I. J. Mathematical Sciences and Computing, **2024, 1, 19-30**
Published Online on February 8, 2024 by MECS Press (http://www.mecs-press.org/)
DOI: 10.5815/ijmsc.2024.01.03

Application of Mathematical Modeling: A Mathematical Model for Dengue Disease in Bangladesh

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Received: 12 October, 2023; Revised: 16 November, 2023; Accepted: 14 January, 2024; Published: 08 February, 2024

Abstract: A virus spread by mosquitoes called dengue fever affects millions of people each year and is a serious threat to world health. More than 140 nations are affected by the illness of dengue fever. Therefore, in this paper, a Susceptible-Infectious-Recovered (SIR) mathematical model for the host (human) and vector (dengue mosquitoes) has been presented to describe the transmission of dengue in Bangladesh. In the model the vector are related with two compartments that are susceptible and infective and host are related with three compartments that are susceptible, infective, and recovered. By these five compartments, five connected nonlinear ordinary differential equations (ODEs) are produced. As a result of non dimensionalization, a system of three nonlinear ODEs has been generated. The reproductive number and equilibrium points have been estimated for different cases. In order to compute the infection rate, data for infected human populations have been gathered from multiple health institutes in Bangladesh. MATLAB has been utilized to construct numerical simulations of different compartments in order to examine the impact of critical parameters on the disease's propagation and to bolster the analytical findings. The simulated outcomes for susceptible, infected, and eliminated in graphical formats have been displayed. The paper's main goal is to emphasize the uniqueness of computational analysis of the SIR mathematical model for the dengue fever.

Index Terms: Dengue Disease, Endemic Equilibrium, Mathematical Model, Reproduction Number, Numerical Simulations.

1. Introduction

In recent decades, infectious diseases have been the primary reason of the high mortality rate. As the twenty-first century began, a number of infectious diseases, such as hepatitis and dengue, spread quickly and killed more people in a number of developing countries. Dengue was initially reported in the Philippines in 1953 and Thailand in 1955. The spread of disease has accelerated recently as a result of climate change and a lack of public awareness. Dengue spreads annually in many tropical and subtropical areas, mainly during the rainy season when the Aede mosquito population is larger. Each year, dengue affects 50–390 million people worldwide and it results in about 25,000 fatalities. The advancement of medical knowledge allowed for the control of infectious diseases. It was anticipated that infectious diseases would vanish after the first half of the 20th century due to advancements in immunization, antibiotics, and improved living circumstances.

Understanding the dynamics of infectious illnesses and assessing control and containment measures need the use of mathematical models. According to their epidemiological status, the population can be categorized into three groups in epidemiological modeling: susceptible (S), infectious (I), and recovered (R). The SI (susceptible-infected), SIS (susceptible-infected-susceptible), and SIR (susceptible-infected-recovered) models are important frameworks in epidemiology that are used to quantitatively describe the spread of infectious illnesses within a community. These models shed light on how illnesses spread, how they endure or disappear, and how treatments might alter their course. Public health responses to illnesses like influenza, HIV/AIDS, dengue and most recently, the COVID-19 pandemic, have all benefited from the use of these models. Researchers can gain a better understanding of elements like disease transmission rates, the effects of vaccination, and the possibility for herd immunity by examining the behavior of these models.

There are differing viewpoints on the use of the mathematical modeling to make executive decisions in various diseases. The previously published papers or articles on a subject provide a useful orientation for the realizing of problems, background for the selection of procedures and data type for the interpretation of the results. In [1], optimal control of SIS and SIR information epidemics has been investigated. The author in [2], proposed how the basic SIR transmission model is analyzed. Also, described a variety of applications, both standard and novel to demonstrate the significance of this method. Matthias *et al*. [3] proposed a model, which describes vaccination and fading immunity, and offered a finite difference strategy for solving it, along with some qualitative results. In [4], the authors described the SIR epidemic model with three components; S, I and R as well as the stability analysis theory to discover the model's equilibrium. An optimal control for a SIR model governed by an ODE system with time delay has been proposed by Moussa *et al*. [5]. In [6, 7, 8, 9], the authors have demonstrated the analytical and numerical solutions of dynamic models for dengue disease. In communicable disease modeling the incidence rate plays a vital role to describe the number of infection per unit time and by which the model gives a qualitative description of the disease dynamics. Treatment is significant in every infectious disease for the infected population to become recovered. Usually, the treatment rate is considered to be proportional to the number of infective individuals [10, 11, 12].

The authors in [13, 14, 15], have used the SIR model for the study of the dynamics of dengue in several countries. The acute phase of the disease lasts 3 to 7 days [16]. After the mosquito consumes contaminated blood, there is an 8–14 day period known as the extrinsic incubation period. The life of a mosquito is infectious [16]. Dengue is a year-round disease with a cyclical distribution pattern in endemic tropical regions. Although the exact causes of dengue have not been explained, the disease's severity is linked to secondary infections [17, 18]. In order to establish strategies for prevention, control, and collaborative treatments, it is imperative to comprehend the disease's dynamics and how it spreads and persists. Numerous models for dengue fever have been proposed in the literature, such as [19, 20, 21, 22, 23], which examine various facets of the disease's behavior and dissemination. A multi-risk SIR model (MR-SIR) where infection, hospitalization and fatality rates vary between groups—in particular between the "young", "the middle-aged" and the "old" has been developed by Acemoglu *et al*. [24]. Several mathematical approaches to study the dengue transmission dynamics which include an age structure in human population have been presented in [25, 26, 27, 28]. On the other hand, in [29], the authors have studied a mathematical modeling and analysis of dengue transmission in Bangladesh with saturated incidence rate and constant treatment function. Syafruddin and Noorani in [30] described the SIR model for spread of dengue fever disease simulated for south Sulawesi, Indonesia and Selangor, Malaysia.

The purpose of this work is to solve the dynamical models for dengue disease and validate through real time data of Dhaka, Bangladesh. 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. Numerical case studies are presented to validate the analytical and numerical results. The parametric study is also performed.

The paper is organized as follows: In section 2, the formulation of the model has been described. SIR model due to KERMACK and MCKENDRICK has been discussed in 2.1. In section 2.2, SIR model for dengue fever disease with model parameters are briefly described. Section 2.3 presents the stability analysis. Descriptions of data for infective population and numerical simulations have been shown in section 3. Finally, a general conclusion has been drawn in section 4.

2. Model Formulation

In this section, we offer mathematical theories that will be useful in resolving the endemic stability of dengue illness.

2.1. SIR Model Due to Kermack and Mckendrick

In this section, a basic SIR Model (Kermack&McKendrick 1927) has been considered. It is used to simulate an outbreak of a variety of infectious diseases in a large population. The population is made up of three categories of people, designated by the letters *S, I* and *R*. All of these are the functions of time t.

Susceptible → Infected → Removed

- *S* stands for susceptibles, or those who are not currently infected but have the potential to get sick

- ϕ represents the infection rate.. Susceptibles interact with the infective, thus becoming infected.
- I stands for infectious number. These people are carriers of the disease and can infect others who are susceptible
- η expressed as the recovery rate. Infected individuals become recovered.
- R is the number of people eliminated.

Becoming infected depends on contact between susceptible and infected. New infections occur as a result of a contact between infective and susceptible. In this model, the rate at which new infections occur is (ϕSI) for some positive constant ϕ (infection rate). When a new illness occurs, the afflicted person passes from the susceptible to the infective class. There is no alternative mechanism for individuals to enter or leave the vulnerable class in this approach. The other procedure involves the removal of infective people to the removed class. Assuming that, this happens at the rate (ηI) for some positive constant η (recovery rate).

$$\frac{dS}{dt} = -\frac{\phi SI}{N}$$
$$\frac{dI}{dt} = \frac{\phi SI}{N} - \eta I$$
$$\frac{dR}{dt} = \eta I$$

This model assumes that the population as a whole is constant. It consists of all susceptible, infected, and recovered individuals.

Total population $N = (S + I + R) \Rightarrow \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \Rightarrow \frac{dN}{dt} = 0 \ \therefore N$ is constant

• If we consider there are 0 infective, that is $I = 0$ then $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$. This implies that nothing changes, so we must have some infectives.

Since $N = S + I + R$, then $R = N - S - I$. Therefore, based on the basic SIR Model of three ordinary differential equations, (1), (2) and (1), two coupled ordinary differential equations have been constructed.

$$\frac{dS}{dt} = -\frac{\phi SI}{N} = 0$$
$$\frac{dI}{dt} = I\left(\frac{\phi S}{N} - \eta\right) = 0$$

To find two possible equilibrium points. This yield $S = 0$ or $I = 0$
Therefore, the equilibrium point is $(S^*, I^*, R^*) = (S, 0, N - S)$

- If S is 0, then$(S^*, I^*, R^*) = (0, 0, N)$. This means that all susceptible individuals have been eliminated at this equilibrium point.
- If $S = N$, then$(S^*, I^*, R^*) = (N, 0, 0)$. This equilibrium point means that there no infection. There is no disease in the whole population.
- If $S \neq N$, then$(S^*, I^*, R^*) = (S, 0, N - S)$. This equilibrium point means that the infected diminish in a number of quantities.

There are three equilibrium points. For each of those equilibrium points, to ascertain the stability using the Jacobian method, assuming

$$U = \frac{dS}{dt} = -\frac{\phi SI}{N} \quad (1)$$

$$V = \frac{dI}{dt} = \frac{\phi SI}{N} - \eta I \quad (2)$$

$$W = \frac{dR}{dt} = \eta I \quad (3)$$

The corresponding Jacobian is

$$\begin{pmatrix} \frac{dU}{dS} & \frac{dU}{dI} & \frac{dU}{dR} \\ \frac{dV}{dS} & \frac{dV}{dI} & \frac{dV}{dR} \\ \frac{dW}{dS} & \frac{dW}{dI} & \frac{dW}{dR} \end{pmatrix} = \begin{pmatrix} \frac{\phi I}{N} & \frac{-\phi S}{N} & 0 \\ \frac{\phi I}{N} & \frac{\phi S}{N} - \eta & 0 \\ 0 & \eta & 0 \end{pmatrix}$$

Now, consider the equilibrium point $\left(S^*, I^*, R^*\right) = \left(0, 0, N\right)$. The corresponding eigenvalues are:

$$\left.\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= -\eta \end{aligned}\right\} \tag{4}$$

Again, for the equilibrium point $(S^*, I^*, R^*) = (0, 0, N)$, corresponding eigenvalues are:

$$\left.\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= \phi - \eta \end{aligned}\right\} \tag{5}$$

Again, for the equilibrium point $(S^*, I^*, R^*) = (S, 0, N - S)$, corresponding eigenvalues are:

$$\left.\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= \frac{\phi S}{N} - \eta \end{aligned}\right\} \tag{6}$$

Basic Reproductive Number R_0

R_0 is defined as the ratio of the infection rate as follows

$$R_0 = \frac{\phi}{\eta} \tag{7}$$

Now, we will see how this reproductive number affects in the model. We will analyze the rate of infection. Equation (2) becomes,

$$\frac{dI}{dt} = \frac{\phi SI}{N} - \eta I = I\left(\frac{\phi S}{N} - \eta\right)$$

Since $I \to 0 \Rightarrow S \to N$, we obtain

$$\frac{dI}{dt} = (\phi - \eta) I$$

Let, $r = \phi - \eta$ which yields $r = \eta(R_0 - 1)$

$$\frac{dI}{dt} = rI \Rightarrow I = e^{rt}k \tag{8}$$

where k is a constant

We can draw the following conclusions from the solution:

- If $R_0 < 1$, then $r < 0$. As a result, the infection declines.
- If $R_0 > 1$, then $r > 0$. As a result, the infection spreads.
- If $R_0 = 1$, then $r = 0$. As a result, the infection never goes away.

Moreover, we can establish a threshold behavior based on R_0 in the manner described below:

- If $R_0 < 1$, then the epidemic does not exist.
- If $R_0 > 1$, then an epidemic occurs.
- If $R_0 = 1$, then nothing has changed.

2.2. SIR Model for Dengue Fever Disease

Although the SIR model is used to determine the stability of a disease in humans, it may also be employed on vectors. Because humans contract the dengue virus through the bite of a mosquito (b). This effect should be reflected in the SIR model. However, we shall overlook the mosquito's recovery rate because mosquitos have a short life span. N_h represents the whole human population, which includes susceptible, infected, and removed individuals (S_h, I_h, R_h). N_v represents the overall vector population, consisting of mosquitoes that are both susceptible and infected (S_v, I_v). In this model, N_h and N_v are assumed to be constants. As a result, take the entire population birth rate as $(\psi_k N_k)$ such that k is either v (vectors) or h (host), σ_k is the death rate. Furthermore, we may begin to see what occurs in category S_h, such that $\left(\frac{\phi_h b I_v}{N_h}\right)$ represents the likelihood of a susceptible host being infected by the virus. As a result, an infected mosquito I_v— interaction between an infected person and a mosquito ϕ_h from biting the human, b —tells us that these interactions to a susceptible $\left(\frac{\phi_h b}{N_h} I_v S_h\right)$— concludes a drop in the rate of susceptible $\frac{d}{dt}(S_h)$. Furthermore, the death of susceptibility reduces it, which is indicated as $\sigma_h S_h$. Going further, the rate of infected individuals $\frac{d}{dt}(I_h)$ (respect to time) decreases by the death of an infected person $\sigma_h I_h$ and the recovery of an infected person $\eta_h I_h$ such that η_h is denoted as the recovery parameter. However, the recovery rate $\frac{d}{dt}(R_h)$ (respect to time) is only decreased by the death of the recovery $\sigma_h R_h$ indicating that it is only enhanced by $\eta_h I_h$. As a result, the model of this interaction is represented by three differential equations.

$$\frac{d}{dt} S_h = \psi_h N_h - \frac{\phi b}{N_h} I_v S_h - \sigma_h S_h \tag{9}$$

$$\frac{d}{dt} I_h = \frac{\phi b}{N_h} I_v S_h - (\sigma_h + \eta_h) I_h \tag{10}$$

$$\frac{d}{dt} R_h = \eta_h I_h - \sigma_h R_h \tag{11}$$

Now, we will discuss the vector model, which will discuss the rate of susceptible and infected vectors. Category S_v, such that $\left(\frac{\phi_v b I_h}{N_h}\right)$ signifies the likelihood of a susceptible mosquito being infected by the virus. Therefore, an infected human I_h —interaction from a mosquito to an infected human β_v from a bite b —tells us that these interactions to a susceptible $\left(\frac{\phi_v b}{N_h} I_h S_v\right)$ — concludes a drop in the rate of susceptible $\frac{d}{dt}(S_v)$. As well, death of a susceptible will decrease it which is denoted as $(\sigma_v S_v)$. Going further, the rate of infected mosquitoes $\frac{d}{dt}(I_v)$ (respect to time) decreases by the death of an infected mosquito $(\sigma_v S_v)$ and we stated earlier that a recovery parameter is not included.

Consequently, two differential equations serve as a representation of the interaction model.

$$\frac{d}{dt} S_v = \psi_v N_v - \frac{\phi_v b}{N_h} I_h S_v - \sigma_v S_v \tag{12}$$

$$\frac{d}{dt} I_v = \frac{\phi_v b}{N_h} I_h S_v - \sigma_v I_v \tag{13}$$

- N_h is the entire population of humans.
- S_h is the quantity of susceptible humans who are not currently ill but could contract the disease.
- I_h is the number of human infectives. They can spread the illness to mosquitoes because they are infected.
- R_h is the number of human removed individuals. These people are incapable of becoming infected or infecting others, regardless of whether they have the disease or not. It's possible that they have a built-in immunity, that they overcame the illness and are safe from getting it again, that they have the illness but are unable to spread it because of their isolation, or that they have passed away. These options are not distinguished by the mathematical model.
- ψ_h is the rate of human births. The entire population N_h is impacted by this parameter.
- σ_h is the rate of human deaths. S_h, I_h and R_h is impacted by this parameter.
- ϕ_h is the rate of human infections.
- η_h is the rate of human recoveries.
- N_v is the entire population of mosquitoes.
- S_v is the quantity of mosquitoes that may become infected but are not currently infected.
- I_v is the quantity of mosquitoes carrying the virus. These mosquitoes are carriers of the disease and can infect humans.
- ϕ_v is the rate of mosquitoes infections.
- σ_v is the rate of mosquitoes deaths.
- ψ_v is the rate of mosquitoes births. The entire population N_v is impacted by this parameter.
- b is the typical amount of mosquito bites.

Assume that $\sigma_k = \psi_k, \sigma_h = \psi_h, \sigma_v = \psi_v$, therefore we have these two models as follows:
for the human population,

$$\frac{d}{dt}S_h = \psi_h N_h - \frac{\phi_h b}{N_h} I_v S_h - \psi_h S_h \tag{14}$$

$$\frac{d}{dt}I_h = \frac{\phi_h b}{N_h} I_v S_h - (\psi_h + \eta_h) I_h \tag{15}$$

$$\frac{d}{dt}R_h = \eta_h I_h - \psi_h R_h \tag{16}$$

for the vector population,

$$\frac{d}{dt}S_v = \psi_v N_v - \frac{\phi_v b}{N_h} I_h S_v - \psi_v S_v \tag{17}$$

$$\frac{d}{dt}I_v = \frac{\phi_v b}{N_h} I_h S_v - \psi_v I_v \tag{18}$$

with the conditions,

$$S_h + I_h + R_h = N_h \Rightarrow R_h = N_h - S_h - I_h \tag{19}$$

$$S_v + I_v = N_v = \frac{A}{\mu_v} \Rightarrow S_v = N_v - I_v = \frac{A}{\mu_v} - S_v \tag{20}$$

Applying equation (19) into equation (11)

$$\begin{gathered}\frac{d}{dt}R_h = \eta_h I_h - \psi_h R_h, \text{ as } \sigma_h = \psi_h \\ \Rightarrow \frac{d}{dt}(N_h - S_h - I_h) = \eta_h I_h - \psi_h (N_h - S_h - I_h) \\ \Rightarrow 0 - \frac{dS_h}{dt} - \frac{dI_h}{dt} = \eta_h I_h - \psi_h N_h + \psi_h S_h + \psi_h I_h\end{gathered}$$

$$\Rightarrow -\frac{dI_h}{dt} = \eta_h I_h - \psi_h N_h + \psi_h S_h + \psi_h I_h + \frac{dS_h}{dt}$$
$$\Rightarrow -\frac{dI_h}{dt} = \eta_h I_h - \psi_h N_h + \psi_h S_h + \psi_h I_h + \psi_h N_h - \frac{\phi_h b}{N_h} I_v S_h - \psi_h S_h \text{ [using(14)]}$$
$$\Rightarrow -\frac{dI_h}{dt} = \eta_h I_h + \psi_h I_h - \frac{\phi_h b}{N_h} I_v S_h$$
$$\Rightarrow \frac{dI_h}{dt} = -\eta_h I_h - \psi_h I_h + \frac{\phi_h b}{N_h} I_v S_h$$

Applying equation (20) into equation (12)

$$\frac{d}{dt} S_v = \psi_v N_v - \frac{\phi_v b}{N_h} I_h S_v - \sigma_v S_v$$
$$\Rightarrow \frac{d}{dt}(N_v - I_v) = \psi_v N_v - \frac{\phi_v b}{N_h} I_h S_v - \sigma_v (N_v - I_v)$$
$$\Rightarrow 0 - \frac{dI_v}{dt} = -\frac{\phi_v b}{N_h} I_h S_v + \psi_v I_v, \text{ as } \sigma_v = \psi_v$$
$$\Rightarrow \frac{dI_v}{dt} = \frac{\phi_v b}{N_h} I_h S_v - \mu_v I_v$$

As a result, these two equations tell us that our conditions can be expressed as,

$$\frac{d}{dt} S_h = \psi_h N_h - \frac{\phi_h b}{N_h} I_v S_h - \psi_h S_h \tag{21}$$

$$\frac{d}{dt} I_h = \frac{\phi_h b}{N_h} I_v S_h - (\psi_h + \eta_h) I_h \tag{22}$$

$$\frac{d}{dt} I_v = \frac{\phi_v b}{N_h} I_h S_v - \psi_v I_v \tag{23}$$

The model given in equations (21), (22) and (23) can be simplified by the following fractional assumptions:

$$x(t) = \frac{S_h}{N_h},\ y(t) = \frac{I_h}{N_h},\ z(t) = \frac{I_v}{N_v}$$

Consequently, the following represents the population of humans and vectors:

$$\begin{aligned} \frac{dx}{dt} &= \psi\big(1 - x(t)\big) - \sigma x(t) z(t) \\ \frac{dy}{dt} &= \sigma x(t) z(t) - \phi y(t) \\ \frac{dz}{dt} &= y(t)\eta\,(1 - z(t)) - \xi z(t) \end{aligned} \tag{24}$$

where $\sigma = \frac{b\phi_h N_v}{N_h}$, $\phi = (\psi_h + \eta_h)$, $\eta = b\phi_v$ and $\xi = \psi_v$

2.3. Stability Analysis

The equilibrium points satisfy the following relations:

$$\frac{dx}{dt} = \frac{dy}{dt} = \frac{dz}{dt} = 0 \tag{25}$$

Putting equation (24) into equation (25) yields,

$$\begin{aligned} \frac{dx}{dt} &= \psi(1 - x(t)) - \sigma x(t) x(t) = 0 \\ \frac{dy}{dt} &= \sigma x(t) z(t) - \phi y(t) = 0 \\ \frac{dz}{dt} &= y(t)\eta\,(1 - z(t)) - \xi z(t) = 0 \end{aligned} \tag{26}$$

Thus two equilibrium points are $(1,0,0)$ and (x_0, y_0, z_0),where

$$x_0 = \frac{\psi\eta + \phi\xi}{\eta(\psi + \sigma)}$$

$$y_0 = \frac{\psi(\eta\sigma - \phi\xi)}{\phi\eta(\psi + \sigma)}$$
$$z_0 = \frac{\psi(\eta\sigma - \phi\xi)}{\sigma(\eta\psi + \phi\xi)}$$

To find the variational matrix we linearize the system given in equation (24), we get the following Jacobian matrix:

$$J(x,y,z) = \begin{pmatrix} -\psi - \sigma z & 0 & -\sigma x \\ \sigma z & -\phi & \sigma x \\ 0 & \eta - z\eta & -\eta y - \xi \end{pmatrix} \tag{27}$$

So, at the first equilibrium point (1,0,0), we obtain

$$J(1,0,0) = \begin{pmatrix} -\psi & 0 & -\sigma \\ 0 & -\phi & \sigma \\ 0 & \eta & -\xi \end{pmatrix} \tag{28}$$

Equation (28) leads to the following characteristic equation.

$$\Rightarrow (-\psi - \lambda)(-\sigma\eta + \phi\xi + \phi\lambda + \xi\lambda + \lambda^2) = 0 \tag{29}$$

The eigenvalues for equation (29) are as follows,

$$\lambda_1 = -\psi$$
$$\lambda_2 = \tfrac{1}{2}(-\phi - \xi - \sqrt{4\sigma\eta + \phi^2 - 2\phi\xi + \xi}$$
$$\lambda_3 = \tfrac{1}{2}(-\phi - \xi + \sqrt{4\sigma\eta + \phi^2 - 2\phi\xi + \xi}$$

We have λ_1 and λ_2 are always negative, because $\psi, \sigma, \phi, \xi, \eta$ are always positive. λ_3 can be either positive or negative.

At the equilibrium point (x_0, y_0, z_0),we have

$$J(x_0,y_0,z_0) = \begin{pmatrix} -\psi - \sigma\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) & 0 & -\sigma\left(\frac{\psi\eta+\phi\xi}{\eta(\psi+\sigma)}\right) \\ \sigma\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) & -\phi & \sigma\left(\frac{\psi\eta+\phi\xi}{\eta(\psi+\sigma)}\right) \\ 0 & \eta - \eta\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) & -\eta\left(\frac{\psi(\eta\sigma-\phi\xi)}{\phi\eta(\psi+\sigma)}\right) - \xi \end{pmatrix}$$

To find the eigenvalues, we set

$$\det\begin{pmatrix} -\psi - \sigma\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) - \lambda & 0 & -\sigma\left(\frac{\psi\eta+\phi\xi}{\eta(\psi+\sigma)}\right) \\ \sigma\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) & -\phi - \lambda & \sigma\left(\frac{\psi\eta+\phi\xi}{\eta(\psi+\sigma)}\right) \\ 0 & \eta - \eta\left(\frac{\psi(\eta\sigma-\phi\xi)}{\sigma(\eta\psi+\phi\xi)}\right) & -\eta\left(\frac{\psi(\eta\sigma-\phi\xi)}{\phi\eta(\psi+\sigma)}\right) - \xi - \lambda \end{pmatrix} = 0 \tag{30}$$

By using computer simulation, we may discover the eigen-values. A decent tool for this is MAPLE. However, if we have a look at some numerical values for the parameters, it becomes simpler to establish the stability.

Reproduction Number R_0

Only when the equilibrium point (x_0, y_0, z_0) is positive does it make sense. It is predicated on a threshold value. Therefore, the threshold parameter is $R = \frac{\sigma\eta}{\xi\phi}$, as a result, the reproduction number is indicated as:

$$R_o = \sqrt{R} \tag{31}$$

3. Numerical Simulations

In this section, the proposed analytical and numerical schemes are applied to solve the model equations. The results are verified for SIR model including human and vector population. The solutions of the SIR model are validated with real time data of dengue cases in Dhaka, Bangladesh. In order to perform the numerical simulations, the data of infected human due to dengue have been collected from Institute of Epidemiology Disease Control and Research (IEDCR), and from Directorate General of Health Services, Bangladesh.

Table 1 summarizes the values of the parameters needed to run the numerical simulations. Due to the large number of mosquitoes involved and the lack of accurate data on the population, we have assumed that the rate of mosquito infection is twice that of human infection.

Table 1. Parameter values

Name of the Parameter	Notation	Base Value
Possibility of vector transmission to host	ϕ_v	0.5
Probability of host-to-vector transmission	ϕ_h	0.5
Daily bites per susceptible mosquito	b_s	0.25
Daily bites per infected mosquito	b_i	1.0
Rate of Contact, Host to Vector	C_{hv}	0.5
Rate of Contact, Vector to Host	C_{vh}	0.5
Human Life Span	$\frac{1}{\psi_h}$	HL
Vector Life Span	$\frac{1}{\psi_v}$	VL
Host Infection Duration	$\frac{1}{\psi_h + \eta_h}$	5.0 Days

3.1. Application of The Model for Dhaka

Dhaka is the capital of Bangladesh. It is Bangladesh's largest metropolitan and 7th most populated city in the world. In July 2023, as per estimation, the population of Dhaka was around 10 million. Heavy summer monsoon rains in Dhaka province provide suitable environment for the spread of dengue as vector population spreads fast in stationary waters. We choose or find the life spans HL and VL in resources. Therefore, HL = 26,250 days and VL = 10 days.

Thus the equilibrium points are:

$$(S_h, I_h, R_h) = (1,0,0) \text{ and } (S_h, I_h, R_h) = (0.8001518, 0.0003797, 0.0001898)$$

Now, we need to calculate the eigen-values for the equilibrium point $(1,0,0)$.

Using MAPLE software, we get the eigen-values for the equilibrium point $(1,0,0)$ are:

$\lambda_1 = -0.315831,\ \lambda_2 = -0.000038$ and $\lambda_3 = 0.0158312$

As one of the eigenvalues at the equilibrium point $(S_h, I_h, R_h) = (1,0,0)$ is positive, so the equilibrium point is a saddle point. The human population is free of dengue disease since 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.

Using MAPLE software, we get the eigen-values for the equilibrium point $(0.8001518, 0.0003797, 0.0001898)$ are:

$$\lambda_1 = -0.300033, \lambda_2 = -0.000101511 - 0.00054443i \text{ and } \lambda_3 = -0.000101511 + 0.00054443i.$$

The eigenvalues are all negative and complex, so the equilibrium point is asymptotically stable and there would occur some cases of dengue fever. Also from equation (31) we get, $R_0 = \sqrt{R} = \sqrt{\frac{\sigma\eta}{\xi\phi}} = \sqrt{\frac{0.05\times0.5}{0.1\times0.2}} = 1.1180$, which is greater than 1.

We will now generate the following case using these parameters.

Let us consider some initial data. Suppose we have $S_h(0) = 72000,\ I_h(0) = 36500,\ R_h(0) = 0$, and $S_v(0) = 100000,\ I_v(0) = 50000$ [31, 32].

Figure 1 shows the number of dengue cases reported in Dhaka. According to figure 1, it is observed that a considerable number of people will recover over time. Days are used to measure time. As a result, it will take around 90 days for the number of infected people to reach zero, and nearly 100 days for the number of infected mosquitos to reach zero. Despite this, we can see that some susceptible persons will not have the sickness by day 100 since there are no more infected mosquitos. As a result, it remains unaltered for susceptible and recoverable in day 100, which sounds reasonable.

In this work, we obtained real time data of Dhaka and used it in SIR model. Afterwards, we solved SIR model and predicted the situation of dengue spread in Dhaka. The considered SIR model can be applied to analyze the transmission of dengue disease in other regions.

3.2. 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 [20]. From equation (31) we get, $R_0 = \sqrt{R} = \sqrt{\frac{\sigma\eta}{\xi\phi}} = \sqrt{\frac{0.05\times 0.5}{0.1\times 0.2}} = 1.1180,$ which is greater than 1. The unstable situation, so there is an endemic. This means that the infection rate is very high, and the transmission of dengue virus can infect more than one person. That is the number of infected human rises with the rise in infected mosquitoes.

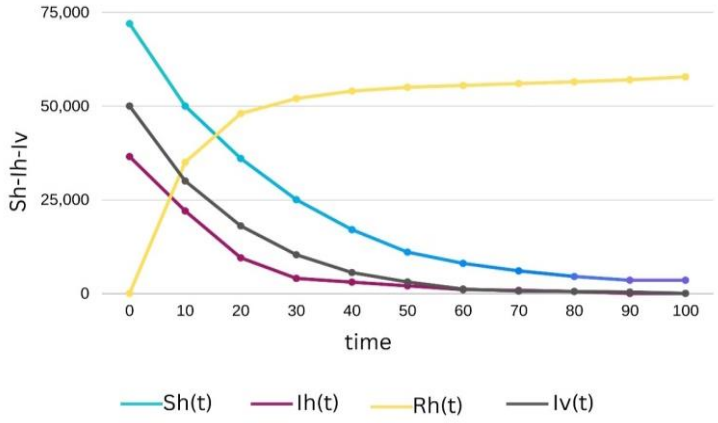

Fig.1. Graphical transmission about suspected, infected, recovered of human population

4. Conclusion

The SIR model with a human and vector population was solved analytically and numerically in this work. A system of coupled non-linear differential equations makes up the model that incorporates the dynamics of the vector population (Susceptible and Infected) and human population (Susceptible, Infected, and recovered). As demonstrated by the findings, the dengue virus is primarily dependent on infected mosquitoes, which have the capacity to spread quickly to a healthy human population. It is significant to note that as the number of infected mosquitoes increases, so does the number of infected humans. The study suggests that significant steps be taken to reduce mosquito reproduction. We considered equilibrium points to analysis stability of the infectious disease dengue. We also draw the conclusion that the SIR model under consideration is applicable for analyzing dengue disease transmission in different areas.

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How to cite this paper: Nazrul Islam, J. R. M. Borhan, Rayhan Prodhan, "Application of Mathematical Modeling: A Mathematical Model for Dengue Disease in Bangladesh", International Journal of Mathematical Sciences and Computing(IJMSC), Vol.10, No.1, pp. 19-30, 2024. DOI: 10.5815/ijmsc.2024.01.03