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Analytical Solution of a Tuberculosis Epidemic Model Using Homotopy Analysis Method

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Abstract

In this paper, we describe a powerful, easy to use analytical technique known as homotopy analysis method (HAM). The HAM is then applied to nonlinear equations describing the transmission dynamics of tuberculosis epidemics. The method yields series solutions that are reasonable and easy to express. Our results reveal that HAM is very effective and simple.

***Keywords*:** tuberculosis, homotopy analysis method, nonlinear equations, mathematical model, epidemics

1.0 Introduction

Over the past decades, analytic solutions of nonlinear equations are obtained by the three traditional non-perturbation methods of Adomian decomposition method [1], Lyapunov artificial small parameter method [2] and δ- expansion method [3]. Unfortunately, these methods have some restrictions. Firstly, they are valid for weakly nonlinear problems. Secondly, none of the methods provide any freedom to choose initial approximations and the governing equations required to approximate the considered nonlinear problem. Besides, all the methods do not provide a convenient way to ensure convergence of solutions.

In order to overcome these limitations, Liao [4] proposed a new analytical approach known as homotopy analysis method (HAM).The method was developed for the purpose of obtaining series solutions to nonlinear equations with strong nonlinearity. As discussed in several articles, HAM has been shown to exhibit several distinct advantages over all previous non-perturbation methods. First, it is valid for many nonlinear equations especially those with strong nonlinearity. Second, HAM gives great freedom to select initial approximations and types of auxiliary sub problem. In addition, it provides a convergence control parameter $\hbar$ that helps to ensure series convergence. Finally it contains homotopy perturbation method develop by He [5] and the three previous non-perturbation methods as pointed out by Sajid and Hayat [6] and other researchers [7-8].

This method has been successfully applied to solve many types of nonlinear problems arising in the field of science, engineering and finance [9-26]. All these successful applications confirm the validity and great potential of HAM for solving nonlinear equations.

In this paper we shall apply the HAM to obtain series solutions of tuberculosis model proposed in Blower et. al [27]. The obtained results will be graphically displayed and discussed quantitavely to illustrate the solutions. The remainder of the paper is organized as follows: In section 2 we state the Blower et. al. model [27]. We go on in section 3 to give a systematic description of the HAM approach. Section 4 deals with the application of HAM to the model equations proposed in [27]. Numerical results are presented in section 5 while section 6 concludes the presentation.

2.0 Mathematical Formulation

The model is [27]

$$S' = \pi - \beta IS - \mu S \tag{2.1}$$
$$E' = (1-\rho)\beta IS - (\mu + v)E \tag{2.2}$$
$$I' = \rho\beta IS + vE - (\mu + \mu_T)I \tag{2.3}$$

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where
S =denotes susceptible class
E =denotes exposed class
I =denotes infected class
π *denotes* rate of recruitment of susceptible individuals
β *denotes* transmission rate of TB
μ *denotes* natural death rate
μ_T = death rate of TB
v = rate of slow progression
ρ = rate of fast progression

In the paper of Blower et. al. [27], the authors gave a qualitative analysis of the equilibrium points of the model and showed that the disease-free equilibrium is locally asymptotically stable if the basic reproduction number R_0 is less than one. It was further shown that the endemic equilibrium is unstable when $R_0 < 1$. In the present paper, we reconsider the model in [27] in order to obtain a purely analytic solution of the model. The method of solution shall be based on homotopy analysis method developed by Liao [4].

3.0 Basic Approach of HAM

Let us consider a nonlinear equation of the form

$$N[y(t)] = 0 \tag{3.1}$$

where N is a nonlinear operator, t denotes the time and $u(t)$ is an unknown function. Let $y_0(t)$ denote an initial approximation of $y(t)$ and L denote an auxiliary linear operator, Liao [9] constructs the zero-order deformation equation

$$(1-q)L[\phi(t;q) - y_0(t)] = q\hbar H(t)N(t;q) \tag{3.2}$$

where $q \in [0,1]$ is the embedding parameter, $\hbar \neq 0$ is a nonzero auxiliary parameter, $H(t) \neq 0$ is a non-zero auxiliary function.

When $q = 0$ and $q = 1$, the zero-order deformation equations becomes respectively

$$\phi(t;0) = y_0(t) \tag{3.3}$$

and

$$\phi(t;0) = y(t) \tag{3.4}$$

Thus, as q increases from 0 to 1, the solution $\phi(t;q)$ varies continuously from the initial approximation $y_0(t)$ to the exact solution $y(t)$. Such a kind of continuous variation is called deformation in topology. Expanding $\phi(t;q)$ by Taylor's series in power series of q, we have

$$\phi(t;q) = y_0(t) + \sum_{m=1}^{\infty} y_m q^m \tag{3.5}$$

where

$$y_m(t) = \frac{1}{m!}\frac{\partial^m \phi(t;q)}{\partial q^m} \tag{3.6}$$

is the deformation derivative.

If the auxiliary linear operator L, the initial approximation $y_0(t)$, the auxiliary parameter $\hbar$ and the auxiliary function $H(t)$ are properly chosen so that

(i) the solution $\phi(t;q)$ of the zero-order deformation equation (3.2) exists for all $q \in [0,1]$.
(ii) the deformation derivative (3.6) exists for all $m = 1,2,...$
(iii) the series (3.5) converges at q=1.

Then, we have the series solution

$$\phi(t;1) = y_0(t) + \sum_{m=1}^{\infty} y_m(t) \tag{3.7}$$

Define the vector

$$\overrightarrow{y_m}(t) = \{y_0(t),\ y_1(t), \dots, y_m(t)\} \tag{3.8}$$

According to the definition (3.6), the governing equation can be derived from the zero-order deformation equation (3.2). Differentiating (3.2) m times with respect to the embedding parameter q, then setting $q = 0$ and finally dividing by $m!$, we obtain the mth order deformation equation

$$L[y_m(t) - \chi_m y_{m-1}(t)] = \hbar H(t) R_m\left(\vec{y}_{m-1}(t)\right) \tag{3.9}$$

where

$$R_m\left(\vec{u}_{m-1}(t)\right) = \frac{1}{(m-1)!}\frac{\partial^{m-1} N[\phi(t;q)]}{\partial q^{m-1}} \tag{3.10}$$

and

$$\chi_m = \begin{cases} 0, & m \leq 1 \\ 1, & m > 1 \end{cases} \tag{3.11}$$

Note that according to the definition (3.10), the right hand side of (3.9) depends only on $y_{m-1}(t)$. Thus, we easily gain the series $y_1(t)$, $y_2(t)$, ... by solving the linear high-order deformation equation (3.9) using symbolic computation software such as Matlab, Maple or Mathematica.

4.0 Application of HAM to solution of Blower et. al. Model

To solve the model equations (2.1) – (2.3) by HAM, we consider equation (2.1) and choose the linear operator

$$L[S(t;q)] = \frac{dS(t;q)}{dt} \tag{4.1}$$

with the property that

$$L[a_1] = 0 \tag{4.2}$$

where a_1 is a constant of integration. The inverse operator L^{-1} is given by

$$L^{-1}(\cdot) = \int_0^t (\cdot)dt \tag{4.3}$$

Let the nonlinear operator be defined as

$$N[S(t;q)] = \frac{dS(t;q)}{dt} - \pi + \beta I(t;q)S(t;q) + \mu S(t;q) \tag{4.4}$$

By constructing the zero-order deformation equation

$$(1-q)L[S(t;q) - s_0(t;q)] = q\hbar H(t)N[S(t;q)] \tag{4.5}$$

we have that for
$q = 0$, then $S(t;0) = s_0(t)$
$q = 1$, then $S(t;1) = s(t)$.
Then, we have the mth order deformation equation

$$L[S_m(t) - \chi_m S_{m-1}(t)] = \hbar H(t) R_m\left(\vec{S}_{m-1}(t)\right), \qquad m \geq 1 \tag{4.6}$$

where

$$R_m\left(\vec{S}_{m-1}(t)\right) = \frac{dS_{m-1}(t)}{dt} - \pi + \rho\beta I_{m-1}(t)S_{m-1}(t) + \mu S_{m-1}(t) \tag{4.7}$$

The solution of the mth order deformation equation (4.6) for $m \geq 1$ and using $\hbar = -1$ and $H(t) = 1$ is given by

$$S_m(t) = \chi_m S_{m-1}(t) - \int_0^t \left(\frac{d}{dt}S_{m-1}(t) - \pi + \rho\beta I_{m-1}(t)S_{m-1}(t) + \mu S_{m-1}(t)\right)dt, \quad m \geq 1 \tag{4.8}$$

Following earlier steps, we get

$$E_m(t) = \chi_m E_{m-1}(t) - \int_0^t \left(\frac{d}{dt}E_{m-1}(t) - (1-\rho)\beta I_{m-1}(t)S_{m-1}(t) + (\mu + v)E_{m-1}(t)\right)dt, \ m \geq 1 \tag{4.9}$$

$$I_m(t) = \chi_m I_{m-1}(t) - \int_0^t \left(\frac{d}{dt}I_{m-1}(t) - \rho\beta I_{m-1}(t)S_{m-1}(t) - vE_{m-1}(t)) - (\mu + \mu_T)I_{m-1}(t)\right)dt, \quad m \geq 1 \tag{4.10}$$

5.0 Numerical Results and Discussion

The following parameters values are considered for numerical results

Table 1: Parameter values for the series solutions

Parameter	Assigned values
S	300
E	7
I	25
β	0.0005
μ	0.01
μ_T	0.003
π	0.3
ρ	0.008

Using the above table, we calculate the 3rd, 4th and 5th terms series approximations for $S(t),\ E(t), and\ \ I(t)$. Series solutions are obtained by Maple 15 software package [28].

3rd terms approximations

$$S_3(t) = \sum_{m=0}^{3} S_m(t) = 300 - 67.27t - 5.395875t^2 - 0.1757564583t^3,$$

$$E_3(t) = \sum_{m=0}^{3} E_m(t) = 7 - 34.2t + 5.6688125t^2 + 0.2795809458t^3,$$

$$I_3(t) = \sum_{m=0}^{3} I_m(t) = 25 - 17.285t + 4.404375t^2 + 2.113624167t^3,$$

4th terms approximations

$$S_4(t) = \sum_{m=0}^{4} S_m(t) = 300 - 67.27t + 5.395875t^2 - 0.1757564583t^3 + 0.5584367383t^4,$$

$$E_4(t) = \sum_{m=0}^{4} E_m(t) = 7 + 34.2t - 5.6688125t^2 + 0.2795809458t^3 - 0.5185765253t^4,$$

$$I_4(t) = \sum_{m=0}^{4} I_m(t) = 25 - 17.285t + 4.404375t^2 + 2.113624167t^3 - 0.3300966248t^4,$$

5th terms approximations

$$S_5(t) = \sum_{m=0}^{5} S_m(t) = 300 - 67.27t + 5.395875t^2 - 0.1757564583t^3 + 0.5584367383t^4 + 0.08035312773t^5,$$

$$E_5(t) = \sum_{m=0}^{5} E_m(t) = 7 + 34.2t + 5.6688125t^2 + 0.2795809458t^3 - 0.5185765253t^4 + 0.07047325499t^5,$$

$$I_5(t) = \sum_{m=0}^{5} I_m(t) = 25 - 17.285t + 4.404375t^2 + 2.113624167t^3 - 0.3300966248t^4 - 0.04623484033t^5,$$

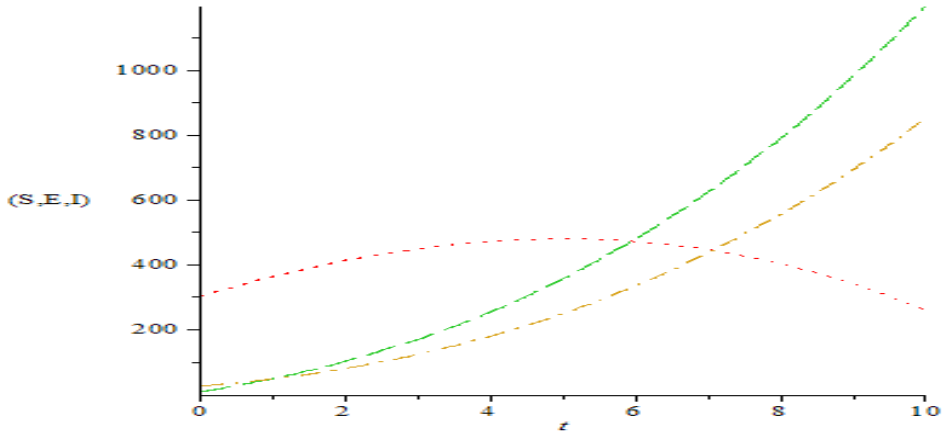

Fig. 1: Plots of 3rd terms approximations for S(t), E(t) and I(t) against time (t). The dash lines denote Exposed (E), dash dot lines denote Infective while dot lines denote Susceptibles

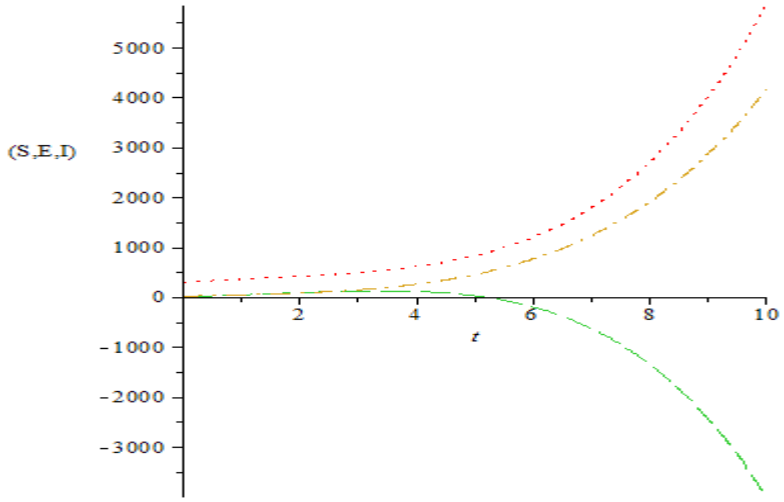

Figure 2: Plots of 4th terms approximations for S(t), E(t) and I(t) against time (t). The dash lines denote exposed (E), dashdot lines denote infectives (I) while dot lines denote Susceptible (S)

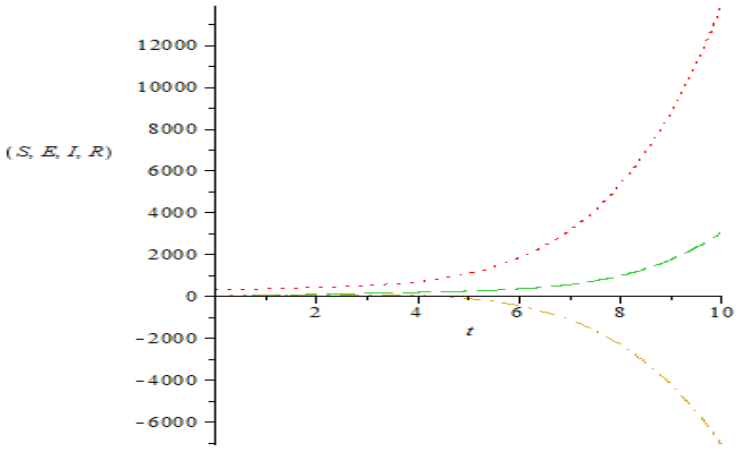

Fig. 3: Plots of 3rd terms approximations for S(t), E(t) and I(t) against time (t). The dash lines denote Exposed (E), dash dot lines denote Infective while dot lines denote Susceptibles

The results show that as the order of approximations increases, the homotopy series solutions converges rapidly. This indicate that the efficiency of HAM can be improved by obtaining higher order approximations. Furthermore, by plotting the 5th terms approximations (Fig. 3), we notice that the infective (I), exposed (E) and removed (R) classes have decreased to zero signifying the end of the epidemics. At this stage, the number of susceptible (S) approach some positive value (3.0105) which is the eventual population who were never infective.
That is,

$$\lim_{t\to\infty} I(t) = \lim_{t\to\infty} I_5(t) = 0 \; and \; \lim_{n\to\infty} S(t) = \lim_{n\to\infty} S_5(t) = 3.0105$$

6.0 Conclusion

The homotopy series solutions obtained for the SEI tuberculosis model by HAM converges very fast using a few iterations. These results show the validity and potential of homotopy analysis method for getting satisfactory approximations to nonlinear equations arising in the mathematical modeling of infectious diseases.

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