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# Application of Homotopy Perturbation Method to Biological Population Model

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## Abstract

In this article, a well-known analytical approximation method, so-called the Homotopy perturbation method (HPM) is adopted for solving the nonlinear partial differential equations arising in the spatial diffusion of biological populations. The resulting solutions are compared with those of the existing solutions obtained by employing the Adomian's decomposition method. The comparison reveals that our approximate solutions are in very good agreement with the solutions by Adomian's method. Moreover, the results show that the proposed method is a more reliable, efficient and convenient one for solving the non-linear differential equations.

**Keywords:** Homotopy perturbation method (HPM); Adomian's decomposition method; biological population model; exact solution

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# 1. Introduction

Many problems arising in scientific fields including mathematical biology, fluid dynamics, visco-elasticity and mathematical physics can be successfully modeled by the use of nonlinear partial differential equations. Several approaches such as the Than method [Evans (2005), Fan (2000)], the Homotopy-Perturbation method [He (1999a, 2000a, 2005), Janalizadeh (2008), Yildirim (2010a, 2010b), Koçak (2009), Ganji (2006)], the Adomian's decomposition method

[Adomian (1988,1994), Gorguis (2006), Momani (2005), Shakeri (2007)], the Variational Iteration Method [(He (1999b, 2000b, 2006), Mohyud-Din (2009), Abdou (2005), Xu (2009), Noor (2008), Shakeri (2007)], and some asymptotic methods [He (2006)] have been used to solve either linear or nonlinear differential equations. Among these methods, the variational iteration method and the homotopy perturbation method are the most efficient, convenient and effective methods for finding the analytical approximate solutions of nonlinear problems.

In this article, the nonlinear degenerate parabolic equations arise in the study of spatial diffusion of biological populations subject to some initial conditions. Consider the first-order time derivative, nonlinear biological model in the following form:

$$\frac{\partial u}{\partial t} = \frac{\partial^2 u^2}{\partial x^2} + \frac{\partial^2 u^2}{\partial y^2} + g(u), \tag{1}$$

with given initial condition u(x, y, 0), where u and g denote the population density and population supply due to births and deaths, respectively.

In this study, g is considered as  $g(u) = hu^k (1 - ru^d)$ , where h, d, k, r are real numbers. It is worth pointing out that there are two examples of constitutive equations for g(u): if h = c, d = 1, r = 0, this leads to Malthusian law [Gurtin (1977)], where c is a constant and  $h = c_1, d = k = 1$ ,  $r = c_2/c_1$ , Verhulst law [Gurtin (1977)],  $c_1, c_2$  are positive constants.

The purpose of this paper is to extend the homotopy perturbation method for computing the approximate analytical solutions of the nonlinear biological population model and then see how these solutions compare with the available exact solutions implemented by Shekeri et al. [Shakeri (2007)] adopting an Adomian decomposition method. The homotopy perturbation method was originally proposed by He for nonlinear differential problems [He (1999a, 2000a)]. It's main feature is the condition of homotopy by introducing an embedment parameter p, which takes the value from 0 to 1. If p = 0, the system of equations (homotopy equations) generally reduces to a very simplified form, which yields a rather simple solution. On the other hand, when p = 1, it turns out to be the original problem and provides the required solution. The approximate solutions obtained using the HPM converges rapidly to the exact solution without any restrictive assumptions, linearization or transformations. In contrast to the traditional perturbation method [Holemen (1995), Nayfeh (2000)], the HPM method does not need a small parameter in the system. The detailed description of HPM is described in Section 2.

This article is organized as follows. Section 2 is devoted to a short description of the analysis of homotopy perturbation method. In Section 3, we present the analytical approximate solutions obtained by implementing the HPM to the nonlinear biological population model followed by the comparison of results between the approximate solutions and the solutions obtained by adopting an Adomian decomposition method. Finally in Section 4, we summarize and discuss the results.

### 2. Analysis of Homotopy Perturbation Method

To illustrate the basis ideas of the homotopy-perturbation method, we consider the following nonlinear differential equation:

$$Lu(\tau) + Nu(\tau) + g(\tau) = 0, \tag{2}$$

with boundary conditions

$$B\left(u,\frac{\partial u}{\partial n}\right) = 0, \qquad \tau \in \Gamma,$$
(3)

where *L* is a linear operator, *N* denotes a non-linear operator, and  $g(\tau)$  is a known analytical function,  $u(\tau)$  is an unknown function,  $\Gamma$  is the boundary of the domain  $\Omega$  and *B* is a boundary operator.

By means of Homotopy perturbation method [He (1999a, 2000a)], we can construct a Homotopy  $v(\tau, p)$  for Equation (2) as follows:

$$v(\tau, p): \Omega \times [0,1] \to R,$$

which satisfies

$$H(v(\tau), p) = (1-p)(Lv(\tau) - Lu_0(\tau)) + p(Lv(\tau) + Nv(\tau) + g(\tau)),$$

$$\tag{4}$$

or

$$H(v(\tau), p) = Lv(\tau) - Lu_0(\tau) + pLu_0(\tau) + p(Nv(\tau) + g(\tau)),$$
(5)

where  $p \in [0,1]$  is an embedding parameter,  $v(\tau)$  is an unknown function and  $u_0$  is an initial approximation that must satisfies the boundary condition (3).

If p = 0, then Equation (5) becomes

$$H(v(\tau),0) = Lv(\tau) - Lu_0(\tau) = 0$$
(6)

and when p = 1, Equation (5) takes the original form of the Equation (2), i.e.,

$$H(v(\tau),1) = Lv(\tau) + Nv(\tau) + g(\tau) = 0.$$
(7)

To solve the problem (2), it is necessary to use the perturbation technique as discussed in Holemen (1995) and Nayfeh (2000). So the combination of the perturbation method and the

homotopy method is known as the homotopy-perturbation method. By applying the perturbation technique the solution of Equation (2) can be expressed as a power series in p

$$v = v_0 + pv_1 + p^2 v_2 + p^3 v_3 + \cdots.$$
(8)

Letting p = 1 in Equation (8), the approximate solution of (2) can be obtained easily as follows

$$u = \lim_{p \to 1} \left( v_0 + p v_1 + p^2 v_2 + p^3 v_3 + \cdots \right) = v_0 + v_1 + v_2 + v_3 + \cdots.$$
(9)

The detailed convergence analysis of the HPM has been discussed in He (1999a, 2000a). The rate of convergence of power series (8), stated in He (1999a), depends upon the nonlinear operator of Equation (2) which satisfies the following two conditions:

- I. The second derivative of nonlinear operator  $Nv(\tau)$  must be small enough, otherwise the parameter may be large, that is, *p* approaches to 1.
- II. The norm of  $L^{-1} \frac{\partial N}{\partial v}$  must be smaller than 1.

## 3. Application of Homotopy Perturbation Method

In this section, the homotopy perturbation method described in the previous section for solving three different types of problems arising in biological population models is applied. Then comparison is made with the available analytical results obtained by Shakeri et al. (2007) using the Adomian's decomposition method to assess the accuracy and the effectiveness of the homotopy perturbation method.

#### Example 1.

Let us consider the following biological population model:

$$u_{t}(x, y, t) = \frac{\partial^{2} u^{2}(x, y, t)}{\partial x^{2}} + \frac{\partial^{2} u^{2}(x, y, t)}{\partial y^{2}} - u(x, y, t) \left(1 + \frac{8}{9}u(x, y, t)\right),$$
(10)

subject to the initial condition  $u(x, y, 0) = \exp\left(\frac{1}{3}(x+y)\right)$ . (11)

According to the homotopy perturbation method, we can construct the homotopy for Equation (10) which satisfies:

$$(1-p)\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial u_0(x,y,t)}{\partial t}\right) + p\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial^2 u^2(x,y,t)}{\partial x^2} - \frac{\partial^2 u^2(x,y,t)}{\partial y^2} + u(x,y,t)\left(1 + \frac{8}{9}u(x,y,t)\right)\right).$$
(12)

Substituting (8) into (12) and equating the terms with identical powers of p, we obtain the following set of linear partial differential equations

$$p^{0}: \frac{\partial u_{0}(x, y, t)}{\partial t} = 0, \qquad u_{0}(x, y, t) = \exp\left(\frac{1}{3}(x+y)\right).$$
(13)

$$p^{1}:\frac{\partial u_{1}(x,y,t)}{\partial t}-\frac{\partial^{2} u_{0}^{2}(x,y,t)}{\partial x^{2}}-\frac{\partial^{2} u_{0}^{2}(x,y,t)}{\partial y^{2}}+u_{0}(x,y,t)+\frac{8}{9}u_{0}^{2}(x,y,t)=0, \quad u_{1}(x,y,0)=0, \quad (14)$$

$$p^{2}: \frac{\partial u_{2}(x, y, t)}{\partial t} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial x^{2}} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial y^{2}} + u_{1} \left( x, y, t \right) + \frac{16}{9} u_{0} \left( x, y, t \right) u_{1} \left( x, y, t \right) = 0,$$

$$u_{2} \left( x, y, 0 \right) = 0,$$
(15)

Solving the above equations, we obtain the following approximations

$$u_0(x, y, t) = \exp\left(\frac{1}{3}(x+y)\right),\tag{16}$$

$$u_1(x, y, t) = -t \exp\left(\frac{1}{3}(x+y)\right),\tag{17}$$

$$u_{2}(x, y, t) = \frac{t^{2}}{2} \exp\left(\frac{1}{3}(x+y)\right),$$
(18)

and so on, in the same manner the rest of the components can be obtained using the Maple package.

According to the HPM, we can obtain the solution in a series form as follows

$$u(x, y, t) = \exp\left(\frac{1}{3}(x+y)\right) - t \exp\left(\frac{1}{3}(x+y)\right) + \frac{t^2}{2!} \exp\left(\frac{1}{3}(x+y)\right) - \cdots$$

$$= \exp\left(\frac{1}{3}(x+y)\right) \left(1 - t + \frac{t^2}{2!} - \cdots\right)$$
  
$$= \exp\left(\frac{1}{3}(x+y)\right) \sum_{n=0}^{\infty} \frac{(-1)^n t^n}{n!},$$
 (19)

which has the exact solution

$$u(x, y, t) = \exp\left(\frac{1}{3}(x+y)\right) \exp(-t) = \exp\left(\frac{1}{3}(x+y) - t\right).$$
 (20)

From the above solution process, it can be seen clearly that, the approximate solution converges very fast to its exact solution. The solution in Equation (20) which obtained by HPM is absolutely same as that of the solution investigated by Shkeri et al. [Shakeri (2007)] using the Adomian decomposition method. Furthermore, the main advantage in using the HPM for solving the considered model is that the exact solutions obtained successfully without requiring a small parameter in the equation and without calculating the complicated Adomian's polynomials.

#### Example 2.

Let us consider the following biological population model:

$$u_t(x, y, t) = \frac{\partial^2 u^2(x, y, t)}{\partial x^2} + \frac{\partial^2 u^2(x, y, t)}{\partial y^2} + hu(x, y, t),$$
(21)

with the initial condition  $u(x, y, 0) = \sqrt{xy}$ .

Similarly, by using the homotopy perturbation method, a homotopy of (21) can be obtained as follows

$$(1-p)\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial u_0(x,y,t)}{\partial t}\right) + p\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial^2 u^2(x,y,t)}{\partial x^2} - \frac{\partial^2 u^2(x,y,t)}{\partial y^2}hu(x,y,t)\right).$$
(22)

Substituting (8) into (22) and equating the terms with identical powers of p, we obtain the following set of linear partial differential equations

$$p^{0}: \quad \frac{\partial u_{0}(x, y, t)}{\partial t} = 0, \quad u_{0}(x, y, t) = \sqrt{xy}, \tag{23}$$

$$p^{1}: \frac{\partial u_{1}(x, y, t)}{\partial t} - \frac{\partial^{2} u_{0}^{2}(x, y, t)}{\partial x^{2}} - \frac{\partial^{2} u_{0}^{2}(x, y, t)}{\partial y^{2}} - hu_{0}(x, y, t) = 0, \quad u_{1}(x, y, 0) = 0, \quad (24)$$

$$p^{2}: \frac{\partial u_{2}(x, y, t)}{\partial t} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial x^{2}} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial y^{2}} - h u_{1}(x, y, t) = 0,$$

$$u_{2}(x, y, 0) = 0,$$
(25)

Using the initial approximation  $u_0(x, y, t) = \sqrt{xy}$ , and solving the above equations, we obtain the approximations as follows

$$u_0(x, y, t) = \sqrt{xy} , \qquad (26)$$

$$u_1(x, y, t) = h\sqrt{xyt},$$
(27)

$$u_{2}(x, y, t) = h^{2} \sqrt{xy} \frac{t^{2}}{2!},$$
(28)

$$u_n(x, y, t) = h^n \sqrt{xy} \frac{t^n}{n!}.$$
(29)

Inserting the values of  $u_0, u_1, u_2, \dots u_n$  in Equation (9), yields the exact solution of (21) as follows

$$u(x, y, t) = \lim_{n \to \infty} \left( \sqrt{xy} + h\sqrt{xy}t + h^2\sqrt{xy}\frac{t^2}{2!} + \dots + h^n\sqrt{xy}\frac{t^n}{n!} \right)$$
$$= \lim_{n \to \infty} \sqrt{xy}\sum_{n=0}^{\infty} \frac{(ht)^n}{n!} = \sqrt{xy}e^{ht},$$
(30)

which is the same exact solution obtained by Shakeri et al. (2007) using the Adomian decomposition method, if we use the parameter h = 1/5.

#### Example 3.

Consider the following biological population model:

$$u_t(x, y, t) = \frac{\partial^2 u^2(x, y, t)}{\partial x^2} + \frac{\partial^2 u^2(x, y, t)}{\partial y^2} + u(x, y, t), \qquad (31)$$

subject to the initial condition  $u(x, y, 0) = \sqrt{\sin x \sinh y}$ .

For solving (31) by the homotopy-perturbation technique we consider the following homotopy

$$(1-p)\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial u_0(x,y,t)}{\partial t}\right) + p\left(\frac{\partial u(x,y,t)}{\partial t} - \frac{\partial^2 u^2(x,y,t)}{\partial x^2} - \frac{\partial^2 u^2(x,y,t)}{\partial y^2}u(x,y,t)\right).$$
(32)

Substituting the value of u from Equation (8) into (32) and equating the terms of the same powers of p, it yields that

$$p^{0}: \frac{\partial u_{0}(x, y, t)}{\partial t} = 0, \quad u_{0}(x, y, t) = \sqrt{\sin x \sinh y}.$$
(33)

$$p^{1}:\frac{\partial u_{1}(x,y,t)}{\partial t}-\frac{\partial^{2} u_{0}^{2}(x,y,t)}{\partial x^{2}}-\frac{\partial^{2} u_{0}^{2}(x,y,t)}{\partial y^{2}}-u_{0}(x,y,t)=0, \qquad u_{1}(x,y,0)=0,$$
(34)

$$p^{2}: \frac{\partial u_{2}(x, y, t)}{\partial t} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial x^{2}} - 2 \frac{\partial^{2} \left( u_{0}(x, y, t) u_{1}(x, y, t) \right)}{\partial y^{2}} - u_{1}(x, y, t) = 0,$$

$$u_{2}(x, y, 0) = 0,$$
(35)

Using the initial approximation  $u_0(x, y, t) = \sqrt{\sin x \sinh y}$ , and solving the above equations, we obtain the approximations as follows

$$u_0(x, y, t) = \sqrt{\sin x \sinh y}, \tag{36}$$

$$u_1(x, y, t) = \sqrt{\sin x \sinh y}t, \tag{37}$$

$$u_2(x, y, t) = \sqrt{\sin x \sinh y} \frac{t^2}{2!},$$
(38)

$$u_n(x, y, t) = \sqrt{\sin x \sinh y} \frac{t^n}{n!}.$$
(39)

Therefore, the exact solution of (31) can be expressed as

$$u(x, y, t) = \lim_{n \to \infty} \left( \sqrt{\sin x \sinh y} + \sqrt{\sin x \sinh y} t + \sqrt{\sin x \sinh y} \frac{t^2}{2!} + \dots \sqrt{\sin x \sinh y} \frac{t^n}{n!} \right)$$
$$= \lim_{n \to \infty} \sqrt{\sin x \sinh y} \left( 1 + t + \frac{t^2}{2!} + \dots + \frac{t^n}{n!} \right) = \sqrt{\sin x \sinh y} e^t.$$
(40)

## 4. Conclusions

The main goal of this work was to employ homotopy perturbation method for finding the approximate analytical solution of biological population models. Three examples were presented in this study to illustrate the reliability and applicability of the method. The analytical solution in each of the examples obtained in terms of an infinite series with easily computable components which converges very rapidly to the exact solution without using any restrictive assumption, perturbation or discretization of the variables. Furthermore, the approximate solutions obtained using HPM are in excellent agreement with those obtained by the decomposition method of Adomian. However, due to its ease in calculations, the HPM is a more reliable and powerful mathematical tool that can be applied to other non-linear partial differential equations.

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