APPROXIMATE ANALYTICAL SOLUTION OF
NON LINEAR EQUATION IN BIOLOGICAL MEMBRANE USING SINGLE PARAMETER HPM

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ABSTRACT

***T**raditional perturbation methods depend on a small parameter which is difficult to be found for real-life nonlinear problems. To overcome this problem, in this article a powerful analytical methods (single parameter homotopy perturbation method (HPM)) is applied to solve nonlinear differential equation in biological membrane. Proper graphs will be used to illustrate the obtained results. The proposed analysis demonstrates reliability and efficiency applicability of the employed method. In this paper we obtained the approximate analytical solutions for the non linear equations under non steady state conditions using single parameter homotopy perturbation method. Simple and approximate polynomial expressions for the concentration of spices are obtained.*

Keywords: Mathematical Modeling; nonlinear equations; single parameter homotopy perturbation method.

1. INTRODUCTION

The transport of molecules across biological membranes is vital to the operation and survival of living cells. The supply of nutrients to the cell, for growth and reproduction, and the transfer of waste products from cell to the extracellular medium, is a complex process that is facilitated by many mechanisms. There is passive transport of molecules due to the combined effects of concentration gradients and electrical potential differences that exist across the cell membrane. Neutral molecules diffuse from regions of high concentration to regions of low concentration. In addition, charged molecules move along a voltage gradient that normally exists across a cell membrane, such as in neural cells and axons. Carrier-mediated transport and active transport are additional mechanisms that facilitate the movement of molecules across cell boundaries. The transport mechanism of molecules may be model using nonlinear ordinary and partial differential equations.

There are many nonlinear equations, which are quite useful and applicable in engineering and physics such as the well-known KdV equation [1], MKdV equation, BBM equation [2], Burgers equation [2], KdV–KSV equation [2], so on. Since solving these equations needs some nonphysical assumptions, some various approximate methods have recently been developed to solve linear and nonlinear differential equations [3–9]. Recently many non linear problems are solved using homotopy perturbation method (HPM) [10–12] and variational iteration method (VIM) [13–15], which are widely applied to various engineering problems [16–30]. In this article the non linear problem in biological membrane is presented and the single parameter homotopy perturbation method are employed to compute an approximation to the solution of the system of nonlinear differential equations governing the problem.

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2. MATHEMATICAL FORMULATION OF THE PROBLEM

The system of equations in biological membrane can be represented as follows:

$$\frac{dy_1}{dt} = y_2 \tag{1}$$

$$\frac{dy_2}{dt} = y_3 \tag{2}$$

$$\frac{dy_3}{dt} = y_4 \tag{3}$$

$$\frac{dy_4}{dt} = -3y_1 + 6y_2 + 2y_3 - 5y_4 + y_5 \tag{4}$$

$$\frac{dy_5}{dt} = -y_5 \tag{5}$$

The initial conditions are:

$$y_1(0) = 0.5, \; y_2(0) = 1, \; y_3(0) = 1.5, \; y_4(0) = 2, \; y_5(0) = 1 \tag{6}$$

where y_i are the concentration of the species in thin membrane.

This problem is nonlinear, however, the following similar transformations may be applied:

$$z = y_1 \tag{7}$$

$$\frac{dz}{dt} = \frac{dy_1}{dt} = y_2 \tag{8}$$

$$\frac{d^2 z}{dt^2} = \frac{dy_2}{dt} = y_3 \tag{9}$$

$$\frac{d^3 z}{dt^3} = \frac{dy_3}{dt} \tag{10}$$

Make the substitutions into the above set of Eqns. (7) – (10) to obtain the below Eqns.

$$\frac{dy_1}{dt} = y_2 \tag{11}$$

$$\frac{dy_2}{dt} = y_3 \tag{12}$$

$$\frac{dy_3}{dt} = 2y_1 + y_2^3 - y_1^2 y_3 \tag{13}$$

Single-parameter hpm solution

The single-parameter HPM solution is quite attractive as it gives a compact analytical solution which can serve several purposes. It can give a deeper insight into the physics of the problem. It can give a rough first-hand idea about the mathematical structure of the solution (for example, presence of boundary layers etc.). It can be launching pad for obtaining a more accurate solution using a numerical iterative technique. Further, if it gives sufficiently accurate results then there is no need to look any further for other solutions. The homotopy perturbation equations corresponding to Eqns. (11) and (13)are written as

$$\frac{dy_1}{dt} + b^2 y_1 + p\left(-y_2 - b^2 y_1\right) = 0 \tag{14}$$

$$\frac{dy_2}{dt} + b^2 y_2 + p\left(-y_3 - b^2 y_2\right) = 0 \tag{15}$$

$$\frac{dy_3}{dt} + b^2 y_3 + p\left(-2y_1 - y_2^3 + y_1^2 y_3 - b^2 y_3\right) = 0 \tag{16}$$

where p is the homotopy perturbation parameter and b is an auxiliary parameter whose value will be calculated by invoking the principle that the solution should be free of the secular terms. Here we take $b^2 = 1$, then the Eqns. (14) – (16) is converted as follows:

$$\frac{dy_1}{dt} + y_1 + p(-y_2 - y_1) = 0 \tag{17}$$

$$\frac{dy_2}{dt} + y_2 + p(-y_3 - y_2) = 0 \tag{18}$$

$$\frac{dy_3}{dt} + y_3 + p(-2y_1 - y_2^3 + y_1^2 y_3 - y_3) = 0 \tag{19}$$

The initial conditions are:

$$y_1(0) = 3, \, y_2(0) = 2, \, y_3(0) = 1 \tag{20}$$

Seeking the perturbation solutions for the concentration of species y_1, y_2 and y_3 as under

$$y_1 = y_{10} + p\, y_{11} + p^2 y_{12} .... \tag{21}$$

$$y_2 = y_{20} + p\, y_{21} + p^2 y_{22} .... \tag{22}$$

$$y_3 = y_{30} + p\, y_{31} + p^2 y_{32} .... \tag{23}$$

Substitute the Eqns. (21) – (23) in Eqns. (17) – (19) we obtain the following systems of equations for zeroth and first order.

Zeroth-order system:

$$\frac{dy_{10}}{dt} + y_{10} = 0 \quad \frac{dy_{20}}{dt} + y_{20} = 0 \quad \frac{dy_{30}}{dt} + y_{30} = 0 \tag{24}$$

The initial conditions are

$$y_{10}(0) = 3, \, y_{20}(0) = 2, \, y_{30}(0) = 1 \tag{25}$$

First-order system:

$$\frac{dy_{11}}{dt} + y_{11} - y_{10} - y_{20} = 0$$

$$\frac{dy_{21}}{dt} + y_{21} - y_{30} - y_{20} = 0 \tag{26}$$

$$\frac{dy_{31}}{dt} + y_{31} - 2y_{10} - y_{20}^3 + y_{10}^2 y_{30} - y_{30} = 0$$

The initial conditions are

$$y_{10}(0) = 0, \, y_{20}(0) = 0, \, y_{30}(0) = 0 \tag{27}$$

The solution of the zeroth-order system is straightforward. We have

$$y_{10}(t) = (y_1)_{in} e^{-t} \quad y_{20}(t) = (y_2)_{in} e^{-t} \quad y_{30}(t) = (y_3)_{in} e^{-t} \tag{28}$$

Substituting for y_{10}, y_{20} and y_{30} in Eq. (26) and solving the differential equations for y_{11}, y_{21} and y_{31} applying the appropriate initial conditions, we get

$$y_{11}(t) = (y_1)_{in} t\, e^{-t} + (y_2)_{in} t\, e^{-t} \tag{29}$$

$$y_{21}(t) = (y_3)_{in} t\, e^{-t} + (y_2)_{in} t\, e^{-t} \tag{30}$$

$$y_{31}(t) = \frac{(y_1)_{in}^2 (y_3)_{in} e^{-3t}}{2} + 2(y_1)_{in} t\, e^{-t} - \frac{(y_2)_{in}^3 e^{-3t}}{2} + (y_3)_{in} t\, e^{-t} + \left[\frac{(y_2)_{in}^3}{2} - \frac{(y_1)_{in}^2 (y_3)_{in}}{2} \right] e^{-t} \tag{31}$$

As pointed out in [18-20], the variant of the HPM introduced above cannot be further extended to obtain the second-order perturbation solution as the latter will have secular terms in its expression. Therefore, we have to terminate our solution at this stage. Truncating the perturbation solution (10) after the first-order terms, and setting $p = 1$, we obtain the final solution as

$$y_1(t) = y_{10} + y_{11} = (y_1)_{in} e^{-t} + (y_1)_{in} t e^{-t} + (y_2)_{in} t e^{-t} \tag{32}$$

$$y_2(t) = y_{20} + y_{21} = (y_2)_{in} e^{-t} + (y_3)_{in} t e^{-t} + (y_2)_{in} t e^{-t} \tag{33}$$

$$y_3(t) = y_{30} + y_{31} = (y_3)_{in} e^{-t} + \frac{(y_1)_{in}^2 (y_3)_{in} e^{-3t}}{2} + 2(y_1)_{in} t e^{-t} - \frac{(y_2)_{in}^3 e^{-3t}}{2} + (y_3)_{in} t e^{-t}$$

$$+ \left[\frac{(y_2)_{in}^3}{2} - \frac{(y_1)_{in}^2 (y_3)_{in}}{2} \right] e^{-t} \tag{34}$$

RESULT AND DISCUSSION

Equations (32)- (34) represent the new analytical expression of concentrations of species in biological membrane. Fig 1 represent the concentration y_1 versus time t for various values of initial concentration. From Fig 1a-1b, it is observed that, the concentration y_1 increases with the initial values of the concentration. Also the concentration y_1 decreases when time increases when initial value is greater than two (refer Fig 1a). But the concentration y_1 initially rises and reaches the maximum value immediately and then decreases gradually.

Fig 2, represent concentration y_2 versus time t. From these figure, it is inferred that when the initial values increases, the concentration is also increases. Fig 3, represent the concentration of y_3 versus time t. Here also the concentration decreases when initial values are increases. Fig 4, represent that the concentration of y_1, y_2 and y_3 versus time t for some initial values.

CONCLUSION

The approximate analytical expression of concentration of species in biological membrane is obtained by solving the nonlinear rate equation using single parameter homotopy perturbation method. First time we attempted the single parameter HPM solution for biological membrane which generally leads to a very good approximate solution in the minimum number of iteration.. Based on the proposed model, nonlinear equation in physical and chemical sciences is solved. These analytical results are useful for experimental data analysis.

APPENDIX A: Basic Concept of Homotopy Perturbation Method

To explain this method, let us consider the following function:
$$D_o(u) - f(r) = 0, \quad r \in \Omega \tag{A1}$$
with the boundary conditions of
$$B_o(u, \frac{\partial u}{\partial n}) = 0, \quad r \in \Gamma \tag{A2}$$

where D_o is a general differential operator, B_o is a boundary operator, $f(r)$ is a known analytical function and Γ is the boundary of the domain Ω. In general, the operator D_o can be divided into a linear part L and a non-linear part N. The eqn. (A.1) can therefore be written as
$$L(u) + N(u) - f(r) = 0 \tag{A3}$$

By the homotopy technique, we construct a homotopy $v(r, p) : \Omega \times [0,1] \to \Re$ that satisfies
$$H(v, p) = (1 - p)[L(v) - L(u_0)] + p[D_o(v) - f(r)] = 0. \tag{A4}$$
$$H(v, p) = L(v) - L(u_0) + pL(u_0) + p[N(v) - f(r)] = 0. \tag{A5}$$

Where $p \in [0, 1]$ is an embedding parameter, and u_0 is an initial approximation of eqn. (A1) that satisfies the boundary conditions. From eqns. (A4) and (A5), we have
$$H(v,0) = L(v) - L(u_0) = 0 \tag{A6}$$
$$H(v,1) = D_o(v) - f(r) = 0 \tag{A7}$$

When $p=0$, the eqns. (A4) and (A5) become linear equations. When $p=1$, they become non-linear equations. The process of changing p from zero to unity is that of $L(v) - L(u_0) = 0$ to $D_o(v) - f(r) = 0$. We first use the embedding parameter p as a "small parameter" and assume that the solutions of eqns. (A.4) and (A.5) can be written as a power series in p:

$$v = v_0 + v_1 p + v_2 p^2 + ... \tag{A8}$$

Setting $p = 1$ results in the approximate solution of the eqn. (A1):

$$u = \lim_{p \to 1} v = v_0 + v_1 + v_2 + ... \tag{A9}$$

This is the basic idea of the HPM.
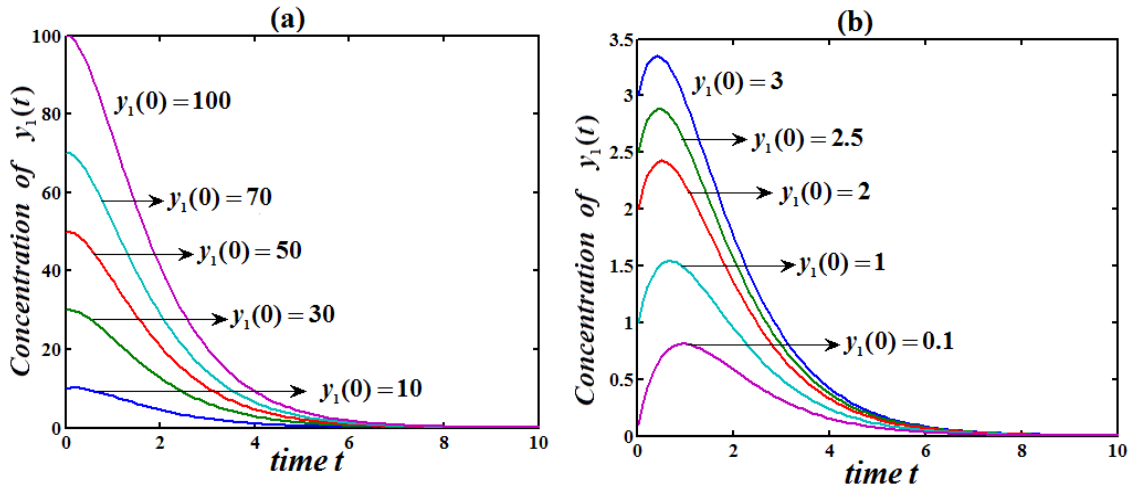
Figure-1: Concentration y_1 versus time t for various value of initial concentration.
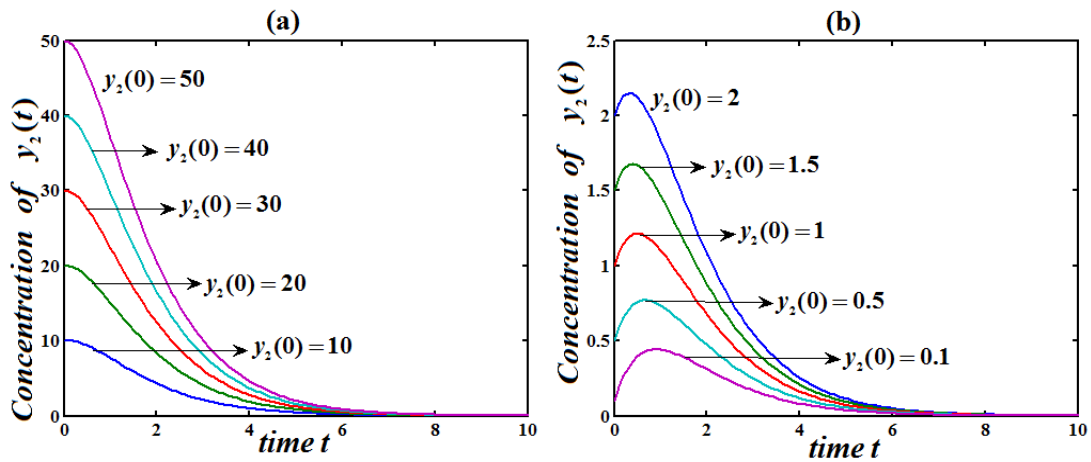

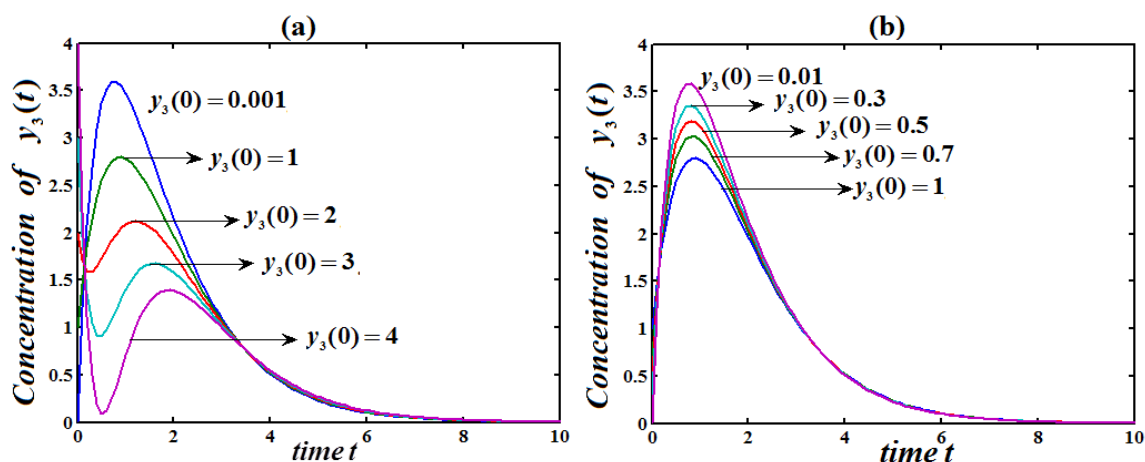**Figure-2:** Concentration y_2 versus time t for various value of initial concentration.

Figure-3: Concentration y_3 versus time t for various value of initial concentration.
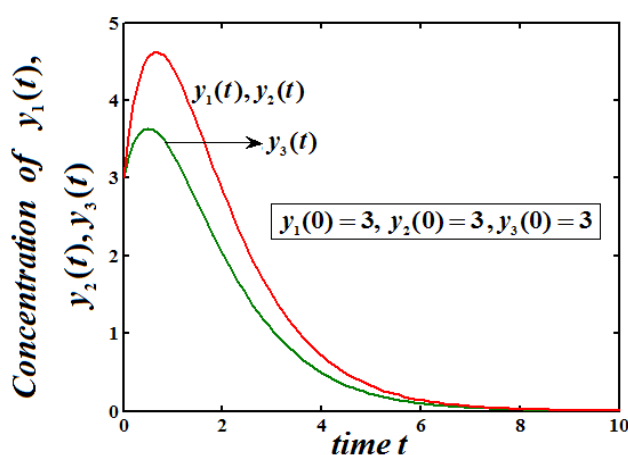
Figure-4: Concentrations y_1, y_2, y_3 versus time t.

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