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Stability Analysis and Solutions of Dynamical Models for Dengue

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Abstract. This paper focuses on the analytical and numerical solutions of dynamic models for dengue fever. The considered model consists of a system of coupled non-linear differential equations. Homotopy Perturbation Method (HPM) and Runge Kutta Method of Order 4 (RK4) are applied to obtain analytical and numerical solutions, respectively. Moreover, the positivity of the solution is proved. The results of the suggested methods are validated with the exact solution for simplified model equations. Furthermore, the proposed methods are applied to the considered model using the real time data of Lahore (years 2011-2014), Pakistan. The results are found to be in agreement with the available exact solution and real time data. HPM results approach the exact solution by including higher order polynomials. The parametric study of dengue cases are performed. Moreover, the synchronization between the simulated results and real time data of dengue cases verifies the correctness of model formulation. On the

basis of these results, it is concluded that RK4 and HPM are suitable techniques to solve a non-linear dynamical system for dengue.

AMS (MOS) Subject Classification Codes: 35S29; 40S70; 25U09
Key Words: Nonlinear dynamical models, Homotopy perturbation method, Reproduction number, RK4.

1. INTRODUCTION

Infectious diseases have been the main cause of high mortality rate during the recent decades. Average life span was reduced due to lack of health facilities. Infectious diseases were controlled with the improvement in medical science. After the first half of 20th century, it was expected that infectious diseases would disappear, because of achievements in vaccination, antibiotics and better life conditions. However, with the start of 21st century, many infectious diseases e.g. dengue, hepatitis spread fast, and mortality rates increased in many developing countries. Many infectious diseases e.g. malaria, tuberculosis, AIDS, yellow fever and Ebola are still not completely controlled [20].
Among the infectious diseases, Dengue Fever (threatening about 2.5 million people all over the world, mostly in South Asia) spread in more than 100 countries, especially with the tropical and warm climates. In many tropical and sub tropical regions, dengue spreads every year, usually during rainy season, when population of Aede mosquito is higher. Dengue was identified in 1779-1780 for the first time in North America, Africa and Asia. In 1998, World Heath Organization, reported about 1.2 million cases in 56 countries. Every year, dengue infects almost 50 million humans. Among the affected humans, almost 0.5 million are affected by Dengue Hemorrhagic Fever (DHF)[5, 20].
Mathematical modeling is an effective tool to test and compare different strategies that are useful in controlling and eliminating epidemics. Numerical computations have gained a significant popularity to solve the nonlinear physical problems in the recent decades [2, 16, 25]. Various epidemiological models have been developed to analyze the infectious diseases. In epidemiological modeling, population can be divided into different groups on the basis their epidemiological status: susceptible (S), infectious (I) and recovered (R). The divisions in an SIR model are supposed to be mutually exclusive and number of individuals shifts from S to I and I to R. The variations in the compartments are based on the disease types. Several forms of compartmental models have been used, for instance, SI (susceptible-infected), SIS (susceptible-infected-susceptible), SIR (susceptible-infected-recovered), SIRS (susceptible-infected-recovered-susceptible) and SEIR (susceptible-exposed-infected-recovered) [5, 6, 17, 18, 23, 24, 26]. The dynamical models contain systems of nonlinear ordinary differential equations (ODEs). The exact solutions are only possible for simplified mathematical models, and therefore numerical methods are used to obtain reliable results [1, 3, 12, 14, 19, 22]. Analytical and numerical methods are effective in analyzing the transmission of infectious diseases. These methods are also helpful in devising measures to eliminate the infectious diseases like dengue.
In mathematics, linearization is used to find the linear approximation of a function at a given point. In dynamical systems, linearization is a method for assessing the local stability of an equilibrium point of a system of nonlinear differential equations or discrete dynamical systems. Linearization is used in engineering, physics, economics, and ecology.

The purpose of this work is to solve the dynamical models for dengue fever and validate through real time data of Lahore, Pakistan (years 2011-2014). The dynamical models can predict how infectious diseases spread to the extent of an epidemic. The SIR model including human and vector (mosquitoes) population is taken into consideration [23]. The positivity of the solution for the considered model is also proved in this study. HPM and RK4 is used to solve the SIR model. Numerical case studies are presented to validate the analytical and numerical results. The simplified model having exact solution is verified with the proposed analytical and numerical techniques. The results are compatible with the real time data. The parametric study is also performed and various aspects of dengue disease are highlighted.

The paper is organized as follows: In section 2, SIR model for dengue fever with model parameters are briefly described. In section 3, stability analysis is presented. In section 4, the positivity of the solution is discussed. Moreover, the procedure of HPM is explained and implemented to the SIR model. In section 5, the numerical test problems employing HPM and RK4 are presented. Finally, section 6 comprises the conclusion, remarks and future prospectives of the current research.

2. The SIR Model with Vector Population

In this research, the SIR model of Side and Noorani is considered [23]. The model identifies two populations: human population (N_1) and vector population (N_2). The human population is further split into three subcategories: susceptible (S_1), the group of people who may potentially get infected with dengue virus; infected (I_1), the group of people infected with dengue virus, and recovered (R_1), the group of people who came back to a normal state of health after infection. The mosquito population is split into two categories: susceptible (S_2) and infected (I_2). The changes in human and vector population can be expressed in mathematical form:
For the human population,

$$\begin{aligned}
\frac{dS_1}{dt} &= \mu_1 N_1 - \frac{\beta_1 b}{N_1} I_2 S_1 - \mu_1 S_1, \\
\frac{dI_1}{dt} &= \frac{\beta_1 b}{N_1} I_2 S_1 - (\mu_1 + \gamma_1) I_1, \\
\frac{dR_1}{dt} &= \gamma_1 I_1 - \mu_1 R_1.
\end{aligned} \tag{2. 1}$$

For the vector population,

$$\begin{aligned}
\frac{dS_2}{dt} &= \mu_2 N_2 - \frac{\beta_2 b}{N_1} I_1 S_2 - \mu_2 S_2, \\
\frac{dI_2}{dt} &= \frac{\beta_2 b}{N_1} I_1 S_2 - \mu_2 I_2,
\end{aligned} \tag{2. 2}$$

with the initial conditions

$$S_1(0) \geq 0, \;\; I_1(0) \geq 0, \;\; R_1(0) \geq 0, \;\; S_2(0) \geq 0, \;\; I_2(0) \geq 0. \tag{2. 3}$$

Moreover,

$$S_1 + I_1 + R_1 = N_1 \Rightarrow R_1 = N_1 - S_1 - I_1,$$
$$S_2 + I_2 = N_2 = \frac{A}{\mu_2} \Rightarrow S_2 = N_2 - I_2 = \frac{A}{\mu_2} - I_2. \quad (2.\ 4)$$

The parameters $\mu_1 N_1$ is the change in the total human population, $\frac{\beta_1 b I_2}{N_1}$ is the probability of susceptible individual being infected with dengue virus, β_1 is the infection probability from infected ones to a susceptible mosquito, b represents a mosquito's average bites and $\mu_1 S_1$ denotes the deaths among susceptible human population. Moreover, the number of deaths in the infected human population is represented by $\mu_1 I_1$, whereas the infected people who recovered from infection is represented by $\gamma_1 I_1$. The parameter R_1 is the total human population that has recovered from infection. The difference between the humans recovered from infection $(\gamma_1 I_1)$ and the total deaths in recovered human population $(\mu_1 R_1)$ is the rate of change for a healthy population.
The parameter $\frac{\beta_2 b I_1}{N_1}$ shows that each individual in the susceptible population has the probability of being bitten by mosquitoes infected with dengue virus, β_2 is the transmission probability from infected human to virtually infected mosquito, $\mu_2 S_2$ is the death toll among the susceptible mosquitoes. The number of deaths in the mosquito population is represented by $\mu_2 I_2$. The model given in Eqs. (2. 1) and (2. 2) can be simplified by assuming following fractions:

$$x_1 = \frac{S_1}{N_1},\ x_2 = \frac{I_1}{N_1},\ x_3 = \frac{R_1}{N_1},\ x_4 = \frac{S_2}{N_2},\ x_5 = \frac{I_2}{N_2}. \quad (2.\ 5)$$

Thus, the human and vector population is given below:

$$\begin{aligned}
\frac{dx_1}{dt} &= \mu_1(1 - x_1(t)) - \alpha x_1(t) x_5(t),\\
\frac{dx_2}{dt} &= \alpha x_1(t) x_5(t) - \beta x_2(t),\\
\frac{dx_3}{dt} &= \gamma_1 x_2(t) - \mu_1 x_3(t),\\
\frac{dx_4}{dt} &= \mu_2(1 - x_4(t)) - \xi x_2(t) x_4(t),\\
\frac{dx_5}{dt} &= \xi x_2(t) x_4(t) - \mu_2 x_5(t), \quad (2.\ 6)
\end{aligned}$$

where $\alpha = \frac{b\beta_1 A}{\mu_2 N_1},\ \ \beta = \gamma_1 + \mu_1,\ \ \xi = b\beta_2$.

3. Stability Analysis

In this section the stability analysis is presented by using linearization method.

Equilibrium points

Let the set Ω be given by
$\Omega = \{(S_1, I_1, R_1, S_2, I_2)/0 \leq I_2 \leq N_2; 0 \leq S_1, I_1; 0 \leq S_2, I_2; S_1 + I_1 + R_1 \leq N_1; S_2 + I_2 \leq N_2\}$ Then we have the following theorem.

3.1. **Theorem.** The system Eq. (2. 6) admits two equilibrium points $F_1 = (1, 0, 0, 1, 0)$ and
$F_2 = (x_{10}, x_{20}, x_{30}, x_{40}, x_{50})$, where $x_{10} = \frac{(\mu_1\xi+\beta\mu_2)}{\xi(\alpha+\mu_1)}$, $x_{20} = \frac{\mu_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}$, $x_{30} = \frac{\gamma_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}$,
$x_{40} = \frac{\mu_2\beta(\alpha+\mu_1)}{\alpha(\mu_1\xi+\beta\mu_2)}$, $x_{50} = \frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)}$.
Proof:
The system Eq. (2. 6) is given as:

$$\begin{aligned}
\frac{dx_1}{dt} &= \mu_1(1 - x_1(t)) - \alpha x_1(t)x_5(t),\\
\frac{dx_2}{dt} &= \alpha x_1(t)x_5(t) - \beta x_2(t),\\
\frac{dx_3}{dt} &= \gamma_1 x_2(t) - \mu_1 x_3(t),\\
\frac{dx_4}{dt} &= \mu_2(1 - x_4(t)) - \xi x_2(t)x_4(t),\\
\frac{dx_5}{dt} &= \xi x_2(t)x_4(t) - \mu_2 x_5(t). \qquad (3.\ 7)
\end{aligned}$$

The equilibrium points satisfy the following relations:

$$\frac{dx_1}{dt} = \frac{dx_2}{dt} = \frac{dx_3}{dt} = \frac{dx_4}{dt} = \frac{dx_5}{dt} = 0. \qquad (3.\ 8)$$

Putting Eq. (3. 7) into Eq. (3. 8) yields,

$$\begin{aligned}
&\mu_1(1 - x_1(t)) - \alpha x_1(t)x_5(t) = 0,\\
&\alpha x_1(t)x_5(t) - \beta x_2(t) = 0,\\
&\gamma_1 x_2(t) - \mu_1 x_3(t) = 0,\\
&\mu_2(1 - x_4(t)) - \xi x_2(t)x_4(t) = 0,\\
&\xi x_2(t)x_4(t) - \mu_2 x_5(t) = 0. \qquad (3.\ 9)
\end{aligned}$$

The first $F_1 = (1, 0, 0, 1, 0)$ is trivial in the sense that all individuals stay healthy. Now to find the second equilibrium point, we consider Eq. (3. 9),

$$\mu_1(1 - x_1(t)) - \alpha x_1(t)x_5(t) = 0, \qquad (3.\ 10)$$

$$\alpha x_1(t)x_5(t) - \beta x_2(t) = 0, \qquad (3.\ 11)$$

$$\gamma_1 x_2(t) - \mu_1 x_3(t) = 0, \qquad (3.\ 12)$$

$$\mu_2(1 - x_4(t)) - \xi x_2(t)x_4(t) = 0, \qquad (3.\ 13)$$

$$\xi x_2(t)x_4(t) - \mu_2 x_5(t) = 0. \qquad (3.\ 14)$$

Adding Eq. (3. 10) and Eq. (3. 11),

$$\begin{aligned}
&\mu_1(1 - x_1(t)) - \beta x_2(t) = 0,\\
&x_2 = \frac{\mu_1(1 - x_1(t))}{\beta}. \qquad (3.\ 15)
\end{aligned}$$

Now adding Eq. (3. 13) and Eq. (3. 14),

$$\begin{aligned}&\mu_2(1-x_4(t))-\mu_2x_5(t)=0,\\&x_4=1-x_5.\end{aligned}\tag{3. 16}$$

Further simplification of Eq. (3. 15) results in the following equation:

$$x_1=\frac{\mu_1-\beta x_2(t))}{\mu_1}.\tag{3. 17}$$

Putting Eq. (3. 17) into Eq. (3. 11) yields,

$$\begin{aligned}&\alpha(\frac{\mu_1-\beta x_2(t))}{\mu_1})x_5(t)-\beta x_2(t)=0,\\&\alpha(\mu_1-\beta x_2(t))x_5(t)-\beta\mu_1x_2(t)=0,\\&\alpha\mu_1x_5(t)-\beta x_2(t)x_5(t)-\beta\mu_1x_2(t)=0.\end{aligned}\tag{3. 18}$$

Simplification of Eq. (3. 14) results in the following equation:

$$x_2(t)=\frac{\mu_2x_5(t)}{\xi(1-x_5)}.\tag{3. 19}$$

Now putting the value of x_2 into Eq. (3. 18),

$$\begin{aligned}&\alpha\mu_1x_5-\alpha\beta x_5\frac{\mu_2x_5}{\xi(1-x_5)}-\beta\mu_1\frac{\mu_2x_5}{\xi(1-x_5)}=0,\\&x_5=\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)}.\end{aligned}\tag{3. 20}$$

Now in Eq. (3. 16) replacing x_5 by its value we get x_4,

$$\begin{aligned}&x_4=1-x_5=1-\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)},\\&x_4=\frac{\mu_2\beta(\alpha+\mu_1)}{\alpha(\mu_1\xi+\beta\mu_2)}.\end{aligned}\tag{3. 21}$$

Similarly by putting the value of x_5 into Eq. (3. 19), we get x_2,

$$\begin{aligned}&x_2=\frac{\mu_2x_5}{\xi(1-x_5)}=\frac{\mu_2\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)}}{\xi(1-\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)})}\\&x_2=\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}.\end{aligned}\tag{3. 22}$$

Now putting the value of x_2 into Eq. (3. 17), we obtain x_1,

$$\begin{aligned}&x_1=\frac{\mu_1-\beta x_2}{\mu_1}=\frac{\mu_1-\beta\frac{\mu_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}}{\mu_1},\\&x_1=\frac{\mu_1\xi+\beta\mu_2}{\xi(\alpha+\mu_1)}.\end{aligned}\tag{3. 23}$$

Then giving the value of x_2 into Eq. (3. 12), we get x_3,

$$\gamma_1 x_2 - \mu_1 x_3 = 0,$$
$$x_3 = \frac{\gamma_1(\alpha\xi - \beta\mu_2)}{\xi\beta(\alpha + \mu_1)}. \tag{3. 24}$$

The second point is $F_2 = (x_{10}, x_{20}, x_{30}, x_{40}, x_{50})$ that corresponds to the endemic state i.e. the case where the disease persists in the two populations.
The obtained values of x_{10}, x_{20}, x_{30}, x_{40} and x_{50} are given below:

$$x_{10} = \frac{(\mu_1\xi + \beta\mu_2)}{\xi(\alpha + \mu_1)}, x_{20} = \frac{\mu_1(\alpha\xi - \beta\mu_2)}{\xi\beta(\alpha + \mu_1)}, x_{30} = \frac{\gamma_1(\alpha\xi - \beta\mu_2)}{\xi\beta(\alpha + \mu_1)},$$
$$x_{40} = \frac{\mu_2\beta(\alpha + \mu_1)}{\alpha(\mu_1\xi + \beta\mu_2)}, x_{50} = \frac{\mu_1(\alpha\xi - \beta\mu_2)}{\alpha(\mu_1\xi + \beta\mu_2)}. \tag{3. 25}$$

Hence it is proved that the system of Eq. (2. 6) has two equilibrium points $F_1 = (1, 0, 0, 1, 0)$ and $F_2 = (x_{10}, x_{20}, x_{30}, x_{40}, x_{50})$.

3.2. **Theorem.** 1 • The equilibrium point $F_1 = (1, 0, 0, 1, 0)$ is a saddle point.
2 • The equilibrium point $F_2 = (x_{10}, x_{20}, x_{30}, x_{40}, x_{50})$ is asymptotically stable.
Here, $x_{10} = \frac{(\mu_1\xi+\beta\mu_2)}{\xi(\alpha+\mu_1)}, x_{20} = \frac{\mu_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}, x_{30} = \frac{\gamma_1(\alpha\xi-\beta\mu_2)}{\xi\beta(\alpha+\mu_1)}, x_{40} = \frac{\mu_2\beta(\alpha+\mu_1)}{\alpha(\mu_1\xi+\beta\mu_2)}$, $x_{50} = \frac{\mu_1(\alpha\xi-\beta\mu_2)}{\alpha(\mu_1\xi+\beta\mu_2)}$.
Proof:
1• To find the variational matrix we linearize the system given in Eq. (2. 6) at the the first equilibrium point F_1, we get the following matrix:

$$\begin{pmatrix} -\mu_1 & 0 & 0 & 0 & -\alpha \\ 0 & -\beta & 0 & 0 & \alpha \\ 0 & \gamma_1 & -\mu_1 & 0 & 0 \\ 0 & -\xi & 0 & -\mu_2 & 0 \\ 0 & \xi & 0 & 0 & -\mu_2 \end{pmatrix} \tag{3. 26}$$

Using MAPLE, Eq. (3. 26) leads to the following characteristic equation.

$$\lambda^5 + (\beta + 2\mu_1 + 2\mu_2)\lambda^4 + (\alpha\xi + 2\beta\mu_2 - \mu_1^2 - \mu_2^2)\lambda^3 - (2\alpha\mu_1\xi + \alpha\mu_2\xi$$
$$- \beta\mu_1^2 - 4\beta\mu_1\mu_2 - \beta\mu_2^2 - 2\mu_1^2\mu_2 - 2\mu_1\mu_2^2)\lambda^2 - (\alpha\mu_1^2\xi + 2\alpha\mu_1\mu_2\xi - 2\beta\mu_1^2\mu_2$$
$$- 2\beta\mu_1\mu_2^2 - \mu_1^2\mu_2^2)\lambda - \alpha\mu_1^2\mu_2\xi + \mu_2^2\mu_1\beta = 0. \tag{3. 27}$$

The parameter values are given in Table 1. The eigenvalues for Eq. (3. 27) are as follows, $\lambda_1 = -0.00004000$, $\lambda_2 = -.55945061$, $\lambda_3 = 0.201167613$, $\lambda_4 = -0.00003990$, $\lambda_5 = -0.0294100$.
As one of the eigenvalues at the equilibrium point F_1 is positive, so the equilibrium point is a saddle point. The human population is free of dengue disease since the the number of infected human is 0 as well as the number of infected mosquito is also 0. Over all human population is healthy and there is no infected human in the population.

Name of parameter	Notation	Value
Host to vector infected rate	γ_1	0.328833
Contact rate, vector to host	$b\beta_1$	0.75000
Contact rate, host to vector	$b\beta_2$	0.375000
Human life span	μ_1	0.000046
Vector life span	μ_2	0.0323

TABLE 1. Parameter Values.

2 • To find the variational matrix we linearize the system given in Eq. (2. 6) at the second equilibrium point F_2, we obtain the following matrix:

$$\begin{pmatrix} \mu_1 - \mu_1\frac{(\alpha\xi-\beta\mu_2)}{(\mu_1\xi+\beta\mu_2)} & 0 & 0 & 0 & -\alpha\frac{(\mu_1\xi+\beta\mu_2)}{\xi(\alpha+\mu_1)} \\ \mu_1\frac{(\alpha\xi-\beta\mu_2)}{(\mu_1\xi+\beta\mu_2)} & -\beta & 0 & 0 & \alpha\frac{(\mu_1\xi+\beta\mu_2)}{\xi(\alpha+\mu_1)} \\ 0 & \gamma_1 & -\mu_1 & 0 & 0 \\ 0 & -\xi\frac{\mu_2\beta(\alpha+\mu_1)}{\alpha(\mu_1\xi+\beta\mu_2)} & 0 & -\mu_2-\mu_1\frac{(\alpha\xi-\beta\mu_2)}{\beta(\alpha+\mu_2)} & 0 \\ 0 & \xi\frac{\mu_2\beta(\alpha+\mu_1)}{\alpha(\mu_1\xi+\beta\mu_2)} & 0 & \mu_1\frac{(\alpha\xi-\beta\mu_2)}{\beta(\alpha+\mu_2)} & -\mu_2 \end{pmatrix} \tag{3. 28}$$

Using MAPLE, Eq. (3. 28) leads to the following characteristic equation:
$\lambda^5-(-\mu_1x_{50}-\xi x_{20}-\beta-2\mu_2)\lambda^4-(\alpha x_{10}\xi x_{10}x_{40}-\mu_1x_{50}\xi x_{20}-\beta\mu_1x_{50}-\beta\xi x_{20}-\mu_1^2x_{50}-2\mu_1\mu_2x_{50}-\mu_2\xi x_{20}-2\beta\mu_2+\mu_1^2-\mu_2^2)\lambda^3-(-\alpha x_{40}x_{10}\xi^2x_{20}+\alpha x_{10}\xi^2x_{10}x_{40}x_{20}+\alpha\mu_2x_{10}\xi x_{10}x_{40}-\beta\mu_1x_{50}\xi x_{20}-\mu_1^2x_{50}\xi x_{20}-\mu_1\mu_2x_{50}\xi x_{20}-\beta\mu_1^2x_{50}-2\beta\mu_1\mu_2x_{50}-\beta\mu_2\xi x_{20}-2\mu_1^2\mu_2x_{50}+\mu_1^2\xi x_{20}-\mu_1\mu_2^2x_{50}+\beta\mu_1^2-\beta\mu_2^2+2\mu_1^2\mu_2)\lambda^2-(-\alpha\mu_1^2x_{10}\xi x_{10}x_{40}-\beta\mu_1^2x_{50}\xi x_{20}-\beta\mu_1\mu_2x_{50}\xi x_{20}-\mu_1^2\mu_2x_{50}\xi x_{20}-2\beta\mu_1^2\mu_2x_{50}+\beta\mu_1^2\xi x_{20}-\beta\mu_1\mu_2^2x_{50}+\mu_1^2\mu_2^2x_{50}+\mu_1^2\mu_2\xi x_{20}+2\beta\mu_1^2\mu_2+\mu_1^2\mu_2^2)\lambda-\alpha\mu_1^2x_{40}x_{10}\xi^2x_{20}+\alpha\mu_1^2x_{10}\xi^2x_{10}x_{40}x_{20}+\alpha\mu_1^2\mu_2x_{10}\xi x_{10}x_{40}+\beta\mu_1^2\mu_2x_{50}\xi x_{20}+\beta\mu_1^2\mu_2^2x_{50}-\beta\mu_1^2\mu_2\xi x_{20}-\beta\mu_1^2\mu_2^2.$

The eigenvalues for equilibrium point F_2 are,
$\lambda_1 = -.358318057$, $\lambda_2 = -0.0000234827 + 0.00353i$, $\lambda_3 = -0.0000400$, $\lambda_4 = -0.0002348 - 0.003533$, $\lambda_5 = -0.0294519$.
The eigenvalues are all negative and complex, so the equilibrium point is asymptotically stable. The second equilibrium point shows that if the number of susceptible human population rises up to 0.07925 of the total human population and the number of infected vector rises up to 0.001425, the infected human population increases up to 0.00011 and the value of recovered persons becomes 0.9206. The equilibrium point F_2 would be stable, and there would occur some cases of dengue fever.

4. NUMERICAL SOLUTION OF SIR MODEL

The exact solution is not always possible, therefore, we use different numerical techniques to solve the problem. There are different numerical methods to solve initial value problems such as Euler method, Bisection method, Newton method, Heun's method and Runge-Kutta methods. In this work, RK4 is applied to solve SIR model given in Eq. (2. 6).

4.1. **Algorithm.** Suppose we have m differential equations:

$$\begin{aligned} y_1' &= g_1(t, y_1, y_2, ..., y_m) \\ y_2' &= g_2(t, y_1, y_2, ..., y_m) \\ . &\quad . \\ . &\quad . \\ y_m' &= g_m(t, y_1, y_2, ..., y_m), \end{aligned}$$

with the initial conditions,

$$y_1(t_0) = y_{10},\ y_2(t_0) = y_{20}, . . .,\ y_m(t_0) = y_{m0}.$$

There is no derivative on the right hand side and all of these m equations are of order one. RK4 formula is as follows:

$$y_{i,n+1} = y_{i,n} + \frac{h}{6}(L_{i,1} + 2L_{i,2} + 2L_{i,3} + L_{i,4}), \tag{4. 29}$$

$$t_{n+1} = t_n + h, \tag{4. 30}$$

where,

$$L_{i,1} = g_i(t_n, y_{1n}, y_{2n}, ..., y_{mn}), \tag{4. 31}$$

$$L_{i,2} = g_i(t_n + \frac{h}{2}, y_{1n} + \frac{h}{2}L_{11}, y_{2n} + \frac{h}{2}L_{21}, ..., y_{mn} + \frac{h}{2}L_{m1}), \tag{4. 32}$$

$$L_{i,3} = g_i(t_n + \frac{h}{2}, y_{1n} + \frac{h}{2}L_{12}, y_{2n} + \frac{h}{2}L_{22}, ..., y_{mn} + \frac{h}{2}L_{m2}), \tag{4. 33}$$

$$L_{i,4} = g_i(t_n + h, y_{1n} + hL_{13}, y_{2n} + hL_{23}, ..., y_{mn} + hL_{m3}). \tag{4. 34}$$

where $y_{i,n+1}$ is the RK4 approximation of $y(t_{i,n+1})$ and h is step size.

5. Analytical Solution of SIR Model

Positivity of solutions:
The solution of the systems given in Eqs. (2. 1) and (2. 2) with positive initial conditions are positive for all $t > 0$.

5.1. **Theorem.** Consider the initial conditions, given in Eq. (2. 4), then the solutions $(S_1, I_1, R_1, S_2, I_2)$ of the systems in Eqs. (2. 1) and (2. 2) are positive, for all $t > 0$.
Proof: We consider,

$$t^* = sup\{t > 0 : S_1 > 0, I_1 \geq 0, R_1 > 0, S(2) > 0, I_2 \geq 0\}.$$

So $t^* > 0$. Now for the first equation of system (2. 1),

$$\begin{aligned} \frac{dS_1}{dt} &= \mu_1 N_1 - \frac{\beta_1 b}{N_1} I_2 S_1 - \mu_1 S_1, \\ &= \mu_1 N_1 - (\frac{\beta_1 b}{N_1} I_2 + \mu_1) S_1, \end{aligned}$$

We let $g(t) = \frac{\beta_1 b}{N_1} I_2$ and $c = \mu_1 N_1$, where c is a constant, the above equation becomes,

$$\frac{d}{dt}(S_1 exp\{\int_0^t g(u)\mathrm{d}u + \mu_1 t\}) = c\, exp\{\int_0^t g(u)\mathrm{d}u + \mu_1 t\},$$

Now taking integration on both sides from $t = 0$ to $t = t^*$

$$S_1(t^*)exp\{\int_0^{t^*} g(u)\mathrm{d}u + \mu_1 t^*\} - S_1(0) = \int_0^{t^*} c\, exp\{\int_0^x g(x)\mathrm{d}x + \mu_1 y\}\mathrm{d}y.$$

Multiplying both sides by $exp\{-\int_0^{t^*} g(u)\mathrm{d}u - \mu_1 t^*\}$,

$$\begin{aligned} S_1(t^*) =& S_1(0)exp\{-\int_0^{t^*} g(u)\mathrm{d}u - \mu_1 t^*\} + exp\{-\int_0^{t^*} g(u)\mathrm{d}u - \mu_1 t^*\} \\ & \times \int_0^{t^*} c\, exp\{\int_0^x g(x)\mathrm{d}x + \mu_1 y\}\mathrm{d}y > 0. \end{aligned}$$

Since $S_1(t^*)$ is the sum of positive terms, so it is positive. Similarly we can prove for the quantities (I_1, R_1, S_2, I_2) are positive for all $t > 0$.

5.2. **Homotopy Perturbation Method.** HPM, introduced by J. He, has been widely applied to obtain approximate series solution of linear and nonlinear differential equations [7, 8]. These articles comprise the relevant literature on the application and convergence of HPM [1, 3, 9, 10, 11, 12]. Firstly, we write the general system of differential equations as follows:

$$\begin{aligned} &\frac{dr_1}{dt} + h_1(t, r_1, r_2, ..., r_m) = f_1(t), \\ &\frac{dr_2}{dt} + h_2(t, r_1, r_2, ..., r_m) = f_2(t), \\ &\quad . \qquad . \qquad . \\ &\quad . \qquad . \qquad . \\ &\frac{dr_m}{dt} + h_m(t, r_1, r_2, ..., r_m) = f_m(t), \end{aligned} \tag{5. 35}$$

with initial conditions,

$$r_1(t_0) = k_1, \quad r_2(t_0) = k_2, ..., \quad r_m(t_0) = k_m. \tag{5. 36}$$

We can write Eq. (5. 35) in the operator form as:

$$\begin{aligned} &L(r_1) + A_1(r_1, r_2, ..., r_m) - f_1(t) = 0, \\ &L(r_2) + A_2(r_1, r_2, ..., r_m) - f_2(t) = 0, \\ &\quad . \qquad . \qquad . \quad . \\ &\quad . \qquad . \qquad . \quad . \\ &L(r_m) + A_m(r_1, r_2, ..., r_m) - f_m(t) = 0. \end{aligned} \tag{5. 37}$$

subject to the conditions in Eq. (5. 36), where $L = \frac{d}{dt}$ is a linear operator and $A_1, A_2, ..., A_m$ are nonlinear operators. Now based on the standard HPM, we present the solution for model equations given in Eq. (5. 37).

We construct a homotopy for Eq. (5. 37) that satisfies the following relations:

$$\begin{aligned}
&L(r_1) - L(r_{1,0}) + pL(r_{1,0}) + p[A_1(r_1, r_2, ..., r_m) - f_1(t)] = 0,\\
&L(r_2) - L(r_{2,0}) + pL(r_{2,0}) + p[A_2(r_1, r_2, ..., r_m) - f_2(t)] = 0,\\
&\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot\\
&\cdot \quad \cdot \quad \cdot \quad \cdot \quad \cdot\\
&L(r_m) - L(r_{m,0}) + pL(r_{m,0}) + p[A_m(r_1, r_2, ..., r_m) - f_m(t)] = 0.
\end{aligned} \tag{5. 38}$$

where $p \in [0, 1]$, is a parameter and $r_{1,0}, r_{2,0}, ..., r_{m,0}$ are initial approximations satisfying the given conditions. Eq. (5. 38) becomes a linear system when $p = 0$ and a nonlinear system when $p = 1$.

$$\begin{aligned}
r_1(t) &= r_{1,0}(t) + pr_{1,1}(t) + p^2 r_{1,2}(t) + ...,\\
r_2(t) &= r_{2,0}(t) + pr_{2,1}(t) + p^2 r_{2,2}(t) + ...,\\
&\cdot \quad \cdot\\
&\cdot \quad \cdot\\
r_m(t) &= r_{m,0}(t) + pr_{m,1}(t) + p^2 r_{m,2}(t) + ...
\end{aligned} \tag{5. 39}$$

where $r_{i,j}$ $(i = 1, 2, ..., m;\ j = 1, 2, ..., m)$ are unknown functions which we have to determine. Now we apply the inverse operator on the above system of equations to obtain the values of unknown $r_{i,j}$ $(i = 1, 2, ..., m;\ j = 1, 2, ..., m)$.

$$L^{-1}(.) = \int_0^t (.)\, \mathrm{d}t. \tag{5. 40}$$

So the $n - term$ approximation to the solutions of Eq. (5. 37) can be expressed as:

$$\begin{aligned}
\phi_{1,n}(t) = r_1(t) = lim_{p\to 1} r_1(t) &= \sum_{k=0}^{n-1} r_{1,k}(t),\\
\phi_{2,n}(t) = r_2(t) = lim_{p\to 1} r_2(t) &= \sum_{k=0}^{n-1} r_{2,k}(t),\\
&\cdot \quad \cdot \quad \cdot \quad \cdot\\
&\cdot \quad \cdot \quad \cdot \quad \cdot\\
\phi_{m,n}(t) = r_m(t) = lim_{p\to 1} r_m(t) &= \sum_{k=0}^{n-1} r_{m,k}(t).
\end{aligned} \tag{5. 41}$$

5.3. **Implementation of HPM.** In this subsection, the proposed HPM is implemented on the SIR model. The simplified form of the model with initial conditions is given below:

$$\begin{aligned}
\frac{dx_1}{dt} &= \mu_1(1 - x_1(t)) - \alpha x_1(t)x_5(t),\\
\frac{dx_2}{dt} &= \alpha x_1(t)x_5(t) - \beta x_2(t),\\
\frac{dx_3}{dt} &= \gamma_1 x_2(t) - \mu_1 x_3(t),\\
\frac{dx_4}{dt} &= \mu_2(1 - x_4(t)) - \xi x_2(t)x_4(t),\\
\frac{dx_5}{dt} &= \xi x_2(t)x_4(t) - \mu_2 x_5(t). \qquad (5.\ 42)
\end{aligned}$$

with initial conditions,

$$x_1(t_0) = k_1,\ x_2(t_0) = k_2,\ x_3(t_0) = k_3,\ x_4(t_0) = k_4,\ x_5(t_0) = k_5. \qquad (5.\ 43)$$

According to HPM, constructing a homotopy for Eq. (5. 42) satisfies the following relations:

$$\begin{aligned}
&x_1' - x_{10}' + p(x_{10}' - \mu_1(1 - x_1) + \alpha x_1 x_5) = 0,\\
&x_2' - x_{20}' + p(x_{20}' - \alpha x_1 x_5 + \beta x_2) = 0,\\
&x_3' - x_{30}' + p(x_{30}' - \gamma_1 x_2 + \mu_1 x_3) = 0,\\
&x_4' - x_{40}' + p(x_{40}' - \mu_2(1 - x_4) + \xi x_2 x_4) = 0,\\
&x_5' - x_{50}' + p(x_{50}' - \alpha x_1 x_5 + \mu_2 x_5) = 0. \qquad (5.\ 44)
\end{aligned}$$

with initial approximation:

$$x_{10}(t) = k_1,\ x_{20}(t) = k_2,\ x_{30}(t) = k_3,\ x_{40}(t) = k_4,\ x_{50}(t) = k_5. \qquad (5.\ 45)$$

$$\begin{aligned}
\text{and}\quad x_1(t) &= x_{1,0}(t) + p x_{1,1}(t) + p^2 x_{1,2}(t) + p^3 x_{1,3}(t) + ...,\\
x_2(t) &= x_{2,0}(t) + p x_{2,1}(t) + p^2 x_{2,2}(t) + p^3 x_{2,3}(t) + ...,\\
x_3(t) &= x_{3,0}(t) + p x_{3,1}(t) + p^2 x_{3,2}(t) + p^3 x_{3,3}(t) + ...,\\
x_4(t) &= x_{4,0}(t) + p x_{4,1}(t) + p^2 x_{4,2}(t) + p^3 x_{4,3}(t) + ...,\\
x_5(t) &= x_{5,0}(t) + p x_{5,1}(t) + p^2 x_{5,2}(t) + p^3 x_{5,3}(t) + ... \qquad (5.\ 46)
\end{aligned}$$

where $x_{i,j}$ $(i = 1, 2, ..., m;\ j = 1, 2, ...m)$ are the functions to be determined. Substituting Eq. (5. 45) and Eq. (5. 46) into Eq. (5. 44) and equating the terms of same powers of p, we have:

$$
\begin{aligned}
&x'_{1,1} - \mu_1 + \mu_1 x_{1,0} + \alpha x_{1,0} x_{5,0} = 0, && x_{1,1}(0) = 0,\\
&x'_{2,1} - \alpha x_{1,0} x_{5,0} + \beta x_{2,0} = 0, && x_{2,1}(0) = 0,\\
&x'_{3,1} - \gamma_1 x_{2,0} + \mu_1 x_{3,0} = 0, && x_{3,1}(0) = 0,\\
&x'_{4,1} - \mu_2 + \mu_2 x_{4,0} + \xi x_{2,0} x_{4,0} = 0, && x_{4,1}(0) = 0,\\
&x'_{5,1} - \xi x_{2,0} x_{4,0} + \mu_2 x_{5,0} = 0, && x_{5,1}(0) = 0,\\
&x'_{1,2} + \mu_1 x_{1,1} + \alpha x_{1,0} x_{5,1} + \alpha x_{1,1} x_{5,0} = 0, && x_{1,2}(0) = 0,\\
&x'_{2,2} - \alpha x_{1,0} x_{5,1} - \alpha x_{1,1} x_{5,0} + \beta x_{2,1} = 0, && x_{2,2}(0) = 0,\\
&x'_{3,2} - \gamma_1 x_{2,1} + \mu_1 x_{3,1} = 0, && x_{3,2}(0) = 0,\\
&x'_{4,2} + \mu_2 x_{4,1} + \xi x_{2,0} x_{4,1} + \xi x_{2,1} x_{4,0} = 0, && x_{4,2}(0) = 0,\\
&x'_{5,2} - \xi x_{2,0} x_{4,1} - \xi x_{2,1} x_{4,0} + \mu_2 x_{5,1} = 0, && x_{5,2}(0) = 0,\\
&x'_{1,3} + \mu_1 x_{1,2} + \alpha x_{1,0} x_{5,1} + \alpha x_{1,1} x_{5,1} + \alpha x_{1,1} x_{5,0} = 0, && x_{1,3}(0) = 0,\\
&x'_{2,3} - \alpha x_{1,0} x_{5,2} - \alpha x_{1,1} x_{5,1} - \alpha x_{1,2} x_{5,0} + \beta x_{2,2} = 0, && x_{2,3}(0) = 0,\\
&x'_{3,3} - \gamma_1 x_{2,2} + \mu_1 x_{3,2} = 0, && x_{3,3}(0) = 0,\\
&x'_{4,3} + \mu_2 x_{4,2} + \xi x_{2,0} x_{4,2} + \xi x_{2,1} x_{4,1} + \xi x_{2,2} x_{4,0} = 0, && x_{4,3}(0) = 0,\\
&x'_{5,3} - \xi x_{2,0} x_{4,2} - \xi x_{2,1} x_{4,1} - \xi x_{2,2} x_{4,0} + \mu_2 x_{5,2} = 0, && x_{5,3}(0) = 0.
\end{aligned} \tag{5. 47}
$$

Solving the above mentioned differential equations, we get:

$$
\begin{aligned}
&x_{1,1} = \int_0^t [\mu_1 - \mu_1 x_{1,0} - \alpha x_{1,0} x_{5,0}]\,\mathrm{d}x, \qquad x_{2,1} = \int_0^t [\alpha x_{1,0} x_{5,0} - \beta x_{2,0}]\,\mathrm{d}x,\\
&x_{3,1} = \int_0^t [\gamma_1 x_{2,0} - \mu_1 x_{3,0}]\,\mathrm{d}x, \qquad x_{4,1} = \int_0^t [\mu_2 - \mu_2 x_{4,0} - \xi x_{2,0} x_{4,0}]\,\mathrm{d}x,\\
&x_{5,1} = \int_0^t [\xi x_{2,0} x_{4,0} - \mu_2 x_{5,0}]\,\mathrm{d}x, \quad x_{1,2} = \int_0^t [-\mu_1 x_{1,1} - \alpha x_{1,0} s_{5,1} - \alpha x_{1,1} x_{5,0}]\,\mathrm{d}x,\\
&x_{2,2} = \int_0^t [\alpha x_{1,0} x_{5,1} + \alpha x_{1,1} x_{5,0} - \beta x_{2,1}]\,\mathrm{d}x, \quad x_{3,2} = \int_0^t [\gamma_1 x_{2,1} - \mu_1 x_{3,1}]\,\mathrm{d}x,\\
&x_{4,2} = \int_0^t [-\mu_2 x_{4,1} - \xi x_{2,0} x_{4,1} - \xi x_{2,1} x_{4,0}]\,\mathrm{d}x,\\
&x_{5,2} = \int_0^t [\xi x_{2,0} x_{4,1} + \xi x_{2,1} x_{4,0} - \mu_2 x_{5,1}]\,\mathrm{d}x,\\
&x_{1,3} = \int_0^t [-\mu_1 x_{1,2} - \alpha x_{1,0} x_{5,1} - \alpha x_{1,1} x_{5,1} - \alpha x_{1,1} x_{5,0}]\,\mathrm{d}x,\\
&x_{2,3} = \int_0^t [\alpha x_{1,0} x_{5,2} + \alpha x_{1,1} x_{5,1} + \alpha x_{1,2} x_{5,0} - \beta x_{2,2}]\,\mathrm{d}x, \quad x_{3,3} = \int_0^t [\gamma_1 x_{2,2} - \mu_1 x_{3,2}]\,\mathrm{d}x,\\
&x_{4,3} = \int_0^t [-\mu_2 x_{4,2} - \xi x_{2,0} x_{4,2} - \xi x_{2,1} x_{4,1} - \xi x_{2,2} x_{4,0}]\,\mathrm{d}s,\\
&x_{5,3} = \int_0^t [\xi x_{2,0} x_{4,2} + \xi x_{2,1} x_{4,1} + \xi x_{2,2} x_{4,0} - \mu_2 x_{5,2}]\,\mathrm{d}x.
\end{aligned}
$$

The parameter values are taken from [13], $k_1 = \frac{7675406}{7675893}$, $k_2 = \frac{487}{7675893}$, $k_3 = 0.0$, $k_4 = 0.944$, $k_5 = 0.056$ as well $\alpha = 0.2925$, $\beta = 0.328879$, $\gamma_1 = 0.328833$, $\xi = 0.375$ yields:
$x_{1,1} = -0.0163790t$, $x_{2,1} = 0.0163593t$, $x_{3,1} = 0.0000197t$, $x_{4,1} = 0.0017876t$, $x_{5,1} = -0.0017876t$, $x_{1,2} = 0.0003959t^2$, $x_{2,2} = -0.0030857t^2$, $x_{3,2} = 0.0026897t^2$, $x_{4,2} = -0.0029245t^2$, $x_{5,2} = 0.0029245t^2$, $x_{1,3} = -0.0002901t^3$, $x_{2,3} = 0.0006284t^3$, $x_{3,3} = -0.0003383t^3$, $x_{4,3} = 0.0003920t^3$, $x_{5,3} = -0.0003920t^3$.
The 4-term solution of HPM is

$$x_1(t) = 0.99994 - 0.0163790t + 0.0003959t^2 - 0.0002901t^3, \tag{5. 48}$$

$$x_2(t) = 0.00006 + 0.0163593t - 0.0030857t^2 + 0.0006284t^3, \tag{5. 49}$$

$$x_3(t) = 0.00 + 0.0000197t + 0.0026897t^2 - 0.0003383t^3,$$

$$x_4(t) = 0.944 + 0.0017876t - 0.0029245t^2 + 0.0003920t^3,$$

$$x_5(t) = 0.056 - 0.0017876t + 0.0029245t^2 - 0.0003920t^3. \tag{5. 50}$$

Here, we calculated the HPM up to 10th term in order to obtain a reliable solution.
In order to obtain numerical results, RK4 is employed to solve the non linear system of ODEs [4].

6. Numerical Test Problem

In this section, the proposed analytical and numerical schemes are applied to solve the model equations. The results are verified for two different models: (1) SI model, (2) SIR model including human and vector population. The results are compared with the exact solution owing to the availability of exact solution for simplified SI model equations. The solutions of the SIR model are validated with real time data of dengue cases in Lahore.

6.1. **Problem 1: SI model.** The purpose of this problem is to validate the results of our proposed HPM and RK4 techniques with the exact solution. The exact solution can only be attained for simplified model equations. Recently, Shabbir et. al [21] extracted the exact solution to the SIR model, which is a particular case of the model given by Kermack and Mekendrick. The model is as follows:

$$\begin{aligned} \frac{dS_1}{dt} &= \mu - \mu S_1 - \alpha S_1 I_1, \\ \frac{dI_1}{dt} &= \alpha S_1 I_1 - \mu I_1, \end{aligned} \tag{6. 51}$$

with the conditions $S_1(0) = S_{1_0}$, $I_1(0) = I_{1_0}$ and $S_1(t) + I_1(t) = N_1$.
The human population (N_1) is taken as constant and is divided into two categories: Susceptible (S_1) and Infected (I_1).
The exact solution of Eq. (6. 51) is given as:

$$\begin{aligned} S_1(t) &= 1 + (N-1)(1-\mu t) - \frac{w}{\alpha + \frac{\omega - \alpha I_0}{I_0 exp(\frac{\alpha(N-1)}{\mu})} exp(-\omega t \frac{\alpha(N-1)}{\mu})}, \\ I_1(t) &= \frac{w}{\alpha + \frac{\omega - \alpha I_0}{I_0 exp(\frac{\alpha(N-1)}{\mu})} exp(-\omega t \frac{\alpha(N-1)}{\mu})}, \ \ where \ \ w = \alpha N_1 - \mu. \end{aligned} \tag{6. 52}$$

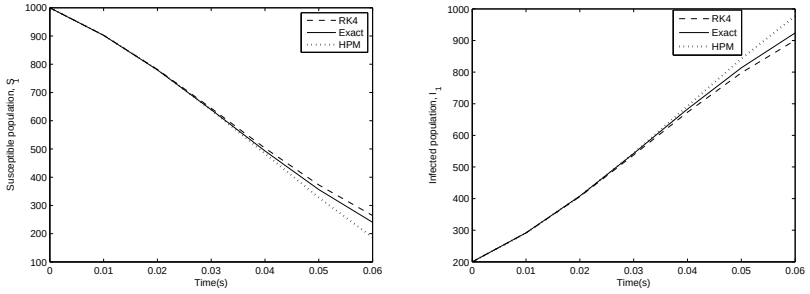


FIGURE 1. Comparison of exact solution with RK4 and HPM.

TABLE 2. Problem 1: Errors of HPM and RK method

t	Susceptive Human S_1		Infected Human I_1	
	$\lvert S_{1exact} - S_{1RK}\rvert$	$\lvert S_{1exact} - S_{1HPM}\rvert$	$\lvert I_{1exact} - I_{1RK}\rvert$	$\lvert I_{1exact} - I_{1HPM}\rvert$
0.10	4.0×10^{-4}	4.0×10^{-4}	4.0×10^{-4}	4.0×10^{-4}
0.015	1.8×10^{-3}	1.6×10^{-3}	1.7×10^{-3}	1.6×10^{-3}
0.020	4.6×10^{-3}	3.5×10^{-3}	4.4×10^{-3}	3.4×10^{-3}
0.025	9.2×10^{-3}	5.1×10^{-3}	8.9×10^{-3}	4.8×10^{-3}
0.030	1.6×10^{-2}	4.0×10^{-3}	1.5×10^{-1}	3.6×10^{-3}
0.035	2.5×10^{-2}	2.7×10^{-3}	2.4×10^{-2}	3.6×10^{-3}
0.040	3.6×10^{-2}	1.8×10^{-2}	3.5×10^{-2}	3.3×10^{-3}
0.045	5.0×10^{-2}	4.6×10^{-2}	4.9×10^{-2}	1.9×10^{-2}
0.050	6.5×10^{-2}	8.7×10^{-2}	6.4×10^{-2}	4.7×10^{-2}

The exact solution of SI model given in Eq. (6. 52) is compared with the solution obtained by using HPM and RK4 methods. The Matlab software is used to solve the above mentioned model.
The initial conditions, $S_{1_0} = 1000$, $I_{1_0} = 200$ and parameter values, $\alpha = 0.04$ and $\mu = 0.5$ are considered. The results are shown in Figure 1.
The solution of HPM is calculated up to the third term. Figure 1, depicts that solutions obtained by HPM and RK4 methods agree well with the exact solution, for step size $\triangle t = 0.03$. Numerical errors of both the methods are presented in Table 2. Therefore, it can be concluded that both methods produce reliable results to solve simplified non linear dynamical models.

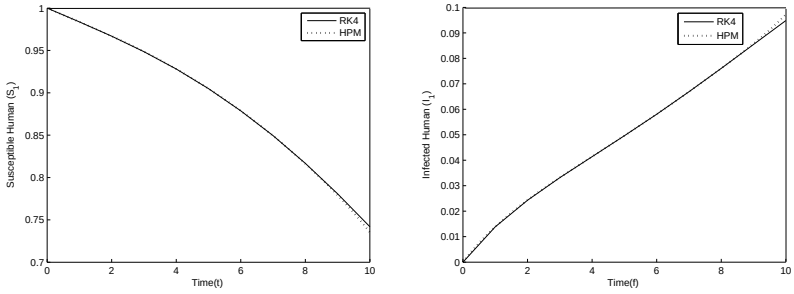
6.2. **Application of the model for Lahore.** Lahore is the capital of Punjab Province. It is Pakistan's second largest metropolitan and 16^{th} most populated city in the world. In July 2014, as per one estimation, the population of Lahore was around 7.566 million. Heavy summer monsoon rains in Punjab province provide suitable environment for the spread of dengue as vector population spreads fast in stationary waters. Annual average temperature during 2011 remained on higher side in most part of the country, which added to the spread of dengue (Climate of Pakistan, 2011). In this study, four years (2011 to 2014) data

of dengue disease has been obtained from District Health Office (DHO) Lahore. The parameter values for host population are extracted from the obtained data, while approximate parameter values are used for vector population.
The SIR model given in Eq. (2. 6) for Lahore is simulated by using RK4 with the conditions $S_1(0) = \frac{7566000}{7566000}$, $I_1(0) = 0$, $R_1(0) = 0$, $S_2(0) = 0.944$ and $I_2(0) = 0.056$, and the parameters $\mu_1 = 0.00004$, $b\beta_1 = 0.75$, $b\beta_2 = 0.375$, $\gamma_1 = 0.328833$ and $\mu_2 = 0.02941$.
The comparison of HPM and RK4 is shown in Figure 2. The solution of both methods shows good synchronization with each other. The solution obtained through HPM is acquired using 10th order polynomial to obtain reliable results. The higher accuracy can be achieved by increasing the order of polynomial in HPM. On the basis of results, it can be concluded that both techniques (HPM and RK4) produce reliable solutions and can be used to solve the nonlinear dynamical system to predict the behavior of infectious diseases. As a classical technique, the solution obtained through RK4 is taken as a benchmark to solve the models used for infectious diseases in the current research.
Figure 3 (Left) shows the number of dengue cases reported in Lahore while Figure 3 (Right) shows the results obtained by RK4. According to Figure 3 (Left), the number of dengue cases reach the highest level in 11 months. Figure 3 (Right), acquired by using the model Eq. (2. 6), depicts that the number of infected human population rises up to 11 percent of the total human population in 13 months. Moreover, the number of infected persons reduce after 20 months. The difference between real data and simulated results is because of the use of approximate parameter values. The simulated results further indicate that the humans are completely recovered in 38 months, that is consistent with the obtained data in Figure 3 (Left), as no dengue case is reported after these particular months. Moreover, the susceptible vector population initially starts decreasing and reach its lowest level where the infected mosquito population is on its peak and after that the susceptible population starts increasing. The number of infected mosquitoes takes 26 months to reach its highest value that is 47 percent of the mosquitoes' total population and it takes more than 60 months to reach its lowest level i.e. zero. It is important to mention that when the number of infected mosquitoes rises, the number of infected human beings also rises.
In SIR model, parameters can be acquired by two ways: 1) extracting from real time data 2) using parameter estimation methods. In this work, we obtained real time data of Lahore and used it in SIR model. Afterwards, we solved SIR model and predicted the situation of dengue spread in Lahore. The considered SIR model can be applied to analyze the transmission of dengue disease in other regions.

6.2.1. *Reproduction rate,* R_0. The reproduction rate (R_0) is used to measure the possible communication of a disease. The R_0 shows the number of infection among the humans as a result of infected mosquitoes [23]. It can be defined mathematically as

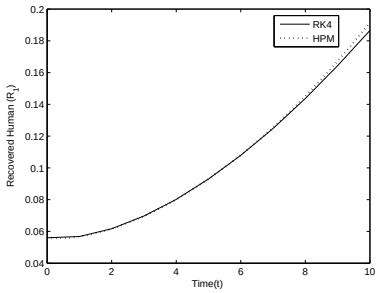
$$R_0 = \frac{b\beta_2 I_2/N_1}{\gamma_1} S_1(0).$$

If the value of R_0 is greater than 1 $(R_0 > 1)$, DF become epidemic [15].
The use of initial and parameter values from the data of dengue cases in Lahore can be rewritten in mathematical form as:
For Lahore, the value of R_0 is $\frac{b\beta_2 I_2/N_1}{\gamma_1} S_1(0) = 1.1375 I_2$.
For different values of I_2, the values of R_0 are given in Table 3. From Table 3, we find that

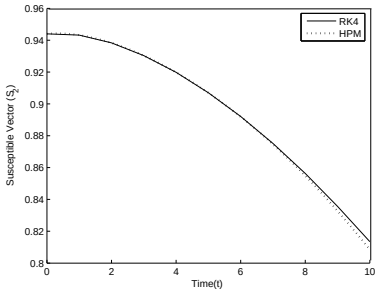


(A) Susceptible human population

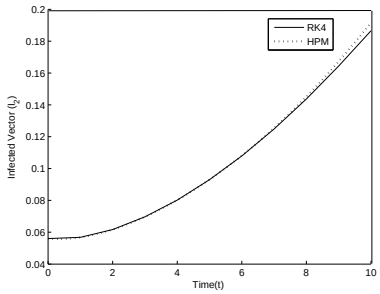
(B) Infected human population



(C) Recovered human population



(D) Susceptible vector population



(E) Infected vector population

FIGURE 2. Approximate Solution of SIR model using 10^{th} term HPM and RK4.

if the number of infected mosquitoes are less than one $(I_2 < 1)$, then $R_0 < 1$, and cases of dengue fever are not worrisome, since the obtained results show that dengue virus has no potential to infect healthy humans. The sketch of the dynamics for Lahore (Pakistan) is given in Figure 4 (upper figures). For $R_0 \leq 1$, Figure 4 (lower figures) depicts the typical behavior of the SIR model and shows the trivial state where the whole human population remains healthy. If the number of infected mosquitoes is more than one $(I_2 > 1)$, then

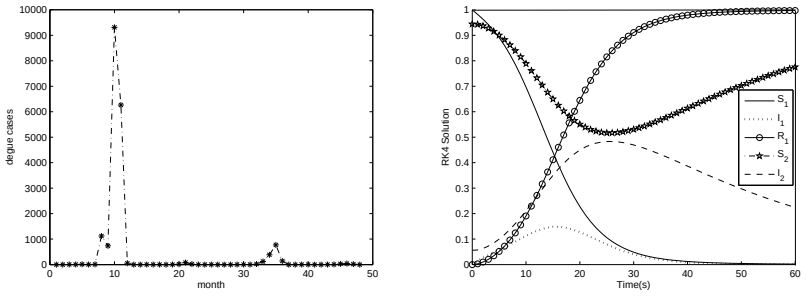


FIGURE 3. Left: Number of cases reported in Lahore, Pakistan, from 2011 to 2014, Right: DF For Lahore with initial conditions $S_1(0) = 1$, $I_1(0) = 0$, $R_1(0) = 0$, $S_2(0) = 0.944$ and $I_2(0) = 0.056$.

$R_0 > 1$ as indicated in Table 3. The results show that the infection rate is very high, and the transmission of dengue virus can infect more than one persons. Figure 4 (lower figures) shows the non-typical behavior and the number of infected human rises with the rise in infected mosquitoes.

I_2value	R_0 values
0.056	0.0637
0.1	0.11375
1	1.1375
5	5.6875

TABLE 3. Re-breeding value R_0 of infected mosquitoes.

6.2.2. *Parametric study of dengue cases.* Effects of different parameters are discussed in this subsection. In the numerical experiments, we change one parameter, while keeping all the other parameters fixed.
In Figure 5, the value of $b\beta_1$ is varied and all the others parameter values are kept fixed. The solution is found for three different values of human to vector contact rate i.e. $b\beta_1$ $(0.65, 0.75, 0.85)$. The variation of susceptible human, infected human and infected vectors population are shown in Figure 5. It is found that as the quantitative values of contact rate from vector to human increase, the number of infected human population also increases along with the increase in number of infected mosquitoes. The susceptible human population decreases more rapidly and approaches close to zero. The decrease in the value of contact rate from vector to human shows a decline in the number of infected human population due to less number of infected vector population. There also occurs a decrease in susceptible to infected human population. Figure 6, presents the results for different values of $b\beta_2$ $(0.3, 0.375, 0.46)$. The results show that when interaction between vector and human increases, the number of virus infected humans also increases. Moreover, the ratio of susceptible individuals also increases. When the value of contact rate (vector to human)

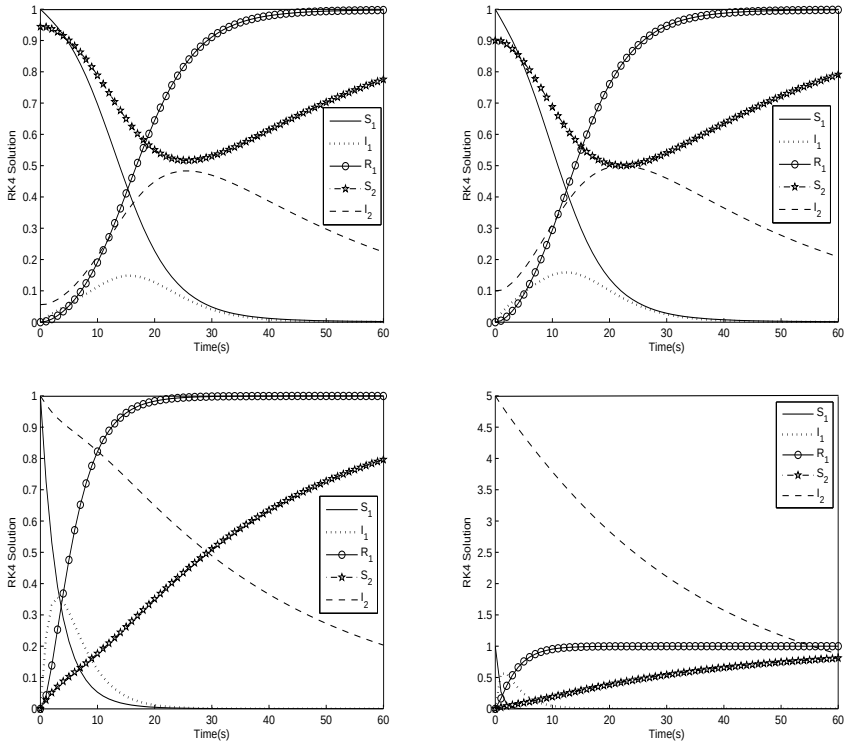


FIGURE 4. Upper figures: For $R_0 < 1$, Lower figures: For $R_0 > 1$.

decreases, the number of infected individuals also decreases. Similarly with the increase in the value of recovery rate γ, presented in Figure 7, the virus-infected human population and infected mosquito population will decrease. There is also a decrease in the number of susceptible individuals.

7. CONCLUSION

In this study, SIR model including human and vector population was solved analytically and numerically. The model contains system of coupled non-linear differential equations which incorporate the human population (Susceptible, Infected, and Recovered) and vector population (Susceptible and Infected) dynamics. HPM was applied to obtain analytical solution, whereas, RK4 was employed to acquire numerical solution. The results were validated with the available exact solution in the literature. Furthermore, HPM and RK4 were implemented to the considered model using the four years $(2011 - 2014)$ data of dengue cases in Lahore, Pakistan. Both schemes were found to be in agreement with available exact solution and real time data. HPM results approach to the exact solution by including higher order polynomials. Synchronization between the simulated results and the real time

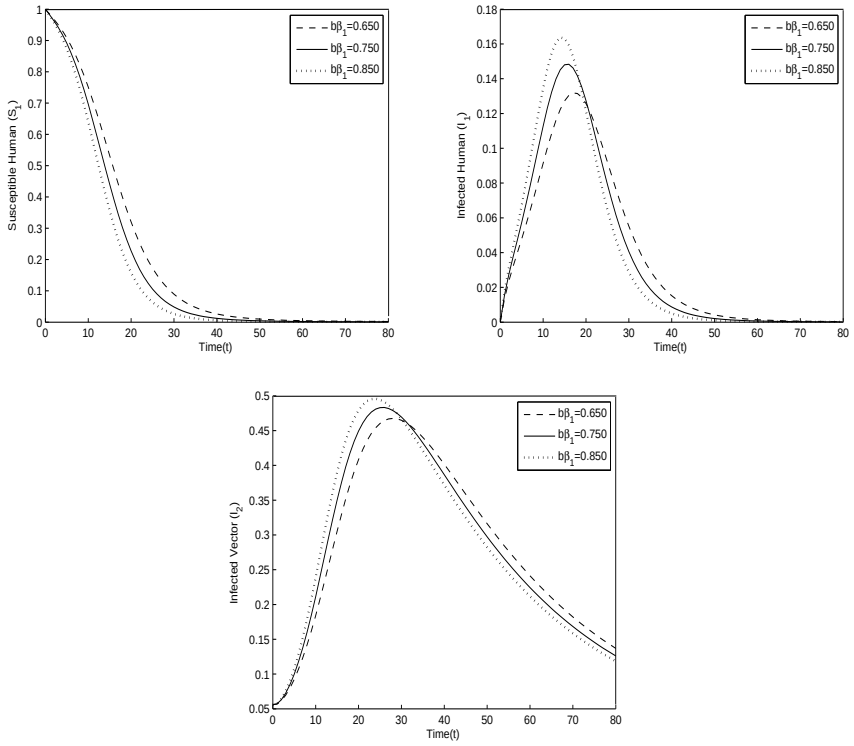


FIGURE 5. Variation of the susceptible human population, infected human population and infected vector population with time for different rate of contact, vector to human ($b\beta_1$), where other parameters are $\mu_1 = 0.000046$, $\mu_2 = 0.0323$, $b\beta_2 = 0.375$ and $\gamma_1 = 0.328833$.

data of dengue cases verified the correctness of model formulation. Furthermore, the parametric study was performed. The reproduction rate (R_0) results showed that dengue virus largely depends upon the infected mosquitoes which have the potential to infect healthy human population rapidly. The study recommends that serious measures should be taken for the reduction of mosquitoes' breeding. We also conclude that the considered SIR model can be applied to analyze the transmission of dengue disease in other regions.
Future researches may explore parameter estimation, inclusion of climate in the SIR model and solution of the optimal control problems to develop the control strategies for the elimination of dengue disease.

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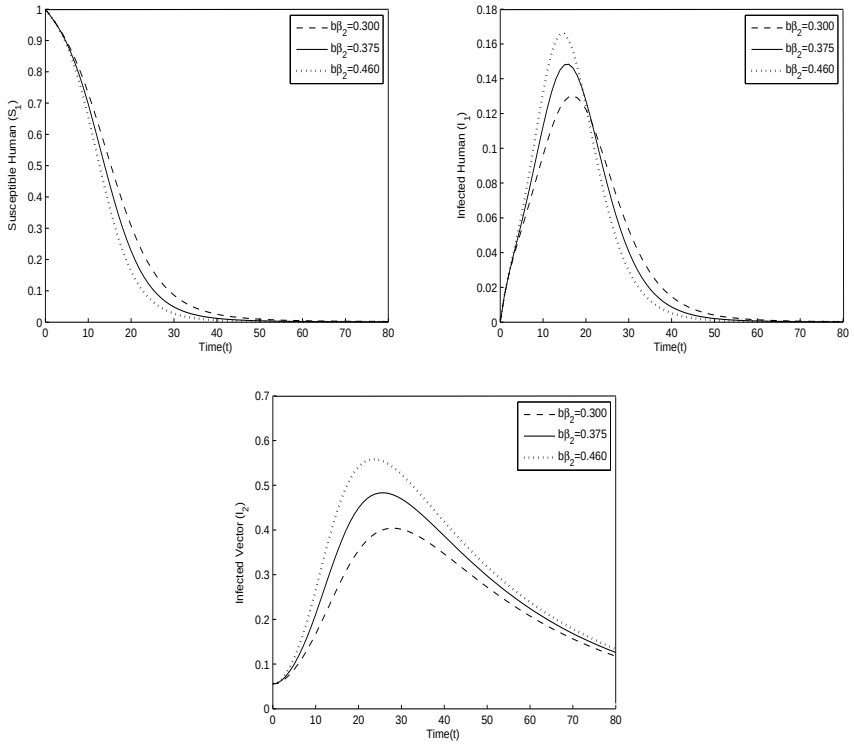

FIGURE 6. Variation of the susceptible human population, infected human population and infected vector population with time for different rate of contact, human to vector ($b\beta_2$), where other parameters are $\mu_1 = 0.000046$, $\mu_2 = 0.0323$, $b\beta_1 = 0.75$ and $\gamma_1 = 0.328833$.

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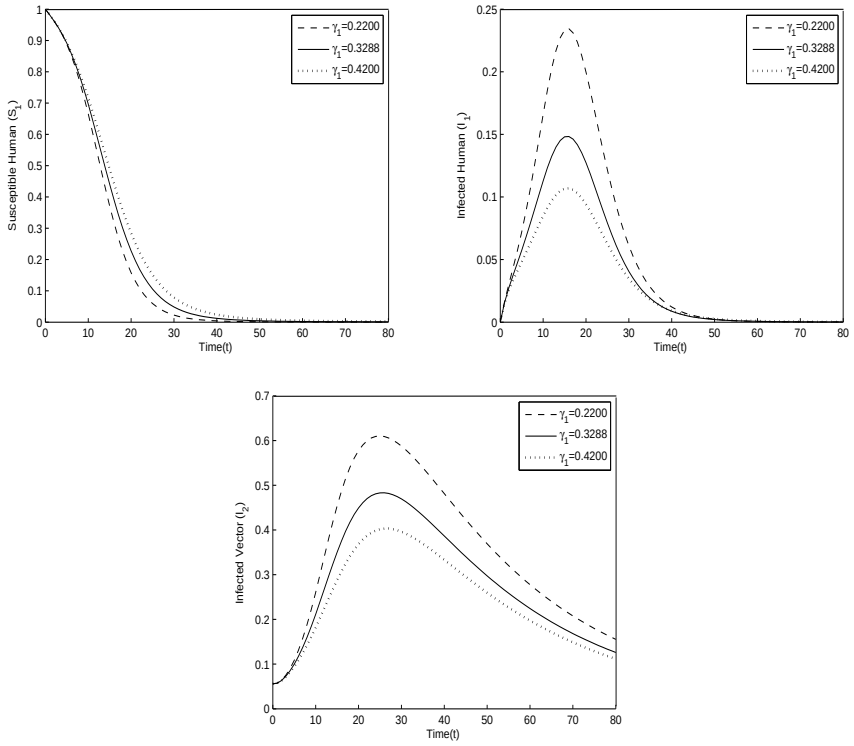

FIGURE 7. Variation of the susceptible human population, infected human population and infected vector population with time for different values of recovered rate (γ_1), where other parameters are $\mu_1 = 0.000046$, $\mu_2 = 0.0323$, $b\beta_1 = 0.75$ and $b\beta_2 = 0.375$.

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