COMPARING THE MULTISTAGE AND PADÉ TECHNIQUES FOR ITERATIVE METHODS IN SOLVING NONLINEAR FOOD CHAIN MODEL

H.M. NOUR, A. ELSAID* AND A. ELSONBATY

Mathematics & Engineering Physics Department, Faculty of Engineering, Mansoura University, Egypt

Abstract. In this article, we illustrate the advantages of using multistage technique to improve the solution obtained via iterative methods for series solution of differential equations. This is accomplished by comparing between the Padé and the multistage techniques when used with the Adomian decomposition method and the differential transformation method. The case study is a system of nonlinear differential equations that describes three species food chain model with Beddington DeAngelis functional response. Numerical simulations illustrate that the multistage technique presents good results in the different cases of the solution of the considered system whereas the Padé technique fails when dealing with the case of periodic solution.

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1. Introduction

Several iterative methods were proposed to solve functional equations, mainly differential equations, in the form of infinite series solution. Yet, a common drawback in these

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*Corresponding author

E-mail addresses: hanour@mans.edu.eg (H.M. Nour), a_elsaid@mans.edu.eg (A. Elsaid), amrelsonbaty@mans.edu.eg (A. Elsonbaty)

methods is the lack of global convergence as the results obtained are accurate only for a small period of time. Two approaches are used to overcome this drawback. The first one is to compute a very large number of the series terms but this leads to computational complexities. The second approach is to use some techniques to improve the obtained solution.

Two of the well known iterative methods are the Adomian decomposition method (ADM) [1] and the differential transformation method (DTM) [2]. To solve differential equations with ADM, an inverse integral operator is applied to a recurrence relation to obtain the terms of the series solution. Whereas the DTM computes the components of the Taylor series solution with the advantage that it can be computerized to greatly reduce the size of computational work.

The Padé approximation is one of the techniques that can be utilized to overcome the lack of global convergence in the iterative methods. Though the ADM-Padé (ADM-P) technique show good results [3], we demonstrate that it fails with periodic solutions whereas the multistage ADM (MADM) [4] and the multistage DTM (MDTM) [5] give good results in all the cases of the solution of the considered system.

The case study of this work is the mathematical model of a predator-prey system for three species food chain model. This type of models is usually characterized by the functional response which is the function that describes the number of preys consumed per predator per unit time for given quantities of prey and predator. The functional response proposed in this article is of the Beddington DeAngelis type as it is considered to be more general than the other types [6] and [7]. This model is a generalization for the host–parasitoid–hyperparasitoid model studied in [8].

This paper is structured as follows; In Section 2, the mathematical model of the food chain we use as a case study is introduced. Section 3 presents the basics of the ADM, the DTM, the Padé approximation, and the multistage technique. Section 4 contains the numerical simulations and results. Section 5 contains the conclusion of this work.

2. Mathematical model

In this paper, we study the nonlinear three species food chain model with the Bedding-ton DeAngelis functional response of the following form

$$\frac{dx}{dt} = x\big[a_1 - b_1 x - \frac{s_1 y}{c_1 + x + d_1 y}\big],$$
$$\frac{dy}{dt} = y\big[-a_2 - b_2 y + \frac{s_2 x}{c_1 + x + d_1 y} - \frac{s_3 z}{c_2 + y + d_2 z}\big], \quad , \qquad (2.1)$$
$$\frac{dz}{dt} = z\big[-a_3 - b_3 z + \frac{s_4 y}{c_2 + y + d_2 z}\big],$$

where x, y, and z represent the population density of the prey, the predator, and the top-predator at time t, respectively. Parameters a_i, b_i, s_i, c_i, and d_i are positive constants. The state space of system (2.1) is given by $R_+^3 = \{(x, y, z) \in R^3 : x \geqslant 0, \ y \geqslant 0, \ z \geqslant 0\}$.

This model can be considered a general form of many food chain models (see [6] and references within). Model (2.1) has at most four non-negative equilibrium points which are:

$E_0 = (0, 0, 0)$, $E_1 = (\frac{a_1}{b_1}, 0, 0)$, $E_2 = (\bar{x}, \bar{y}, 0)$, and the positive equilibrium point $E_3 = (x^*, y^*, z^*)$, see [6] and [7].

3. Methods of solution

3.1 Adomian decomposition method

Consider the standard operator

$$Lu + Ru + Nu = g, \qquad (3.1)$$

where u is the unknown function, L is the highest order derivative which is assumed to be easily invertible, R is a linear differential operator of order less than the order of L, Nu represents the nonlinear terms, and g is the source term. By applying the inverse operator L^{-1} to both sides of equation (3.1) we obtain

$$u = v - L^{-1}(Ru) - L^{-1}(Nu), \qquad (3.2)$$

where the function v represents the terms arising from integrating the source term g and from using the auxiliary conditions. The standard Adomian method defines the solution

u by the series

$$u = \sum_{n=0}^{\infty} u_n, \tag{3.3}$$

and the nonlinear term by the series

$$Nu = \sum_{n=0}^{\infty} A_n, \tag{3.4}$$

where A_n are the Adomian polynomials determined formally from the relation[1]

$$A_n = \frac{1}{n!} \left[\frac{d^n}{d\lambda^n} [N(\sum_{i=0}^{\infty} \lambda^i u_i)] \right]_{\lambda=0}, \quad n = 0, 1, ... \tag{3.5}$$

The solution components u_0, u_1, u_2, $\ldots$, are then determined recursively by using the relation

$$\begin{cases} u_0 = v \\ u_{k+1} = -L^{-1}Ru_k - L^{-1}A_k, \ k \geq 0 \end{cases} \tag{3.6}$$

where u_0 is referred to as the zeroth component.

By replacing each nonlinear term in system (2.1) by its corresponding Adomian polynomials and applying the inverse operator, which is an integral operator from t_0 to t, a truncated series solution is thus obtained as

$$x_N = \sum_{n=0}^{N} x_n, \ y_N = \sum_{n=0}^{N} y_n, \ and \ z_N = \sum_{n=0}^{N} z_n, \tag{3.7}$$

3.2 Differential transformation method

The DTM is a semi analytical–numerical technique which uses the form of polynomials as the approximation to the exact solution. It is an iterative procedure for obtaining Taylor series solutions of functional equations. The differential transformation of an analytic function $u(t)$ is defined by

$$U(k) = \frac{1}{k!} [\frac{d^k u(t)}{dt^k}]_{t=t_0}, \ k = 1, 2, ... \tag{3.8}$$

The inverse differential transformation of $U(k)$ is defined by

$$u(t) = \sum_{k=0}^{\infty} U(k)(t - t_0)^k, \tag{3.9}$$

In real applications, the function $u(t)$ is expressed by the truncated finite series of the form

$$u(t) = \sum_{k=0}^{N} U(k)(t - t_0)^k. \tag{3.10}$$

Let $u(t)$, $v(t)$ and $w(t)$ be three uncorrelated functions of time t and $U(k)$, $V(k)$, and $W(k)$ are their corresponding differential transforms. Then the following basic properties of the differential transformation hold ([5], [9], and references therein)

1- If $u(t) = v(t) \pm w(t)$, then $U(k) = V(k) \pm W(k)$.

2- If $u(t) = av(t)$, then $U(k) = aV(k)$, where a is a constant.

3- If $u(t) = v(t)w(t)$, then $U(k) = \sum_{k_i=0}^{k} V(k_i)W(k - k_i)$.

4- If $u(t) = t^n$, then $U(k) = \delta(k - n)$ where $\delta(k - n) = \{\begin{smallmatrix} 1 & k=n \\ 0 & k \neq n \end{smallmatrix}$.

Also, algorithms are available for computing the differential transform of general analytic nonlinear functions and for arbitrary order differential equations[10].

In system (2.1) we have

$$X(0) = x_0 = x(t_0), Y(0) = y_0, \ Z(0) = z_0,$$
$$X(1) = x_0\left[a_1 - b_1 x_0 - \frac{s_1 y_0}{c_1 + x_0 + d_1 y_0}\right],$$
$$Y(1) = y_0\left[-a_2 - b_2 y_0 + \frac{s_2 x_0}{c_1 + x_0 + d_1 y_0} - \frac{s_3 z_0}{c_2 + y_0 + d_2 z_0}\right], \tag{3.11}$$
$$Z(1) = z_0\left[a_3 - b_3 z_0 - \frac{s_4 y_0}{c_2 + y_0 + d_2 z_0}\right].$$

To write the iterative scheme of system (2.1) in a more compact form, we define the following terms

$$\Psi_X(i) = (i + 1)X(i + 1),$$
$$\Omega_{X,Y}(i) = \sum_{m=0}^{i} X(m)Y(i - m), \ and \tag{3.12}$$
$$\Phi_{j,X,Y}(i) = c_j\delta(i) + X(i) + d_jY(i), \ \delta(k) = \{\begin{smallmatrix} 1 & k=0 \\ 0 & k \neq 0 \end{smallmatrix}.$$

The following equations describe the iterative scheme of system (2.1) for $k = 1, 2, ...$

$$
\begin{aligned}
X(k+1) = {} & \frac{1}{(k+1)\Phi_{1,X,Y}(0)}\Big[\sum_{n=0}^{k}(a_1 X(n) - b_1\Omega_{X,X}(n))\Phi_{1,X,Y}(k-n) \\
& -s_1\Omega_{Y,X}(k) - \sum_{n=0}^{k-1}\Psi_X(n)\Phi_{1,X,Y}(k-n)\Big],
\end{aligned} \tag{3.13}
$$

$$
\begin{aligned}
Y(k+1) = {} & \frac{1}{(k+1)\Phi_{1,X,Y}(0)\Phi_{2,Y,Z}(0)} \\
& \Big[\sum_{n=0}^{k}\sum_{l=0}^{n}(-a_2 Y(l) - b_2\Omega_{Y,Y}(l))\Phi_{2,Y,Z}(n-l)\Phi_{1,X,Y}(k-n) \\
& +\sum_{n=0}^{k}(s_2\Omega_{Y,X}(n)\Phi_{2,Y,Z}(k-n) - s_3\Omega_{Z,Y}(n)\Phi_{1,X,Y}(k-n)) \\
& -\sum_{n=0}^{k-1}\Psi_Y(n)\Phi_{2,Y,Z}(k-n)\Phi_{1,X,Y}(0) \\
& -\sum_{n=0}^{k-1}\sum_{l=0}^{n}\Psi_Y(l)\Phi_{2,Y,Z}(n-l)\Phi_{1,X,Y}(k-n),
\end{aligned} \tag{3.14}
$$

$$
\begin{aligned}
Z(k+1) = {} & \frac{1}{(k+1)\Phi_{2,Y,Z}(0)}\Big[\sum_{n=0}^{k}(-a_3 Z(n) - b_3\Omega_{Z,Z}(n))\Phi_{2,Y,Z}(k-n) \\
& +s_4\Omega_{Z,Y}(k) - \sum_{n=0}^{k-1}\Psi_Z(n)\Phi_{2,Y,Z}(k-n)\Big].
\end{aligned} \tag{3.15}
$$

In the following subsections, the two improvement techniques we considered (the Padé approximation and the multistage technique) are presented.

3.3 Padé approximation

The Padé approximants are a particular type of rational fraction approximation which idea is to match the Taylor series expansion as far as possible [11]. The L, M Padé approximant to $U(t) = \sum_{n=0}^{\infty} u_n t^n$ is uniquely determined for given L and M and is denoted by

$$
[L/M] = \frac{P_L(t)}{Q_M(t)} = \frac{\sum_{n=0}^{L} p_n t^n}{\sum_{n=0}^{M} q_n t^n}. \tag{3.16}
$$

The normalization condition $Q_M(0) = 1$ is imposed such that $Q_M(t)$ and $P_L(t)$ have no common factors [11] and [12]. The Padé approximant for the truncated sum $U_k(t) = \sum_{n=0}^{K} u_n t^n$ is the same as for $U(t)$ when $K \geq L + M$ [12].

The diagonal approximant $[M/M]$ is usually the most accurate Padé approximant [13]. Therefore, we construct the diagonal approximants in the following numerical simulations such that the series in (3.7) are transformed as follows

$$x_N^* = \frac{\sum_{n=0}^{M} d_n t^n}{\sum_{n=0}^{M} e_n t^n}, \quad y_N^* = \frac{\sum_{n=0}^{M} f_n t^n}{\sum_{n=0}^{M} g_n t^n}, \quad and \quad z_N^* = \frac{\sum_{n=0}^{M} h_n t^n}{\sum_{n=0}^{M} k_n t^n}. \tag{3.17}$$

where $N \geq M + M$.

3.4 Multistage technique

The other technique used to increase the accuracy of iterative methods is to divide the interval $[t_0, T)$ into m subintervals, $[t_0, t_1)$, $[t_1, t_2)$, ..., $[t_{m-1}, T)$. Then the $N + 1$ terms partial sums $x_N^1 = \sum_{n=0}^{N} x_n^1$, $y_N^1 = \sum_{n=0}^{N} y_n^1$, and $z_N^1 = \sum_{n=0}^{N} z_n^1$ are obtained as the system solution for the first subinterval $[t_0, t_1)$. Then, the solutions x_N^1, y_N^1, and z_N^1 are used to obtain a new initial condition for the next subinterval $[t_1, t_2)$ and another solution x_N^2, y_N^2, and z_N^2 for subinterval $[t_1, t_2)$ is obtained. This procedure is applied over the m successive subintervals, and the obtained solutions for each subinterval $[t_{p-1}, t_p)$ can be used to obtain the initial condition at t_p for the next subinterval $[t_p, t_{p+1})$.

4. Numerical implementation

In this section, we present the numerical results obtained when model (2.1) is solved by ADM, DTM, MADM, MDTM, ADM-P, and 4th order Runge–Kutta method (RK4). Three sets of values are assigned to the system parameters to illustrate three cases of the solution stability [6] and [14].

Case	a_1	b_1	a_2	b_2	a_3	b_3	s_1	s_2	s_3	s_4	c_1	d_1
1	1	1	0.4	1	0.1	0.5	2	2	2	2	1	1
2	1	1	0.4	1	1.5	0.5	2	2	2	1	1	1
3	1	1	1	0	1	0	1	10	10	2	0	1

c_2	d_2	$x(0)$	$y(0)$	$z(0)$
1	4	0.3	0.5	0.4
1	4	0.3	0.5	0.4
0	1	0.7046	0.2941	0.2853

Case 1 represents an asymptotically stable coexistence equilibrium point of the model. Case 2 and Case 3 correspond to a ratio-dependent food chain model with positive periodic solution and asymptotically stable equilibrium point, respectively.

MADM and MDTM are used with $N = 6$ and $h = 0.4$; ADM-P has $M = 3$; RK4 step is 0.01. We show ADM-P for $[M/M]$, $[M - 1/M]$, and $[M/M - 1]$ as in some cases the last two give better results.

Fig.1 to Fig. 3 have the legend shown in Fig. 1-a. In numbering the figures (a), (b), and (c) represent the solution of Case 1, Case 2, and Case 3, respectively.
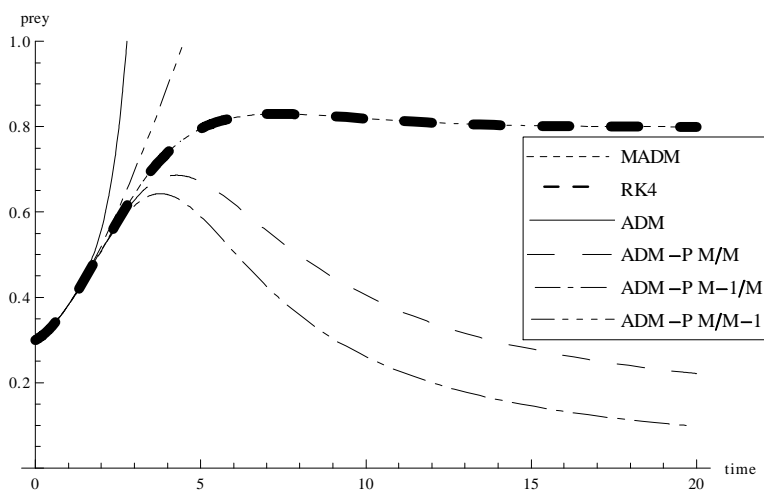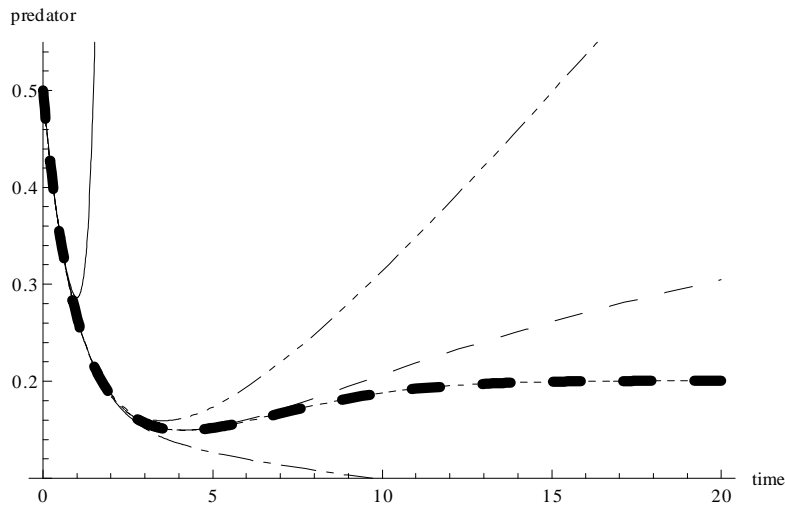

Fig. 1-a.
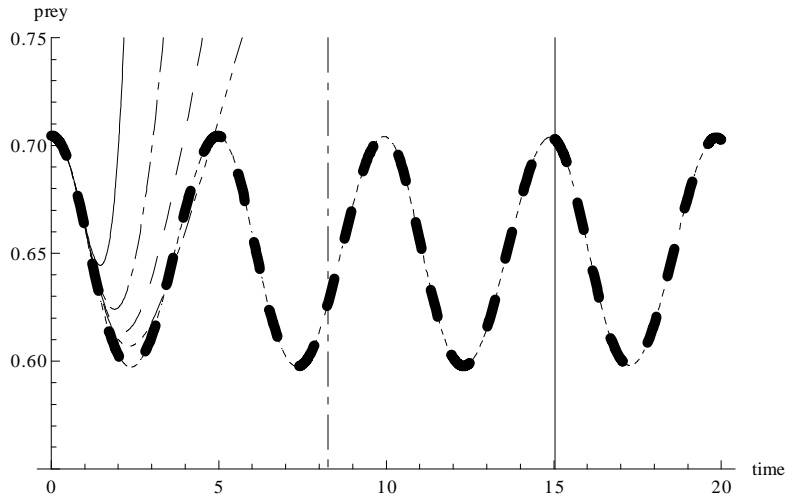
Fig. 1-b.
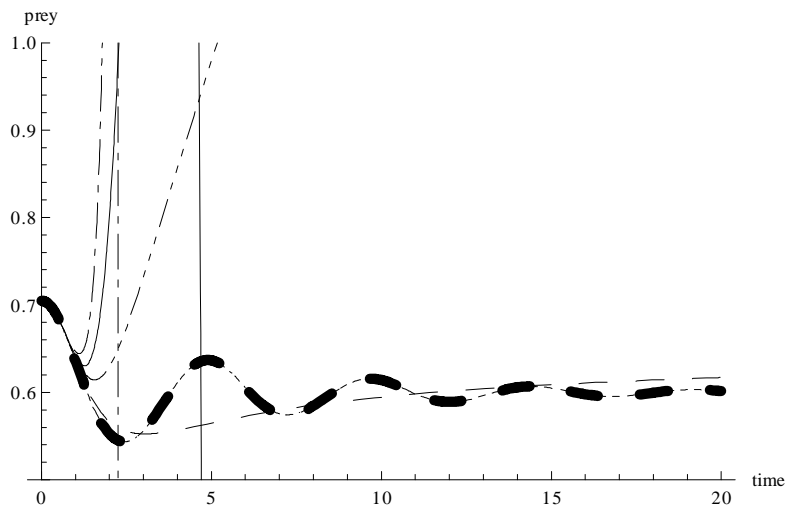
Fig. 1-c.

Fig. 1 Prey population density using ADM-P and MADM.

predator

Fig. 2-a.

predator

Fig. 2-b.

predator

Fig. 2-c.

Fig. 2 Predator population density using ADM-P and MADM.

top-predator

Fig. 3-a.

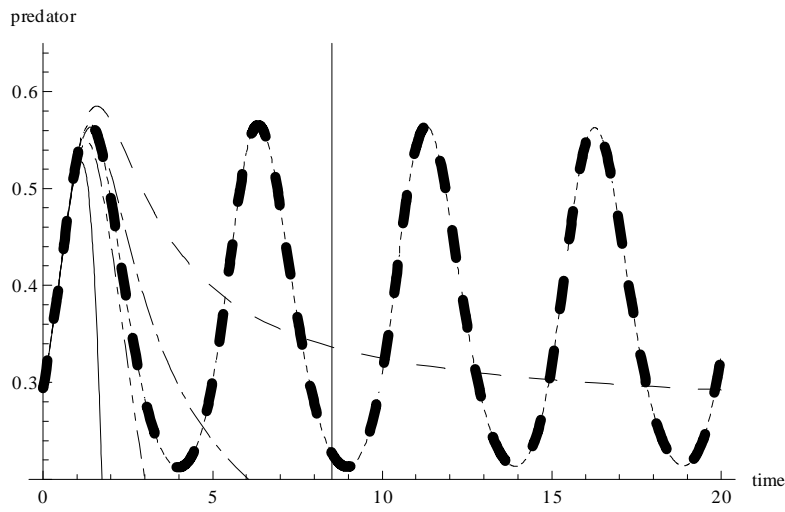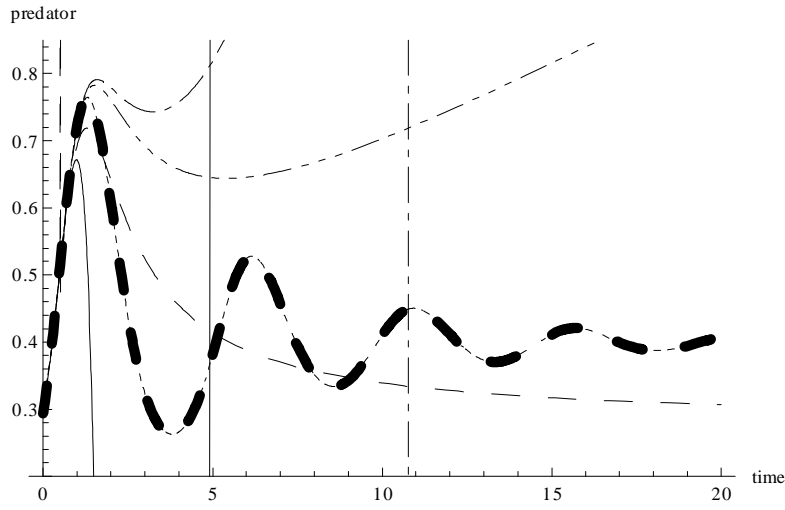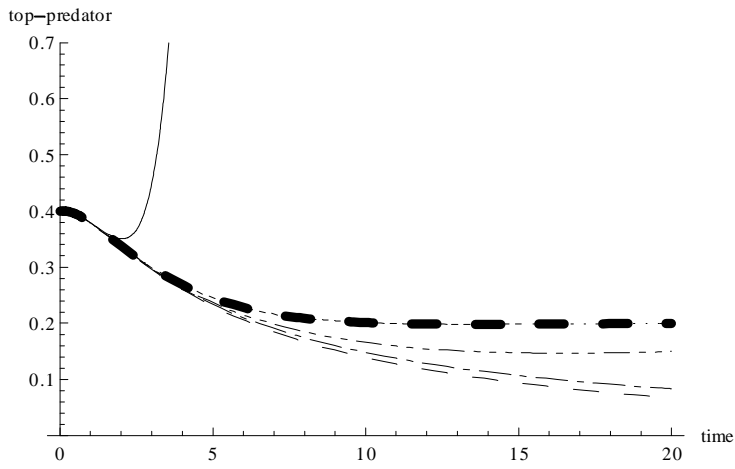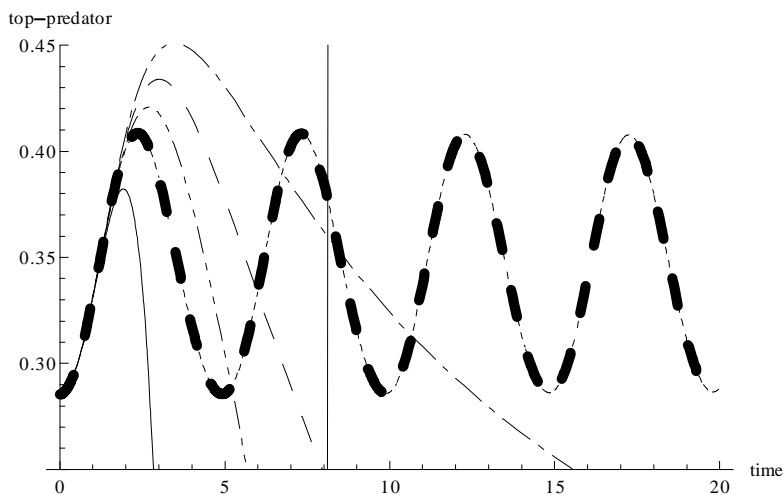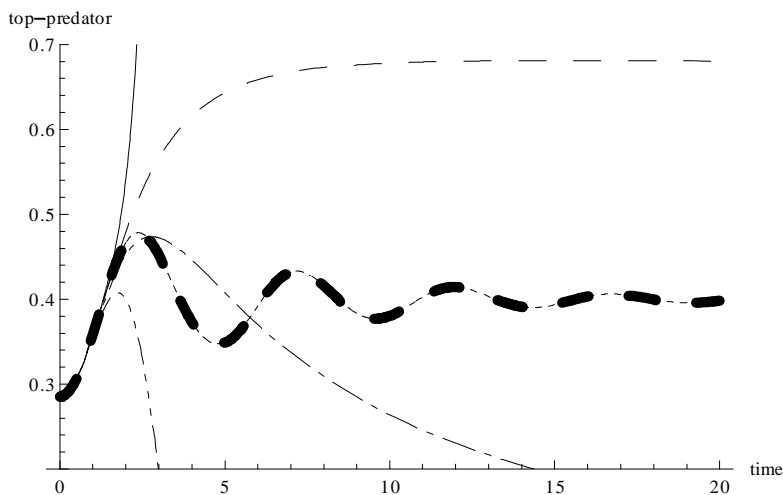Fig. 3-b.

Fig. 3-c.

Fig. 3 Top-predator population density using ADM-P and MADM.

Fig1, Fig2, and Fig3 show that ADM solution diverges as time increases and does not preserve the positivity, boundedness, nor the periodic behavior of the solution. The ADM-P has a better performance than ADM solution but it does not preserve the periodic behavior in Case 2 and Case 3. On the other hand, the solution obtained by MADM is more accurate in all cases and with a time step $h = 0.4$, it coincides with the solution obtained using RK4 with time step equals 0.01.

The terms of the series solution obtained using DTM and MDTM are identical to those obtained by ADM and MADM, respectively. This asserts the fact that DTM solution

shows the same disadvantages of ADM solution and MDTM, as MADM, gives more accurate solution.

5. Conclusion

In this work, it is shown that though the ADM-P solution is more accurate than both ADM and DTM, it also diverges after a period of time. More importantly, it does not preserve the periodic behavior of the solution. Both the MADM and the MDTM presented accurate results in simulating all cases of the solution, including periodic type, for the system of nonlinear differential equations. These two methods also inherits the advantage of giving a functional form of the solution within each time interval. Also, the accuracy of the two methods can be controlled via changing truncation order N or subinterval width h. Yet, there is no formula that shows how to choose the more suitable h or N.

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