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Computational analysis of the sir mathematical model for the dengue fever

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COMPUTATIONAL ANALYSIS OF THE SIR MATHEMATICAL MODEL FOR THE DENGUE FEVER

A Thesis

by

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ABSTRACT

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Dengue fever is a disease affecting people in more than 100 countries. Here we consider a host and vector model for the transmission of dengue fever. This SIR model consists of three compartments of susceptible, infective and removed for host (human) and two compartments of susceptible and infective for vector (dengue mosquitoes). These five compartments yield five coupled nonlinear ordinary differential equations (ODEs). After non-dimensionalization, we have a system of three nonlinear ODEs. Reproductive number and two equilibrium points are calculated for various cases. Simulation is carried out for susceptible, infective and removed and the results are presented in graphical forms for various scenarios.

DEDICATION

This thesis is dedicated to my family. My parents, Margarita Diaz and Jose de Jesus Diaz, my many thanks for their love as great parents. As well, my sister who supported me when I was small and push me to greatness. Last but not least, my big brother Jesse Diaz. He passed away July 1st, 2002. He accomplished great achievements in academics, and he is a huge inspiration in my academic life.

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CHAPTER I

INTRODUCTION

Although, various endemic disease are present around the world, there are several mathematical models that are used to analyze an endemic disease. One of the most popular mathematical models is known as an SIR model, which means Susceptible, Infected, and Removed Model. Thanks to Kermack and McKendrick in 1927 (Kermack & McKendrick, 1927) who constructed a basic SIR Model—which opened many doors. SIR Models are constructed by Ordinary Differential Equations, and the model can be constructed in many possible ways. There are several parameters that can be included in an epidemic or endemic case. These parameters are well defined, if they make sense with the interaction of humans and the disease. The idea behind this model is to analyze the stability of the disease: will the disease die out or will it expand. If the disease expands, then the infection will increase. If the disease dies out, then we have a massive population recovering from the disease.These equations consider the rate of susceptibles, infected, and removed individuals respect to time. However, we need useful data to determine the stability of a real epidemic or endemic case thus we can have an estimation of the stability of the disease in a selected population. Therefore, the data will be analyzed with Autonomous Systems, Jacobian, and Eigen Value Analysis thus we can process useful conclusions that determine the outcome of an outbreak or not. Kermack and McKendrick work has evolved into a biological response on certain diseases. As time develop, the SIR models grew more accurate to a real endemic/epidemic case. In year 2012, a paper has been published about an endemic in South Sulawesi (Noorani & Side, 2013). The model they used was from Bailey in 1975 (Bailey,1975)**.** This model contains mathematical analysis of the stability of the dengue virus. It considers the

process of vector and human interactions. During the interactions—the dengue virus spreads. Dengue fever is commonly known around the globe. The dengue virus is spread by mosquitoes, therefore dengue fever is a mosquito-borne disease. Mosquitoes can obtain the disease from an infected human, or/and vectors (born with the disease) can spread the disease to a human (Epidemiology, 2014). If mosquitoes can genetically carry the virus, the population of vectors can expand. The expansion occurs on a climate change. Usually when heavy amount of rainfall in the subtropical and tropical areas happen, they tend to reproduce. Mosquitoes tend to lay their eggs on stagnant or fresh water. Once the egg hatches, a larvae appears. They're known as "wringlres". Wringlres can live for months. If the temperature of the water is cold, they prefer to live longer. If the temperature is hot, they tend to form their third stage, pupa stage. Later on, an adult mosquito emerges from the pupa and they're ready to feed. Only females feed on blood. Males feed on nectar. Anyways, mosquitoes tend to grow base on the climate change and mosquitoes will reproduce faster, which the infection rate increases**.** (Murray & Quam & Wilder, 2013). Anyways, mosquitoes live longer in the subtropical and tropical regions in the globe, because that is the best environment for a mosquito to live. 40% of the world's population live in these areas (Division of Vector-Borne Disease, 2015). Among these areas, there are several organizations surveillance the vectors expansion, virus expansion, and human fatalities/infectious. Central Disease Control, World Health Organizations, and The Dengue Branch located in San Juan, Puerto Rico has current data of this surveillance (Epidemiology, 2014). Thailand has been keeping records yearly of the dengue virus**.** Recently they have reported 91,418 cases with 91 deaths, October 2015 (Thaivbd, 2015). We find the stability of different cases with these three models to see what is the difference, what is more accurate, what is more relevant. We will use Maple Software to determine the stability of several cases.

CHAPTER II

MATHEMATICAL THEORIES

In this chapter, we introduce mathematical theories which will be helpful to solve the stability of the dengue fever endemic.

Stability of a System of Ordinary Differential Equations

Consider a system

$$\begin{aligned} x'(t) &= f(x,y) \\ y'(t) &= g(x,y) \end{aligned} \tag{1}$$

f and g contain partial derivatives, and they're continuous. Thus, the **equilibrium point** can be obtained by setting

$$\begin{aligned} x'(t) &= f(x,y) = 0 \\ y'(t) &= g(x,y) = 0 \end{aligned}$$

i.e., a point (x_0,y_0) where $f(x_0,y_0) = 0$ and $g(x_0,y_0) = 0$. (Sanchez, 1979).

Using Taylor's theorem for two variables, we have

$$\begin{aligned} f(x,y) &\approx f(x_0,y_0) + \frac{\partial f(x_0,y_0)}{\partial x}(x-x_0) + \frac{\partial f(x_0,y_0)}{\partial y}(y-y_0) + \\ g(x,y) &\approx g(x_0,y_0) + \frac{\partial g(x_0,y_0)}{\partial x}(x-x_0) + \frac{\partial g(x_0,y_0)}{\partial y}(y-y_0) + \end{aligned}$$

Since $f(x_0,y_0) = 0$ and $g(x_0,y_0) = 0$, linearization yields us

$$\begin{pmatrix} x' \\ \\ y' \end{pmatrix} = \begin{pmatrix} \frac{\partial f(x_0,y_0)}{\partial x} & \frac{\partial f(x_0,y_0)}{\partial y} \\ \\ \frac{\partial g(x_0,y_0)}{\partial x} & \frac{\partial g(x_0,y_0)}{\partial y} \end{pmatrix} \begin{pmatrix} x \\ \\ y \end{pmatrix}$$

Therefore, you can analyse the stability by finding the eigenvalues of the following Jacobian J:

$$J = \begin{pmatrix} f_x & f_y \\ g_x & g_y \end{pmatrix} \tag{2}$$

At the equilibrium point, we have

$$J = \begin{pmatrix} f_x\,(x_0,y_0) & f_y\,(x_0,y_0) \\ \\ g_x\,(x_0,y_0) & g_y\,(x_0,y_0) \end{pmatrix} \tag{3}$$

The eigenvalues are obtained from

$$det(J - \lambda I_1) = 0 \qquad \text{where } I_1 \text{ is the identity matrix.}$$

$$\Rightarrow \begin{vmatrix} f_x(x_0,y_0) - \lambda & f_y(x_0,y_0) \\ g_x(x_0,y_0) & g_y(x_0,y_0) - \lambda \end{vmatrix} = 0 \tag{4}$$

Solving (4), we obtain two eigen values λ_1, λ_2. Now we consider various scenarios:

- **Case 1 :** λ_1, λ_2 **are real**

  (i)If λ_1, λ_2 are distinct and not equal to 0.

  (a) $\lambda_1 < \lambda_2 < 0$, then it is stable node.

  (b) $0 < \lambda_1 < \lambda_2$, then it is unstable node.

  (c) $\lambda_2 < 0 < \lambda_1$, then it is a saddle point.

  (ii) If $\lambda_1 = \lambda_2 \neq 0$ and

  (a) $\lambda_1 < 0$, then it is stable.

  (b) $0 < \lambda_1$, then it is unstable.

  (iii) If one λ_i=0, then we have to due further investigation.

- **Case 2 :** λ_1, λ_2 **are complex conjugat**e

  We have $\lambda_1 = r + ic$ and $\lambda_2 = r - ic$. Therefore, we can have multiple cases such that

  (i)λ_1, λ_2 are purely imaginary, it is stable and center node

  (ii) It is an unstable spiral point if $r > 0$

  (iii) It is an stable spiral point if $r < 0$

CHAPTER III

SIR MODEL DUE TO KERMACK AND MCKENDRICK

In this section, we will consider a basic SIR Model (Kermack & McKendrick, 1927). It is used to model an epidemic of various infectious diseases in a large population. The population consists of three types of individuals whose numbers are denoted by *S, I* and *R*. All these are functions of time *t*.

- Susceptible $\rightarrow$ Infected $\rightarrow$ Removed

- *S* is the number of susceptibles, who are not infected but could become infected.
- β is the infection rate. Susceptibles interact with the infective, thus becoming infected.
- *I* is the number of infectives. These individuals have the disease and can transmit it to the susceptibles.
- γ is the recovery rate. Infected individuals become recovered.
- *R* is the number of individuals removed.
- The model considered below assumes a time scale short enough that births and deaths (other than deaths from this disease) can be neglected.

Figure 1: Basic SIR

Becoming infected depends on contact between Susceptibles and Infecteds. New infections occur as a result of a contact between infectives and susceptibles. In this model, the rate at which new infections occur is βSI for some positive constant β (infection rate).

When a new infection occurs, the individual infected moves from the susceptible class to infective class. In this model, there is no other way individuals can enter or leave the susceptible class. The other process is that infective individuals are removed to the removed class. Assuming that this happens at the rate γI for some positive constant γ (recovery rate)

$$\frac{dS}{dt} = -\frac{\beta SI}{N} \tag{5}$$

$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I \tag{6}$$

$$\frac{dR}{dt} = \gamma I \tag{7}$$

In this model, we consider that the total population is constant. It is consist of the total of susceptible, infected, and recovered.

- Total population $N = S + I + R$ is constant.

Adding (5), (6) and (7), we have

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \Longrightarrow \frac{dN}{dt} = 0 \Longrightarrow N \text{ is constant.}$$

- Another detail is that there are 0 infectives, ($I = 0.$) $\frac{dS}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$. Thus 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 3 ordinary differential equations, (5), (6) and (7), we can construct two coupled ODE's. We concentrate on the following equation as $R = N - S - I$:

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta SI}{N} \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \end{aligned}$$

We set

$$\begin{aligned} \frac{dS}{dt} &= -\tfrac{\beta SI}{N} &&= 0 \\ \frac{dI}{dt} &= \tfrac{\beta SI}{N} - \gamma I &&= 0 \end{aligned}$$

to find two possible equilibrium points. This yield

$$\begin{aligned} I(\frac{\beta S}{N} - \gamma) &= 0 \\ \Rightarrow I &= 0 \end{aligned}$$

We see that I is always 0.

That is

$$\begin{aligned} \frac{-\beta SI}{N} &= 0 \\ \Rightarrow S &= 0 \\ & \textit{or} \\ I &= 0 \end{aligned}$$

Therefore, the equilibrium point is based on $(S^*, I^*, R^*) = (S, 0, N-S)$

- If S is 0, then we have $(S^*, I^*, R^*) = (0, 0, N)$. This equilibrium point means that all susceptible individuals are removed.

- If S=N, then we have $(S^*, I^*, R^*) = (N, 0, 0)$. This equilibrium point means that there is no infection. The entire population is disease free.

- If $S \neq N$, then we have $(S^*, I^*, R^*) = (S, 0, N - S)$. This equilibrium point means that the infected diminish in a number of quantity.

Since we have all three equilibrium points, we can determine the stability by the jacobian method.

Recall (5) (6) (7) ,

$$\begin{aligned} \frac{dS}{dt} &= -\frac{\beta SI}{N} \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\ \frac{dR}{dt} &= \gamma I \end{aligned}$$

Writing

$$\begin{aligned} A = \frac{dS}{dt} &= -\frac{\beta SI}{N} \\ B = \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\ C = \frac{dR}{dt} &= \gamma I \end{aligned}$$

the jacobian is

$$\begin{pmatrix} \frac{dA}{dS} & \frac{dA}{dI} & \frac{dA}{dR} \\ \frac{dB}{dS} & \frac{dB}{dI} & \frac{dB}{dR} \\ \frac{dC}{dS} & \frac{dC}{dI} & \frac{dC}{dR} \end{pmatrix} = \begin{pmatrix} \frac{-\beta I}{N} & \frac{-\beta S}{N} & 0 \\ \frac{\beta I}{N} & \frac{\beta S}{N} - \gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}$$

Let s work with equilibrium $(S^*, I^*, R^*) = (0, 0, N) \Rightarrow$

$$\Rightarrow \begin{pmatrix} \frac{dA}{dS} & \frac{dA}{dI} & \frac{dA}{dR} \\ \frac{dB}{dS} & \frac{dB}{dI} & \frac{dB}{dR} \\ \frac{dC}{dS} & \frac{dC}{dI} & \frac{dC}{dR} \end{pmatrix} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & -\gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}$$

Lets find the eigen values.

$$\Rightarrow det \begin{pmatrix} -\lambda & 0 & 0 \\ 0 & -\gamma - \lambda & 0 \\ 0 & \gamma & -\lambda \end{pmatrix} = \lambda^2(-\lambda - \gamma) = 0$$

The eigen values are

$$\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= -\gamma \end{aligned} \tag{8}$$

Now lets work with the equilibrium $(S^*, I^*, R^*) = (N, 0, 0)$

$$\Rightarrow \begin{pmatrix} \frac{dA}{dS} & \frac{dA}{dI} & \frac{dA}{dR} \\ \frac{dB}{dS} & \frac{dB}{dI} & \frac{dB}{dR} \\ \frac{dC}{dS} & \frac{dC}{dI} & \frac{dC}{dR} \end{pmatrix} = \begin{pmatrix} 0 & -\beta & 0 \\ 0 & \beta - \gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}$$

Lets find the eigen values.

$$\Rightarrow det \begin{pmatrix} -\lambda & -\beta & 0 \\ 0 & \beta-\gamma-\lambda & 0 \\ 0 & \gamma & -\lambda \end{pmatrix} = \lambda^2(\beta-\gamma-\lambda) = 0$$

The eigen values are

$$\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= \beta-\gamma \end{aligned} \tag{9}$$

Now lets work with the equilibrium $(S^*, I^*, R^*) = (S, 0, N-S)$

$$\Rightarrow \begin{pmatrix} \frac{dA}{dS} & \frac{dA}{dI} & \frac{dA}{dR} \\ \frac{dB}{dS} & \frac{dB}{dI} & \frac{dB}{dR} \\ \frac{dC}{dS} & \frac{dC}{dI} & \frac{dC}{dR} \end{pmatrix} = \begin{pmatrix} 0 & -\frac{\beta S}{N} & 0 \\ 0 & \frac{\beta S}{N}-\gamma & 0 \\ 0 & \gamma & 0 \end{pmatrix}$$

Lets find the eigen values.

$$\Rightarrow det \begin{pmatrix} -\lambda & -\frac{\beta S}{N} & 0 \\ 0 & \frac{\beta S}{N}-\gamma-\lambda & 0 \\ 0 & \gamma & -\lambda \end{pmatrix} = \lambda^2(\beta-\gamma-\lambda) = 0$$

The eigen values are

$$\begin{aligned} \lambda_1 &= 0 \\ \lambda_2 &= 0 \\ \lambda_3 &= \frac{\beta S}{N} - \gamma \end{aligned} \tag{10}$$

Now lets analyse the eigen values of (8), (9) and (10). Although we see eigen values equal to 0, therefore we need to do further analysis. Base on how the solution of the differential equation looks like, we can determine the stability. The solution of the infection rate can explain the stability.

Basic Reproductive Number R_0

R_0 is defined as the ratio of the infection rate to the recovery rate. i.e

$$R_0 = \frac{\beta}{\gamma} \tag{11}$$

Lets see how this reproductive number affects the model. We analyze the rate of infection. We have (6)

$$\begin{aligned} \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I \\ &= I(\frac{\beta S}{N} - \gamma) \end{aligned}$$

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

$$\frac{dI}{dt} = (\beta - \gamma)I$$

Let $r = \beta - \gamma$. which yields $r = \gamma(\frac{\beta}{\gamma} - 1)$ Thus we get

$$r = \gamma(R_0 - 1) \tag{12}$$

Now we have

$$\begin{aligned} \frac{dI}{dt} &= rI \\ \Rightarrow I &= k_1 \exp(rt) \end{aligned} \tag{13}$$

From the solution (32), we can conclude the following

- If $R_0 < 1$, then $r < 0$. Therefore, the infection decreases
- If $R_0 > 1$, then $r > 0$. Therefore, the infection increases
- If $R_0 = 1$, then $r = 0$. Therefore, the infection remains constant. .

Furthermore, we can determine a threshold behavior—based on R_0.

- If $R_0 < 1$, then there is no epidemic.
- If $R_0 > 1$, then there is an epidemic.
- If $R_0 = 1$, then there is a no change.

CHAPTER IV

SIR MODEL WITH BIRTH AND DEATHS

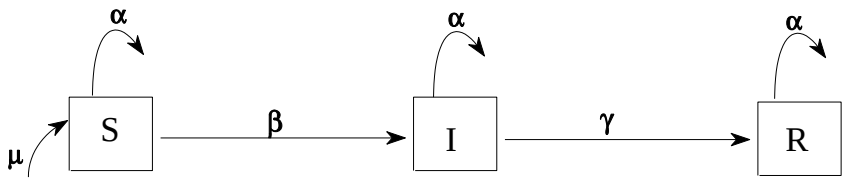
In this model, birth and death scenarios are included. This model contains extra information than a basic SIR Model. We still consider the same parameters in the SIR Model, but we add two extra parameters.

- μ is the birth rate. This parameter interacts with the total population N.
- α is the death rate. This parameter interacts with any individual. He or she maybe a susceptible to the disease, infected or recovered.

Thus, the system of ordinary differential equations for this model is

$$\begin{aligned} \frac{dS}{dt} &= \mu N - \frac{\beta SI}{N} - \alpha S \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I - \alpha I \\ \frac{dR}{dt} &= \gamma I - \alpha R \end{aligned} \tag{14}$$

Figure 2: SIR with Birth and Death



The rate of a susceptible $\frac{dS}{dt}$ tells us that a selected population contains a birth rate μN, thus some susceptibles interacting with infected individuals at a contact rate—are decreasing the rate of susceptible individuals $-\frac{\beta SI}{N}$. As well, some of these susceptibles can die at some point which decreases the rate of susceptibles individuals $-\alpha S$. The rate of infected individuals $\frac{dI}{dt}$, tells us that it begins with susceptibles becoming infected $\frac{\beta SI}{N}$, however it decreases with infected individuals being recovered and dying $-\gamma I - \alpha I$. Further more, the rate of recovery individuals $\frac{dR}{dt}$, tell us that it increases as infected individuals recover γI , and the rate of recovery individuals decrease by death $-\alpha R$. Assuming birth rate and death rate are the same$\mu = \alpha$, we have

$$\begin{aligned} \frac{dS}{dt} &= \mu N - \frac{\beta SI}{N} - \mu S \\ \frac{dI}{dt} &= \frac{\beta SI}{N} - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I - \mu R \end{aligned} \tag{15}$$

Therefore, we have that the total population is constant and N=S+I+R. Thus, the rate of N is 0 because the derivative of a constant is 0; $\frac{dN}{dt} = 0$. This is true, because of $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$

Finding the equilibrium points.

We let

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \tfrac{\beta SI}{N} - \alpha S &= 0 \\
\frac{dI}{dt} &= \tfrac{\beta SI}{N} - \alpha I - \gamma I &= 0 \\
\frac{dR}{dt} &= \gamma I - \alpha R &= 0
\end{aligned}$$

Let $\mu = \alpha$, therefore N is constant.

$$\begin{aligned}
\frac{dS}{dt} &= \mu N - \tfrac{\beta SI}{N} - \mu S &= 0 \\
\frac{dI}{dt} &= \tfrac{\beta SI}{N} - \mu I - \gamma I &= 0 \\
\frac{dR}{dt} &= \gamma I - \mu R &= 0
\end{aligned}$$

Algebraically we find two equilibrium points.

$$\begin{aligned}
S' &= N \\
I' &= 0 \\
R' &= 0
\end{aligned} \tag{16}$$

and

$$\begin{aligned}
S^* &= \frac{\gamma + \mu}{\beta} \\
I^* &= \frac{\mu(\beta - \gamma - \mu)}{\beta(\gamma + \mu)} \\
R^* &= \frac{\gamma(\beta - \gamma - \mu)}{\beta(\gamma + \mu)}
\end{aligned} \tag{17}$$

Now we can formulate the jacobian out of the differential system.

$$J = \begin{pmatrix} -\mu - \frac{\beta I}{N} & -\frac{\beta S}{N} & 0 \\ \frac{\beta I}{N} & \frac{\beta S}{N} - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{pmatrix}$$

Now, Lets find the eigen values for (16). We get

$$J(S', I', R') = \begin{pmatrix} -\mu & -\beta & 0 \\ 0 & \beta - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{pmatrix}$$

Now find the eigen values

$$det \begin{pmatrix} -\mu - \lambda & -\beta & 0 \\ 0 & \beta - \mu - \gamma - \lambda & 0 \\ 0 & \gamma & -\mu - \lambda \end{pmatrix} = 0$$

$\Rightarrow$

$$\begin{aligned} \lambda_1 &= -\mu \\ \lambda_2 &= \beta - \gamma - \mu \\ \lambda_3 &= -\mu \end{aligned} \tag{18}$$

Now, lets find the eigen values for (18). We get

$$J(S^*, I^*, R^*) = \begin{pmatrix} -\mu - \frac{\beta}{N}\left(\frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)}\right) & -\frac{\beta}{N}\left(\frac{\gamma+\mu}{\beta}\right) & 0 \\ \frac{\beta}{N}\left(\frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)}\right) & \frac{\beta}{N}\left(\frac{\gamma+\mu}{\beta}\right) - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{pmatrix}$$

$$= \begin{pmatrix} -\mu - \frac{R_0(\beta-\gamma-\mu)}{N\beta} & -\frac{\beta}{NR_0} & 0 \\ \frac{R_0(\beta-\gamma-\mu)}{N\beta} & \frac{\beta}{NR_0} - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{pmatrix}$$

Such that $R_0 = \frac{\beta}{\gamma+\mu}$. We will later talk about the reproduction number.

Anyways, apply the determinant on the jacobian above.

$$det \begin{pmatrix} -\mu - \frac{R_0(\beta-\gamma-\mu)}{N\beta} & -\frac{\beta}{NR_0} & 0 \\ \frac{R_0(\beta-\gamma-\mu)}{N\beta} & \frac{\beta}{NR_0} - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{pmatrix} = 0$$

Reproduction Number R_0

Base on (S', I', R'), we have two eigen values that are negative. We are one step closer to verify that this model is stable. However, it really depends what λ_2 is because it can't either be negative or positive. Therefore, if we find out what β is then we can determine the stability of λ_2. So, we must include the reproduction number such that it represents the average number of infected individuals that appear from a single infected case. Thus, the reproduction number is defined by $R_0 = \frac{\beta}{\mu+\gamma}$ so $\lambda_2 = (\mu + \gamma)(R_0 - 1)$. Then, we have two cases such that $R_0 < 1$ and $R_0 > 1$. If $R_0 < 1$, then the model is stable. If $R_0 > 1$, then the model is unstable.

CHAPTER V

SIR MODEL FOR DENGUE FEVER DISEASE

Although, the SIR model is used to identify the stability of a disease on a human, it as well can be used on a vector (Bailey, 1975). Since humans get the dengue virus by the bite of a mosquito (b) , the SIR model should reflect this effect. However, we will disregard the recovery rate for the mosquitoes because mosquitoes tend to live a short life span (Lee, 2009). The total population of humans is represented by N_h, which consists of the susceptible, infected, and removed individuals (S_h, I_h, R_h). The total vector population is represented by N_v, which consists of the susceptible and infected mosquitoes (S_v, I_v). In this model, it is assumed that N_h and N_v are constants. Therefore, consider total population birth rate as ($\mu_k N_k$) such that k is either v (vectors) or h (host). α_k is the death rate, and k is either v or h. Furthermore, we can start to see what happens in category S_h, such that $\frac{\beta_h b I_v}{N_h}$ denotes the probability of a susceptible host to be infected by the virus. Therefore, an infected mosquito I_v—interaction from an infected individual to a mosquito β_h from biting the human b—tells us that these interactions to a susceptible $\frac{\beta_h b}{N_h} I_v S_h$ — concludes decrease in the rate of susceptibles $\frac{d}{dt} S_h$. As well, death of a susceptible will decrease it which is denoted as $\alpha_h S_h$. Going further, the rate of infected individuals $\frac{d}{dt} I_h$(respect to time) decreases by the death of an infected person $\alpha_h I_h$ and the recovery of an infected person $\gamma_h I_h$such that $\gamma_h$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 $\alpha_h R_h$such that it is obvious it only increase by $\gamma_h I_h$. Therefore, the model of this interaction is represented with three differential equations which are (Noorani & Side, 2013)

$$\frac{d}{dt}S_h = \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \alpha_h S_h \quad (19)$$

$$\frac{d}{dt}I_h = \frac{\beta_h b}{N_h} I_v S_h - (\alpha_h + \gamma_h) I_h \quad (20)$$

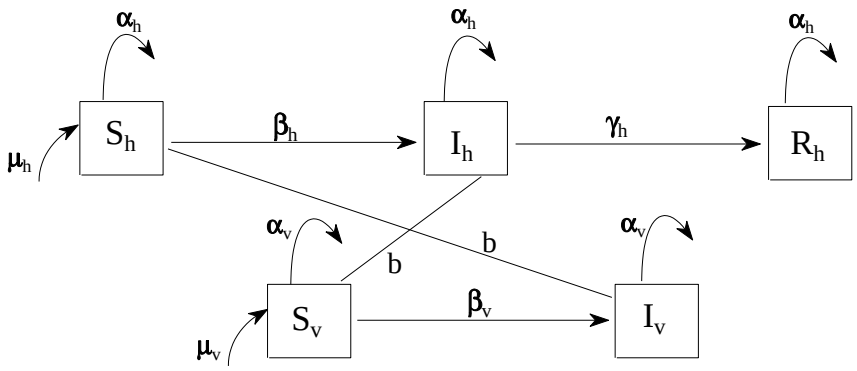
$$\frac{d}{dt}R_h = \gamma_h I_h - \alpha_h R_h \quad (21)$$

Now, we will mention the vector model which will talk about the rate of the susceptible and infected vector. Category S_v, such that $\frac{\beta_v b I_h}{N_h}$ denotes the probability of a susceptible mosquito to be 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 $\frac{\beta_v b}{N_h} I_h S_v$ — concludes decrease in the rate of susceptibles $\frac{d}{dt}S_v$. As well, death of a susceptible will decrease it which is denoted as $\alpha_v S_v$. Going further, the rate of infected mosquitoes $\frac{d}{dt}I_v$(respect to time) decreases by the death of an infected mosquito $\alpha_v I_v$ and we stated earlier that a recovery parameter is not included. Therefore, the model of this interaction is represented with two differential equations which are

$$\frac{d}{dt}S_v = \mu_v N_v - \frac{b\beta_v}{N_h} I_h S_v - \alpha_v S_v \quad (22)$$

$$\frac{d}{dt}I_v = \frac{\beta_v b}{N_h} I_h S_v - \alpha_v I_v \quad (23)$$

Figure 3: SIR for Dengue Fever



- N_h is the total human population.
- S_h is the number of human susceptibles, who are not infected but could become infected.
- I_h is the number of human infectives. These individuals have the disease and can transmit it to the mosquitoes.
- R_h is the number of human removed individuals. These may or may not have the disease, but they can't become infected and they can't transmit the disease to others. They may have a natural immunity, or they may have recovered from the disease and are immune from getting it again, or they may have the disease but are incapable of transmitting it (because they may have been placed in isolation), or they may have died. The mathematical model doesn't distinguish among those possibilities.
- μ_h is the birth rate for humans. This parameter interacts with the total population N_h
- α_h is the death rate for humans. This parameter interacts with $S_h,\ I_h$ and R_h.
- β_h is the infection rate for humans.
- γ_h is the recovery rate for humans.

- N_v is the total mosquito population
- S_v is the number of mosquitoes, who are not infected but could become infected.
- I_v is the number of infected mosquitoes. These mosquitoes have the disease and can transmit it to the humans.
- β_v is the infection rate for mosquitoes
- α_v is the death rate for mosquitoes.
- μ_v is the birth rate for mosquitoes. This parameter interacts with the total population N_v.
- b is the average of a mosquito bite.

However, we can as well assume that $\alpha_k = \mu_k$ therefore we have these two models now.

$$\begin{aligned} \frac{d}{dt}S_h &= \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h && (24) \\ \frac{d}{dt}I_h &= \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \gamma_h) I_h && (25) \\ \frac{d}{dt}R_h &= \gamma_h I_h - \mu_h R_h && (26) \end{aligned}$$

and

$$\begin{aligned} \frac{d}{dt}S_v &= \mu_v N_v - \frac{b\beta_v}{N_h} I_h S_v - \mu_v S_v && (27) \\ \frac{d}{dt}I_v &= \frac{\beta_v b}{N_h} I_h S_v - \mu_v I_v && (28) \end{aligned}$$

Figure 3 presents the interactions of these variables.

Considering these conditions,

$$S_h + I_h + R_h = N_h \quad \Rightarrow \quad R_h = N_h - S_h - I_h \tag{29}$$

$$S_v + I_v = N_v = \frac{A}{\mu_v} \quad \Rightarrow \quad S_v = N_v - I_v = \frac{A}{\mu_v} - I_v \tag{30}$$

it will rearrange both models into combining both into a single model of understanding the stability of human and mosquito populations.

Therefore, (29) will be applied to (21) and (30) will be applied to (22).

Applying (29) to (21)

$$\begin{aligned}
\frac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h \\
= \frac{d}{dt}(N_h - S_h - I_h) &= \gamma_h I_h - \mu_h (N_h - S_h - I_h) \\
= 0 - \frac{dS_h}{dt} - \frac{dI_h}{dt} &= \gamma_h I_h - \mu_h N_h + \mu_h S_h + \mu_h I_h \\
\Rightarrow -\frac{dI_h}{dt} &= \gamma_h I_h - \mu_h N_h + \mu_h S_h + \mu_h I_h + \frac{\partial S_h}{\partial t} \\
-\frac{dI_h}{dt} &= \gamma_h I_h - \mu_h N_h + \mu_h S_h + \mu_h I_h + \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h \\
-\frac{dI_h}{dt} &= \gamma_h I_h + \mu_h I_h - \frac{\beta_h b}{N_h} I_v S_h \\
\Rightarrow \frac{dI_h}{dt} &= -\gamma_h I_h - \mu_h I_h + \frac{\beta_h b}{N_h} I_v S_h
\end{aligned}$$

Applying **(30)** to **(22)**

$$
\begin{aligned}
\frac{dS_v}{dt} &= \mu_v N_v - \frac{b\beta_v}{N_h} I_h S_v - \mu_v S_v \\
= \frac{d}{dt}(N_v - I_v) &= \mu_v N_v - \frac{b\beta_v}{N_h} I_h S_v - u_v(N_v - I_v) \\
= 0 - \frac{dI_v}{dt} &= -\frac{b\beta_v}{N_h} I_h S_v + \mu_v I_v \\
\Rightarrow \frac{dI_v}{dt} &= \frac{b\beta_v}{N_h} I_h S_v - \mu_v I_v
\end{aligned}
$$

Thus, these two equations that were just formed, tells us that our conditions can be formulated into

$$
\begin{aligned}
\frac{d}{dt} S_h &= \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h && (31) \\
\frac{d}{dt} I_h &= \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \gamma_h) I_h && (32) \\
\frac{d}{dt} I_v &= \frac{\beta_v b}{N_h} I_h S_v - \mu_v I_v && (33)
\end{aligned}
$$

Now we will nondimensionalize this model.

$$
x(t) = \frac{S_h}{N_h}, \quad y(t) = \tfrac{I_h}{N_h}, \quad z(t) = \frac{I_v}{N_v} = \frac{I_v}{A/\mu_v} \tag{34}
$$

thus we get from (31)

$$
\begin{aligned}
\frac{d}{dt}S_h &= \mu_h N_h - \frac{\beta_h b}{N_h} I_v S_h - \mu_h S_h \\
\Rightarrow \frac{d}{dt}\frac{S_h}{N_h} &= \mu_h - \frac{\beta_h b S_h I_v}{N_h N_h} - \mu_h \frac{S_h}{N_h} \\
= \frac{dx}{dt} &= \mu_h - x(t)\frac{\beta_h b I_v}{N_h}\frac{N_v}{N_v} - \mu_h x(t) \\
&= \mu_h - x(t)z(t)\frac{\beta_h b N_v}{N_h} - \mu_h x(t) \\
&= \mu_h(1 - x(t)) - \alpha x(t) z(t) \\
s.t \quad let \quad \alpha &= \frac{b\beta_h A}{\mu_v N_h}
\end{aligned}
$$

From (32)

$$
\begin{aligned}
\frac{d}{dt}I_h &= \frac{\beta_h b}{N_h} I_v S_h - (\mu_h + \gamma_h) I_h \\
\Rightarrow \frac{d}{dt}\frac{I_h}{N_h} &= \frac{\beta_h b S_h I_v}{N_h N_h} - (\mu_h + \gamma_h)\frac{I_h}{N_h} \\
= \frac{dy}{dt} &= x(t)\frac{\beta_h b I_v}{N_h}\frac{N_v}{N_v} - (\mu_h + \gamma_h) y(t) \\
&= x(t)z(t)\frac{\beta_h b N_v}{N_h} - \beta y(t) \\
&= \alpha x(t) z(t) - \beta y(t) \\
s.t \quad let \quad \beta &= (\mu_h + \gamma_h)
\end{aligned}
$$

From (33)

$$\begin{aligned}
\frac{d}{dt}I_v &= \frac{\beta_v b}{N_h}I_h S_v - \mu_v I_v \\
\Rightarrow \frac{d}{dt}\frac{I_v}{N_v} &= \frac{\beta_v b I_h S_v}{N_h N_v} - \frac{\mu_v I_v}{N_v} \\
(let \quad \gamma = b\beta_v, \quad \delta = \mu_v) & \\
\Rightarrow \frac{dz}{dt} &= y(t)\frac{\gamma S_v}{N_v} - z(t)\delta \\
&= y(t)\gamma\frac{N_v - I_v}{N_v} - z(t)\delta \\
&= y(t)\gamma(1 - z(t)) - \delta z(t)
\end{aligned}$$

thus formulate a nondimensionalize model.

$$\frac{dx}{dt} = \mu(1 - x(t)) - \alpha x(t)z(t) \tag{35}$$

$$\frac{dy}{dt} = \alpha x(t)z(t) - \beta y(t) \tag{36}$$

$$\frac{dz}{dt} = \gamma(1 - z(t))y(t) - \delta z(t) \tag{37}$$

Defining

- $\alpha = \frac{b\beta_h A}{\mu_v N_h}$
- $\beta = (\mu_h + \gamma_h)$
- $\gamma = b\beta_v$
- $\delta = \mu_v$
- $\mu = \mu_h$

we find the equilibrium points. We need the set the above equations to 0. Therefore,

$$\begin{aligned}
\frac{dx}{dt} &= \mu(1-x(t)) - \alpha x(t)z(t) &= 0 \\
\frac{dy}{dt} &= \alpha x(t)z(t) - \beta y(t) &= 0 \\
\frac{dz}{dt} &= \gamma(1-z(t))y(t) - \delta z(t) &= 0
\end{aligned}$$

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

$$\begin{aligned}
x_0 &= \frac{\mu\gamma + \beta\delta}{\gamma(\mu+\alpha)} \\
y_0 &= \frac{\mu(\gamma\alpha - \beta\delta)}{\beta\gamma(\mu+\alpha)} \\
z_0 &= \frac{\mu(\gamma\alpha - \beta\delta)}{\alpha(\gamma\mu + \beta\delta)}
\end{aligned}$$

Now considering the jacobian of nondimensionalize model, we have

$$J(x,y,z) = \begin{pmatrix} -\mu - \alpha z & 0 & -\alpha x \\ \alpha z & -\beta & \alpha x \\ 0 & \gamma - z\gamma & -\gamma y - \delta \end{pmatrix} \tag{38}$$

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

$$J(1,0,0) = \begin{pmatrix} -\mu & 0 & -\alpha \\ 0 & -\beta & \alpha \\ 0 & \gamma & -\delta \end{pmatrix} \tag{39}$$

To find the eigen values, we set

$$\begin{vmatrix} -\mu-\lambda & 0 & -\alpha \\ 0 & -\beta-\lambda & \alpha \\ 0 & \gamma & -\delta-\lambda \end{vmatrix} = 0 \tag{40}$$

This yields

$$\Rightarrow \quad (-\lambda-\mu)(-\alpha\gamma+\beta\delta+\beta\lambda+\delta\lambda+\lambda^2) \quad = 0 \tag{41}$$

The three eigen values are

$$\begin{aligned} \lambda_1 &= -\mu \\ \lambda_2 &= \frac{1}{2}\left(-\beta-\delta-\sqrt{4\alpha\gamma+\beta^2-2\beta\delta+\delta}\right) \\ \lambda_3 &= \frac{1}{2}(-\beta-\delta+\sqrt{4\alpha\gamma+\beta^2-2\beta\delta+\delta} \end{aligned} \tag{42}$$

We have $\lambda_1$and λ_2 are always negative, because μ, β, δ are always positive. λ_3 can be either positive or negative.

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

$$J(x_0, y_{0,} z_0) \quad = \quad \begin{pmatrix} -\mu-\alpha\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) & 0 & -\alpha\left(\frac{\mu\gamma+\beta\delta}{\gamma(\mu+\alpha)}\right) \\ \alpha\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) & -\beta & \alpha\left(\frac{\mu\gamma+\beta\delta}{\gamma(\mu+\alpha)}\right) \\ 0 & \gamma-\gamma\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) & -\gamma\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\beta\gamma(\mu+\alpha)}\right)-\delta \end{pmatrix} \tag{43}$$

Find the eigen values

$$det \begin{pmatrix} -\mu - \alpha\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) - \lambda & 0 & -\alpha\left(\frac{\mu\gamma+\beta\delta}{\gamma(\mu+\alpha)}\right) \\ \alpha\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) & -\beta-\lambda & \alpha\left(\frac{\mu\gamma+\beta\delta}{\gamma(\mu+\alpha)}\right) \\ 0 & \gamma - \gamma\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\alpha(\gamma\mu+\beta\delta)}\right) & -\gamma\left(\frac{\mu(\gamma\alpha-\beta\delta)}{\beta\gamma(\mu+\alpha)}\right) - \delta - \lambda \end{pmatrix} = 0 \quad (44)$$

You can find the eigen values by computer simulation. Maple is a good program to do this. However, it is more easier to determine the stability if we consider some numerical values on the parameters.

Reproduction Number R_0(SoeWono & Supriatna, 2001)

The equilibrium point (x_0, y_0, z_0) only makes sense if its positive. It is based on a threshold parameter. Therefore, the threshold parameter is $R = \frac{\alpha\gamma}{\delta\beta}$ thus the reproduction number is denoted as

$$R_0 = \sqrt{R} \quad (45)$$

You can immediately tell that the equilibrium point (x_0, y_0, z_0) must be positive.

- If $R \leq 1$, then $(1, 0, 0)$ is globally asymptotically stable.
- If $R > 1$, then $(x_0$,y_0, $z_0)$ is globally asymptotically stable, and $(1, 0, 0)$ is unstable.
- If $R < 1$, then $(x_0$,y_0, $z_0)$ is unstable. Although, we wont consider this one because we will always get negative values in $(x_0$,y_0, $z_0)$.

CHAPTER VI

RESULTS AND DISCUSSION

In this section, we will provide some numerical data for the SIR Model for Dengue Fever Disease. In Boutayeb and Derouich paper, they denoted a numerical value that is given (Boutayeb & Derouich, 2006). These numerical values are constructed for the purpose of other authors (Boutayeb & Derouich, 2006) (Noorani & Side, 2013). These numerical values are in Table 1. We will use this data and other resources to compute some simulations.

Table 1: Basic Parameters

Name of the Parameter	Notation	Base Value
Transmission probability of vector to host	β_v	.75
Transmission probability of host to vector	β_h	.75
Bites per susceptible mosquito per day	b_s	.5
Bites per infectious mosquito per day	b_i	1
Contact Rate, Host to Vector	C_{hv}	.375
Contact Rate, Vector to Host	C_{vh}	.75
Human Life Span	$\frac{1}{\mu_h}$	HL
Vector Life Span	$\frac{1}{\mu_v}$	VL
Host Infection Duration	$\frac{1}{\mu_h+\gamma_h}$	3 days

HL and VL are the Life Spans we choose or find in resources. Suppose we analyse the population of Hidalgo County. Record shows that Hidalgo County, Texas has total population of 815, 996 in 2013. Therefore, lets consider some parameters with this population thus lets say there are 100000 mosquitoes in Hidalgo. Lets consider HL = 25,000 days and VL = 12 days. 12 days are consider

to be the minimum number of days that a mosquito lives (Lee, 2009) (Noorani & Side, 2013). This yields

$$\begin{aligned}
\frac{dx}{dt} &= .00004(1-x(t)) - .091912x(t)z(t) \\
\frac{dy}{dt} &= .091912x(t)z(t) - .33333y(t) \\
\frac{dz}{dt} &= .375(1-z(t))y(t) - .083333z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) = (1, 0, 0)$$

and

$$(S_h, I_h, R_h) = (.8060070125, .00002344798, .0001055048)$$

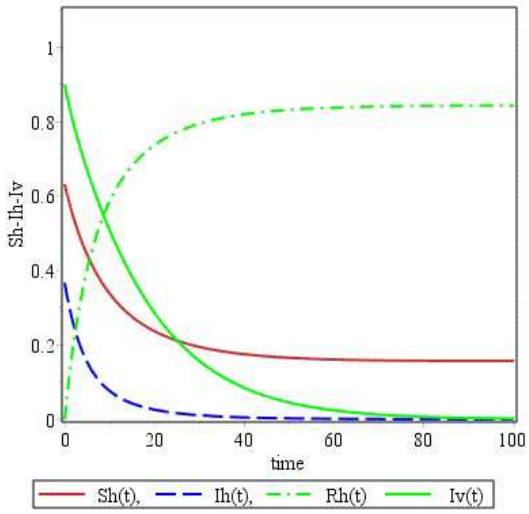
The Eigen Values for (1,0,0) are $\lambda = -.00004029008863$, $\lambda = -.432145935102$, $\lambda = .015479268472$. This is unstable.

The Eigen Values for (.8060070125,.00002344798,.0001055048) are $\lambda = -.00002773486 + .0008037760i$, $\lambda = -.00002773486 - .0008037760i$, $\lambda = -.4166699769$. This is unstable $R_0 = 1.1139$, so there is an endemic. We will produce two cases with these parameters.

Case 1.

Lets consider some initial data. Suppose we have $S_h(0) = 515996$, $I_h(0) = 300000$, $R_h(0) = 0$ and $S_v(0) = 10000$, $I_v(0) = 90000$. Base on Figure 4, we can analyze this initial data.

Figure 4: Case 1 for Hidalgo

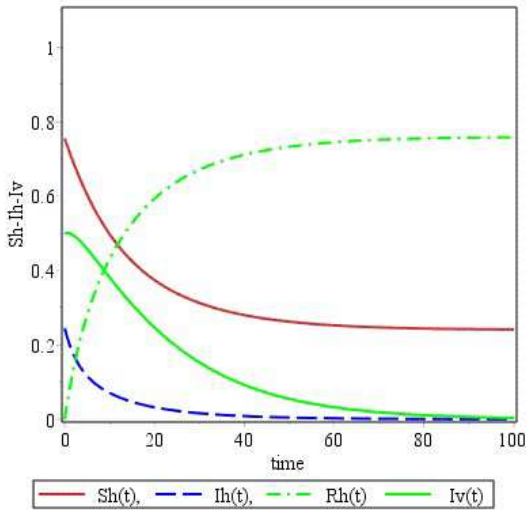


This Figure tells us that a large amount of individuals will recover, respect to time. Time is consider to be number of days. Thus approximately it will take 80 days for the number of infected to go to 0 and close to 100 days for infected mosquitoes to go to 0. Although, we see that some susceptibles will not get infected by day 100 because there is no more infected mosquitoes. Thus, it remains constant for Susceptible and recoverable in day 100 which looks reasonable to conclude. We can't conclude that this model will be accurately correct in a real situation for hidalgo–of this large amount—because the parameters were used inappropriate.

Case 2.

Lets consider some initial data. Suppose we have $S_h(0) = 615996$, $I_h(0) = 200000$, $R_h(0) = 0$ and $S_v(0) = 50000$, $I_v(0) = 50000$. Base on Figure 5, we can analyze this initial data.

Figure 5: Case 2 for Hidalgo



This Figure tells us that a large amount of individuals will recover, respect to time. Time is consider to be number of days. Thus approximately it will take 76 days for the number of infected humans go to 0 and more than 100 days for infected mosquitoes to go to 0. Although, we see that some susceptibles will not get infected by more than day 100 because there is no more infected mosquitoes. Thus, it remains constant for Susceptible and recoverable more than day 100 which looks reasonable to conclude. Again, we can't conclude that this model will be accurately correct in a real situation for hidalgo–of this large amount—because the parameters were used inappropriate. Furthermore, looking at Figure 4 and 5, we see that more infected mosquitoes will die out quickly than less infected mosquitoes.

Now lets consider a different population for mosquitoes, however we will still use the same values for HL and VL. Lets say there are 10000 mosquitoes in Hidalgo. This yields

$$\begin{aligned}
\frac{dx}{dt} &= .00004(1-x(t)) - .009191x(t)z(t) \\
\frac{dy}{dt} &= .009191x(t)z(t) - .33333y(t) \\
\frac{dz}{dt} &= .375(1-z(t))y(t) - .083333z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) \quad = \quad (1, 0, 0)$$

and

$$(S_h, I_h, R_h) \quad = \quad (8.02841043, -.000849525838, . - .00383753666)$$

The Eigen Values for (1,0,0) are $\lambda = -.00004029008863$, $\lambda = -.346433688377903$, $\lambda = -.0702329782520966$. This is a stable node. $R_0 = .35225$

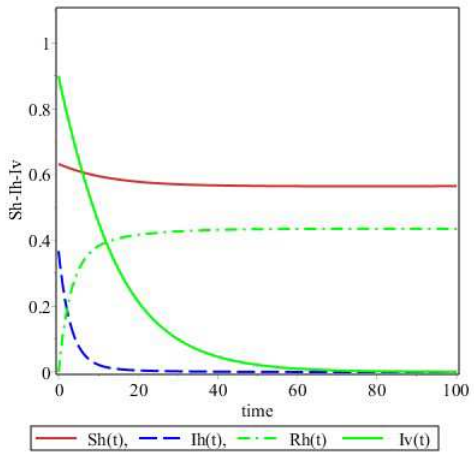
We wont consider the eigen values for (8.02841043,-.000849525838,.-.00383753666). They have negative values.

We will produce two cases again.

Case 3.

Lets consider some initial data. Suppose we have $S_h(0) = 515996$, $I_h(0) = 300000$, $R_h(0) = 0$ and $S_v(0) = 1000$, $I_v(0) = 9000$. Base on Figure 6, we can analyse this initial data.

Figure 6: Case 3 for Hidalgo

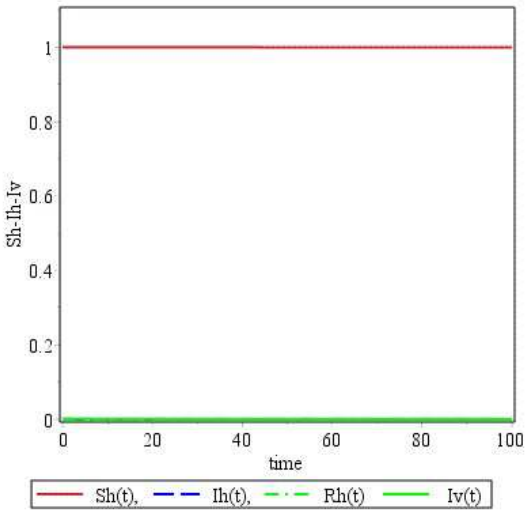


This Figure tells us that a large amount of infected individuals will go to 0 quickly. Thus approximately it will take 25 days for the number of infected humans go to 0 and 90 days for infected mosquitoes to go to 0. Although, we see that small numbers of susceptibles not being infected thus we get about 57% of the population remain unaffected by the disease. As well, approximately 43% will remain removed and we can conclude that these calculations meet very well in time. Again, we can't conclude that this model will be accurately correct in a real situation for hidalgo–of this large amount—because the parameters were used inappropriate. It seems unrealistic for a large amount of individuals to be infected compare to a small number of infected mosquitoes.

Case 4.

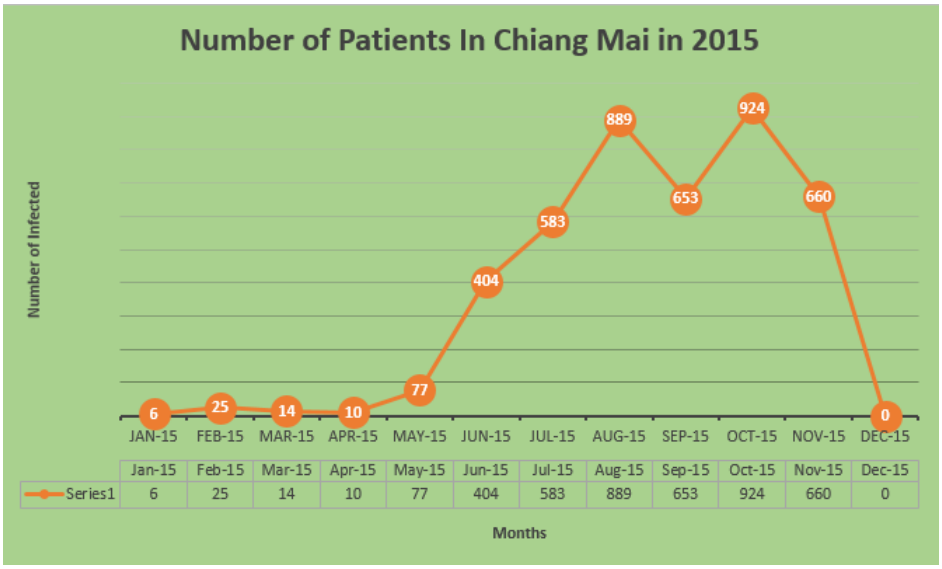
Lets consider some initial data. Suppose we have $S_h(0) = 815896$, $I_h(0) = 100$, $R_h(0) = 0$ and $S_v(0) = 9990$, $I_v(0) = 10$. Base on Figure 7, we can analyse this initial data.

Figure 7: Case 4 for Hidalgo



This Figure tells us that a small amount of infected individuals will go to 0 real quick. You have approximately 100% population to be unaffected. Therefore, there are approximately 0 removed and infected individuals and infected mosquitoes in a small amount of days. You really can't tell what day, but this seems more of a reasonable conclusion for a real scenario in hidalgo, compare to the other cases. Hidalgo has had very little cases of dengue fever in 2003-2012. They reported about 5 cases in total in 2003-2012 (Dengue Cases Reported in Texas by County 2003-2012, 2013). Therefore, we can consider an initial data of 5 infected individuals with 5-10 mosquitoes, but we will get the same figure like figure 7. Thus, we can conclude that Hidalgo in 2003-2012 is considered a disease free case instead of an endemic case which we can see based on the analysis of the stability of the equilibrium points. Again, we can't conclude that this model will be precisely correct in a real situation for hidalgo–of this small amount of cases—because the parameters were used inappropriate. However,we can say Hidalgo remained close to a 100% disease free based on 2003-2012 data (Dengue Cases Reported in Texas by County 2003-2012, 2013) and analyzing a statement that may seem relevant with the SIR Mathematical Model of Dengue Fever.

Figure 8: Number of Patients in 2015 at Chiang Mai



Now we will consider a country that contains dengue fever cases. In Chiang Mai in Thailand, it has been reported around 4000 and more cases of the dengue fever in 2015 (Thaivbd, 2015). Base on Figure 8, we consider all the reported cases in Chiang Mai in 2015, however we do not have the data for December 15. We do expect a decrease by December, because we always see less patients in that month (Polwaing, 2015). Suppose we analyze the population of Chiang Mai. Record shows that Chiang Mai has total population of 343,585 in 2015 (Thaivbd, 2015). Therefore, lets consider some parameters with this population however the parameters are much different than Table 1. We will consider numerical values that are useful for Chiang Mai epidemiology (Polwaing, 2015). Table 2. contains these numerical values.

Table 2: Numerical Values For Chiang Mai 1

Name of Parameter	Notation	Base Value
Transmission probability of vector to host	β_v	.75
Transmission probability of host to vector	β_h	.75
Bites per susceptible mosquito per day	b_s	.5
Bites per infectious mosquito per day	b_i	1
Contact Rate, Host to Vector	C_{hv}	.375
Contact Rate, Vector to Host	C_{vh}	.75
Human Life Span	$\frac{1}{\mu_h}$	25000days
Mortality Rate of Vectors	μ_v	VL
Recovery Rate	γ_h	.143
Host Infection Duration	$\frac{1}{\mu_h+\gamma_h}$	$\frac{1}{.00004+.143} \approx 6.99105$

Lets consider VL = 12 days. 12 days are consider to be–a minimum number of days that a mosquito lives (Lee, 2009) (Noorani & Side, 2013). Lets consider 20,000 mosquitoes. Thus we get

$$\begin{aligned} \frac{dx}{dt} &= .00004(1-x(t)) - .043657x(t)z(t) \\ \frac{dy}{dt} &= .043657x(t)z(t) - .14304y(t) \\ \frac{dz}{dt} &= .375(1-z(t))y(t) - .083333z(t) \end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) = (1, 0, 0)$$

and

$$(S_h, I_h, R_h) = (-.00003999997121, -.244574341115242, .018200977985241)$$

The Eigen Values for (1,0,0) are $\lambda = .7283438410$, $\lambda = .00007596641692$, $\lambda = .000341732055$. This is unstable.

We wont consider the eigen values for (-.00003999997121,-.244574341115242,.018200977985241). They have negative values.

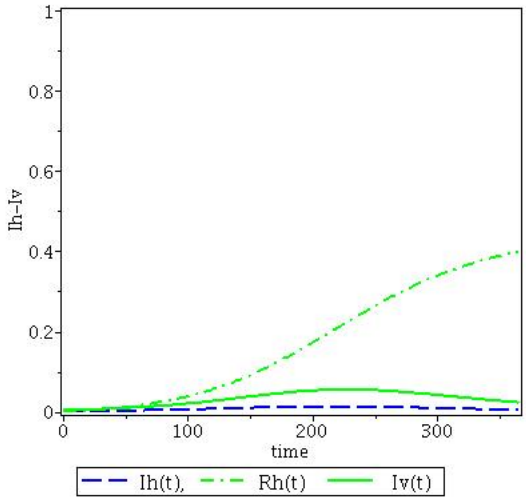
This is unstable $R_0 = 1.171942$, so there is an endemic. We will produce one case with these parameters.

Case 1.

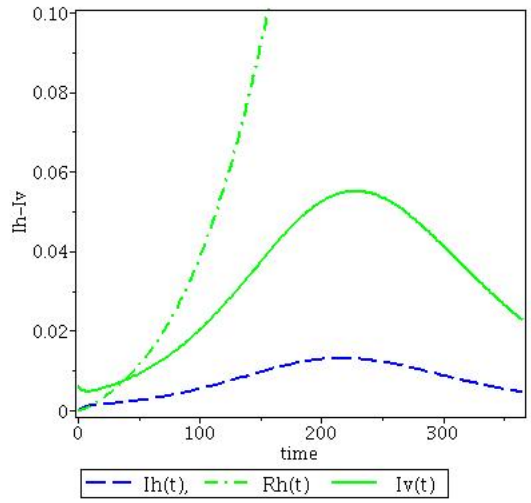
Lets consider some initial data. In the first week of January, 2015 in Chiang Mai, they reported 1 patient (Thaivbd, 2015). Lets consider $S_h(0) = 343,584$, $I_h(0) = 1$, $R_h(0) = 0$ and $S_v(0) = 19875$, $I_v(0) = 125$. Base on Figure 9, we can analyse this initial data.

Figure 9 tells us that there are approximately a maximum of 4,638 infected people, which doesn't match with the data of Figure 8. As well, there is approximately a maximum of 1200 infected mosquitoes. Again, we can't conclude that this analysis is precisely correct in a real situation—because the parameters were used inappropriate. However, the domain of the graph in Figure 9 (0-365), gives a close axis of symmetry when a person and a mosquito is usually at there max. Usually, August (213-243 days) contains the most infected persons in Chiang Mai (Polwaing, 2015), and usually infected mosquitoes are increasing through June - August (151-243 days) (Polwaing, 2015).

Figure 9: Case 1 for Chiang Mai



(a) Zoom Figure 9



Now what if we consider more mosquitoes? We will still consider the same numerical values in Table 2., and we will consider 22500 mosquitoes. This yields

$$\begin{aligned}
\frac{dx}{dt} &= .00004(1-x(t)) - .049114x(t)z(t) \\
\frac{dy}{dt} &= .049114x(t)z(t) - .14304y(t) \\
\frac{dz}{dt} &= .375(1-z(t))y(t) - .083333z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) = (1, 0, 0)$$

and

$$(S_h, I_h, R_h) = (-.00003999997121, -.252144063217938, .0257707000879377)$$

The Eigen Values for (1,0,0) are $\lambda = .6474826029$, $\lambda = .00009857859908$, $\lambda = .0004434069989$ This is unstable.

We wont consider the eigen values for (-.00003999997121,-.252144063217938,.0257707000879377). They have negative values.

This is unstable $R_0 = 1.243032$, so there is an endemic. We will produce one case with these parameters.

Case 2.

Lets consider same initial data Case 1, but we consider different mosquito population. In the first week of January, 2015 in Chiang Mai, they reported 1 incident (RESOURCE). Lets consider

$S_h(0) = 343,584$, $I_h(0) = 1$, $R_h(0) = 0$ and $S_v(0) = 22375$, $I_v(0) = 125$. Base on Figure 10, we can analyse this initial data.

Figure 10: Case 2 for Chiang Mai

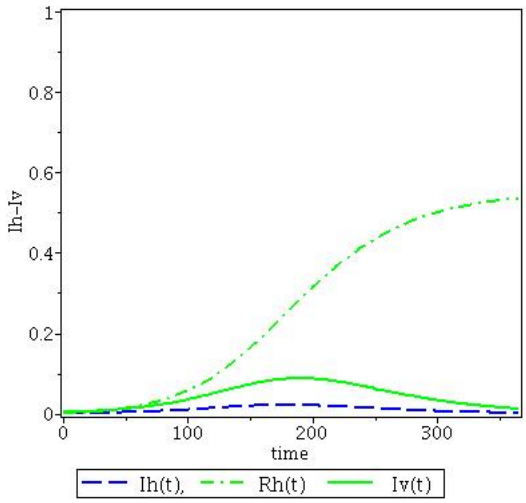


Figure 10 contains an unreasonable axis of symmetry when infected people and mosquitoes are usually at their max, because it shifted the graph to the left. It does not match with data in Figure 8.

Now we will consider less mosquito population. Lets consider 16,000 mosquitoes. Now we have

$$\begin{aligned}
\frac{dx}{dt} &= .00004(1 - x(t)) - .034926x(t)z(t) \\
\frac{dy}{dt} &= .034926x(t)z(t) - .14304y(t) \\
\frac{dz}{dt} &= .375(1 - z(t))y(t) - .083333z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) \quad = \quad (1, 0, 0)$$

and

$$(S_h, I_h, R_h) \quad = \quad (-.00003999997121, -.231459324834017, .00508596170401712)$$

The Eigen Values for (1,0,0) are $\lambda = .9102215000$, $\lambda = .00002510582112$, $\lambda = .0001129634329$. This is unstable.

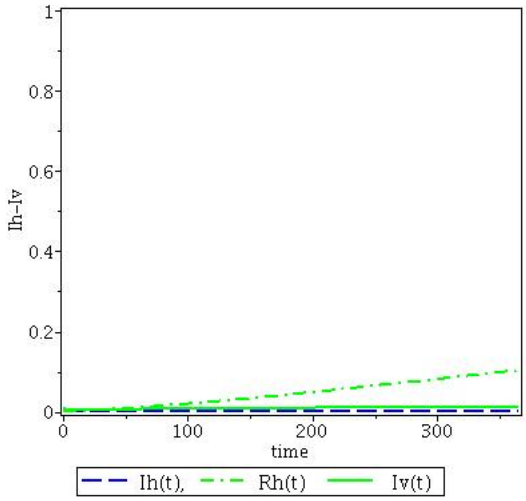
We wont consider the eigen values for (-.00003999997121,-.231459324834017,.00508596170401712). They have negative values.

This is unstable $R_0 = 1.048216$, so there is an endemic. We will produce one case with these parameters.

Case 3.

Lets consider same initial data Case 1, but we consider different mosquito population. $S_h(0) = 343,584$, $I_h(0) = 1$, $R_h(0) = 0$ and $S_v(0) = 15875$, $I_v(0) = 125$. Base on Figure 11, we can analyse this initial data.

Figure 11: Case 3 for Chiang Mai



(a) Zoom Figure 11

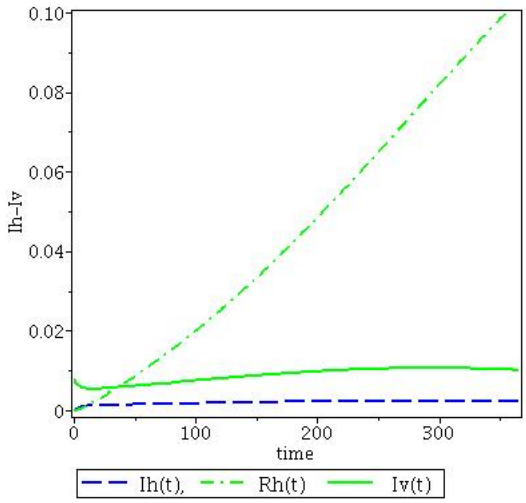


Figure 11 tells us that there are approximately a maximum of 900 infected people, which almost match with the data of Figure 8. Figure 8 contains most infected persons around 212-303. Figure 11—almost contains—similar—- infected people during those days. As well, there is approximately a maximum of 160 infected mosquitoes. Again, we can't conclude that this analysis is precisely correct in a real situation—because the parameters were used inappropriate. However, is the closest numerical solution that matches with Chiang Mai case in 2015, but we see more mosquitoes approximately 260-325 days. Infected mosquitoes are usually increasing through June

- August (151-243 days) (Polwaing, 2015). Is it possible that this year (2015), it increase to October? We don't know base on the model we are analyzing.

Now we will consider a different life span for the mosquitoes.Let VL = 20 days, and we consider the same number of mosquitoes with the same numerical values in Table 2. This yields

$$\begin{aligned}
\frac{dx}{dt} &= .00004(1-x(t)) - .043657x(t)z(t) \\
\frac{dy}{dt} &= .043657x(t)z(t) - .14304y(t) \\
\frac{dz}{dt} &= .375(1-z(t))y(t) - .05000z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) = (1, 0, 0)$$

and

$$(S_h, I_h, R_h) = (-0.00003999997121, -.232665549044702, .039625519244702)$$

The Eigen Values for (1,0,0) are $\lambda = .4373724596$, $\lambda = .0001573341773$, $\lambda = .001178615556$. This is unstable.

We wont consider the eigen values for (-0.00003999997121,-.232665549044702,.039625519244702). They have negative values.

This is unstable $R_0 = 1.512970$, so there is an endemic. We will produce one case with these

parameters.

Case 4.

Lets consider same initial data Case 1, but we consider different mosquito population. Lets consider $S_h(0) = 343,584$, $I_h(0) = 1$, $R_h(0) = 0$ and $S_v(0) = 19,875$, $I_v(0) = 125$. Base on Figure 12, we can analyse this initial data.

Figure 12: Case 4 for Chiang Mai

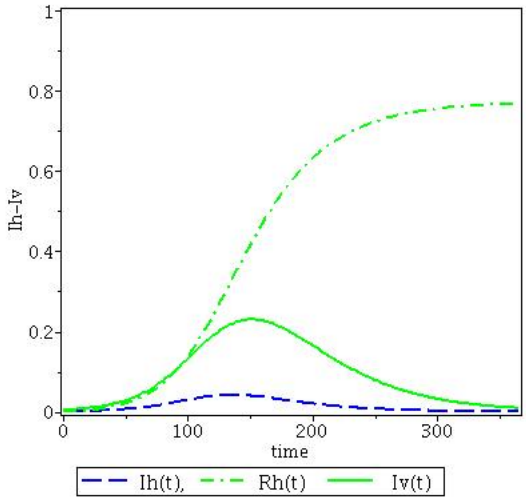


Figure 12. has no biological meaning to study. However, a larger life span in this model, will shift the curve more to the left. Although, the numerical values for Chiang Mai considers a death parameter of .000035 thus we will test this out. Since, our model assumes death and birth to be the same, we will consider human life span to equal .000035 base on Table 3.

Table 3: Numerical Values For Chiang Mai 2

Name of Parameter	Notation	Base Value
Transmission probability of vector to host	β_v	.75
Transmission probability of host to vector	β_h	.75
Bites per susceptible mosquito per day	b_s	.5
Bites per infectious mosquito per day	b_i	1
Contact Rate, Host to Vector	C_{hv}	.375
Contact Rate, Vector to Host	C_{vh}	.75
Human Life Span	$\frac{1}{\mu_h}$	$\frac{1}{.000035}$
Mortality Rate of Vectors	μ_v	VL
Recovery Rate	γ_h	.143
Host Infection Duration	$\frac{1}{\mu_h+\gamma_h}$	$\frac{1}{.00004+.143} \approx 6.991296$

Lets consider VL = 12 days. 12 days are consider to be the minimum number of days that a mosquito lives (Lee, 2009) (Noorani & Side, 2013). Lets consider 20,000 mosquitoes. Thus we get

$$\begin{aligned} \frac{dx}{dt} &= .000035(1-x(t)) - .043657x(t)z(t) \\ \frac{dy}{dt} &= .043657x(t)z(t) - .143035y(t) \\ \frac{dz}{dt} &= .375(1-z(t))y(t) - .083333z(t) \end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) = (1, 0, 0)$$

and

$$(S_h, I_h, R_h) \;=\; (-.00003499999844, -.244571255304007, .018202921174007)$$

The Eigen Values for (1,0,0) are $\lambda = .7282871761$, $\lambda = .00006648686236$, $\lambda = .0002991013923$. This is unstable.

We wont consider the eigen values for (-.00003499999844,-.244571255304007,.018202921174007). They have negative values.

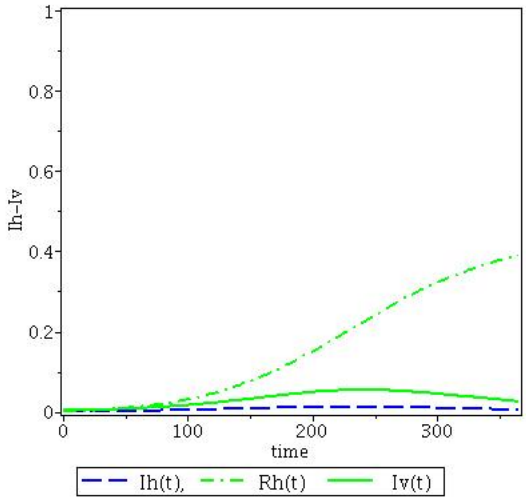
This is unstable $R_0 = 1.171962$, so there is an endemic. We will produce one case with these parameters.

Case 5.

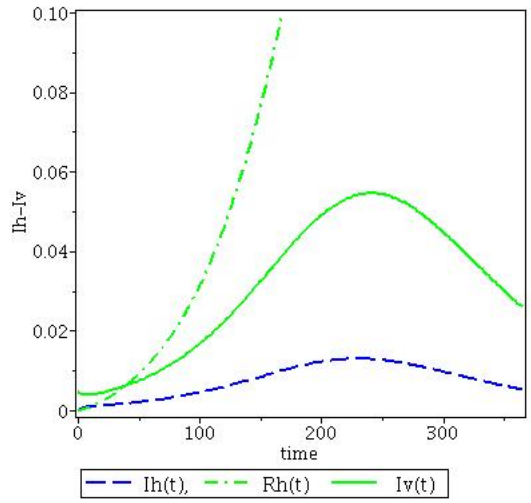
Lets consider some initial data. Lets consider $S_h(0) = 343,583$, $I_h(0) = 2$, $R_h(0) = 0$ and $S_v(0) = 19900$, $I_v(0) = 100$. Base on Figure 13, we can analyze this initial data.

Figure 13 tells us that there are approximately a maximum of 4,810 infected people. As well, there is approximately a maximum of 1200 infected mosquitoes. Again, we can't conclude that this analysis is precisely correct in a real situation—because the parameters were used inappropriate. However, the domain of the graph in Figure 13 (0-365), gives a close axis of symmetry when a person and a mosquito is usually at there max. Usually, August (213-243 days) contains the most infected persons in Chiang Mai (Polwaing, 2015), and usually infected mosquitoes are increasing through June - August (151-243 days) (Polwaing, 2015).

Figure 13: Case 5 for Chiang Mai



(a) Zoom Figure 13



Now consider VL = 14 days with 20000 mosquitoes. This yields

$$\begin{aligned}
\frac{dx}{dt} &= .000035(1-x(t)) - .043657x(t)z(t) \\
\frac{dy}{dt} &= .043657x(t)z(t) - .143035y(t) \\
\frac{dz}{dt} &= .375(1-z(t))y(t) - .071429z(t)
\end{aligned}$$

We use MAPLE software, which yields these two equilibrium points

$$(S_h, I_h, R_h) \quad = \quad (1, 0, 0)$$

and

$$(S_h, I_h, R_h) \quad = \quad (-.00003499999844, -.240097751896423, .0256341796664228)$$

The Eigen Values for (1,0,0) are $\lambda = .6243605874$, $\lambda = .00009191721450$, $\lambda = .0004823326191$. This is unstable.

We wont consider the eigen values for (-.00003499999844,-.240097751896423,.0256341796664228). They have negative values.

This is unstable $R_0 = 1.265864$, so there is an endemic. We will produce one case with these parameters.

Case 6.

Lets consider some initial data. Lets consider $S_h(0) = 343,583$, $I_h(0) = 2$, $R_h(0) = 0$ and $S_v(0) = 19900$, $I_v(0) = 100$. Base on Figure 14, we can analyst this initial data.

Figure 14: Case 6 for Chiang Mai

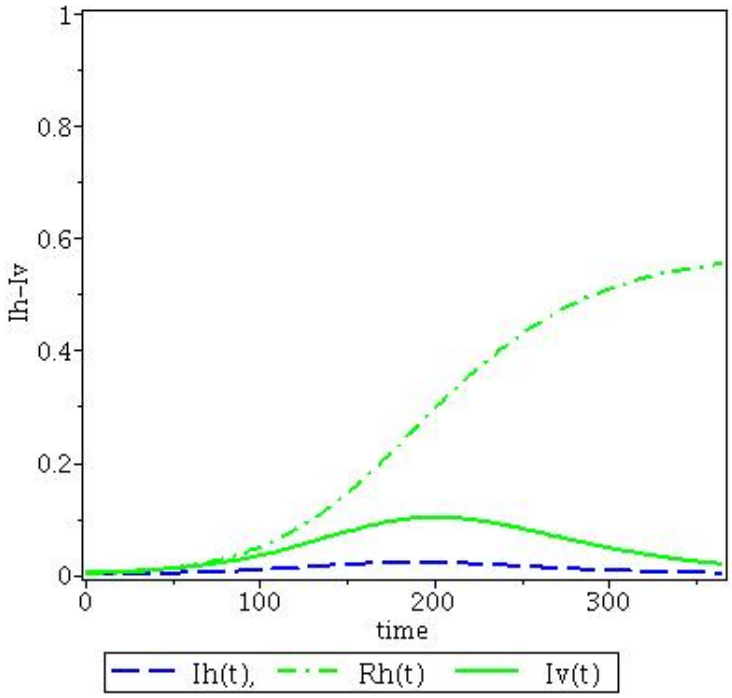


Figure 14 biologically is unreasonable (Polwiang, 2015).

Base on all the figures we constructed, we realize a larger life span and mosquito population—will shift the curve of the graph in this model—to an unreasonable biological matter when infected humans and mosquitoes are at their max.

CHAPTER VII

FUTURE WORK

Based on Polwiang's paper in 2015, he worked with a temperature mathematical model that is similar to the SIR for dengue fever but more accurate. (Polwiang, 2015). They denoted that mosquitoes, respect to time and temperature, will change the mosquito population, mortality rate, and infection rate. This is true based on the biological perspectives (Biology, n.d.). Anyways, they used data from reported cases in Chiang Mia in Thailand, and these cases contain data from 2004-2014. Furthermore, we will consider useful parameters that is used Chiang Mia cases (Polwiang, 2015) and we will introduce an idea that considers Chiang Mia incidences in 2015 (Thaivbd, 2015). However, we will consider a small time interval where it lies when mosquitoes are at their peek, thus we can fix a constant temperature during the time interval. If we do allow a constant temperature with a small time interval, then it wont do much effect towards the independent variables for the SIR Model for Dengue Fever. Although, we can't consider anything above it or before that time interval thus we will analyse a small interval only (initial value problems, IVP). The time interval we chose is from July-September. This time lies when infected mosquitoes are higher than any other month and large amounts of incidents in Chiang Mai (Polwiang, 2015). So, we took the average mean temperature for all three months in 2015 which you can see Table 4 (Weather Underground, 2015). This temperature helps us calculate the mortality rate of the mosquito Aedes Aegypti (Galvani & Macoris & Yang, 2009) (Polwiang,2015).

$$\begin{aligned} \mu_v(T) &= .8692 - .159T + .01116T^2 - 3.408 \times 10^{-4}T^3 + 3.809 \times 10^{-6}T^4 \\ & such \quad that \\ 10.54^\circ C < & \quad T \quad < 33.4^\circ C \end{aligned}$$

Table 4: Average Temperatures for Chiang Mia in 2015

Month	Average Mean Temperature
July	84^oF
August	84^o F
September	84^oF
Average	84^o F

July-September averages out 84^oF, and we will consider it constant for July-September.

$$\begin{aligned} 84^\circ F \quad & \Rightarrow \quad 28.8889^\circ C \\ \Rightarrow \quad \mu_v(28.8889) & = .026027 \end{aligned}$$

We want to use $\mu_v = .026027$ to a similar SIR mathematical model for the Dengue Fever that considers better parameters to calculate a close approximation to real data–respect to time. However, we want to construct IVP only on July-September and try to match it with Chiang Mai 2015 data.

As well, calculate reproduction number from interventions and foward and see in reality if its unstable or stable.

CHAPTER VIII

CONCLUSION

Here we have considered a mathematical model for the transmission of dengue fever in human by using host and vector concept. For three compartments of susceptible, infective and removed for host (human) and two compartments of susceptible and infective for vector (dengue mosquitoes), we have obtained five nonlinear ordinary differential equations (ODEs). After non-dimensionalization, we have a system of three nonlinear ODEs. Reproductive number, R0 and two equilibrium points E1, E2 are calculated for various cases using Maple. Computational results are presented in graphical forms for various scenarios for susceptible, infective and removed and the results. It is observed that when $R0 \leq 1$, E1 is stable and when $R0 > 1$, E2 is stable.

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BIOGRAPHICAL SKETCH

Joseph Diaz, born August 14, 1991, grew up in Weslaco, TX. He graduated from South Texas College with a Certificate, May 2010. Later, he graduated from Weslaco High School, June 2010, and was in the top 10%. After high school, he attended in University of Texas-Pan American, August 2010 and he graduated with Bachelors of Science in Applied Mathematics, December 2013. He further progress his studies, and he decided to pursue a Masters of Science in Mathematical Science with Concentration in Applied Mathematics from the University of Texas Rio Grande Valley in 2015. Thus, he accomplished his Masters degree in December 2015. While pursuing his Masters degree, he served as a graduate teaching assistant. He was a member in the Society for Industrial and Applied Mathematics and SPIE. His permanent mailing address 8701 Big Valley, Dr. Weslaco Tx.