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Approximate Series Solution of a Tuberculosis Vaccination Model using Homotopy Analysis Method

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Abstract In this paper, we employed a very powerful, non-perturbation method known as the homotopy analysis method (HAM) to obtain an approximate series solutions of non-linear equations describing the transmission dynamics of tuberculosis (TB) epidemic. We obtained fast convergent series solutions which further confirmed the ability and efficiency of HAM in solving many nonlinear problems arising in mathematical modeling of tuberculosis disease. All computations were accomplished using Maple 18 computation software.

Keywords tuberculosis, mathematical model, homotopy analysis method, series solution, non- linear equations

1. Introduction

Tuberculosis (TB) is a bacteria disease caused by Mycobacterium tuberculosis which mainly affects the lungs [1]. It is usually transmitted if the air particles produced by infected persons are inhaled when they laugh, sing, sneeze or cough. Nearly 20 years after the World Health Organization declaration of TB as a global emergency, the epidemic remains a health problem as revealed by the very slow incidence decline (estimated at 1.8% per year), the high mortality worldwide, the delay in diagnosis that perpetuate transmission in the communities and the 90% multi-drug resistant TB cases that are not on proper treatment [2].

Mathematical models in various forms have been used to gain significant insights into the epidemiology of the disease. These models have contributed greatly in identifying the groups of the population that are at a higher risk, estimating the incidence and prevalence of TB and predicting optimal strategies needed for TB diagnosis and treatment.

In this paper, we describe a non-perturbation method namely the homotopy analysis method (HAM) and apply it to give series solutions of nonlinear equations of a mathematical model of tuberculosis epidemic. In tradition, perturbation techniques such as Adomian decomposition method, Lyapunov artificial small parameter method and δ-expansion method are widely applied to give analytic approximations of nonlinear problems. Compared with previous perturbation methods, the HAM is independent of any small physical parameters and is valid for mostly nonlinear equations especially those with strong nonlinearities. More importantly, it provides a simple way to ensure the convergence of series solutions. Furthermore, as pointed out by Liao and Tan [3], the HAM gives great freedom to select initial guess, auxillary linear operator, types of governing equations of auxillary sub-problems and also some auxillary parameters so that one can approximate a nonlinear problem more effectively by means of better base functions.

HAM has been used widely to solve different types of nonlinear problems in science and engineering.

Liao [4] applied HAM to obtain a purely analytic solution for Blasius flow problem which is a 2-dimensional laminar flow over a semi-infinite flat plate. This explicit analytic solution is valid in the whole region of the considered physical parameter and gives an analytic value which is in perfect agreement with Howarth [5] numerical results.

Liao [6] by means of HAM gave a drag formula for a sphere in a uniform stream which agrees with experimental results in a considerable larger region of Renolds number than those of all reported drag formula.

Liao and Tan [3] solved the second order 2-dimensional Gelfand equations by means of a 4th order auxillary linear operator in the frame of HAM. This shows that using homotopy analysis method, we have much larger freedom to solve a nonlinear problems and thereby become much easier to find solutions of many nonlinear problems hitherto neglected by previous perturbation and numerical methods.

Awawdeh et al [7] investigated the accuracy of HAM for solving a system of 1st order nonlinear differential equations for the spread of a non-fatal disease. The HAM approximations to the solution of the model are reliable and confirm its validity for nonlinear problems.

Matinfar and Saeidy [8] obtained the solutions of some fourth order parabolic partial differential equations in fluid mechanics by the HAM. The analytical results reveal that HAM is very effective and simple.

Vahdati et al [9] applied HAM to SIR epidemic model of nonlinear differential equations. The authors obtained fast convergence series solutions which further confirm the potential of HAM in handling nonlinear problems.

2. Extension and Modification of Blower et al Model

Considering the model of Blower et al. [10] given by

$$S' = \pi - \beta IS - \mu S \quad (1)$$

$$L' = (1-\rho)\beta IS - (\mu + v)L \quad (2)$$

$$I' = \rho\beta IS + vL + (\mu + \mu_T)L \quad (3)$$

where S, L, I denotes the number of susceptible, latently infected and actively infected individuals respectively while other parameters are as given in Blower et al. [10]. Using the assumption that latent TB is completely undetectable during the course of infection and therefore, may be ignored. We replace the latently infected class (L) with the vaccinated class (V). Then, the differential equations for the proposed SVI model are

$$S' = (1-\gamma)\pi - sI - \beta IS - \mu S \quad (4)$$

$$V' = n(1-\gamma)\pi - qV - (1-f_1)\beta IV - \mu V \quad (5)$$

$$I' = \rho\beta IS + \rho(1-f_1)(1-f_2)\beta IV + (\mu + \mu_T + s)I \quad (6)$$

All the parameters are positive constants with the following interpretations

s denotes treatment rate
q denotes rate of waning of vaccine
γ denotes proportion of recruitment due to immigration
n denotes proportion of immigrants that are vaccinated
f_1 denotes efficacy rate of vaccine in protecting against initial infection
f_2 denotes efficacy rate of vaccine in slowing down progression to active TB
μ denotes natural death rate
π denotes recruitment rate of susceptible individuals
μ_T denotes death rate due to TB
v denotes rate of slow progression
ρ denotes rate of fast progression
β denotes transmission rate

In this paper, we provide series solutions for model system (4) – (6) using the techniques of homotopy analysis method described in the next section.

3. Homotopy Analysis Method

Consider the following nonlinear differential equation

$$N[v(t)] = 0 \quad (7)$$

where N is a nonlinear operator, t is independent variable and $v(t)$ is an unknown function. Based on the homotopy method in topology, Liao [3-4] constructs the so-called deformation equation

$$(1-q)L[\theta(t;r) - v_0(t)] = q\hbar H(t)N[\theta(t;r)] \quad (8)$$

where $r \in [0,1]$ is the embedding parameter, $\hbar \neq 0$ is an auxillary parameter, $H(t) \neq 0$ is an auxillary function, $v_0(t)$ is an initial approximation of the exact solution $v(t)$ and L is an auxillary linear operator with the property that $L[v(t)] = 0$ when $v(t) = 0$. When $r = 0$, the zero-order deformation equation (8) becomes

$$\theta(t;0) = v_0(t) \tag{9}$$

and when $r = 1$, equation (8) takes the form

$$\theta(t;1) = v(t) \tag{10}$$

Thus, as r increases from 0 to 1, $\theta(t;r)$ varies continuously from the initial approximation $v_0(t)$ to the exact solution $v(t)$. Expanding $\theta(t;r)$ by Taylor's series with respect to r, we obtain

$$\theta(t;r) = v_0(t) + \sum_{k=1}^{\infty} v_k(t) r^k \tag{11}$$

where

$$v_k(t) = \frac{1}{k!} \frac{\partial^k \theta(t;r)}{\partial r^k}\bigg|_{r=0} \tag{12}$$

If the auxillary linear operator, the initial approximation, the auxiliary parameter $\hbar$ and the auxillary function $H(t)$ are properly chosen, the series (11) converges at $r = 1$. Then, as proved by Liao [6]

$$v(t) = v_0(t) + \sum_{k=1}^{\infty} v_k(t) \tag{13}$$

must be one of the solutions of the original nonlinear equation (7).

According to definition (12), the governing equations of $v_k(t)$ can be deduced from the zero-order deformation (8). Define the vector

$$\vec{v}_n(t) = \{v_0(t), v_1(t), v_2(t), \cdots, v_n(t)\} \tag{14}$$

Differentiating equation (8) k times with respect to the embedding parameter r, then dividing by $k!$ and finally setting $r = 0$, we have the kth-order deformation equation

$$L[v_k(t) - \chi_k v_{k-1}(t)] = \hbar H(t) R_k(\vec{v}_{k-1}) \tag{15}$$

where

$$R_k(\vec{v}_{k-1}) = \frac{1}{(k-1)!} \frac{\partial^{k-1} N[\theta(t;r)]}{\partial r^{k-1}} \tag{16}$$

and

$$\chi_k = \begin{cases} 0, & k \leq 1 \\ 1, & k > 1 \end{cases} \tag{17}$$

It should be noted that $v_k(t)$, $k \geq 1$ is governed by the linear equation (15) together with the linear boundary conditions that come from the original nonlinear problem and can be solved directly by symbolic computation software such as Maple, Matlab or Mathematical. In the next section, all computations were accomplished using Maple 18 to ensure high accuracy results.

4. Application of HAM to the SVI Model

In this section, we employ HAM to solve the model equations (4) – (6). Considering equation (4), we choose the linear operator as

$$L\{S(t,r)\} = \frac{dS(t,r)}{dt} \tag{18}$$

with the property that

$$L[A] = 0 \tag{19}$$

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

$$L^{-1}(\cdot) = \int_0^t (\cdot) dt \tag{20}$$

We now define a nonlinear operator

$$N[S(t;r) = \frac{dS(t;r)}{dt} - (1-\gamma)\pi + sI(t;r) + \beta I(t;r)S(t;r) + \mu S(t;r) \tag{21}$$

By using the above definition, we construct the zero-order deformation equation as

$$(1-r)N[S(t;r) - s_0(t;r)] = r\hbar H(t) N[S(t;r)] \tag{22}$$

For $r = 0$ and $r = 1$, we obtain

$$S(t;0) = s_0(t), \; S(t;r) = s(t) \tag{23}$$

respectively.

Then, we have the kth order deformation equation

$$L[S_k(t) - \chi_k S_{k-1}(t)] = \hbar H(t) R_k\left(\vec{S}_{k-1}(t)\right), \quad k \geq 1 \tag{24}$$

where

$$R_k\left(\vec{S}_{k-1}(t)\right) = \frac{d}{dt} S_{k-1}(t) - (1-\gamma)\pi + sI_{k-1}(t) + \beta I_{k-1}(t)S_{k-1}(t) + \mu S_{k-1}(t) \tag{25}$$

From the kth order deformation equation (24), the solutions of equations (4)-(6) fir $k \geq 1$ and using $\hbar = -1$ and $H(t) = 1$ are obtained as follows

$$S_k(t) = \chi_k S_{k-1}(t) - \int_0^t \left[\frac{d}{dt} S_{k-1}(t) - (1-\gamma)\pi - sI_{k-1}(t) + \beta I_{k-1}(t)S_{k-1}(t) + \mu S_{k-1}(t)\right] dt \tag{26}$$

$$V_k(t) = \chi_k V_{k-1}(t) - \int_0^t \left[\frac{d}{dt} V_{k-1}(t) - n(1-\gamma)\pi + qV_{k-1}(t) + (1-f_1)\beta I_{k-1}(t)V_{k-1}(t) + \mu V_{k-1}(t)\right] dt \tag{27}$$

$$I_k(t) = \chi_k I_{k-1}(t) - \int_0^t \left[\frac{d}{dt} I_{k-1}(t) - \rho\beta I_{k-1}(t)S_{k-1}(t) \rho(1-f_1)(1-f_2)\beta I_{k-1}(t)V_{k-1}(t) - (\mu + \mu_T + s)I_{k-1}(t)\right] dt \tag{28}$$

5. Numerical Results and Discussion

For numerical results, the following parameter values are considered

Table 1: Parameters and their Assigned Values

Parameters	Values
S	50
V	20
I	15
π	0.003
γ	0.07
s	0.21
β	0.008
μ	0.01
μ_T	0.005
ρ	0.06
v	0.03
f_1	0.004
f_2	0.003
q	0.007
n	0.1

The $1^{st} - 5^{th}$ terms approximations for $S(t), V(t)$ and $I(t)$ are calculated and presented below.

1^{st} terms approximation

$$S_1(t) = \sum_{k=0}^{1} S_k(t) = 50 - 3.413t,$$

$$V_1(t) = \sum_{k=0}^{1} V_k(t) = 20 - 0.35183236t,$$

$$I_1(t) = \sum_{k=0}^{1} I_k(t) = 15 + 3.41172450t,$$

2nd terms approximations:

$$S_2(t) = \sum_{k=0}^{2} S_k(t) = 50 - 3.413t - 0.38892256\,t^2,$$

$$V_2(t) = \sum_{k=0}^{2} V_k(t) = 20 - 0.35183236t - 0.22091496t^2,$$

$$I_2(t) = \sum_{k=0}^{2} I_k(t) = 15 + 3.41172450t + 0.38818481t^2,$$

3rd terms approximations:

$$S_3(t) = \sum_{k=0}^{3} S_k(t) = 50 - 3.413t - 0.38892256\,t^2 - 0.02639151t^3,$$

$$V_3(t) = \sum_{k=0}^{3} V_k(t) = 20 - 0.35183236t - 0.22091496t^2 + 0.00038875322t^3,$$

$$I_3(t) = \sum_{k=0}^{3} I_k(t) = 15 + 3.41172450t + 0.38818481t^2 + 0.029196389t^3,$$

4th terms approximations:

$$S_4(t) = \sum_{k=0}^{4} S_k(t) = 50 - 3.413t - 0.38892256\,t^2 - 0.02639151t^3 + 0.056710493t^4,$$

$$V_4(t) = \sum_{k=0}^{4} V_k(t) = 20 - 0.35183236t - 0.22091496t^2 + 0.00038875322t^3 + 0.0088460811t^4,$$

$$I_4(t) = \sum_{k=0}^{4} I_k(t) = 15 + 3.41172450t + 0.38818481t^2 + 0.029196389t^3 + 0.096743255t^4,$$

5th terms approximations:

$$S_5(t) = \sum_{k=0}^{5} S_k(t) = 50 - 3.413t - 0.38892256\,t^2 - 0.02639151t^3 + 0.056710493t^4, + 0.030482657t^5$$

$$V_5(t) = \sum_{k=0}^{5} V_k(t) = 20 - 0.35183236t - 0.22091496t^2 + 0.00038875322t^3 + 0.0088460811t^4 + 0.006652814t^5,$$

$$I_5(t) = \sum_{k=0}^{5} I_k(t) = 15 + 3.41172450t + 0.38818481t^2 + 0.029196389t^3 + 0.096743255t^4 - 0.076350118t^5,$$

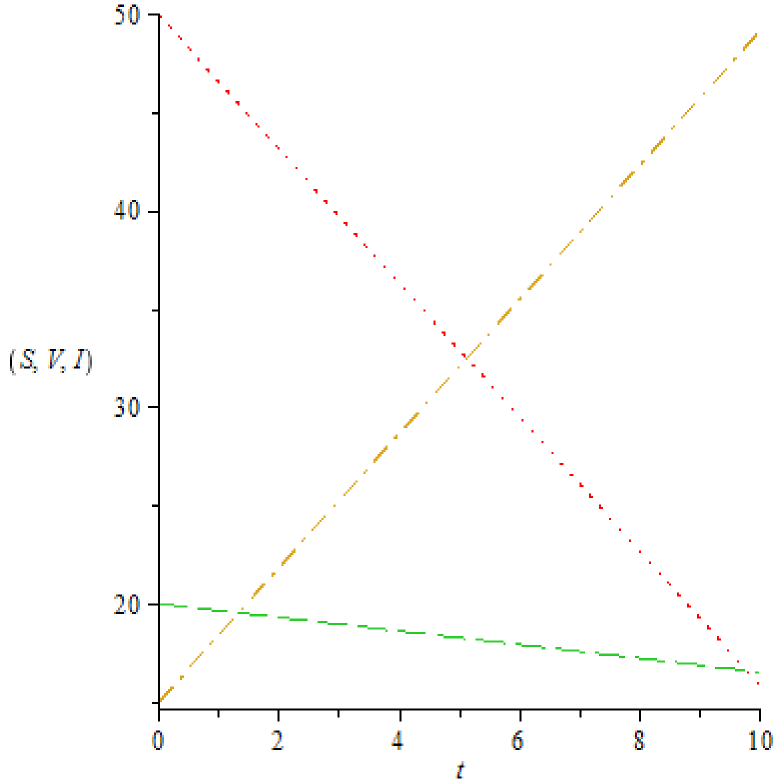

Figure 1: Plots of 1st approximations for $S(t)$, $V(t)$ and $I(t)$ against $time(t)$ for $\hbar = -1$

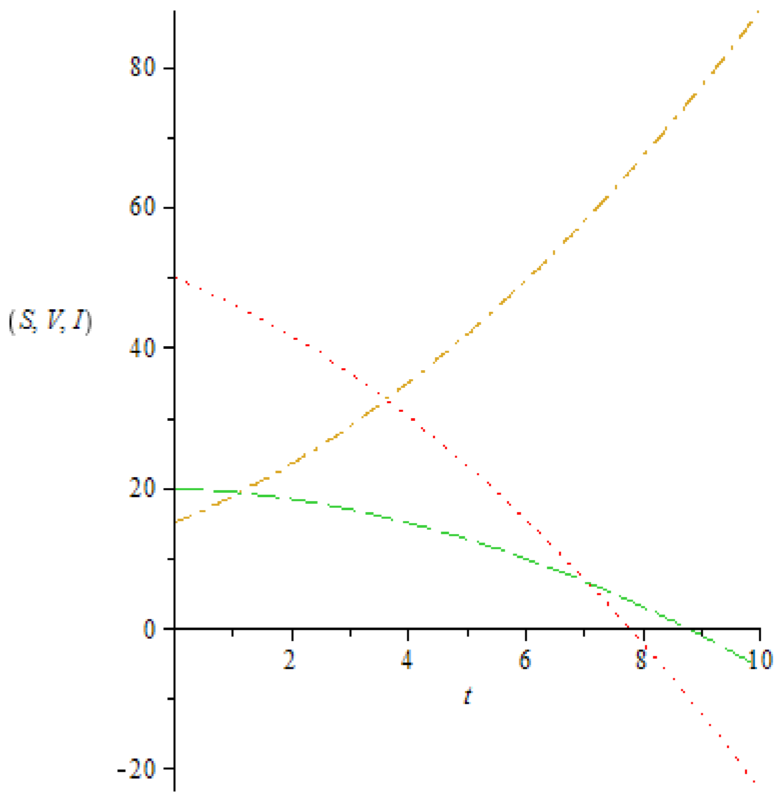

Figure 2: Plots of 2nd terms approximations for $S(t)$, $V(t)$ and $I(t)$ against $time(t)$ for $\hbar = -1$

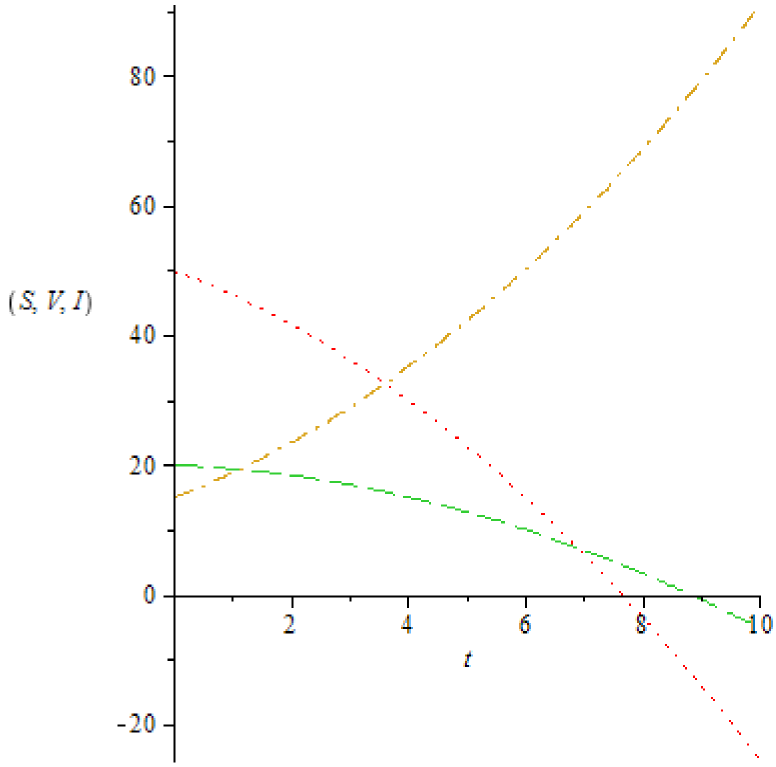

Figure3: Plots of 3rd terms approximations for $S(t)$, $V(t)$ and $I(t)$ against $time(t)$ for $\hbar = -1$

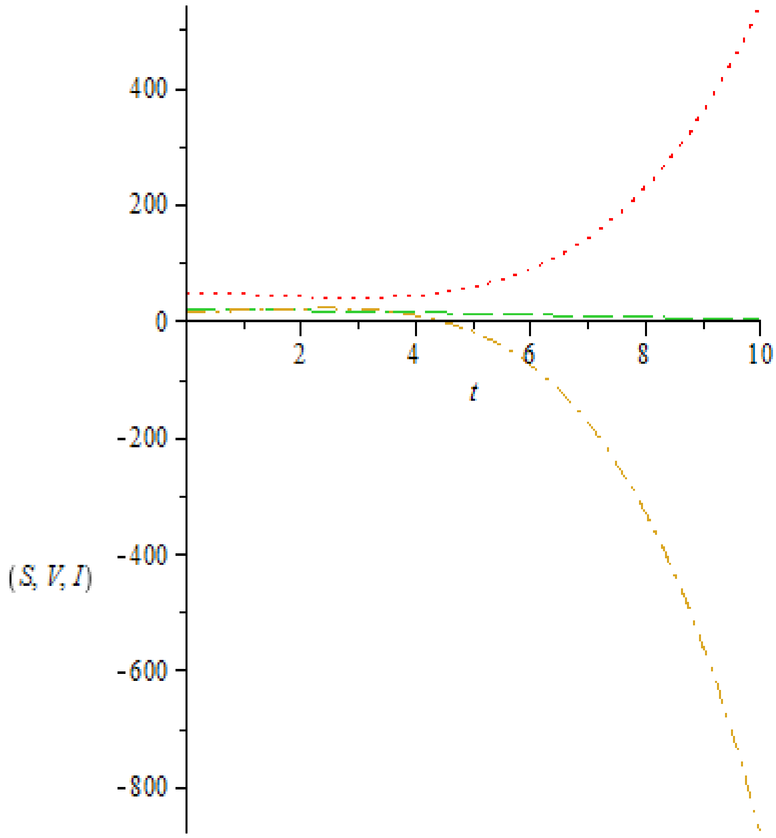

Figure 4 : Plots of 4th terms approximations for $S(t)$, $V(t)$ and $I(t)$ against $time(t)$ for $\hbar = -1$

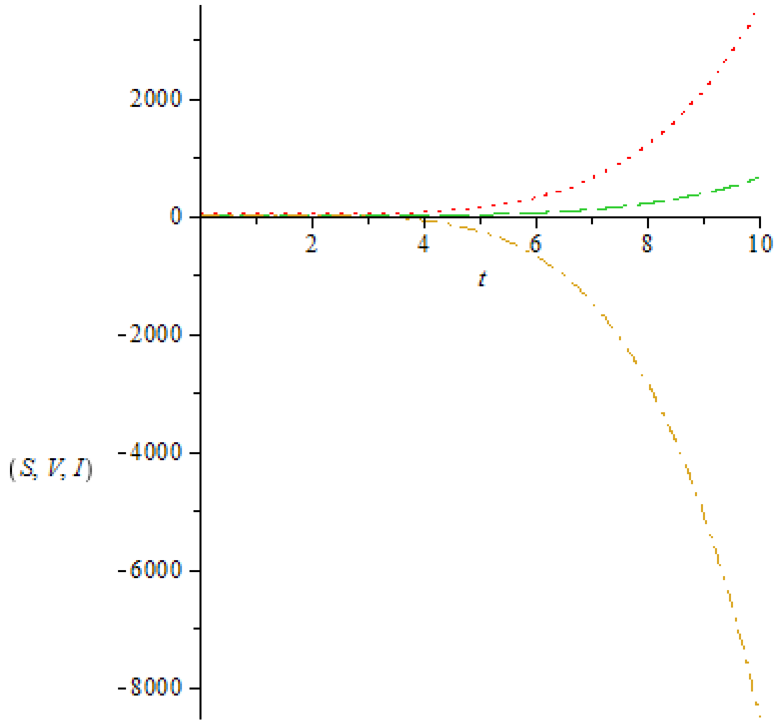

Figure 5: Plots of 5th terms approximations for $S(t), V(t)$ and $I(t)$ against time (t) for $\hbar = -1$

The numerical results show that HAM approximations to the solution of the model is good and easy to express. Furthermore, the plots show that HAM yields rapidly convergent series solutions as the order of approximations increases. It could be observed from the figures that the series solutions converge at the 5^{th} order approximations of S(t), V(t) and I(t). Figure 5 also illustrates the end of the epidemic since as time goes on $(t \to \infty)$, the number of infective (I) decreases to zero while the number of susceptible (S) approaches some positive value (4.4708) which is the eventual population of those who were not infected with TB disease.

6. Conclusion

The HAM approximations obtained for the SVI model converge rapidly using a few iterations. These results further confirm HAM as a powerful device for solving many functional equations such as ordinary, partial, integral and nonlinear differential equations in disease dynamics models.

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