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Abdolsaeed Alavi
Payame Noor University

Asghar Ghorbani
Ferdowsi University of Mashhad

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An Approximate Analytical Algorithm for Solving The Multispecies Lotka-Volterra Equations

Abdolsaeed Alavi

Department of Mathematics
Payame Noor University
Bandare Torkman, Iran
alavi601@yahoo.com

Asghar Ghorbani*

Department of Applied Mathematics
School of Mathematical Sciences
Ferdowsi University of Mashhad
Mashhad, Iran
as_gh56@yahoo.com

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* Corresponding author

Abstract

In this paper, a new efficient method called the parametric iteration method (PIM) is applied to accurately solve the multispecies Lotka–Volterra equations (MLVEs). Some cases of MLVEs are highlighted in order to show the simplicity and efficiency of the method. The results obtained in this work demonstrate that the present algorithm is a powerful analytic tool for the solution of MLVEs.

Keywords: Piecewise-truncated parametric iteration method, Parametric iteration method, Multispecies Lotka–Volterra equations, Runge–Kutta method

MSC 2010 No.: 35E15, 35F55, 35G25

1. Introduction

In this paper, we study the analytical approximate solution of the multispecies Lotka–Volterra equations of the type

$$\frac{dN_i}{dt} = N_i \left[b_i + \sum_{j=1}^m a_{ij} N_j \right], \quad i = 1, 2, \dots, m \quad (1)$$

with the initial conditions

$$N_i(0) = c_i, \quad i = 1, 2, \dots, m, \quad (2)$$

by a new analytical method based on the parametric iteration method (PIM) proposed in [Saber-Nadjafi and Ghorbani (2010)]. Here, a_{ij} , b_i and c_i are real constants. These equations model the dynamic behaviour of an arbitrary number of competitors [Hofbauer and Sigmund (1988)]. Though originally formulated to describe the time history of a biological system, these equations find their application in a number of engineering fields such as simultaneous chemical and nonlinear control. In fact, the one-predator one-prey Lotka–Volterra model is one of the most popular ones to demonstrate a simple nonlinear control system. The accurate solutions of the LVEs may become a difficult task either if the equations are stiff (even with a small number of species), or when the number of species is large [Olek (1994)]. These kinds of equations have been solved using the approximate analytical methods such as the variational iteration method (VIM) [Batiha et al. (2007)] and homotopy perturbation method (HPM) [Chowdhury et al. (2007)]. However, the convergence region and rate of the corresponding results is small. In order to overcome these shortcomings, a new analytic algorithm is proposed to simulate (1).

In our previous paper [Saber-Nadjafi and Ghorbani (2010)], we proposed a new approximate analytical algorithm based on the PIM called the piecewise-truncated PIM (PTP) for solving the Abel differential equations. The new algorithm analytically approximates the solution of an initial value problem of ODEs in a sequence of subintervals, which is continuous everywhere. The local convergence and the stability of the algorithm were discussed in details [Saber-Nadjafi and Ghorbani (2010)]. One of the main advantages of the PTP algorithm is its ability in providing us a continuous representation of the approximate solution, which allows better information of the solution over the time interval. In this paper, an application of this algorithm to solve MLVEs is introduced. Some cases of the MLVEs are examined to illustrate the efficiency and accuracy of this method, and in all cases, the present technique performed excellently.

2. The Basic Idea of the New Method

In this section, we describe the PIM and PTP algorithms for solving the nonlinear system (1). The method gives rapidly convergent successive approximations of the exact solution if such a solution exists, otherwise approximations may be used for numerical purposes. Also, it has been shown in [Ghorbani (2008) and Saberi-Nadjafi and Ghorbani (2010)] that the PIM logically contains the approximate analytical method of the VIM, which is widely used in approximate calculations.

The idea of the PIM is very simple and straightforward. To explain the basic idea of the PIM, we first consider (1) as follows:

$$L[N_i(t)] + N[N_i(t)] = f_i(t), \quad i = 1, 2, \dots, m, \quad (3)$$

where L , with the property $Lg \equiv 0$ when $g \equiv 0$, denotes the so-called auxiliary linear operator with respect to N_i , N is a nonlinear operator with respect to N_i and $f_i(t)$ is the source term. Then, we construct a family of iterative processes for Equation (3) as [Saberi-Nadjafi and Ghorbani (2010)]:

$$L[N_{i,n+1}(t) - N_{i,n}(t)] = hH_i(t)A[N_{i,n}(t)], \quad i = 1, 2, \dots, m, \quad (4)$$

with the initial condition

$$N_{i,n+1}(t_0) = N_i(t_0), \quad \forall n, \quad (5)$$

where

$$A[N_{i,n}(t)] = L[N_{i,n}(t)] + N[N_{i,n}(t)] - f_i(t) \equiv \frac{dN_{i,n}}{dt} - N_{i,n} \left[b_i + \sum_{j=1}^m a_{ij} N_{j,n} \right], \quad (6)$$

and $N_{i,0}(t)$ is the initial guess (which can be freely chosen with possible unknown constants, or it can also be solved from its corresponding linear homogeneous equation $L[N_{i,0}(t)] = 0$) and the subscript n denotes the n th iteration.

The $h \neq 0$ and $H_i(t) \neq 0$ denote the so-called auxiliary parameter and auxiliary function, respectively, which can be identified easily and efficiently by the techniques proposed in [Saberi-Nadjafi and Ghorbani (2010)]. In this work, for simplicity, we take $H_i(t) = 1, i = 1, \dots, m$.

It should be emphasized that though we have the great freedom to choose the auxiliary linear operator \mathcal{L} , the auxiliary parameter h and the initial approximation $N_{i,0}(t)$, which is fundamental to the validity and flexibility of the PIM, we can also assume that all of them are properly chosen so that solution of (4) exists, as will be shown in this paper later. Accordingly, the successive approximations $N_{i,n}(t)$ ($n \geq 1$) of the PIM in the auxiliary parameter h will be

readily obtained by choosing the zeroth component. Consequently, the exact solution may be obtained by using

$$N_i(t) = \lim_{n \rightarrow \infty} N_{i,n}(t), \quad i = 1, \dots, m. \quad (7)$$

Now, in order to avoid expensive computational work for solving (4) via the PIM, it is straightforward to use the set of base functions

$$\{t^k \mid k = 0, 1, 2, \dots\}, \quad (8)$$

to represent $N_i(t)$, i.e.,

$$N_i(t) = \sum_{k=0}^{\infty} \gamma_{i,k} t^k, \quad \gamma_{i,k} \in \mathbb{R}. \quad (9)$$

In view of the solution expression (8) and according to the initial condition (5), it is straightforward to choose

$$L[N_{i,n}(t)] = N'_{i,n}(t), \quad (10)$$

with the property (where d_i is the integral constant)

$$L[d_i t] = 0, \quad (11)$$

as the auxiliary linear operator, and to choose an initial approximation of $N_i(t)$, which is the solution of the corresponding linear homogeneous equation $L[N_{i,0}(t)] = 0$ as

$$N_{i,0}(t) = c_i. \quad (12)$$

According to (4) and (10), the solution of the equation (4) becomes

$$N_{i,n+1}(t) = N_{i,n}(t) + h \int_0^t \left\{ \frac{dN_{i,n}(s)}{ds} - N_{i,n}(s) \left[b_i + \sum_{j=1}^m a_{ij} N_{j,n}(s) \right] \right\} ds, \quad i = 1, \dots, m. \quad (13)$$

Therefore, the successive approximations $N_{i,n}(t)$ ($n \geq 1$) of the PIM iterative relation of (13) in the auxiliary parameter h will be readily obtained, especially by means of symbolic computation software such as Maple, Mathematica, Matlab and others.

In general, the application of the PIM to solve the MLVEs leads to calculation of unneeded terms. The repeated calculations may or may not lead to faster convergence. In order to completely eliminate these repeated calculations, using the integration by parts and Taylor series

around 0, the following improved version of the PIM called the truncated PIM (TP) is proposed for solving the MLVEs of (1) [Saber-Nadjafi and Ghorbani (2010)]:

$$\begin{aligned} N_{i,0}(t) &= c_i, \\ N_{i,1}(t) &= N_{i,0}(t) - h \int_0^t G_{i,0}(s) ds, \\ N_{i,n+1}(t) &= N_{i,n}(t) + (1+h)[N_{i,n}(t) - N_{i,n-1}(t)] - h \int_0^t \{G_{i,n}(s) - G_{i,n-1}(s)\} ds, \quad n \geq 1, \end{aligned} \quad (14)$$

where $i = 1, 2, \dots, m$ and

$$N_{i,n}(s) \left[b_i + \sum_{j=1}^m a_{ij} N_{j,n}(s) \right] = G_{i,n}(s) + O(s^{n+1}). \quad (15)$$

Here, we assume that the right hand (1) in each of iterations of the PIM is an analytic function. It is worth mentioning that the TP formula (14) can cancel all the repeated calculations and terms that are not needed. Furthermore, it is capable of solving strongly nonlinear problems with the complicated variable coefficients in a straightforward manner. Besides, this modified method reduces the volume of calculations and constructs a sequence which converges to the exact solution rapidly.

By using the TP algorithm (14), we obtain a series solution, which in practice is a truncated series solution. Unfortunately, this series solution gives a good approximation to the exact solution in a small region of t . An easy and reliable way of ensuring the validity of the approximations (14) for large t (i.e., $[0, T]$) is to determine the solution in a sequence of equal subintervals t , i.e. $I_k = [t_k, t_{k+1}]$ where $\Delta t = t_{k+1} - t_k$, $k = 0, 1, 2, \dots, M-1$, with $t_N = T$. According to [Saber-Nadjafi and Ghorbani (2010)], therefore, we can obtain the following n_{k+1} -order piecewise approximation $N_{i,n_{k+1}}^{k+1}(t)$ on I_k for Equation (14), which was called the piecewise TP (PTP):

$$\begin{cases} N_{i,n+1}^{k+1}(t) = N_{i,n}^{k+1}(t) + (1+h)[N_{i,n}^{k+1}(t) - N_{i,n-1}^{k+1}(t)] - h \int_{t_k}^t \{G_{i,n}^{k+1}(s) - G_{i,n-1}^{k+1}(s)\} ds, \\ N_{i,0}^{k+1}(t) = N_{i,n_k}^k(t_k) = c_{i,k}, \quad n = 0, 1, \dots, n_{k+1} - 1, \\ N_{i,n}^{k+1}(s) \left[b_i + \sum_{j=1}^m a_{ij} N_{j,n}^{k+1}(s) \right] = G_{i,n}^{k+1}(s) + O((s - t_k)^{n+1}), \quad k = 0, 1, \dots, M-1, \end{cases} \quad (16)$$

where $N_{i,n_0}^0(t_0) = N_i(t_0) = c_i = c_{i,0}$. Now, we can obtain the n_{k+1} -order PTP approximation $N_{i,n_{k+1}}^{k+1}(t)$ on $[t_k, t_{k+1}]$. Thus, in the light of (16) for $k = 0, 1, \dots, M-1$, the approximate analytical solution of (1) on the entire interval $[0, T]$ can easily be obtained. It should be emphasized that the PIM and TP algorithms provide analytical solutions in $[0, T]$, while the PTP technique provides analytical solutions in $[t_k, t_{k+1}]$, which are continuous at the end points of each interval, i.e., $N_{i,n_k}^k(t_k) = c_{i,k} = N_{i,n_{k+1}}^{k+1}(t_k)$, $k = 0, 1, \dots, M-1$.

Following the present subsection, the n_{k+1} -order approximate analytical solution via the PTP method for Equation (1) can be written as:

$$N_{i,n_{k+1}}^{k+1}(t) = \sum_{r=0}^{n_{k+1}} \frac{\gamma_{i,r}^k(t_k, c_1, \dots, c_m)}{r!} (t - t_k)^r + O[(t - t_k)^{n_{k+1}+1}], \quad t \in I_k = [t_k, t_{k+1}], \quad (17)$$

where $\gamma_{i,r}^k(t_k, c_1, \dots, c_m)$ is a coefficient dependent of t_k and c_1, \dots, c_m . The expression (17) demonstrates that the n_{k+1} -order PTP method has an error per step of the order of $(\Delta t)^{n_{k+1}+1}$, while the total accumulated error is of order $(\Delta t)^{n_{k+1}}$.

3. Choosing h and Δt in a Geometric Form

We mentioned that the PTP algorithm, in the present paper, uses a fixed number of approximations n and a fixed step size $\Delta = \Delta t$ to run the iterative procedure (16). So, it is important to ensure that the numerical result obtained using the PTP algorithm (i.e., $c_{i,k}$), which is as a series in the auxiliary parameter h and the fixed step size Δ is convergent in a large enough region whereby the convergence region and rate are dependent upon the h and Δ . Most important, however, is to choose the value of h in relation to Δ to make sure that the numerical result converges fast enough in a sufficiently large region. Since we have a family of solution expressions in the auxiliary parameter h and the step size Δ , hence, regarding h and Δ as independent variables, a simple and practical way of selecting h in relation to Δ is to plot the curves of the resulting series ($c_{i,k}$) with respect to h and Δ .

Thus, if the series is convergent, there exists a segment in its figure called *the $h\Delta$ -curves* that corresponds to a region of h and Δ . For brevity, we call such a region the valid region of h with relation to Δ , i.e., $R_{h\Delta}$. Accordingly, if we set h and Δ values in $R_{h\Delta}$, we are quite sure that the corresponding solution series converges. In order to ensure that the numerical results of the PTP algorithm converge in the whole spatial and temporal regions, in most cases, we can find a proper value of h in relation to Δ . Therefore, the $h\Delta$ -curves provide us with a convenient way to show the influence of h and Δ on the convergence of the PTP algorithm.

In general, by means of the curves of $c_{i,k}$ versus h and Δ , only h and only Δ , it is straightforward to know the corresponding valid regions of $h\Delta$, h and Δ . Choosing a value in

the valid region, we can ensure that the corresponding solution series is convergent. In this manner, we can direct and modify the convergence region and rate of solution series. Thus, the auxiliary parameter h plays an important role within the frame of the PTP algorithm.

4. Some Illustrative Cases

In this section, to give a clear overview of the content of this study, several modeling cases of the MLVEs will be tested by the PTP algorithm, which will ultimately show the simplicity, efficiency and accuracy of this method. Moreover, the obtained results reveal that the approach is easy to implement and accurate when applied to the MLVEs of (1) and avoids tedious computational work. It is noticeable that these equations have been solved by some authors using some available approximate analytical methods [Batiha et al. (2007) and Chowdhury et al. (2007)]. However, the corresponding approximate solutions are valid for a very small interval. In order to completely overcome this disadvantage, here we utilize the PTP algorithm to acquire satisfactory solutions of these equations.

Case 1. One species ($m = 1$)

In the one-species case, Equation (1) reduces to one species competing for a given finite source of food [Batiha et al. (2007) and Chowdhury et al. (2007)]:

$$\frac{dN_1}{dt} = N_1(b + aN_1), \quad a < 0, \quad b > 0, \quad N_1(0) > 0, \quad (18)$$

where a and b are arbitrary constants ($a = -3$ and $b = 1$). In order to solve Equation (18) by using the PTP algorithm, according to (16), we can obtain the following PTP approximations in the subintervals I_k :

$$N_{1,1}^{k+1}(t) = c_{1,k} + hc_{1,k}(-1 + 3c_{1,k})(t - t_k), \quad (19)$$

$$N_{1,2}^{k+1}(t) = c_{1,k} + [h + h(1 + h)]c_{1,k}(-1 + 3c_{1,k})(t - t_k) + \frac{1}{2}h^2c_{1,k}(6c_{1,k} - 1)(-1 + 3c_{1,k})(t - t_k)^2, \quad (20)$$

⋮

where $k = 0, 1, 2, \dots, M - 1$, $c_{1,0} = N_1(0) = 0.1$ and

$$c_{1,k+1} = N_{1,n_{k+1}}^{k+1}(t_{k+1}), \quad k = 0, 1, \dots, M - 1, \quad n_{k+1} = 1, 2, \dots \quad (21)$$

To investigate the valid region of the solution obtained in (20) via the second order PTP algorithm, here we plot the curve of $c_{1,3}$ and $c_{1,4}$ with respect to h and Δ , as shown in Figures 1 and 2. According to this curve, it is easy to discover the valid region of (20). We point out that the valid region becomes more accurate as the number n_{k+1} increases. It is usually convenient to investigate the stability region of the PTP method by means of such kinds of curves.

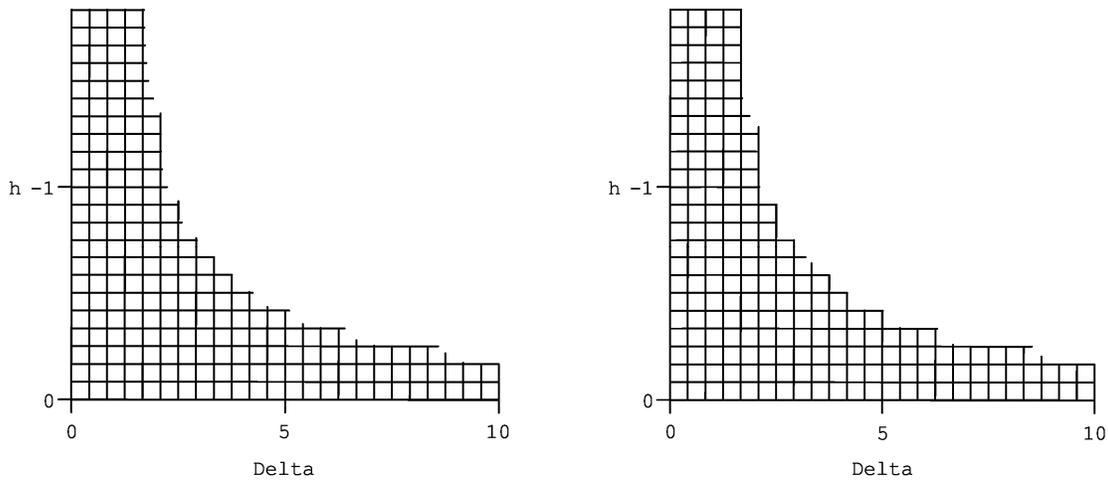


Figure 1. (Plotting the $h\Delta$ -curves) the valid region of h with relation to the step size Δ (Delta) for Case 1 by using the second order PTP solution where left: the curve $c_{1,3}$ and right: the curve $c_{1,4}$

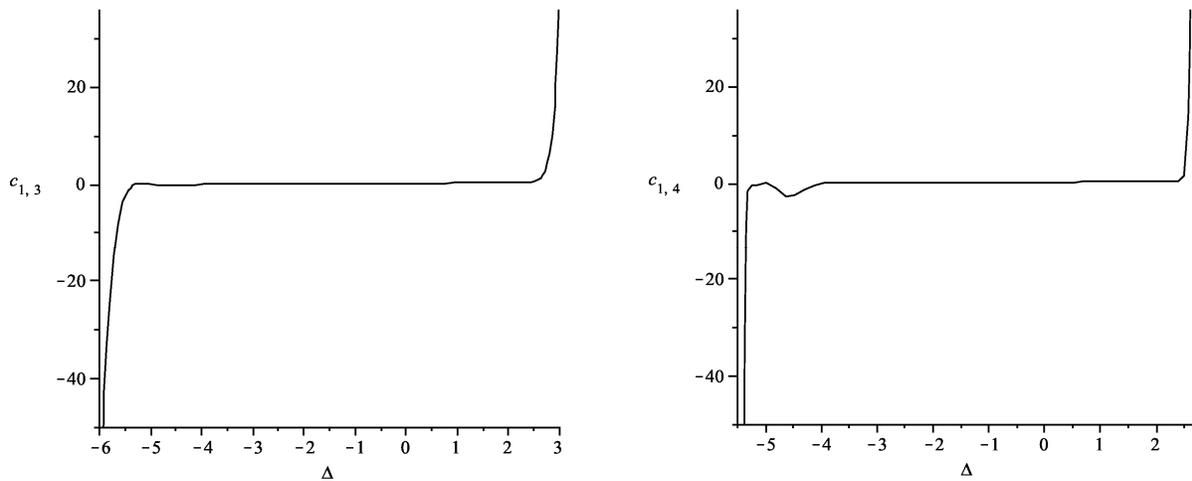


Figure 2. (Plotting the Δ -curves), the valid region Δ of the second order PTP algorithm when $h = -1$ for solving the equation (18) of Case 1 where left: the curve $c_{1,3}$ and right: the curve $c_{1,4}$

Figure 3 shows the approximate solution obtained for Equation (18) using the second order PTP algorithm (16) when $h = -1$, $\Delta = 0.1$, $M = 1000$ and $T = 100$ versus the numerical RK78 solution of (18) and also the difference between the second order PTP solution and the numerical RK78 solution. It must be emphasized that only the second order term of our algorithm was used in evaluating the approximate solution for Figure 3. It is easy to conclude from the numerical results in Figure 3 that our approximate analytical solution using the PTP algorithm is in excellent agreement with the numerical values in the large interval of t .

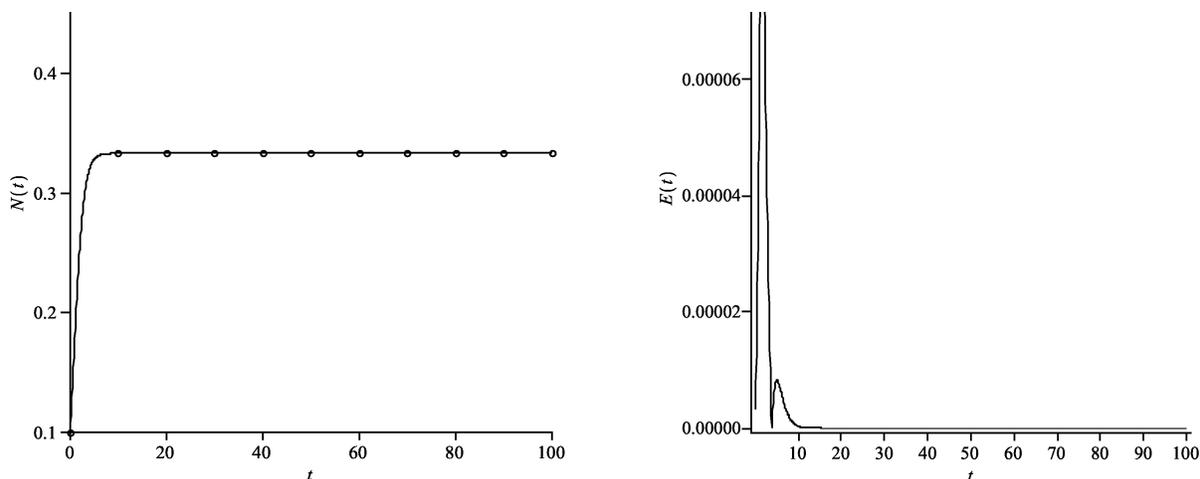


Figure 3. Approximate solution (left) and absolute error (right) of the second order PTP algorithm when $h = -1$ and $\Delta = 0.1$ for the case of the one species where Solid line: $N(t)$ and Circle symbols: $N_{RK78}(t)$

Case 2. Two species ($m = 2$)

The Lotka–Volterra equations modelling two species competing for a common ecological niche are [Batiha et al. (2007) and Chowdhury et al. (2007)]:

$$\begin{cases} \frac{dN_1}{dt} = N_1(b_1 + a_{11}N_1 + a_{12}N_2), \\ \frac{dN_2}{dt} = N_2(b_2 + a_{21}N_1 + a_{22}N_2), \end{cases} \quad (22)$$

where the constants are chosen as

$$a_{11} = -0.0014, a_{12} = -0.0012, a_{21} = -0.0009, a_{22} = -0.001, b_1 = 0.1 \text{ and } b_2 = 0.08.$$

To solve Equation (22) via the PTP algorithm (16), proceeding as before, we consider a second order PTP approximation. The approximate solution and absolute error of the second-order PTP solution when $h = -1$, $\Delta = 0.1$, $M = 1000$ and $T = 100$ are given in Figure 4. From the numerical results in Figure 4, it is easy to conclude that our approximate analytical solution using the PTP algorithm is in good agreement with the numerical values in the large interval of t .

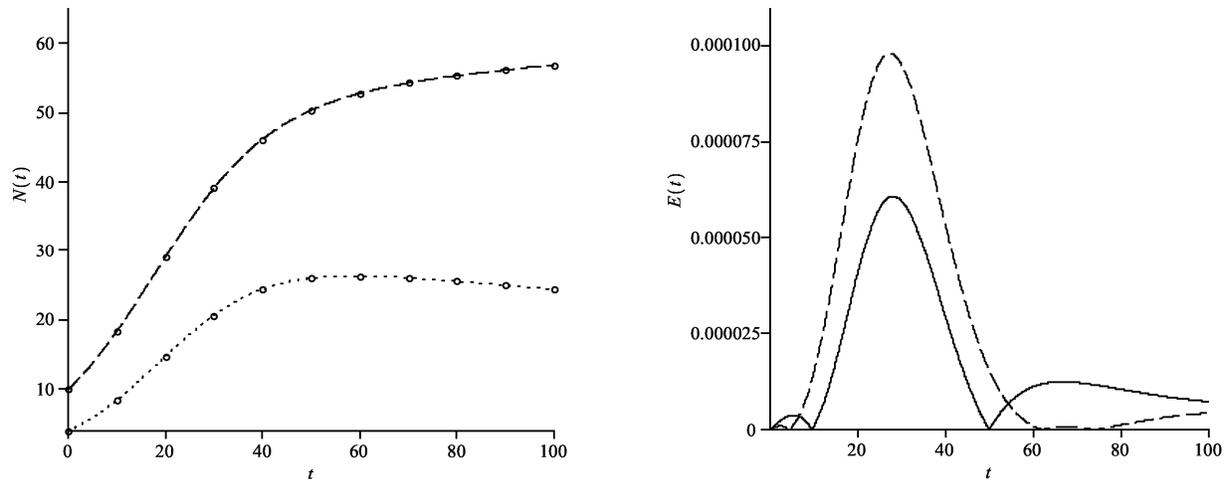


Figure 4. Approximate solution and absolute error of the second order PTP algorithm (lines) when $h = -1$ and $\Delta = 0.1$ versus the numerical RK78 solution (symbols) for the case of the two species

Case 3. Three species ($m = 3$)

The following version of the Lotka–Volterra equations modelling three species shall be used [Batiha et al. (2007)]:

$$\begin{cases} \frac{dN_1}{dt} = N_1(1 - N_1 - aN_2 - bN_3), \\ \frac{dN_2}{dt} = N_2(1 - bN_1 - N_2 - aN_3), \\ \frac{dN_3}{dt} = N_3(1 - aN_1 - bN_2 - N_3), \end{cases} \quad (23)$$

where $a = 0.1$ and $b = 0.1$, [Batiha et al. (2007) and Chowdhury et al. (2007)]. To solve Equation (23) through the PTP algorithm (16), proceeding as before, we consider a second order PTP approximation. Figure 5 reveals the approximate solution and absolute error of the second order PTP algorithm when $h = -1$, $\Delta = 0.1$, $M = 1000$ and $T = 100$ versus the numerical RK78 solution. It is convenient to conclude that our approximate analytical solution using the PTP algorithm is in superior agreement with the numerical values in the large interval of t .

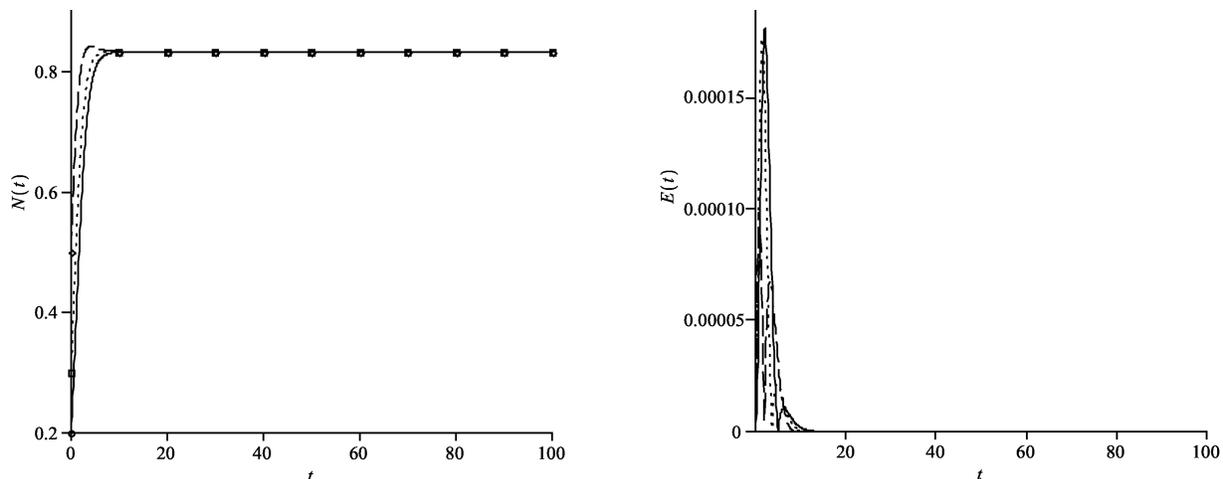


Figure 5. Approximate solution and absolute error of the second order PTP algorithm (lines) when $h = -1$ and $\Delta = 0.1$ versus the numerical RK78 solution (symbols) for the case of the three species

Remark 1.

We mention that all the results here were computed using the Maple 11. Most mentionable, however, is the fact that the authors only used the PTP algorithm with the fixed number of approximations and fixed step sizes in solving the cases given here. Although, the authors believe that the best PTP algorithm can be achieved by using a variable number of approximations and a variable step size in the series solution to obtain a specified tolerance.

Remark 2.

The convergence of the numerical classical RK4 method for solving Equation (1) depends mainly on choosing the step size Δt . While, the present PTP algorithm is rather free of this shortcoming, using for instance the classical RK4 method with $\Delta t = 3$ and greater, to solve the case 1 leads to the divergent results. As, the convergent results of utilizing the second order PTP algorithm with the fixed step sizes $\Delta t = 5, 10$ have been given in Figure 6 below.

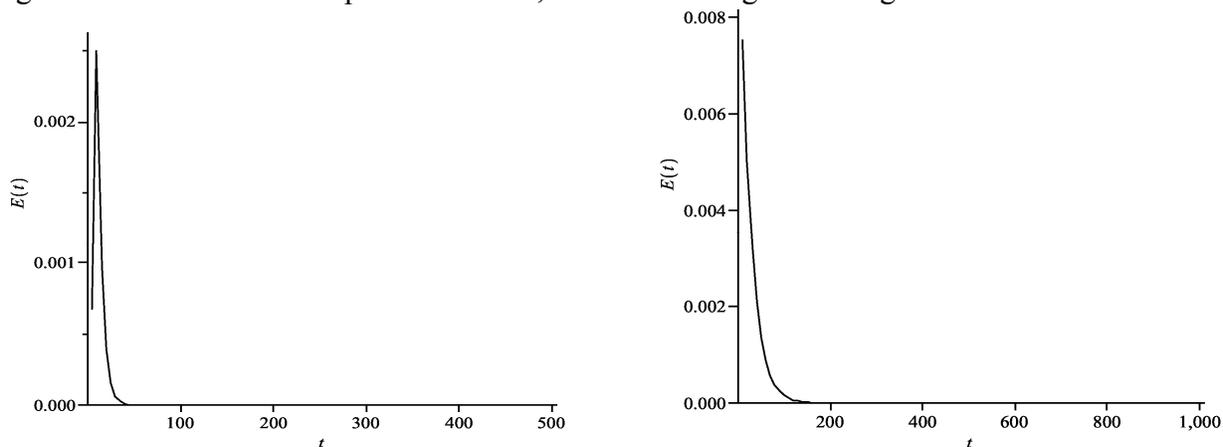


Figure 6. The absolute errors of the second order PTP algorithm when (left) $h = -0.325$ and (right) $h = -0.15$ for two large values of the fixed step size Δ for Case 1

In closing our analysis, we point out that several modeling cases of the MLVEs were tested using the PTP algorithm proposed in this paper, and the obtained results have shown excellent performance. As a result, it is easy to conclude that the PTP algorithm is a useful analytical tool for solving the MLVEs.

5. Concluding Remarks

It is shown that the solution obtained by the classical RK4 was not valid for large step size. In this paper, we proposed a technique which treated the PIM as an algorithm in a sequence of intervals for getting highly accurate approximate analytical solutions of the multispecies Lotka–Volterra equations. Unlike the purely numerical methods like the classical RK4, the solutions here are readily given in series form. Moreover, we gave a geometric scheme for determining the so-called valid region of the auxiliary parameter and the fixed step size. The obtained numerical results demonstrate that the PTP algorithm is easy to implement, accurate when applied to the MLVEs and avoids tedious computational work. This confirms our belief that the developed approach is a promising analytic tool to solve the MLVEs and more promising because it can further be applied to a wider class of nonlinear population ordinary models with highly accuracy.

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