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A Galerkin-like approach to solve continuous population models for single and interacting species

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Abstract

In this paper, we present a Galerkin-like approach to numerically solve continuous population models for single and interacting species. After taking inner product of a set of monomials with a vector obtained from the problem under consideration, the problem is transformed to a nonlinear system of algebraic equations. The solution of this system gives the coefficients of the approximate solutions. Additionally, the technique of residual correction, which aims to increase the accuracy of the approximate solution by estimating its error, is discussed in some detail. The method and the residual correction technique areillustrated with two examples. The results are also compared with numerous existing methods from the literature.

Keywords: Continuous population models; Galerkin method; logistic equation; predator-prey equation; residual error correction.

MSC :65L03 and 92D30.

1. Introduction

The utilization of differential equations in order to model biological and ecological phenomena has a fairly long history. One of the oldest, simplest and the most famous examples is the so called logistic equation first proposed by Verhulst (1845), (1847) in order to model the population growth of a certain species with respect to time. This equation is given by

$$\frac{\mathrm{d}x}{\mathrm{d}t} = rx - rx^2 \tag{1}$$

under the initial condition $x(0) = x_0$ and in the interval $0 \le t \le T$. Here $x = x(t)$ is the ratio of the population at time t to the maximum sustainable population and r is the rate of maximum population growth. This equation is separable and of first order with exact solution $x(t) = \dfrac{1}{1+\left(\dfrac{1}{x_0}-1\right)e^{-rt}}$. Logistic equation was rediscovered in 1911 by McKendrick & Kesava Pai (1911) for the growth of bacteria. Several years later, it was made popular by the work of Pearl & Reed (1922) on the population growth of the United States of America since 1790. Lastly, Lotka derived the equation again in his book (Lotka, 1925), which was the first one written on mathematical biology.

Population models where two animal species are in a predator-prey relation are present in the environment have also attracted the attention of scientists beginning from 1910s. The first such model was proposed by Lotka (1910) in relation to autocatalytic chemical reactions. Lotka then extended his work to organic systems (Lotka, 1920) and finally used his model to analyze predator-prey relations in his book (Lotka, 1925). The same model was discovered independently by Volterra (1927), who made a statistical analysis of the fish catches in the Adriatic sea circa 1926. The outcome of these studies is what is called the *Lotka-Volterra equations* given by

$$\begin{aligned} \frac{\mathrm{d}p}{\mathrm{d}t} &= ap - bpq \\ \frac{\mathrm{d}q}{\mathrm{d}t} &= cpq - dq \end{aligned} \tag{2}$$

with the initial conditions $p(0) = \lambda_p, q(0) = \lambda_q$. Here $p(t)$ and $q(t)$ respectively represent the prey and predator populations at time t according to some scale, and a, b, c, d are real parameters describing the interaction of the two species. These real parameters vary according to which species are in consideration. This constant coefficient nonlinear model, also known as *predator-prey equations* or *Lotka-Volterra equations*, is the basis of many predator-prey models that have been developed since then. A derivation of this system can be found in Volterra & Brelot (1931) and Hirsch & Smale (1974).

The problem of finding approximate solutions of the system (2) has so far attracted the attention of many researchers; as a result, many numerical methods present in the literature have been applied to this system. Among such methods we can count Adomian decomposition method (Pamuk, 2005), homotopy perturbation method (Pamuk & Pamuk, 2010), Bessel collocation method (Yüzbaşı, 2012a) and a nonstandard scheme (Mickens, 2003) similar to the finite difference method. Lotka-Volterra equations, where several predator species are competing for a common source of food have also been investigated by several authors. Such studies include approximate solutions using Adomian decomposition method (Olek, 1994), variational iteration method (Batiha *et al.,* 2007) and a modified version of He's homotopy perturbation method (Chowdhury & Rahman, 2012). For several other uses of some of these methods, the interested reader may refer to Jamshidi & Ganji (2010); Bayat *et al.* (2012); Bayat *et al.* (2015); He (2007); Wu (2011); Xu & Zhang (2009). In addition, some authors have investigated the analytical and dynamical aspects of Lotka-Volterra systems. The reader who is interested in such studies can see Gander (1994); Grozdanovski & Shepherd (2008); Murty & Rao (1987); Kim & Choo (2015).

The main interest of this study is to adopt a Galerkin-like approach in order to numerically solve the Lotka-Volterra predator-prey model given by Equation (2). In order to measure the accuracy of the method, we will also apply it to the logistic model given by Equation (1). The proposed scheme was also used by Türkyılmazoğlu (2014) in order to solve high-order Fredholm integro-differential equations.

The outline of the paper is as follows: In Section 2, we give an outline of the method. In Section 3, a technique to improve solutions is discussed. Section 4 contains two examples and their approximate solutions as well as comparison with other methods. Finally, Section 5 draws some conclusions as to the effectiveness of the scheme outlined in this paper.

2. Method of solution

In this section, we outline the procedure we will use to find approximate solutions of models (1) and (2). The method basically comprises determining an integer N and taking inner product of an expression obtained from the equations with the elements of the set of monomials $\{1,t,t^2,...,t^N\}$. This then gives rise to a set of nonlinear algebraic equations in the coefficients of the approximate solution polynomials. Although the procedure is essentially the same for models (1) and (2), for the sake of clarity we will describe them separately. All the calculations will be expressed in terms of matrices, which makes computer implementation somewhat easier. As expressed earlier, this method was used in Türkyılmazoğlu (2014), where the problem in question was solving a class of Fredholm integral equations.

2.1 Solution method for single species model

To begin with, we assume that the unique solution $x(t)$ of Equation (1) can be expressed as a polynomial of degree N, namely

$$x_N(t)=\sum_{k=0}^{N}a_k t^k=\mathbf{T}_N(t)\cdot\mathbf{A},$$

where

$$\mathbf{T}_N(t)=[1\quad t\quad t^2\quad \dots\quad t^N],\ \mathbf{A}=[a_0\quad a_1\quad a_2\quad \dots\quad a_N]^T.$$

The output of the method will be the unknown coefficients a_i. The derivative $x_N'(t)$ can also be expressed as the product of matrices as follows: If $\mathbf{B}$ is the $(N+1)\times(N+1)$ matrix defined by $\mathbf{B}_{i,i+1}=i$ for $i=1,2,\dots,N$ and $\mathbf{B}_{i,j}=0$ elsewhere, explicitly given by

$$\mathbf{B}=\begin{bmatrix}0&1&0&\dots&0\\0&0&2&\dots&0\\\vdots&\vdots&\vdots&\ddots&\vdots\\0&0&0&\dots&N\\0&0&0&\dots&0\end{bmatrix}$$

then we have $x_N'(t)=\mathbf{T}_N(t)\mathbf{BA}$. As for the nonlinear term rx^2, we proceed by defining a new matrix as follows: We denote by $\tilde{\mathbf{A}}$ the $(2N+1)\times(N+1)$ matrix with $A_{ij}=a_{i-j}$ if $j\le i\le j+N$ and $A_{ij}=0$ otherwise. Explicitly, we define $\tilde{\mathbf{A}}$ by

$$\tilde{\mathbf{A}} = \begin{bmatrix} a_0 & 0 & 0 & \dots & 0 \\ a_1 & a_0 & 0 & \dots & 0 \\ a_2 & a_1 & a_0 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ a_N & a_{N-1} & a_{N-2} & \dots & a_0 \\ 0 & a_N & a_{N-1} & \dots & a_1 \\ 0 & 0 & a_N & \dots & a_2 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & 0 & \dots & a_N \end{bmatrix}.$$

Then since $x_N(t)^2$ is a polynomial of degree $2N$ formed by multiplying $x_N(t)$ by itself, it is easy to verify the equality

$$x_N(t)^2 = \mathbf{T}_{2N}(t)\tilde{\mathbf{A}}\mathbf{A}.$$

Next step is to substitute the matrix expressions for $x_N(t), x_N^{'}(t)$ and $x_N(t)^2$ into Equation (1). Doing this, since the polynomial x_N is assumed to solve the equation, we obtain the equality

$$(\mathbf{T}_N(t)\mathbf{B} - r\mathbf{T}_N(t) + r\mathbf{T}_{2N}(t)\tilde{\mathbf{A}})\mathbf{A} = 0, \tag{3}$$

where we took the common factor $\mathbf{A}$ out of brackets. Next step is applying inner product to the equation with the elements of the set $\{1, t, t^2, \dots, t^N\}$, where the inner product is defined by

$$< f, g >= \int_a^b f(x)g(x)\mathrm{d}x.$$

Here, f and g are functions from the Hilbert space $L^2[0,T]$. In order to express the result of this inner product in a simple matrix form, we give the left-hand side of Equation (3) a name by introducing the notation

$$\mathbf{G}(t) := \mathbf{T}_N(t)\mathbf{B} - r\mathbf{T}_N(t) + r\mathbf{T}_{2N}(t)\tilde{\mathbf{A}}.$$

Then, noticing that the entries of $\mathbf{A}$ are just unknown constants, since integration is a linear operation we have the equality

$$< t^i, \mathbf{G}(t)\mathbf{A} > = < t^i, \mathbf{G}(t) > \mathbf{A}$$

which holds for all $i = 0, 1, \dots, N$. For each i, the application of this inner product yields a nonlinear equation in the unknowns $a_0, a_1, \dots, a_N$. This nonlinearity is brought about by the term $r\mathbf{T}_{2N}(t)\tilde{\mathbf{A}}$ of $\mathbf{G}(t)$. Since there are a total of $N+1$ such equations, we arrive at a system of $N+1$ nonlinear equations, which can be expressed in terms of matrices as $\mathbf{WA} = \mathbf{0}$, where each side is a vector of length $N+1$ and the entries of $\mathbf{W}$ are explicitly given as $\mathbf{W}_{i,j} =< t^{i-1}, \mathbf{G}(t)_{1,j} >$. Notice that some of the entries of $\mathbf{W}$ are constants while some of them contain expressions linear in some a_i. Since the approximate solution $x_N(t)$ of Equation (1) should satisfy the initial condition $x_N(0) = x_0$, we substitute one row of the system $\mathbf{WA} = \mathbf{0}$ with the vector equivalent of this initial condition. This vector equivalent form can be simply expressed as

$$\mathbf{T}_N(0)\mathbf{A} = \begin{bmatrix} 1 & 0 & 0 & \cdots & 0 \end{bmatrix}\mathbf{A} = x_0.$$

For the sake of being deterministic, we choose the last row of $\mathbf{W}$ as the row to be replaced and substitute the above vector for this last row. Consequently, we obtain the nonlinear system

$$\tilde{\mathbf{W}}\mathbf{A} = \begin{bmatrix} 0 & 0 & \cdots & 0 & x_0 \end{bmatrix}^T, \tag{4}$$

where $\tilde{\mathbf{W}}$ is the *modified* form of $\mathbf{W}$, explicitly given by

$$\tilde{\mathbf{W}} = \begin{bmatrix} < 1, \mathbf{G}(t)_{1,1} > & < 1, \mathbf{G}(t)_{1,2} > & \dots & < 1, \mathbf{G}(t)_{1,N+1} > \\ < t, \mathbf{G}(t)_{1,1} > & < t, \mathbf{G}(t)_{1,2} > & \dots & < t, \mathbf{G}(t)_{1,N+1} > \\ \vdots & \vdots & \vdots & \vdots \\ < t^{N-1}, \mathbf{G}(t)_{1,1} > & < t^{N-1}, \mathbf{G}(t)_{1,2} > & \dots & < t^{N-1}, \mathbf{G}(t)_{1,N+1} > \\ 1 & 0 & \dots & 0 \end{bmatrix}.$$

Let us once again note that $\tilde{\mathbf{W}}$ contains terms which are linear in some a_i; therefore the system (4) is nonlinear. Solving it yields the unknown constants $a_0, a_1, \dots, a_N$, hence the approximate solution $x_N(t) = \sum_{k=0}^{N} a_k t^k$.

2.2 Solution method for predator-prey model

Our method for the model (2) will be more or less the same as the single species model (1), except that this time two equations are concerned, so a small arrangement will be necessary. To begin with, let $p_N(t)$ and $q_N(t)$ denote the approximate solutions for the prey and predator populations at time t, respectively. As before, we have

$$p_N(t)=\sum_{k=0}^{N}p_k t^k \text{ and } q_N(t)=\sum_{k=0}^{N}q_k t^k,$$

which can be expressed in terms of matrices as $p_N(t)=\mathbf{T}_N(t)\mathbf{P}$ and $q_N(t)=\mathbf{T}_N(t)\mathbf{Q}$. This time there are $2N+2$ unknown constants to be determined, which are $p_0,p_1,\dots,p_N$ and $q_0,q_1,\dots,q_N$. Following the same procedure as in the single species case, we arrive at the matrix equations

$$\begin{aligned}\left(\mathbf{T}_N(t)\mathbf{B}-a\mathbf{T}_N(t)+b\mathbf{T}_{2N}(t)\tilde{\mathbf{Q}}\right)\mathbf{P}=0,\\ \left(\mathbf{T}_N(t)\mathbf{B}+c\mathbf{T}_N(t)-d\mathbf{T}_{2N}(t)\tilde{\mathbf{P}}\right)\mathbf{Q}=0.\end{aligned}\tag{5}$$

Here $\tilde{\mathbf{P}}$ and $\tilde{\mathbf{Q}}$ are $(2N+1)\times(N+1)$ matrices with $P_{ij}=p_{i-j},Q_{ij}=q_{i-j}$ if $j\le i\le j+N$ and $P_{ij}=Q_{ij}=0$ otherwise, just as we defined $\tilde{\mathbf{A}}$ for the single species case. Adopting a similiar notation, this time we define

$$\begin{aligned}\mathbf{G}^p(t)&:=\mathbf{T}_N(t)\mathbf{B}-a\mathbf{T}_N(t)+b\mathbf{T}_{2N}(t)\tilde{\mathbf{Q}},\\ \mathbf{G}^q(t)&:=\mathbf{T}_N(t)\mathbf{B}+c\mathbf{T}_N(t)-d\mathbf{T}_{2N}(t)\tilde{\mathbf{P}}.\end{aligned}$$

Then, performing the inner products of the expressions in Equations (5) with the monomials $1,t,\dots,t^N$, we obtain two nonlinear systems which can be expressed as

$$\mathbf{W}^p\mathbf{P}=\mathbf{0},\mathbf{W}^q\mathbf{Q}=\mathbf{0},\tag{6}$$

where $\mathbf{W}^p_{i,j}=<t^{i-1},\mathbf{G}^p(t)_{1,j}>$ and $\mathbf{W}^q_{i,j}=<t^{i-1},\mathbf{G}^q(t)_{1,j}>$ Then, as before we feed the initial conditions $p(0)=\lambda_p,q(0)=\lambda_q$ to the system 6. This amounts to replacing the last rows of $\mathbf{W}^p$ and $\mathbf{W}^q$ with the row $[1\ \ 0\ \ \cdots\ \ 0]$ and replacing the last entry of the zero vectors on the right-hand side of system (6) with λ_p and λ_q, respectively. These substitutions then give rise to the following two systems:

$$\tilde{\mathbf{W}}^p\mathbf{P}=[0\ \ \dots\ \ 0\ \ \lambda_p]^T,\tilde{\mathbf{W}}^q\mathbf{Q}=[0\ \ \dots\ \ 0\ \ \lambda_q]^T.\tag{7}$$

Here each system is a nonlinear system of $N+1$ equations in $2N+2$ unknowns. This comes from the fact that $\tilde{\mathbf{W}}^p$ has entries containing some q_i and $\tilde{\mathbf{W}}^q$ has entries containing some p_i. Therefore, on the whole there are $2N+2$ nonlinear equations in $2N+2$ unknowns. Although the systems (7) are thus perfectly sufficient for the purpose of determining the unknown coefficients p_i and q_i for $i=0,1,\dots,N$, one might desire to express these two systems in the form of a single system of equations just like the system (4). For that purpose we will define three new matrices by means of concatenating the already defined ones. First is the new $(2N+2)\times(2N+2)$ coefficient matrix formed by using the separate coefficient matrices $\tilde{\mathbf{W}}^p$ and $\tilde{\mathbf{W}}^q$ as follows:

$$\tilde{\mathbf{W}}^{pq}:=\begin{bmatrix}\tilde{\mathbf{W}}^p & \mathbf{0}_{(N+1)\times(N+1)}\\ \mathbf{0}_{(N+1)\times(N+1)} & \tilde{\mathbf{W}}^q\end{bmatrix},$$

where $\mathbf{0}_{(N+1)\times(N+1)}$ stands for the $(N+1)\times(N+1)$ square matrix with all entries equal to zero. Second matrix is just the length-$2N+2$ vector of unknowns given explicitly as

$$\mathbf{U}:=[\mathbf{P}\quad\mathbf{Q}]=[p_0\quad p_1\quad\cdots\quad p_N\quad q_0\quad q_1\quad\cdots\quad q_N]^T.$$

Third matrix is the right-hand side of the new system, formed by concatenating the right-hand sides of the systems (7) in the same manner:

$$\mathbf{F}:=[0\quad\cdots\quad 0\quad\lambda_p\quad 0\quad\cdots\quad 0\quad\lambda_q]^T.$$

After these preparations the aforementioned single system of $2N+2$ equations in the $2N+2$ unknowns is given by

$$\tilde{\mathbf{W}}^{pq}\mathbf{U}=\mathbf{F}.$$

Solving this system yields the unknowns $p_0,p_1,\dots,p_N,q_0,q_1,\dots,q_N$ and hence the approximate solutions $p_N(t)=\sum_{k=0}^{N}p_k t^k$ and $q_N(t)=\sum_{k=0}^{N}q_k t^k$.

3. Error estimation and residual correction

In this section, we outline a method known as *residual correction*, the purpose of which is to obtain better solutions using the existing ones. This technique is based on the observation that substitution of an approximate solution in the equation gives rise to a new equation, similar to the original one in structure, in the error of that particular approximate solution. Then, the same method of solution is used to solve the new equation, thus yielding an *estimation* of the error function. Residual correction has been employed in connection with many numerical methods and many different kinds of equations. An example of how it is utilized in the case of other kinds of equations, e.g. Riccati type differential equation systems, can be found in (Yüzbaşı, 2012b).

Although the idea behind the technique of residual correction is essentially the same for the single species model (1) and the predator-prey model (2), we treat the two cases separately for the sake of completeness.

3.1 The case of single species model

Now, we consider the logistic model given by Equation (1) with its exact solution $x(t)$ and its approximate solution $x_N(t) = \sum_{k=0}^{N} a_k t^k$ obtained by the method of the previous section. We then consider the error of this solution given by $e_N(t) = x(t) - x_N(t)$. Note that we can express $x(t)$ in terms of $e_N(t)$ and $x_N(t)$ as $x(t) = x_N(t) + e_N(t)$. On the other hand, since $x(t)$ is the exact solution, it satisfies the logistic equation. This gives us the following:

$$\begin{aligned} x'(t) - rx(t) + rx^2(t) &= (x_N'(t) + e_N'(t)) - r(x_N(t) + e_N(t)) \\ &\quad + r(x_N(t) + e_N(t))^2 \\ &= e_N'(t) - re_N(t) + re_N(t)^2 + 2rx_N(t)e_N(t) + R_N(t) = 0. \end{aligned} \tag{8}$$

This is a first order nonlinear equation in the unknown function e_N with nonhomogeneous term

$$R_N(t) = x_N'(t) - rx_N(t) + rx_N(t)^2.$$

This nonhomogeneous term is called the *residual* of the approximate solution $x_N(t)$. In general, the residual of a function f related to a certain equation is simply the resulting function after substituting f in that particular equation. The residual of the exact solution of any equation is thus zero.

Next step in the technique of residual correction is just to apply the method of Section 2 to Equation (8). Since Equation (8) is not the same as the logistic Equation (1), a short explanation is in order. The difference comes from the additional terms $2rx_N(t)e_N(t)$ and $R_N(t)$. Before following the footsteps of the method of Section 2, we take the nonhomogeneous term $R_N(t)$ to the right-hand side and write Equation (8) as

$$e_N'(t) - re_N(t) + re_N(t)^2 + 2rx_N(t)e_N(t) = -R_N(t) \tag{9}$$

with the initial condition

$$e_N(0) = x(0) - x_N(t) = 0 - 0 = 0.$$

We then pick a positive integer M and decide to approximate the solution $e_N(t)$ to this equation with the M-th degree polynomial $e_{NM}(t) = \sum_{k=0}^{M} e_{N,k} t^k$. Next, in the style of Section 2, we write Equation (9) in terms of matrices. The matrix equivalent of $e_{NM}(t)$ is $\mathbf{T}_M(t)\mathbf{E}$, where $\mathbf{E}$ is a column matrix of $M+1$ entries with i-th entry equal to the unknown $e_{N,i-1}$. In this case, we are left with

$$\begin{aligned} \left(\mathbf{T}_M(t)\mathbf{B} - r\mathbf{T}_M(t) + r\mathbf{T}_{2M}(t)\tilde{\mathbf{E}} + 2r\mathbf{T}_{N+M+1}(t)\tilde{\mathbf{A}}\right)\mathbf{E} = \\ -R_N(t), \end{aligned} \tag{10}$$

where $\tilde{\mathbf{E}}$ is a $(2M+1)\times(M+1)$ matrix with $\tilde{\mathbf{E}}_{ij} = e_{N,i-j}$ if $j \le i \le j+M$ and $\tilde{\mathbf{E}}_{ij} = 0$ otherwise. Notice that this time $\mathbf{B}$ is a $(M+1)\times(M+1)$ matrix and $\tilde{\mathbf{A}}$ is a $(N+M+1)\times(M+1)$ matrix with $A_{ij} = a_{i-j}$ if $j \le i \le j+N$ and $A_{ij} = 0$ otherwise. Notice also that the entries of $\tilde{\mathbf{A}}$ are known this time since we have already computed $x_N(t)$. Defining

$$\mathbf{G}(t) := \mathbf{T}_M(t)\mathbf{B} - r\mathbf{T}_M(t) + r\mathbf{T}_{2M}(t)\tilde{\mathbf{E}} + 2r\mathbf{T}_{2M}(t)\tilde{\mathbf{P}}$$

and taking inner product of Equation (10) with the set $\{1,t,t^2,\dots,t^M\}$ yields the nonlinear system $\mathbf{WE}=\mathbf{R}$, where $\mathbf{W}$ is a $(M+1)\times(M+1)$ matrix with $\mathbf{W}_{i,j}=<t^{i-1},\mathbf{G}(t)_{1,j}>$ and $\mathbf{R}$ is a column matrix of length-M+1 with $\mathbf{R}_{i,1}=<t^{i-1},-R_N(t)>$. Since we would like the approximate solution $e_{NM}(t)$ for $e_N(t)$ to satisfy the initial condition $e_N(0)=0$ as well, we feed the matrix equivalent, which is $\mathbf{T}_M(0)\mathbf{E}=0,$ to the system $\mathbf{WE}=\mathbf{R}$. To this end, replacing the last rows $\mathbf{W}$ and the last entry of $\mathbf{R}$ with $\mathbf{T}_M(0)$ and 0, respectively, yields the final (nonlinear) system

$$\tilde{\mathbf{W}}\mathbf{E}=\tilde{\mathbf{R}}.$$

Solving this we acquire the coefficients $e_{N,0},e_{N,1},\dots,e_{N,M}$ and hence the approximation $e_{NM}(t)$ to the error function $e_N(t)$.

A useful remark about residual correction is now in order. The function $e_{NM}(t)$ that we have found as the approximate solution to Equation (9) is our *estimation* to the exact error function $e_N(t)=x(t)-x_N(t)$. We will use this estimation to set up a new approximate solution $x_{NM}(t)$, which is hopefully, compared to $x_N(t)$, a better approximation to the exact solution $x(t)$ of the logistic Equation (1). Since $x(t)=x_N(t)+e_N(t)$ and $e_{NM}(t)$ is our estimation for $e_N(t)$, this new approximate solution is just

$$x_{NM}(t)=x_N(t)+e_{NM}(t).$$

The approximate solution $x_{NM}(t)$ thus obtained is called the *corrected solution*. The accuracy of this corrected solution is directly related to the accuracy of our estimation $e_{NM}(t)$ for the error function $e_N(t)$. Namely, we have

$$\begin{aligned}x_{NM}(t)-x(t)&=(x_N(t)+e_{NM}(t))-(x_N(t)+e_N(t))\\&=e_{NM}(t)-e_N(t).\end{aligned}\tag{11}$$

Therefore, the error in $x_{NM}(t)$ is simply the same as the error in $e_{NM}(t)$, which is natural since knowing the error function exactly means knowing the exact solution. This situtation shows the importance of the technique of residual correction. The numerical examples that will be presented in the subsequent section will give an idea as to its effectiveness. In what follows, the actual error of $x_{NM}(t)$ given in Equation (11) will be denoted by $E_{NM}(t)$.

3.2 The case of predator-prey model

In the same fashion as we did for the single species model, we now start by considering the error functions of the solutions belonging to the Lotka-Volterra equations given by (2). Let the error function corresponding to the prey population be $e_{p,N}(t)=p(t)-p_N(t)$ and the error function corresponding to the predator population be $e_{q,N}(t)=q(t)-q_N(t)$. Since $p(t)$ and $q(t)$ are the exact solutions, after some simplifications their substitution into (2) will give rise to the following two equations

$$\begin{aligned}&e'_{p,N}(t)-ae_{p,N}(t)+b(e_{p,N}(t)e_{q,N}(t)\\&+q_N(t)e_{p,N}(t)+p_N(t)e_{q,N}(t))+R_N^p(t)=0,\end{aligned}\tag{12}$$

$$\begin{aligned}&e'_{q,N}(t)+de_{q,N}(t)-c(e_{p,N}(t)e_{q,N}(t)\\&+q_N(t)e_{p,N}(t)+p_N(t)e_{q,N}(t))+R_N^q(t)=0\end{aligned}\tag{13}$$

with the initial conditions $e_{p,N}(0)=e_{q,N}(0)=0.$ Here

$$\begin{aligned}R_N^p(t)&=p'_N(t)-ap_N(t)+bp_N(t)q_N(t),R_N^q(t)\\&=q'_N(t)+cq_N(t)-dp_N(t)q_N(t)\end{aligned}$$

are the residual functions of approximate prey population $p(t)$ and approximate predator population $q(t)$, respectively. Choosing a positive integer M, let $e_{p,NM}(t)$ and $e_{q,NM}(t)$ denote the approximate solutions to Equations (12) and (13) given by

$$e_{p,NM}(t)=\sum_{k=0}^{M}e_{p,N,k}t^k=\mathbf{T}_M(t)\mathbf{E}^p$$

and

$$e_{q,NM}(t)=\sum_{k=0}^{M}e_{q,N,k}t^k=\mathbf{T}_M(t)\mathbf{E}^q,$$

where $e_{p,N,0},\dots,e_{p,N,M}$ and $e_{q,N,0},\dots,e_{q,N,M}$ are unknown constants to be determined. Then, the matrix expressions of Equations (12) and (13) become

$$\left(\mathbf{T}_M(t)\mathbf{B}-a\mathbf{T}_M(t)+b\mathbf{T}_{2M}(t)\tilde{\mathbf{E}}^q+b\mathbf{T}_{N+M}(t)\tilde{\mathbf{Q}}\right)\mathbf{E}^p$$
$$+b\mathbf{T}_{N+M}(t)\tilde{\mathbf{P}}\mathbf{E}^q=-R_N^p(t),$$
$$\left(\mathbf{T}_M(t)\mathbf{B}+d\mathbf{T}_M(t)-c\mathbf{T}_{2M}(t)\tilde{\mathbf{E}}^p-c\mathbf{T}_{N+M}(t)\tilde{\mathbf{P}}\right)\mathbf{E}^q$$
$$-c\mathbf{T}_{N+M}(t)\tilde{\mathbf{Q}}\mathbf{E}^p=-R_N^q(t).$$

This time, $\tilde{\mathbf{E}}^p$ and $\tilde{\mathbf{E}}^q$ are $(2M+1)\times(M+1)$ matrices with $\tilde{\mathbf{E}}_{ij}^p=e_{p,N,i-j}$ and $\tilde{\mathbf{E}}_{ij}^q=e_{q,N,i-j}$ if $j\le i\le j+M$ and $\tilde{\mathbf{E}}_{ij}^p=\tilde{\mathbf{E}}_{ij}^q=0$ otherwise, whereas $\tilde{Q}$ and $\tilde{P}$ are $(N+M+1)\times(M+1)$ with entries as defined earlier. Proceeding as we did earlier, as a preparation to taking inner product we introduce some new notation as follows:

$$\mathbf{G}^{p1}(t):=\mathbf{T}_M(t)\mathbf{B}-a\mathbf{T}_M(t)+b\mathbf{T}_{2M}(t)\tilde{\mathbf{E}}^q+b\mathbf{T}_{N+M}(t)\tilde{\mathbf{Q}},$$
$$\mathbf{G}^{p2}(t):=b\mathbf{T}_{N+M}(t)\tilde{\mathbf{P}},$$
$$\mathbf{G}^{q1}(t):=\mathbf{T}_M(t)\mathbf{B}+d\mathbf{T}_M(t)-c\mathbf{T}_{2M}(t)\tilde{\mathbf{E}}^p-c\mathbf{T}_{N+M}(t)\tilde{\mathbf{P}},$$
$$\mathbf{G}^{q2}(t):=-c\mathbf{T}_{N+M}(t)\tilde{\mathbf{Q}}.$$

Then, taking inner product of both equations with the set $\left\{1,t,\dots,t^M\right\}$ yields the two systems

$$\mathbf{W}^{p1}\mathbf{E}^p+\mathbf{W}^{p2}\mathbf{E}^q=\mathbf{R}^p$$

and

$$\mathbf{W}^{q1}\mathbf{E}^q+\mathbf{W}^{q2}\mathbf{E}^p=\mathbf{R}^q,$$

where the coefficient matrices $\mathbf{W}$ are $(M+1)\times(M+1)$ with $\mathbf{W}_{jk}^{pi}=<\mathbf{G}^{pi}(t)_{1,k},t^{j-1}>$ and $\mathbf{W}_{jk}^{qi}=<\mathbf{G}^{qi}(t)_{1,k},t^{j-1}>$ for $i=1,2$. Likewise, the right-hand sides of the two systems are determined by $\mathbf{R}_{j,1}^p=<-R_N^p(t),t^{j-1}>$ and $\mathbf{R}_{j,1}^q=<-R_N^q(t),t^{j-1}>$ for $j=1,2,\dots,M+1$. Then, there still remain to feed the initial conditions $e_{p,NM}(0)=0$ and $e_{q,NM}(0)=0$ to the systems. For that purpose, we replace the last rows of $\mathbf{W}^{p1}$, $\mathbf{W}^{p2}$, $\mathbf{W}^{q1}$ and $\mathbf{W}^{q2}$ with $\mathbf{T}_M(0)$, thus forming the matrices $\tilde{\mathbf{W}}^{p1}$, $\tilde{\mathbf{W}}^{p2}$, $\tilde{\mathbf{W}}^{q1}$ and $\tilde{\mathbf{W}}^{q2}$, and replacing the first entries of $\mathbf{R}^p$ and $\mathbf{R}^q$ with 0, thus forming $\tilde{\mathbf{R}}^p$ and $\tilde{\mathbf{R}}^q$. After these operations we are left with the following two modified systems:

$$(1)\ \tilde{\mathbf{W}}^{p1}\mathbf{E}^p+\tilde{\mathbf{W}}^{p2}\mathbf{E}^q=\tilde{\mathbf{R}}^p,\ (2)\ \tilde{\mathbf{W}}^{q1}\mathbf{E}^q+\tilde{\mathbf{W}}^{q2}\mathbf{E}^p=\tilde{\mathbf{R}}^q. \quad (14)$$

Each of these two systems consists of $M+1$ nonlinear equations in the unknown coefficients $e_{p,N,i}$ and $e_{q,N,i}$ for $i=0,1,\dots,M$. Solving systems (14), we obtain these $2M+2$ coefficients and hence the estimated error functions $e_{p,NM}(t)$ and $e_{q,NM}(t)$. Finally, using these estimations of the actual error functions $e_{p,N}(t)$ and $e_{q,N}(t)$, we obtain the new approximate solutions $p_{NM}(t)=p_N(t)+e_{p,NM}(t)$ and $q_{NM}(t)=q_N(t)+e_{q,NM}(t)$ for the prey population $p(t)$ and the predator population $q(t)$. Next section will give an idea on how much accuracy is provided by the residual correction technique applied to the predator-prey model (2).

4. Numerical examples

In this section we consider two examples, one a single species model and the other a predator-prey model. To each of these examples we find a number of approximate solutions using the method of Section 2 and compare the results with a few methods from the literature. In addition, we apply residual correction to these numerical solutions and thus investigate how much improvement is provided by this technique in each case.

Example 1: Let us consider the following logistic equation studied in Pamuk (2005); Pamuk & Pamuk (2010); Yüzbaşı (2012a):

$$\frac{\mathrm{d}x}{\mathrm{d}t} = x - x^2, x(0) = 2. \tag{15}$$

This is Equation (1) with $r = 1$ and $x_0 = 2$. The exact solution is $x(t) = \dfrac{2}{2 - e^{-t}}$. Let us take $N = 3$ and numerically solve it using our method. Our purpose is to obtain $x_3(t) = a_0 + a_1 t + a_2 t^2 + a_3 t^3$ by determining the coefficients a_0, a_1, a_2 and a_3. We begin with writing Equation (15) in matrix form. To this end, we have

$$\mathbf{T}_3(t) = \begin{bmatrix} 1 \\ t \\ t^2 \\ t^3 \end{bmatrix}^T, \mathbf{B} = \begin{bmatrix} 0 & 1 & 0 & 0 \\ 0 & 0 & 2 & 0 \\ 0 & 0 & 0 & 3 \\ 0 & 0 & 0 & 0 \end{bmatrix}, \mathbf{A} = \begin{bmatrix} a_0 \\ a_1 \\ a_2 \\ a_3 \end{bmatrix},$$

$$\tilde{\mathbf{A}} = \begin{bmatrix} a_0 & 0 & 0 & 0 \\ a_1 & a_0 & 0 & 0 \\ a_2 & a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 & a_0 \\ 0 & a_3 & a_2 & a_1 \\ 0 & 0 & a_3 & a_2 \\ 0 & 0 & 0 & a_3 \end{bmatrix}.$$

Thus, the matrix expression 3 for Equation (15) becomes

$$\begin{bmatrix} a_0 - 1 + a_1 t + a_2 t^2 + a_3 t^3 \\ 1 + (a_0 - 1)t + a_1 t^2 + a_2 t^3 + a_3 t^4 \\ 2t + (a_0 - 1)t^2 + a_1 t^3 + a_2 t^4 + a_3 t^5 \\ 3t^2 + (a_0 - 1)t^3 + a_1 t^4 + a_2 t^5 + a_3 t^6 \end{bmatrix}^T \begin{bmatrix} a_0 \\ a_1 \\ a_2 \\ a_3 \end{bmatrix} = 0.$$

Taking inner product of this equation with the set $\{1, t, t^2, t^3\}$ yields the following nonlinear equations in a_0, a_1, a_2, a_3:

$$(1)\ a_0^2 - a_0 + \frac{a_1}{2} + a_0 a_1 \frac{a_1^2}{3} + \frac{2a_2}{3} + \frac{2a_0 a_2}{3} + \frac{a_1 a_2}{2} + \frac{a_2^2}{5} + \frac{3a_3}{4} + \frac{a_0 a_3}{2} + \frac{2a_1 a_3}{5} + \frac{a_2 a_3}{3} + \frac{a_3^2}{7} = 0.$$

$$(2)\ -\frac{a_0}{2} + \frac{a_0^2}{2} + \frac{a_1}{6} + \frac{2a_0 a_1}{3} + \frac{a_1^2}{4} + \frac{5a_2}{12} + \frac{a_0 a_2}{2} + \frac{2a_1 a_2}{5} + \frac{a_2^2}{6} + \frac{11a_3}{6} + \frac{2a_0 a_3}{5} + \frac{a_1 a_3}{3} + \frac{2a_2 a_3}{7} + \frac{a_3^2}{8} = 0.$$

$$(3)\ -\frac{a_0}{3} + \frac{a_0^2}{3} + \frac{a_1}{12} + \frac{a_0 a_1}{2} + \frac{a_1^2}{5} + \frac{3a_2}{10} + \frac{2a_0 a_2}{5} + \frac{a_1 a_2}{3} + \frac{a_2^2}{7} + \frac{13a_3}{30} + \frac{a_0 a_3}{3} + \frac{2a_1 a_3}{7} + \frac{a_2 a_3}{4} + \frac{a_3^2}{9} = 0.$$

$$(4)\ -\frac{a_0}{4} + \frac{a_0^2}{4} + \frac{a_1}{20} + \frac{2a_0 a_1}{5} + \frac{a_1^2}{6} + \frac{7a_2}{30} + \frac{a_0 a_2}{3} + \frac{2a_1 a_2}{7} + \frac{a_2^2}{8} + \frac{5a_3}{14} + \frac{2a_0 a_3}{7} + \frac{a_1 a_3}{4} + \frac{2a_2 a_3}{9} + \frac{a_3^2}{10} = 0.$$

The initial condition $x_3(0) = 2$ simply means $a_0 = 2$, so we simply replace the last equation with $a_0 = 2$. Solving the remaining three equations under the constraint $a_0 = 2$ yields the solution $a_1 = -1.8519683183$, $a_2 = 1.7592176788$, $a_3 = -0.6819806307$. As a result, the approximate solution to Equation (15) becomes

$$x_3(t) = 2 - 1.8519683183t + 1.7592176788t^2 - 0.6819806307t^3.$$

This scheme can be implemented for any value of the parameter N. We applied it to Equation (15) for $N = 5, 6, 8, 10$ and the results are as follows:

$$x_5(t) = 2 - 1.9866363518t + 2.7596921681t^2 - 2.8848489480t^3 + 1.8494306309t^4 - 0.5122378725t^5,$$

$$x_6(t) = 2 - 1.9962749995t + 2.9095764496t^2 - 3.6011827843t^3 + 3.3067174321t^4 - 1.8407187161t^5 + 0.4472822911t^6,$$

$$x_8(t) = 2 - 1.9996012716t + 2.9856043501t^2 - 4.1583695620t^3 + 5.1879423127t^4 - 5.1643541739t^5 + 3.6033394438t^6 - 1.5105852289t^7 + 0.2814238033t^8,$$

$$x_{10}(t) = 2 - 1.9983956978t + 2.9465515044t^2 - 3.7497963961t^3 + 3.2040718121t^4 - 0.1106999873t^5 - 3.1477448760t^6 + 2.2159209023t^7 + 1.3282519525t^8 - 2.1932690836t^9 + 0.7305095435t^{10}.$$

In order to measure the accuracy of these solutions, we consider the absolute actual error functions given by $|e_N(t)| = |x(t) - x_N(t)|$. Since the exact solution is available in this case, we can easily obtain the actual error functions for any N value and compare these functions with the actual error functions resulting from the application of other numerical methods. In Table 1, the absolute actual error functions for Equation (15) resulting from the Adomian decomposition method (Pamuk, 2005), He's Homotopy perturbation method (Pamuk & Pamuk, 2010), Bessel collocation method (Yüzbaşı, 2012a) and the present method are compared for various choices of the parameter N and for several values of time t. The interested reader can find the details of these methods in Adomian (1988); He (1999); Yüzbaşı (2012a). As for the results of the comparison, it is seen that the errors resulting from the present method is smaller than the errors of the other methods obtained with the same value of the parameter N. In addition, the present scheme has the advantage that its absolute error functions behave rather smoothly in the interval [0,1]; as can be seen from Table 1, $|e_N(t)|$ values do not exhibit dramatic changes for the test values chosen from this interval. Another important observation we can make is that increasing N does not necessarily mean reduced errors, as $|e_{10}(t)| \geq |e_8(t)|$ for all t values.

We also try to improve the already obtained solutions $x_3(t)$ and $x_6(t)$ by the technique of residual correction described in Section 3.1. For this purpose we choose $M = 5,6,8$ for $N = 3$ and $M = 7,8,9$ for $N = 6$. The process simply consists of calculating the estimated error function $e_{NM}(t)$ for each choice of (N, M) pairs and then setting up the new approximate solution $x_{NM}(t) = x_N(t) + e_{NM}(t)$. For instance, for $N = 3$ and $M = 5$ we obtain the estimated error function $e_{35}(t)$ as follows:

$$e_{35}(t) = -0.1346680335t + 1.0004744894t^2 - 2.2028683174t^3$$
$$+1.8494306311t^4 - 0.5122378726t^5.$$

Therefore, since $x_3(t)$ was calculated earlier, the corresponding corrected solution becomes

$$x_{35}(t) \;=\; x_3(t) + e_{35}(t)$$
$$= 2 - 1.9866363518t + 2.7596921681t^2 - 2.8848489482t^3$$
$$+1.8494306311t^4 - 0.5122378726t^5.$$

The other corrected solutions can be calculated in a similar manner. In order to understand how much better these corrected solutions are in comparison to the previously obtained solutions $x_N(t)$, it will be useful to compare the error functions, in the manner that was described at the end of Section 3.1. Namely, since $E_{NM}(t)$ is the actual error of the corrected solution $x_{NM}(t)$, comparing it to the actual error $e_N(t)$ of $x_N(t)$ will reveal the effectiveness of residual correction. In Figure 1, the absolute actual error functions $|e_3(t)|$ and $|e_6(t)|$ of the approximate solutions $x_3(t)$ and $x_6(t)$ are compared with the absolute actual error functions $|E_{NM}(t)|$ corresponding to their three improvements. It is seen that both for $N = 3$ and $N = 6$, residual correction significantly reduces the absolute error values.

Since the remark we made just before Section 3.2 relates the success of residual correction process to that of the error estimations $e_{NM}(t)$, it can be interesting to compare the error functions $e_N(t)$ to our estimations $e_{NM}(t)$ for these functions. In Table 2, the actual

Table 1. Absolute error values at some points for Example 1.

t	ADM (actual errors)		Present method (actual errors)		HPM (actual errors)	
	$\lvert e_3(t)\rvert$	$\lvert e_5(t)\rvert$	$\lvert e_3(t)\rvert$	$\lvert e_5(t)\rvert$	$\lvert e_6(t)\rvert$	$\lvert e_8(t)\rvert$
0	0	0	0	0	0	0
0.2	0.0077	6.4611E-4	0.0014	3.1731E-4	1.8643E-4	1.5521E-5
0.4	0.1014	0.0337	0.0071	2.4464E-4	0.0194	0.0064
0.6	0.4341	0.3253	0.0034	5.3748E-5	0.2816	0.2110
0.8	1.1884	1.5830	0.0054	2.3628E-4	1.8270	2.4338
1	2.5587	5.3254	1.3094E-4	4.7008E-8	7.6829	15.991
t	Present method (actual errors)			BCM (actual errors)		
	$\lvert e_6(t)\rvert$	$\lvert e_8(t)\rvert$	$\lvert e_{10}(t)\rvert$	$\lvert e_3(t)\rvert$	$\lvert e_6(t)\rvert$	
0	0	0	0	0	0	
0.2	4.5167E-5	2.9698E-6	1.0794E-5	0.0098	1.4442E-4	
0.4	6.0264E-5	3.7031E-6	1.8150E-5	0.0086	6.9504E-5	
0.6	6.9106E-5	2.8054E-6	1.7900E-5	0.0026	3.9746E-5	
0.8	5.6255E-5	1.8500E-6	1.4082E-5	0.0065	1.1093E-4	
1	5.7946E-10	6.0696E-11	3.2620E-10	0.0787	0.0022	

Table 2. Actual errors and their estimations at some points for some values of the parameters N and M for Example 1.

t	Act. error $\lvert e_3(t)\rvert$	Est.error $\lvert e_{35}(t)\rvert$	Est.error $\lvert e_{38}(t)\rvert$	Act. error $\lvert e_6(t)\rvert$	Est.error $\lvert e_{67}(t)\rvert$	Est.error $\lvert e_{69}(t)\rvert$
0	0	0	0	0	0	0
0.2	0.0014250	0.0017424	0.0014243	4.5166E-5	4.9201E-5	4.7665E-5
0.4	0.0070806	0.0073252	0.0070770	6.0264E-5	6.7237E-5	6.4123E-5
0.6	0.0033512	0.0034050	0.0033516	6.9105E-5	7.3236E-5	7.2861E-5
0.8	0.0053863	0.0056226	0.0053883	5.6255-5	6.0710E-5	5.8792E-5
1	1.3094E-4	1.E3089-4	1.3094E-4	5E-10	1.4E-9	1.4E-9

absolute error functions $|e_3(t)|$ and $|e_5(t)|$ are compared with their two improvements. It is seen that as M gets larger, the estimated error values $e_{NM}(t)$ gets closer to the actual error $e_N(t)$. For a fixed N, this explains why $x_{NM}(t)$ turns out to be a better approximation to the exact solution $x(t)$ as we increase M.

Our last comments on Example 1 will be about the graph of the solution. Figure 2 depicts the exact solution along with the approximate solutions we have found for three different values of N. Since the approximate solutions are close to the exact solution, the graphs of these four solutions are seen as a single graph. The population of the animal species exhibits a decrease in the interval [0,1] although the pace of this decrease is in decrease itself. This is brought about by the fact that the derivative of the population with respect to time, which is $x-x^2$, is negative and decreasing on the interval $(1,2]$. Since the exact solution $x(t)=\dfrac{2}{2-e^{-t}}$ is also decreasing with a limiting value $\lim\limits_{t\to\infty} x(t)=1$, the solution function will exhibit a decrease with a decreasing speed on the whole half real-line $t\in[0,\infty)$.

Example 2: Secondly, let us consider the system

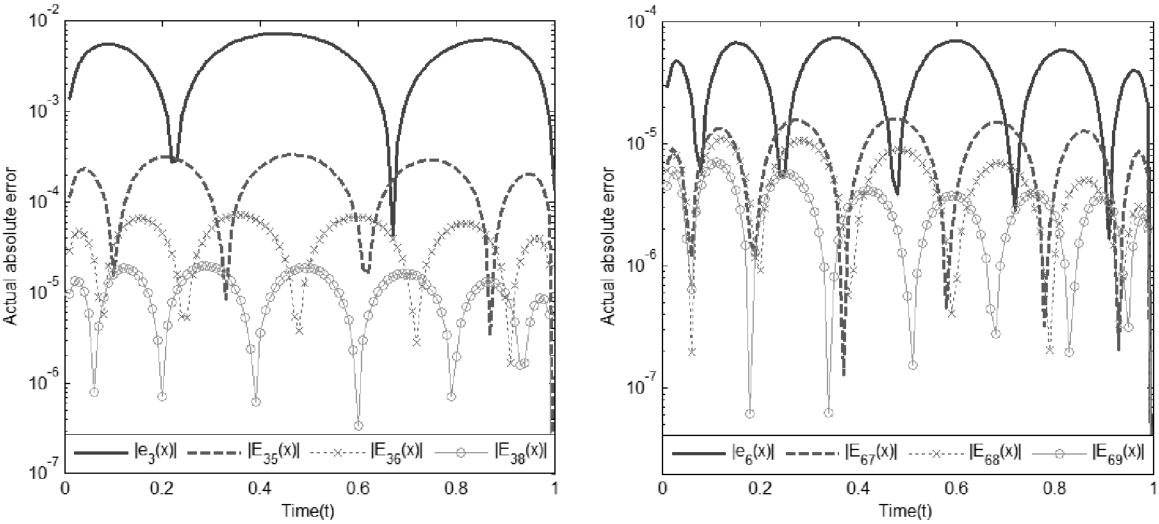

Fig. 1. Comparison of the actual absolute errors of the approximate solutions $x_3(t), x_6(t)$ and their three improvements for Example 1.

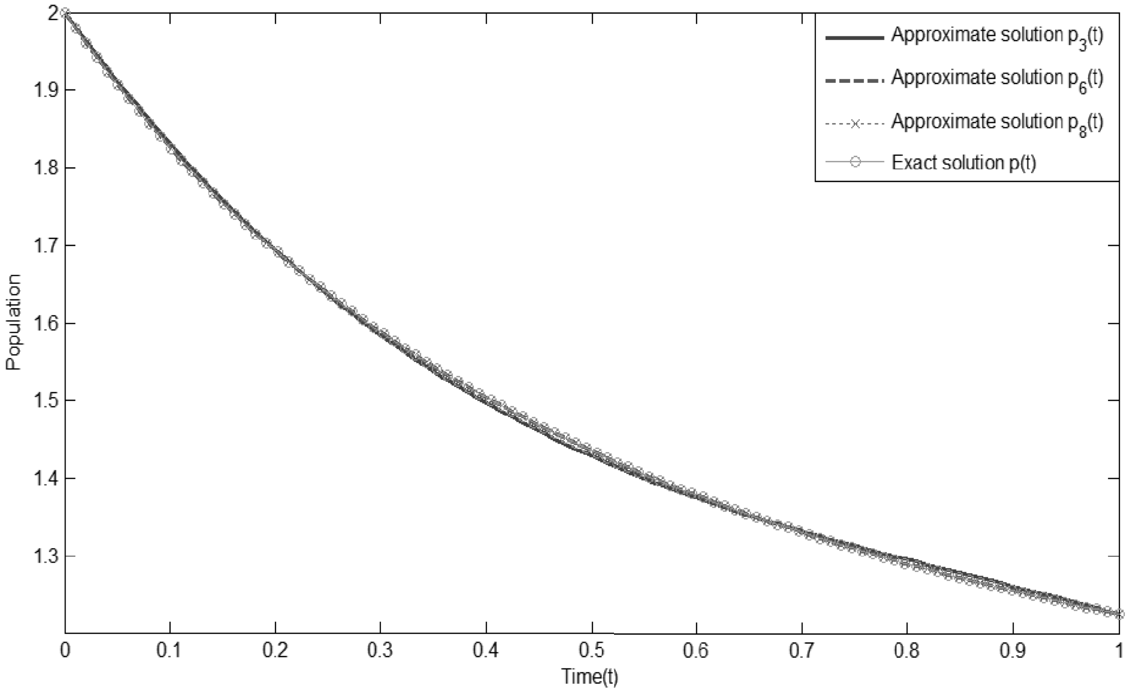

Fig. 2. Graph of the exact and approximate solutions in Example 1.

$$\frac{\mathrm{d}p}{\mathrm{d}t} = p(1-q)$$
$$\frac{\mathrm{d}q}{\mathrm{d}t} = q(p-1) \qquad (16)$$
$$p(0)=1.3,\ q(0)=0.6,$$

where the interval of interest is $0 \le t \le 1$. We will try to determine the approximate prey population $p_N(t)$ and the approximate predator population $q_N(t)$ for various values of N. Let us choose $N = 3, 6, 9$ for this purpose. Implementing the method of Section 2.2 yields

$$p_3(t) = 1.3 + 0.5152921081t + 0.0240177066t^2 - 0.1913425996t^3,$$
$$q_3(t) = 0.6 + 0.1740260386t + 0.2107064508t^2 + 0.0222944792t^3$$

for $N = 3$,

$$p_6(t) = 1.3 + 0.5199732156t - 0.0123927898t^2 - 0.1166191035t^3 - 0.0353749396t^4 - 0.0301148315t^5 + 0.0225265020t^6,$$
$$q_6(t) = 0.6 + 0.1799909007t + 0.1831379366t^2 + 0.0464137281t^3 + 0.0097060534t^4 - 0.0015396911t^5 - 0.0106851417t^6$$

for $N = 6$, and

$$p_9(t) = 1.3 + 0.5200767436t - 0.0146831992t^2 - 0.1031704747t^3 - 0.0521358765t^4 - 0.1156822100t^5 + 0.3599968478t^6 - 0.4917152562t^7 + 0.3317554219t^8 - 0.0864439383t^9,$$
$$q_9(t) = 0.6 + 0.1801015370t + 0.1801637338t^2 + 0.0741284681t^3 - 0.1186959070t^4 + 0.3367987634t^5 - 0.5428370460t^6 + 0.4951584135t^7 - 0.2516069868t^8 + 0.0538128009t^9$$

for $N = 9$. As for the accuracy of these approximate solutions, we cannot measure it by their error functions since we do not have the exact solutions this time. Instead, we can consider the resdiual functions corresponding to each approximate solution; if the residual of a particular approximate function at a particular point is smaller in absolute value than that of another solution, then we accept that solution as being closer to the exact solution at that particular point. Therefore, it is reasonable to do the thing that we did for the actual error functions in Example 1 for the residuals of the approximate solutions in this case. We obtain those residuals by just substituting the approximate solutions in the related equation in system (16). For instance, the residual of $p_3(t)$ is

$$R_3^p(t) = \frac{\mathrm{d}p_N}{\mathrm{d}t} - p_N(t)(1-q_N(t))$$
$$= -0.0047078919 + 0.0681524201t - 0.2200422511t^2 + 0.2182749404t^3 - 0.0167497396t^4 - 0.0397816577t^5 - 0.0042658836t^6.$$

The residuals of several approximate solutions obtained by Adomain decomposition method (Pamuk, 2005), Homotopy perturbation method (Pamuk & Pamuk, 2005), Bessel collocation method (Yüzbaşı, 2012a) and the present method are compared in Table 3. The results of the present method clearly outperform those of ADM and HPM (which are the same since these two methods give the same approximate solution for $N = 3$ and $N = 4$) with only a few exceptions. It is also seen from the table that the present method gives worse results for $N = 9$ than for $N = 6$, which means that increasing N does not necessarily yield better solutions. This is also apparent from Figure 3, where absolute residuals of the approximate prey and predator populations are given together for three different N values. In adition, results of the present method are comparable to those of BCM for $N = 3$ and $N = 6$. The residuals of the solutions obtained by ADM and HPM have been calculated using the approximate solutions given in Pamuk & Pamuk (2010). These solutions are

$$p_3(t) = 1.3 + 0.52t - 0.013t^2 - 0.1122t^3,$$
$$q_3(t) = 0.6 + 0.18t + 0.183t^2 + 0.0469t^3$$

for $N = 3$, and

$$p_4(t) = 1.3 + 0.52t - 0.013t^2 - 0.1122t^3 - 0.0497t^4,$$
$$q_4(t) = 0.6 + 0.18t + 0.183t^2 + 0.0469t^3 + 0.0099t^4$$

for $N = 4$. Note that these approximate solutions have been found without any restrictions on t; therefore, they can be used to approximate the populations of both species in any time instant t. Our method, on the other hand, fixes a time interval and computes the approximate solutions for that time interval. For instance, if one desires to approximate the predator and prey populations in Equation (16) corresponding to some $t' > 1$, one should work the algorithm from the beginning using an interval which contains that t' value. As a result, one will get different approximate solutions than those we have obtained.

Just like we did for the case of single species logistic equation of Example 1, we can try to improve our approximate solutions by applying residual correction to them. Following the method described in Section 3.2, we can find estimations to the error functions $e_{p,N}(t)$ and $e_{q,N}(t)$ and use these estimations to obtain new approximate solutions to the system (16). For example, taking $N = 3$ and $M = 4$ one obtains

$$e_{p,34}(t) = 0.0023030232t - 0.0162542904t^2 \\ +0.0295874683t^3 - 0.0156052449t^4$$

as the estimated error for the approximate prey population $p_3(t)$, and

Table 3. Residual errors of the approximate solutions of Example 2 obtained by ADM, HPM, BCM and the present method for several values of the parameter *N*.

t	Pr.meth. $\lvert R_3^p(t)\rvert$	Pr.meth. $\lvert R_3^q(t)\rvert$	Pr.meth. $\lvert R_6^p(t)\rvert$	Pr.meth. $\lvert R_6^q(t)\rvert$	Pr.meth. $\lvert R_9^p(t)\rvert$	Pr.meth. $\lvert R_9^q(t)\rvert$
0	0.0047	0.0060	2.6784E-5	9.0993E-6	7.6744E-5	1.0154E-4
0.2	0.0018	0.0020	5.9021E-6	2.9613E-7	3.3657E-5	2.1011E-5
0.4	4.6228E-4	0.0025	4.1061E-6	1.1935E-6	3.8455E-5	1.0573E-5
0.6	0.0013	0.0016	1.0997E-6	3.9849E-6	3.8341E-5	4.9394E-6
0.8	2.7085E-4	0.0036	1.9543E-7	5.9873E-6	4.8856E-5	1.5034E-6
1	8.7994E-4	0.0098	9.3932E-6	2.6586E-5	1.5824E-4	2.1079E-5

t	BCM $\lvert R_3^p(t)\rvert$	BCM $\lvert R_3^q(t)\rvert$	BCM $\lvert R_6^p(t)\rvert$	BCM $\lvert R_6^q(t)\rvert$	ADM $\lvert R_3^p(t)\rvert$	ADM $\lvert R_3^q(t)\rvert$
0	0	0	0	0	0	0
0.2	0.0022	5.3700E-4	3.1839E-6	5.9124E-7	1.5892E-4	3.1236E-4
0.4	0.0011	4.1061E-4	2.6961E-6	3.3081E-7	0.0125	0.0023
0.6	0.0015	8.1424E-4	3.6045E-6	5.6621E-8	0.0412	0.0068
0.8	0.0060	0.0049	8.8329E-6	1.5379E-6	0.0942	0.0126
1	0.0210	0.0282	3.2721E-4	1.8044E-4	0.1741	0.0149

t	HPM $\lvert R_3^p(t)\rvert$	HPM $\lvert R_3^q(t)\rvert$	HPM $\lvert R_4^p(t)\rvert$	HPM $\lvert R_4^q(t)\rvert$	ADM $\lvert R_4^p(t)\rvert$	ADM $\lvert R_4^q(t)\rvert$
0	0	0	0	0	0	0
0.2	1.5892E-4	3.1236E-4	0.0014	3.1834E-6	0.0014	3.1834E-6
0.4	0.0125	0.0023	0.0116	1.5680E-4	0.0116	1.5680E-4
0.6	0.0412	0.0068	0.0391	0.0014	0.0391	0.0014
0.8	0.0942	0.0126	0.0909	0.0067	0.0909	0.0067
1	0.1741	0.0149	0.0228	0.0228	0.0228	0.0228

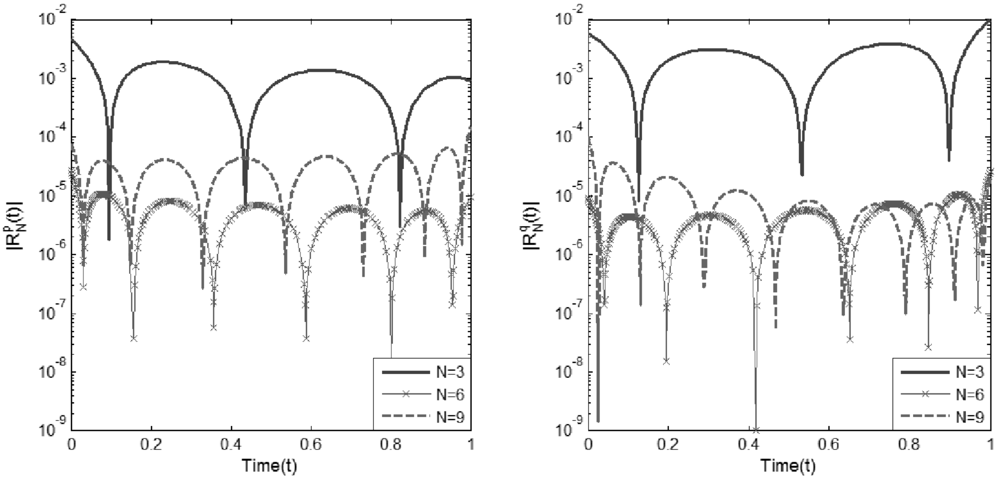

Fig. 3 Comparison of the absolute residual errors of the approximate prey and predator populations obtained with $N = 3,6$ and 9 in Example 2.

Table 4. Comparison of the residual errors of corrected approximate solutions corresponding to some values of the parameters N and M in Example 2.

t	$\left\|R_{34}^{p}(t)\right\|$	$\left\|R_{34}^{q}(t)\right\|$	$\left\|R_{35}^{p}(t)\right\|$	$\left\|R_{35}^{q}(t)\right\|$	$\left\|R_{36}^{p}(t)\right\|$	$\left\|R_{36}^{q}(t)\right\|$
0	0.0024	0.0020	5.3329E-4	2.5069E-4	2.6879E-5	9.0707E-6
0.2	0.0010	9.2266E-4	8.3180E-5	4.0044E-5	5.8891E-6	2.9767E-7
0.4	5.3526E-4	4.5956E-4	1.6642E-4	7.9522E-5	4.0815E-6	1.1848E-6
0.6	7.1710E-4	6.4139E-4	1.6721E-4	8.0307E-5	1.0754E-6	3.9721E-6
0.8	0.0011	0.0010	8.5019E-5	4.1883E-5	2.0282E-7	5.9840E-6
1	0.0029	0.0026	5.2294E-4	2.4034E-4	9.1717E-6	2.6778E-5

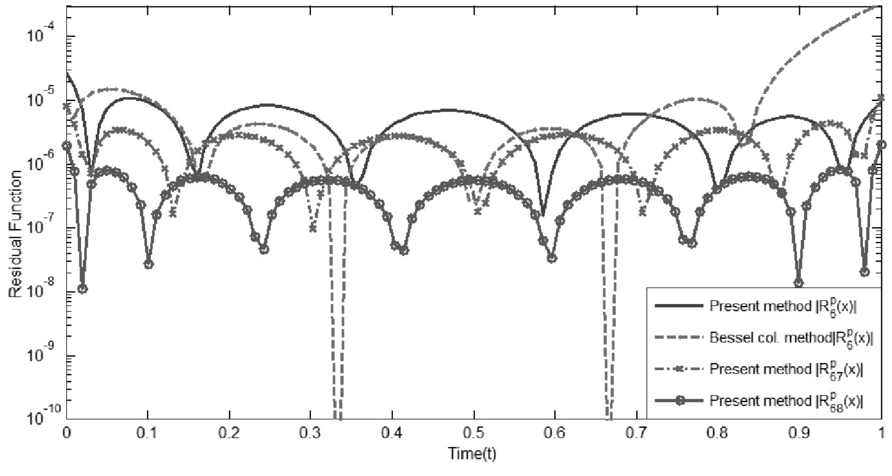

Fig. 4. Comparison of the residual errors of approximate prey population $p_6(t)$ obtained by the present method and its two improvements with Bessel collocation method in Example 2.

$$e_{q,34}(t) = 0.0080525260t - 0.0474485435t^2 + 0.0778400345t^3 - 0.0384465258t^4$$

as the estimated error for the approximate predator population $q_3(t)$. As explained in Section 3.2, using these estimations yields

$$\begin{aligned} p_{34}(t) &= p_3(t) + e_{p,34}(t) \\ &= 1.3 + 0.5175951313t + 0.0077634161t^2 \\ &\quad -0.1617551312t^3 - 0.0156052449t^4 \end{aligned}$$

as a new approximation for the prey population $p_3(t)$, and

$$\begin{aligned} q_{34}(t) &= q_3(t) + e_{q,34}(t) \\ &= 0.6 - 0.0156052449t + 0.1632579072t^2 \\ &\quad +0.1001345138t^3 - 0.0384465258t^4 \end{aligned}$$

as a new approximation for the predator population $q_3(t)$. For $N = 3$, similarly we have obtained new approximate solutions taking $M = 5, 6$ and then we obtained the residual functions $R^p_{NM}(t)$ and $R^q_{NM}(t)$ corresponding to these approximate solutions. The values of these residual functions are shown in Table 4. Values show a significant improvement in the solutions as we increase the parameter M.

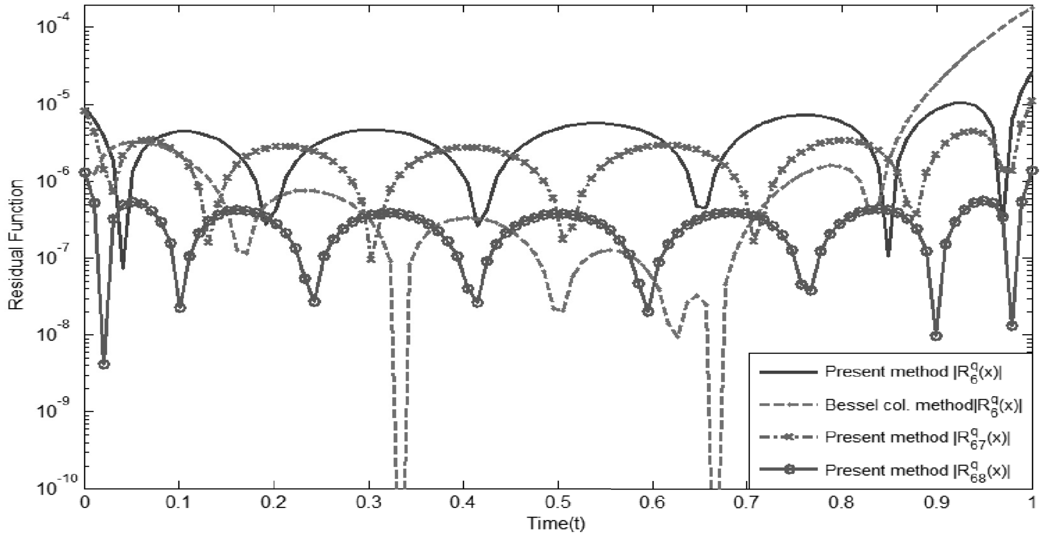

Fig. 5. Comparison of the residual errors of approximate predator population $q_6(t)$ obtained by the present method and its two improvements with Bessel collocation method in Example 2.

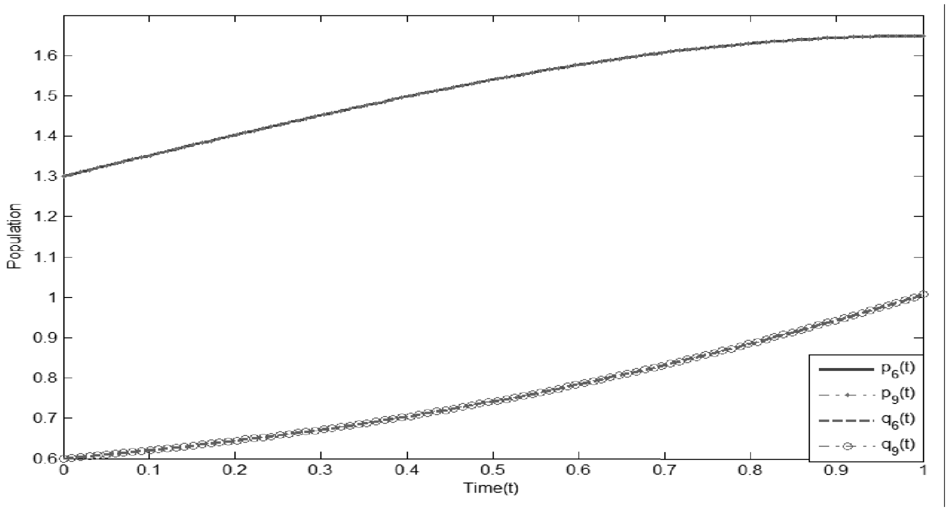

Fig. 6. Graph of predator and prey populations obtained with $N = 6, 9$ in Example 2.

Since residual correction turns out to be very effective for the predator-prey model, one can think of utilizing it to improve the approximate solutions $p_6(t)$ and $q_6(t)$. Doing so for $M=7$ and 8, we obtained new approximate solutions $p_{67}(t), q_{67}(t), p_{68}(t)$ and $q_{68}(t)$. Figures 4 and 5 show that solutions thus obtained tend out to have smaller residuals as we increase M. Especially for $M=8$ the residuals of our corrected solutions are smaller than those of Bessel collocation method for most values of t. Thus, residual correction is a highly effective technique in case of the predator-prey model, just as it was for the single species model.

Lastly, since determining the solution of any equation means determining the values of the unknown function over a set of real numbers, it is natural to investigate the predator and prey populations subject to the system (16). Figure 6 depicts the approximate predator and prey populations for Example 2 obtained by $N=6$ and $N=9$. Since the solutions for these two values are very close as Table 3 shows, the corresponding solutions appear as a single function. The figure and the expressions we had found for $p_6(t)$ and $p_9(t)$ show that the prey population starts with the initial value of 1.3 and becomes approximately equal to 1.648 for $t=1$ after it increases over the entire interval [0,1]. Likewise, the predator population starts with the initial value 0.6 and becomes approximately equal to 1.007 for $t=1$ after it increases over the same interval. The difference lies in the fact that the graph of the prey population is concave (has negative second derivative) while the graph of the predator population is convex. Therefore, we can anticipate that the populations of the two species will be equal at some time t in the future.

5. Conclusion

In this paper, we outlined a numerical method based on inner product to solve two population models. The models we considered were Verhulst's logistic equation and the predator-prey model of Lotka and Volterra. After describing the solution method in detail, we also explained a technique known as residual correction, which relies on estimating the error function accurately and is used to obtain better solutions using the already obtained ones. Then, we applied the method to two examples, one being a single species model and the other a predator-prey model. Results of our simulation revealed that the scheme of this paper gives better or comparable solutions with respect to some other methods in the literature. Numerical results also show that in case the results obtained by the present method perform slightly poor, we can rely on residual correction to obtain solutions which perform fairly well. Furthermore, the technique of residual correction is computationally as easy as the method itself, as Section 3.2 shows. When we put all these facts together, it can be concluded that the scheme outlined in this paper is an easy-to-implement method, which can be relied on in order to solve problems of the type considered in this study with a high level of accuracy.

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نهج Galerkin-like لحل نماذج سكانية مستمرة لأنواع أحادية ومتفاعلة

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خلاصة

نقدم في هذا البحث نهج (Galerkin-like) لحل رقمي لنماذج سكانية مستمرة لأنواع أحادية ومتفاعلة. بعد أخذ حاصل الضرب الداخلي لمجموعة أحادية الحدود بمتجه تم الحصول عليه من المشكلة قيد الدراسة، تم تحويل المشكلة إلى منظومة لا خطية من المعادلات الجبرية. يقدم الحل لهذه المنظومة معاملات الحلول التقريبية. بالإضافة إلى ذلك، وبشيء من التفصيل تمت مناقشة تقنية تصحيح البواقي التي تهدف إلى زيادة دقة الحل التقريبي من خلال تقدير خطئه. تم توضيح الطريقة وتقنية تصحيح البواقي بمثالين. وكذلك تمت مقارنة النتائج مع طرق عديدة منشورة.