Research Journal of Recent Sciences _____ ISSN 2277-2502
Vol. **2(8),** 66-71, August **(2013)** *Res.J.Recent Sci.*

Analytical Solution of the Leptospirosis Epidemic model by Homotopy Perturbation method

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Available online at: www.isca.in
Received 24th February 2013, revised 25th March 2013, accepted 21st April 2013

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 easly 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[1-4]. Pongsuumpun et al[5]., developed a mathematical model to study the dynamical behavior of Leptospirosis disease. Triampo et al[6]., considered a deterministic models for the transmission of Leptospirosis disease by collecting some real data. Zaman[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 non-linear 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[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[10], introduced Homotopy Perturbation Method (HPM) and its application in several problems[11,12]. Ali et al[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[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 leptoapirosis disease1. 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 frame work: 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[8,9] , for solving the non linear differential equations.

$$B(m) = f(d), \quad d \in \Lambda \tag{1}$$

subject to the boundary conditions

$$\psi\left(m, \frac{\partial m}{\partial n}\right) = 0, \qquad d \in \Omega \tag{2}$$

Here B represents the general differential operator, ψ is the boundary operator, $f(d)$ is the analytic function, Ω is the boundary of the domain Λ, $\frac{\partial}{\partial n}$ represents the differentiation along the normal vector Λ drawn outward. The operator B is divided in two parts, H is linear and K is nonlinear to get the following equation

$$H(m) + K(m) = f(d) \tag{3}$$

Define the homotopy $v(r,p): \Lambda \times [0,1] \to \mathbb{R}$, that satisfies

$$F(v,p) = (1-p)[H(v) - H(m_o)] + p[B(v) - f(d)] = 0, \tag{4}$$

Which can be written as

$$F(v,p) = H(v) + pH(m_o) + p[K(m) - f(d)] = 0, \tag{5}$$

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 obatin

$$F(v,1) = [B(v) - f(d)].$$

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

$$v = v_o + pv_1 + p^2 v_2 + p^3 v_3 \ldots, \tag{6}$$

when p approaches 1 the equation (4) becomes the original equation (3) and (7) becomes the approximate solution of (3) is given by

$$m = lim_{p \to 1} v = v_o + pv_1 + p^2 v_2 + p^3 v_3 \ldots, \tag{7}$$

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

In order to formulate our problem, we assume that $S_h(t)$ represents number of susceptible human at time t; $I_h(t)$ represents number of infected human in the population, which is infected from the leptospirosis disease at time t; $R_h(t)$ represents number of human in the population which is recovered at time t. The total population size is $N_h(t)=S_h(t)+I_h(t)+R_h(t)$. 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 $N_v(t)$ with $N_v(t)=P_v(t)+M_v(t)$. By the interaction of both human and vector population we get the following system of five differential equations is given by:

$$\frac{dS_h}{dt} = b_1 - \mu_h S_h - \beta_2 S_h M_v - \beta_1 S_h I_h + \lambda_h R_h,$$

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

$$\frac{dR_h}{dt} = \gamma_h I_h - (\mu_h + \lambda_h) R_h, \tag{8}$$

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

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

With the initial conditions

$$S_h(0) \geq 0, I_h(0) \geq 0, R_h(0) \geq 0, \; P_v(0) \geq 0, M_v(0) \geq 0 \tag{9}$$

$b_1$represents the growth rate of human population. The direct transmission between susceptible human and infected vector is represented by β_1. The transmission rate of the vector is shown by β_2. The natural death rate for the human is μ_h. The disease death rate for the human is represented by δ_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. β_3 is the transmission coefficient between susceptible vector and infected human. The rate of recovery from the infection is shown by γ_h. The individuals are susceptible again at λ_h .

Now, we apply the homotopy perturbation techniques to our model (8). We assume for simplifications

$$S_h^*(t) = S, I_h^*(t) = I, R_h^*(t) = R, P_v^*(t) = P \; and \; M_v^*(t) = M$$

Now we define the operator $\mathcal{L} = \frac{d}{dt}$. The initial data we consider is given by

$$\begin{aligned}
&\mathcal{L}S(t) - \mathcal{L}S^o(t) = p\left(b_1 - \mu_h S_h - \beta_2 SM - \beta_1 SI + \lambda_h R - \mathcal{L}S^o(t)\right),\\
&\mathcal{L}I(t) - \mathcal{L}I^o(t) = p(\beta_2 SM + \beta_1 SI - (\mu_h + \delta_h + \gamma_h)I - \mathcal{L}I^o(t)),\\
&\mathcal{L}R(t) - \mathcal{L}R^o(t) = p(\gamma_h I - (\mu_h + \lambda_h)R - \mathcal{L}R^o(t)),\\
&\mathcal{L}P(t) - \mathcal{L}P^o(t) = p(b_2 - \gamma_v P_v - \beta_3 PI - \mathcal{L}P^o(t))\\
&\mathcal{L}M(t) - \mathcal{L}M^o(t) = p(\beta_3 PI - \gamma_v M - \delta_v M - \mathcal{L}M^o(t))
\end{aligned} \tag{11}$$

$$S_h^*(t) = S(0), \; I_h^*(t) = I(0), \; R_h^*(t) = R(0), P_v^*(t) = P(0) \; and M_v^*(t) = M(0) \tag{12}$$

Assume the solution of the system (11) in the form

$$\begin{aligned}
S^*(t) &= S_0^*(t) + pS_1^*(t) + p^2 S_2^*(t) + \cdots,\\
I^*(t) &= I_0^*(t) + pI_1^*(t) + p^2 I_2^*(t) + \cdots,\\
R^*(t) &= R_0^*(t) + pR_1^*(t) + p^2 R_2^*(t) + \cdots,\\
P^*(t) &= P_0^*(t) + pP_1^*(t) + p^2 P_2^*(t) + \cdots,\\
M^*(t) &= M_0^*(t) + pM_1^*(t) + p^2 M_2^*(t) + \cdots,
\end{aligned} \tag{13}$$

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

$$\begin{aligned}
&\mathcal{L}S(t) - \mathcal{L}S^o(t) = 0,\\
&\mathcal{L}I(t) - \mathcal{L}I^o(t) = 0\\
&\mathcal{L}R(t) - \mathcal{L}R^o(t) = 0\\
&\mathcal{L}P(t) - \mathcal{L}P^o(t) = 0\\
&\mathcal{L}M(t) - \mathcal{L}M^o(t) = 0.
\end{aligned} \tag{14}$$

And

$$\mathcal{L}S_1^*(t) = (b_1 - \beta_2 S_o^*(t)M_o^*(t) - \beta_1 S_o^*(t)I_o^*(t) - \mu_h S_o^*(t) + \lambda_h R_o^*(t) - \mathcal{L}S_o^*(t)),$$
$$\mathcal{L}I_1^*(t) = (\beta_2 S_o^*(t)M_o^*(t) + \beta_1 S_o^*(t)I_o^*(t) - (\mu_h + \delta_h + \gamma_h)I_o^*(t) - \mathcal{L}I_o^*(t)),$$
$$\mathcal{L}R_1^*(t) = (\gamma_h I_o^*(t) - (\mu_h + \lambda_h)R_o^*(t) - \mathcal{L}R_o^*(t)), \quad (15)$$

$$\mathcal{L}P_1^*(t) = (b_2 - \gamma_v P_o^*(t) - \beta_3 P_o^*(t)I_o^*(t) - \mathcal{L}P_o^*(t)),$$

$$\mathcal{L}M_1^*(t) = (\beta_3 P_o^*(t)I_o^*(t) - (\gamma_v + \delta_v)M_o^*(t) - \mathcal{L}M_o^*(t)),$$

With the initial conditions

$$S_1^*(t) = 0,\ I_1^*(t) = 0,\ R_1^*(t) = 0,\ P_1^*(t) = 0,\ and M_1^*(t) = 0, \quad (16)$$

And

$$\mathcal{L}S_2^*(t) = -\beta_2\left(S_o^*(t)M_1^*(t) + S_1^*(t)M_o^*(t)\right) - \beta_1(S_o^*(t)I_1^*(t) + S_1^*(t)I_o^*(t)) - \mu_h S_1^*(t) + \lambda_h R_1^*(t)),$$

$$\mathcal{L}S_2^*(t) = \beta_2\left(S_o^*(t)M_1^*(t) + S_1^*(t)M_o^*(t)\right) + \beta_1(S_o^*(t)I_1^*(t) + S_1^*(t)I_o^*(t)) - (\mu_h + \delta_h + \gamma_h)I_1^*(t)),$$

$$\mathcal{L}R_2^*(t) = \gamma_h I_1^*(t) - (\mu_h + \lambda_h)R_1^*(t), \quad (17)$$

$$\mathcal{L}P_2^*(t) = -\gamma_v P_1^*(t) - \beta_3(P_o^*(t)I_1^*(t) + P_1^*(t)I_o^*(t)),$$

$$\mathcal{L}M_2^*(t) = \beta_3(P_o^*(t)I_1^*(t) + P_1^*(t)I_o^*(t)) - (\gamma_v + \delta_v)M_1^*(t),$$

With the initial conditions

$$S_2^*(t) = 0,\ I_2^*(t) = 0,\ R_2^*(t) = 0,\ P_2^*(t) = 0,\ and M_2^*(t) = 0, \quad (18)$$

In similarway, we get

$$\mathcal{L}S_3^*(t) = -\beta_2\left(S_o^*(t)M_2^*(t) + S_1^*(t)M_1^*(t) + S_o^*(t)M_2^*(t)\right) - \beta_1(S_o^*(t)I_2^*(t) + S_1^*(t)I_1^*(t) + S_2^*(t)I_2^*(t)) - \mu_h S_2^*(t) + \lambda_h R_2^*(t)),$$

$$\mathcal{L}I_3^*(t) = \beta_2\left(S_o^*(t)M_2^*(t) + S_1^*(t)M_1^*(t) + S_o^*(t)M_2^*(t)\right) \quad (19)$$
$$+\beta_1(S_o^*(t)I_2^*(t) + S_1^*(t)I_1^*(t) + S_2^*(t)I_2^*(t)) - (\mu_h + \delta_h + \gamma_h)I_2^*(t)),$$

$$\mathcal{L}R_3^*(t) = \gamma_h I_2^*(t) - (\mu_h + \lambda_h)R_2^*(t),$$

$$\mathcal{L}P_3^*(t) = -\gamma_v P_2^*(t) - \beta_3(P_o^*(t)I_2^*(t) + P_1^*(t)I_1^*(t) + P_2^*(t)I_o^*(t)),$$

$$\mathcal{L}M_3^*(t) = \beta_3(P_o^*(t)I_2^*(t) + P_1^*(t)I_1^*(t) + P_2^*(t)I_o^*(t)) - (\gamma_v + \delta_v)M_2^*(t),$$

with initial condition

$$S_2^*(t) = 0,\ I_2^*(t) = 0,\ R_2^*(t) = 0,\ P_2^*(t) = 0,\ and\ M_2^*(t) = 0, \quad (20)$$

To find the solution, we consider p=1 inthesystem (11), we get

$$\begin{aligned} S^*(t) &= S_0^*(t) + S_1^*(t) + S_2^*(t) + \cdots, \\ I^*(t) &= I_0^*(t) + I_1^*(t) + I_2^*(t) + \cdots, \\ R^*(t) &= R_0^*(t) + R_1^*(t) + R_2^*(t) + \cdots, \\ P^*(t) &= P_0^*(t) + P_1^*(t) + P_2^*(t) + \cdots, \\ M^*(t) &= M_0^*(t) + M_1^*(t) + M_2^*(t) + \cdots, \end{aligned} \quad (21)$$

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

Zeroth order Problem or P^0

$$S_0^*(t) = 130, \quad I_o^*(t) = 80, \quad R_o^*(t) = 100, \quad P_o^*(t) = 220, \quad and\ M_o^*(t) = 200,$$

First order Problem or P^1

$$\begin{aligned} S_1^*(t) &= (b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)t, \\ I_1^*(t) &= ((\beta_2 d_1 d_5 + \beta_1 d_1 d_2) - (\mu_h + \delta_h + \gamma_h)d_2)t, \\ R_1^*(t) &= (\gamma_h d_2 - (\mu_h + \lambda_h)d_3)t, \\ P_1^*(t) &= (b_2 - \gamma_v d_4 - \beta_3 d_4 d_2)t, \\ M_1^*(t) &= (\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)t, \end{aligned} \quad (22)$$

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.

Second order solution or P^2

$$S_2^*(t) = 130 = d_1,\ I_2^*(t) = 80 = d_2,\ R_2^*(t) = 100 = d_3,\ Q_2^*(t) = 220 = d_4,\ and\ W_2^*(t) = 200 = d_5, \quad (23)$$

$$S_2^*(t) = -\mu_h\{(b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)\}\frac{t^2}{2}\ \beta_2\left\{d_1(\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)\frac{t^2}{2} + d_5(b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)\frac{t^2}{2}\right\}$$
$$- \beta_1\left\{d_1(\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)\frac{t^2}{2} + d_2(b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)\frac{t^2}{2}\right\} + \lambda_h\{(\gamma_h d_2 - (\mu_h + \lambda_h)d_3)\}\frac{t^2}{2},$$

$$I_2^*(t) = \beta_2\left\{d_1(\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)\frac{t^2}{2} + d_5(b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)\frac{t^2}{2}\right\}\ \beta_1\left\{d_1(\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)\frac{t^2}{2}\right.$$
$$\left. + d_2(b_1 - \mu_h d_1 - \beta_2 d_1 d_5 - \beta_1 d_1 d_2 + \lambda_h d_3)\frac{t^2}{2}\right\}(\mu_h + \delta_h + \gamma_h)\{(\beta_2 d_1 d_5 + \beta_1 d_1 d_2) - (\mu_h + \delta_h + \gamma_h)d_2)\}\frac{t^2}{2},$$

$$R_2^*(t) = \gamma_h\left\{(\beta_2 d_1 d_5 + \beta_1 d_1 d_2) - (\mu_h + \delta_h + \gamma_h)d_2)\frac{t^2}{2}\right\} - (\mu_h + \lambda_h)\left\{(\gamma_h d_2 - (\mu_h + \lambda_h)d_3)\frac{t^2}{2}\right\}, P_2^*(t) =$$
$$-\gamma_v\left\{(b_2 - \gamma_v d_4 - \beta_3 d_4 d_2)\frac{t^2}{2}\right\}\ \beta_3\left\{d_2(b_2 - \gamma_v d_4 - \beta_3 d_4 d_2)\frac{t^2}{2}\ d_4(\beta_2 d_1 d_5 + \beta_1 d_1 d_2) - (\mu_h + \delta_h + \gamma_h)d_2)\frac{t^2}{2}\right\}, M_2^*(t) = \beta_3\left\{d_2(b_2 - \gamma_v d_4 - \beta_3 d_4 d_2)\frac{t^2}{2} + d_4(\beta_2 d_1 d_5 + \beta_1 d_1 d_2) - (\mu_h + \delta_h + \gamma_h)d_2)\frac{t^2}{2}\right\} - (\gamma_v + \delta_v)\{(\beta_3 d_4 d_2 - (\gamma_v + \delta_v)d_5)\}\frac{t^2}{2}. \quad \textbf{(24)}$$

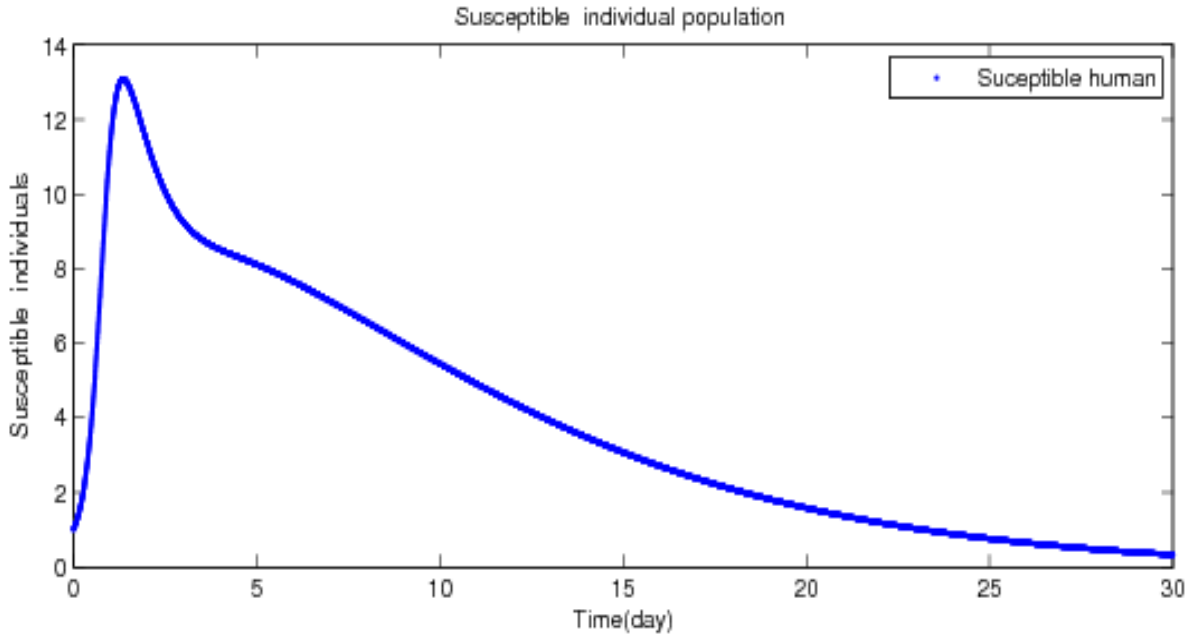

Figure-1
The plot represents the population of susceptible human in the model

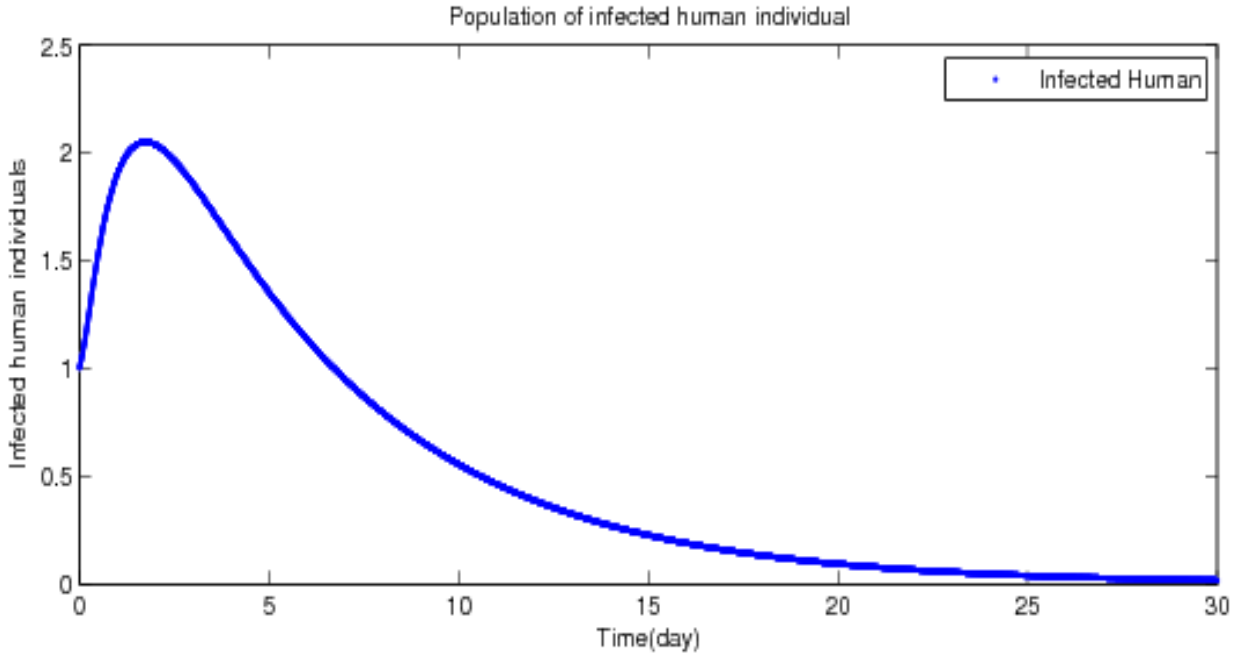

Figure-2
The represents the population of infected human in the model

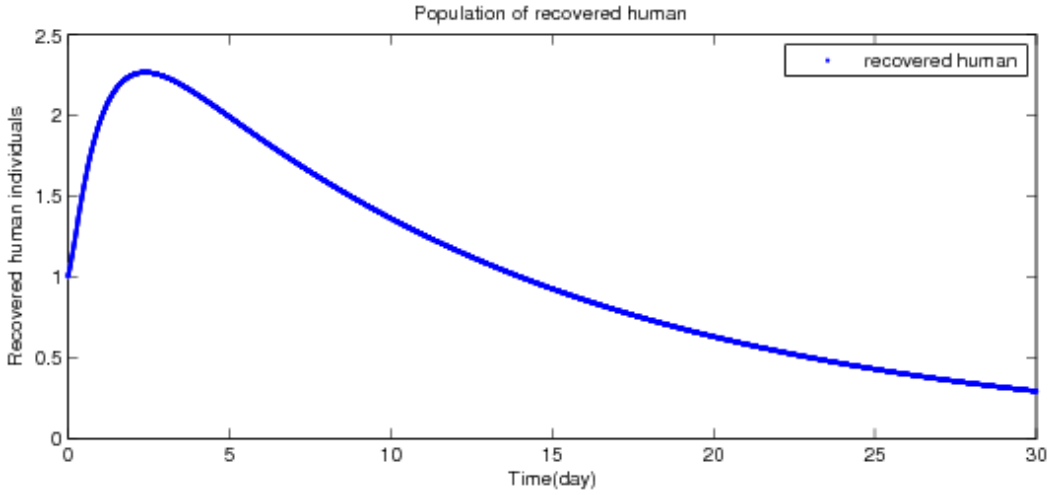

Figure-3
The represents the population of recovered human in the model

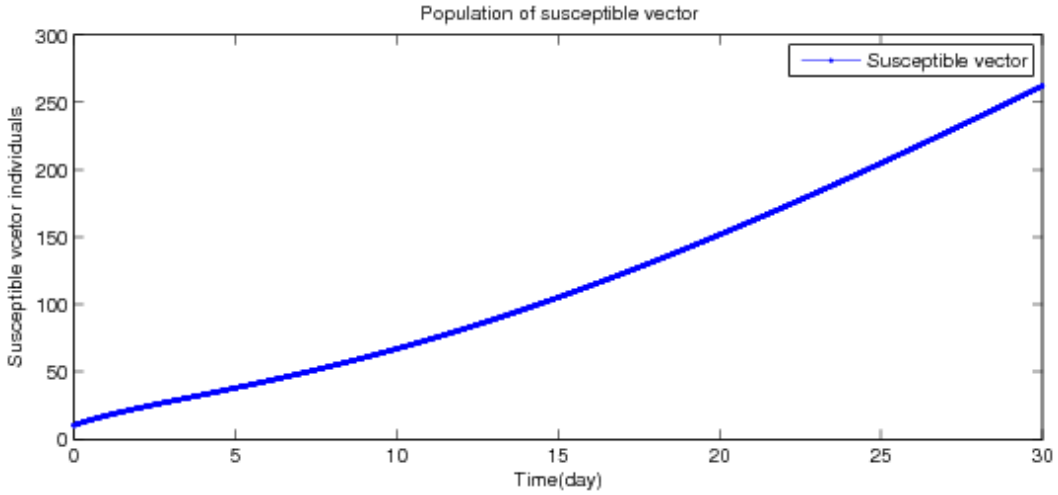

Figure-4
The plot shows the population of susceptible vector in the model

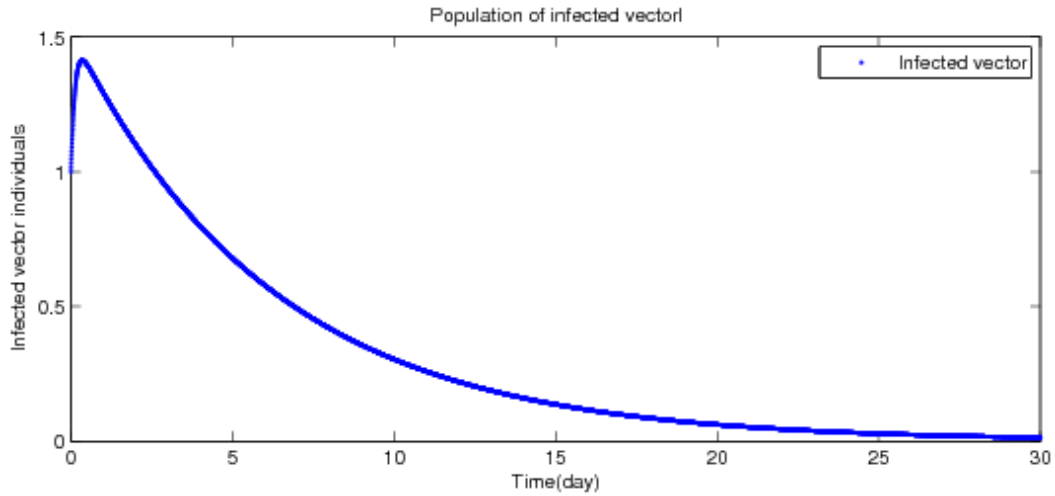

Figure-5
The plot shows population of infected vector in the model

Table-1
Parameter values used for the Numerical Simulation

δ_v	Disease death rate of Vector	0.0094
δ_h	Disease death rate of a human	0.0000001
b_1	Recruitment rate of human population	1.6
β_1	Direct transmission between susceptible human and infected human	0.00005
β_3	Transmission between susceptible vector and infected human	0.0078
β_2	Transmission between susceptible human and infected vector	0.0098
μ_h	A natural death rate of a human	0.0034
b_2	Birth rate for vector population	1.2
γ_v	Natural death rate of vector	0.0017
λ_h	The rate at which the individuals become susceptible again	0.00067
γ_h	A recovery rate of infection of human	0.007

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.

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