Analytical Solution of the Leptospirosis Epidemic model by Homotopy Perturbation method

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Abstract

In this paper, we consider a mathematical model of leptospirosis disease consisting of differential equations. We apply the Homotopy perturbation method to the proposed model to find both the analytic and approximate solutions. From our solutions, we obtained that Homotopy perturbation method is one of the most important method, like just few perturbation terms are sufficient for obtaining a reasonable accurate solution. The solution obtain from this method is good as compared to other standard numerical methods.

Keywords: Leptospirosis, mathematical model, Homotopy Perturbation Method, numerical simulations

Introduction

The infection of Leptospirosis disease is a globally important. Because the infection of the disease occurs in developed and industrialized countries as well as rural regions in the world. The people infected from this disease easily are rice planters, sewer cleaners, workers cleaning canals, agriculture labors. In order to understand the dynamics of this infectious disease, several authors proposed different mathematical models\textsuperscript{1-14}. Pongsuumpun et al\textsuperscript{5}, developed a mathematical model to study the dynamical behavior of Leptospirosis disease. Triampo et al\textsuperscript{6}, considered a deterministic models for the transmission of Leptospirosis disease by collecting some real data. Zaman\textsuperscript{7}, studied the dynamical behavior of Leptospirosis and applied optimal control theory to control the spread of this disease in the community.

Most of the biological problems in the form of mathematical models are inherently nonlinear. Therefore it’s not only difficult but always impossible to find the exact solutions that represent the complete biological phenomena. So, the scientists are in search to find such numerical methods or perturbations method to find the exact solution and approximate solution to these nonlinear problems. In the numerical methods, stability and convergence should be considered so as to avoid divergence or inappropriate results. While, in the analytical perturbation method, we need to exert the small parameter in the equation. Therefore, finding the small parameter and exerting it into the equation are difficulties of this method. However, there are some limitations with the common perturbation method, like the common perturbation method is based upon the existence of a small parameter, which is difficult to apply to real world problems. Therefore, many different powerful mathematical methods have been recently introduced to vanish the small parameters, such as artificial parameter method\textsuperscript{8,9}.

The Homotopy Analysis Method (HAM) is one of the wellknown methods to solve the nonlinear equations. In the last decade, the idea of homotopy was combined with perturbation. The fundamental work was done by Liao and He. This method involves a free parameter, whose suitable choice results into fast convergence. First time He\textsuperscript{10}, introduced Homotopy Perturbation Method (HPM) and its application in several problems\textsuperscript{11,12}. Ali et al\textsuperscript{13}, presented the solution of multi points boundary values by using Optimal Homotopy Analysis Method (OHAM). These methods are independent of the assumption of small parameter as well as they covered all the advantages of the perturbation method. Some other relevant work can be find by other researchers\textsuperscript{14-17}.

The motivation of this paper is to present the application of the analytic homotopy perturbation method (HPM) to solve a model of epidemic leptospirosis disease\textsuperscript{1}. First, we formulate our problem and then apply the HPM to find the analytical as well as numerical solutions. Finally, we also estimates the parameter in the model for the numerical simulation.

The paper is organized as follows. Section 2 is devoted to the basic idea of HPM and the mathematical formulation of the model. In Section 3 the model is solve by HPM. We present the numerical solution and discussion in section 4.

Basic idea of Homotopy Perturbation Method (HPM) and model framework: In this section, first we explain the Homotopy perturbation method in detail and then we apply the technique of HPM to our proposed Leptospirosis epidemic model. HPM was first time introduced by He\textsuperscript{8,9}, for solving the non linear differential equations.

\[ B(m) = f(d), \quad d \in \Lambda \] (1)
subject to the boundary conditions
\[ \psi \left( m \frac{\partial n}{\partial n} \right) = 0, \quad d \in \Omega \]  

Here B represents the general differential operator, \( \psi \) is the boundary operator, \( f(d) \) is the analytic function, \( \Omega \) is the boundary of the domain \( \Lambda, \frac{\partial}{\partial n} \) represents the differentiation along the normal vector \( \Lambda \) drawn outward. The operator B is divided in two parts, H is linear and K is nonlinear to get the following equation
\[ H(m) + K(m) = f(d) \]  

Define the homotopy \( v(r, p) : \Lambda \times [0,1] \rightarrow \mathbb{R} \), that satisfies
\[ F(v, p) = (1 - p)[H(v) - H(m_o)] + p[B(v) - f(d)] = 0, \]  

Which can be written as
\[ F(v, p) = H(v) + p(H(m_o) + p[K(m) - f(d)]) = 0, \]  

Where \( m_o \) shows the initial approximation of (5) and \( p \) is the embedding parameter such that \( p \in [0,1] \). It is obvious that
\[ F(v, 0) = [H(v) - H(m_o)] \]

For \( p=0 \) we get,
\[ F(v, 0) = [H(v) - H(m_o)] \]

while for \( p=1 \) we obtain
\[ F(v, 1) = [B(v) - f(d)]. \]

Applying the perturbation technique by considering parameter \( p \) for small value then the solution of equation (4) can be obtained in \( p \) series is given by
\[ v = v_o + pv_1 + p^2v_2 + p^3v_3 \ldots \]  

when \( p \) approaches 1 the equation (4) becomes the original equation (3) and (7) becomes the approximate solution of (3) is given by
\[ m = \lim_{p \rightarrow 1} v = v_o + pv_1 + p^2v_2 + p^3v_3 \ldots \]

The series (7) is convergent for most of cases see [8,9].

In order to formulate our problem, we assume that \( S_o(t) \) represents number of susceptible human at time \( t \); \( I_o(t) \) represents number of infected human in the population, which is infected from the leprosy disease at time \( t \); \( R_o(t) \) represents number of human in the population which is recovered at time \( t \). The total population size is \( N_o(t) = S_o(t) + I_o(t) + R_o(t) \). For vector population, let \( P_v(t) \) are susceptible vector and \( M_v(t) \) are infected vector at time \( t \). The total population size of vector population is denoted by \( N_v(t) = P_v(t) + M_v(t) \). By the interaction of both human and vector population we get the following system of five differential equations is given by:

\[ \frac{dS_h}{dt} = b_1 - \mu_s S_h - \beta_2 S_h M_v - \beta_1 S_h I_h + \lambda_h R_h, \]

\[ \frac{dI_h}{dt} = \beta_2 S_h M_v + \beta_1 S_h I_h - (\mu_h + \delta_h + \gamma_h) I_h, \]

\[ \frac{dR_h}{dt} = \gamma_h I_h - (\mu_h + \lambda_h) R_h, \]

\[ \frac{dP_v}{dt} = b_2 - \gamma_v P_v - \beta_3 P_v I_h, \]

\[ \frac{dM_v}{dt} = \beta_3 P_v I_h - \gamma_v M_v - \delta_v M_v, \]

With the initial conditions
\[ S_h(0) \geq 0, I_h(0) \geq 0, R_h(0) \geq 0, \quad P_v(0) \geq 0, M_v(0) \geq 0 \]

\( b_1 \) represents the growth rate of human population. The direct transmission between susceptible human and infected vector is represented by \( \beta_1 \). The transmission rate of the vector is shown by \( \beta_2 \). The natural death rate for the human is \( \mu_h \). The disease death rate for the human is represented by \( \delta_h \). The natural mortality rate for vector population is \( \gamma_v \). \( \delta_v \) represents the disease related death rate for vector. \( b_2 \) represent the population growth rate for the vector. \( \beta_3 \) is the transmission coefficient between susceptible vector and infected human. The rate of recovery from the infection is shown by \( \gamma_h \). The individuals are susceptible again at \( \lambda_h \).

Now, we apply the homotopy perturbation techniques to our model (8). We assume for simplifications
\[ S_h(t) = S, I_h(t) = I, R_h(t) = R, P_v(t) = P \text{ and } M_v(t) = M \]

Now we define the operator \( \mathcal{L} = \frac{d}{dt} \). The initial data we consider is given by
\[ \mathcal{L}(S(t) - L^\alpha(t)) = p(\mu_S S_h - \beta_2SM - \beta_1SI + \lambda_h R - L^\alpha(t)), \]
\[ \mathcal{L}(I(t) - L^\alpha(t)) = p(\mu_H I_h - (\mu_h + \delta_h + \gamma_h) I_h - L^\alpha(t)), \]
\[ \mathcal{L}(R(t) - L^\alpha(t)) = p(\gamma_h I_h - (\mu_h + \lambda_h) R - L^\alpha(t)), \]
\[ \mathcal{L}(P(t) - L^\alpha(t)) = p(b_2 - \gamma_v P_v - \beta_3 PI - L^\alpha(t)), \]
\[ \mathcal{L}(M(t) - L^\alpha(t)) = p(\beta_3 PI - \gamma_v M - \delta_v M - L^\alpha(t)) \]

\[ S_h(t) = S(0), I_h(t) = I(0), R_h(t) = R(0), P_v(t) = P(0) \text{ and } M_v(t) = M(0) \]

Assume the solution of the system (11) in the form
\[ S(t) = S_0(t) + pS_1(t) + p^2S_2(t) + \cdots \]

\[ I(t) = I_0(t) + pI_1(t) + p^2I_2(t) + \cdots \]

\[ R(t) = R_0(t) + pR_1(t) + p^2R_2(t) + \cdots \]

\[ P(t) = P_0(t) + pP_1(t) + p^2P_2(t) + \cdots \]

\[ M(t) = M_0(t) + pM_1(t) + p^2M_2(t) + \cdots \]

By considering equation (13) in equation (11), comparing the same coefficient, we obtain

\[ \mathcal{L}(S(t) - L^\alpha(t)) = 0, \]
\[ \mathcal{L}(I(t) - L^\alpha(t)) = 0 \]
\[ \mathcal{L}(R(t) - L^\alpha(t)) = 0 \]
\[ \mathcal{L}(P(t) - L^\alpha(t)) = 0 \]
\[ \mathcal{L}(M(t) - L^\alpha(t)) = 0. \]

And
With the initial conditions
\[ S_1(t) = 0, \quad I_1(t) = 0, \quad R_1(t) = 0, \quad P_1(t) = 0, \quad \text{and} \quad M_1(t) = 0, \]  \tag{16}

And
\[ L \int_{(t)} = -\beta_2(S_0(t)M_1(t) + S_1(t)M_0(t)) - a_1(S_1(t)I_1(t) + S_1(t)I_1(t) + \mu_0 S_0(t) + \lambda_n R_1(t)), \] 
\[ L \int_{(t)} = \beta_2(S_0(t)M_2(t) + S_1(t)M_1(t) + S_2(t)M_2(t) - \mu_0 S_2(t) + \lambda_n R_1(t)), \] 
\[ L \int_{(t)} = \beta_2(S_0(t)M_2(t) + S_1(t)M_1(t) + S_2(t)M_2(t) - \mu_0 S_2(t) + \lambda_n R_1(t)), \] 
\[ L \int_{(t)} = \gamma_0 I_1(t) + (\mu_0 + \lambda_n) R_1(t), \] 
\[ L \int_{(t)} = -\gamma_0 P_1(t) - \beta_3(P_0(t)I_1(t) + P_1(t)I_0(t)), \] 
\[ L \int_{(t)} = \beta_2(P_0(t)I_1(t) + P_1(t)I_0(t)), \] 
\[ L \int_{(t)} = \beta_2(P_0(t)I_1(t) + P_1(t)I_0(t)), \] 
\[ L \int_{(t)} = \beta_2(P_0(t)I_1(t) + P_1(t)I_0(t)), \] 
\[ L \int_{(t)} = \gamma_0 I_1(t) + (\mu_0 + \lambda_n) R_1(t), \] 
\[ L \int_{(t)} = \mu_0 S_0(t) - (\lambda_n + \gamma_n) R_1(t), \] 
\[ L \int_{(t)} = \mu_0 S_0(t) - (\lambda_n + \gamma_n) R_1(t), \] 
\[ L \int_{(t)} = \gamma_0 I_1(t) + (\mu_0 + \lambda_n) R_1(t), \] 
\[ L \int_{(t)} = \gamma_0 I_1(t) + (\mu_0 + \lambda_n) R_1(t), \] 
\[ L \int_{(t)} = \gamma_0 I_1(t) + (\mu_0 + \lambda_n) R_1(t), \] 

In order to obtain the solution to the zero order problem, we consider the following cases.

**Zeroth order Problem or P**
\[ S_0(t) = 130, \quad I_0(t) = 80, \quad R_0(t) = 100, \quad P_0(t) = 220, \quad \text{and} \quad M_0(t) = 200, \] 

**First order Problem or P**
\[ S_1(t) = (b_1 - \mu_0 d_1 - \beta_2 d_1 d_2 - \beta_1 d_1 d_2 + \lambda_n d_3) t, \] 
\[ I_1(t) = ((\beta_2 d_4 d_2 + \beta_1 d_4 d_2) - (\mu_0 + \lambda_n + \gamma_n) d_2) t, \] 
\[ R_1(t) = (\gamma_0 d_2 - (\mu_0 + \lambda_n d_2)), \] 
\[ P_1(t) = (b_2 - \gamma_0 d_4 - \beta_3 d_4 d_2), \] 
\[ M_1(t) = (\beta_3 d_4 d_2 - (\gamma_0 + \delta_0) d_5), \] 

**Numerical Results**
In this section, we discuss the numerical solution of the proposed model. First, we solve the model numerically and then discuss these results. For numerical simulation we consider the parameter values presented in table 1. The numerical results are presented in figure-1, 2 and 3 show the population of susceptible human, infected human and recovered human, respectively. Figure-4 and 5 show the population of susceptible vector and infected vector.
The plot represents the population of susceptible human in the model

$$R_z^2(t) = \gamma_h \left\{ \left( \beta_2 d_5 + \beta_3 d_4 d_2 \right) \left( \mu_h + \delta_h + \gamma_h d_2 \right) \right\} - \left( \mu_h + \lambda_h \right) \left( \gamma_f d_2 - \left( \mu_h + \lambda_h d_2 \right) \right),$$

$$P_z^2(t) = -\gamma_f \left\{ \left( \beta_2 d_5 + \beta_3 d_4 d_2 \right) \left( \mu_h + \delta_h + \gamma_h d_2 \right) \right\},$$

$$M_z^2(t) = \beta_3 \left( \beta_2 d_5 + \beta_1 d_4 d_2 \right)$$

(24)

**Figure-1**

The plot represents the population of susceptible human in the model

**Figure-2**

The represents the population of infected human in the model
Figure-3
The represents the population of recovered human in the model

Figure-4
The plot shows the population of susceptible vector in the model

Figure-5
The plot shows population of infected vector in the model
2. References

Leptospirosis is a zoonotic disease which is found mostly areas. The model is formulated and applied the homotopy perturbation technique and the numerical as well as their analytical solution was obtained. The model is solved up to second order by the Homotopy perturbation method. The homotopy perturbation method gives a good result for the non-linear system, with a few iterations.

**Table-1  
Parameter values used for the Numerical Simulation**

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\delta_v$</td>
<td>Disease death rate of Vector</td>
</tr>
<tr>
<td>$\delta_h$</td>
<td>Disease death rate of a human</td>
</tr>
<tr>
<td>$b_1$</td>
<td>Recruitment rate of human population</td>
</tr>
<tr>
<td>$\beta_1$</td>
<td>Direct transmission between susceptible human and infected human</td>
</tr>
<tr>
<td>$\beta_2$</td>
<td>Transmission between susceptible human and infected vector</td>
</tr>
<tr>
<td>$\beta_3$</td>
<td>Transmission between susceptible vector and infected human</td>
</tr>
<tr>
<td>$\mu_n$</td>
<td>A natural death rate of a human</td>
</tr>
<tr>
<td>$b_2$</td>
<td>Birth rate for vector population</td>
</tr>
<tr>
<td>$\gamma_v$</td>
<td>Natural death rate of vector</td>
</tr>
<tr>
<td>$\lambda_n$</td>
<td>The rate at which the individuals become susceptible again</td>
</tr>
<tr>
<td>$\gamma_h$</td>
<td>A recovery rate of infection of human</td>
</tr>
</tbody>
</table>

**Conclusion**

In this paper, we considered an epidemic model represented the interaction of the leptospirosis infected vector and human population. Leptospirosis is a zoonotic disease which is found mostly areas. The model is formulated and applied the homotopy perturbation technique and the numerical as well as their analytical solution was obtained. The model is solved up to second order by the Homotopy perturbation method. The homotopy perturbation method gives a good result for the non-linear system, with a few iterations.

**References**


