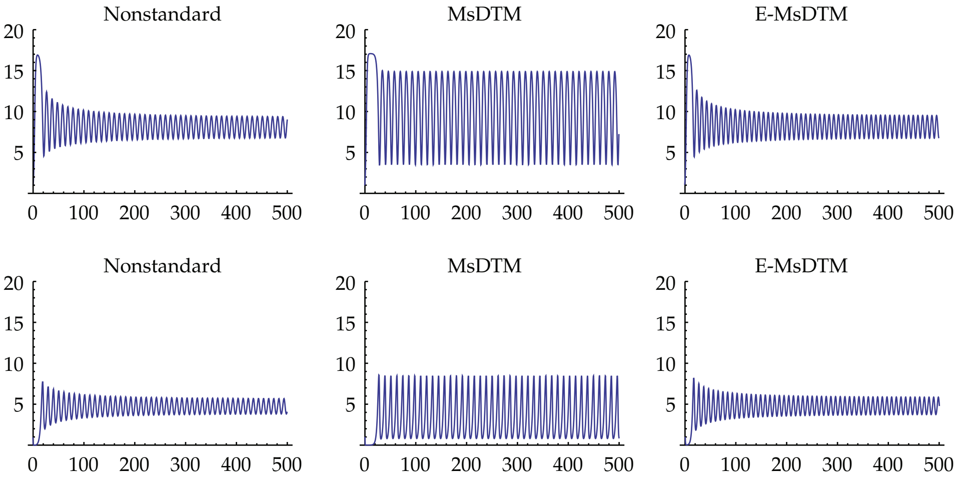


Figure 9: $x(t)$ (Top) and $y(t)$ (Bottom); nonstandard scheme (Left, $h = 0.01$), MsDTM (Middle, $h = 0.25$), E-MsDTM (Right, $h = 0.25$); $k = 17.1$.

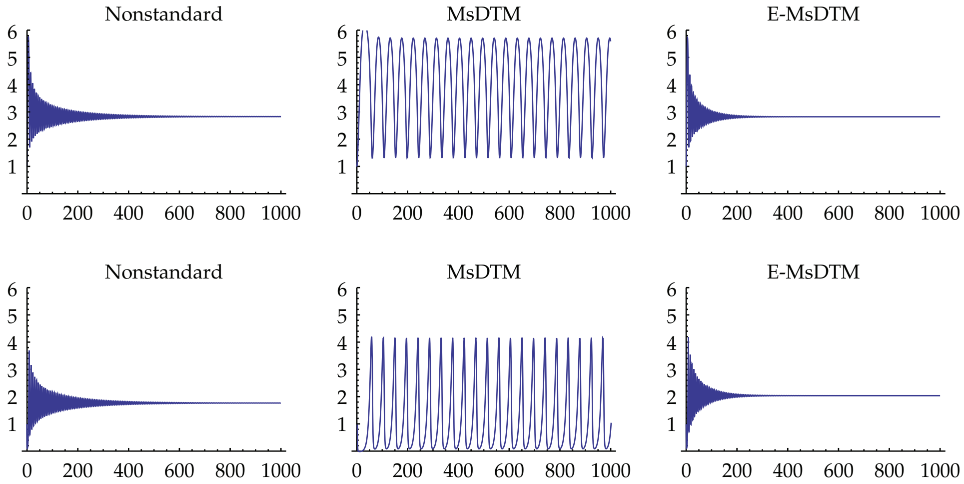


Figure 10: $x(t)$ (Top) and $y(t)$ (Bottom); nonstandard scheme (Left, $h = 0.01$), MsDTM (Middle, $h = 0.2$), E-MsDTM (Right, $h = 0.2$); $k = 32\sqrt{2}/7 - 0.1$.

For the Holling-type prey-predator model (1.2), the parameters are set by $r = 1$, $m = 1$, $\mu = 9$ and $D = 1$. For the Holling-type II ($p = 1$), it has been known [18] that the model (1.2) has at least one limit cycle if $k > 17$ and no limit cycle if $k \leq 17$ and the critical point (x^*, y^*), where $(x^*)^p = D/(m\mu - D)$, $y^* = r\mu x^*(1 - x^*/k)/D$ is globally asymptotically stable if $8 < k \leq 17$ and unstable if $k > 17$. The results obtained by the nonstandard numerical scheme [18], MsDTM and E-MsDTM are demonstrated in Figures 8 and 9. Here, the time step $h = 0.01$ is used in nonstandard scheme, $h = 0.25$ in both MsDTM and E-MsDTM. Only one iteration is employed in both MsDTM, and E-MsDTM. As shown in Figures 8 and 9, all results by nonstandard scheme and E-MsDTM are good agreement. However, the numerical results by MsDTM present a wrong dynamical behavior. For Holling-type III ($p = 2$), it is shown in Figures 10 and 11 that all numerical results by nonstandard scheme and E-MsDTM show the

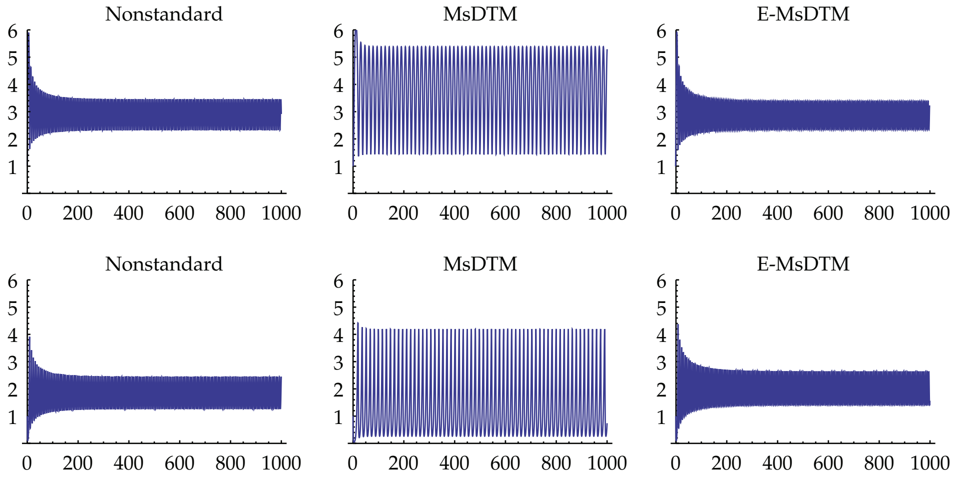


Figure 11: $x(t)$ (Top) and $y(t)$ (Bottom); nonstandard scheme (Left, $h = 0.01$), MsDTM (Middle, $h = 0.125$), E-MsDTM (Right, $h = 0.125$) $k = 32\sqrt{2}/7 + 0.1$.

accurate dynamical behavior, but the result by MsDTM does not. Moreover, E-MsDTM gives the approximate solutions with a coarse time step $h = 0.125$, which shows that E-MsDTM is very effective method.

5. Conclusion

In this paper, we propose an efficient computational algorithm, namely the enhanced multi-stage differential transform method for solving several prey-predator systems. The basic idea of the MsDTM is to apply the standard DTM to each sub-domain by updating an initial condition. However, it is shown that the standard initial updating gives a numerical inefficiency for the complex nonlinear systems. In E-MsDTM, an initial condition at each sub-domain is updated by using the integral operator which is equivalent to the system. For all illustrative examples the E-MsDTM yields accurate and stable numerical solutions in comparison with the ones obtained by other methods such as the standard MsDTM and MVIM. Also, the E-MsDTM gives almost the same results at low computational cost compared with ones obtained by RK4 and nonstandard numerical scheme. Thus, it can be concluded that the E-MsDTM is an effective numerical tool for solving differential equations. Here, all computations are performed by using Mathematica 8.0.

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References

[1] F. Kangalgil and F. Ayaz, “Solitary wave solutions for the KdV and mKdV equations by differential transform method,” *Chaos, Solitons and Fractals*, vol. 41, no. 1, pp. 464–472, 2009.

[2] A. S. V. Ravi Kanth and K. Aruna, “Differential transform method for solving linear and non-linear systems of partial differential equations,” *Physics Letters. A*, vol. 372, no. 46, pp. 6896–6898, 2008.

[3] I. H. A. Hassan, “Comparison differential transformation technique with Adomian decomposition method for linear and nonlinear initial value problems,” *Chaos, Solitons and Fractals*, vol. 36, no. 1, pp. 53–65, 2008.

[4] F. Ayaz, “Solutions of the system of differential equations by differential transform method,” *Applied Mathematics and Computation*, vol. 147, no. 2, pp. 547–567, 2004.

[5] I. H. A. Hassan, “Different applications for the differential transformation in the differential equations,” *Applied Mathematics and Computation*, vol. 129, no. 2-3, pp. 183–201, 2002.

[6] M. J. Jang, C. L. Chen, and Y. C. Liu, “Two-dimensional differential transform for partial differential equations,” *Applied Mathematics and Computation*, vol. 121, no. 2-3, pp. 261–270, 2001.

[7] B. Jang, “Solving a class of two-dimensional linear and nonlinear Volterra integral equations by the differential transform method,” *Journal of Computational and Applied Mathematics*, vol. 233, no. 2, pp. 224–230, 2009.

[8] B. Jang, “Solving linear and nonlinear initial value problems by the projected differential transform method,” *Computer Physics Communications*, vol. 181, no. 5, pp. 848–854, 2010.

[9] H. Koçak and A. Yıldırım, “An efficient algorithm for solving nonlinear age-structured population models by combining homotopy perturbation and Padé techniques,” *International Journal of Computer Mathematics*, vol. 88, no. 3, pp. 491–500, 2011.

[10] A. Yildirim and Y. Cherruault, “Analytical approximate solution of a SIR epidemic model with constant vaccination strategy by homotopy perturbation method,” *Kybernetes*, vol. 38, no. 9, pp. 1566–1575, 2009.

[11] A. Gökdoğan, M. Merdan, and A. Yildirim, “A multistage differential transformation method for approximate solution of Hantavirus infection model,” *Communications in Nonlinear Science and Numerical Simulation*, vol. 17, no. 1, pp. 1–8, 2012.

[12] A. Gökdoğan, M. Merdan, and A. Yildirim, “Adaptive multi-step differential transformation method to solving nonlinear differential equations,” *Mathematical and Computer Modelling*, vol. 55, no. 3-4, pp. 761–769, 2012.

[13] Z. M. Odibat, C. Bertelle, M. A. Aziz-Alaoui, and G. H. E. Duchamp, “A multi-step differential transform method and application to non-chaotic or chaotic systems,” *Computers & Mathematics with Applications*, vol. 59, no. 4, pp. 1462–1472, 2010.

[14] V. S. Ertürk, Z. M. Odibat, and S. Momani, “An approximate solution of a fractional order differential equation model of human T-cell lymphotropic virus I (HTLV-I) infection of CD4+ T-cells,” *Computers & Mathematics with Applications*, vol. 62, no. 3, pp. 996–1002, 2011.

[15] V. S. Erturk, G. Zaman, and S. Momani, “A numeric-analytic method for approximating a giving up smoking model containing fractional derivatives,” *Computers & Mathematics with Applications*. In press.

[16] V.S. Erturk, G. Zaman, and S. Momani, “Application of multi-step differential transform method for the analytical and numerical solutions of the density dependent Nagumo telegraph equation,” *Romanian Journal of Physics*. In press.

[17] S. M. Goh, M. S. M. Noorani, and I. Hashim, “Prescribing a multistage analytical method to a prey-predator dynamical system,” *Physics Letters, Section A*, vol. 373, no. 1, pp. 107–110, 2008.

[18] S. M. Moghadas, M. E. Alexander, and B. D. Corbett, “A non-standard numerical scheme for a generalized Gause-type predator-prey model,” *Physica D*, vol. 188, no. 1-2, pp. 134–151, 2004.

[19] B. Batiha, M. S. M. Noorani, I. Hashim, and E. S. Ismail, “The multistage variational iteration method for a class of nonlinear system of ODEs,” *Physica Scripta*, vol. 76, no. 4, pp. 388–392, 2007.

[20] B. Batiha, M. S. M. Noorani, and I. Hashim, “Variational iteration method for solving multispecies Lotka-Volterra equations,” *Computers & Mathematics with Applications*, vol. 54, no. 7-8, pp. 903–909, 2007.