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On the Homotopy Analysis Method for PSTIR Typhoid 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 of mathematical model of typhoid fever 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. Thus, this method is valid for nonlinear problems with strong nonlinearity.

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

1.0 Introduction

Typhoid fever has continued to be a health problem in developing countries where there is poor sanitation, poor standard of personal hygiene and prevalence of contaminated food. It is endemic in many parts of the developing world, and as global travel increases, illness do occur around the world in span of a day [1].
In urban areas where sewage disposal is lacking or inadequate water supplies get contaminated and thus cause the outbreaks of typhoid. It is endemic in South and Central America, South East, the Middle East and Far East Asia, and the Indian subcontinent. The existing estimate of the global burden of typhoid fever is 16 million illnesses and 600,000 deaths annually [2].
Several mathematical models have been developed on this disease [3 - 10]. In reference [9], the author proposed a mathematical model of the type P S, I, T. They divide the total human population into four subclass, i.e., Susceptible, Protected, Infected, Treated and Recovered. The basic reproduction number is computed using the next generation matrix approach. Stability analysis of the model is carried out to determine the conditions that favors the spread of the disease. Complementing the work of [9], we constructed a mathematical model of the type PSITR we added recovered compartment in which all treated recovered but after some time the recovered loss immunity and return back to susceptible.

2.0 Description and Formulation of the Model

$P(t)$ is the compartment used for those that have been vaccinated against the disease and loses protection over a period of time. S(t) is used to represent the number of individuals that are prone to the disease at time t. I(t) denote the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible categories. $T(t)$ denote the number of individuals who have been infected with the disease and are treated. $R(t)$ is the compartment used for those individuals who have been infected and then recovered from the disease. Susceptible individuals are recruited into the population at rate $(1-\sigma)\Lambda$. Susceptible individual aquired typhoid fever at a constant rate α .Hence We propose the above model with the following equations.

$$\frac{dP}{dt} = \sigma\Lambda - (\gamma + \mu)P \quad (1)$$

$$\frac{dS}{dt} = (1-\sigma)\Lambda + \gamma P - \alpha SI - \mu S + kR \quad (2)$$

$$\frac{dI}{dt} = \alpha SI - (\delta + \beta + \mu)I \quad (3)$$

$$\frac{dT}{dt} = \beta I - (\mu + \varepsilon)T \quad (4)$$

$$\frac{dR}{dt} = \varepsilon T - \mu R - kR \quad (5)$$

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3.0 Homotopy Analysis Method (HAM)

The homotopy analysis method (HAM) is an analytic approximation method for highly nonlinear equations in science, finance and engineering. HAM transfers a nonlinear problem into an infinite number of linear sub problems. It was first proposed by Liao in 1992 in his PhD dissertation, and modified and developed in [11 - 14].

3.1 Mathematical Formulation

Consider a nonlinear differential equation of the form

$$N[u(t)] = 0 \tag{6}$$

where N is a nonlinear operator, $u(t)$ is an unknown function and t is an independent variable.

Let $u_0(t)$ denote an initial approximation of the exact solution $u(t)$, L an auxiliary linear operator, $h \neq 0$ and $H(t) \neq 0$ denote an auxiliary parameter and auxiliary function respectively. Using the embedding parameter $r \in [0,1]$, we construct a zero-order deformation equation

$$(1-r)L[\phi(t;r) - u_0(t)] = rH(t)N[\phi(t;r)] \tag{7}$$

As pointed out in [14], we have great freedom to choose the initial approximation $u_0(t)$, the auxiliary linear operator L, the non-zero auxiliary (convergent-control) parameter and the auxiliary function $H(t)$. It is this kind of freedom and flexibility that allows us to control and adjust the convergence region and rate of homotopy solution of the considered nonlinear problem [12].

When $r = 0$, equation (7) becomes

$$\phi(t;0) = u_0(t) \tag{8}$$

When $r = 1$, the zero-order deformation equation (7) is equivalent to

$$\phi(t,1) = u(t) \tag{9}$$

Therefore, according to equations (8) and (9), as the embedding parameter r increases from 0 to 1, $\phi(t;r)$ varies continuously from the initial approximation $u_0(t)$ to the exact solution $u(t)$. In topology, this kind of continuous variation is called deformation.

If the initial approximation, auxiliary linear operator, auxiliary parameter h and auxiliary function $H(t)$ are properly chosen, then the homotopy solution $\phi(t;r)$ of the zero-order deformation equation (7) exists for all $r \in [0,1]$ and besides its mth-order deformation derivative

$$u_m(t) = \frac{1}{m!}\frac{\partial^m \varphi(t;r)}{\partial r^m}\bigg|_{r=0} \tag{10}$$

for $m \geq 1$.

By Taylor's theorem, we expand the homotopy $\phi(t;r)$ in a power series of the embedding parameter r as follows

$$\varphi(t;r) = u_o(t) + \sum_{m=1}^{\infty} u_m(t) r^m$$

where

$$u_m(t) = \frac{1}{m!}\frac{\partial^m \varphi(t;r)}{\partial r^m}\bigg|_{r=0} \tag{11}$$

Assuming that the auxiliary parameter h, the auxiliary function $H(t)$, the initial approximation $u_0(t)$ and the linear operator L are so properly chosen so that the solution series (10) converges at $r = 1$. Then, at $r = 1$, the series (10) becomes

$$\varphi(t;1) = u_o(t) + \sum_{m=1}^{\infty} u_m(t) \tag{12}$$

Therefore, equation (9), 11) can be re-written as

$$\varphi(t) = u_o(t) + \sum_{m=1}^{\infty} u_m(t)$$

which is the approximate solution series of the nonlinear equation (6) by homotopy analysis method.

Define the vector

$$\vec{U}(t) = \{u_o(t), u_1(t), \ldots, u_n(t)\}$$

Now, according to the definition (10), the related governing equations of $u_m(t)$ can be derived from the zero-order deformation equation (7).

Differentiating the zero-order deformation (7) m times with respect to r and then dividing by $m!$ and finally setting $r = 0$, we have the mth-order deformation equation

$$L[u_m(t) - \chi_m u_{m-1}(t)] = hH(t)Q_m(\vec{u}_{m-1}) \tag{13}$$

Where

$$Q_m(\vec{u}_{m-1}) = \frac{1}{(m-1)!}\frac{\partial^{m-1} N[\varphi(t;r)]}{\partial p^{m-1}}|_{p=0}$$

$$\chi_m = \begin{cases} 0, \ m-1 \\ \\ 1, \ m \succ 1 \end{cases} \quad (14)$$

At this stage, all the solution series $u_1(t)$, $u_2(t)$, $\cdot u_3(t)$ . . . , of $u_m(t)$ can easily be gained by solving the linear high-order deformation equation (12) by means of symbolic computation software such as Matlab, Maple and Mathematica.
Hence, the mth-order approximation of

$u_m(t)$

is given by

$$u(t) \approx \sum_{n=0}^{\infty} u_n(t)$$

4.0 Solution of the PSITR Typhoid Model by HAM

We consider the following nonlinear system of first-order differential equations describing the transmission dynamics of typhoid fever

$$\frac{dP}{dt} = \sigma\Lambda - (\gamma + \mu)P \quad (15)$$

$$\frac{dS}{dt} = (1-\sigma)\Lambda + \gamma P - \alpha SI - \mu S + kR \quad (16)$$

$$\frac{dI}{dt} = \alpha SI - (\delta + \beta + \mu)I \quad (17)$$

$$\frac{dT}{dt} = \beta I - (\mu + \varepsilon)T \quad (18)$$

$$\frac{dR}{dt} = \varepsilon T - \mu R - kR \quad (19)$$

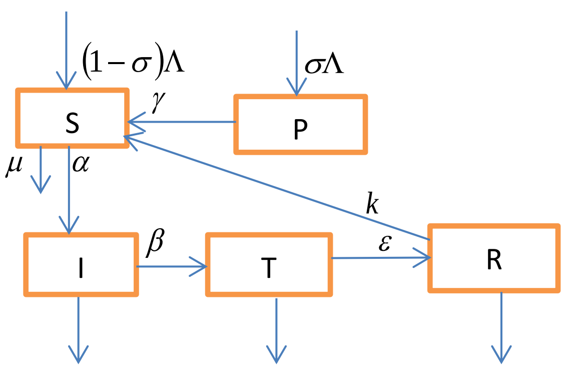

Figure 1

Table 1: Model parameters and their interpretations

Parameter	Description
Λ	Recruitment rate
σ	Adjustment parameter
μ	Natural death rate
δ	Disease induced death rate
γ	Loss of protection
β	Rate of treatment
α	Contact rate of infection
k	relapse rate
ε	Progression rate from T to R

Solving (15) by HAM we choose a linear operator

$$L(S(t;r)] = \frac{dS}{dt}(t;r) \tag{20}$$

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

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

Define the non linear operator

$$N[P(t;r)] = \frac{dP}{dt}(t;r) - \sigma\Lambda + (\gamma+\mu)P(t;r)$$

From the above definition we construct the zeroth-order deformation equation

$$(1-r)L[P(t;r) - p_0(t;r)] = rH(t)N(P(t;r))$$

Where p_0 is the initial approximation of $P(t)$

As the embedding parameter r increases from 0 to 1 we have

$$p(t,0) = p_0(t), \quad p(t,1) = p(t)$$

Thus, we obtain the mth-order(high order) deformation

$$[L[P_m(t) - X_m P_{m-1}(t)] = hH(t)Q_m(P_{m-1}(t)),\ m \geq 1 \tag{21}$$

Where

$$Q_m(P_{m-1}(t)) = \frac{dP_{m-1}(t)}{dt} - \sigma\Lambda + (\gamma+\mu)P_{m-1}, m \geq 1$$

and X_m is defined by equation (13)

By the concept of h-curves (Liao, 2009a), we simply need to replace the values of h while setting $H(t) = 1$ to obtain solutions of the mth-order deformation equations for various values of h. If we choose $h = -1$, then we have the solution of the mth-order deformation equation (20) as

$$P(t) = X_m P_{m-1}(t) - \int_0^t \left[\frac{d}{dt}P_{m-1}(t) - \sigma\Lambda + (\gamma+\mu)P_{m-1}\right]dt\ \ m \geq 1 \tag{22}$$

By observing all other steps in (14) - (20), the solutions of the mth-order deformation equations of $S_m(t)$, $I_m(t)$, $T_m(t)$ and $R_m(t)$ for $h = -1$ are respectively

$$S(t) = X_m S_{m-1}(t) - \int_0^t \left[\frac{d}{dt}S_{m-1}(t) - (1-\sigma)\Lambda + \alpha S_{m-1}(t)I_{m-1}(t) + \mu S_{m-1}(t) - \gamma P_{m-1}(t) + kP_{m-1}(t)\right]dt\ \ m \geq 1 \tag{23}$$

$$I(t) = X_m I_{m-1}(t) - \int_0^t \left[\frac{d}{dt}I_{m-1}(t) - \alpha S_{m-1}(t)I_{m-1}(t) + (\delta+\beta+\mu)I_{m-1}(t)\right]dt\ \ m \geq 1 \tag{24}$$

$$T(t) = X_m T_{m-1}(t) - \int_0^t \left[\frac{d}{dt}\ T_{m-1}(t) - \beta I_{m-1}(t) + (\mu+\varepsilon)T_{m-1}(t)\right]dt\ \ m \geq 1 \tag{25}$$

$$R(t) = X_m R_{m-1}(t) - \int_0^t \left[\frac{d}{dt}\ R_{m-1}(t) - \varepsilon T_{m-1}(t) + (\mu+k)R_{m-1}(t)\right]dt\ \ m \geq 1 \tag{26}$$

5.0 Numerical Results and Discussion

For numerical results, the following values for parameters are considered considered for the disease free equilibrium state . First to third terms approximations for P(t), S(t), I(t), T(t) and R(t) are calculated and presented below.

Table 2: Parameter values used for series solution

Parameters	Assigned values
P	50
S	200
I	100
T	60
R	30
Λ	0.2
σ	0.3
μ	0.12
δ	0.1
γ	0.15
β	0.6
α	0.14
ε	0.5
k	0.02

Using Maple 15 computation software the 1st to 3rd terms approximation for $P(t)$, $S(t)$, $I(t)$, $T(t)$ and $R(t)$ were calculated. The series solution were obtained for $h=-1$. For the graphs, solid line; Protected, dot lines: Susceptibles; dash lines: Infected; dashdot lines: Treated; long dash lines: Recovered.

1st terms approximations

$$P_1(t) = 50 - 1.29t$$
$$S_1(t) = 200 - 27.6t$$
$$I_1(t) = 100 - 5.4t$$
$$T_1(t) = 60 - 9.72t$$
$$R_1(t) = 30 - 0.03t$$

2nd terms approximations

$$P_2(t) = 50 - 1.29t + 10.174156t^2$$
$$S_2(t) = 200 - 27.6t + 26.6t^2$$
$$I_2(t) = 100 - 5.4t + 2.214t^2$$
$$T_2(t) = 60 - 9.72t + 4.6332t^2$$
$$R_2(t) = 30 - 0.03t + 0.018t^2$$

3rd terms approximations

$$P_3(t) = 50 - 1.29t + 10.174156t^2 - 0.015235t^3$$
$$S_3(t) = 200 - 27.6t + 26.6t^2 + 21.3341393t^3$$
$$I_3(t) = 100 - 5.4t + 2.214t^2 - 0.6361733333t^3$$
$$T_3(t) = 60 - 9.72t + 4.6332t^2 - 1.40022328t^3$$
$$R_3(t) = 30 - 0.03t + 0.018t^2 + 0.030048t^3$$

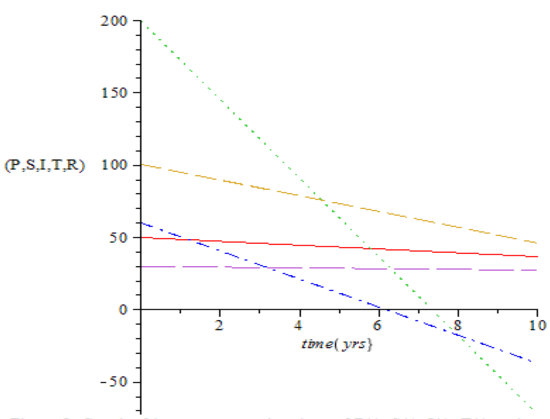

Figure 2: Graph of 1st term approximations of P(t), S(t), I(t), T(t) and R(t) for $\hbar=-1$

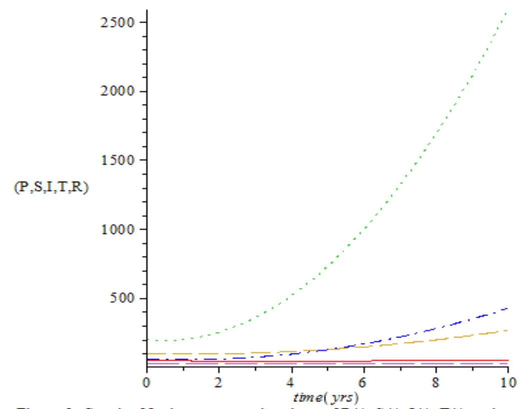

Figure 3: Graph of 2nd term approximations of P(t), S(t), I(t), T(t) and R(t) for $\hbar=-1$

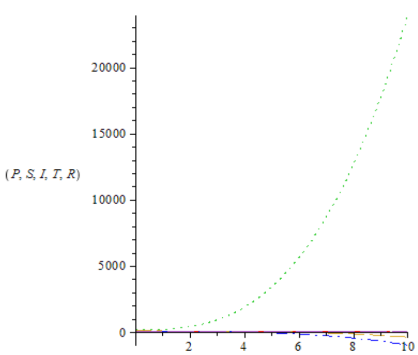

Figure 4: Graph of 3rd term approximations of P(t), S(t), I(t), T(t) and R(t) for $\hbar=-1$

6. Discussion and Conclusion

The Homotopy Analysis Method (HAM) yields rapidly convergent series solution by using a few iterations. Homotopy analysis method has been successfully applied to approximately solve a system of nonlinear equations in typhoid fever dynamics. The results show the potential and efficiency of HAM in solving nonlinear problems. we can then conclude that HAM is very efficient and accurate in solving PSITR model. From our numerical example, we demonstrated the ability of HAM to converge very fast, we saw that the HAM converges in just three iterations we can then conclude that HAM is very efficient and accurate in solving PSITR model.

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