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- [1] D.H. Ackeley, G.E. Hilton and T.J. Sejnovski, A learning algorithm for Bolzmann machine, *Cognitive Science*, 62 (1985), 147-169.
- [2] D.O. Hebb, *Organization of Behaviour*, Wiley, New York, 1949.

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A Single Species Population Model in Polluted Environment Solved by Homotopy Analysis Method

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Abstract

In this article, the homotopy analysis method is applied to obtain approximate analytical solution for a single species population model with viral infection in polluted environment. The resulting solutions are compared with the numerical method. The comparison reveals that our approximate solutions are in very good agreement with the solutions by numerical method. Moreover, The result show that the homotopy analysis method is very effective and simple for solving the nonlinear ordinary differential equation systems.

Mathematics Subject Classification: 34A34, 92D25, 92D30, 93C15

Keywords: Homotopy analysis method, Single-species population, Approximate solution, Nonlinear ODEs

1 Introduction

Pathogen pollution is the introduction of a pathogenic parasite to a new (or naive) host species or population. Pathogens include those organisms such as viruses, bacteria, and protozoan which can cause sickness or death in other

species. Despite their small size, they can have enormous on the environment. Pathogens can also have large economic impacts when the disease affects domestic animals such as the Newcastles disease outbreaks in California and the Nipah virus in Malaysia and Singapore. Both had devastating economic impacts in which millions of infected and potentially infected animals were slaughtered [2]. Theory on the effects of parasites on host population dynamics has received much attention and focused on issues such as how the parasite induced reduction of the host fecundity and survival rates change the host population dynamics and how such dynamics be applied to predict threats to biodiversity in general and endangered species in particular [3]. Besides the study of effect of parasite, effect of environmental pollution is also a great challenge in the study of the population dynamics in a polluted environment. A great quantity of the pollutant enters into the environment one after another which seriously threaten the survival of the exposed populations including human population. The problem of estimating quantitatively the effect of a pollutant on a population by mathematical models is a relatively new field. In recent years, many attempts have been made to develop realistic mathematical models for investigating the effect of environmental pollution. The threshold of survival for a system of two species in polluted environment was studied by [8]. A spatial structure has been carried out by [12], to describe the dynamics of a population in a polluted environment. Recently few interesting mathematical models with combined effects of disease and toxicant were studied by [10], for completing and prey predator dynamics. The mathematical model by considering the combined effect of both the infection and the toxicant through food intake and environment toxicant was studied by [1]. This model is in the form of nonlinear. We know that except a limited number of these problems, most of them do not have analytical solution.

Therefore, the nonlinear equation should be solved using other methods. Some of them are solved using numerical techniques. In the numerical method, stability and convergence should be considered to avoid divergence or inappropriate result. In the analytical perturbation method, we should exert the small parameter in the equation. Therefore, finding the small parameter and exerting it into the equation are difficulties of this method [11]. Many different mathematical methods have been recently introduced to eliminate the small parameter. In 1992, Liao [7] has proposed a new analytical method called the homotopy analysis method, which introduce an embedding parameter to construct a homotopy and then analyzes it by means of Taylor formula. The homotopy analysis method contains the auxiliary parameter, which provides us with a simple way to adjust and control the convergence region of solution series. Therefore, unlike the perturbation method, this method is independent of small parameters and can overcome the restrictions of the perturbation methods. The method has been used by many authors [5], [9] in a wide variety

of scientific and engineering applications to solve different types of governing differential equations. In this paper, the basic idea of the homotopy analysis method is introduced and then, the nonlinear equation of a model is solved through the homotopy analysis method.

The purpose of this paper is to extend the homotopy analysis method for computing the approximate analytical solution of a single species population model in polluted environment and then see how these solutions compare with the solutions by numerical method.

2 The mathematical model

Formulation of a single species population model with viral infection in polluted environment is given by Chauhan and Misra [1]. Let $H(t)$ and $P(t)$ be a single species animal population in terrestrial ecosystem and a virus biomass, respectively, at time t . In the absence of virus biomass, the single species population density grows according to a logistic curve. In the presence of virus biomass, we assume that total population $H(t)$ is divided into two classes, namely the susceptible population class denoted by S and the infected population class denoted by I such that $H(t) = S(t) + I(t)$. The susceptible population is assumed to grow logistically and become infected under the attack of many viruses particles. Virus enters into susceptible individual, and then starts its replication inside the susceptible individual (now infected). From the above assumptions, the model equations are:

$$\begin{aligned}\frac{dS}{dt} &= \alpha S \left(1 - \frac{H}{C}\right) - KSP \\ \frac{dI}{dt} &= KSP - \lambda I \\ \frac{dP}{dt} &= -KSP - \mu P + b\lambda I.\end{aligned}\tag{1}$$

Various constants in equation (1) are described as:

- C : carrying capacity of a single species animal population
- α : birth rate of a single species animal population
- K : rate of infection (effective animal population contact rate with viruses)
- λ : natural death rate of infected population
- μ : mortality rate of virus biomass due to natural death
- b : the virus replication factor.

Now, let $X(t)$ is the concentration of pollutant in the environment at time t , and $U(t)$ is the concentration of pollutant in the organism at time t . The system (1) under the effect of pollutant can be given by the following system

of ordinary differential equations:

$$\frac{dS}{dt} = \alpha S \left(1 - \frac{H}{C}\right) - KSP - r_1US, \quad (2)$$

$$\frac{dI}{dt} = KSP - \lambda I - r_2UI, \quad (3)$$

$$\frac{dP}{dt} = -KSP - \mu P + b\lambda I, \quad (4)$$

$$\frac{dX}{dt} = Q - eX, \quad (5)$$

$$\frac{dU}{dt} = a_1X + \frac{d_1\eta\beta}{a_1} - (l_1 + l_2)U. \quad (6)$$

The first two terms on the right hand side of equation (6) denote the organismal net uptake of pollutant from the environment and the food chain, respectively. The second terms on the right hand side of equation (6) represents the organismal net loss of pollutant due to metabolic processing and other causes. The positive constant, e , is the loss rate of toxicant from the environment due to the processes such as biological transformation, chemical hydrolysis, volatilization, microbial degradation, including other processes. The constant exogenous input rate of the pollutant into the environment is represented by Q . The parameters $a_1, d_1, \eta, \beta, l_1$ and l_2 are positive constant. The parameter a_1 is environmental pollutant uptake rate per unit mass organism, η , the concentration of the pollutant in resource, β , the average rate of the food intake per unit mass organism, d_1 , the uptake rate of pollutant in food per unit mass organism, l_1 and l_2 are organismal net ingestion and depuration rates of pollutant, respectively. Positive parameters r_1 and r_2 denotes the loss rates from susceptible and infected populations respectively due to effect of pollutant.

3 Analysis of method

We considered the following a general nonlinear differential equation

$$A[u(t)] = 0, t \in \Omega, \quad (7)$$

where A is a nonlinear operator, $u(t)$ is an unknown function, t is an independent variable, and Ω is the domain. We constructed a homotopy $v(t, p) : \Omega \times [0, 1] \rightarrow \mathbb{R}$ which satisfies

$$H(v, p) = (1 - p)L[v(t, p) - v_0(t)] + phA[v(t, p)]$$

where $p \in [0, 1]$ is an embedding parameter, L denotes an auxiliary linear operator, h is a nonzero auxiliary parameter, and v_0 is an initial approximation

of the exact solution. By equating to zero the homotopy function, the zero-order deformation equation is constructed as

$$(1-p)L[v(t,p) - v_0(t)] = -phA[v(t,p)]. \quad (8)$$

Setting $p = 0$, the zero-order deformation equation (8) becomes

$$L[v(t,0) - v_0(t)] = 0. \quad (9)$$

Using (9), by linearity

$$v(t,0) = v_0(t).$$

When $p = 1$, the zero-order deformation equation (8) is reduced to

$$A[v(t,1)] = 0,$$

which is exactly the same as the nonlinear equation (7), provided $v(t,1) = u(t)$. Thus, as p increases from 0 to 1, the solution $v(t,p)$ varies continuously from the initial approximation $v_0(t)$ to the exact solution $u(t)$. Expanding $v(t,p)$ by Taylor's series in power series of p , we have

$$v(t,p) = v_0(t) + \sum_{m=1}^{\infty} v_m(t) p^m, \quad (10)$$

where

$$v_m(t) = \frac{1}{m!} \frac{\partial^m v(t,p)}{\partial p^m} \Big|_{p=0}.$$

The auxiliary linear operator L , the initial approximation v_0 , and the auxiliary parameter h are properly chosen so that the solution $v(t,p)$ of the zero-order deformation equation (8) exists for all p and the series (10) converges at $p = 1$. Then we have the approximate solution of equation (7), i.e.

$$u(t) = v_0(t) + \sum_{m=1}^{\infty} v_m(t). \quad (11)$$

When $h = -1$ are chosen, equation (8) becomes

$$(1-p)L[v(t,p) - v_0(t)] = pA[v(t,p)]$$

which is used in the homotopy perturbation method [4]. The term v_m can be determined by the so-called high-order deformation described below. Differentiating equation (8) m times with respect to p , then setting $p = 0$ and dividing them by $m!$, we obtain the m th-order deformation equation

$$L[v_m(t) - \chi_m v_{m-1}(t)] = -hR_m(\vec{v}_{m-1}(t)) \quad (12)$$

where $\vec{v}_m = (v_0(t), v_1(t), v_2(t), \dots, v_m(t))$,

$$R_m(\vec{v}_{m-1}(t)) = \frac{1}{(m-1)!} \frac{\partial^{m-1} A[v(r, p)]}{\partial p^{m-1}} \Big|_{p=0} \quad (13)$$

and

$$\chi_m = \begin{cases} 0 & , m \leq 1 \\ 1 & , m > 1. \end{cases}$$

The right hand side of (12) depends only on the terms v_{m-1} . Thus, we easily gain the series v_1, v_2, \dots by solving the linear high-order deformation equation (12) using symbolic computation software such as Maple and Mathematica. By varying L, v_0 , and h , we can adjust the region in which the series is convergent. In order to determine the optimum value of h , we can plot the so-called h -curves of the solution. These curves are obtained by plotting the h -curves of $v''(0)$ or $v'''(0)$ as suggested by Liao [6].

4 Application of method

In this section, the homotopy analysis method described in the previous section for solving a single species population model in polluted environment is applied. Then comparison is made with the numerical method to assess the accuracy and the effectiveness of the homotopy analysis method. System (2) - (6) will be solved by generalizing the described homotopy analysis method. The linear operators L_1, L_2, L_3, L_4 and L_5 can be defined as below

$$L_1 = L_2 = L_3 = L_4 = L_5 = \frac{d}{dt}.$$

From system (2) - (6) nonlinear operators A_1, A_2, A_3, A_4 , and A_5 can be defined as

$$\begin{aligned} A_1(\phi_1) &= \frac{d\phi_1}{dt} - \alpha\phi_1 \left(1 - \frac{\phi_1 + \phi_2}{C}\right) + K\phi_1\phi_3 + r_1\phi_5\phi_1, \\ A_2(\phi_2) &= \frac{d\phi_2}{dt} - K\phi_1\phi_3 + \lambda\phi_2 + r_2\phi_5\phi_2, \\ A_3(\phi_3) &= \frac{d\phi_3}{dt} + K\phi_1\phi_3 + \mu\phi_3 - b\lambda\phi_2, \\ A_4(\phi_4) &= \frac{d\phi_4}{dt} - Q + e\phi_4, \\ A_5(\phi_5) &= \frac{d\phi_5}{dt} - a_1\phi_4 - \frac{d_1\eta\beta}{a_1} + (l_1 + l_2)\phi_5. \end{aligned}$$

Using the above definition, we construct the zeroth-order deformation equation as follows

$$(1-p)L_i[\phi_i(t, p) - \phi_{i,0}(t)] = -phA_i[\phi_i(t, p)], \quad i = 1, 2, 3, 4, 5.$$

Then, we obtain the m th-order deformation equation

$$L[\phi_{i,m}(t) - \chi_m \phi_{i,m-1}(t)] = -h R_{i,m}(\vec{\phi}_{i,m-1}) \tag{14}$$

where

$$\begin{aligned} R_{1,m} &= \frac{d}{dt} \phi_{1,m-1} - \alpha \phi_{1,m-1} + \frac{\alpha}{C} \sum_{n=0}^{m-1} \phi_{1,n} (\phi_{1,m-n-1} + \phi_{2,m-n-1}) \\ &\quad + K \sum_{n=0}^{m-1} \phi_{1,n} \phi_{3,m-n-1} + r_1 \sum_{n=0}^{m-1} \phi_{5,n} \phi_{1,m-n-1}, \\ R_{2,m} &= \frac{d}{dt} \phi_{2,m-1} - K \sum_{n=0}^{m-1} \phi_{1,n} \phi_{3,m-n-1} + \lambda \phi_{2,m-1} + r_2 \sum_{n=0}^{m-1} \phi_{5,n} \phi_{2,m-n-1}, \tag{15} \\ R_{3,m} &= \frac{d}{dt} \phi_{3,m-1} + K \sum_{n=0}^{m-1} \phi_{1,n} \phi_{3,m-n-1} + \mu \phi_{3,m-1} - b \lambda \phi_{2,m-1}, \\ R_{4,m} &= \frac{d}{dt} \phi_{4,m-1} - Q(1 - \chi_m) + e \phi_{4,m-1}, \\ R_{5,m} &= \frac{d}{dt} \phi_{5,m-1} - a_1 \phi_{4,m-1} - \frac{d_1 \eta \beta}{a_1} (1 - \chi_m) + (l_1 + l_2) \phi_{5,m-1}, \end{aligned}$$

and initial condition: $\phi_{i,m}(0) = 0, m = 1, 2, \dots, i = 1, 2, 3, 4, 5,$

$$\phi_{1,0} = S(0), \phi_{2,0} = I(0), \phi_{3,0} = P(0), \phi_{4,0} = X(0), \phi_{5,0} = U(0).$$

Now, the solution of the m th-order deformation equation (14) for $m \geq 1$ becomes

$$\phi_{i,m}(t) = \chi_m \phi_{i,m-1}(t) - h \int R_{i,m}(\vec{\phi}_{i,m-1}) dt \tag{16}$$

Suppose given the following data: the initial number of susceptible individual in the location $S(0) = 40$; the initial number of infected individual $I(0) = 8$; initial number of virus biomass $P(0) = 500$. The initial concentration of pollutant in the environment $X(0) = 10$ and in the organism $U(0) = 20$. The following parameter values used for numerical simulation: $C = 100, \alpha = 0.1, K = 0.001, \lambda = 0.24628, \mu = 0.14925, \beta = 0.12, b = 10, r_1 = 0.01, r_2 = 0.011, Q = 2, e = 0.1, a_1 = 1, d_1 = 0.21, \eta = 1, l_1 + l_2 = 0.5$. By using equation (15)

and (16), we successively obtain

$$\begin{aligned}
 \phi_{1,1}(t) &= (155.52h^2 + 103.68h + 103.68h^3 + 25.92h^4)t \\
 \phi_{1,2}(t) &= (60.51h^2 + 80.68h^3 + 30.25h^4)t^2 \\
 &\vdots \\
 \phi_{2,1}(t) &= (-97.62h^2 - 65.08h - 65.08h^3 - 16.27h^4)t \\
 \phi_{2,2}(t) &= (-70.64h^2 - 94.18h^3 - 35.32h^4)t^2 \\
 &\vdots \\
 \phi_{3,1}(t) &= (449.54h^2 + 299.69h + 299.69h^3 + 74.92h^4)t \\
 \phi_{3,2}(t) &= (201.62h^2 + 268.83h^3 + 100.81h^4)t^2 \\
 &\vdots \\
 \phi_{4,1}(t) &= (-6.h^2 - 4.h - 4.h^3 - h^4)t \\
 \phi_{4,2}(t) &= (-0.30h^2 - 0.40h^3 - 0.15h^4)t^2 \\
 &\vdots \\
 \phi_{5,1}(t) &= (-0.15h^2 - 0.10h - 0.10h^3 - 0.025h^4)t \\
 \phi_{5,2}(t) &= (2.96h^2 + 3.95h^3 + 1.48h^4)t^2 \\
 &\vdots
 \end{aligned}$$

and so on. In the same manner the rest of the components can be obtained using the symbolic package. According to the homotopy analysis method, we can obtain the solution in a series form as follows:

$$\begin{aligned}
 S(t) &= \phi_1(t, 1) = \phi_{1,0} + \phi_{1,1} + \phi_{1,2} + \dots, \\
 I(t) &= \phi_2(t, 1) = \phi_{2,0} + \phi_{2,1} + \phi_{2,2} + \dots, \\
 P(t) &= \phi_3(t, 1) = \phi_{3,0} + \phi_{3,1} + \phi_{3,2} + \dots, \\
 X(t) &= \phi_4(t, 1) = \phi_{4,0} + \phi_{4,1} + \phi_{4,2} + \dots, \\
 U(t) &= \phi_5(t, 1) = \phi_{5,0} + \phi_{5,1} + \phi_{5,2} + \dots.
 \end{aligned} \tag{17}$$

Note that the equation (17) contains the auxiliary parameter h . To obtain an appropriate range for h , we consider the h -curves. Plotted in Figure 1, by discovering the valid region of h which corresponds to the line segments nearly parallel to the horizontal axis. In Figure 1, we demonstrate the h -curves of $S''(0)$, $I''(0)$, and $P''(0)$ given by 10th-order homotopy analysis method solution (17). From these curves, it is clear that we must choose h between about -2.7 and 1.0 to obtain valid results.

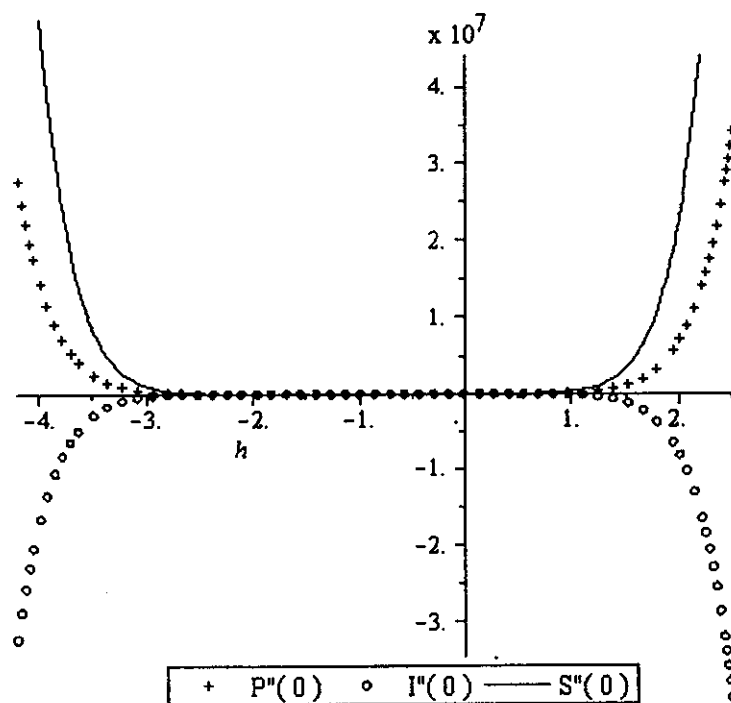


Figure 1. The h -curves of 10th-order approximate solutions obtained by the homotopy analysis method.

The comparison of the results of the homotopy analysis method and numerical solution is given in Table 1. The explicit Runge-Kutta method in symbolic computation package has been used to find numerical solution of $S(t)$, $I(t)$, $P(t)$, $X(t)$, and $U(t)$. Table 1 shows the absolute error between the homotopy analysis method and the numerical solution for $h = -1$ and $h = -0.8$. It can be seen from Table 1 that the choice of $h = -0.8$ is a suitable one. As it can be seen in Table 1, there exists a very good agreement between homotopy analysis method result and numerical solutions.

Table 1. Comparison between absolute error of homotopy analysis method (HAM) and numerical method (NM) for $h = -0.8$ and $h = -1$.

t	$ S(t)_{HAM} - S(t)_{NM} $		$ I(t)_{HAM} - I(t)_{NM} $		$ P(t)_{HAM} - P(t)_{NM} $	
	$h = -0.8$	$h = -1$	$h = -0.8$	$h = -1$	$h = -0.8$	$h = -1$
0	0	0	0	0	0	0
0.2	2.7×10^{-7}	3.3×10^{-7}	3.5×10^{-7}	4.9×10^{-7}	2.1×10^{-6}	6.5×10^{-6}
0.4	7.7×10^{-7}	8.5×10^{-7}	1.4×10^{-6}	1.3×10^{-6}	6.8×10^{-6}	4.0×10^{-6}
0.6	9.5×10^{-7}	2.1×10^{-6}	2.0×10^{-6}	2.8×10^{-6}	7.8×10^{-6}	7.3×10^{-6}
0.8	1.1×10^{-6}	2.8×10^{-5}	1.9×10^{-6}	3.4×10^{-5}	2.8×10^{-6}	5.9×10^{-5}
1.0	8.6×10^{-7}	3.1×10^{-4}	5.4×10^{-6}	3.7×10^{-4}	6.0×10^{-6}	6.1×10^{-4}
1.2	1.9×10^{-8}	2.2×10^{-3}	2.2×10^{-6}	2.6×10^{-3}	1.3×10^{-5}	4.3×10^{-3}
1.4	9.2×10^{-7}	1.1×10^{-2}	4.1×10^{-6}	1.4×10^{-2}	6.6×10^{-6}	2.2×10^{-2}
1.6	3.5×10^{-6}	4.7×10^{-2}	2.9×10^{-6}	5.6×10^{-2}	2.8×10^{-5}	9.3×10^{-2}
1.8	4.8×10^{-5}	1.7×10^{-1}	6.2×10^{-5}	1.9×10^{-1}	1.5×10^{-4}	3.3×10^{-1}
2.0	3.2×10^{-4}	5.1×10^{-1}	3.9×10^{-4}	6.1×10^{-1}	6.4×10^{-4}	1.0×10^0

5 Conclusions

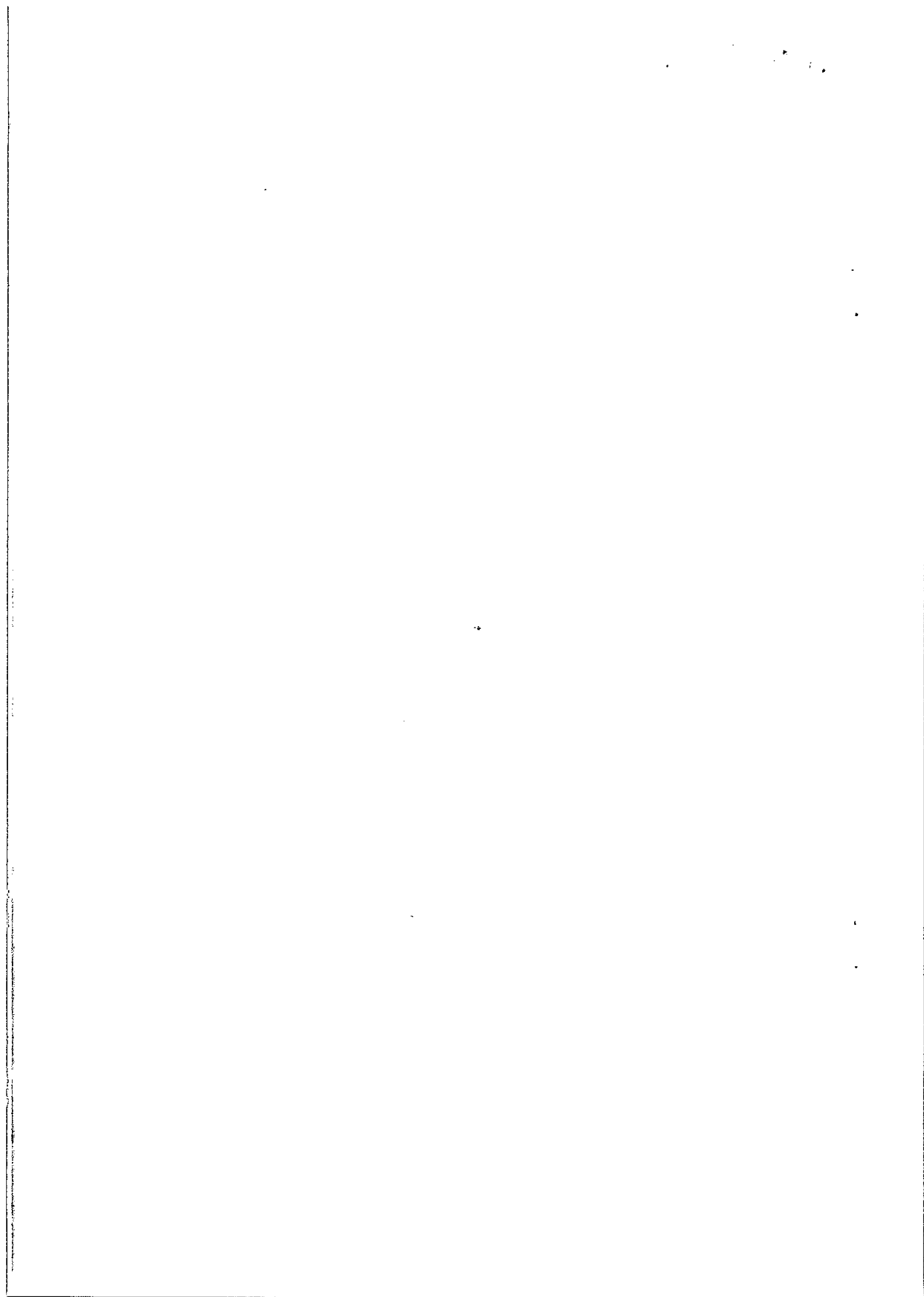
In this paper, homotopy analysis method has been successfully applied to find the approximate analytical solution of a single species population model with viral infection in polluted environment. The method is very effective and easy to use. The calculations involved in homotopy analysis method are simple and straightforward. The solutions obtained by homotopy analysis method contain the auxiliary parameter which plays an important role within the frame of the method. In addition, our analytical approximate solution shown that for nonlinear ordinary differential equation systems just a few iterations of homotopy analysis method gives a good result. It is demonstrated that homotopy analysis method is a powerful and efficient tool for solving the nonlinear ordinary differential equation systems.

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