On the Homotopy Analysis Method for an Seir Tuberculosis Model

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Abstract In this paper, we provide a very accurate, non-perturbative, semi-analytical solution to a system of nonlinear first-order differential equations modeling the transmission of tuberculosis (TB) in a homogeneous population. Our analysis is based on Homotopy Analysis Method (HAM). Maple 15 software is used to carry out the computations. Our results show the validity and potential of HAM for computing the solution of nonlinear equations.

Keywords: uberculosis, homotopy analysis method, series solution, nonlinear equations, mathematical model

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1. Introduction

Infection with tuberculosis (TB) is caused by a bacterial known as Mycobacterium Tuberculosis [1,2,3]. Globally, TB is one of the greatest diseases of public concern because the pandemic is a substantial threat to socioeconomic development imposing a heavy burden on families, communities and economies [4,5,6]. In 1993, the World Health Organisation (WHO) declared TB a global emergency and about 2 billion people were estimated to be globally infected with TB that year [7]. However, with drastic global treatment measures, the incidence of TB has reduced across the globe. According to a recent global TB reports, 9.4 million people acquired the disease in 2008 resulting in 1.8 million deaths while the number of active cases has reduced to 5.7 million in 2011 with 1.4 million deaths showing that TB mortality has decreased by 22% globally since 2008 [8,9].

Mathematical models have been widely used in different forms for studying the transmission dynamics of TB epidemics [10-17]. However, the dilemma with many models in epidemiology is sometimes how to obtain analytic solutions of the nonlinear equations describing the dynamics of these diseases [18].

In 1992, a non-perturbative method known as homotopy analysis method (HAM) was proposed by Liao [19].This method was based on homotopy, an important part of topology [20]. HAM is a general analytic technique developed for the purpose of obtaining approximate analytic series solutions to different types of nonlinear equations especially those with strong nonlinearity. This method has been successfully applied to solve many types of nonlinear problems arising in the field of science, engineering and finance [21-38]. The HAM offers certain advantages over previous non-perturbative methods. Firstly, its validity does not depend upon small parameters of the considered nonlinear problem. Secondly, it provides a simple way to ensure the convergence of series solutions. Furthermore, we have great freedom to choose auxiliary linear operator so that one can approximate a nonlinear equation more efficiently by means of better base functions. Equal importantly, a few new solutions of some nonlinear problems which are neglected by all other analytic and numerical techniques are found using HAM. In addition, as proved in [25], HAM logically contains the three traditional non-perturbation methods such as Lyapunov artificial small parameter method [39], δexpansion method [40] and Adomian decomposition method [41]. The homotopy perturbation method developed in [42] is also a special case of HAM as pointed out by Sajid and Hayat [43], Liang and Jeffery [44] and other researchers.

2. Mathematical Formulation

In this paper, we consider the following TB epidemic model proposed by Egbetade and Ibrahim [45]

$$S' = (1 - \gamma)\pi + sI - \beta IS - \mu S \tag{2.1}$$

$$E' = (1 - \rho)\beta IS - (\mu + \upsilon)E$$
 (2.2)

$$I' = d\rho IS + D\upsilon E - (\mu + \mu_T + s)I$$
 (2.3)

$$R' = \varepsilon I - sI - \beta IR - \mu R \tag{2.4}$$

where S= number of susceptible who do not have the disease but could get it

E= number of exposed who are infected but are yet to show any sign of symptoms

I= number of infectives who have the disease and can transmit it to others

R= number of recovered or removed who can not get the disease or transmit it.

 γ = proportion of recruitment due to immigration

 π = rate of recruitment of susceptible individuals

- S= treatment rate of TB
- β = transmission rate of TB
- μ = natural death rate
- μ_T = death rate of TB
- v = rate of slow progression
- ρ = rate of fast progression
- D= detection rate of TB

 ε = rate at which susceptible individuals recover.

In section 3, we shall apply the homotopy analysis method described in the next section to solve equations (2.1) - (2.4).

3. Homotopy Analysis Method

For the sake of completeness and readability of the present work, we give below a systematic description of the procedures of HAM.

Consider a nonlinear equation of the form

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

where N is a nonlinear operator, t denotes the time and u(t) is an unknown function. Let $u_0(t)$ denote an initial approximation of u(t) and L denote an auxiliary linear operator, Liao [21] constructs the zero-order deformation equation.

$$(1-p)L[\phi(t;p)-u_0(t)] = phH(t)N(t;p) \quad (3.2)$$

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

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

$$\phi(t;0) = u_0(t) \tag{3.3}$$

and

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

Thus, as p increases from 0 to 1, the solution $\phi(t; p)$ varies continuously from the initial approximation $u_0(t)$ to the exact solution u(t). Such a kind of continuous variation is called deformation in topology. Expanding $\phi(t; p)$ by Taylor's series in power series of p, we have

$$\phi(t;p) = u_0(t) + \sum_{m=1}^{\infty} u_m p^m$$
(3.5)

where

$$u_m(t) = \frac{1}{m!} \frac{\partial^m \phi(t; p)}{\partial p^m}$$
(3.6)

If the auxiliary linear operator N, the initial approximation $u_0(t)$, the auxiliary parameter h and the auxiliary function H(t) are properly chosen so that

(1) the solution $\phi(t; p)$ of the zero-order deformation equation (3.2) exists for all $p \in [0,1]$.

(2) the deformation derivative (3.6) exists for all m = 1, 2, ...

(3) the series (3.5) converges at p=1.

Then, we have the series solution

$$\phi(t;1) = u_0(t) + \sum_{m=1}^{\infty} u_m(t)$$
(3.7)

Define the vector

$$\vec{u}_m(t) = \{u_0(t), u_1(t), \dots, u_m(t)\}$$
 (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 p, then setting p = 0 and finally dividing by m!, we obtain the m th order deformation equation

$$L\left[y_m(t) - \chi_m u_{m-1}(t)\right] = hH(t)Q_m\left(\vec{u}_{m-1}(t)\right) \quad (3.9)$$

where

$$Q_m(\vec{u}_{m-1}(t)) = \frac{1}{(m-1)!} \frac{\partial^{m-1} N[\phi(t;p)]}{\partial p^{m-1}} \quad (3.10)$$

and

$$\chi_m = \begin{cases} 0, & m \le 1 \\ 1, & m > 1 \end{cases}$$
(3.11)

Note that according to the definition (3.10), the right hand side of (3.9) depends only on $u_{m-1}(t)$. Thus, we easily gain the series $u_1(t), u_2(t), \ldots$ by solving the linear high-order deformation equation (3.9) using symbolic computation software such as Matlab, Maple or Mathematica.

4. Solution of SEIR Model by HAM

To solve the model equation (2.1) - (2.4) by HAM, we consider equation (2.1) and choose the linear operator

$$N[S(t;p)] = \frac{dS(t;p)}{dt}$$
(4.1)

with the property that

$$N[c_1] = 0 \tag{4.2}$$

where c_1 is a constant of integration. The inverse operator N^{-1} is given by

$$N^{-1}(\bullet) = \int_0^t (\bullet) dt \tag{4.3}$$

Let the nonlinear operator be defined as

is the deformation derivative.

$$N[S(t;p)] = \frac{dS(t;p)}{dt} - (1-\gamma)\pi - sI(t;p) + \beta I(t;p)S(t;p) + uS(t;p)$$
(4.4)

By constructing the zero-order deformation equation

$$(1-p)N[S(t;p)-s_0(t;p)] = phH(t)N[S(t;p)] (4.5)$$

we have that for

p = 0, then $S(t;0) = s_0(t)$

p=1, then S(t;1) = s(t)

Then, we have the m th order deformation equation

$$N[S_m(t) - \chi_m S_{m-1}(A)] = hH(t)Q(\bar{S}_{m-1}(t)), m \ge 1 (4.6)$$

where

$$Q_m(\vec{S}_{m-1}(t)) = \frac{dS_{m-1}(t)}{dt} - (1-\gamma)\pi - sI_{m-1}(t) + \beta I_{m-1}(t)S_{m-1}(t) + \mu S_{m-1}(t)$$
(4.7)

The solution of the *m*th order deformation equation (4.6) for $m \ge 1$ and using h = -1 and H(t) = 1 is given by

$$S_{m}(t) = \chi_{m}S_{m-1}(t)$$

-
$$\int_{0}^{t} \left(\frac{\frac{d}{dt}S_{m-1}(t) - (1-\gamma)\pi}{-sI_{m-1}(t) + \beta I_{m-1}(t)S_{m-1}(t)}\right) dt, m \ge 1$$

(4.8)
+ $\mu S_{m-1}(t)$

Following earlier steps, we get

$$E_{m}(t) = \chi_{m} E_{m-1}(t) - \int_{0}^{t} \left(\frac{d}{dt} E_{m-1}(t) - (1-\rho)\beta I_{m-1}(t) S_{m-1}(t) + (\mu+\nu)E_{m-1}(t) \right) dt, m \ge 1$$

$$(4.9)$$

$$I_{m}(t) = \chi_{m}I_{m-1}(t)$$

$$-\int_{0}^{t} \left(\frac{d}{dt}I_{m-1}(t) - d\rho\beta I_{m-1}(t)S_{m-1}(t) - d\rho\beta I_{m-1}(t)S_{m-1}(t) - d\nu E_{m-1}(T) - (\mu + \mu_{T} + \varepsilon)I_{m-1}(t) + sI_{m-1}(t)\right) dt, m \ge 1$$
(4.10)

$$R_{m}(t) = \chi_{m}R_{m-1}(t) - \varepsilon I_{m-1}(t) - \varepsilon I_{m-1}(t) + sI_{m-1}(t) + sI_{m-1}(t) + \mu R_{m-1}(t) dt, m \ge 1$$

$$(4.11)$$

5. Numerical Results and Discussion

For numerical results, the following values for parameters are considered.

 Table 1. Parameter values for the series solutions

Parameter	Assigned values
S	20
Е	10
I	15
R	5
β	0.02
γ	0.08
8	0.2
μ	0.1
μτ	0.03
U	0.04
3	0.3
d	0.4
π	0.3
ρ	0.05

For high accuracy of results, we use Maple 15 computation software [46].For the graphs, dot lines: Susceptibles; dash lines: Exposed; dashdot lines: Infectives; longdash lines: Recovered. The 5^{th} , 6^{th} , 7^{th} and 8^{th} terms approximations for S(t), E(t), I(t) and R(t) are calculated and presented below.

5th terms approximations

$$S_5(t) = 20 - 4.724t + 0.5782t^2 + 0.00844498667t^3$$
$$- 0.00251226171t^4 - 0.00034215451t^5$$

$$E_5(t) = 10 + 4.46t - 0.266284t^2 + 0.0116749093t^3$$

 $+ 0.00338895936t^4 - 0.0006101162407t^5$

$$I_5(t) = 15 + 3.66t + 0.4487436t^2 + 0.03337370672t^3$$

 $+0.00194694054t^4 + 0.000106838353t^5$

$$R_5(t) = 5 - 0.5t + 0.1t^2 - 0.00111333333t^3 - 0.000599807669t^4 + 0.000090582606t^5$$

6th terms approximations

$$S_6(t) = 20 - 4.724t + 0.5782t^2 + 0.00844498667t^3 - 0.00251226171t^4 - 0.00034215451t^5 - 0.00005700487683t^6$$

$$\begin{split} E_6(t) &= 10 + 4.46t - 0.266284t^2 \\ &\quad + 0.0116749093t^3 + 0.00338895936t^4 \\ &\quad - 0.0006201162407t^5 + 0.00001953571468t^6 \\ I_6(t) &= 15 + 3.66t + 0.4487436t^2 \end{split}$$

$$+ 0.03337370672t^{3} + 0.00194694054t^{4} + 0.000106838353t^{5} + 0.00000197134589t^{6}$$

$$R_6(t) = 5 - 0.5t + 0.1t^2$$

- 0.00111333333t^3 - 0.000599807669t^4
+ 0.0000090582606t^5 + 0.00000235519466t^6

7th terms approximations



Figure 2. Plots of 6^{th} terms approximations for S(t), I(t) and R(t) against time(t)



Figure 3. Plots of 7^{th} terms approximations for S(t), E(t), I(t) and R(t) against time(t)



Figure 4. Plots of 8^{th} terms approximations for S(t), E(t), I(t) and R(t) against time(t)

From the various order of approximations, the HAM yields convergent series solutions that are reasonable and easy to express. The plots show that while the number of susceptible (S) decreases the population who are infectives (I) increases in the period of the epidemic. Meanwhile, the number of exposed (E) increases while the number of recovered (R) decreases. However, from figure 4, as the infection dies out (i.e. as $I\rightarrow 0$, the number of susceptible, exposed and recovered increases. In particular, as $I\rightarrow 0$, S approaches some positive value S=6.0513 which is the eventual population who were never infective.

6. Conclusion

In this paper, the HAM has been successfully applied to approximately solve a system of nonlinear equations in

$$S_{7}(t) = 20 - 4.724t + 0.5782t^{2} + 0.00844498667t^{3}$$

-0.00251226171t⁴ -0.00034215451t⁵
-0.00005700487683t⁶, +0.0000106219886t⁷
$$E_{7}(t) = 10 + 4.46t - 0.266284t^{2} + 0.0116749093t^{3}$$

+0.00338895936t⁴ -0.0006201162407t⁵
+0.00001953571468t⁶ -0.000006581417588t⁷
$$I_{7}(t) = 15 + 3.66t + 0.4487436t^{2} + 0.03337370672t^{3}$$

+0.00194694054t⁴ + 0.000106838353t⁵
+0.00000197134589t⁶ - 0.00009629017459t⁷
$$R_{7}(t) = 5 - 0.5t + 0.1t^{2} - 0.0011133333t^{3}$$

-0.000599807669t⁴ + 0.000090582606t⁵

$$+0.00000235519466t^{6}+0.00005687282t^{7}$$

8th terms approximations

$$S_8(t) = 20 - 4.724t + 0.5782t^2 + 0.00844498667t^3 - 0.00251226171t^4 - 0.00034215451t^5 - 0.00005700487683t^6 + 0.0000106219886t^7 + 0.000049876956t^8$$

$$E_8(t) = 10 + 4.46t - 0.266284t^2$$

 $+0.0116749093t^{3}+0.00338895936t^{4}$

$$+0.000106838353t^{5}+0.00000197134589t^{6}$$

$$-0.00009629017459t^7 + 0.00000286668947t^8$$

$$I_8(t) = 15 + 3.66t + 0.4487436t^2$$

$$+0.03337370672t^{3}+0.00194694054t^{4}$$

 $+0.000106838353t^{5}+0.00000197134589t^{6}$

$$-0.00009629017459t^7 + 0.00000286668947t^8$$

 $R_8(t) = 5 - 0.5t + 0.1t^2$

$$-0.00111333333t^3 - 0.000599807669t^4$$

 $+0.0000090582606t^{5}+0.00000235519466t^{6}$

 $+0.00005687282t^7 + 0.00000127768296t^8$



Figure 1. Plots of 5^{th} terms approximations for S(t), I(t) and R(t) against time(t)

tuberculosis dynamics. The results show the potential and efficiency of HAM in solving nonlinear problems. We thus conclude that, combined with high performance computer and symbolic computation software such as Maple and so on, the homotopy analysis method might become a new powerful analytic tool to get satisfactory approximations for nonlinear problems in science and engineering.

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