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Application of Homotopy Perturbation Method to Vector Host Epidemic Model with Non-Linear Incidences

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Abstract

In this paper, we consider an epidemic model of vector host with non-linear incidences. The spread of the disease is due to the vector such as malaria, dengue and yellow fever. We use the homotopy perturbation method to the consider model to obtain their analytical and numerical solution. Due to the importance of homotopy method a just few perturbation terms are sufficient for a reasonably accurate solution. The numerical results are presented for justification.

Keywords: Vector-host, mathematical model, Homotopy Perturbation method, numerical simulations.

Introduction

For understanding the epidemiology of infectious disease mathematical models played an important role for the infectious diseases[1,2]. This provides us the qualitative descriptions of the complicated, non-linear process of disease transmission, and also help us to obtain the dynamics of the disease and enable us to make the decision of Public health policy. World Health Statistics (2008)[3] show, that some vector-borne infectious diseases as malaria, dengue and yellow fever, continue to threaten throughout the public health of many people. Most of the biological problems are inherently nonlinear. The Scientist is in search to find such Numerical methods or Perturbation method to find the exact approximate solution to these non-linear problems. Most of the nonlinear problems have not solved exactly to find their exact solution, only a few numbers of non-linear of problems have the exact solution. So these non-linearproblems can be solved by Numerical or traditional methods. To use analytical perturbation method, a small parameter is inserted in the equation and making use of small parameter and exerting it into the equation are the difficulties of this method. Therefore, many different powerful mathematical methods have been recently introduced to vanish the small parameters, such as artificial parameter method[4,5]. Zaman[6] considered the model, to study the approximate solution with HPM and compare with other standard methods.

The Homotopy Analysis Method (HAM) is the well known method used for to solve the non linear equations. In the last decade, the idea of homotopy was combined with perturbation. The fundamental work was done by Liao and He. He introduced Homotopy Perturbation Method (HPM) and its application are in several problems in detail the reader are referred to[7,8,9] while Ali et al.[10], Presented the solution of multi point boundary values by using Optimal Homotopy Analysis Method (OHAM).These methods are free of the assumption of a such a small parameter.

In this paper, we consider the model presented in[11], by applying the Homotopy perturbation method, to find the approximate solution. First, we formulate our problem and then apply the HPM to find the analytical as well as numerical solutions.

The paper is organized as follows. Section 2 is devoted to the mathematical formulation of the model and basic idea of HPM. In Section 3 the model is solved by HPM. In Section 4 we present the solution of the model numerically with a discussion and conclusion. Finally, the references are presented.

Basic idea of Homotopy perturbation method (HPM) and model framework: In this section, we explain the Homotopy perturbation method in detail and then we apply thetechnique of HPM to our proposed epidemic model. HPM was first timeintroduced by the He[7,8] for solving the nonlinear differential equations.

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

boundary conditions is

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

Here B represents the general differential operator, ψ is the boundary operator, the analytic function is $f(d)$, Ω is the boundary of the domain Λ, $\frac{\partial}{\partial n}$ and represent the differentiation along the normal vector drawn outward from Λ. The operator B is divided in two parts, H is linear and K is nonlinear. So we get Equation namely (3) in the following form:

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

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

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

In simplified form we write it as:

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

Here m_o shows the initial approximation of (5) and p is the embedding parameter, $p \in [0,1]$. We see that

$$F(v,0) = [H(v) - H(m_o)] = 0, F(v,1) = [B(v) - f(d)] = 0 \quad (6)$$

for putting p=0, we obtain, $F(v,0) = [H(v) - H(m_o)]$ and using p=1, we get, $F(v,1) = [B(v) - f(d)]$.

Applying the perturbation technique, consider p is the smallest parameter then the solution of equation (4) can be considered as series in p, which is given by

$$v = v_o + pv_1 + p^2 v_2 + p^3 v_3 \ldots, \quad (7)$$

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

$$m = \lim_{p\to 1} v = v_o + pv_1 + p^2 v_2 + p^3 v_3 \ldots, \quad (8)$$

The series (8) is convergent for most of the cases, for reader sees[7,8] .

Now we formulate our problem here, assume that $S_h(t)$ is the number of susceptible human at time t; $I_h(t)$ is the number of infected human at time *t* and $R_h(t)$ represents is the recovered individuals.The total population size is denoted by N_1, with $N_1 = S_h(t) + I_h(t) + R_h(t)$. For vector population, let $S_v(t)$ are susceptible vector and $I_v(t)$ are infectious vector at time *t* and $d = \gamma_o + \gamma_1$.The total population size of vector population is denoted by N_2 with $N_2(t) = S_v(t) + I_v(t)$.

The governing differential equation is given by

$$\begin{aligned} S_h' &= \mu K - \frac{\beta_h S_h I_v}{1+\alpha_1 I_v} - \mu S_h, \\ I_h' &= \frac{\beta_h S_h I_v}{1+\alpha_1 I_v} - (\mu + d) I_h\,, \\ R_h' &= dI_h - \mu R_h, \\ S_v' &= \Lambda - \frac{\beta_v S_v I_h}{1+\alpha_2 I_h} - nS_v \\ I_v' &= \frac{\beta_v S_v I_h}{1+\alpha_2 I_h} - nI_v. \end{aligned} \quad (9)$$

With the initial conditions

$$S_h(0) \geq 0, I_h(0) \geq 0,\ R_h(0) \geq 0,\ S_v(0) \geq 0\,, I_v(0) \geq 0 \quad (10).$$

The parameters used in the model (9), μK is the recruitment rate of human population, β_h represent the transmission rate from vector to human, β_v is the transmission from human to vector, the natural death rate for the human is denoted by μ, γ_1 represent the treatment rate for human, the rate of recovery from infection is shown by γ_o. The natural mortality rate for vector is *n*, the level at which the force of infection saturated is denoted by α_1 *and* α_2 and the birth rate for the vector is Λ.

Solution of Model by HPM

In this section, we use the model (9) by applying the homotopy perturbation method. For this first we choose $S_h^*(t) = S, I_h^*(t) = I, R_h^*(t) = R, S_v^*(t) = Q$ *and* $I_v^*(t) = W$ and then apply the method, which is given by:

$$\begin{aligned} \mathcal{L}S(t) - \mathcal{L}S^o(t) &= p\left(\mu K - \frac{\beta_h SW}{1+\alpha_1 W} - \mu S - \mathcal{L}S^o(t)\right), \\ \mathcal{L}I(t) - \mathcal{L}I^o(t) &= p\left(\frac{\beta_h SW}{1+\alpha_1 W} - (\mu + d)I - \mathcal{L}I^o(t)\right), \\ \mathcal{L}R(t) - \mathcal{L}R^o(t) &= p(dI - \mu R - \mathcal{L}R^o(t)), \\ \mathcal{L}Q(t) - \mathcal{L}Q^o(t) &= p\left(\Lambda - \frac{\beta_v QI}{1+\alpha_2 I} - nQ - \mathcal{L}Q^o(t)\right) \\ \mathcal{L}W(t) - \mathcal{L}W^o(t) &= p\left(\frac{\beta_v QI}{1+\alpha_2 I} - nW - \mathcal{L}W^o(t)\right) \end{aligned} \quad (11)$$

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

$$S_o(t) = S(0),\ I_o(t) = I(0),\ R_o(t) = R(0),\ Q_o(t) = Q(0),\ and\ W_o(t) = W(0), \quad (12)$$

Assuming the solution of (11) in the form

$$\begin{aligned} S^*(t) &= S_0^*(t) + pS_1^*(t) + p^2 S_2^*(t) + \cdots, \\ I^*(t) &= I_0^*(t) + pI_1^*(t) + p^2 I_2^*(t) + \cdots, \\ R^*(t) &= R_0^*(t) + pR_1^*(t) + p^2 R_2^*(t) + \cdots, \\ Q^*(t) &= Q_0^*(t) + pQ_1^*(t) + p^2 Q_2^*(t) + \cdots, \\ W^*(t) &= W_0^*(t) + pW_1^*(t) + p^2 W_2^*(t) + \cdots, \end{aligned} \quad (13)$$

Making use of (13) in (11) and comparing the coefficient of the same power, we get

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

And

$$\begin{aligned} \mathcal{L}S_1^*(t) &= \left(\mu K - \frac{\beta_h S_o^*(t)\, Q_o^*(t)}{1+\alpha_1 Q_o^*(t)} - \mu S_o^*(t) - \mathcal{L}S_o^*(t)\right), \\ \mathcal{L}I_1^*(t) &= \left(\frac{\beta_h S_o^*(t) Q_o^*(t)}{1+\alpha_1 Q_o^*(t)} - (\mu + d) I_o^*(t) - \mathcal{L}I_o^*(t)\right), \\ \mathcal{L}R_1^*(t) &= \left(dI_o^*(t) - \mu R_o^*(t) - \mathcal{L}R_o^*(t)\right), \\ \mathcal{L}Q_1^*(t) &= \left(\Gamma - \frac{\beta_v I_o^*(t) Q_o^*(t)}{1+\alpha_2 I_o^*(t)} - nQ_o^*(t) - \mathcal{L}Q_o^*(t)\right), \\ \mathcal{L}W_1^*(t) &= \left(\frac{\beta_v I_o^*(t) Q_o^*(t)}{1+\alpha_2 I_o^*(t)} - nW_o^*(t) - \mathcal{L}W_o^*(t)\right), \end{aligned} \quad (15)$$

With the conditions

$$S_1^*(t) = 0,\ I_1^*(t) = 0,\ R_1^*(t) = 0,\ Q_1^*(t) = 0,\ and W_1^*(t) = 0, \quad (16)$$

And

$$\mathcal{L}S_2^*(t) = (-\frac{\beta_h[S_o^*(t)Q_1^*(t) + S_1^*(t)Q_o^*(t)\,]}{\alpha_1 Q_1^*(t)} - \mu S_1^*(t)),$$

$$\mathcal{L}S_2^*(t) = (\frac{\beta_h[S_o^*(t)Q_1^*(t) + S_1^*(t)Q_o^*(t)\,]}{\alpha_1 Q_1^*(t)} - (\mu+d)I_1^*(t)),$$

$$\mathcal{L}R_2^*(t) = \left(dI_1^*(t) - \mu R_1^*(t)\right), \tag{17}$$

$$\mathcal{L}Q_2^*(t) = (-\frac{\beta_v[I_o^*(t)Q_1^*(t) + I_1^*(t)Q_o^*(t)]}{1+\alpha_2 I_1^*(t)} - nQ_1^*(t)),$$

$$\mathcal{L}W_2^*(t) = (\frac{\beta_v[I_o^*(t)Q_1^*(t) + I_1^*(t)Q_o^*(t)]}{1+\alpha_2 I_1^*(t)} - nW_1^*(t)),$$

with the conditions

$$S_2^*(t) = 0,\ I_2^*(t) = 0,\ R_2^*(t) = 0,\ Q_2^*(t) = 0,\ and\ W_2^*(t) = 0, \tag{18}$$

In similar fashion, we obtain

$$\mathcal{L}S_3^*(t) = (-\frac{\beta_h[S_2^*(t)Q_o^*(t) + S_1^*(t)Q_1^*(t) + S_o^*(t)Q_2^*(t)]}{\alpha_1 Q_2^*(t)} - \mu S_2^*(t)),$$

$$\mathcal{L}I_3^*(t) = (\frac{\beta_h[S_2^*(t)Q_o^*(t) + S_1^*(t)Q_1^*(t) + S_o^*(t)Q_2^*(t)]}{\alpha_1 Q_2^*(t)} - (\mu+d)I_2^*(t)),$$

$$\mathcal{L}R_3^*(t) = \left(dI_2^*(t) - \mu R_2^*(t)\right) \tag{19}$$

$$\mathcal{L}Q_3^*(t) = (-\frac{\beta_v[I_2^*(t)Q_1^*(t) + I_1^*(t)Q_1^*(t) + I_o^*(t)Q_2^*(t)]}{1+\alpha_2 I_1^*(t)} - nQ_2^*(t)),$$

$$\mathcal{L}W_3^*(t) = (-\frac{\beta_v[I_2^*(t)Q_1^*(t) + I_1^*(t)Q_1^*(t) + I_o^*(t)Q_2^*(t)]}{1+\alpha_2 I_1^*(t)} - nW_2^*),$$

To find the solution, we put p=1 in the system (13), we get

$$S^*(t) = S_0^*(t) + S_1^*(t) + S_2^*(t) + \cdots,$$
$$I^*(t) = I_0^*(t) + I_1^*(t) + I_2^*(t) + \cdots,$$
$$R^*(t) = R_0^*(t) + R_1^*(t) + R_2^*(t) + \cdots, \tag{20}$$
$$Q^*(t) = Q_0^*(t) + Q_1^*(t) + Q_2^*(t) + \cdots,$$
$$W^*(t) = W_0^*(t) + W_1^*(t) + W_2^*(t) + \cdots,$$

The convergence of HPM is rapid, for a few iterations of both linear and non-linear.

Zeroth order solution or P^0

$$S_2^*(t) = 130, \quad I_2^*(t) = 80, \quad R_2^*(t) = 100, \quad Q_2^*(t) = 220, \quad and\ W_2^*(t) = 200,$$

First order solution or P^1

$$S_1^*(t) = \left(\mu K - \frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - \mu e_1\right)t,$$

$$I_1^*(t) = \left(\frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - (\mu+d)e_2\right)t,$$

$$R_1^*(t) = (de_2 - \mu e_3)t,$$

$$Q_1^*(t) = \left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)t,$$

$$W_1^*(t) = \left(\frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_5\right)t,$$

Numerical Results

In this section, we solve our proposed model numerically by using the Runge-Kutta order 4 scheme with the positive initial conditions. In the numerical simulation the values assigned to the parameter are presented in table-1. The solution of the model is presented in the form of plots. In our simulations the figure-1 representst the susceptible human individuals in the model. Figure-2 represents the infected human individuals. Figure-3 shows the population of recovered human. The population of susceptible vector is shown in figure-4 and the population of infected vector is represented by figure-5.

Second order solution or P^2

$$S_2^*(t) = 130 = e_1, \quad I_2^*(t) = 80 = e_2, \quad R_2^*(t) = 100 = e_3, \quad Q_2^*(t) = 220 = e_4, \quad and\ W_2^*(t) = 200 = e_5,$$

$$S_2^*(t) = -\left\{\frac{\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)e_1\beta_h + \left(\mu K - \frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - \mu e_1\right)e_4\beta_h}{\alpha_1\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)}\right\}\frac{t^2}{2} - \mu\left(\mu K - \frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - \mu e_1\right)\frac{t^2}{2},$$

$$I_2^*(t) = -\left\{\frac{\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)e_1\beta_h + \left(\mu K - \frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - \mu e_1\right)e_4\beta_h}{\alpha_1\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)}\right\}\frac{t^2}{2} - (\mu+d)\left(\frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - (\mu+d)e_2\right)\frac{t^2}{2},$$

$$R_2^*(t) = \left\{d\left(\frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - (\mu+d)e_2\right)\frac{t^2}{2} - \mu(de_2 - \mu e_3)\frac{t^2}{2}\right\},$$

$$Q_2^*(t) = -\beta_v\left\{\frac{\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)e_2 + \left(\frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - (\mu+d)e_2\right)e_4}{\alpha_2\left(\frac{\beta_h e_1\, e_5}{1+\alpha_1 e_5} - (\mu+d)e_2\right)}\right\}\frac{t^2}{2} - n\left(\Lambda - \frac{\beta_v e_2\, e_4}{1+\alpha_2 e_2} - ne_4\right)\frac{t^2}{2},$$

$$W_2^*(t) = \beta_v \left\{ \frac{\left(\Lambda - \frac{\beta_v e_2 e_4}{1+\alpha_2 e_2} - n e_4\right) e_2 + \left(\frac{\beta_h e_1 e_5}{1+\alpha_1 e_5} - (\mu + d) e_2\right) e_4}{\alpha_2 \left(\frac{\beta_h e_1 e_5}{1+\alpha_1 e_5} - (\mu + d) e_2\right)} \right\} \frac{t^2}{2} - n\left(\frac{\beta_v e_2 e_4}{1+\alpha_2 e_2} - n e_5\right)\frac{t^2}{2}.$$

Table-1
Parameter and their values used in the numerical solution

μK	Represent the intrinsic growth rate of the human population	3
β_h	Transmission rate from vector to human	0.0046
β_v	Transmission from human to vector	0.00098
μ	A natural deathrate of a human	0.0034
γ_1	Treated rate of human	0.0012
γ_o	A recovery rate of infection of human	0.00007
n	The mortality rate of vector	0.00068
α_1, α_2	The level at which the force of infection saturates	0.0089
Λ	Recruitment rate of vector	2

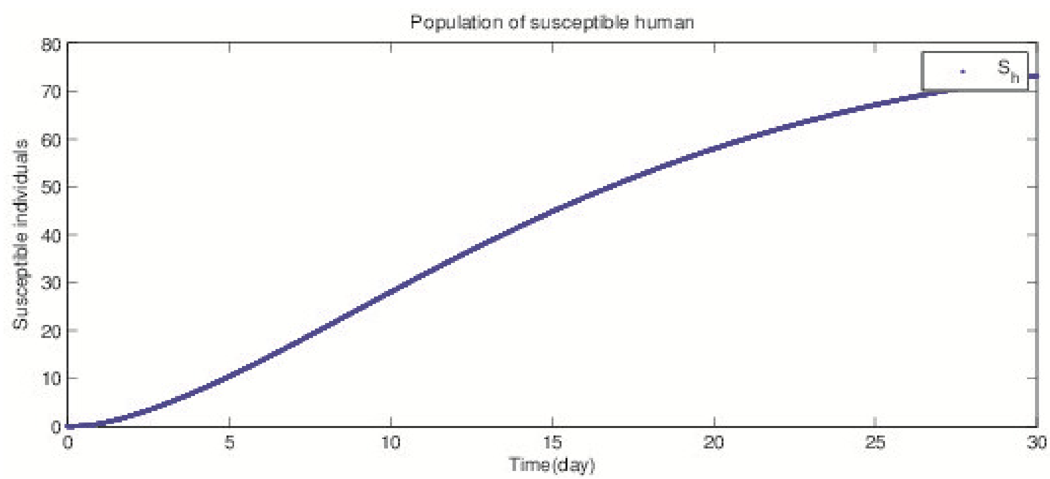

Figure-1
Shows the susceptible individuals

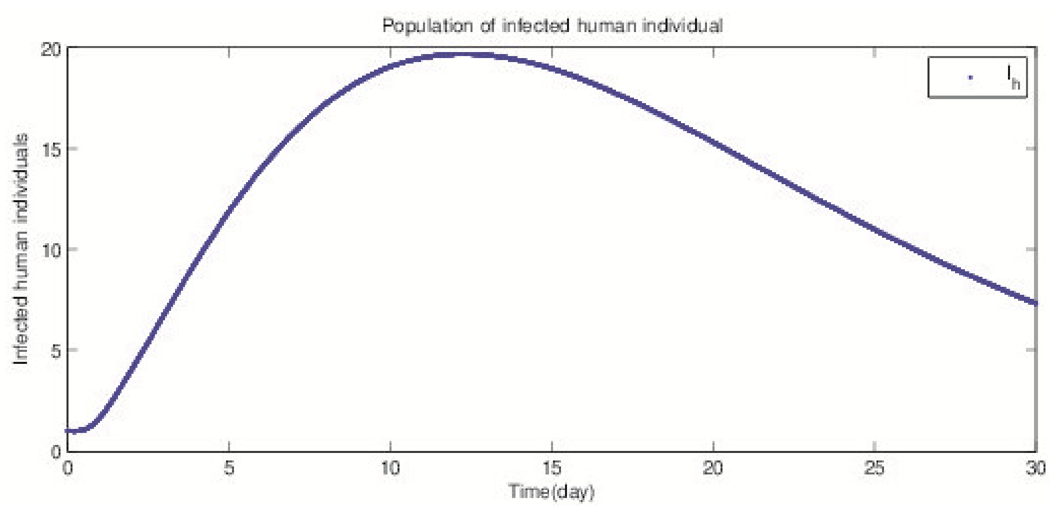

Figure-2
Represent the Infected human individuals in the population.

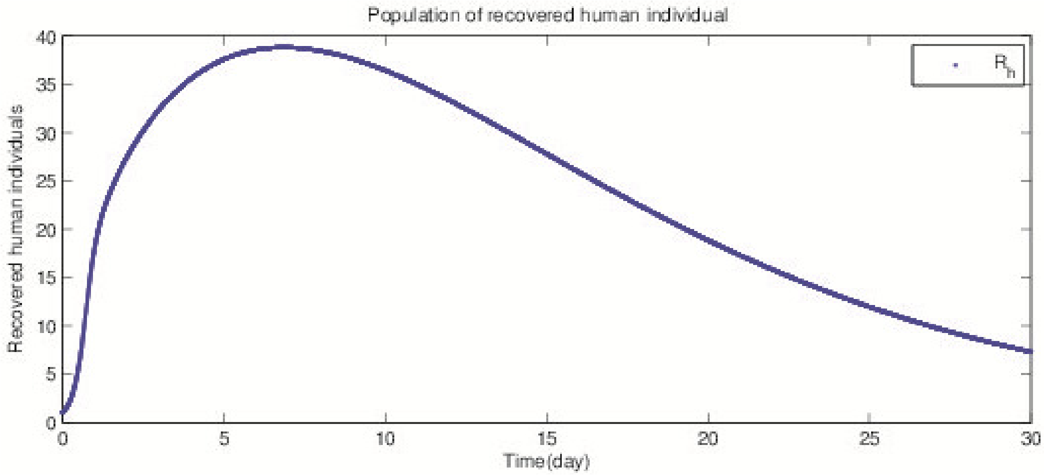

Figure-3
Represent the population of recovered individuals

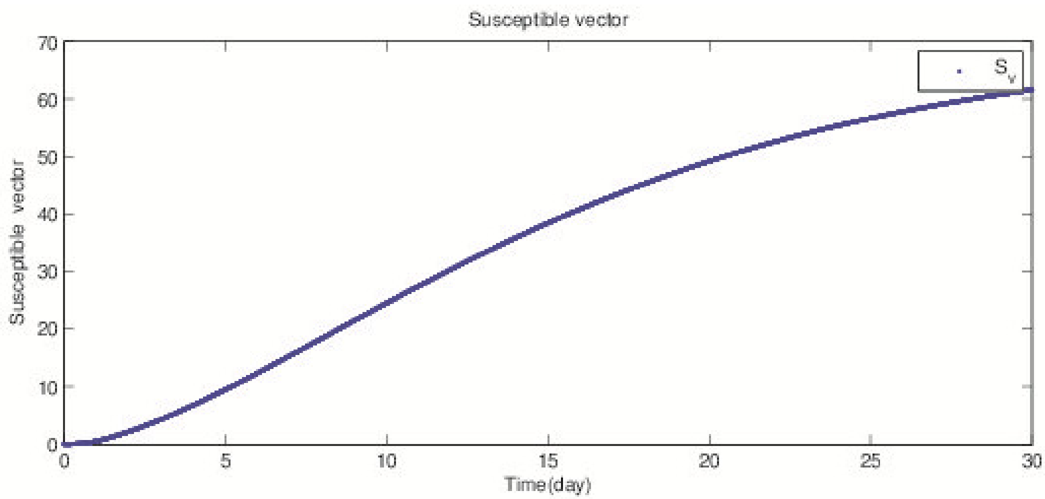

Figure-4
Represent the population of susceptible individuals

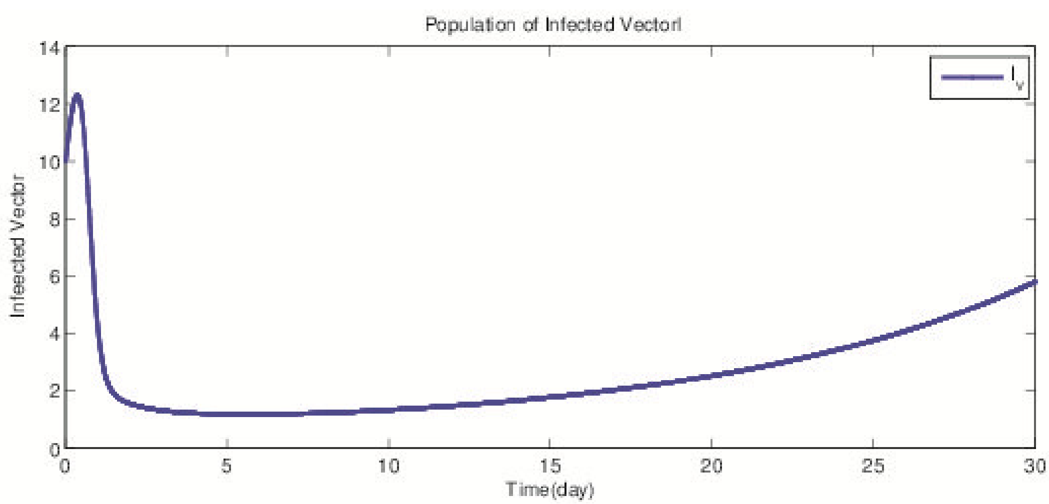

Figure-5
Represent the population of infected individuals

Conclusion

In this paper, we have presented an epidemic model and applied the homotopy perturbation techniques. First, we have explained the techniques in detail and then we applied to our proposed model. The importance of homotopy perturbation method is that for a system of nonlinear differential equation just a few iterations is enough for a best and reliable results. We have formulated the problem, and then by comparing the coefficient, the solution to the zeroth, first and second order was obtained. The obtained zeroth order solution, was used to obtain the first order solution. Similarly the second order solution was obtained by using the first order. Then we solved the model numerically and the results are presented in the form of plots for justification purpose.

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