Mathematical Models for Infectious Disease Dynamics:

A Case of Dengue Fever Transmission in Thailand

Collins Bekoe

A Thesis Submitted in Partial Fulfillment of the Requirements for the Degree of

Master of Science in Applied Mathematics

Prince of Songkla University

2017

Thesis Title	Mathematical Models for Infectious Disease Dynamics: A Case of Dengue Fever Transmission in Thailand
Author	Mr. Collins Bekoe
Major Program	Applied Mathematics

Major Advisor

……
(Dr. Pakwan Riyapan)

Co-advisor

……
(Dr. Tatdow Pansombut)

……
(Asst. Prof. Dr. Aniruth Phon-On)

Examining Committee:

…… Chairperson
(Dr. Nifatamah Makaje)

……
(Dr. Pakwan Riyapan)

……
(Dr. Tatdow Pansombut)

……
(Asst. Prof. Dr. Aniruth Phon-On)

……
(Asst. Prof. Dr. Konvika Kongkul)

The Graduate School, Prince of Songkla University, has approved this thesis as partial fulfillment of the requirements for the Master of Science Degree in Applied Mathematics.

……
(Assoc. Prof. Dr. Teerapol Srichana)
Dean of Graduate School

This is to certify that the work here submitted is the result of the candidate's own investigations. Due acknowledgement has been made of any assistance received.

……. Signature

(Dr. Pakwan Riyapan)

Major Advisor

……. Signature

(Dr. Tatdow Pansombut)

Co – Advisor

……. Signature

(Asst. Prof. Dr. Aniruth Phon-On)

Co –Advisor

……..... Signature

(Mr. Collins Bekoe)

Candidate

I hereby certify that this work has not been accepted in substance for any other degree, and is not being currently submitted in candidature for any degree.

…….. Signature

(Mr. Collins Bekoe)

Candidate

ชื่อวิทยานิพนธ์ ตัวแบบเชิงคณิตศาสตร์สำหรับพลศาสตร์ของโรคติดเชื้อ: กรณีการแพร่เชื้อของโรคไข้เลือดออกในประเทศไทย

ผู้เขียน Mr. Collins Bekoe

สาขาวิชา คณิตศาสตร์ประยุกต์

ปีการศึกษา 2559

บทคัดย่อ

โรคไข้เลือดออกเป็นโรคติดเชื้อที่เกิดจากเชื้อไวรัสเดงกี โดยมียุงลายตัวเมียเป็นพาหะของโรค ในงานวิจัยฉบับนี้ ผู้วิจัยได้ทำการศึกษาพลวัตรของการระบาดของโรคไข้เลือดออกในประเทศไทย สำหรับจังหวัดเชียงใหม่ จันทบุรี และ ร้อยเอ็ด โดยใช้ตัวแบบเชิงคณิตศาสตร์ของประชากรคนและยุง ซึ่งเขียนในรูประบบสมการเชิงอนุพันธ์แบบไม่เชิงเส้นจำนวน 7 สมการ ทั้งนี้ผู้วิจัยได้วิเคราะห์ความเสถียรภาพของจุดสมดุลที่ได้จากตัวแบบเชิงคณิตศาสตร์ดังกล่าวและค่าระดับการติดเชื้อของโรค ($R_{\circ}$) พร้อมทั้งหาผลเฉลยเชิงตัวเลขของตัวแบบเชิงคณิตศาสตร์ด้วยวิธีสมการเชิงผลต่างอันตะแบบไม่มาตรฐานและแสดงผลด้วยกราฟ นอกจากนี้ผู้วิจัยได้นำข้อมูลจากสำนักระบาดวิทยาประเทศไทยมาแสดงในแผนที่เฉพาะเรื่อง เพื่อแสดงการกระจายของจำนวนผู้ติดเชื้อไข้เลือดออกเฉลี่ยในช่วง พ.ศ. 2546 ถึง พ.ศ. 2558 ของแต่ละจังหวัด โดยเปรียบเทียบกับจำนวนผู้ติดเชื้อไข้เลือดออกเฉลี่ยของประเทศในช่วงเวลาเดียวกัน

Thesis Mathematical Models for Infectious Disease Dynamics: A Case of Dengue Fever Transmission in Thailand

Author Mr. Collins Bekoe

Major Program Applied Mathematics

Academic Year 2016

ABSTRACT

Dengue fever is an infectious disease caused by the dengue virus, which has female mosquitoes as carriers. In this thesis, we study the dynamics of dengue fever transmission in Thailand, considering Chiang Mai, Chanthaburi, and Roi Et provinces, by using a mathematical model for human and mosquito populations consisting of seven nonlinear differential equations. We also analyze the stability of equilibrium points and the basic reproduction number R_o. The model is solved numerically by using a nonstandard finite difference scheme and the numerical solutions are shown by graphs. Moreover, by using the data obtained from the Thai Bureau of Epidemiology, we show the thematic map of distribution of the average number of dengue fever cases for 2003-2015 for each province in Thailand in relation to the country's average number of cases in the same period of time.

Acknowledgement

First and foremost, I would like to thank the Almighty God for seeing me through this study. I would like to show my profound gratitude to my advisors, Dr. Pakwan Riyapan, Dr. Tatdow Pansombut and Asst. Prof. Dr. Aniruth Phon – On for their guidance, advice, encouragement and motivation for my study. Their efforts are deeply appreciated and I am happy to have them through this study.

I would like to also thank the Applied Mathematics program committee chaired by Dr. Nifatamah Makaje for giving me the opportunity to enhance my knowledge through this program. I will like to appreciate the Department of Mathematics and Computer Science headed by Asst. Prof. Dr. Areeyuth Sama-Ae for providing me with a conducive atmosphere to do my study.

I would like to acknowledge the Higher Education Research and Promotion and Thailand's Education Hub for Southern Region of ASEAN Countries Project Office of Higher Education Commission for funding my studies. I am also grateful to the Faculty of Science and Technology and the Office of the Graduate School, Pattani campus.

I appreciate my colleagues and friends in Applied Mathematics as well as the Research Methodology Program for being there when I needed them most. Special thanks to Mr. Sampurna Kakchapti, Mr. Bright Emmanuel Owusu, Benjamin Attah Owusu, Cornelia Afia Appianing, George Gyamfi, Nitinun Pongsiri, Syafika Ulfah, Saeful Bahtiar, Farida, and Sureeluk for their enormous help and assistance.

Finally, I would like to thank my parents, Mr. Christian Kofi Darko and Mrs. Beatrice Darko not forgetting my brothers and sisters in the persons of Angelina Darko, Christopher Darko, Cynthia Darko, Christian Asare-Darko, Matilda Serwaa Darko, and Clement Ansah Darko as well as Mavis Owusu Damprane. Their help and support throughout my entire educational life will never be forgotten. God richly bless them.

Collins Bekoe

Table of Contents

List of Figures

List of Tables

Chapter 1

INTRODUCTION

1.1 Overview

1.1.1 Mathematical Models

Infectious disease still remains a problem in the world today. Diseases such as Ebola, Yellow fever, HIV/AIDS, Malaria, Dengue fever and others still cause deaths in developing countries. Despite many successes made in the control and prevention of such diseases, they still remain an enormous threat to humanity. Over a couple of years now, mathematical models have been widely used in the study of the dynamics and patterns of the spread of infectious diseases from microbiology to epidemiology. Mathematical models for the study of infectious disease dynamics have been applied in the filled of immunology and public health. A good mathematical model can be used to study the patterns and understand the spread of diseases within a population with the estimation of parameters and comparing of hypotheses (Hethcote, 2000). The practical challenges in formulating a good mathematical model arise from establishing the necessary data in managing increasingly large volume of information. Theoretical challenges require the study and formulation of nonlinear systems in which these infectious diseases evolve and spread.

The dynamics of the diseases are modelled and formulated into systems of nonlinear differential equations based on some assumptions. Different parameters in the model describe the rate at which the disease spread, the survival rate of the disease, the recovery rate, lifespan of the population, rate of loss of immunity over time and other factors that are specific with a particular disease. Changing these

parameters give epidemiologists the necessary information as to how the spread of such diseases can be controlled either through vaccination or isolation of infected individuals. These parameters also allow mathematical epidemiologists to predict whether the disease would die out over time or can attain an epidemic level.

1.1.2 Dengue Fever and Dengue Hemorrhagic Fever

Infectious diseases that can be modelled using differential equations include Ebola, HIV/AIDS, Malaria, Tuberculosis, Dengue fever, and many others. One of such diseases worth studying is dengue fever, which according to the World Health Organisation, 50-100 million cases occur each year worldwide.

Dengue fever is a disease transmitted by the female Aedes Agypti mosquitoes. The disease is sometimes called “break bone fever” because of its associated joint pains and sometimes rashes. The World Health Organization describes four immunologically distant virus serotypes. The serotypes are Dengue Virus 1 (DEN-1), Dengue Virus 2 (DEN-2), Dengue Virus 3 (DEN-3), and Dengue Virus 4 (DEN-4) (WHO, 2015). Dengue can affect all age groups, that is from infants to adults, and symptoms appear 3-14 days after a person is bitten by an infected mosquito.

An infected person experiences a life-long immunity when he/she recovers from the infection of one of the four dengue virus serotypes (DEN-1, DEN-2, DEN-3, DEN-4) and this is known as homologous immunity. It means that the individual would not be able to get the disease again from the same serotype. As a result the infected person may not be immune to the other three serotypes and this is known as heterologous immunity. The person therefore becomes susceptible in getting the severe form of dengue fever (dengue hemorrhagic fever) in about 12 weeks. The dengue hemorrhagic fever (DHF) is accompanied by vomiting, nausea, and fainting

because of fluid leakage, which causes low blood pressure. The infected person suffers from the fluid leakage for some few days and can lead to death. About 5% of all the cases that are reported at various hospitals are normally classified as dengue hemorrhagic fever.

1.1.3 History of Dengue Fever

The origin of the word Dengue may be difficult to trace but an old theory surrounding the name is that it was derived from the Swahili phrase "Ka – dinga pepo", which means "cramp – like seizure caused by an evil spirit". Also, the Swahili word "dinga" may have originated from the Spanish word "dengue" which means fastidious or careful, describing the gait of a person suffering the bone pain of dengue fever. The slaves in West Indies who suffered from the disease were said to have the posture and gait of a dandy, and so the disease was named "dandy fever".

Dengue fever was first confirmed in 1789 by Benjamin Rush (Dengue Virus Net, 2016), who called it "break bone fever" because of symptoms of myalgia and arthralgia. The epidemiology and spread by the mosquito were known in the 20th century.

Currently, about 40% of the world's population approximately 2.5 billion people live in areas of high risk of dengue fever transmission. The disease has spread to more than 100 countries in Asia, the Pacific, Africa, the Caribbean and the Americas (Dengue Virus Net).

1.1.4 Biological Notes on *Aedes Agypti*

There are many species of mosquitoes; Anopheles quadrimaculatus, culex pipiens, and Aedes Aegypti (Asian tiger mosquito) are among the most common. The

Anopheles is a malaria carrier. Figure 1 shows the image of an Aedes Agypti, the principal vector of dengue virus. The mosquito originated from the African forest but is now living in among humans (Gubler and Clark, 1996). In its original habitat, the Aedes Aegypti breeds in fruit husks, holes in trees and rocks, and natural water – holding containers. In a domestic environment, humans beings are the perfect providers of breeding sites. The nature of the human environment provides a breeding atmosphere for the mosquitoes. The mosquitoes normally breed and lay eggs using rain-collecting containers such as old buckets and tires in the streets, flower-pot saucers, discarded barrels, etc. Places like cupboards and drawers provide a safe-haven for them to hide and multiply.

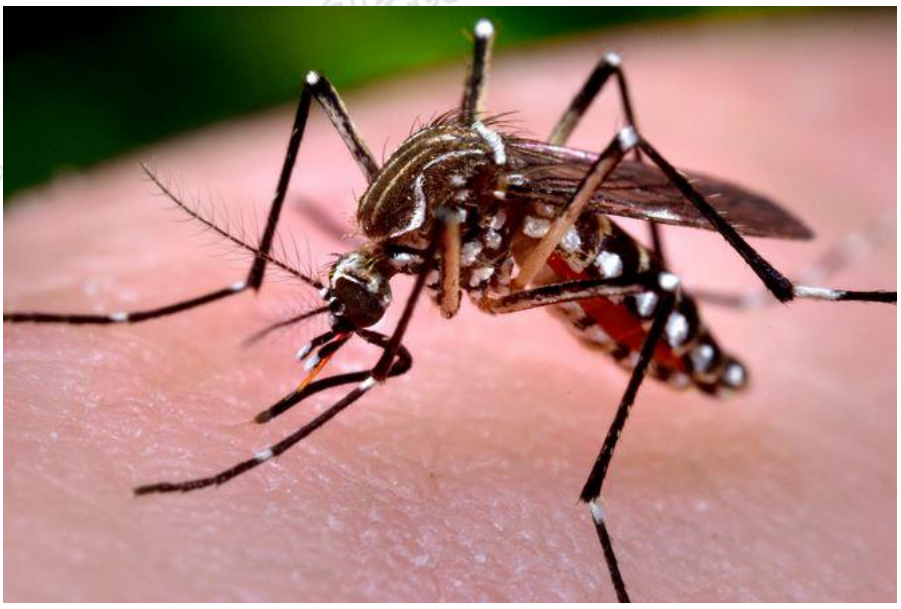


Figure 1. An Aedes Agypti

Source: VectorBase (2015)

According to Oxitech, only the female Aedes Agypti bites. The blood proteins in humans are needed by the female mosquito in order to lay eggs. The male mosquito does not need the blood proteins but rather require carbohydrates, which comes from

nectar from flowers and plants (a natural sugar source). The spread of the dengue virus in a population begins when a female bites and sucks blood from a human suffering from dengue. The mosquito then becomes infected with the dengue virus and in about 8-10 days later, the dengue virus circulates through the mosquito's salivary system. The virus remains in the mosquito's saliva and gets transmitted to a healthy human when the mosquito bites. The female Aedes Aegypti remains infected for its entire lifetime and after every bite, the virus is being transmitted to a new person (Chamberlain and Sudia, 1961). The life cycle of the mosquito is shown in Figure 2.

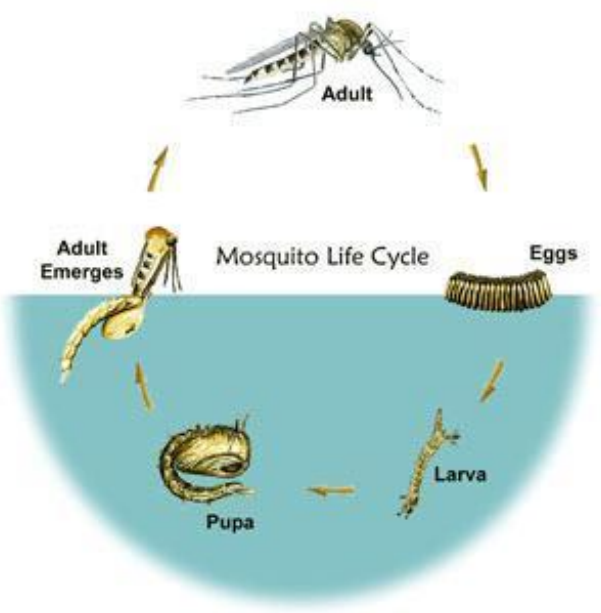


Figure 2. The life cycle of the mosquito

Source: Environmental Protection Agency, USA (2015)

1.1.5 Transmission of Dengue Fever

According to the World Health Organization, dengue fever is transmitted by the female Aedes Aegpti mosquito. Humans get the virus when they are bitten by the female mosquito. A mosquito with the dengue virus is able to transmit it after 8 – 10 days' incubation period. It remains infected in its entire life span.

The main carriers and multipliers of dengue fever virus are the infected symptomatic or asymptomatic humans. Infected people can transmit the infection (4 – 5 days; maximum 12 days) through the Aedes Aegypti when they begin to show symptoms. Figure 3 shows the transmission of dengue fever by the female Aedes Aegypti.

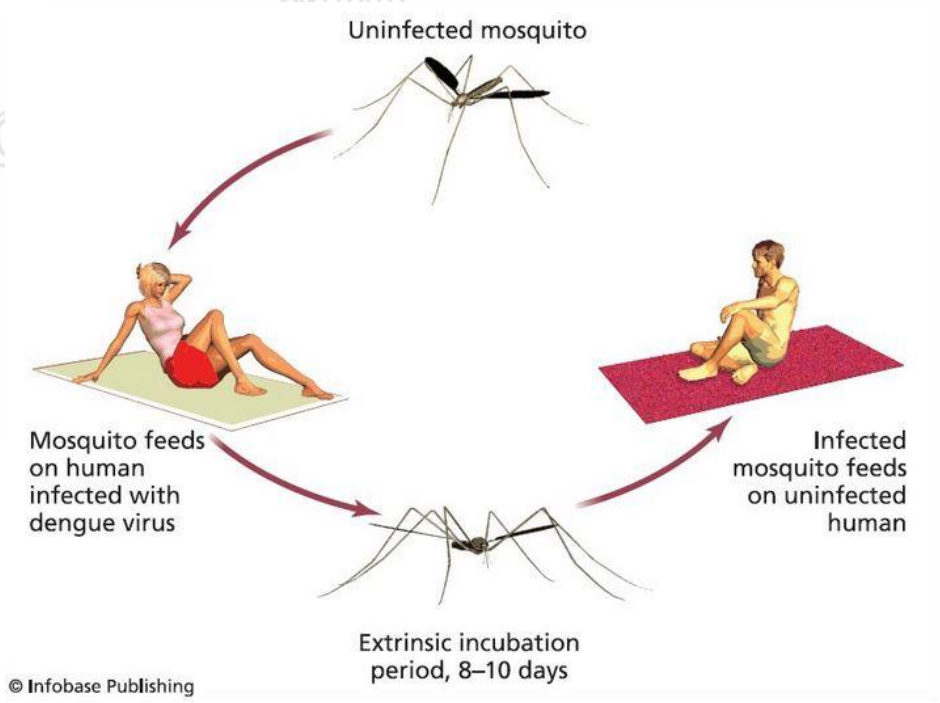


Figure 3. Transmission of dengue fever

Source: Infobase Publishing

1.1.6 Signs and Symptoms of Dengue Fever

Dengue fever is a disease that affects all age groups but seldom causes death according to the World Health Organization. The symptoms of dengue fever is characterized by high fever $\left(40^0 C / 104^0 F\right)$ and any of the following: pain behind the eyes, joint pains, severe headache, vomiting, rash and nausea. The signs and symptoms associated with dengue fever is usually between 2 – 7 days which right after a 4 to 10 – days incubation period.

On the other hand, sever dengue is deadly due to patients suffering from fluid accumulation, sever bleeding etc. In about 3 – 7 days after the first symptoms appear, the patient's temperature may drop below $38^0 C / 100^0 F$ and abdominal pains, continuous vomiting, bleeding gums, restlessness, and fatigue follow this. At this point, the patient is at risk of death if proper medical care is not provided.

1.1.7 Treatment and Vaccines of Dengue Fever

According to the World Health Organization, dengue fever does have a specific. However, medical interventions by heath professionals who are familiar with the progression and effects of dengue fever can save lives. In addition, maintaining and monitoring the volume of the patient's body fluid is essential in caring for a person suffering the dengue disease.

The first dengue vaccine, Dengvaxia (CYD – TDV) by Sanofi Pasteur (Sanofi Pasteur, 2015) has been used in the vaccination of people aged 9 – 45 years in late 2015. In addition, various tetravalent live – attenuated vaccines are in development.

1.1.8 Areas of High Risk

The global burden and transmission of dengue is formidable and almost half of the total people in the world live in areas where dengue is prevalent. Severe dengue (dengue hemorrhagic fever) was first reported in the Philippines and Thailand during the 1950's epidemics. Various statistics confirm how severe the spread of dengue fever is throughout the world. Figure 4 shows the distribution of global dengue risk from 2000 to 2008. The two curves separate countries of risk of dengue transmission from countries of no risk. In 1998, about 616,000 dengue fever cases were recorded in America, of with 11,000 of the cases were classified as hemorrhagic which was twice the number of cases of dengue hemorrhagic fever recorded in the same region in 1995. In 2001, 400,000 dengue hemorrhagic fever cases were recorded in Southeast Asia, while in 2002, 500,000 people were infected in Rio de Janeiro. The epidemic spread to Florida, Southern Texas, and some other states at the time.

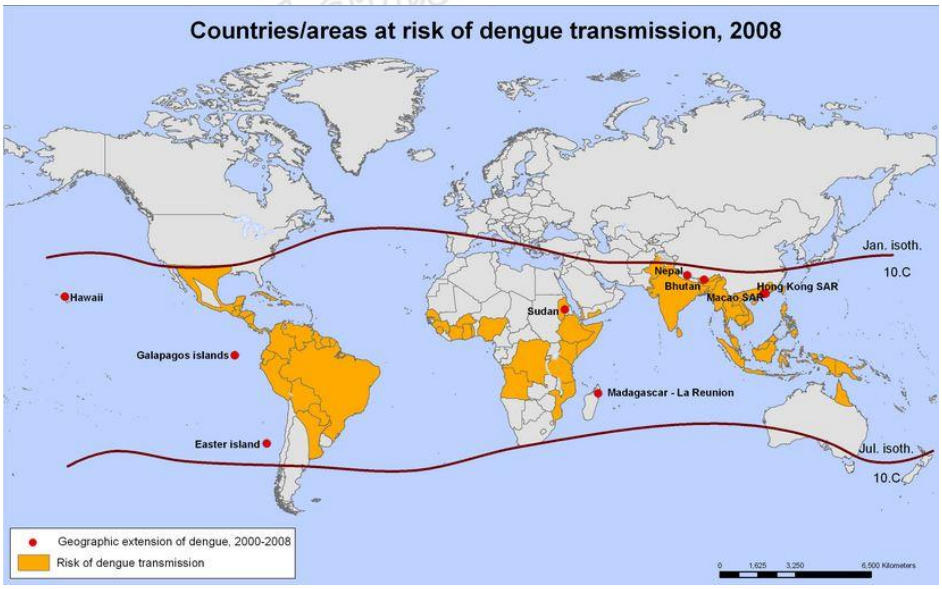


Figure 4. Areas of high risk of dengue fever

Source: World Health Organization, 2008

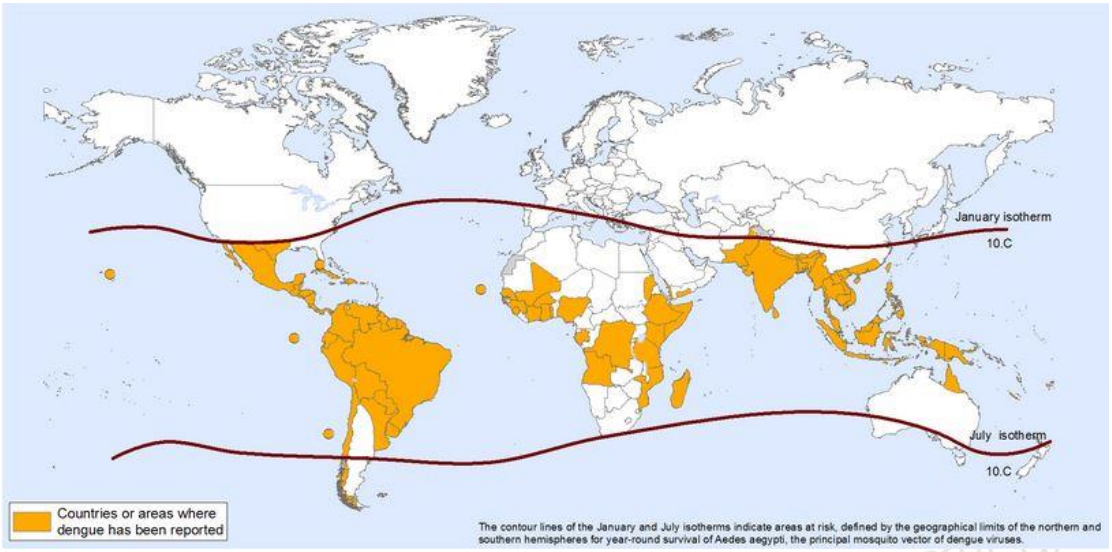


Figure 5. Areas of high risk of dengue fever

Source: World Health Organization, 2013

1.2 Statement of the Problem

Dengue is still health priority in Thailand and the four serotypes circulate in urban and rural areas. According to the World Health Organization, Thailand was the sixth among 30 most highly endemic countries in the world (see Figure 6) between 2004 and 2010 with an average of 74,292 cases and 83 deaths.

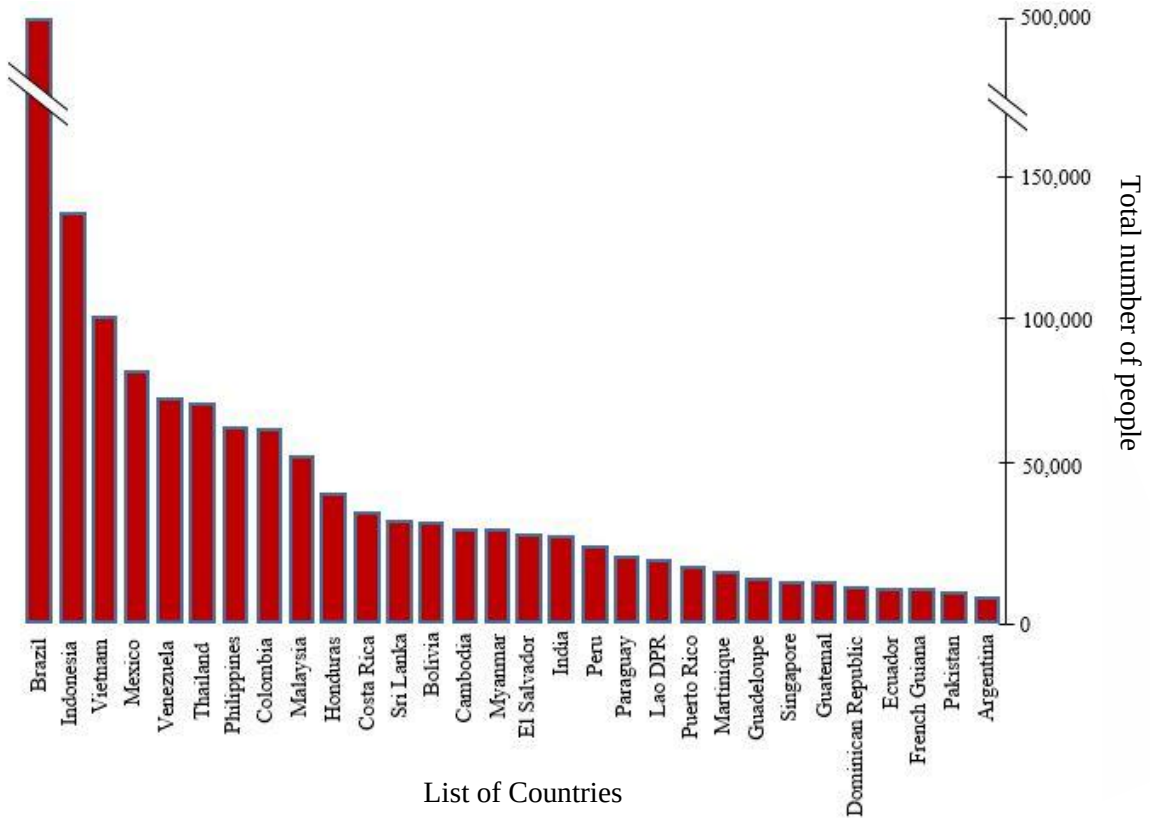


Figure 6. Average number of dengue cases in 30 most endemic countries

Source: World Health Organization (2004)

In 2013, Thailand recorded its worst dengue epidemic in more than 20 years with 87,502 (234.1 cases per 100,000 inhabitants) cases and 6 deaths.

The Bureau of Epidemiology, Ministry of Public Health, Thailand in their National Disease Surveillance report (number 506) reported that 17805 cases of dengue fever have been reported among 76 provinces from 1st January 2016 to 8th August 2016. The Bureau of Epidemiology puts the morbidity rate at 27.34/100,000 population with 3 deaths.

The top five morbidities rated by province at the time were from Maehongsorn (110.36 / 100,000 population), Chiang Mai (67.46/100,000 population.), Bungkan (67.44/100,000 population.), Chanthaburi (65.00/100,000 population.), and Surin

(57.27/100,000 population.). Overall, the northern part of Thailand recorded the highest morbidity rate of 34.66/100,000 population, the northeast had 26.48/100,000 population, the central part had 25.64/100,000 population and the southern part with a 24.00/100,000 population.

1.3 Objectives of the Study

1.1 To study mathematical models for infectious disease dynamics.

1.2 To apply the susceptible, exposed and infected (SEI) model for the human population and the aquatic, susceptible, exposed and infected (ASEI) model for the mosquito population to the problems of dengue fever transmission in Thailand.

1.3 To analyze the simulated results when the model is applied to the real data.

1.4 Expected Advantages of the Study

1.1 Appropriate mathematical models can help understand the interactions between the various compartments coupled with their equilibrium analysis.

1.2 The transmission and spread of dengue fever can be understand to help inform public health interventions for a likely outcome of an epidemic.

1.3 Numerical analysis can help the understanding of the system for better conclusions to be drawn.

1.5 Methodology

Kermack and McKendrick (1927) formulated the SIR model meaning the susceptible, the infected and the recovered for people living with infectious disease in a closed population (i.e., no immigration or emigration) over time. The model assumed that the population size is fixed (i.e., no births, deaths due to disease, or

deaths by natural causes), and the incubation of the infectious agent is instantaneous. They assumed a completely homogeneous population with no age, spatial, or social structure. The model divides the population into compartments with individuals that are identical in terms of their status with respect to the infection.

However, an $SEI + ASEI$ model would be used to study the dynamics of dengue fever transmission in Thailand. The model presents two populations: the host (human) and vector (mosquito) populations. The human population is made up of three epidemiological compartments, which are the susceptible, exposed and infected. The mosquito population is made of four epidemiological compartments namely, the aquatic phase, susceptible, exposed and infected.

The interactions between these compartments are studied by using a system of differential equations. The mathematical model would be solved and analysed by the deterministic approach. Numerical simulations would be carried out using Octave computational software.

1.6 Theoretical Approaches

In this section, the theoretical approaches to the various computations and analysis would be discussed briefly. It would comprise of the general background behind the equilibrium analysis of the model, the stability analysis, the basic reproduction number and numerical method that would be used to solved the model equations.

1.6.1 The Equilibrium Analysis

The general nth order system of continuous differential equations is of the form:

$$\begin{aligned}
\dot{x}_1(t) &= f_1(x_1(t), x_2(t), ..., x_n(t)),\\
\dot{x}_2(t) &= f_1(x_1(t), x_2(t), ..., x_n(t)),\\
&\vdots\\
\dot{x}_n(t) &= f_n(x_n(t), x_n(t), ..., x_n(t)).
\end{aligned}$$

The above system can be written in the matrix form as

$$\dot{X}(t) = f(x(t), t),$$

where $X = [x_1, x_2, ..., x_n]^T$ and $f = [f_1, f_2, ..., f_n]^T$. T means transpose of the vector f (E.M Lungu et al, 2007).

Definition (E. M lungu et al, 2007)**:** *A vector $\bar{X}$ is said to be an equilibrium point of a dynamical system if the state vector is equal to $\bar{X}$ and continuous to be equal to $\bar{X}$ for all the time (future).*

Consider the dynamical system

$$\dot{X}(t) = f(x(t), t).$$

An equilibrium point of the above system would be a state $\bar{X}$ that satisfies

$$f(\bar{X}, t) = 0, \text{ for all time } t.$$

Equilibrium points for a dynamical system maybe none, one or any number in virtually a spatial pattern in state space. The equilibrium points of a linear system are generally the solutions to the linear equations. However, this is not the case of a nonlinear system. Finding solutions to the nonlinear system involves solving polynomials of higher degree which is not the case in the linear system. Also, in the nonlinear case, the distribution of the equilibrium points is more complex than the linear system (E.M Lungu et al, 2007).

In epidemiology, the system of nonlinear equations gives two equilibrium points: the disease free and the endemic equilibrium points. These equilibrium points

are obtained by equating the system of equations to zero and solving for the variables of interest. It is biologically meaningful to always consider only nonnegative solution of the nonlinear system of differential equations.

1.6.2 The Stability Analysis

Consider the Jacobian matrix J of the system f .

$$J = \begin{pmatrix} \frac{\partial f_1}{\partial x_1} & \frac{\partial f_1}{\partial x_2} & \cdots & \frac{\partial f_1}{\partial x_n} \\ \frac{\partial f_2}{\partial x_1} & \frac{\partial f_2}{\partial x_2} & \cdots & \frac{\partial f_2}{\partial x_n} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1} & \frac{\partial f_n}{\partial x_2} & \cdots & \frac{\partial f_n}{\partial x_n} \end{pmatrix}.$$

The stability analysis can be done on the linearized system based on the following.

1. In the nonlinear system, $\bar{x}$, the equilibrium point is asymptotically stable, if all eigenvalues of J are specifically in the left half plane, that is if they have all strictly negative real parts .

2. The equilibrium point $\bar{x}$ is unstable in the nonlinear system if at least one eigenvalue of J has a positive real part.

3. The equilibrium point $\bar{x}$ may be either stable, asymptotically stable or unstable for the nonlinear system if the eigenvalues of J are all in the left half –plane (strictly negative real part) but at least there is one eigenvalue with a zero real part.

1.6.3 The Basic Reproduction Number, R_o

Diekmann and Heesterbeek (1990) and Van den Driessche and Watmough (2002) have shown that the basic reproduction number R_0 is equal to the spectral ratio of the matrix $J_F J_V^{-1}$, where $F(z)$ is the rate of appearance of new infections, $V(z)$ is the rate of transfer of individuals in and out of the infected compartment and z describes the linearization of the reduced system around the disease free equilibrium. Note that the spectral ratio of any matrix is equal to the largest eigenvalue.

Therefore, the basic reproduction number, R_0, according to Driessche et al. (2002) can be calculated as

$$R_0 = \rho\left(J_F J_V^{-1}\right)$$

where J_F and J_V are the Jacobian matrices associated with $F(z)$ and $V(z)$ while ρ denotes the spectral radius of the matrix $\left(J_F J_V^{-1}\right)$. The matrix F and V would be calculated in Chapter 3 of this study.

1.6.4 The Numerical Method

Usually nonlinear differential equations are used to model several physical phenomena. Previous studies by several researchers have shown various attempts that have been made in solving such problems by replacing the nonlinear equations with its related linear equations. These linear equations approximate the actual equations in manner that has close properties with the dynamics of the actual phenomena. As a result, other researchers have suggested various forms of approximations as such

linearization are not always feasible. Studies by Mickens (1981), Fatunla (1988), Mickens (1994) and Lubuma (2003) have used discrete models for nonlinear differential equations.

A nonstandard numerical scheme developed by Mickens (1994) would be used in section 3.7 in Chapter 3 to solve the nonlinear differential equations representing the evolution of the different compartments of the $SEI + ASEI$ model.

Solutions to compartmental models are usually found by using standard numerical methods like Euler or the Runge Kutta methods. ODE45 function in a computational software like MATLAB is also usually used to solve epidemic models involving ordinary differential equations. However, these standard numerical methods can lead to numerical instabilities for some parameter values (Dumont, 2008).

Mickens (1994) developed the non-standard finite difference scheme based on some rules. The general form of the non-standard scheme is written as

$$y_{n+1} = F(h, y_n).$$

Mickens' stated five rules and they are as follows:

Frist rule

The first rule states that the order of the discrete derivative should be exactly the same as the order of the corresponding derivatives of the differential equation.

Consider the example below (Sunday, 2010)

$$\frac{dy}{dx} = -y. \qquad \text{(a)}$$

Applying the central difference scheme to equation (a) gives

$$\frac{y_{n+1} - y_{n-1}}{2h} = -y_n. \qquad \text{(b)}$$

It can therefore be seen that equation (b) if of the second order while equation (a) is of the first order. This can lead to numerical instability as it violates the principle of uniqueness.

Second rule

The second rule introduces a complex analytic function of h in the denominator which expresses the step size with a complicated function than what the standard methods use.

As an example, consider the logistic equation below.

$$\frac{dy}{dx} = y(1-y).$$

Having $\frac{dy}{dx} \to \frac{y_{n+1} - y_n}{\phi(\lambda, h)}$. (c)

Where $\phi(\lambda, h)$ the denominator function has the property that $\phi(\lambda, h) = h + O(h^2)$

The variable λ in equation (c) is fixed as the variable h approaches zero $(h \to 0)$.

If the denominator function for equation, (c) is given by $D_1 = e^h - 1.$ (d)

Then substituting equation (d) into (c) gives

$$\frac{y_{n+1} - y_n}{e^h - 1} = y_n(1 - y_{n+1}). \qquad \text{(e)}$$

As Mickens stated in 1999, the selection of the denominator is an ‘art’ and that the differential equation must be examined for which the exact schemes are known.

Third rule

The third rule states that the nonlinear terms must be generally approximated in a non – local way whiles implicitly dealing with the linear terms.

For example, in equation (e), there is an assumption that $y^2 \cong y_n y_{n+1}$.

The nonlinear terms y^2, y^3 can therefore be modeled as

$$y^2 \cong y_n y_{n+1},$$
$$y^2 \cong y_n \left(\frac{y_{n+1} + y_n}{2} \right),$$
$$y^3 \cong y_n^2 y_{n+1},$$
$$y^3 \cong y_n^2 \left(\frac{y_{n+1} + y_n}{2} \right).$$

Fourth rule

Differential equations having special solutions must be accompanied by finite difference models with special discrete solutions.

Fifth rule

The solution to the finite – difference equation should correspond to the solution of the differential equations.

The nonstandard numerical scheme is required to be qualitatively stable in relation with monotone dependence on the initial value according to Anguelov et al. (2001). That is

$$\frac{\partial F(h, y)}{\partial y} \geq 0, \ y \in \mathbb{R}, h > 0.$$

As an application in an epidemiological model, consider the standard SIR model developed by Kermack and Mckendn'ck (1927) as follows:

$$\frac{dS}{dt} = -bSI,$$
$$\frac{dI}{dt} = bSI - \gamma R,$$
$$\frac{dR}{dt} = \gamma R.$$

Where S is the susceptible compartment, I is the infected compartment, R is the recovered compartment, b is the transmission rate and γ is the recovery rate.

Let S^n, I^n and R^n be the approximations of $S(t_n)$, $I(t_n)$ and $R(t_n)$, respectively for $n = 0,1,2...$ and $\Delta t > 0$, the step size of the scheme.

Applying the Mickens' third rule gives,

$$\frac{S^{n+1} - S^n}{\Delta t} = -bS^{n+1}I^n,$$
$$\frac{I^{n+1} - I^n}{\Delta t} = bS^{n+1}I^{n+1} - \gamma R^n,$$
$$\frac{R^{n+1} - R^n}{\Delta t} = \gamma R^{n+1}.$$

Re-arranging the terms for the susceptible compartment gives,

$$\frac{S^{n+1} - S^n}{\Delta t} = -bS^{n+1}I^n,$$
$$S^{n+1} - S^n = -bS^{n+1}I^n\Delta t,$$
$$S^{n+1} + bS^{n+1}I^n\Delta t = S^n,$$
$$S^{n+1}\left(1 + bI^n\Delta t\right) = S^n,$$
$$S^{n+1} = \frac{S^n}{1 + bI^n\Delta t}.$$

Re-arranging the terms for the infected compartment gives,

$$\frac{I^{n+1}-I^{n}}{\Delta t}=bS^{n+1}I^{n+1}-\gamma R^{n},$$
$$I^{n+1}-I^{n}=bS^{n+1}I^{n+1}\Delta t-\gamma R^{n},$$
$$I^{n+1}-bS^{n+1}I^{n+1}\Delta t=I^{n}-\gamma R^{n}\Delta t,$$
$$I^{n+1}\left(1-bS^{n+1}\Delta t\right)=I^{n}-\gamma R^{n}\Delta t,$$
$$I^{n+1}=\frac{I^{n}-\gamma R^{n}\Delta t}{1-bS^{n+1}\Delta t}.$$

Re-arranging the terms for the recovered compartment gives,

$$\frac{R^{n+1}-R^{n}}{\Delta t}=\gamma R^{n+1},$$
$$R^{n+1}-R^{n}=\gamma R^{n+1}\Delta t,$$
$$R^{n+1}-\gamma R^{n+1}\Delta t=R^{n},$$
$$R^{n+1}\left(1-\gamma\Delta t\right)=R^{n},$$
$$R^{n+1}=\frac{R^{n}}{1-\gamma\Delta t}.$$

Finally, three compartments are put together as follows:

$$S^{n+1}=\frac{S^{n}}{1+bI^{n}\Delta t}, \tag{f}$$

$$I^{n+1}=\frac{I^{n}-\gamma R^{n}\Delta t}{1-bS^{n+1}\Delta t}, \tag{g}$$

$$R^{n+1}=\frac{R^{n}}{1-\gamma\Delta t}. \tag{h}$$

The right hand side of the above equation (g) is positive if $\gamma R^{n}\Delta t > I^{n}$ in the numerator term and $bS^{n+1}\Delta t > 1$ in the denominator term. Similarly, in equation (h), the right hand side is positive if $\gamma\Delta t > 1$ in the numerator term. This means that

positive initial values will give positive approximations, which will always lie in a feasible region.

Organization of the Study

The thesis is made up of 5 main chapters. Chapter 1 presents the general overview of the mathematical models for infectious disease dynamics as well as an in-depth background of dengue fever transmission. The objectives, expected advantages, methodology, theoretical approaches and organization of the study are described in the chapter. Related studies by other researches would be reviewed in Chapter 2. Chapter 3 would present the mathematical model formulation and equilibrium and stability analysis of the model. The numerical simulations and results are presented in Chapter 4. Conclusions and recommendations for further studies are presented in Chapter 5.

Chapter 2

LITERATURE REVIEW

Over the past few decades, the incidence of infectious diseases has increased resulting in researches in mathematical models for studying the patterns of the transmission dynamics. This chapter presents studies and researches that have been carried out in the field of mathematical epidemiology. The chapter focuses primarily on the mathematical models for infectious disease dynamics and specifically dengue fever transmission models.

2.1 Mathematical Models for Infectious Diseases

Feng et al. (2000) used differential equations to describe the transmission dynamics of Tuberculosis (TB). The interest of the research was to study mathematical models to understand the long term behavior of the transmission dynamics of the disease, thus if the disease would develop into an epidemic or it would die out. In the study, the effects of the variable periods of latency on the dynamics of Tuberculosis were considered with an *SEIS* model. In the model, the possibility of re – infection was considered meaning individuals moved back to the susceptible (S) compartment from both the exposed (E) and the infectious compartment after treatment. It was concluded that the introduction of an arbitrarily distributed incubation period (latent) to the basic tuberculosis model did not have a significant impact on the dynamics of TB. However, the spread of disease degenerate into an epidemic or dies out regardless of the shape of the incubation period distribution.

Dumont et al. (2008) presented a mathematical model of Chikungunya disease. The study proposed a model which comprised human and mosquito populations for the epidemics of Chikungunya. The basic reproduction number (R_0), was calculated and it showed a disease – free equilibrium existed which was locally asymptotically stable. This is evident if the basic reproduction number is less than 1. The study showed the global asymptotic stability of the disease – free equilibrium. Several simulations of the basic reproduction number based on a proposed numerical scheme that is qualitatively stable was presented. It was concluded that the basic reproduction number (R_0) varies from place to place and that destroying breeding sites may help in the control of the disease.

2.2 Dengue Fever Transmission Dynamic Models

Derouich et al. (2003) presented a research on dengue fever and dengue Hemorrhagic fever using a compartmental model which involved nonlinear equations for both the human and mosquito populations. It is shown that between 40% and 50% was the infection rate among susceptible individuals. This however can increase to 80% - 90% in times when the condition for the transmission is favorable. The study proposed a model where two different virus serotypes acting at different time periods. The latent period during the susceptible – infective interaction was assumed to be not crucial. This was done by excluding the exposed compartment and using the standard SIR model. Considering a succession of two epidemics by two different virus serotypes, a random fraction, p of the susceptible humans could be immunized against all four serotypes in the first epidemic. Again, a proportion of the population of susceptible could be globally immunized against the four virus serotypes during the

second epidemic. This was an assumption that was considered. The MATLAB programming software was used to carry out simulations with different parameter values in each model in order to illustrate the dynamics of each epidemic. The complexity of the dengue epidemics as shown in the research indicates that vector control remains insufficient since it only delays the outbreak of the epidemic. Although the proposed model suggests the reduction of susceptible through vaccination, it was stated that such strategy is unlikely to be applicable in the short term. An intermediate solution proposed to combine environmental prevention and partial vaccination to avoid the hemorrhagic form of the disease caused by different viruses.

Pinho et al. (2010) analysed dengue transmission using a mathematical model by comparing two dengue epidemics in Salvador and Brazil from 1995 to 1996 and then in 2002. The aim of the study was to understand the dynamics of the two epidemics in a way of investigating the effect the vector control and the susceptible population have on the decrease in the occurrence rate as well as the duration of the outbreak. A compartmental model comprising of the human and the mosquito population was presented with vector control parameters.

The basic reproduction number and the force of infection were obtained using real data for two epidemics. It was found that the value of the basic reproduction number was greater than one for the epidemics in 1993 to 1996 for different values of the vector control parameters. It indicated that other strategies like the control of the aquatic stage of the mosquito would be effective.

Syafruddin and Noorani (2012) presented systems of differential equations that studies the transmission of dengue fever. The SEIR vector transmission of dengue fever was used to determine the dynamic behavior of the system. In the research, they stated that the difference between the standard SIR model and the SEIR model is the inclusion of the latent period as a variable in the SEIR model. Assumptions made in the study were that a number of people in the population have already been infected while others have not. In addition, the spread of the virus is continuous throughout the population but the number of mosquitoes is constant. Another assumption is that there is no re-infection as everyone treated of the disease enjoys a lifetime immunity. Numerical simulations using the ODESOLVE in MATLAB were used for the stability analysis of the system. They concluded that the infection to human is based on data as the dengue virus infection occurs when there is continuous correlation between human and mosquito.

Khalid *et al.* (2015) presented a mathematical model based on the standard SIR model for dengue fever transmission. The spread of serotype 1 of the dengue virus between the subject and the vector was generated using the SIR mathematical model. In this research, the SIR model was used to describe the two kinds of populations involving human (N_h) and vector (N_v). The human population was distinguished into three groups: people already living without the virus (Susceptible, S_h), people who are already infected with the virus (Infected, I_h), and those who have recovered (Removed, R_h). The vector population of mosquitoes N_v was also put into two groups: mosquitoes that may be infected with the virus (Susceptible, S_v) and those infected with the virus (Infected, I_v). In the model, it is assumed that some

people already have the disease while others do not have. The transmission of the virus is continuous and grows in the population while the vector population remains constant. The model was solved by using the perturbation iteration Algorithm (PIA) and the 4th – order Runge – Kutta method. The research showed that the PIA method achieved more accuracy in the solution than the RK4 in the basic spread of dengue fever.

2.3 Basic Reproduction Number

Favier *et al*. (2006) presented a study on the early determination of the reproductive number for vector – bone disease that is a case of dengue in Brazil. The study focused on a new method for deriving the reproductive number for vector – borne diseases from the early epidemic curves with incubations in the vectors and in the hosts. The model was applied to several dengue epidemics in different climatic regions in Brazil. It was shown that the new method led to higher estimates of the reproductive number than previous models and that the Aedes Aegypti densities, the meeting of more compatible strains of viruses and mosquitoes may lead to re – emergence of urban yellow fever epidemics.

Jafaruddin *et al.* (2015) presented an estimation of the basic reproductive ratio (R_0) for dengue fever at the take – off period of dengue infection. In the study, two different constructions for estimating the basic reproductive number which was derived from a dynamical system of host – vector dengue transmission model was proposed. In the construction of the estimates, it was assumed that the rates of infection for mosquito and human compartment might be different. Also, a more realistic condition in which the dynamics of an infected human compartment are

intervened by the dynamics of an infected mosquito compartment and vice versa was included in the estimation of (R_0). The construction was applied to a real dengue epidemic data from SB hospital, Bandung, Indonesia during the November 2008 to December 2012 outbreak. Two scenarios to determine the take – off rate of infection at the beginning of the dengue epidemics for estimating (R_0) was proposed. It was concluded that the second approach in the construction of (R_0) was more realistic as it took into account the presence of infective mosquitoes in the early growth rate of infected humans and vice versa.

Noor *et al.* (2015) used a mathematical model to study dengue fever epidemics in different hospitals of Lahore (Pakistan) during 2010/2011 outbreak period. The model was used to compartmentalize the human population into three compartments and the vector population into two compartments. The model showed that there is a basic reproduction number (R_0) that determines the transmission rate of dengue disease. An explicit formula was derived in the calculation of the basic reproduction number. The value of the basic reproduction number was obtained by using data from different hospitals in Lahore. Numerical simulations were carried out in MATLAB in the calculation of the basic reproduction number against the real data in Lahore. It was found that dengue was epidemic in Lahore and much attention in the control of the disease was needed.

2.4 Control Strategies for Dengue Fever and Aedes Agypti

Burattini *et al.* (2007) applied a mathematical model for dengue infection by taking into account the seasonal variation in incidence and characteristics of dengue

fever for the 2004 and 2005 epidemics in Singapore. The study aimed at comparing the impact of several possible alternative controls strategies based on the reproduction number and also to understand the causes of dengue resurgence to Singapore in the last decade. Through simulation, it was shown that a set of possible control strategies which confirmed the intuitive belief killing adult mosquitoes is the most effective strategy to control an ongoing epidemic. Also, it was shown that the control of immature forms was very efficient in the prevention of dengue epidemics. Lastly, it was concluded that the best strategy is to combine both adulticide and larvicide control measure during an outbreak.

Chapter 3

METHODOLOGY

3.1 Introduction

Dengue fever transmission can be studied using deterministic or stochastic models. The models work by defining compartments for individuals of a population based on how susceptible they are to the disease under consideration. Deterministic models use a set of differential equations to study the interactions between these compartments based on some assumptions.

This chapter presents the susceptible, exposed and infected compartments for the human population as well as the aquatic, susceptible, exposed and infected compartments for the mosquito population. The $SEI + ASEI$ model with vector control represents the dynamics of dengue fever transmission as the disease is between the interaction of host (human) and vector (mosquito). This model presents a set of seven nonlinear differential equations. The equilibrium points together with their stability analysis would be discussed. In addition, an expression that would be used to find the basic reproduction number would be formulated.

3.2 Preliminaries

Mathematical epidemiology studies how a disease is spread in a population and also the factors that determine or influence this distribution. This is done by developing mathematical models using differential equations.

Human disease does not happen in a vacuum. It is as a result of the interaction of the host (infected person), the agent (e.g. viruses) and the environment (e.g.

contaminated water supply). As explained in Chapter 1 under section 1.1.5, dengue fever transmission is from an infected human to a vector (mosquito) then to a healthy human. When dengue fever is in a population, those who are susceptible become exposed for a time period after a mosquito bite. These exposed individuals after an incubation period then show signs of infection and transmission continuous through as more individuals get bitten by an infected mosquito. Thus, for Dengue fever to spread in a population, there should be an interaction between the human and mosquito populations.

This chapter therefore presents a detailed information on the transmission of the disease by using a set of differential equations.

3.3 Model Formulation

3.3.1 Assumptions of the model

The system of differential equations that would be used to study the transmission dynamics of dengue fever would be formulated by keeping in mind the following assumptions.

1. A number of people in the population is already with the infection.
2. The probability of getting the infection is not dependent on age, sex, social status or race.
3. The human and mosquito populations have equal rate of transmitting the disease to the other.
4. There are no re – infections of the disease.
5. The vector (mosquito) population remains constant.

3.3.2 Description of the $SEI + ASEI$ Model

The $SEI + ASEI$ model describes two populations: the host (human) and vector (mosquito) populations.

The human population is made of three epidemiological compartments. They are susceptible (those who are capable of getting the infection), exposed (those who are latently infected but are not infectious) and infected (those who are infectious and are showing signs of infection).

The mosquito population however is made up of four compartments. They are aquatic phase (the eggs that hatch into the adult mosquitoes), susceptible (mosquitoes that are capable of getting the infection), exposed (mosquitoes that are latently infected) and infected (mosquitoes that are infectious and can transmit the infection).

The dynamics of the transmission between the human and the mosquito population is described in Figure 7. All the parameters shown in Figure 7 have been explained in Table 1.

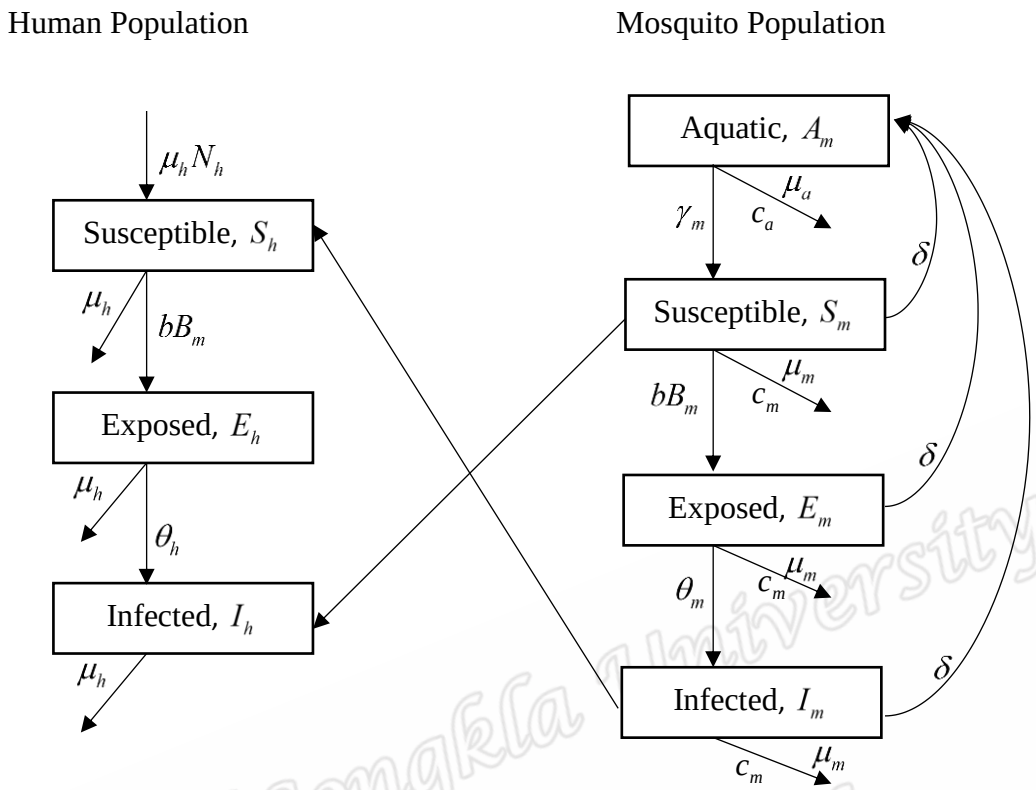


Figure 7. A compartmental model for dengue fever disease

3.3.3 Model Equations

This section explains the formulation of the SEI+ASEI model with each of the terms from the various compartments. As it has been assumed that there are some people in the population with the disease, the transmission of the disease starts with an infected human being bitten by a susceptible mosquito with an average bite per day of b and an infective contact rate of B_m . This rate can be represented as $\frac{bB_m S_m I_h}{N_h}$. The susceptible mosquitoes (S_m) get reduced by a mosquito mortality rate of μ_m and a control effort rate of c_m. The susceptible compartment then joins the exposed compartment with the rate $\frac{bB_m S_m I_h}{N_h}$ and are moved to the infected compartment with

an extrinsic incubation period of θ_m. The adult mosquito at the exposed (E_m) and infected compartment (I_m) die at the rate of μ_m.

The susceptible human (S_h) gets the infection through the bite of an infected mosquito and then join the exposed compartment (E_h) at the rate $\frac{bB_mS_hI_m}{N_h}$. The exposed human becomes infectious after an incubation period of θ_hE_h. There is a human mortality rate of (μ_h) which reduces the various compartments at a point in time. Some individuals recover at the infected compartment (I_h) at the recovery rate of α_h.

The interaction between the human and mosquito populations showing the dynamics of the transmission can be summed up in the following system of differential equations.

$$\frac{dS_h}{dt} = \mu_h\left(N_h - S_h\right) - \frac{bB_mS_hI_m}{N_h}, \tag{1}$$

$$\frac{dE_h}{dt} = \frac{bB_mS_hI_m}{N_h} - \left(\theta_h + \mu_h\right)E_h, \tag{2}$$

$$\frac{dI_h}{dt} = \theta_hE_h - \left(\alpha_h + \mu_h\right)I_h, \tag{3}$$

$$\frac{dA_m}{dt} = k\delta(t)\left(1 - \left(\frac{A_m}{C}\right)\right)M - \left(\gamma_m(t) + \mu_a(t) + c_a(t)\right)A_m, \tag{4}$$

$$\frac{dS_m}{dt} = \gamma_m(t)A_m - \frac{bB_mS_mI_h}{N_h} - \left(\mu_m(t) + c_m(t)\right)S_m, \tag{5}$$

$$\frac{dE_m}{dt} = \frac{bB_m S_m I_h}{N_h} - \left(\theta_m(t) + \mu_m(t) + c_m(t)\right)E_m, \tag{6}$$

$$\frac{dI_m}{dt} = \theta_m(t)E_m - \left(\mu_m(t) + c_m(t)\right)I_m. \tag{7}$$

From equations (1) to (7), $N_h = S_h + E_h + I_h$ is constant and $M = S_m + E_m + I_m$ is also constant. Table 3 shows the parameters used in equations (1) to (7) and their interpretations.

Table 1. Parameters interpretation of the model

Parameter	Biological Meaning
δ	Average oviposit rate
μ_m	Average mosquito mortality rate
μ_a	Average aquatic mortality rate
γ_m	Average aquatic transition rate
θ_m	Extrinsic incubation
μ_h	Human mortality rate
θ_h	Intrinsic incubation rate
α_h	Recovery rate
k	Fraction of female mosquitoes hatched from all eggs
C	Mosquito carrying capacity
b	Average bite per mosquito per day
B_m	Effective contact rate
c_a, c_m	Control effort rates

3.4 Equilibrium and Stability Analysis of the SEI + ASEI model

In this section, the equilibrium points of equations (1) to (7) is computed and the stability analysis is discussed based on section 1.6.1 in Chapter 1.

A point $E = (S_h^*, E_h^*, I_h^*, A_m^*, S_m^*, E_m^*, I_m^*)$ is said to be an equilibrium point for the system of nonlinear equations in equations (1) to (7) if it satisfies the following.

$$
\begin{aligned}
&\mu_h\left(N_h - S_h\right) - \frac{bB_m S_h I_m}{N_h} = 0,\\
&\frac{bB_m S_h I_m}{N_h} - \left(\theta_h + \mu_h\right)E_h = 0,\\
&\theta_h E_h - \left(\alpha_h + \mu_h\right)I_h = 0,\\
&k\delta(t)\left(1 - \left(\frac{A_m}{C}\right)\right)M - \left(\gamma_m(t) + \mu_a(t) + c_a(t)\right)A_m = 0,\\
&\gamma_m(t)A_m - \frac{bB_m S_m I_h}{N_h} - \left(\mu_m(t) + c_m(t)\right)S_m = 0,\\
&\frac{bB_m S_m I_h}{N_h} - \left(\theta_m(t) + \mu_m(t) + c_m(t)\right)E_m = 0,\\
&\theta_m(t)E_m - \left(\mu_m(t) + c_m(t)\right)I_m = 0.
\end{aligned}
\tag{8}
$$

From equation (8), the disease free and the endemic equilibrium points can be considered. A disease free equilibrium point is obtained when $I_h = I_m = 0$ whereas an endemic equilibrium point is obtained $I_h \neq 0$ or $I_m \neq 0$ (that is $I_h > 0$ or $I_m > 0$)

$$E_1 = \left(S_h^*, 0, 0, 0, 0, 0, 0\right),$$

$$E_2 = \left(S_h^*, 0, 0, A_m^*, S_m^*, 0, 0\right),$$

$$E_3 = \left(S_h^*, E_h^*, I_h^*, A_m^*, S_m^*, E_m^*, I_m^*\right).$$

Equilibrium points E_1 and E_2 are referred to as the disease-free equilibrium point and the equilibrium point E_3 is called the endemic equilibrium point. It should be noted that, E_1 is not biological realistic as there are no mosquitoes in the

population. However, equilibrium points E_2 and E_3 are biological realistic with both mosquitoes and human coexisting in the population.

3.5 Stability Analysis of the Equilibrium Points

The stability analysis of the disease-free and endemic equilibrium points would be computed by finding the Jacobian matrix associated with equations (1) to (7). The equilibrium points of the disease-free and endemic equilibrium would then be substituted into the Jacobian matrix. The matrix equation would then be solved to obtain the various eigenvalues. The equations (1) to (7) are shown below.

$$
\begin{aligned}
f_1(E) &= \frac{dS_h}{dt} = \mu_h\left(N_h - S_h\right) - \frac{bB_m S_h I_m}{N_h}, \\
f_2(E) &= \frac{dE_h}{dt} = \frac{bB_m S_h I_m}{N_h} - \left(\theta_h + \mu_h\right)E_h, \\
f_3(E) &= \frac{dI_h}{dt} = \theta_h E_h - \left(\alpha_h + \mu_h\right)I_h, \\
f_4(E) &= \frac{dA_m}{dt} = k\delta(t)\left(1 - \left(\frac{A_m}{C}\right)\right)M - \left(\gamma_m(t) + \mu_a(t) + c_a(t)\right)A_m, \\
f_5(E) &= \frac{dS_m}{dt} = \gamma_m(t)A_m - \frac{bB_m S_m I_h}{N_h} - \left(\mu_m(t) + c_m(t)\right)S_m, \\
f_6(E) &= \frac{dE_m}{dt} = \frac{bB_m S_m I_h}{N_h} - \left(\theta_m(t) + \mu_m(t) + c_m(t)\right)E_m, \\
f_7(E) &= \frac{dI_m}{dt} = \theta_m(t)E_m - \left(\mu_m(t) + c_m(t)\right)I_m.
\end{aligned}
\tag{9}
$$

The Jacobian matrix associated with system of equation (9) is,

$$J=\begin{bmatrix} \frac{\partial f_1}{\partial S_h} & \frac{\partial f_1}{\partial E_h} & \frac{\partial f_1}{\partial I_h} & \frac{\partial f_1}{\partial A_m} & \frac{\partial f_1}{\partial S_m} & \frac{\partial f_1}{\partial E_m} & \frac{\partial f_1}{\partial I_m} \\ \frac{\partial f_2}{\partial S_h} & \frac{\partial f_2}{\partial E_h} & \frac{\partial f_2}{\partial I_h} & \frac{\partial f_2}{\partial A_m} & \frac{\partial f_2}{\partial S_m} & \frac{\partial f_2}{\partial E_m} & \frac{\partial f_2}{\partial I_m} \\ \vdots & \vdots & \vdots & \vdots & \vdots & \vdots & \vdots \\ \frac{\partial f_6}{\partial S_h} & \frac{\partial f_6}{\partial E_h} & \frac{\partial f_6}{\partial I_h} & \frac{\partial f_6}{\partial A_m} & \frac{\partial f_6}{\partial S_m} & \frac{\partial f_6}{\partial E_m} & \frac{\partial f_6}{\partial I_m} \\ \frac{\partial f_7}{\partial S_h} & \frac{\partial f_7}{\partial E_h} & \frac{\partial f_7}{\partial I_h} & \frac{\partial f_7}{\partial A_m} & \frac{\partial f_7}{\partial S_m} & \frac{\partial f_7}{\partial E_m} & \frac{\partial f_7}{\partial I_m} \end{bmatrix}.$$

The Jacobian matrix J can therefore be obtained as follows,

$$J(E)=\begin{pmatrix} J_1 & J_2 & J_2 & 0 & 0 & 0 & J_3 \\ -J_1 & J_4 & J_5 & 0 & 0 & 0 & -J_3 \\ 0 & J_6 & J_7 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & J_8 & J_9 & J_9 & J_9 \\ J_{10} & J_{10} & J_{11} & J_{12} & J_{13} & 0 & 0 \\ -J_{10} & -J_{10} & -J_{11} & 0 & J_{14} & J_{15} & 0 \\ 0 & 0 & 0 & 0 & 0 & J_{16} & J_{17} \end{pmatrix},$$

where

$$J_1 = \frac{-bB_m I_m (E_h + I_h)}{(S_h + E_h + I_h)^2}, \qquad J_{10} = \frac{bB_m S_m I_h}{(S_h + E_h + I_h)^2},$$

$$J_2 = \mu_h + \frac{bB_m I_m S_h}{(S_h + E_h + I_h)^2}, \qquad J_{11} = \frac{-bB_m S_m (S_h + E_h)}{(S_h + E_h + I_h)^2},$$

$$J_3 = \frac{-bB_m S_h}{S_h + E_h + I_h}, \qquad J_{12} = \gamma_m$$

$$J_4 = \frac{-bB_m I_m S_h}{(S_h + E_h + I_h)^2} - \theta_h - \mu_h, \qquad J_{13} = \frac{-bB_m I_h}{(S_h + E_h + I_h)} - c_m - \mu_m,$$

$$J_5 = \frac{-bB_m S_h I_m}{(S_h + E_h + I_h)^2}, \qquad J_{14} = \frac{bS_m I_h}{S_h + E_h + I_h},$$

$$J_6 = \theta_h, \qquad J_{15} = -\theta_m - \mu_m - c_m,$$

$$J_7 = -\alpha_h - \mu_h, \qquad J_{16} = \theta_m,$$

$$J_8 = -(\gamma_m + c_a + \mu_a) - \frac{[k\delta E_m + \delta k I_m + \delta k S_m]}{C}, \qquad J_{17} = -\mu_m - c_m.$$

$$J_9 = \frac{-k\delta}{C}(-C + A_m),$$

The equilibrium points would be computed in the next section.

3.5.1 The Disease-Free Equilibrium Point(DFE)

From equation (8), the disease free can be found by solving for the variables of interest. As stated earlier, a disease free equilibrium point is obtained when there is no disease in the population or $I_h = I_m = 0$. In that case, two equilibrium points E_1 and E_2 are obtained as follows.

$$E_1 = \left(S_h^*, 0, 0, 0, 0, 0, 0\right),$$

$$E_2 = \left(S_h^*, 0, 0, A_m^*, S_m^*, 0, 0\right).$$

Therefore, substituting $I_h = I_m = 0$ into equation (8), gives the following

$$\mu_h\left(N_h - S_h\right) = 0,$$

$$k\delta\left(1 - \left(\frac{A_m}{C}\right)\right)\left(S_m + E_m + I_m\right) - \left(\gamma_m + \mu_a + c_a\right)A_m = 0,$$

$$\gamma_m A_m - \left(\mu_m + c_m\right)S_m = 0.$$

Solving for S_h^*, A_m^* and S_m^* , gives the following solutions.

$$S_h^*(t) = N_h,$$

$$A_m^*(t) = \frac{C\left[k\delta - \left(\gamma_m + \mu_a + c_m\right)\left(\frac{\mu_m + c_m}{\gamma_m}\right)\right]}{k\delta},$$

$$S_m^*(t) = \frac{k\delta - \left(\gamma_m + \mu_a + c_a\right)\left(\frac{\mu_m + c_m}{\gamma_m}\right)}{k\delta\left(\frac{\mu_m + c_m}{\gamma_m C}\right)}.$$

When $S_m = 0, A_m = 0$. However at the disease-free equilibrium $S_m, A_m \neq 0$. This would then be substituted into the Jacobian matrix $J(E)$ in order to find the corresponding eigenvalues.

3.5.2 Stability Analysis of the Diseases –Free Equilibrium Point

At the disease-free equilibrium, $I_h = I_m = 0$. Substituting $I_h = I_m = 0$ into the Jacobian matrix associated with equations (1) to (7) gives, With the equilibrium point $E_2 = \left(S_h^*, 0, 0, A_m^*, S_m^*, 0, 0\right).$, the Jacobian matrix associated with it is

$$J(\tilde{E}) = \begin{pmatrix} 0 & J_1 & J_1 & 0 & 0 & 0 & -J_2 \\ 0 & J_3 & 0 & 0 & 0 & 0 & J_2 \\ 0 & J_4 & J_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & J_6 & J_7 & J_7 & J_7 \\ 0 & 0 & J_8 & J_9 & J_{10} & 0 & 0 \\ 0 & 0 & -J_8 & 0 & 0 & J_{11} & 0 \\ 0 & 0 & 0 & 0 & 0 & J_{12} & J_{10} \end{pmatrix}.$$

where

$$J_1 = \mu_h, \qquad J_7 = \frac{-k\delta(-C + A_m)}{C},$$

$$J_2 = bB_m, \qquad J_8 = \frac{-bB_m S_m}{S_h},$$

$$J_3 = -(\theta_h + \mu_h), \qquad J_9 = \gamma_m,$$

$$J_4 = \theta_h, \qquad J_{10} = -\mu_m - c_m,$$

$$J_5 = -(\alpha_h + \mu_h), \qquad J_{11} = -\theta_m - \mu_m - c_m,$$

$$J_6 = -\left[\frac{\delta k S_m + C\gamma_m + Cc_a + C\mu_a}{C}\right], \qquad J_{12} = \theta_m.$$

It is difficult to find the eigenvalues of the above matrix as the system is made up of seven nonlinear differential equation. This would result in polynomial of order 7 and cannot be computed easily by hand. Therefore, the Maple computational software would be used to find the eigenvalues of the Jacobian matrix of the DFE in Chapter 4.

3.5.3 The Endemic Equilibrium Point (EE)

The endemic equilibrium point describes a state in the population whereby the disease persists and is spreading. Therefore an endemic equilibrium point is obtained

$I_h \neq 0$ or $I_m \neq 0$ (that is $I_h > 0$ or $I_m > 0$). The endemic equilibrium point is obtained as follows:

$$E_3 = \left(S_h^*, E_h^*, I_h^*, A_m^*, S_m^*, E_m^*, I_m^*\right).$$

The solutions to the variables of interest from equilibrium point (E_3) are found by solving equation (10). That is equating system of equation (9) to zero.

$$\begin{aligned}
&\mu_h\left(N_h - S_h^*\right) - \frac{bB_m S_h^* I_m^*}{N_h} = 0,\\
&\frac{bB_m S_h^* I_m^*}{N_h} - \left(\theta_h + \mu_h\right)E_h^* = 0,\\
&\theta_h E_h^* - \left(\alpha_h + \mu_h\right)I_h^* = 0,\\
&k\delta\left(1 - \left(\frac{A_m}{C}\right)\right)M - \left(\gamma_m + \mu_a + c_a\right)A_m^* = 0,\\
&\gamma_m A_m^* - \frac{bB_m S_m^* I_h^*}{N_h} - \left(\mu_m + c_m\right)S_m^* = 0,\\
&\frac{bB_m S_m^* I_h^*}{N_h} - \left(\theta_m + \mu_m + c_m\right)E_m^* = 0,\\
&\theta_m E_m^* - \left(\mu_m + c_m\right)I_m^* = 0.
\end{aligned} \tag{10}$$

An analytical solution to equation (10) is difficult to obtain and the eigenvalues would be calculated and shown in the next chapter when the model parameters are found.

3.5.4 Stability Analysis of the Endemic Equilibrium Point

At the endemic equilibrium, $I_h \neq 0$ or $I_m \neq 0$ (that is $I_h > 0$ or $I_m > 0$). Substituting equilibrium point (E_3) into the Jacobian matrix associated with equations (1) to (7) gives,

$$J = \begin{pmatrix} J_1 & J_2 & J_2 & 0 & 0 & 0 & J_3 \\ -J_1 & J_4 & J_5 & 0 & 0 & 0 & -J_3 \\ 0 & J_6 & J_7 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & J_8 & J_9 & J_9 & J_9 \\ J_{10} & J_{10} & J_{11} & J_{12} & J_{13} & 0 & 0 \\ -J_{10} & -J_{10} & -J_{11} & 0 & J_{14} & J_{15} & 0 \\ 0 & 0 & 0 & 0 & 0 & J_{16} & J_{17} \end{pmatrix}.$$

where

$$J_1 = \frac{-bB_m I_m^* \left(E_h^* + I_h^*\right)}{\left(S_h^* + E_h^* + I_h^*\right)^2}, \qquad J_{10} = \frac{bB_m S_m^* I_h^*}{\left(S_h^* + E_h^* + I_h^*\right)^2},$$

$$J_2 = \mu_h + \frac{bB_m I_m^* S_h^*}{\left(S_h^* + E_h^* + I_h^*\right)^2}, \qquad J_{11} = \frac{-bB_m S_m^* \left(S_h^* + E_h^*\right)}{\left(S_h^* + E_h^* + I_h^*\right)^2},$$

$$J_3 = \frac{-bB_m S_h^*}{S_h^* + E_h^* + I_h^*}, \qquad J_{12} = \gamma_m$$

$$J_4 = \frac{-bB_m I_m^* S_h^*}{\left(S_h^* + E_h^* + I_h^*\right)^2} - \theta_h - \mu_h, \qquad J_{13} = \frac{-bB_m I_h^*}{\left(S_h^* + E_h^* + I_h^*\right)} - c_m - \mu_m,$$

$$J_5 = \frac{-bB_m S_h^* I_m^*}{\left(S_h^* + E_h^* + I_h^*\right)^2}, \qquad J_{14} = \frac{bS_m^* I_h^*}{S_h^* + E_h^* + I_h^*},$$

$$J_6 = \theta_h, \qquad J_{15} = -\theta_m - \mu_m - c_m,$$

$$J_7 = -\alpha_h - \mu_h, \qquad J_{16} = \theta_m,$$

$$J_8 = -(\gamma_m + c_a + \mu_a) - \frac{\left[k\delta E_m^* + k\delta I_m^* + k\delta S_m^*\right]}{C}, \quad J_{17} = -\mu_m - c_m.$$

$$J_9 = \frac{-k\delta}{C}\left(-C + A_m^*\right),$$

The eigenvalues associated with the Jacobian matrix of the disease-free equilibrium would be the only one to be calculated as the study is mainly on when there is no disease in the population.

3.6 The Basic Reproduction Number

The basic reproduction number R_o is an estimation that gives the average number of people an infected person can transmit the disease to in a completely susceptible population.

In finding the basic reproduction number, the terms in which the infection is progressing would be considered as described in section 1.6.3 in Chapter 1. That is E_h, I_h, E_m and I_m. Where $\dot{x}_i = f_i(x) - (V_i^-(x) - V_i^+(x)), i = 1,...,4.$

$F_i(x)$ represents the rate of appearance of new infections in compartment i.

$V_i^+(x)$ is the rate of transfer of individuals into compartment i by any means.

$V_i^-(x)$ is the rate of transfer of individuals out compartment i by any means.

Therefore, from equations (2), (3), (6) and (7) we obtain,

$$\frac{dE_h}{dt} = \frac{bB_m S_h I_m}{N_h} - (\theta_h + \mu_h) E_h,$$
$$\frac{dI_h}{dt} = \theta_h E_h - (\alpha_h + \mu_h) I_h,$$
$$\frac{dE_m}{dt} = \frac{bB_m S_m I_h}{N_h} - (\theta_m(t) + \mu_m(t) + c_m(t)) E_m,$$
$$\frac{dI_m}{dt} = \theta_m(t) E_m - (\mu_m(t) + c_m(t)) I_m.$$

$$\frac{dx}{dt} = F(x) - V(x) \text{ where } x^T = (E_h, I_h, E_m, I_m).$$

and $V(x) = V_i^-(x) - V_i^+(x)$ is the rate of transfer of individuals in and out of the infected compartment.

$$F(x) = \begin{pmatrix} \frac{bB_m S_h I_m}{N_h} \\ 0 \\ \frac{bB_m S_m I_h}{N_h} \\ 0 \end{pmatrix}, \qquad V(x) = \begin{pmatrix} (\theta_h + \mu_h) E_h \\ -\theta_h E_h + (\alpha_h + \mu_h) I_h \\ (\theta_m + \mu_m + c_m) E_m \\ -\theta_m E_m + (\mu_m + c_m) I_m \end{pmatrix}.$$

Calculating the Jacobian matrix associated with F and V.

$$J_v(x) = \begin{pmatrix} \theta_h + \mu_h & 0 & 0 & 0 \\ -\theta_h & \alpha_h + \mu_h & 0 & 0 \\ 0 & 0 & \theta_m + \mu_m + c_m & 0 \\ 0 & 0 & -\theta_m & \mu_m + c_m \end{pmatrix},$$

$$J_F(x)=\begin{pmatrix} 0 & 0 & 0 & \frac{bB_mS_h}{N_h} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{bB_mS_m}{N_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

Then computing J_v^{-1}, we get

$$J_v^{-1}=\begin{pmatrix} \frac{1}{\theta_h+\mu_h} & 0 & 0 & 0 \\ \frac{\theta_h}{(\theta_h+\mu_h)(\alpha_h+\mu_h)} & \frac{1}{\alpha_h+\mu_h} & 0 & 0 \\ 0 & 0 & \frac{1}{\theta_m+\mu_m+c_m} & 0 \\ 0 & 0 & \frac{\theta_m}{(\theta_m+\mu_m+c_m)(\mu_m+c_m)} & \frac{1}{\mu_m+c_m} \end{pmatrix}.$$

Calculating $J_F\left(X_{DFE}\right)J_V^{-1}\left(X_{DFE}\right)$ gives

$$J_F\left(X_{DFE}\right)J_V^{-1}\left(X_{DFE}\right)=\begin{pmatrix} 0 & 0 & \frac{bB_mS_h\theta_m}{N_h(\theta_m+\mu_m+c_m)(\mu_m+c_m)} & \frac{bB_mS_h}{N_h(\mu_m+c_m)} \\ 0 & 0 & 0 & 0 \\ \frac{bB_mS_m\theta_h}{N_h(\theta_h+\mu_h)(\alpha_h+\mu_h)} & \frac{bB_mS_m}{N_h(\alpha_h+\mu_h)} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

where $J_F\left(X_{DFE}\right)$ is the Jacobian matrix associated with F and $J_V^{-1}\left(X_{DFE}\right)$ is the inverse of the Jacobian matrix associated with matrix V.

The characteristic polynomial

$$p(\lambda)=\lambda^2\left[\lambda^2-\left(\frac{bB_mS_h\theta_m}{N_h(\theta_m+\mu_m+c_m)(\mu_m+c_m)}\right)\left(\frac{bB_mS_m\theta_h}{N_h(\theta_h+\mu_h)(\alpha_h+\mu_h)}\right)\right].$$

Therefore, the basic reproduction number (R_o) according to Driessche et al. (2002), can be written as follows:

$$R_o = \rho\left(J_F J_v^{-1}\right) \tag{11}$$

$$p(\lambda) = \lambda^2\left[\lambda^2 - \left(\frac{bB_m S_h \theta_m}{N_h(\theta_m + \mu_m + c_m)(\mu_m + c_m)}\right)\left(\frac{bB_m S_m \theta_h}{N_h(\theta_h + \mu_h)(\alpha_h + \mu_h)}\right)\right],$$

$$\rho(J_F J_V^{-1}) = \sqrt{\frac{b^2 B_m^2 S_h S_m \theta_m \theta_h}{S_h^2(\theta_m + \mu_m + c_m)(\mu_m + c_m) N_h(\theta_h + \mu_h)(\alpha_h + \mu_h)}}.$$

Where J_F and J_V are the Jacobian matrices associated with F and V. The linearization of the reduced system around the disease free equilibrium is described by F and V. Note that at the disease-free equilibrium $N_h = S_h$ because all the compartments are zero except S_h. We therefore obtain

$$R_o = \pm\sqrt{\frac{b^2 B_m^2 S_m \theta_m \theta_h}{S_h\left(\theta_m + \mu_m + c_m\right)\left(\mu_m + c_m\right)\left(\theta_h + \mu_h\right)\left(\alpha_h + \mu_h\right)}}. \tag{12}$$

Furthermore, according to Driessche et al., (2002), if $R_o < 1$, then the DFE is locally stable, and if $R_o > 1$, then it is locally unstable which results in an outbreak if a virus is introduced into the population.

Theorem 1 (P. van den Dreiessche et al. 2002). Consider the disease transmission model given by equations (1) to (7). If x_0 is a DFE of the model, then x_0 is locally asymptotically stable if $R_0 < 1,$ but unstable if $R_0 > 1,$ where R_0 is defined by (12).

3.6.1 Biological Interpretation of R_o

The basic reproduction number, which is the number of cases generated by one case during the infection period from equation (12), has a biological meaning. The biological meaning can be explained terms wise from equations (1) to (6) as it depends on parameters from the human and the mosquito compartment. It also depends on the fraction between the susceptible mosquito and the total population of the human compartment. Again it depends on the square of the biting rate and the square of the effective contact rate, $b^2B_m^2$, meaning that only two bites from the same mosquito would result in a new case of dengue.

The next section would concentrate on the numerical solution of the mathematical model described in equations (1) to (7).

3.7 Numerical Solution to the Model

In this section, the numerical method described in section 1.6.4 in Chapter 1 is used to solve the mathematical model in equations (1) to (7).

This is a robust scheme that maintains the positivity as the dynamics properties of the solutions as well as $S_h + E_h + I_h = N_h$.

Using the Mickens' second rule, equations (1) to (7) can be written as the following.

$$\frac{S_h^{n+1} - S_h^n}{\Delta t} = \mu_h N_h - \mu_h S_h^{n+1} - \frac{bB_m S_h^{n+1} I_m^n}{N_h},$$

$$\frac{E_h^{n+1} - E_h^n}{\Delta t} = \frac{bB_m S_h^{n+1} I_m^n}{N_h} - \left(\theta_h + \mu_h\right) E_h^{n+1},$$

$$\frac{I_h^{n+1}-I_h^n}{\Delta t}=\theta_h E_h^{n+1}-\left(\alpha_h+\mu_h\right)I_h^{n+1}.$$

$$\frac{A_m^{n+1}-A_m^n}{\Delta t}=k\delta\left(S_m^n+E_m^n+I_m^n\right)-\left(\frac{k\delta}{C}\left(S_m^n+E_m^n+I_m^n\right)+\left(\gamma_m+\mu_a+c_a\right)\right)A_m^{n+1},$$

$$\frac{S_m^{n+1}-S_m^n}{\Delta t}=\gamma_m A_m^{n+1}-\frac{bB_m S_m^{n+1}I_h^n}{N_h}-\mu_m S_m^{n+1}-c_m S_m^{n+1},$$

$$\frac{E_m^{n+1}-E_m^n}{\Delta t}=\frac{bB_m S_m^{n+1}I_h^n}{N_h}-\left(\theta_m+\mu_m+c_m\right)E_m^{n+1},$$

$$\frac{I_m^{n+1}-I_m^n}{\Delta t}=\theta_m E_m^{n+1}-\left(\mu_m+c_m\right)I_m^{n+1}.$$

Δt is the time-step, $S_h^n, E_h^n, I_h^n, A_m^n, S_m^n, E_m^n$ and I_m^n are approximations of $S_h(t_n), E_h(t_n), I_h(t_n), A_m(t_n), S_m(t_n), E_m(t_n)$ and $I_m(t_n)$.

The susceptible human

$$S_h^{n+1}-S_h^n=\mu_h N_h\Delta t-\mu_h S_h^{n+1}\Delta t-\frac{bB_m S_h^{n+1}I_m^n\Delta t}{N_h},$$

$$S_h^{n+1}+\mu_h S_h^{n+1}\Delta t+\frac{bB_m S_h^{n+1}I_m^n\Delta t}{N_h}=\mu_h N_h\Delta t+S_h^n,$$

$$S_h^{n+1}\left(1+\mu_h\Delta t+\frac{bB_m I_m^n\Delta t}{N_h}\right)=\mu_h N_h\Delta t+S_h^n,$$

$$S_h^{n+1}=\frac{\mu_h N_h\Delta t+S_h^n}{1+\mu_h\Delta t+\frac{bB_m I_m^n\Delta t}{N_h}}.$$

The exposed human

$$\frac{E_h^{n+1}-E_h^n}{\Delta t}=\frac{bB_m S_h^{n+1}I_m^n}{N_h}-\left(\theta_h+\mu_h\right)E_h^{n+1},$$

$$E_h^{n+1} - E_h^n = \frac{bB_m S_h^{n+1} I_m^n}{N_h}\Delta t - \left(\theta_h + \mu_h\right) E_h^{n+1}\Delta t,$$

$$E_h^{n+1} + \left(\theta_h + \mu_h\right) E_h^{n+1}\Delta t = \frac{bB_m S_h^{n+1} I_m^n}{N_h}\Delta t + E_h^n,$$

$$E_h^{n+1}\left(1 + \left(\theta_h + \mu_h\right)\Delta t\right) = \frac{bB_m S_h^{n+1} I_m^n}{N_h}\Delta t + E_h^n,$$

$$E_h^{n+1} = \frac{\dfrac{bB_m S_h^{n+1} I_m^n}{N_h}\Delta t + E_h^n}{1 + \left(\theta_h + \mu_h\right)\Delta t}.$$

The infected human

$$\frac{I_h^{n+1} - I_h^n}{\Delta t} = \theta_h E_h^{n+1} - \left(\alpha_h + \mu_h\right) I_m^{n+1},$$

$$I_h^{n+1} - I_h^n = \theta_h E_h^{n+1}\Delta t - \left(\alpha_h + \mu_h\right) I_m^{n+1}\Delta t,$$

$$I_h^{n+1} + \left(\alpha_h + \mu_h\right) I_h^{n+1}\Delta t = \theta_h E_h^{n+1}\Delta t + I_h^n,$$

$$I_h^{n+1}\left(1 + \left(\alpha_h + \mu_h\right)\Delta t\right) = \theta_h E_h^{n+1}\Delta t + I_h^n,$$

$$I_h^{n+1} = \frac{\theta_h E_h^{n+1}\Delta t + I_h^n}{1 + \left(\alpha_h + \mu_h\right)\Delta t}.$$

The aquatic phase

$$\frac{A_m^{n+1} - A_m^n}{\Delta t} = k\delta\left(S_m^n + E_m^n + I_m^n\right) - \left(\frac{k\delta}{C}\left(S_m^n + E_m^n + I_m^n\right) + \left(\gamma_m + \mu_a + c_a\right)\right) A_m^{n+1},$$

$$A_m^{n+1} - A_m^n = k\delta\left(S_m^n + E_m^n + I_m^n\right)\Delta t - \left(\frac{k\delta}{C}\left(S_m^n + E_m^n + I_m^n\right) + \left(\gamma_m + \mu_a + c_a\right)\right) A_m^{n+1}\Delta t,$$

$$A_m^{n+1}\left(1 + \left(\frac{k\delta}{C}\left(S_m^n + E_m^n + I_m^n\right) + \left(\gamma_m + \mu_a + c_a\right)\right)\Delta t\right) = k\delta\left(S_m^n + E_m^n + I_m^n\right)\Delta t + A_m^n,$$

$$A_m^{n+1} = \frac{k\delta\left(S_m^n + E_m^n + I_m^n\right)\Delta t + A_m^n}{1 + \left(\dfrac{k\delta}{C}\left(S_m^n + E_m^n + I_m^n\right) + \left(\gamma_m + \mu_a + c_a\right)\right)\Delta t}.$$

The susceptible mosquito

$$\frac{S_m^{n+1}-S_m^n}{\Delta t}=\gamma_m A_m^{n+1}-\frac{bB_m S_m^{n+1}I_h^n}{N_h}-\mu_m S_m^{n+1}-c_m S_m^{n+1},$$

$$S_m^{n+1}-S_m^n=\gamma_m A_m^{n+1}\Delta t-\frac{bB_m S_m^{n+1}I_h^n}{N_h}\Delta t-\Delta t\mu_m S_m^{n+1}-\Delta t c_m S_m^{n+1},$$

$$S_m^{n+1}+\frac{bB_m S_m^{n+1}I_h^n}{N_h}\Delta t+\Delta t\mu_m S_m^{n+1}+\Delta t c_m S_m^{n+1}=\gamma_m A_m^{n+1}\Delta t+S_m^n,$$

$$S_m^{n+1}\left(1+\frac{bB_m I_h^n}{N_h}\Delta t+\Delta t\mu_m+\Delta t c_m\right)=\gamma_m A_m^{n+1}\Delta t+S_m^n,$$

$$S_m^{n+1}=\frac{\gamma_m A_m^{n+1}\Delta t+S_m^n}{1+\Delta t\left(\frac{bB_m I_h^n}{N_h}+\mu_m+c_m\right)}.$$

The exposed mosquito

$$\frac{E_m^{n+1}-E_m^n}{\Delta t}=\frac{bB_m S_m^{n+1}I_h^n}{N_h}-\left(\theta_m+\mu_m+c_m\right)E_m^{n+1},$$

$$E_m^{n+1}-E_m^n=\frac{bB_m S_m^{n+1}I_h^n}{N_h}\Delta t-\left(\theta_m+\mu_m+c_m\right)E_m^{n+1}\Delta t,$$

$$E_m^{n+1}+\left(\theta_m+\mu_m+c_m\right)E_m^{n+1}\Delta t=\frac{bB_m S_m^{n+1}I_h^n}{N_h}\Delta t+E_m^n,$$

$$E_m^{n+1}\left(1+\left(\theta_m+\mu_m+c_m\right)\Delta t\right)=\frac{bB_m S_m^{n+1}I_h^n}{N_h}\Delta t+E_m^n,$$

$$E_m^{n+1} = \frac{\frac{bB_m S_m^{n+1} I_h^n}{N_h}\Delta t + E_m^n}{1+\left(\theta_m + \mu_m + c_m\right)\Delta t}.$$

The infected mosquito

$$\frac{I_m^{n+1} - I_m^n}{\Delta t} = \theta_m E_m^{n+1}\Delta t - \left(\mu_m + c_m\right) I_m^{n+1}$$

$$I_m^{n+1} - I_m^n = \theta_m E_m^{n+1}\Delta t - \left(\mu_m + c_m\right) I_m^{n+1}\Delta t,$$

$$I_m^{n+1} + \left(\mu_m + c_m\right) I_m^{n+1}\Delta t = \theta_m E_m^{n+1}\Delta t + I_m^n,$$

$$I_m^{n+1}\left(1+\left(\mu_m + c_m\right)\Delta t\right) = \theta_m E_m^{n+1}\Delta t + I_m^n,$$

$$I_m^{n+1} = \frac{\theta_m E_m^{n+1}\Delta t + I_m^n,}{1+\left(\mu_m + c_m\right)\Delta t}.$$

Human Population

$$\left.\begin{aligned} S_h^{n+1} &= \frac{\mu_h N_h \Delta t + S_h^n}{1+\mu_h\Delta t + \frac{bB_m I_m^n \Delta t}{N_h}}. \\ E_h^{n+1} &= \frac{\frac{bB_m S_h^{n+1} I_m^n}{N_h}\Delta t + E_h^n}{1+\left(\theta_h + \mu_h\right)\Delta t}. \\ I_h^{n+1} &= \frac{\theta_h E_h^{n+1}\Delta t + I_h^n}{1+\left(\alpha_h + \mu_h\right)\Delta t}. \end{aligned}\right\} \quad (13)$$

Mosquito Population

$$\left.\begin{aligned}
A_m^{n+1} &= \frac{K\delta\left(S_m^n + E_m^n + I_m^n\right)\Delta t + A_m^n}{1+\left(\frac{K\delta\left(S_m^n + E_m^n + I_m^n\right)}{C} + \left(\gamma_m + \mu_a + c_a\right)\right)\Delta t}, \\
S_m^{n+1} &= \frac{\gamma_m A_m^{n+1}\Delta t + S_m^n}{1+\Delta t\left(\frac{bB_m I_h^n}{N_h} + \mu_m + c_m\right)}, \\
E_m^{n+1} &= \frac{\frac{bB_m S_m^{n+1} I_h^n \Delta t}{N_h} + E_m^n}{1+\left(\theta_m + \mu_m + c_m\right)\Delta t}, \\
I_m^{n+1} &= \frac{\theta_m E_m^{n+1}\Delta t + I_m^n}{1+\left(\mu_m + c_m\right)\Delta t}.
\end{aligned}\right\} \quad (14)$$

Since from the equation, we have a positive right – hand side, then positive approximations for any positive initial data which would be located in the feasible region can be obtained. These numerical results would be used in the simulations that would be carried out in section 4.5 in Chapter 4.

Chapter 4

RESULT AND DISCUSSION

In this chapter, the epidemiology of dengue fever in Thailand would be analyzed and discussed. Various simulations would be run to gain some understanding of the transmission patterns in Thailand. This chapter will analyze and discuss the transmission of the disease in a population when human and mosquitos are interacting together.

4.1 Data for the Simulation

Data obtained from the Bureau of Epidemiology detailing the number of dengue fever cases that have been reported in all 76 provinces from 2003 to 2015, have been grouped into zones and all also into regions. The data is a monthly data with each year starting from January and ending in December. The data shows the number of cases as well as deaths recorded in each month for all the 76 provinces.

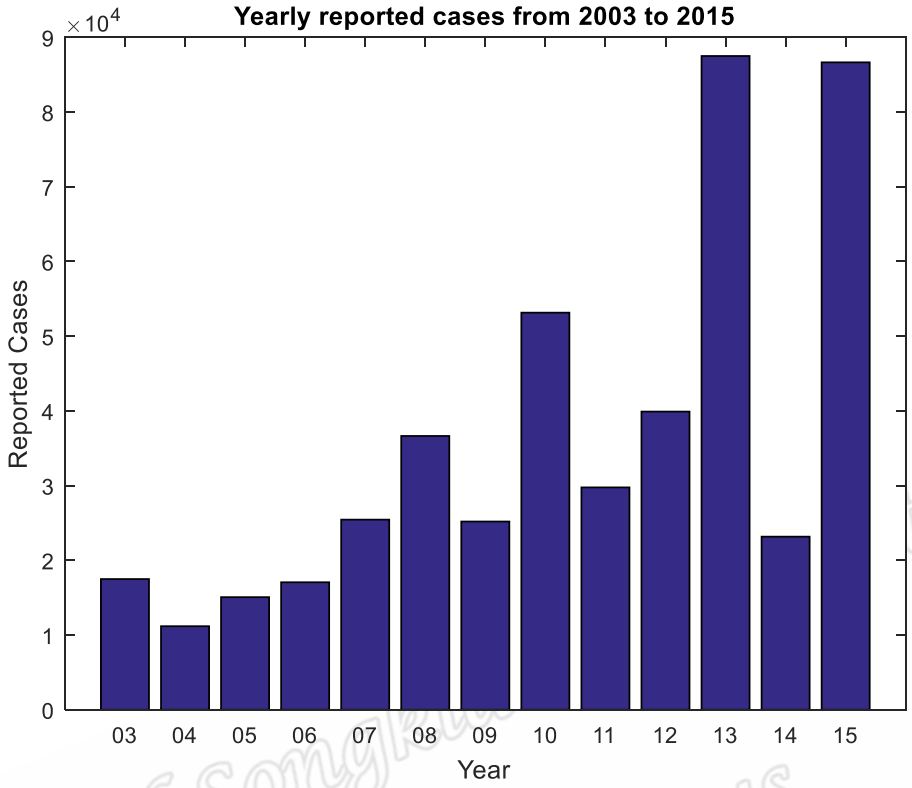


Figure 8. Total number of reported cases from all 76 provinces from 2003 to 2015

Figure 8 shows the plots of the number of reported cases from 2003 to 2015. From the figure, it can be seen that dengue fever incidence was highest in 2013 and also 2015.

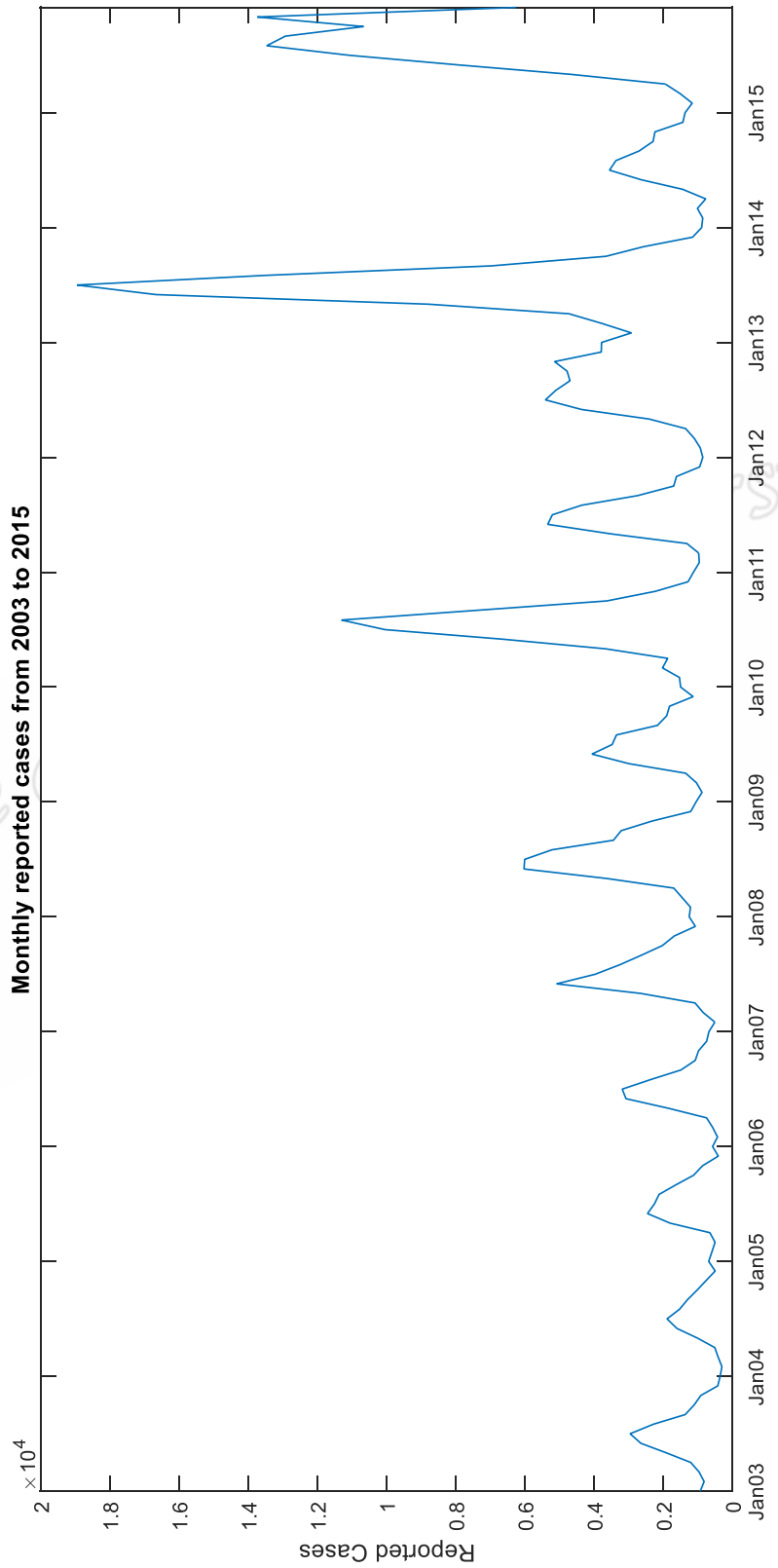


Figure 9. Number of Monthly cases from January 2003 to December 2015

Figure 9 shows the total number of monthly reported from 2003 to 2015. It can clearly be seen that dengue fever incidence starts peaking from May through to August each year with July as the month that records the highest number of cases.

4.2 Graphical Analysis of the Data

The obtained data is transformed for further analysis in order to understand the transmission pattern of dengue fever in Thailand. The year was divided into periods with the first period beginning from January to April. The second period continues from May to August, and the third period starts from September to December.

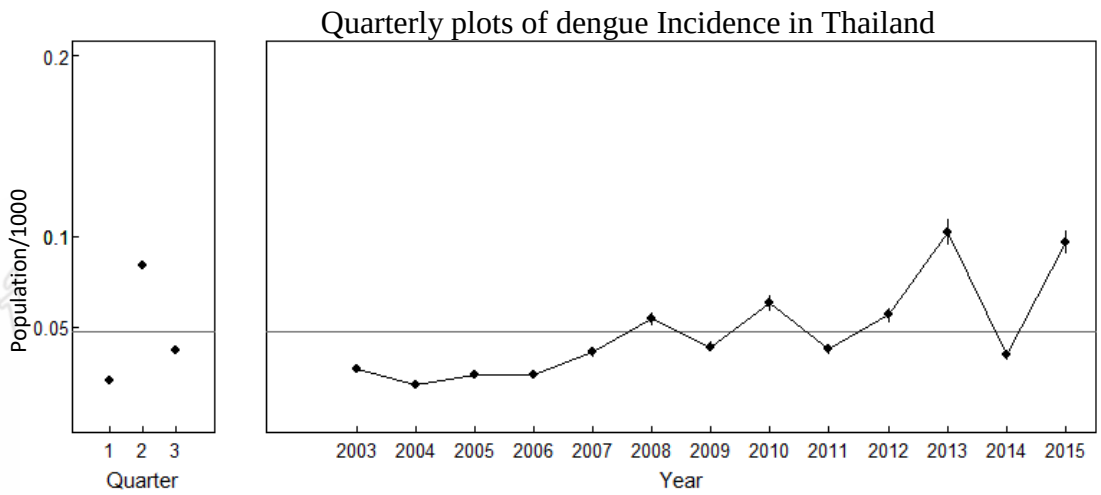


Figure 10. 95% confidence intervals of the annual reported cases in Thailand by quarter and year

Figure 10 shows the plot of the dengue fever cases for the three periods in the year on the left panel and yearly plots on the right panel. It can clearly be seen that dengue fever is highest in the second period, which is May, June, July, and August every year. The horizontal line represents the overall mean annual incidence rate (0.04 per 1,000)

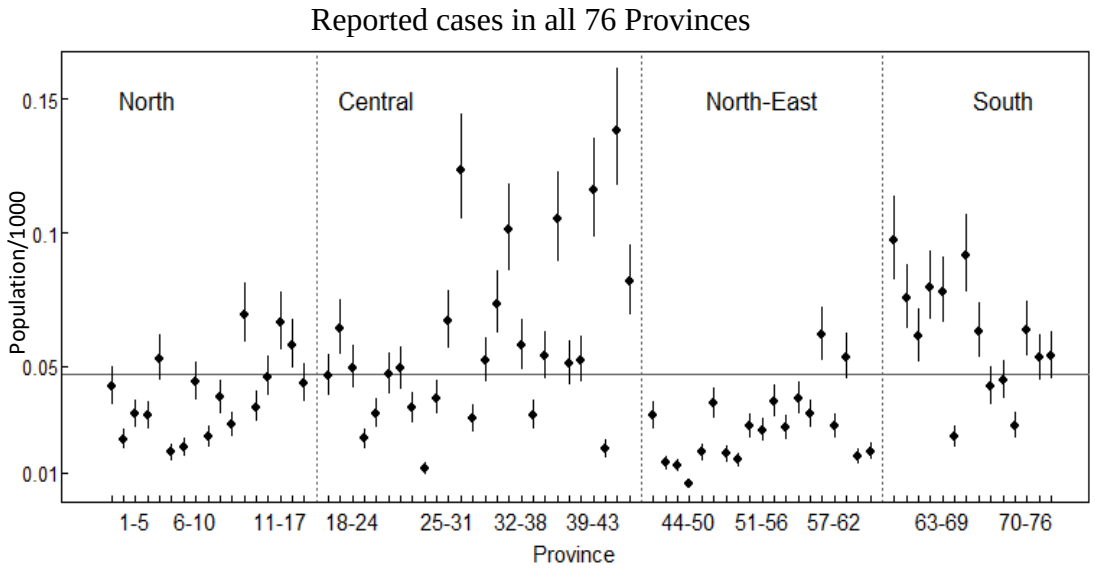


Figure 11. Dengue fever casess by province in Thailand

The analysis continues with the investigation of the dengue incidence in all the 76 provinces from 2003 and 2015. Figure 11 shows the graphs of the total number of cases that have been reported in all 76 provinces from 2003 to 2015. Every province is given an ID starting from 1 to 76 and this can be seen in Table 4. The horizontal line is the mean indicating the number of average cases reported. Provinces like Ratchaburi (ID=29), Samut Sakhon(ID=33), Prachin Buri (ID=37), Chanthaburi (ID=40), and Rayong (ID=42) had a much higher dengue fever incidence as compared to the other provinces by using the mean line. Chumphon (ID=63), Ranong (ID=64), Nakhon Si Thammarat (ID=66), Phatthalung (ID=67), and Roi Et (ID=54) provinces had lower than average (mean line) incidence rates.

Table 2 shows the list of the provinces in Thailand with an ID which would be used later in the analysis of the incidence rate of Dengue fever in Thailand.

Table 2 List of the 76 provinces and their IDs

ID	Province	**ID**	Province	**ID**	Province
1	Chiang Mai	27	Kanchanaburi	53	Maha Sarakham
2	Chiang Rai	28	Nakhon Pathom	54	Roi Et
3	Lampang	29	Ratchaburi	55	Buri Ram
4	Lamphun	30	Suphan Buri	56	Chaiyaphum
5	Mae Hong Son	31	Phetchaburi	57	Nakhon Ratchasima
6	Nan	32	Prachuap Khiri Khan	58	Surin
7	Phayao	33	Samut Sakhon	59	Amnat Charoen
8	Phrae	34	Samut Songkhram	60	Si Sa Ket
9	Phetchabun	35	Chachoengsao	61	Ubon Ratchathani
10	Phitsanulok	36	Nakhon Nayok	62	Yasothon
11	Sukhothai	37	Prachin Buri	63	Chumphon
12	Tak	38	Sa Kaeo	64	Ranong
13	Uttaradit	39	Samut Prakan	65	Surat Thani
14	Kamphaeng Phet	40	Chanthaburi	66	Nakhon Si Thammarat
15	Nakhon Sawan	41	Chon Buri	67	Phatthalung
16	Phichit	42	Rayong	68	Trang
17	Uthai Thani	43	Trat	69	Krabi
18	Bangkok	44	Loei	70	Phangnga
19	Ang Thong	45	Nong Bua Lam Phu	71	Phuket
20	Nonthaburi	46	Nong Khai	72	Narathiwat
21	P. Nakhon S. Ayutthaya	47	Udon Thani	73	Pattani
22	Pathum Thani	48	Kalasin	74	Yala
23	Chai Nat	49	Mukdahan	75	Satun
24	Lop Buri	50	Nakhon Phanom	76	Songkhla
25	Saraburi	51	Sakon Nakhon		
26	Sing Buri	52	Khon Kaen		

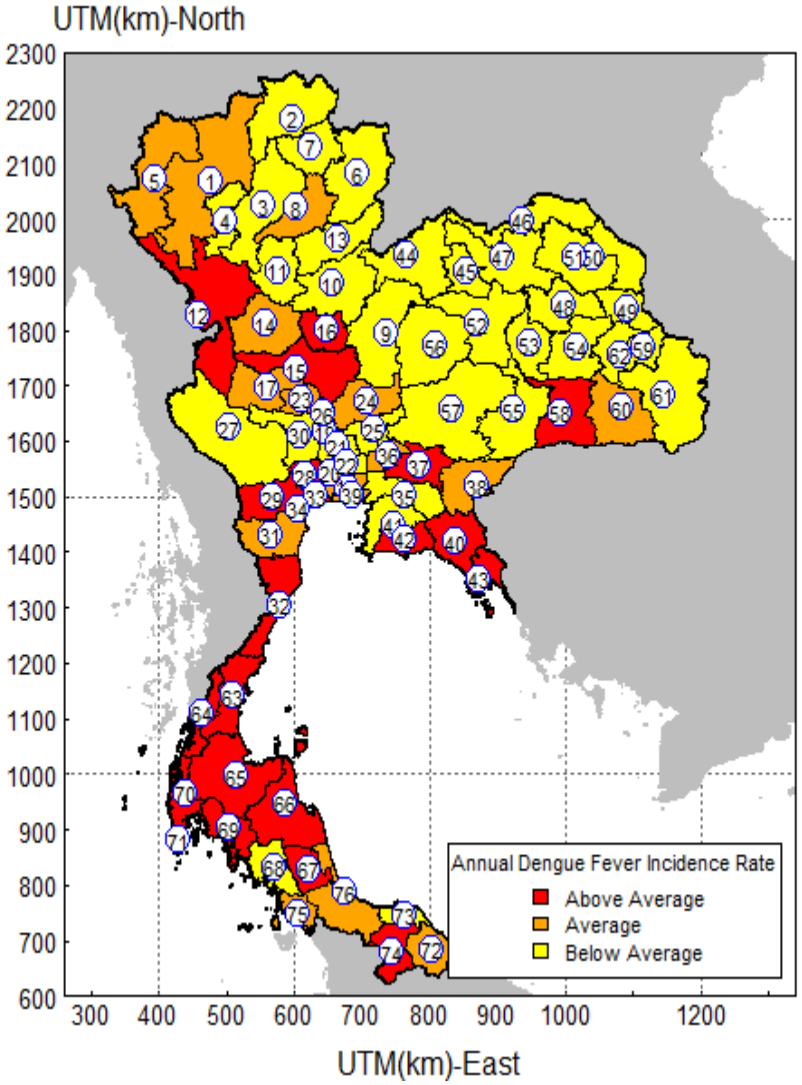


Figure 12. Thematic Map showing dengue fever distribution in Thailand

From the plots obtained from the Figure11, it can be seen that some of the provinces' incidence rates are below and above the average line. Figure 12 therefore shows the thematic map of Thailand showing of the number cases reported in all the 76 provinces with the province ID's shown in Table 2, the provinces that are above (red shade), on the average line (orange shade) and below the average line (yellow shade) are indicated on the map.

4.3 Parameter Models

Entomological parameters on the various stages of the adult mosquito as well as some parameter value pertaining to the human population in Table 3 was not available. The parameters are average oviposit rate, average mosquito mortality rate, average aquatic mortality rate, average aquatic transition rate, extrinsic, and intrinsic incubation rate. Also, the recovery rate, fraction of female mosquitos hatched from all eggs, mosquito carrying capacity, average bite per mosquito per day, effective contact rate, and control efforts rates were also not available. Therefore, parameter values chosen from the ranges of possible values, indicated in Pinho et al., (shown in Range column in Table 3), will be used but they will be adjusted to mimic the transmission pattern of the data obtained from the Bureau of Epidemiology. The adjusted values are in the Values column (4th column) in Table 3. The total human population in the model equation is obtained from the total population of each province in the data.

Table 3. Parameter values for numerical simulations as used by Pinho, et al.

Biological Meaning	Parameter	Range	Values
Average oviposit rate	δ	0-11.2 day^{-1}	4
Average mosquito mortality rate	μ_m	0.02-0.09 day^{-1}	0.02
Average aquatic mortality rate	μ_a	0.01-0.47 day^{-1}	0.01
Average aquatic transition rate	γ_m	0-0.19 day^{-1}	0.12
Extrinsic incubation	θ_m	0.02-0.2 day^{-1}	0.02
Human mortality rate	μ_h	0.0143-0.0167 year^{-1}	0.0143
Intrinsic incubation rate	θ_h	0.083-0.17 day^{-1}	0.083
Recovery rate	α_h	0.083-0.17 day^{-1}	0.083
Fraction of female mosquitoes hatched from all eggs	k	0-1	0.5
Mosquito carrying capacity	C	–	0.918455
Average bite per mosquito per day	b	0-1	0.5
Effective contact rate	B_m		0.4
Control efforts rate for aquatic phase	c_a	0-1	0
Control efforts rate for adult mosquito	c_m	0-1	0

4.4 Model Simulation

The simulations for the model were carried out in Octave programming software version 4.2.0. All scripts and graphs were produced in Octave. The parameters for the simulations were from Table 3 under section 4.4. Equations (13) and (14) from section 3.7 in Chapter 3 were used in the numerical computations. The numerical simulations were carried out for 365 days and an array with zero entries of size 365×1 was created in order to hold the values for the various compartments for both the human and mosquito populations (see appendix).

Thailand recorded its highest ever dengue case with 87,502 cases in 2013 and among the zones created by the bureau of epidemiology in partitioning the various provinces, zone 15 out a total of 18 zones was the one with the highest number of cases. Zone 15 had four provinces which are Chiang Mai, Lampang, Lamphun, and Mae Hong Son. Chiang Mai recorded 8,713 cases as against 2,547 for Lampang, 917 for Lamphun, and 1,473 for Mae Hong Son from a total of 13,650 cases. It could be seen from Figure 11 that some provinces such as Ratchaburi, Samut Sakhon, and Prachin Buri recorded much higher cases than others when compared with the average number of cases across all provinces. Some provinces such as Sing Buri, Chon Buri, and Udon Thani recorded much lower than the average number of cases reported when compared with the average line. The study selects one province to represent each group of provinces, which are the provinces on the average line, below the average line, and above the average line. The study considered Chiang Mai as the province that is on the average line, Chanthaburi as the province that is above the average line, and Roi Et as the province that is below the average line.

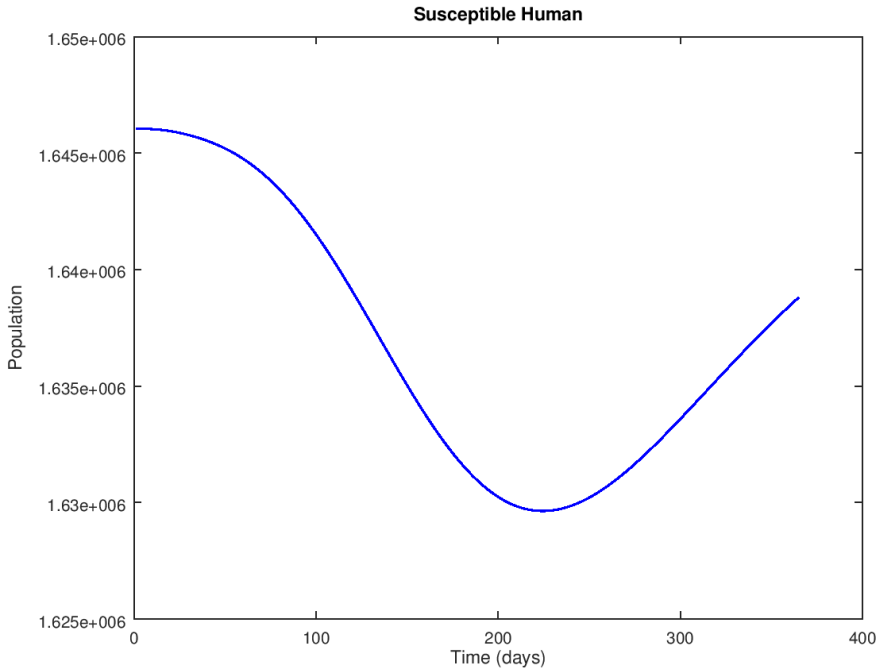
The simulations were done from 2003 to 2015 with the total population of Chiang Mai in each year as N_h in equation (1) to (7).

The various parameters are predefined in the script in order to make them available for the simulation. The simulations for both the human and mosquito populations are done for 365 days representing 1 year using equations (13) and (14) respectively. The simulated compartments are plotted to show a graphical representation of the transmission dynamics of the infection. For the human population, the susceptible compartment is plotted separately as the scale is bigger than the exposed and infected compartment. The mosquito compartment has two separated figures representing the aquatic stage and the susceptible compartment with the exposed and infected compartment plotted together. All programming codes and scripts are shown in the appendix.

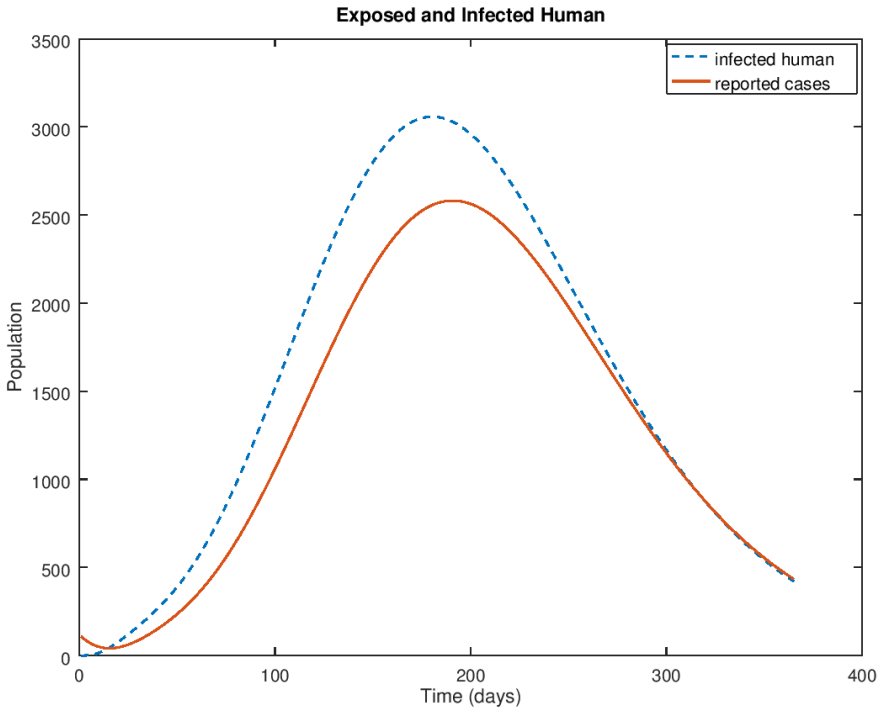
After obtaining the parameters for the simulation, the eigenvalues associated with the disease-free equilibrium can be calculated as follows

$$DFE = 1000000 \times \begin{bmatrix} 0.0000 \\ 0.0000 \\ 0.0000 \\ 0.0000 \\ 0.0000 \\ -9.7699 \\ 0.0000 \end{bmatrix}.$$

The graphs below therefore show the simulations that were carried out for all the compartments representing the human and mosquito populations.



(a)



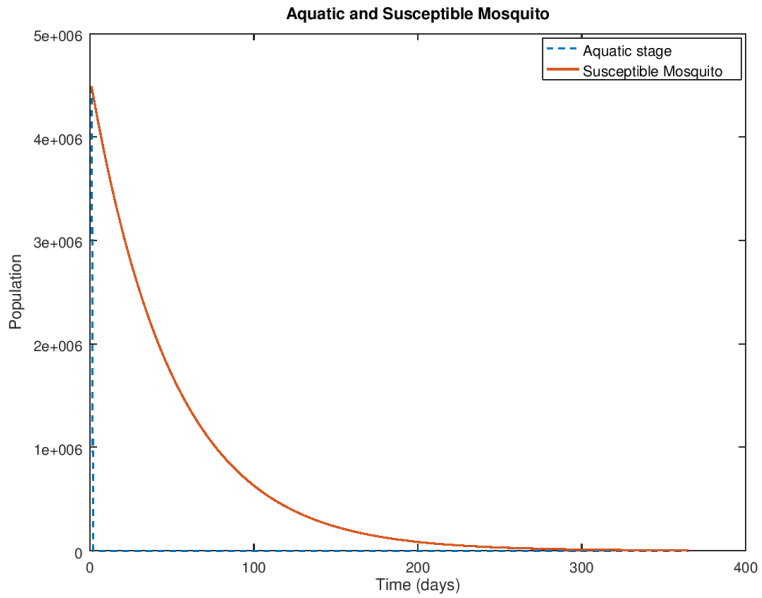
(b)

Figure 13. Simulation of the Human Compartment for Chiang Mai Province for 2013

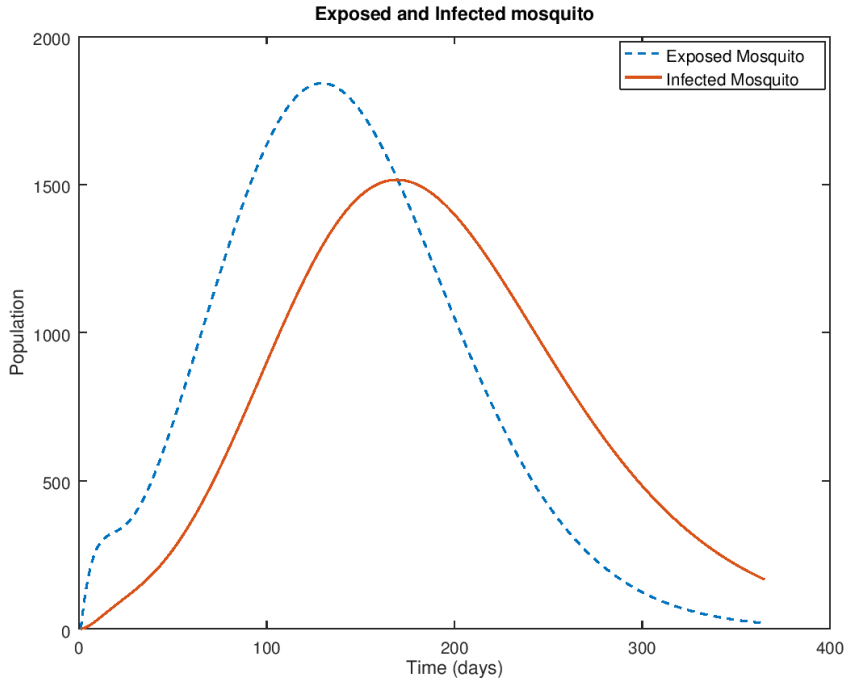
Figure 13 shows the numerical simulations of the Human Compartment for Chiang Mai Province for the year 2013. The simulations were carried out on a daily basis for one year. The total number of people (both susceptible and infected) in Chiang Mai at the beginning of the year 2013 is 1,650,894. The initial number of infected people for the simulation was the total number of cases reported in December 2012, which is 107. Figure 13(a) shows the graph of the susceptible human population and 13(b) show the graphs of the exposed and infected human compartment. The y-axis indicates the total population and the x-axis represents the time for the simulation in day. The parameters used in the simulation are from Table 3.

From Figure 13(a), the number of susceptible people reduces as the disease spreads in the population from an initial number of 1,646,144 from the start of the simulation to about 1,585,000 people at the 247^{th} day and starts increasing after the 250^{th} day to approximately 1,613,000 people. However, in Figure 13(a), a corresponding increase in the exposed compartment can be seen from 0 at the beginning to about 3,050 people at the 155^{th} day of the simulation which then decreases to about 500 people at the end of the simulation. The reason can be that those who get bitten by the mosquitoes get exposed for an incubation period before they show signs of infection. These people then become infected and thereby join the infected compartment as shown in Figure 13(b). The number of infected people increase from the initial 107 number at the first day to about 2,550 people at the 195^{th} day of the simulation which represents the month of June and July. This result is consistent with the statistical result obtained in Figure 10. From the Infected compartment in Figure 13(b), Dengue fever is the highest in the second period of every year with an increase in the number of cases from May through June and with a

peak in July and then a decline in August which is around the 250th day of the simulation.



(a)



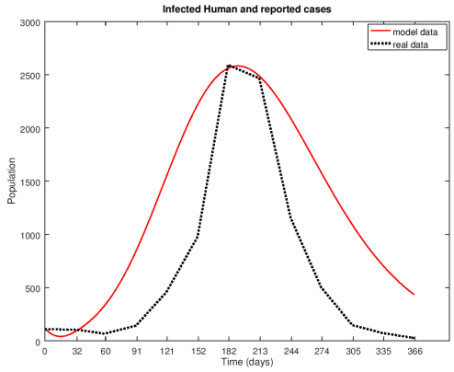
(b)

Figure 14. Simulation of the Mosquito Compartment for Chiang Mai Province for 2013

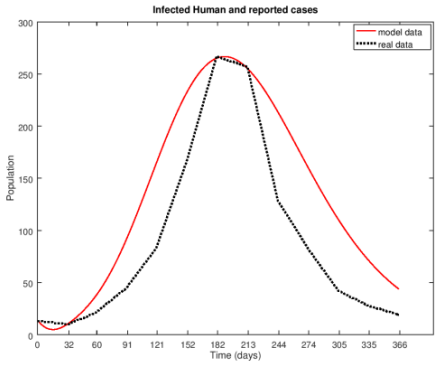
Figure 14 shows the simulations of the mosquito compartment corresponding to the human compartment in Figure 13 for Chiang Mai Province. The simulations were done for the Aquatic Phase, Susceptible Mosquito, Exposed, and Infected Mosquito of the model as shown in Figures 14(a) and 14(b), respectively. From Figure 14(a), the total number of the Aquatic Phase of the mosquito and the Susceptible ones starts decreasing from the start of the simulation as the Aquatic phase becomes the adult mosquitoes and therefore joins the Susceptible compartment. The mosquitoes in the Susceptible compartment get exposed to the disease whenever they bite and thus there is an increase in the number of exposed mosquitoes. This is evident in Figure 14(b). The number, however, decreases after the 120th day. The exposed mosquitos that become infected after the incubation period joins the Infected human compartment and an increase in that number can be seen in Figure 14(b). It should be noted that there is a correlation between the period where there is an increase in the Infected compartment for the human population and the infected mosquito as more mosquitos that bite would result in more humans getting the infection. Figure 13(b) and Figure 14(b) shows this correlation.

4.5 Comparison of Real Data and Simulated Data

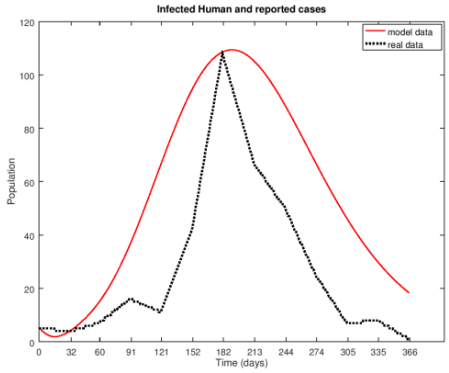
The simulations that were carried out are compared with the real data. This is done by using the graph from the infected compartment and comparing it with the monthly number of cases for Chiang Mai, Chanthaburi and Roi Et provinces.The data obtained from the Bureau of Epidemiology is a monthly data. The data was then interpolated to be a daily data so that it can easily be compared to the daily simulated data obtained from the infected compartment.



(a) Chiang Mai, 2013



(b) Chanthaburi, 2010



(c) Roi Et, 2009

Figure 15. Comparison between the Infected Compartment and Number of Reported Cases for Chiang Mai in 2013, Chanthaburi in 2016, and Roi Et Provinces in 2009

Figure 15 shows the graph of the infected compartment from the model and the number of reported cases for Chiang Mai, Chanthaburi, and Roi Et provinces respectively. The average bite of the mosquito in the model is adjusted to get a graph that mimics the graph of the infected compartment. The highest number of infected people is achieved in the graph corresponding to the model in Figure 15. However, the deviation from the real data can be attributed to the parameters used in the simulation as it can sometimes over estimate the simulated values. This is because it has been assumed that the there is a homogenous mixing of the infected people as well as the mosquito population.

4.6 Numerical Estimation of the Basic Reproduction Number

The basic reproduction number (R_0), an important expression in Mathematical Epidemiology, describes the number of Infected cases generated on the average during the course of an infection. The basic reproduction number for Chiang Mai province was calculated using equation (12). As stated earlier, the infection would result into an endemic situation when $R_0 > 1$ and would die out quickly when $R_0 < 1$. Generally, the bigger than R_0, the harder it becomes to control the infection. In getting an estimate for the basic reproduction number, the graphs were plotted to get a graph that mimics the number of reported cases and after that the parameters that were then substituted in equation (12) to calculate R_o. This was achieved by keeping all the parameters in Table 3 constant and changing only b, the average bite per mosquito per day.

Figures 16, 17, and 18 are the plots of the infected compartments together with the total number of cases that was reported from 2003 to 2015 for Chiang Mai province. It should be noted that some of the parameters like the biting rate and mortality rate of the mosquito have an effect on the transmission of the disease and as the result can cause deviation of the simulated data from the real data.

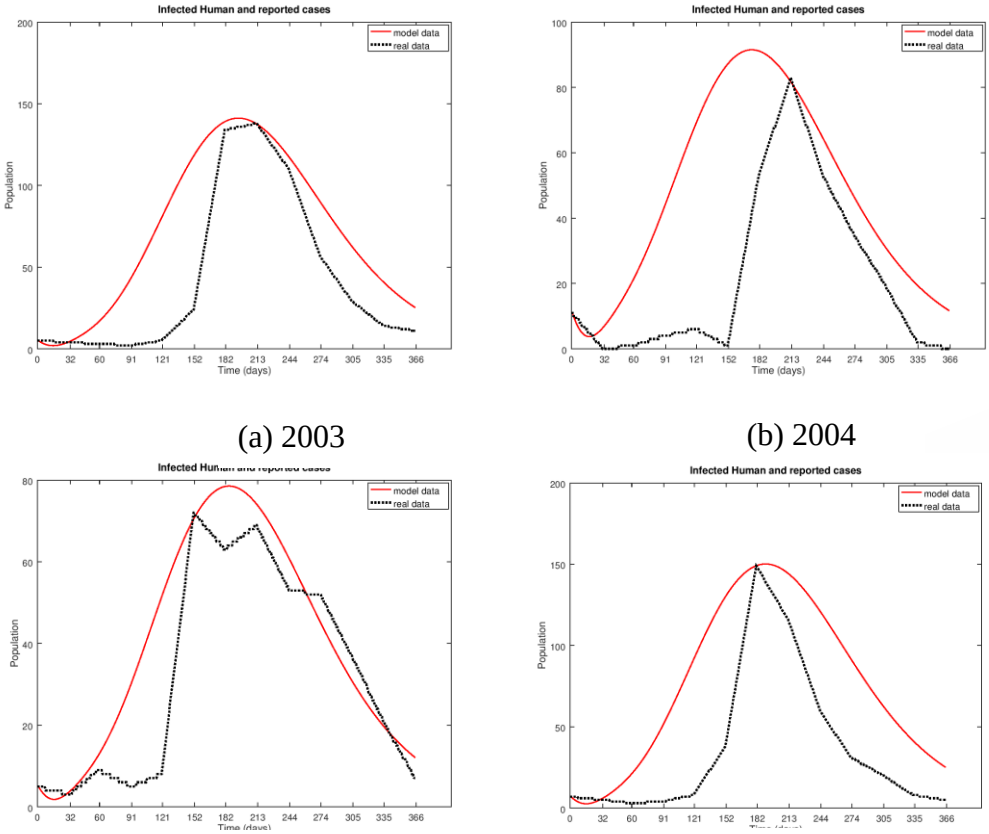


Figure 16. Graph of Infected compartment versus reported number of cases for 2003, 2004, 2005, and 2006 for Chiang Mai Province

In getting an estimate of the basic reproduction number, the graph of the infected compartment together with the number of reported cases are plotted with the model parameters. The various parameters are kept constant, except the parameter b, (average bite per mosquito per day). Figures 16(a), 16(b), 16(c), and 16(d) show the simulation for 2003, 2004, 2005, and 2006, respectively. The graph arising from the model data is shown as the solid line whereas the graph arising from the real data is shown as the dashed line.

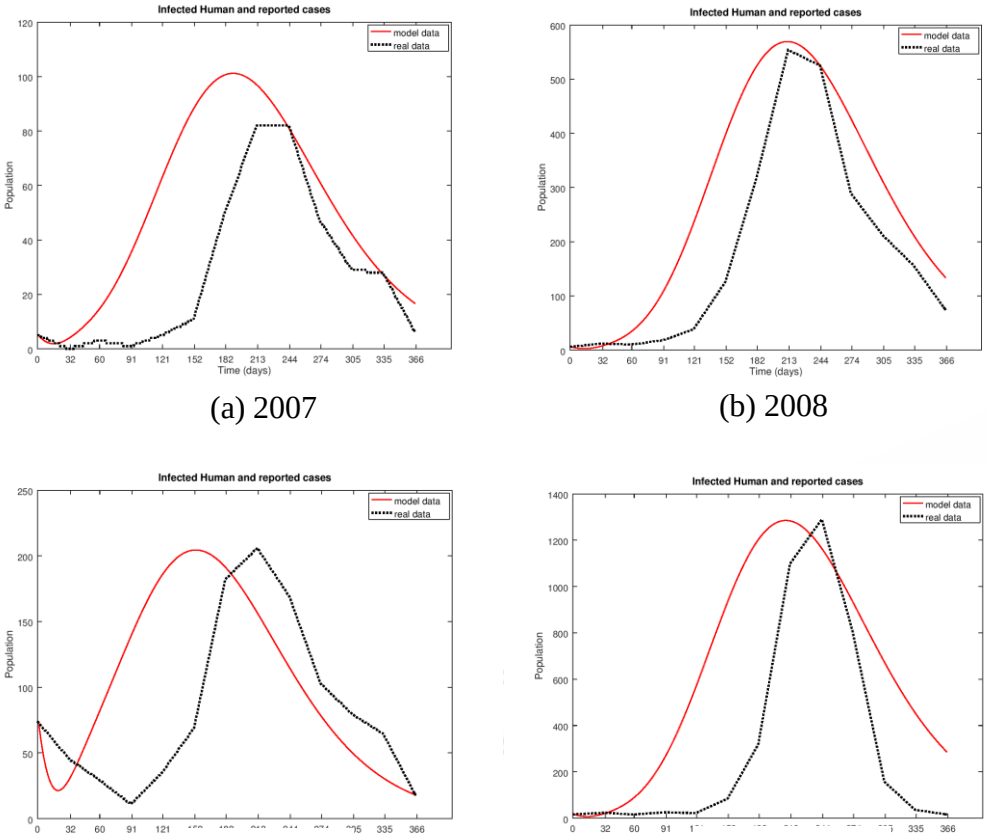
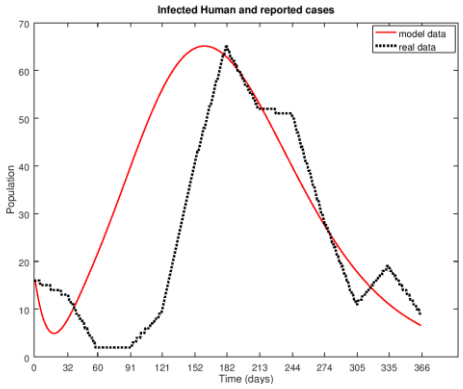
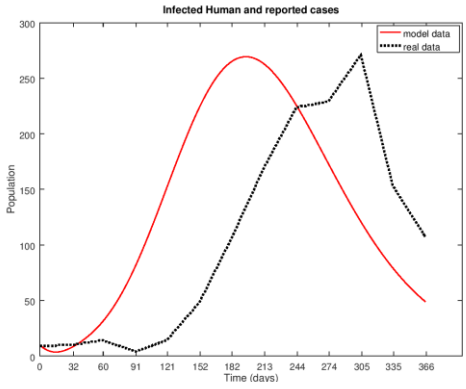


Figure 17. Graph of Infected compartment versus reported number of cases for 2007, 2008, 2009, and 2010 for Chiang Mai Province

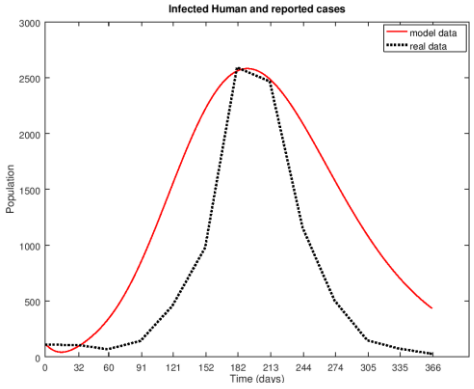
Figures 17(a), 17(b), 17(c), and 17(d) show the graph of the infected compartment and the number of reported cases for Chiang Mai in 2007, 2008, 2009, and 2010 respectively. Figure 17(b) follows the same pattern described under Figure 16.



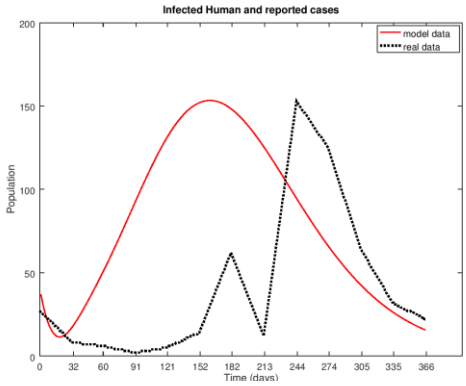
(a) 2011



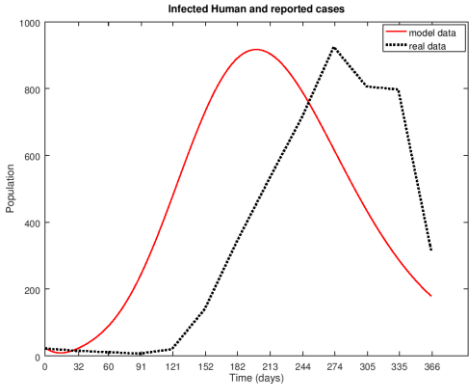
(b) 2012



(c) 2013



(d) 2014



(e) 2015

Figure 18. Graph of Infected compartment versus reported number of cases for 2011, 2012, 2013, 2014, and 2015 for Chiang Mai Province

The simulations for the rest of the years are shown in Figure 18. Figures, 18(a), 18(b), 18(c), 18(d), and 18(e) show the graphs of the infected compartment and the real data for Chiang Mai in 2011, 2012, 2013, 2014, and 2015, respectively. An

estimate of the basic reproduction number and the parameter b, corresponding to each year is shown in Table 4.

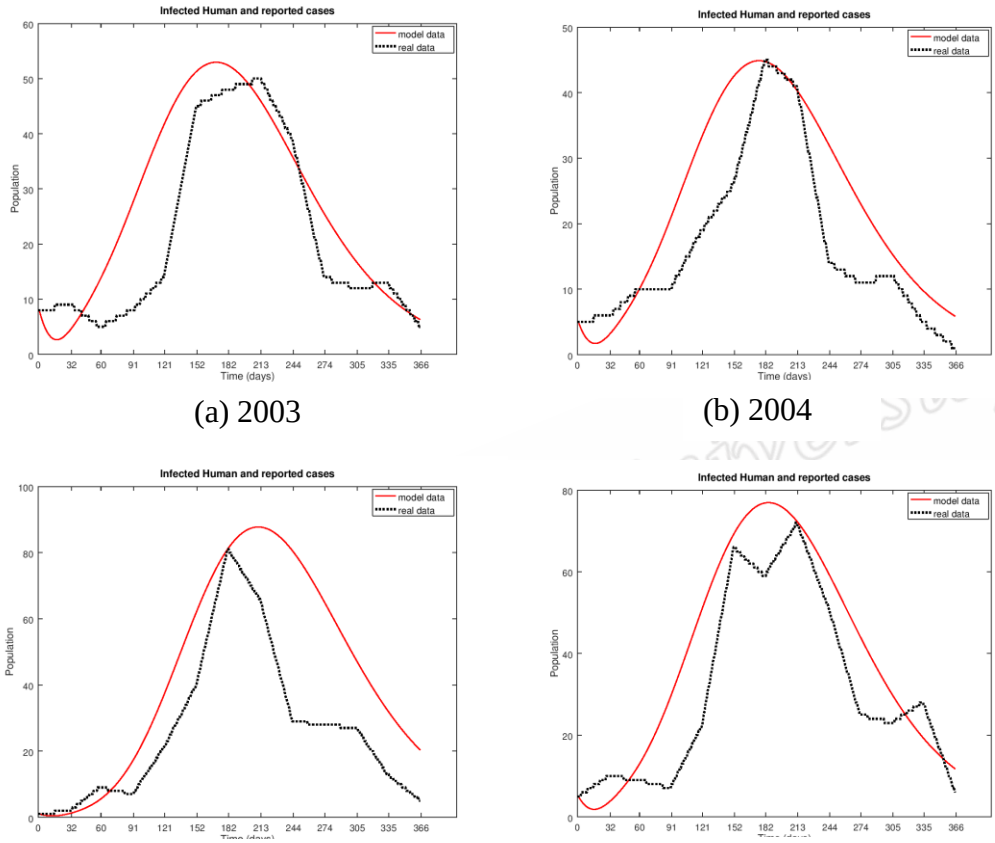
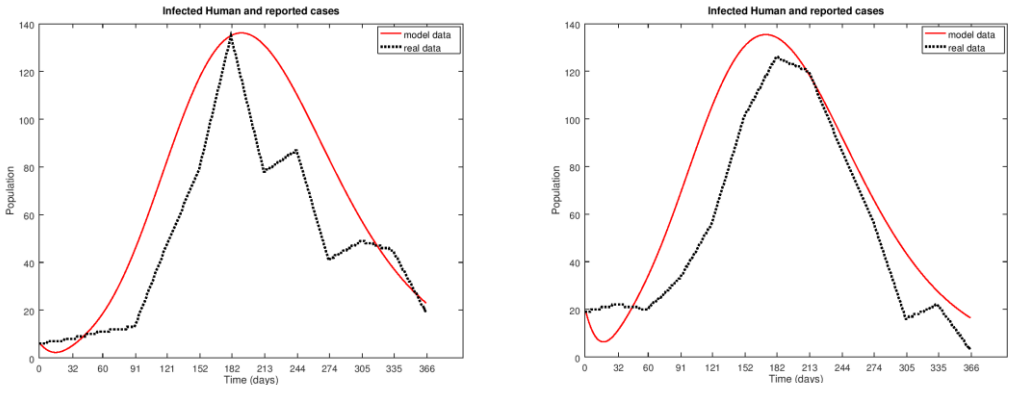


Figure 19. Graph of Infected compartment versus reported number of cases for 2003, 2004, 2005 and 2006 for Chanthaburi Province

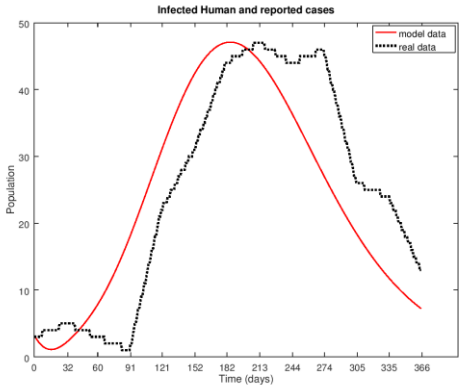
The simulations were repeated for Chanthaburi province, which is part of the provinces that was above the mean line in Figure 11. An estimate of the basic reproduction number has been obtained from 2003 to 2015. All the parameters were kept constant except the parameter b, (average bite per mosquito per day). Figure 19 shows the graph of the real data versus the simulated form 2003 to 2006. From the figure, it can be seen that the number of infected people always starts increasing from the first four months and then peaks in the sixth to seventh month. However, there are

sometimes that the number of infected people from the simulated data are larger than the number of infected people from the real data and this is because of the parameters involved in the simulation.

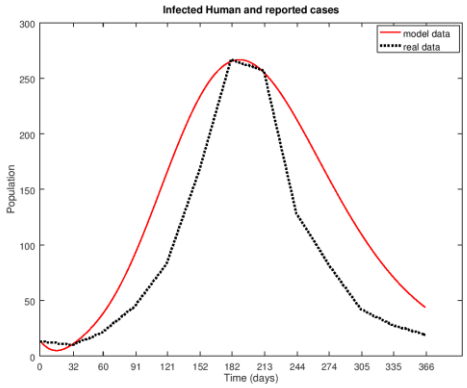


(a) 2007

(b) 2008



(c) 2009

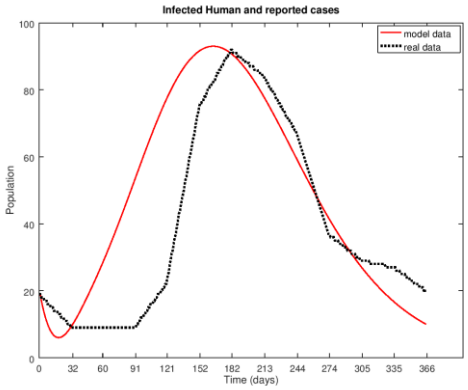


(d) 2010

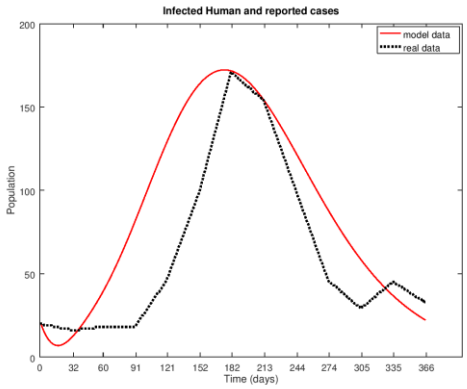
Figure 20. Graph of Infected compartment versus reported number of cases for 2007, 2008, 2009, and 2010 for Chanthaburi Province

Figures 20(a), 20(b), 20(c), and 20(d) show the graph of the infected compartment and the number of reported cases for Chanthaburi province in 2007, 2008, 2009, and 2010, respectively. The simulations were carried out with the same

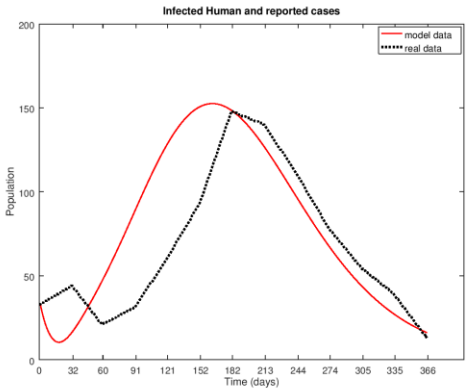
parameter values except the average bit per mosquito per day. The result follows a similar pattern with Figure 19.



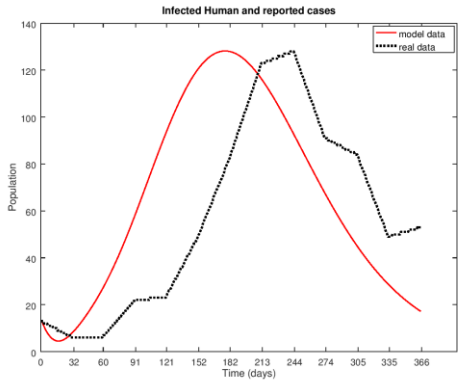
(a) 2011



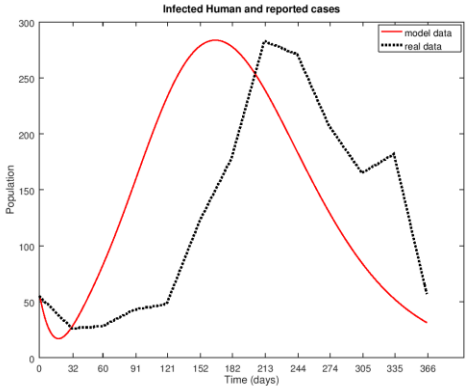
(b) 2012



(c) 2013



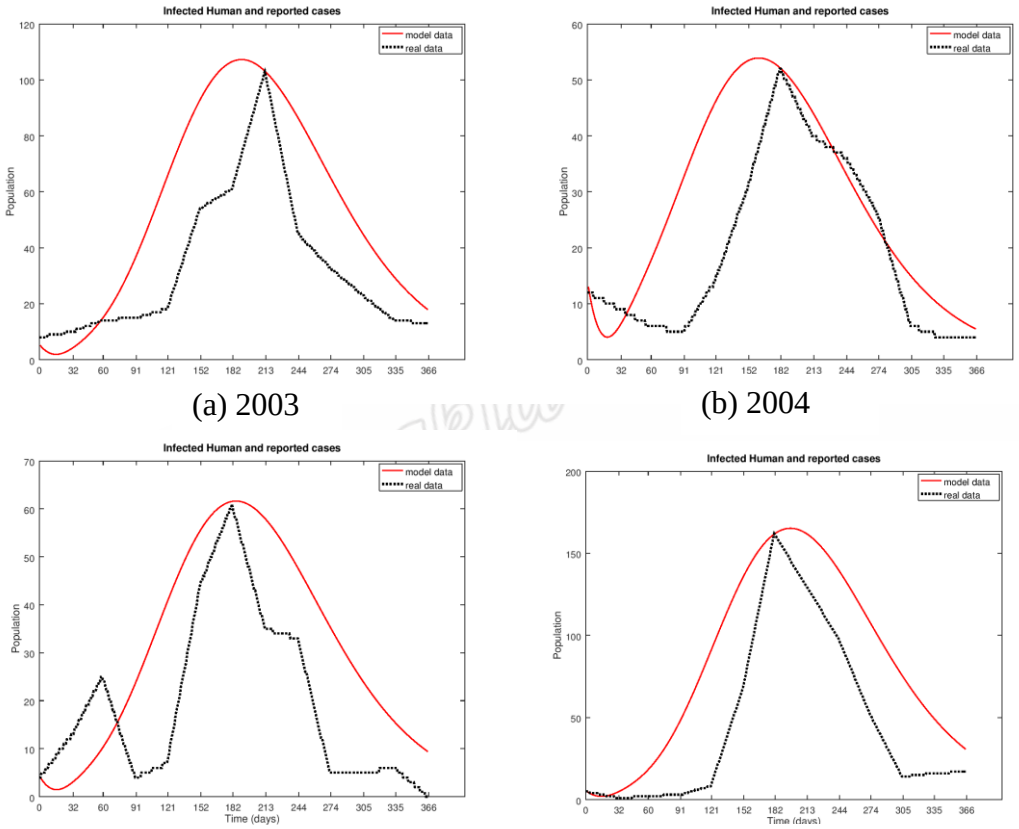
(d) 2014



(e) 2015

Figure 21. Graph of Infected compartment versus reported number of cases for 2011, 2012, 2013, 2014, and 2015 for Chanthaburi Province

Figure 21 shows the simulations for Chanthaburi province for 2011, 2012, 2013, 2014, and 2015. The graphs represents the simulations for the real and simulated data. The province is part of the areas that have reported higher numbers of infected people over the years.

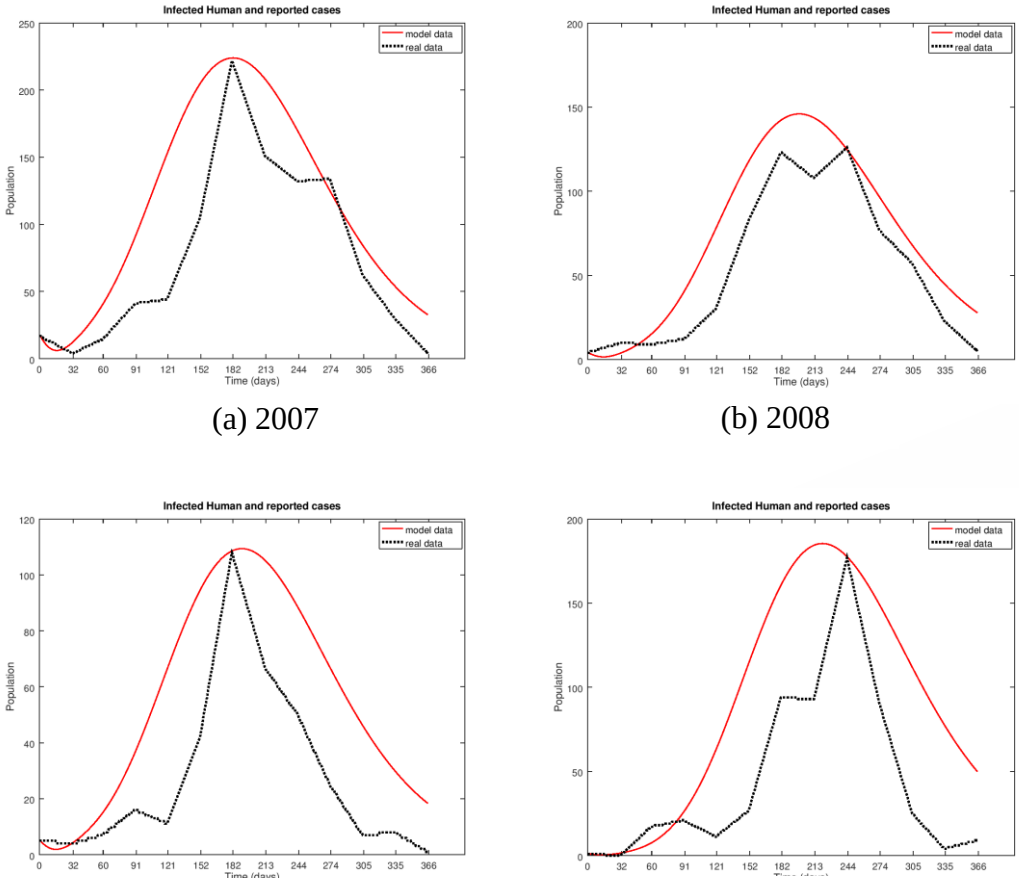


(a) 2003 (b) 2004

(c) 2005 (d) 2006

Figure 22. Graph of Infected compartment versus reported number of cases for 2003, 2004, 2005, and 2006 for Roi Et Province

Figures 22(a), 22(b), 22(c), and 22(d) show the graph of the infected compartment and the number of reported cases for Roi Et province which was below the average line in Figure 11 for 2003, 2004, 2005, and 2006, respectively. The simulation were carried out with the same parameter values except the average bit per mosquito per day. The result follows a similar pattern with Figure 19.

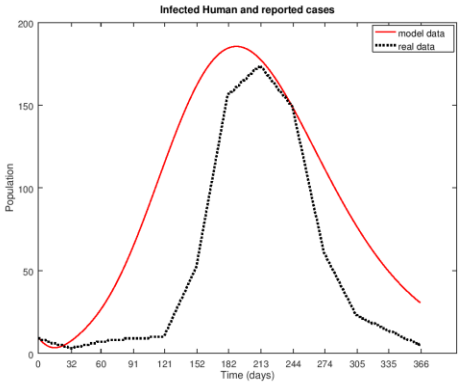


(a) 2007 (b) 2008

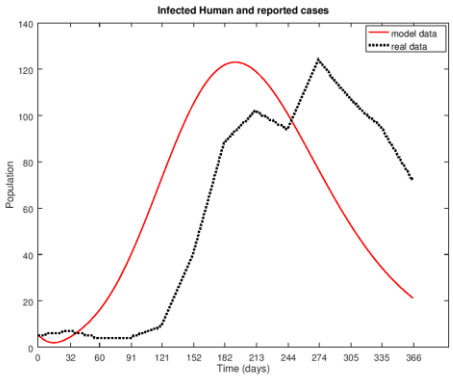
(c) 2009 (d) 2010

Figure 23. Graph of Infected compartment versus reported number of cases for 2007, 2008, 2009, and 2010 for Roi Et Province

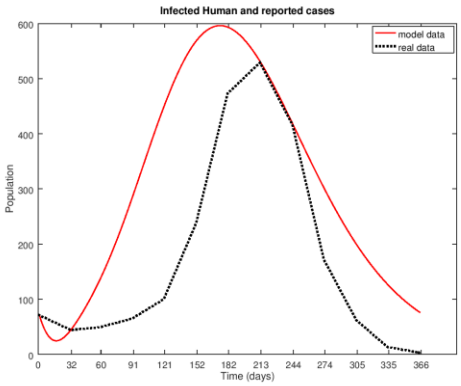
Figure 23 shows the simulations for Roi Et province for 2007, 2008, 2009, and 2010. The graphs represents the simulations for the real and simulated data. The province is part of the areas that have reported much lower cases over the years according to Figure 12.



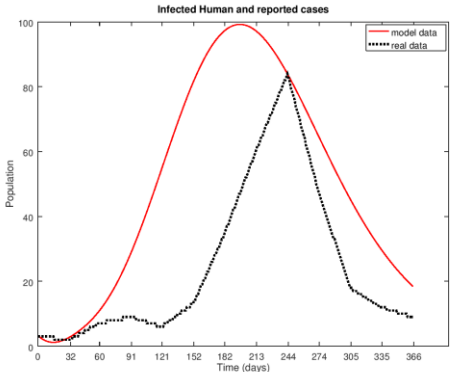
(a) 2011



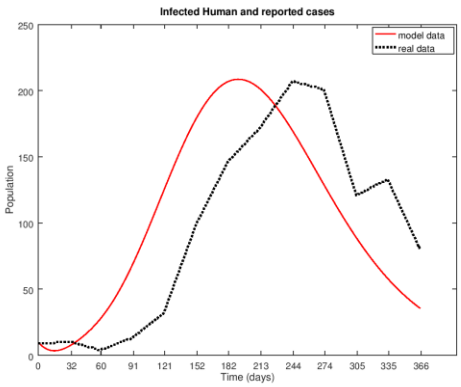
(b) 2012



(c) 2013



(d) 2014



(e) 2015

Figure 24. Graph of Infected compartment versus reported number of cases for 2011, 2012, 2013, 2014, and 2015 for Roi Et Province

Figure 24 shows the graph of the real data versus the simulated from 2011 to 2015 for Roi Et province. From the figure, that the number of infected people always starts increasing from the first four months and then peaks in the sixth to seventh

month. The simulated results are essential for understanding and interpreting the transmission pattern of the disease.

The resulting numerical values are shown in Table 4.

Table 4. The estimated basic reproduction number for Chiang Mai, Chanthaburi, and Roi Et province from 2003 to 2015

	Chiang Mai		Chanthaburi		Roi Et	
Year	b	R_o	b	R_o	b	R_o
2003	0.507	0.7381	0.432	0.73629	0.493	0.7365
2004	0.444	0.7375	0.448	0.73275	0.407	0.73623
2005	0.477	0.7365	0.564	0.73869	0.476	0.73418
2006	0.493	0.7363	0.476	0.73383	0.515	0.73333
2007	0.49	0.7370	0.496	0.73507	0.468	0.73690
2008	0.568	0.7384	0.436	0.73867	0.52	0.73676
2009	0.385	0.7330	0.477	0.73637	0.494	0.73858
2010	0.557	0.7367	0.491	0.73754	0.601	0.73601
2011	0.406	0.7335	0.416	0.73815	0.491	0.73893
2012	0.51	0.7370	0.446	0.73431	0.5	0.73728
2013	0.5	0.7389	0.413	0.73713	0.444	0.73622
2014	0.407	0.7361	0.453	0.73720	0.515	0.73354
2015	0.527	0.7351	0.421	0.73571	0.497	0.73768

Table 4 shows an estimate of the basic reproduction number and the parameter b, the average bite per mosquito per day corresponding to all the years from 2003 to 2015 for Chiang Mai, Chanthaburi, and Roi Et provinces. In 2003, the average bite per mosquito per day is estimated to be 0.507 and its corresponding R_o is estimated as 0.7381 for Chiang Mai province.

Different factors contribute to the dynamic nature of the simulations but this study will concentrate on entomological factors as any policy to control the disease in a short and long term would be about controlling the mosquito and breeding sites.

Therefore, in section 4.7, we will explore how control factors affect the number of infected humans.

4.7 Control Efforts for the Model

The $SEI + ASEI$ model has parameters to control the infection during the epidemic. The control parameters c_m and c_a are used to control the aquatic stage and the adult mosquito respectively. This is done through simulation to know the amount of areas in the province to be controlled with larvicide and insecticides. The values of c_m and c_a lie between 0 and 1. This means that a control value of zero means there is no control whereas a control value of one means a perfect control. However in this study only the control effort c_m for the adult mosquito would be considered. The simulations are carried out for Chiang Mai province for the years 2003, 2006, 2008, 2010, and 2013. The resulting graphs are shown in Figure 25.

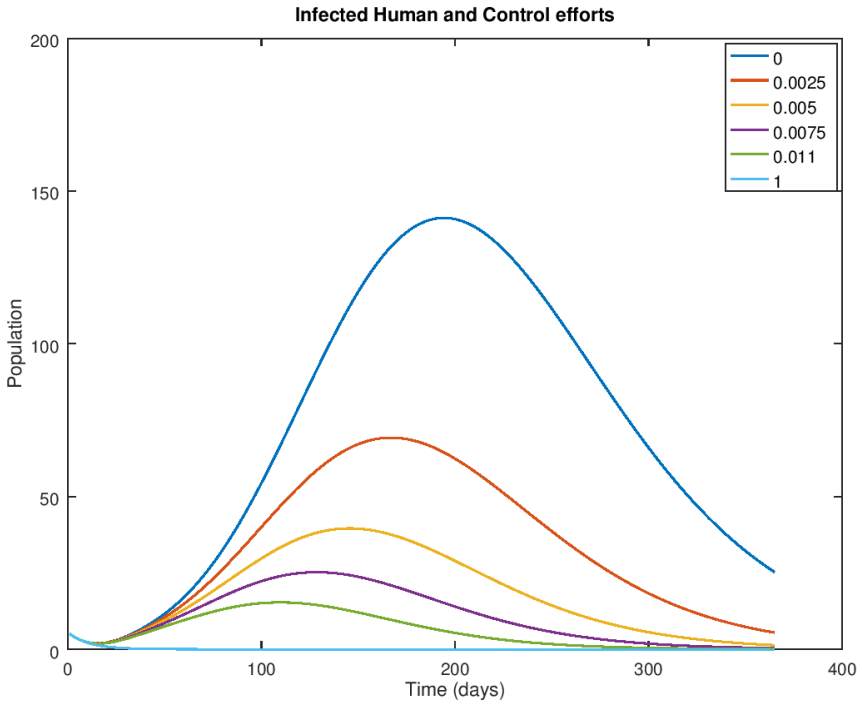


Figure 25. Control Efforts for Chiang Mai province, 2003

Figure 25 shows the graphs of the simulations carried out for Chiang Mai, with control efforts in 2003. Control efforts targeting the adult mosquito were used and the corresponding change in the number of infected individuals are shown in the figures. It should be noted that the control efforts are used of reduce the number of infected individual during the entire simulation. As a result, there is a corresponding decrease in the estimate of the basic reproduction number. The control effort values used and the corresponding estimate of the basic reproduction number is shown in Table 5.

Table 5. Control efforts and basic reproduction number for Chiang Mai in 2003

Control efforts	R_o
0	0.7381
0.0025	0.7172
0.005	0.7100
0.0075	0.6892
0.011	0.6771
1	0.0129

Table 5 shows the values of the control efforts used and their corresponding estimated value of the basic reproduction number. Each control value reduces the estimate of the basic reproduction number.

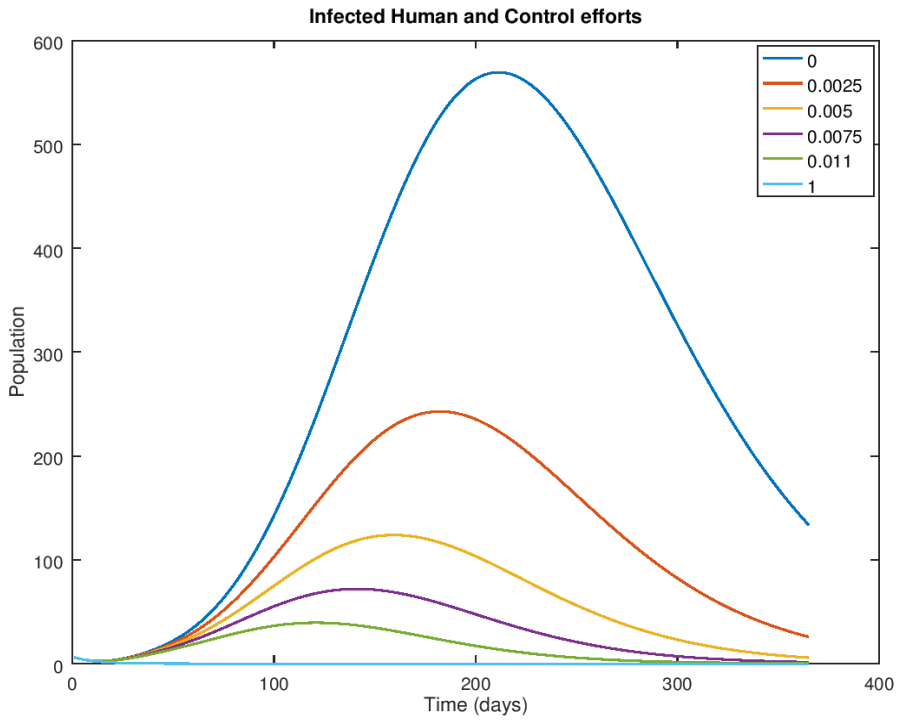


Figure 26. Control Efforts for Chiang Mai province, 2008

Figure 26 shows the graphs of the simulations carried out for Chiang Mai, with control efforts in 2008. The legend on the figure shows each control parameter and the effect it has on the number infected people in the population. The control effort values used and the estimate of the basic reproduction number are shown in Table 6.

Table 6. Control efforts and basic reproduction number for Chiang Mai in 2008

Control efforts	R_o
0	0.7384
0.0025	0.7195
0.005	0.7082
0.0075	0.6944
0.011	0.6788
1	0.0153

Table 6 shows the values of the control efforts used and their corresponding estimated value of the basic reproduction number for Chiang Mai province in 2008. Each control value reduces the estimate of the basic reproduction number.

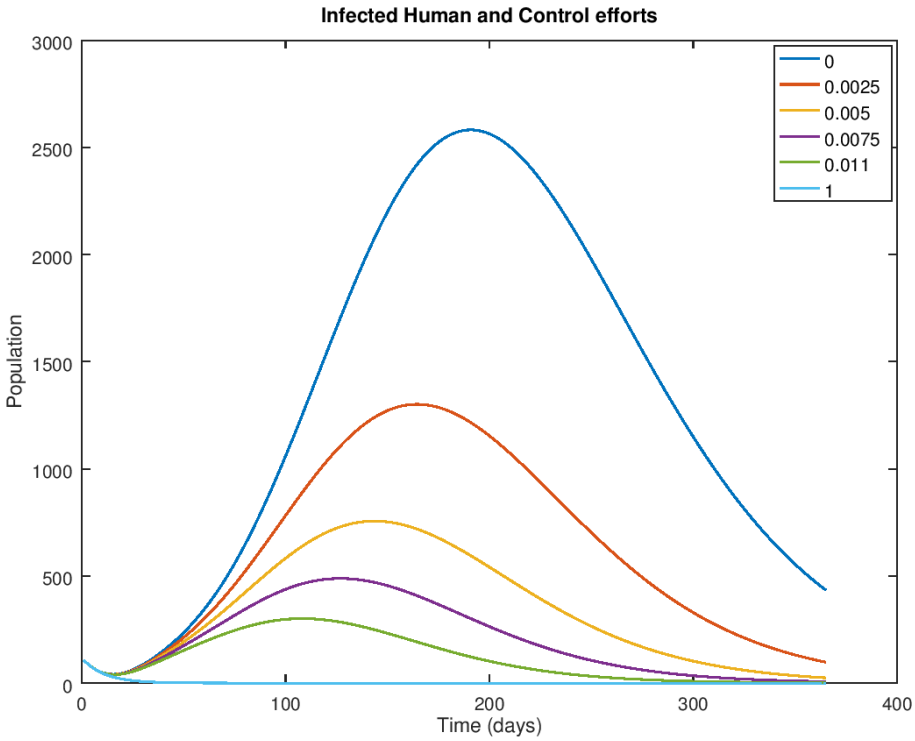


Figure 27. Control Efforts for Chiang Mai province, 2013

Figure 27 shows the graphs of the simulations carried out for Chiang Mai, with control efforts in 2013. The legend on the figure shows each control parameter and the effect it has on the number of infected individuals in the population. Every control effort reduces the total number of infected individuals in the population. The control effort values used and the corresponding estimate of the basic reproduction number are shown in Table 7.

Table 7. Control efforts and basic reproduction number for Chiang Mai in 2013

Control efforts	R_o
0	0.7389
0.0025	0.7245
0.005	0.7032
0.0075	0.6932
0.011	0.6835
1	0.0126

Table 7 shows the values of the control efforts used and their corresponding estimated value of the basic reproduction number. Each control value reduces the estimate of the basic reproduction number which gives the estimates of the number of secondary infection in a population when an infected person in introduced. In the real situation, this is a fact and it has been shown numerically.

When these plots are generated for different provinces for different years, the results would be similar to the ones presented in Figures 25, 26, and 27. The reason is that the control parameters are supposed to reduce the number of infected people over time and as a result whenever c_m, the control effort for the adult mosquito increases, there is a corresponding decrease in the number of infected individuals.

The next chapter discusses the conclusions and some recommendations from the study.

Chapter 5

CONCLUSIONS

In this chapter, conclusions, recommendations as well as further research would be discussed. This would provide more information for the government, public health agencies and other stakeholders to make better policies in determining how to allocate resources for dengue fever treatment and control in Thailand.

5.1 Conclusions

In order to control and prevent the transmission of dengue fever in Thailand, there is the need to understand the transmission patterns and the prevalence of the disease. Many infectious diseases have been modeled using differential equations. The purpose of this study was to examine and discuss in detail a mathematical model for the transmission of the dynamics of dengue fever in Thailand using differential equations. A number of assumptions were made in order for the mathematical model to be applicable in the study area. The nature of dengue fever satisfies the $SEI + ASEI$ model as it describes the interaction between humans and mosquitos in population. The population comprising of human and mosquito were categorized in susceptible, exposed, infected and then another compartment for the aquatic phase of the mosquito's life. All the parameters used in the model are described in section 4.4 in Chapter 4 of the study.

Data from the bureau of epidemiology, Ministry of Public Health, Thailand was obtained from 2003 to 2015 and it was used to understand the transmission pattern of the disease. It was seen that dengue fever is highest in the second period of every year. There is always an increase in the number of cases from the month of May

through June with a peak in July and then declines in August. Also, the distribution of the disease in all the 76 provinces for the 13-year period was also shown. This was done according to regional demarcations and it was seen that dengue fever has been prevalent in the central region of Thailand. A thematic map representing this distribution was presented to give a graphical view of dengue fever in Thailand. This result is good for the government, Public Health professionals, and other stake holders in the control of the disease.

Simulations were carried out in order to understand how the disease spreads in the population. Chiang Mai, Chanthaburi, and Roi Et provinces were used as case studies for all the numerical simulations. A non-standard numerical scheme has been used to obtain the numerical solution of the system of differential equations. The simulations show that an increase in the average bite per mosquito per day results in an increase in the number of infected people. Also, an increase in the number of infected mosquito has a direct correlation in the increase in the number of infected people.

An important estimate in epidemiology is the basic reproduction number (R_0) and in theory, it has been shown that when $R_0 < 1$, the disease free equilibrium is locally asymptotic stable. Estimates of the basic reproduction number for the Chiang Mai, Chanthaburi, and Roi Et province have been shown. The estimated value for the basic reproduction number for Chiang Mai , Chanthaburi, and Roi Et province was relatively small as all the values were less than one. The thematic map obtained shows the provinces that recorded higher number of reported cases when compared with the average number of cases recorded from 2003 to 2015 .

This result is therefore important for epidemiologists in the control of dengue fever in this province and other provinces as well.

In order to understand how the disease can be curbed, the mathematical model makes use of control parameters targeting the adult mosquito. In controlling the epidemics, the control parameters showed good results, as each control parameter value was able to reduce the number of infected individuals throughout the simulation.

From the various simulations, it was seen that, the transmission of the disease depends largely on the average bite of the mosquitoes as well as the average mosquito mortality rate.

5.2 Recommendations

After a careful analysis, the study recommends the following in order to control the spread of the disease.

- The various simulations showed that the transmission of the disease is largely dependent on the average bite of the mosquito. Therefore, it recommended that people put in measures like sleeping in treated mosquito nets.
- As the study provided an estimate of the basic reproduction numbers, epidemiologist can use such information to know on the average how many people would be infected when one infected person is introduced into the population.
- The government should intensify the education on dengue fever incidence to sensitize people in the provinces of its existence.

- The government and other policy makes should increase the control efforts to further reduce the number of infected people in the population.
- Special attention should be given to the provinces in the Central as well as the southern part of the Kingdom as an initial assessment of the data obtained showed that the number of reported cases of dengue fever is higher as compared to the average number of cases reported across all the provinces from 2003 to 2015.
- Entomological data pertaining to Thailand is not available in most endemic provinces and it would be recommended that detailed studies be carried out to make this data more readily available to mathematical epidemiologist for future studies.

5.3 Further Study

Further research work is recommended in order to in-cooperate more parameters in the model to represent the more heterogeneous nature of the real world situation. This study however, considered three provinces from the North, Central and North-East part of Thailand, and thus the incidence of dengue fever could be more understood when the simulations are carried out for most of the provinces in all the regions. The choice of parameters for future work should done on the basis of detailed simulations by varying almost all the parameters involved and then comparing them to the real data in order to get the graph that best fits the real data.

Also, the non-standard finite difference scheme need to be investigated further in order to generally apply it to epidemic models to ensure numerical stability in the results.

REFERENCES

Anguelov, R. and Lubuma, J. M. S. 2003. Nonstandard Finite Difference Method by Nonlocal Approximation. Mathematics and Computers in Simulation. 6, 465-475.

Anguelov, R. and May, R.M. 1991. Infectious Disease of Humans: Dynamics and Control. Oxford University Press.

Badshah, N., Shah, H. and Javid, M. 2015. Estimation of Basic Reproduction Number for Dengue Fever in Lahore, Pakistan. Sains Malaysiana. 44(10), 1423–1430.

Burattini, M. N., Chen, M., Chow A., Coutinho, F. A., Goh, K. T., Lopez, L. F., Ma, S., and Massad E. 2008. Modelling the Control Strategies against Dengue in Singapore. Epidemiology and Infection. 136(3), 309-19.

Chamberlain, R. and Sudia, W. 1961. Mechanism of Transmission of viruses by mosquitoes. Annual Review of Entomology. 6, 371–390.

Dengue Virus Net. 2016. History of Dengue. Available online: http://www.denguevirusnet.com/history-of-dengue.html [January 29, 2016].

Derouich, M., Boutayeb, A. and Twizell, E.H. 2003. A Model of Dengue Fever. Biomedical Engineering Online. 2(4).

Diekmann, O., Heesterbeek, J. A. P. and Metz, J. A. J. 1990. On the definition and the Computation of the Basic Reproduction ratio R_o in Models for Infectious

Diseases in Heterogeneous Populations. Journal of Mathematical Biology. 28(4), 365-82.

Driessche Van den, P. and Watmough, J. 2002. Reproduction Numbers and Sub-Threshold Endemic Equilibria for Compartmental Models of Disease Transmission. Mathematical Biosciences. 180, (2002) 29–48.

Dumont, Y., Chiroleu, F. and Domerg, C. 2008. On a Temporal Model for the Chikungunya Disease: Modeling, Theory and Numerics. Mathematical Biosciences. 213(1), 80-91.

Lungu, E. M., Kgosimore, M. and Nyabadza, F. 2007. Lecture Notes: Mathematical Epidemiology. Department of Mathematics, University of Botswana.

Fatunla, S. O. 1998. Numerical Methods for Initial Value Problems in Ordinary Differential Equations. Academic Press Inc., New York.

Favier, C., Degallier, N., Rosa – Freitas, M. G., Boulangeer, J. P., Costa Lima, J. R., Luitgards-Moura, J. F., Menkes, C. E., Mondet, B., Oliveira, C., Weimann, E. T. and Tsouris, P. 2006. Early Determination of the Reproductive Number for Vector-Borne Diseases: The Case of Dengue in Brazil. Tropical Medicine and International Health. 11(3), 332-40.

Feng, Z., Castilla-Chavez, C. and Capurro A., F. 2000. A Model for Tuberculosis with Exogenous Reinfection. Theoretical Population Bioloy. 57, 235-247.

Gubler, D.J. and Clark, G.G. 1996. Community Involvement in the Control of Aedes Aegypti. Acta Tropica. 61, 169–179.

Hethcote, H.W. 2000. The Mathematics of Infectious Diseases, SIAM. 42, pp. 599-653.

Jafaruddin, Indratno, S. W., Nuraini, N., Supriatna, A. K. and Soewono, E. 2015. Estimation of the Basic Reproductive Ratio for Dengue Fever at the Take-Off Period of Dengue Infection. Computational and Mathematical Methods in Medicine 1-14. Doi: 10.1155/2015/206131

Kermack, W. O. and Mckendn'ck, A. G. 1927. A Contribution to the Mathematical Theory of Epidemics. Proceedings of the Royal Society of London. Series A, Mathematical and Physical Character. 115(772), 700-721.

Khalid, M., Sultana, M. and Khan, F. S. 2015. Numerical solution of SIR Model of Dengue Fever. International Journal of Computer Applications. 118(21).

Mickens, R. E., 2002. Nonstandard Finite Difference Schemes for Differential Equations. Journal of Difference Equations and Applications 823-847. Doi: 10.1080/1023619021000000807

Mickens, R. E., 1981. NonLinear Oscillations. Cambridge University Press, New York.

Noor, B., Hassan, S., and Muhammad, J. 2015. Estimation of Basic Reproduction Number for Dengue fever in Lahore, Pakistan. Sains Malaysiana. 44(10), 1423-1430.

Pinho, S. T. R., Ferreira, C. P., Esteva, L., Barreto, F. R., Morato, V. C., Teixeira, M. G. L. 2010. Modelling the Dynamics of Real Dengue Epidemics.

Philosphical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences. 368, 5679-5693.

Sanofi Pasteur, Dengvaxia, World's First Dengue Vaccine, Approved in Mexico 2015. Available online: http://www.sanofipasteur.com/en/articles/dengvaxia-world-s-first-dengue-vaccine-approved-in-mexico.aspx [March 14, 2016].

Sunday, J. 2010. On Exact Finite-Difference Scheme for Numerical Solution of Initial Value Problems in Ordinary Differential Equations. Pacific Journal of Science and Technology. 11(2), 260-267.

Syafruddin, S. and Noorani, M.S. 2012. SEIR model for transmission of dengue fever in Selangor, Malaysia. International Journal of Modern Physics: Conference Series 380-389. Doi: 10.1142/S2010194512005454

Thailand Bureau of epidemiology. 2016. National trustworthy and competent authority in epidemiological surveillance and investigation. Available online: http://203.157.15.110/boe/home.php [January 1, 2016].

United States Environmental Protection Agency. 2015. Mosquito life cycle. Available online: https://www.epa.gov/mosquitocontrol/mosquito-life-cycle [November 8, 2015].

VectorBase, Bioinformatics Resource for Invertebrate Vectors of Human Pathogens. 2015. Available online: https://www.vectorbase.org/organ- isms/aedes-aegypti [December 29, 2015].

World Health Organization - Dengue and Severe Dengue, fact sheet N°117, May 2015. 2015. Available online: http://www.who.int/mediacentre/factsheets/fs117/en/ [October 8, 2015].

World Health Organization. 2012. Global Strategy for Dengue Prevention Control 2012-2020. Geneva, pp. 2 – 4.

Appendix

Appendix

Octave Code for Simulation

```
% This program is free software: you can redistribute it and/or modify
%     it under the terms of the GNU General Public License as published by
%     the Free Software Foundation, either version 3 of the License, or
%     (at your option) any later version.
%
%     This program is distributed in the hope that it will be useful,
%     but WITHOUT ANY WARRANTY; without even the implied warranty of
%     MERCHANTABILITY or FITNESS %FOR A PARTICULAR PURPOSE.  See
the
%     GNU General Public License for more details.
%
%     You should have received a copy of the GNU General Public License
%     along with this program.  %If not, see <http://www.gnu.org/licenses/>.
% for plotting the main Simulation for all compartments

clear,clc
clear,clc
disp('************************************************************')
disp('Topic: Mathematical Models for Infectious Disease Dynamics:')
disp('A case of Dengue Fever Transmission in Thailand. ')
disp('************************************************************')
disp('  ')
disp('Student: Collins Bekoe')
disp('  ')
disp('Advisors: Dr. Pakwan Riyapan')
disp('          Dr. Tatdow Pansombut')
disp('          Asst. Prof. Dr. Aniruth Phon-On')
disp('  ')
disp('************************************************************')
```

```
disp('      Faculty of Science and Technology')
disp('Department of Mathematics and Computer Science')
disp('        Prince of Songkla University')
disp('          Date: 10th March, 2016.')
disp('************************************************************')
disp('')
deltaT = 1;
Sh = zeros(365,1);  %array to hold the number of susceptible during the iteration
Eh = zeros(365,1);
Ih = zeros(365,1);
Am = zeros(365,1);
Sm = zeros(365,1);
Em = zeros(365,1);
Im = zeros(365,1);
% Nh = 1599538;  % 2003
% Nh = 1616995;  % 2004
% Nh = 1640390;  % 2005
% Nh = 1654154;  % 2006
% Nh = 1661349;  % 2007
% Nh = 1667358;  % 2008
% Nh = 1651433;  % 2009
% Nh = 1636514;  % 2010
% Nh = 1643312;  % 2011
% Nh = 1650894;  % 2012
 Nh = 1646144;  % 2013
% Nh = 1672586;  % 2014
% Nh = 1678284;  % 2015

b = 0.5;  %original value % average bite per mosquito per day
k = 0.5;  %fraction of female mosquitos hatched from all eggs
Eh(1) = 0; %initial value of the exposed human
%Ih(1) = 5;      % 2003
```

```
% Ih(1) = 11;   % 2004
% Ih(1) = 5;    % 2005
% Ih(1) = 7;    % 2006
% Ih(1) = 5;    % 2007
% Ih(1) = 6;    % 2008
% Ih(1) = 74;   % 2009
% Ih(1) = 17;   % 2010
% Ih(1) = 16;   % 2011
% Ih(1) = 9;    % 2012
 Ih(1) = 107;  % 2013
% Ih(1) = 37;   % 2014
% Ih(1) = 22;   % 2015
Sh(1) = Nh-Eh(1)-Ih(1); %initial value of the susceptible human
Am(1) = b*Nh;  %initial number of mosquitoes at the aquatic stage


Em(1) = 0;  %initial value of the exposed mosquito
Im(1) = 0;  %initial value of the infected mosquito
delta = 4; % average oviposition rate
miuM = 0.02;  % average mosquito mortality rate
miuA = 0.01;  %average aquatic mortality rate
gammaM = 0.12; % average aquatic transition rate
thetaM = 0.02; %extrinsic incubation period
miuH = 0.0143;  %human mortality rate
thetaH = 0.083; %intrinsic incubation rate
alphaH = 0.083; %recovering rate
C = 0.918455;  %Mosquito carrying capacity
Bm = 0.4; %0.4;    %effective contact rates
cA = 0;  %control efforts at the aquatic stage

cM =[0]; % Control efforts for Chiang Mai
Rm = (k*delta*gammaM)/((miuM+cM)*(gammaM+miuA+cA));
```

```
Sm(1) = (b*Nh*gammaM*(C*(1-(1/Rm))))/(miuM+cM);
%Simulating on a daily basis for all compartment
for u =1:1
for n = 1:364;

 % Human Population
Sh(n+1) = (miuH*Nh*deltaT+Sh(n))/(1+(miuH*deltaT+(b*Bm*Im(n)*deltaT)/Nh));
Eh(n+1) = (((deltaT*b*Bm*Sh(n+1)*Im(n))/Nh)+Eh(n))/(1+(thetaH+miuH)*deltaT);
Ih(n+1) = ((thetaH*Eh(n+1))*deltaT+Ih(n))/(1+(alphaH+miuH)*deltaT);
% Mosquito Population
Am(n+1) =
(k*delta*(Sm(n)+Em(n)+Im(n))*deltaT+Am(n))/(1+((k*delta*(Sm(n)+Em(n)+Im(n))
)/C+(gammaM+miuA+cA))*deltaT);
Sm(n+1) =
(gammaM*Am(n+1)*deltaT+Sm(n))/(1+(((b*Bm*Ih(n))/Nh)+miuM+cM(u))*deltaT)
;
Em(n+1) =
((((b*Bm*Sm(n+1)*Ih(n))/Nh)*deltaT)+Em(n))/(1+(thetaM+miuM+cM(u))*deltaT);
Im(n+1) = (thetaM*Em(n+1)*deltaT+Im(n))/(1+(miuM+cM(u))*deltaT);

R_o(n) =
sqrt((b^2*Bm^2*Sm(n)*thetaH*thetaM)/(Sh(n)*(thetaH+miuH)*(alphaH+miuH)*(th
etaM+miuM+cM(1))*(miuM+cM(1))));
end
end

%find the day in the year in which we have the maximum number of
%infected human, then output the reproduction number of that day
[max_Ih,index_max_Ih] = max(Ih);
reproduction_number = R_o(index_max_Ih)

%plotting the graph for each comapartment
```

```
figure(1)
plot(Sh,'b','LineWidth',1);
xlabel('Time (days)');
ylabel('Population');
title('Susceptible Human');% Population with no control');

figure(2) %graph of exposed human population
plot(Eh,'--','LineWidth',1); hold on
xlabel('Time (days)');
ylabel('Population');
%title('Exposed Human');% Population with no control');

plot(Ih,'-','LineWidth',1); hold off
xlabel('Time (days)');
legend('exposed human','infected human');
ylabel('Population');
title('Exposed and Infected Human'); % Population with no control');

%monthly_data=[5 4 3 2 5 24 134 138 110 57 29 14 11]; %Chiang Mai  2003
% monthly_data=[11 0 1 4 6 1 53 83 53 35 19 2 0]; %Chiang Mai  2004
% monthly_data=[5 3 9 5 8 72 63 69 53 52 37 21 7]; %Chiang Mai  2005
% monthly_data=[7 5 3 4 8 38 149 116 60 31 20 8 5]; %Chiang Mai  2006
% monthly_data=[5 0 3 1 5 11 50 82 82 47 29 28 6]; %Chiang Mai  2007
% monthly_data=[6 12 10 18 38 126 316 554 525 289 212 156 74]; %Chiang Mai
2008
% monthly_data=[74 45 30 11 35 69 182 206 169 103 79 64 17]; %Chiang Mai  2009
% monthly_data=[17 23 16 25 22 84 319 1099 1290 806 157 36 16]; %Chiang Mai
2010
% monthly_data=[16 13 2 2 9 40 65 52 51 29 11 19 9]; %Chiang Mai  2011
% monthly_data=[9 10 14 4 14 48 105 169 224 229 271 154 107]; %Chiang Mai
2012
```

```
 monthly_data=[107 106 67 142 455 978 2592 2466 1155 505 147 73 27]; %Chiang Mai  2013
% monthly_data=[27 8 6 2 5 14 62 12 153 125 64 32 22]; %Chiang Mai  2014
% monthly_data=[22 15 11 7 20 140 340 530 715 925 806 797 316]; %Chiang Mai 2015

%num_of_days contains the number of days per month from Jan-Dec, except for
%the first element which is a dummy
num_of_days=[0 31 28 31 30 31 30 31 31 30 31 30 31];

%last_day_in_month contains the ith day which represents the end of each
%months.   For example, last_day_in_month(0) is Dec 31, 2012,
%                  last_day_in_month(32) is Jan 31, 2013,
%                  last_day_in_month(60) is Feb 28, 2013,
%                  last_day_in_month(366) is Dec 31, 2013,
last_day_in_month=zeros(1,13);

% daily_data_2013 contains the daily number of cases lineraly interpolated
% from the monthly data by assuming that the monthly data collected at the
% last day of the month
daily_data= zeros(1,365);
daily_data(1) = monthly_data(1);
i=2;

for m=2:13
   step=(monthly_data(m)-monthly_data(m-1))/num_of_days(m);
   for d=1:num_of_days(m)
      if d == num_of_days(m)
         daily_data(i) = monthly_data(m);
         last_day_in_month(m) = i;
      else
         daily_data(i) = daily_data(i-1) + step;
```

```
        end
        i=i+1;
    end
end

%round to get the number of cases as integers
daily_data = round(daily_data);
x_axis = 0:365;

% plot(x_axis , daily_data,':k','LineWidth',2);
% set(gca,'XTick',last_day_in_month)
% xlabel('Time (days)'); % x-axis label
% ylabel('Population') % y-axis label
% legend('model data','real data');

figure(4) %graph of Aquatic phase
plot(Am,'--','LineWidth',1); hold on
xlabel('Time (days)');
ylabel('Population');
%title('Aquatic Phase');

%figure(5) %graph of susceptible mosquito
plot(Sm,'-','LineWidth',1); hold off
xlabel('Time (days)');
legend('Aquatic stage','Susceptible Mosquito');
ylabel('Population');
title('Aquatic and Susceptible Mosquito'); % Comapartmet');

figure(6) %graph of exposed mosquito
%plot(Em,'g','LineWidth',1); %hold on
plot(Em,'--','LineWidth',1);hold on
xlabel('Time (days)');
```

```
ylabel('Population');

 %graph of infected mosquito
plot(Im,'-','LineWidth',1); hold off
xlabel('Time (days)');
legend('Exposed Mosquito','Infected Mosquito');
ylabel('Population');
title('Exposed and Infected mosquito'); % Compartment');
```

Vitae

Name : Collins Bekoe

Student ID : 5720320706

Educational Attainment:

Degree	Name of Institution	Year
B. Sc. (Mathematics)	Kwame Nkrumah Uni. Of Science and Technology	2013

Scholarship Awards during Enrolment

Thailand's Education Hub for Southern Region of ASEAN Countries (TEH-AC), Graduate School, Prince of Songkla University.

Graduate School Dissertation Funding for Thesis Fiscal Year 2016, Prince of Songkla University.