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Solutions of the SIR-B Cholera Model Using Homotopy Analysis Method

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Abstract
Homotopy analysis method (HAM) is a well-known device for solving a wide range of functional equations such as partial and ordinary differential equations, integral equations and so on. In this article, we adopt homotopy analysis method to obtain the solutions of a system of first order nonlinear ordinary differential equations arising from transmission dynamics of cholera disease. The method provides a direct scheme for solving the problem without linearization, perturbation, massive computation and transformation. Numerical simulations are carried out and graphical results are presented to illustrate the solutions. The results obtained confirm the power and accuracy of homotopy analysis method in solving differential equations.
Keywords: Homotopy analysis method (HAM), cholera, simulations

1. Introduction

Cholera is an acute intestinal water-borne infectious disease caused by the bacterium *vibrio cholerae* (Wang and Modnak, 2011). It is a very serious problem in many developing countries due to inadequate access to safe drinking water supply, improper treatment of reservoirs and improper sanitation (Fatima, Krishnarajah, Jaffar, and Adam, 2014). While cholera has been a recognized disease for about 200 years, the control of deadly outbreaks remains a challenge in less developed countries. Highlighted by the 2008 outbreak in Zimbabwe, a new focus on cholera management has emerged due to a rise in cholera incidence. The recent outbreaks have caused enormous loss of life and financial devastation to families and healthcare systems (Neilan, Schaefer, Gaff, Fister. and Lenhart, 2010).

In order to gain deeper understanding of cholera dynamics, a good number of mathematical models have been proposed and analyzed. For example, Codeco (2001) extended the work of Capasso and Paveri-Fontana (1979) and explicitly accounted for the role of the aquatic reservoir in the transmission of cholera. The researcher also included the susceptible population into the model to consider the long-term dynamics of cholera, and like Capasso and Paveri-Fontana (1979) , the model assumed the ingestion of contaminated water as the only transmission route for cholera. Using similar nonlinear incidence as in Codeco (2001),

Hartley, Morris and Smith, (2006) incorporated a hyper-infective stage of *V. cholerae* (i.e freshly shed *vibrios*) into their model with a view to implicitly highlight the importance of human-to-human interaction in cholera epidemics.

Tien and Earn (2010) published a water-borne disease model which also included the dual transmission pathways, with bilinear incidence rates for both the environment-to-human and human-to-human infection routes. No saturation effect was considered in their study. Tian& Wang (2011) proposed a generalized cholera model. The model unified previous mathematical models by introducing a general incidence function f(I,B) which can include multiple transmission pathways, and a general pathogen growth rate h(I,B) which can represent varying environmental factors such as cholera ecology in water and climatological influence.

In 1992, Liao employed the basic ideas of the homotopy in topology to propose a general analytic method for nonlinear problems namely, homotopy analysis method (HAM) (Liao, 2003, 2004). As mentioned by Hassan and El-Tawil (2018), the advantages of the HAM over traditional non-perturbation methods have made it a popular technique in the field of science, engineering and finance. These advantages include its:(a) validity which does not depend upon small parameters of the considered nonlinear problem; (b) rapid rate of convergence of series solutions; (c) freedom to choose auxiliary linear operator so that one can approximate a nonlinear equation more efficiently by means of better base functions; (d) ability to find solutions to some nonlinear problems which are neglected by all other analytic and numerical techniques.

Apart from these advantages, HAM logically contains the three traditional non-perturbation methods (Lyapunov artificial small parameter method, δ- expansion method and Adomian decomposition method). The homotopy perturbation method is also a special case of HAM. The HAM was employed by Awawdeh *et al.* (2013) and by Vehdati *et al.* (2013) to solve the system of nonlinear ordinary differential equations resulting from a non-fatal disease in a population which is assumed to have constant size over the period of the epidemic. The authors appraised the HAM and concluded that the analytical approximations to the solutions of the epidemic models are reliable and confirm the power and ability of the HAM as an easy device for computing the solution of nonlinear problems since the difficulties and massive computational work that usually arise from parallel techniques and finite-difference method are avoided. Some of the recent applications of the HAM can be found (Ibrahim et al, 2017; Egbetade *et al.*, 2018; Naeem *et al.,* 2018; Bakare *et al.,* 2018)

2. The Basic Approach of the Homotopy Analysis Method

Suppose $P[y(t)] = 0$; P , $y(t)$, and t are an operator, unknown function and the independent variable respectively. Suppose also that $y_0(t)$, $H(t) \neq 0$ and L represent an initial guess of the actual solution $y(t)$, an auxiliary function and an auxiliary linear operator with the condition $L[y(t)] = 0$ whenever $y(t) = 0; h \neq 0$ denotes an auxiliary parameter. By employing $n \in [0,1]$ as an embedding parameter, we come about a homotopy

$$(1-n)L\left[\phi(t;n) - y_0(t)\right] - nhH(t)P\left[\phi(t;n)\right] = H\left[\phi(t;n); y_0(t), H(t), h, n\right], \qquad (1)$$

Based on the strength of HAM, there is no restriction or limitation to the choice of $y_0(t), L, h,$ and $H(t)$. Reducing the homotopy (1) to zero, we have

$H\left[\phi(t;n); y_o(t), H(t)\, h, n\right] = 0$, which leads us to zero-order deformation system

$$(1-n)L\left[\phi(t;n) - y_0(t)\right] = nhH(t)P\left[\phi(t;n)\right] \qquad (2)$$

If $n = 0$ then the system (2) becomes

$$\phi(t;0) = y_0(t) \qquad (3)$$

Since $h \neq 0$ and $H(t) \neq 0$ so if $n = 1$ then the system (2) reduces to

$$\phi(t;1) = y(t) \qquad (4)$$

As the embedding parameter n moves from zero to one, there exists continuous variation in $\phi(t;n)$ from the initial approximation $y_0(t)$ to the exact solution $y(t)$ according to Liao (2003, 2004). The continuous variation is what we called deformation in homotopy. It is possible to expand $\phi(t;n)$ in power series of n using the Taylor's series theorem. By that

$$\phi(t;n) = y_0(t) + \sum_{r=1}^{\infty} y_r(t)n^r \qquad (5)$$

where

$$y_r(t) = \frac{1}{r!}\frac{\partial^r\phi(t;n)}{\partial n^r}\Bigg|_{n=0} \qquad (6)$$

The values for $y_0(t)$, L, h and $H(t)$ must be properly chosen to ensure that:

(i) The solution $\phi(t;n)$ of the system (2) exists $\forall\ n \in [0,1]$.

(ii) The deformation derivative $\dfrac{\partial^r\phi(t;n)}{\partial n^r}\Bigg|_{n=0}$ occurs for $r = 1, 2\ldots$

(iii) The power series system (5) of $\phi(t;n)$ converges at $n = 1$.

Going by the above three assumptions, there exists the solution series

$$\phi(t;1) = y_0(t) + \sum_{r=1}^{\infty} y_r(t) \qquad (7)$$

By the definition in Liao (2007), $y_r(t)$ can be obtained from the system (5). Differentiating the system (5) r times with respect to n and dividing the result by $r!$ and then reducing n to zero (i.e. $n = 0$), we come about the r th-order deformation equation

$$L\left[y_r(t) - \Omega_r y_{r-1}(t)\right] = hH(t)\Re_r\left(y_{r-1}(t)\right) \qquad (8)$$

So that

$$\Re_r\left(y_{r-1}(t)\right) = \frac{1}{(r-1)!}\frac{\partial^{r-1}}{\partial n^{r-1}}P[\phi(t;n)], \qquad (9)$$

where $\Omega_r = 0$ whenever $r \leq 1$ and $\Omega_r = 1$ if $r > 1$.

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Remark:

Equation (8) is governed by the linear operator L while the term $\Re_r\left(y_{r-1}(t)\right)$ in the system (8) can be expressed in terms of the system (9) for nonlinear operator P. By the implication of equation (9), the RHS of equation (8) depends on $y_{r-1}(t)$. Hence, $y_1(t), y_2(t),\dots$ can be obtained by solving equation (8) one by one.

3. Application of the Homotopy Analysis Method

Homotopy analysis method provides a direct scheme for obtaining the solution of nonlinear differential equations without perturbation, linearization or massive computation. In order to investigate the advantages and validity of HAM in solving nonlinear equations, we propose the following system of first order ordinary differential equations describing the transmission dynamics of cholera disease and use HAM to attempt its solutions.

$$\left.\begin{aligned}\frac{dS}{dt} &= -\lambda S - \mu_d S \\[2mm] \frac{dI}{dt} &= \lambda S - \gamma I - \left(\mu_c + \mu_d\right)I \\[2mm] \frac{dR}{dt} &= \gamma I - \mu_d R \\[2mm] \frac{dB}{dt} &= \varepsilon I - \delta B\end{aligned}\right\} \tag{10}$$

where $S(t), I(t), R(t)$ and $B(t)$ are compartments for each state variable and they represent the number of susceptible individuals at time t, the number of infected individuals at time t, the number of recovered individuals at time t and the population of bacteria in the aquatic environment at time t respectively. $S(t)$ is the population of individuals who have not been infected at time t but are capable of being infected, $I(t)$ is the population of individuals who have been infected at time t and are capable of spreading the infection to those in the susceptible category. $R(t)$ is the population of individuals who have been infected with the disease at one time or the other and have been permanently recovered from it. The recovered individuals cannot be re-infected again. λ, μ_c, μ_d, ε, δ and γ are parameters representing force of infection, human death rate due to the disease, human death rate unrelated to the disease, rate at which infectious individuals contributes to the growth of pathogen, natural death rate of the pathogen, and human recovery rate unrelated to the treatment respectively. λ is a function of $B(t)$ i.e. force of infection depends on the rate of exposure to contaminated water.

To solve (10) by HAM, we choose the linear operator

$$L\left(S(t;\text{n})\right) = \frac{dS}{dt}(t;\text{n})\,, \tag{11}$$

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with the property $L(c_1) = 0$, where c_1 is the constant of integration. The inverse operator L^{-1} is given by

$$L^{-1}(*) = \int_0^t (*)\,dt \qquad (12)$$

Define the nonlinear operator

$$P[S(t;\mathrm{n})] = \frac{dS}{dt}(t;\mathrm{n}) + \lambda S(t;\mathrm{n}) + \mu_d\, S(t;\mathrm{n})\,. \qquad (13)$$

From equation (13), we construct the zeroth-order deformation equation

$$(1-n)L\big[\mathrm{S}(t;\mathrm{n}) - S_0(t;\mathrm{n})\big] = nhH(t)P\big[S(t;\mathrm{n})\big], \qquad (14)$$

where $S_0(t)$ is an initial approximation $S(t)$.

As the embedding parameter n increases from 0 to 1, we have

$$\left.\begin{array}{l} S(t;0) = S_0(t) \\ S(t;1) = S(t) \end{array}\right\}, \qquad (15)$$

thus, we obtain the rth-order (higher order) deformation equation

$$L\big[S_r(t) - X_r S_{r-1}\big] = hH(t)Q_r\big[(S_{r-1}(t))\big],\ \ r \geq 1. \qquad (16)$$

Where

$$Q_r(S_{r-1}(t)) = \frac{dS_{r-1}(t)}{dt} + \lambda S_{r-1}(t) + \mu_d S_{r-1}(t),\ \ r \geq 1. \qquad (17)$$

By the concept of *h*-curves in [18], we replace the value of *h* by setting $H(t) = 1$ to obtain solution of the $rth-order$ deformation equations for various values of h. Chosen $h = -1$, then we have the solution of the $rth-order$ deformation equation (17) as

$$S_r(t) = X_r S_{r-1}(t) - \left[\int_0^t \frac{dS_{r-1}(t)}{dt} + \lambda S_{r-1}(t) + \mu_d S_{r-1}(t)\right],\ \ r \geq 1 \qquad (18)$$

By observing all the steps in equations (11) – (18), the solutions for the $rth-order$ deformation equations $I_r(t)$, $R_r(t)$ and $B_r(t)$ for $h = -1$ are respectively

$$I_r(t) = X_r I_{r-1}(t) + \left[\int_0^t \frac{dI_{r-1}(t)}{dt} + \lambda S_{r-1}(t) - \gamma I_{r-1}(t) - (\mu_c + \mu_d)I_{r-1}(t)\right],\ \ r \geq 1 \qquad (19)$$

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$$R_r(t) = X_r R_{r-1}(t) + \left[\int_0^t \frac{d R_{r-1}(t)}{dt} + \gamma I_{r-1}(t) - \mu_d R_{r-1}(t) \right], \quad r \geq 1 \qquad (20)$$

$$B_r(t) = X_r B_{r-1}(t) + \left[\int_0^t \frac{d B_{r-1}(t)}{dt} + \varepsilon I_{r-1}(t) - \delta B_{r-1}(t) \right], \quad r \geq 1 \qquad (21)$$

The concept of *h*-curves enables us to regulate the convergence region of the so-called homotopy analysis solution. Going by the concept, we can choose a suitable range for *h* that guarantees the convergence of the series solutions.

4. Simulation and discussion

The definitions for the state variables and parameters are stated in section 3. We shall consider the following values for both the state variables and the parameters to conduct the simulation.

Table 1: Variables / Parameters and their assigned values

Variables / Parameters	Value	Source
S(0)	70	Assumed
I(0)	5	Assumed
R(0)	25	Assumed
B(0)	3	Assumed
μ_c	0.015	Kadaleka, (2011)
μ_d	0.02	Kadaleka, (2011)
δ	0.4	Isere *et al.* (2014)
γ	0.2	Assumed
ε	10	Isere *et al.* (2014)
λ	0.161	Al-Arydah*et al.* (2013)

The 10th terms analytical approximations to the solutions of *S(t),I(t),R(t)* and *B(t)* are computed with the aid of mathematical software (Mathematica) and the results are stated below:

$S(t)$= $70 - 12.67t + 1.14663t^2 - 0.0691803t^3 + 0.00313041t^4 - 0.000113321t^5 + 3.41851 \times 10^{-6}t^6$

$\qquad -8.83929 \times 10^{-8}t^7 + 1.99989 \times 10^{-9}t^8 - 4.022 \times 10^{-11}t^9 - 7.27982 \times 10^{-13}t^{10}$

$I(t)$= $5 + 10.095t - 2.2061t^2 + 0.234347t^3 - 0.0165524t^4 + 0.000878762t^5 - 0.0000374589t^6$

$\qquad +1.33618 \times 10^{-6}t^7 - 4.10291 \times 10^{-8}t^8 + 1.10709 \times 10^{-9}t^9 - 2.66642 \times 10^{-11}t^{10}$

$R(t)$= $25 + 0.5t + 1.0045t^2 - 0.15377t^3 + 0.0124862t^4 - 0.000712041t^5 + 0.0000316655t^6$

$\qquad -1.16073 \times 10^{-6}t^7 + 3.63062 \times 10^{-8}t^8 - 9.92438 \times 10^{-10}t^9 + 2.41267 \times 10^{-11}t^{10}$

$B(t)$= $3 + 4.88t + 40.7155t^2 - 12.7823t^3 + 1.8641t^4 - 0.182233t^5 + 0.0136135t^6$

$$-0.000831425t^7 + 0.0000432414t^8 - 1.96743 \times 10^{-6}t^9 + 7.98043 \times 10^{-8}t^{10}$$

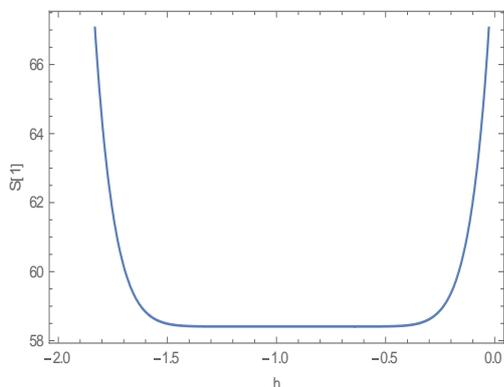The *h*-curves of 10th order approximations for each *S(t),I(t),R(t)* and *B(t)* are displayed below
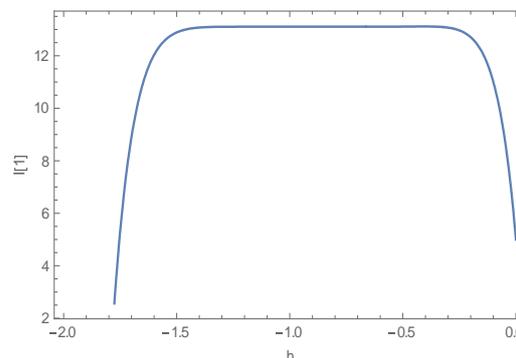

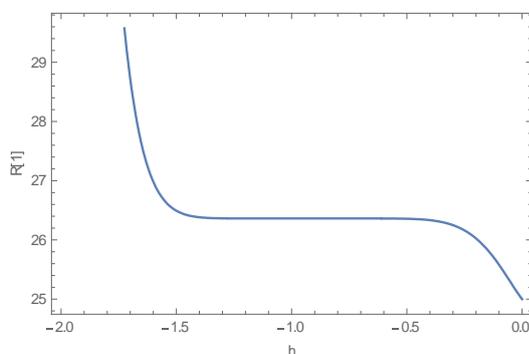Figure 1: *h*-curve for *S(t)*

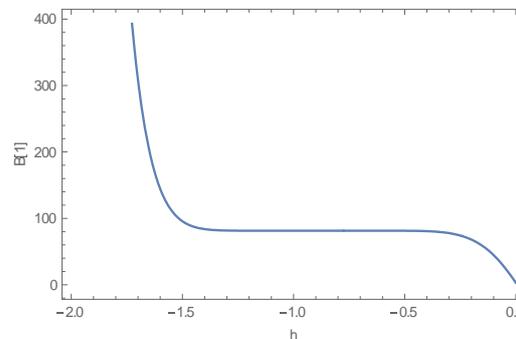Figure 2: *h*-curve for *I(t)*

Figure 3: *h*-curve for *R(t)*

Figure 4: *h*-curve for *B(t)*

The range of *h* that guarantees the convergence of solution for *S(t)* is $-1.5 \leq h \leq -0.5$, for *I(t)* is $-1.8 \leq h \leq -0.1$, for *R(t)* is $-1.5 \leq h \leq -0.4$ and for *B(t)* is $-1.5 \leq h \leq -0.3$. These results are similar to the results obtained by Vehdati*et al.* (2013).

5. Conclusion

Homotopy analysis method is a well-known and powerful method for obtaining the solutions of a large class of linear and nonlinear equations. In this work, we applied homotopy analysis method to solve a system of first order ordinary differential equations arising from *SIR-B* compartmental cholera model. Going by the concept of *h*-curve proposed by Liao (2009), we were able to determine the convergence region for the series solutions of the cholera model. Based on the outcome of the work, homotopy analysis method is a powerful tool that is suitable for the analysis of epidemic models.

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