Homotopy Perturbation Method for Mathematical Modelling of Dengue Fever

S Rekha¹, P Balaganesan¹ and J Renuka²

¹Department of Mathematics, AMET Deemed to be University, Chennai —603112, Tamil Nadu, India.
²Department of Mathematics, Women’s Christian College, Chennai —600006, Tamil Nadu, India.

Email: ndstvu@gmail.com

Abstract: Dengue fever is a viral mosquito-transmitted infection that has become a major international infection in recent years. The leading cause of disease and death in tropical and sub-tropical regions is a public health concern. Models from mathematical epidemiology, such as the classical SIR-model and its variants, are used to characterize the spread of Dengue in a given population. The mathematical modelling of Dengue Fever is formulated into a first-order nonlinear differential equation. Homotopy Perturbation Method approaches the analytical solution of the model (HPM), and also simulation results are identified. Finally, the analytical solutions, simulation results are compared, and satisfactory agreement is noted.

Keywords: Dengue, Homotopy Perturbation Method, SIR-UV model, Disease-free equilibrium, Endemic equilibrium.

1. Introduction
Dengue fever is a mosquito-borne tropical disease caused by the dengue virus. It is estimated that every year, there are about 390 million dengue infections with more than 12,000 deaths per year, cf. World Health Organization (2016a). Symptoms typically begin three to fourteen days after infection[1]. These may include a high fever, headache, vomiting, muscle and joint pains, and a characteristic skin rash[1-2]. Recovery generally takes two to seven days. In a small proportion of cases, the disease develops into severe dengue, also known as dengue hemorrhagic fever, resulting in bleeding, low levels of blood platelets and blood plasma leakage, or into dengue shock syndrome, where dangerously low blood pressure occurs[1,2].

At present, there is no specific treatment for dengue fever. Recently, a first vaccine has been developed and is now at an early stage of clinical trials. Hence, the main method to control and prevent the spread of the dengue virus is to combat vector mosquitoes through several measures including insecticides and preventing mosquitoes from accessing egg-laying habitats like in-and outdoor containers with stagnant water. The Aedes mosquito vector of dengue is also highly sensitive to climate conditions, and studies suggest that climate change is likely to continue to increase exposure to dengue, cf. World Health Organization (2016b).

Other methods of prevention include reducing mosquito habitat and limiting exposure to bites. This may be done by getting rid of or covering standing water and wearing clothing that covers much of the body. Treatment of acute dengue is supportive and includes giving fluid either by mouth or intravenously for the mild or moderate disease. For more severe cases, a blood transfusion may be required. About half a million people require hospital admission every year[1,2].
A vaccine for dengue fever has been approved and is commercially available in a number of countries[3,4]. As of 2018, the vaccine is only recommended in individuals who have been previously infected or, in populations with a high rate of prior infection by age nine[5-6]. Paracetamol (acetaminophen) is recommended instead of nonsteroidal anti-inflammatory drugs (NSAIDs) for fever reduction and pain relief in dengue due to an increased risk of bleeding from NSAID use [7, 8].

In recent years, mathematical modelling has become an essential tool for the understanding of infectious diseases epidemiology and dynamics. A series of deterministic and nowadays also stochastic models have been proposed to describe the host and vector population, see, e.g. Wijaya et al. (2015), Rocha et al. (2013), Altmeier (2016) and references therein. Dengue fever dynamic is well known to be particularly complex with large fluctuations of disease incidences. The integration of climatic factors into mathematical models for vector-borne diseases is a rather new development.

In [9], introduced a model for dengue dynamics, including the effect of the precipitation amount on the infection rate. Since the vector mosquitoes breed in an aquatic environment, rainfall leads to an increase of the mosquito population and hence to an increased infection rate. Using available data of both, recorded dengue infections and local precipitation from the city of Semarang at the northern coast of Java island, Indonesia, [9] proposed a disease model with an infection rate depending on the rainfall.

The analytical solution of this dengue fever SIR–UV model is approached by homotopy perturbation method, which was introduced by He [10-15], in the year 1998. In this method, the solution is considered as the summation of an infinite series which converges rapidly to the exact solutions. This technique has been employed to solve a large variety of linear and nonlinear equations. This scheme is used for solving nonlinear boundary value problems [16], nonlinear fractional partial differential equations [17], and nonlinear Hirota–Satsuma coupled KdV partial differential equations [18]. This method is also adopted for solving the pure strong nonlinear second-order differential equations [19]. Also, this author employed the homotopy-perturbation method for solving the complex-valued differential equations with strong cubic nonlinearity [20]. Some other applications of this method are as follows, such as homotopy perturbation method is described to solve nonlinear differential equations [21]. Also used for travelling wave solutions of nonlinear wave equations [22], nonlinear convective–radioactive cooling equation, nonlinear heat equations (porous media equation) and nonlinear heat equations with cubic nonlinearity [23]. The authors of [24] employed He’s homotopy perturbation method to compute an approximation to the solution of the system of nonlinear ordinary differential equations governing the problem of the spread of a nonfatal disease in a population which is assumed to have constant size over the period of the epidemic. In general, this method has been successfully applied to solve many types of linear and nonlinear problems in science and engineering by many authors [25].

2. Problem Description and Main Results

2.1 Dengue fever (SIR-UV) Model Description and Formula

In this section[15], to describe the dynamics of dengue within-host and vector populations, we recall the classical SIR-UV model introduced by Kermack and McKendrick (1927). The model is divided into the host population and vector population at any time ‘t’ into five components with respect to disease status in the system. The host population is assumed as N. It is divided into components of Susceptible host (S), Infected host (I) and Recovered host (R), which implies $N(t) = S(t) + I(t) + R(t)$. The vector population is denoted as M. It is divided into components of Virus-free vectors (U) and Virus-carrying vectors (V). The total vector population $M = U + V$. The parameters $\beta$ and $\theta$ denote the rates for vector-to-host or host-to-vector infection, and $\gamma$ equals to the recovery rate. By $\mu$, we denote the reproduction and mortality rate of the host. Assuming $\psi = \rho M$ where $\psi$ is the vector reproduce at
a constant rate and drop out with mortality rate. The below figure 1 [15] is the flow chart of Dengue fever (SIR-UV) model.

![Figure 1. Flow chart of Dengue fever (SIR-UV) Model](image)

2.2 Analysis of Dengue fever (SIR-UV) Model

In this section [15], we have described the dynamics of dengue within host and vector populations.

\[
\frac{dS}{dt} = \mu (N - S) - \frac{\beta}{M} SV \\
\frac{dI}{dt} = \frac{\beta}{M} SV - (\gamma + \mu) I \\
\frac{dR}{dt} = \gamma I - \mu R \\
\frac{dU}{dt} = \psi - \frac{\theta}{N} UI - \rho U \\
\frac{dV}{dt} = \frac{\theta}{N} UI - \rho V
\]

Where, \( \mu = 0.00004214 \), \( N = 1500000 \), \( \beta = 0.167 \), \( M = 1000000 \), \( \gamma = 0.03333 \), \( \psi = 10000 \), \( \theta = 0.2 \), \( \rho = 0.1 \).

With the initial condition, \( (S, I, R, U, V) = (1, 1, 0, 1, 1) \) when \( t = 0 \),

The analytical solution is obtained by Homotopy Perturbation Method,

\[
S(t) = -1499999.011e^{(-0.0000421t)} + 1500000 - 25.05e^{(-0.1000421t)} + 25.06e^{(-0.10000t)} \\
I(t) = 1.02378859e^{(-0.033372t)} + 37.57309629e^{(-0.1000421t)} - 37.58685e^{(-0.10000t)} \\
R(t) = -1.000025049e^{(-0.033372t)} + 1.0000167e^{(-0.0000421t)} + 0.0000084e^{(-0.1000421t)} \\
U(t) = -99998.40e^{(-0.10000t)} + 100000 - 0.3996e^{(-0.133372t)} - 0.2001165e^{(-0.03342t)} \\
V(t) = 0.40035265e^{(-0.10000t)} + 0.3995308661e^{(-0.133372t)} + 0.20011648e^{(-0.033372t)}
\]
2.3 Numerical Simulation for Dengue fever (SIR-UV) Model

In this model, numerical solution is found by MATLAB programming, and it is compared with analytical solution for parameters in table 1. For this study, we used the values of parameters in table 1 referred in [15]. The following figures illustrate the simulation showing the comparison of the analytical solution and numerical solution for various values the parameters.

**S - Susceptible host:**

![Figure 2: Simulation showing the increasing effect of infection on Susceptible host of Dengue fever for various values of $\beta$.](image1)

![Figure 3: Simulation showing the increasing effect of infection on Susceptible host of Dengue fever for various values of $M$.](image2)

![Figure 4: Simulation showing the increasing effect of infection on susceptible host of Dengue fever for various values of $\mu$.](image3)

![Figure 5: Simulation showing the increasing effect of infection on susceptible host of Dengue fever for various values of $N$.](image4)
**I - Infected host**

**Figure 6.** Simulation showing the decreasing effect of infection on infected host of dengue fever for various values of $\gamma$.

**Figure 7.** Simulation showing the increasing effect of infection on infected host of Dengue fever for various values of $M$.

**Figure 8.** Simulation showing the increasing effect of infection on infected host of Dengue fever for various values of $\beta$.

**Figure 9.** Simulation showing the decreasing effect of infection on infected host of Dengue fever for various values of $\mu$.
**R - Recovered hosts**

![Graph showing the increasing effect of infection on recovered host of Dengue fever for various values of $\gamma$.](image)

**Figure 10.** Simulation showing the increasing effect of infection on recovered host of Dengue fever for various values of $\gamma$.

**U - Virus Free host**

![Graph showing the increasing effect of infection on Virus-Free vector of Dengue fever for various values of $N$.](image)

**Figure 12.** Simulation showing the increasing effect of infection on Virus-Free vector of Dengue fever for various values of $N$.

**Figure 11.** Simulation showing the increasing effect of infection on recovered host of Dengue fever for various values of $\mu$.

**Figure 13.** Simulation showing the decreasing effect of infection on Virus-Free vector of Dengue fever for various values of $\rho$. 
V- Virus Carrying vectors

Figure 14. Simulation showing the increasing effect of infection on Virus-Free vector of Dengue fever for various values of ψ.

Figure 15. Simulation showing the increasing effect of infection on Virus-Free vector Dengue fever for various values of θ.

Figure 16. Simulation showing the increasing effect of infection on Virus-Carrying vector of Dengue fever for various values of N.

Figure 17. Simulation showing the decreasing effect of infection on Virus-Carrying vector of Dengue fever for various value ρ.
Figure 18. Simulation showing the increasing effect of infection on Virus-Carrying vector of Dengue fever for various values of $\theta$.

Table 1. Variable and Parameter values used in stimulation

| Parameters | Description                                           | Value                |
|------------|-------------------------------------------------------|----------------------|
| $\mu$      | Reproduction and mortality rate of the host           | 0.00004214           |
| $\gamma$   | Recovery rate                                         | 0.03333              |
| $\rho$     | Drop out with mortality rate                          | 0.1                  |
| $\theta$   | Rates for host-to-vector infection                    | 0.2                  |
| $\beta$    | Rates for vector-to-host infection                    | 0.167                |
| $N$        | Host population                                      | 1500000              |
| $M$        | Vector Population                                     | 1000000              |
| $\psi$     | The vector reproduce at a constant rate               | 10000                |

2.4 Disease - Free Equilibrium

We obtain the disease-free equilibrium of the Dengue fever (SIR-UV) only model by setting the system of non-equation of the model to zero. At disease-free equilibrium, there are no infections and recovery, therefore by eqn(1).

$$\mu(N - S) - \frac{\beta}{M} SV = 0$$

$$S = \frac{\mu N}{\mu - \frac{\beta}{M}}$$

$$\xi_{0t} = (S^*, I^*, R^*, U^*, V^*) = \left( \frac{\mu N}{\mu - \frac{\beta}{M}}, 0, 0, 0, 0 \right)$$
2.5 Endemic Equilibrium

The endemic equilibrium points are computed by setting the system of differential equations in the Dengue fever (SIR-UV) to zero. The endemic equilibrium points are as follow:

\[ S^* = \frac{\mu N}{\mu - \frac{\gamma}{M}}; \quad I^* = \frac{\psi}{\beta M} \frac{SV}{\gamma + \mu}, \quad R^* = \frac{\gamma I}{\mu}, \quad U^* = \frac{\psi}{\beta N} \frac{U_1}{I - \rho V}, \quad V^* = \frac{\theta}{\beta} \frac{U_1}{N} \]

\[ \xi_d = (S^*, I^*, R^*, U^*, V^*) = \left( \frac{\mu N}{\mu - \frac{\gamma}{M}} \frac{SV}{\gamma + \mu}, \frac{\psi}{\beta M} \frac{U_1}{I - \rho V}, \frac{\gamma I}{\mu}, \frac{\psi}{\beta N} \frac{U_1}{I - \rho V}, \frac{\theta}{\beta} \frac{U_1}{N} \right) \]

3. Results and Discussions

The approximate analytical solutions for the concentration of Susceptible host, Infected host, Recovered host, Virus-free vectors and Virus-carrying vectors for various values of parameters are coincided with simulation results.

It is observed in figures 2-5, the x-axis and y-axis represent, time ‘t’ and susceptible host, respectively. If the time ‘t’ periodically increases with period 20, then the graph of y is a straight line passing through origin also it makes an angle 45°approximately with x-axis, for various values of \( \beta = 0.167, 0.274, 0.37; M = 100000, 150000, 200000; = 0.0004214, 0.0004230, 0.0004260 \) and \( N = 1500000, 1550000, 1600000 \), respectively also in figure 5, there is small increase in the susceptible host as N increases.

In figures 6-9, x-axis and y-axis represents time ‘t’ and the infected host, respectively. If the time ‘t’ periodically increases with period 20, illustrates the decreasing effect of infection on the infected host for various values of recovery rate \( \gamma \), vector population \( M \), vector-host infection rate \( \beta \) and host population \( N \), respectively also in figure 6, there is a small decrease in the infected host as \( \gamma \) increases.

In figures 10 and 11, x-axis and y-axis represents time ‘t’ and recovery host, respectively. If the time ‘t’ periodically increases with period 20, shows the increasing effect of infection on the recovery host for various values of the recovery rate \( \gamma \) and reproduction and mortality rate of the host \( \mu \), respectively. Also in figure 10, there is an increasing effect of infection on the recovered host by changing the values of the parameter \( \gamma \).

In figures 12 and 15 the increasing values of the host population \( N \) and rates for host-to-vector infection \( \theta \), on the concentration of virus free host \( U \) shows an increasing effect. In figure 13, there is a decreasing rate of effect of infection on Virus-Free vector for values of \( \rho = 0.1, 0.2 \) and 0.3, also we observe that as time increases \( U \) remains a constant. Figure 14, shows the increasing effect of infection on virus-free vectors \( U \) by changing the values of vector reproduce \( \psi \), also we observe that as time increases \( U \) remains a constant.
Figure 16, illustrates the decreasing effect of Virus-Carrying Vectors $V$ as time increases for various values of the host population $N$. Figure 17, exhibits the decreasing effect of infection on virus carrying vector as time increases for various values of drop out with mortality rate. Figure 18, shows the increasing effect of infection on Virus-Carrying vector by changing the values of rates for host-to-vector infection.

4. Conclusion
In this paper, the mathematical modeling of Dengue fever (SIR-UV) is analyzed. The mathematical modeling of Dengue fever (SIR-UV) is formulated into first order non-linear differential equation. The system of non-linear equation is solved using the homotopy perturbation method. Finally, the analytical solutions, simulation results are compared and satisfactory agreement is noted.

Acknowledgments: The authors are also thankful to Shri J. Ramachandran, Chancellor, Col. and Dr.G.Thiruvasagam, Vice-Chancellor, Academy of Maritime Education and Training (AMET), Chennai, Tamil Nadu.

Ethical Clearance: Taken from AMET University, Chennai.

Source of funding: Self

Conflict of interest: Nil

Data Availability: The data supporting this deterministic model are taken from previously published articles and they have been duly cited in this paper. Those parameter values taken from published articles are cited in Table 1 of this paper. These published articles are also cited at relevant places within the text as reference.

Appendixes (a) Mat Lab coding of Mathematical Modelling of Dengue fever(SIR-UV) model is located in the supplementary file section.

References:
[1] He J H, Homotopy perturbation technique, Comp. Meth. Appl. Mech. Eng. 178 (1999) 257-262.
[2] He J H, A coupling method of homotopy technique and a perturbation technique for non linear problems, Int. J. Non linear Mech. 35 (2000) 37-43.
[3] He J H, Homotopy perturbation method: A new nonlinear analytical technique, Appl. Math. Comput. 135 (2003) 73-79.
[4] Rajendran L, Rahamathunissa G, The Application of He’s variational iteration method to nonlinear boundary value problems in enzyme-substrate reaction diffusion processes: Part 1. The steady-state amperometric response, Journal of Mathematical Chemistry 44 (2008) 849-861.
[5] Saranya K, Mohan V, Kizek R, Fernandez C and Rajendran L, Unprecedented homotopy perturbation method for solving nonlinear equations in the enzymatic reaction of glucose in a spherical matrix, Bioprocess and Biosystems Engineering 41(2), (2018), 281-294.
[6] Rajendran L, Anitha S, Reply to “Comments on analytical solution of amperometric enzymatic reaction sbased on Homotopy perturbation method,” by Ji-Huan He, Lu-Feng Mo Electrochimica Acta 102 (2013) 474 - 476.
[7] "Dengue and severe dengue Fact sheet N°117". WHO. May 2015. Archived from the original on 2 September 2016. Retrieved 3 February 2016.
[8] Kularatne SA (September 2015) "Dengue fever". BMJ.
[9] "World's first dengue fever vaccine launched in the Philippines". CNN. Archived from the original on 18 October 2016. Retrieved 17 October 2016.
[10] "Dengue and severe dengue". www.who.int. Retrieved 29 February 2020.
[11] "First FDA-approved vaccine for the prevention of dengue disease in endemic regions". FDA (Press release). 1 May 2019. Retrieved 4 May 2019.
appendix A.

Dengue fever - MATLAB CODING

function Dengue1
options= odeset ('RelTol',1e-6,'Stats','on');
%initial conditions
Xo = [1,1,0,1,1];
tspan = [0,120];
tic
[t,X] = ode45(@TestFunction,tspan,Xo,options);
toc
figure
hold on
plot(t, X(:,1),'-')
plot(t, X(:,2),'-')
plot(t, X(:,3),'-')
plot(t, X(:,4),'-')
plot(t, X(:,5),'-')
legend('x1','x2','x3','x4','x5')
ylabel('x')
xlabel('t')
return

function [dx_dt] = TestFunction(t,x)
m=0.00004214;N=1500000;E=0.167;M=100000;g=0.03333;S=10000;T=0.2;r=0.1;
dx_dt(1) = (((m*N)-(m*x(1)))-((E/M)*x(1)*x(5)));  
dx_dt(2) = (((E/M)*x(1)*x(5))-((g*x(2))-(m*x(2))));  
dx_dt(3) = ((g*x(2))-(m*x(3)));  
dx_dt(4) = (((T/N)*x(4)*x(2))-(r*x(4))));  
dx_dt(5) = (((T/N)*x(4)*x(2))-(r*x(5))));  
dx_dt = dx_dt';
return