ANALYSIS OF MALARIA TRANSMISSION DYNAMICS IN HUMAN AND MOSQUITO POPULATIONS

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Abstract

This mini-thesis presents a deterministic mathematical model for the spread of malaria in human and mosquito populations. The human population is divided into four compartments while mosquito population is divided into three compartments. Susceptible humans can be infected when they are bitten by an infected mosquito, they then progress through the exposed, infected, recovered before going back to the susceptible class. Susceptible mosquitoes can be exposed to the disease and once they are exposed, they can be infected, and remain infected until they die. Basic reproduction number, R_0 was established and used to determine whether the disease dies out or persists in the population. It was shown that the disease-free equilibrium point is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$. Quantitative analysis of the model was carried out to confirm the findings from qualitative analysis. Result obtained indicate that the findings of quantitative analysis correspond to the findings of qualitative analysis. It was proven qualitatively that $R_0 < 1$, which corresponds to the results of the sensitivity analysis, that was carried out quantitatively. It was recommended that future work can be done to investigate the stability of the endemic equilibrium point.

Keywords: Reproduction number, Routh-Hurwitz criterion, Mathematical model, Local stability, Steady states.

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Dedication

My work is dedicated to the Almighty God, my husband Mr. Epuli II Nkalle, my children Tida, Golda and Ruth.

Declaration

I, Hilma Yvonne Shaanika, hereby declare that this study, ”Analysis of malaria transmission dynamics in human and mosquito populations” is my own work and is a true reflection of my research, and that this work, or any part thereof has not been submitted for a degree at any other institution.

Hilma Yvonne Shaanika		April 2024
Name of Student	Signature	Date

Acronyms

DFE: Disease Free Equilibrium

DTM: Differential Transformation Method

ODE: Ordinary Differential Equation

SEIR: Susceptible Exposed Infected Recovered (Humans)

SIR: Susceptible Infected Recovered (Mosquitoes)

VIM: Variation Iteration Method

WHO: World Health Organisation

List Of Symbols

E_0 : Disease free equilibrium

E_e : Endemic equilibrium

R_0 : Basic Reproduction number

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Chapter 1

Introduction

This chapter includes the background of the study, problem statement, objectives of the study, significance of the study, research methods and mini-thesis organisation.

1.1 Background of the Study

Mathematical modelling involves formulating real-life situations into a mathematical equation. In mathematics we have different types of models, such as linear, static, explicit, discrete models just to mention a few, and modelling requires steps or process to follow such as: analysis of the problem, formulation of the model, verification and interpretation of the model solution. In this mini-thesis we are conducting the analysis of malaria transmission dynamics in human and mosquito populations. Malaria is one of the deadliest infectious diseases and has claimed millions of lives around the world [17]. Malaria is caused by plasmodium parasites and transmitted to humans through bites of infectious female anopheles mosquitoes [14]. Plasmodium parasites are single

celled parasites that cannot survive outside their host [24]. Though the disease has been identified hundreds of years back and many prevention and treatment methods have been developed it remains a major public health problem [14]. The World Health Organisation (WHO) estimated that there were 219 million cases of malaria world wide resulting in 660000 million deaths in the year 2010 [16, 27], Moreover WHO estimated 249 million cases of malaria world wide resulting in 608000 in the year 2022 [19]. However, other researchers have estimated that the number of cases of falciparum malaria alone lies between 350 and 550 million and deaths rose from 1.0 million in 1990 to 1.24 million in 2010. Further, these estimations give evidence that the WHO's statistical figures are much lower than the actual ones [11, 15, 18] . Majority of malaria cases accounting about 65 percent occur in children below 15 years old [15]. About 125 million pregnant women are at risk of the infection in Sub-Saharan Africa and the maternal malaria is leading to an estimated 0.2 million infant deaths each year [27]. There are about 10,000 malaria cases per year in Western Europe and 1300 – 1500 in the United States. About 900 people died of the disease in Europe during the decade from 1993 to 2003 [27].

Mathematical models are particularly helpful as they consider and include the relative effects of various sociological, biological, and environmental factors on the spread of a disease. The models have been playing an important role in the development of various controlling techniques for malaria epidemic. Analysis of mathematical models is important because it helps in understanding the spread of diseases in general, and malaria in particular, so that suitable control techniques can be adopted for controlling the disease [27]. The main goal of our research is to analyse malaria transmis-

sion dynamics in human and mosquito populations. Many research articles have been published on Malaria modelling. In this research, we use mathematical modelling to analyse malaria transmission dynamics in human population as well as contribution from mosquitoes in the process.

1.2 Problem Statement

Our research will focus on a model of malaria transmission dynamics that captures latency, relapse and migration in human population. To the best of our knowledge, this has not been addressed before.

1.3 Objectives of the Study

The main goal of the research was to analyse malaria transmission dynamics in human and mosquito populations.

The main objectives of the study are to:

(a) Formulate a plausible model (capturing latency, relapse and migration in the human population) and indicate conditions under which the corresponding problem is well posed.

(b) Provide an insight on what to expect from the disease dynamics in the human population in the long run.

(c) Find the conditions under which the disease dies out or persists in the human population.

(d) Provide an insight on a few ways to proceed in order to control the spread of the disease.

(e) Conduct quantitative analysis of the model, part of which includes generating graphs and providing interpretations in order to get insight on recommendations and directions towards subsequent research.

1.4 Significance of the Study

According to the estimations of World Health Organization (WHO) in 2015, 3.2 billion people were at risk of infection from malaria and 2.4 million new cases were detected with 438000 cases of death [28]. Moreover, sub-Saharan Africa remains the most vulnerable region with high rate of deaths due to malaria [24]. With this high death rate due to malaria, it is important to explore various scenarios of malaria transmission dynamics so that public health personnel may use output from the study to find ways of controlling the spread of the disease.

1.5 Research Methods

Both quantitative and qualitative approaches will be used in this research. Qualitative approach evolves around stability analysis of our model while quantitative approach evolves around simulations and interpretation of the resulting graphs as well as sensitivity analysis.

To check whether our problem is well posed, from a mathematical perspective, we will

provide conditions under which the dynamical system (system of ordinary differential equations in this case) describing our model is positively invariant, meaning the variables of our model are positive at any point in time (since they describe biological concepts), given that these variables actually change with time, starting with positive values.

To provide an insight on what to expect in the long run, we will proceed by finding equilibrium points and discussing their stability.

To check if the disease dies out or persists in the population, we will check the stability of the disease-free equilibrium (equilibrium point for which there is no disease in the population). This can be addressed by finding under which condition the basic reproduction number of our model is less than 1.

The basic reproduction number R_0 is a threshold for many epidemiological models as it determines whether the disease dies out or remains in the population as time evolves. The basic reproduction number in any epidemiological model, including our model, can be derived using the next generation matrix approach.

To provide an insight on how to proceed in order to control the spread of the disease, we will conduct sensitivity analysis of the basic reproduction number against the model parameters. This will be achieved by finding the sensitivity index of the reproduction number against each parameter that can be controlled. This will indeed guide us on how to tune these parameters in order to steer the variables of our model towards the desired state.

As part of the quantitative approach we will perform numerical simulations of the model, in order to confirm the findings from theoretical results. We will use MATLAB

programming language to perform the simulations and the parameter values will be from different sources in the literature, or assumed whenever necessary, based on their meaning and their feasible sets (ranges).

1.6 Mini-Thesis Organisation

This mini-thesis is organised as follows: In chapter 1 we deal with the background of the study. Chapter 2 deals with literature review. Chapter 3 covers preliminaries, in which some basic definitions, propositions and some theorems are given. In chapter 4, we elaborate on the formulation and qualitative analysis of the model, where we discuss about positivity and boundedness of the solutions, disease free equilibrium, endemic equilibrium, the basic reproduction number of the SEIR-SEI model of malaria transmission, stability analysis of the disease free equilibrium point. Chapter 5 deals with quantitative analysis of the model. Finally we conclude with Chapter 6.

1.7 Conclusion

In conclusion this chapter has laid the foundation for our mini-thesis, highlighting the background of the study, problem statement, objectives and significance of the study, research methods and the organisation of our mini-thesis.

Chapter 2

Literature Review

2.1 Review of Malaria Models

The concept of malaria models, could be traced back in early 1911, commencing with the Ross model, Susceptible-Infected-Recovered (SIR) model, which segment the host and vectors population into three groups [21]. Due to the limited predictability of the Ross model that fail to document proof for campaigns for mosquito eradication, George Macdonald complemented the Ross model, named Ross Macdonald model by using real data and incorporating an additional compartment for the latency period [13]. By combining the different compartments susceptible (S), exposed (E), infected (I) and recovered (R), the following mathematical model have been developed among which include,SI, SIRS, SEIR, SEIRS and SEI [10].

2.2 Mathematical Models of Malaria Transmission

A lot of papers have been published on analysis of mathematical models of malaria transmission dynamics in human and mosquito populations as follows:

AL Mojeeb and IK Adu [14] applied an SEIR model to malaria transmission between mosquito and human populations, conducted stability analysis, and numerical simulation using MATLAB to confirm the analytic results. Their findings were that malaria may be controlled by reducing the contact rate between humans and mosquitoes, as well as by using active malaria drugs, insecticides and treated mosquito nets.

Wedajo et.al. [28] applied SIR model to malaria transmission between mosquitoes and human populations, with the inclusion of infected immigrants. They discussed local and global stability of equilibrium points. From the numerical results, it was found that prevention of infected immigrant has a strong impact on the malaria disease control.

S Olaniyi and OS Obabiyi [17] explored a malaria transmission model where the forces of infection are nonlinear. Stability analysis of the disease-free equilibrium is investigated and the model results provide stability conditions based on the value of the basic reproduction number.

Abioye et.al. [3] used Differential Transformation Method (DTM) to analyse mathematical models of malaria in human and mosquito populations. Next generation matrix method was used to derive the basic reproduction number (R_0). They also compared the DTM solution of the model with fourth order Runge Kutta Method (RK4) which is embedded in maple 18 to see the behaviour of parameters used in the model. Their

findings were that the two methods used: MATLAB and maple 18, follow the same pattern which was found to be efficient and accurate.

Wedajo et.al. [26] studied the impact of migration of susceptible population on the dynamics of malaria transmission. The validity of the model was proved by verifying positivity of the solution. They derived the equilibrium points. The basic reproduction number of the model was determined so as to study the effect of the migration parameter on the malaria outbreak. They concluded that in order to keep the malaria outbreak under control, the migration parameter is to be minimised.

KT Akinfe and AC Loyinmi [6] considered a SEIR-SEI vector-host mathematical model. They assessed the positivity and boundedness of the solution. They obtained a solution to the model using the Variational Iteration Method (VIM) to each population compartment and verified the efficacy, reliability and validity of the proposed method by comparing the respective solutions via tables and combined plots with MATLAB.

Zaman et.al. [29] presented the analysis of a SEIR epidemic model with time delay. They assumed that the susceptible population evolves according to the logistic equation with saturated non-linear incidence. The disease-free equilibrium is locally asymptotically stable when $R_0 < 1$ and locally asymptotically unstable , when $R_0 > 1$. For $R_0 > 1$, the endemic equilibrium is locally and globally stable. Finally, they derived numerical solutions.

Zhang et.al. [30] explored the dynamics of a SEIR epidemic model with saturated incidence rate and saturated treatment function. The basic reproduction number was determined. Sufficient conditions were established for the existence of backward bifurcation. The local asymptotic stability of equilibriums was verified by analysing the

disease-free equilibrium points and using the Routh-Hurwitz criterion. Their study indicated that they should improve the efficiency and enlarge the capacity of the treatment to control the spread of the disease.

Akinboro et.al. [5] investigated the application of difference transformation method and variational iteration method. Variational Iteration Method (VIM) uses the general lagrange multiplier to construct the correction functional for the problem, while Differential Transformation Method uses the transformed function of the original non-linear system. The result revealed that both methods are in complete agreement, accurate and efficient for solving systems of ordinary differential equations (ODE).

Abboubakar et.al. [2] studied the modelling effects of malaria infection on mosquito biting behaviour and attractiveness of humans. They used next generation matrix method to derive the basic reproduction number (R_0). They conducted numerical simulations to show that increasing the relative attractiveness of infectious humans, increases R_0 but reduces the equilibrium prevalence of infectious humans, decreasing the biting rate of exposed mosquitoes increases R_0, and the equilibrium prevalence of infectious humans and mosquitoes has no impact on R_0.

van den Driessche and Watmough [9] studied reproduction numbers and sub-threshold endemic equilibria for a compartmental model of disease transmission. They established that if $R_0 < 1$, then the disease free equilibrium is locally asymptotically stable, whereas, if $R_0 > 1$ then it is unstable. They concluded that their results are significant for disease control.

Murray et.al. [15] wrote on global malaria mortality between 1980 and 2010: a systematic analysis for the global burden of disease. They attempted to identify all available

data on causes of death for 187 countries from 1980 - 2010 from vital registration, verbal autopsy, mortality surveillance, censuses, surveys, hospitals, police records, and mortuaries. They assessed data quality for completeness, diagnostic accuracy, missing data, stochastic variations, and probable causes of death. Their findings were that in 2010 there were 53.8 millions deaths globally.

Traore et.al. [24] formulated a mathematical model of ordinary differential equations describing the dynamics of malaria transmission with age structure for the vector population. They considered the biting rate of mosquitoes as a positive periodic function which depends on the climate factors. They derived basic reproduction numbers R_0, and they showed that R_0, is the threshold parameter between the extinction and the persistence of the disease.

Wedajo et.al. [26] studied the impact of susceptible human immigrants on the spread and dynamics of malaria transmission. They proved the validity of the model, by verifying positivity of the solution. They carried out the mathematical analysis of the model, including equilibrium points. They determined the basic reproduction number (R_0) in order to study the effect of the migration parameter on the malaria outbreak. They suggested that in order to keep the malaria outbreak under control, the migration parameter is required to be minimised.

We have undertaken comprehensive exploration of existing research and knowledge in the field of malaria transmission dynamics. The review has highlighted the global need to understand and combat the deadly disease that continues to affect millions of lives. However Our research will focus on a model that captures latency, relapse and migration in human population. To the best of our knowledge, this has not been addressed

before.

Chapter 3

Preliminaries on Dynamical Systems

In this chapter we recall various concepts on dynamical systems, all of which will be helpful throughout the remainder of the mini-thesis.

3.1 Basic Concepts

A dynamical system is defined to be a system that evolves with time. There are two types of dynamical systems namely discrete-time and continuous-time dynamical systems. Discrete-time dynamical systems are governed by difference equations while continuous-time dynamical systems are governed by differential equations. This mini-thesis focuses on continuous-time dynamical systems.

Definition 1

A dynamical system is a state space S, a set of times T and a rule R for evolution, $R : S \times T \to S$ that gives the consequent(s) to a state $s \in S$. A dynamical system can be considered to be a model describing the temporal evolution of a system [12].

Definition 2

An equilibrium point x^* for a dynamical system $\dot{x} = f(x)$ is a point for which $f(x^*) = 0$ [20].

Definition 3

In epidemiological models the basic reproduction number often denoted by, R_0 is defined as the average number of secondary infections produced by a single infectious host introduced into a totally susceptible population [7]. To determine the basic reproduction number (R_0), we need to follow the steps for the next generation approach as follows: The basic reproduction number is defined as the largest eigenvalue of the next generation matrix. The formulation of this matrix involves determining two classes viz, infected and non-infected from the model. That is, the basic reproduction number cannot be determined from the structure of the mathematical model alone but depends on the definition of infected and uninfected compartments. Assuming that there are n compartments in the model of which the first m compartments are of infected individuals. $V_i(x) = V_i^-(x) - V_i^+(x)$ where $V_i^+(x)$ is the rate of transfer of individuals into i^{th} compartment by all other means and $V_i^-(x)$ is the rate of transfer of individuals out i^{th} compartment; it is assumed that each function is continuously differentiable at least twice in each variable. The disease transmission model consists of nonnegative initial conditions together with the following system of equations: $\dot{x} = F_i(x) - V_i(x), i = 1,2,3,...,n$ where $\dot{x}$ is the rate of change of x. The next step is the computation of the square matrices $\mathbf{F}$ and $\mathbf{V}$ of order $m \times m$, where m is the number of infected classes, defined by $\mathbf{F} = [\frac{\partial F_i}{\partial x_j}(E_0)]$ and $\mathbf{V} = [\frac{\partial V_i}{\partial x_j}(E_0)]$ with $1 \leq i, j \leq m$. $\mathbf{F}$ is a matrix for partial derivatives of vector F_i with respect to the variables x_j, evaluated

at the disease-free equilibrium point denoted as E_0 , $\mathbf{V}$ is a nonsingular matrix and E_0 is the disease-free equilibrium point (DFE). The matrix $\mathbf{FV}^{-1}$ is called the next generation matrix for the model. Finally the basic reproduction number (R_O) is given by $R_0 = \rho(\mathbf{FV}^{-1})$ where $\rho(\mathbf{FV}^{-1})$ denotes the spectral radius of the matrix $\mathbf{FV}^{-1}$ and the spectral radius is the biggest eigenvalue of the next generation matrix [27].

Definition 4

The disease - free equilibrium (DFE), denoted by E_0 is an equilibrium state of the epidemiological system where there is no disease strain present in the population [1].

Definition 5

The endemic equilibrium point (E_e) is a positive steady state solution of the epidemiological system where the disease persists in the population [4].

Definition 6

Let $f_1,...,f_n$ be n real-valued functions of n variables $x_1,...,x_n$, having first order partial derivatives at a point $a = (a_1,...,a_n)$ Then the matrix

$$\begin{bmatrix} \frac{\partial f_1(a)}{\partial x_1} & \frac{\partial f_1(a)}{\partial x_2} & \cdots & \frac{\partial f_1(a)}{\partial x_n} \\ \frac{\partial f_2(a)}{\partial x_1} & \frac{\partial f_2(a)}{\partial x_2} & \cdots & \frac{\partial f_2(a)}{\partial x_n} \\ \vdots & \vdots & \vdots & \vdots \\ \frac{\partial f_n(a)}{\partial x_1} & \frac{\partial f_n(a)}{\partial x_2} & \cdots & \frac{\partial f_n(a)}{\partial x_n} \end{bmatrix}$$

is called the jacobian matrix of the functions $f_1,...,f_n$ at $(a_1,...,a_n)$ [25].

Definition 7

Let A be an $n \times n$ matrix.

An eigenvalue of A is a scalar λ such that the equation $Av = \lambda v$ has a non-trivial solution. if $Av = \lambda v$ for $v \neq 0$, we say that λ is the eigen value for v [8].

In epidemiology the application of eigenvalues can be regarded as a vital tool in

analysing a system of disease transmission, eigenvalues are used as indicators in determining the stability of an equilibrium of the epidemic system, it can also be used as the measure of the basic reproduction number [22].

3.2 Stability Criteria

Proposition 1

An equilibrium point x^* for a dynamical system $\dot{x} = f(x)$ is said to be locally stable if all the eigenvalues of the Jacobian matrix evaluated at that equilibrium point have negative real parts [20].

Theorem 1

The disease - free equilibrium E_0 $(4.1.1) - (4.1.7)$, is said to be locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$ [2]. Proof, see theorem 4.3.1 from page $36 - 39$.

Routh-Hurwitz Criterion

The Routh-Hurtwitz criterion is a stability criterion which helps to know the signs of eigenvalues without exactly solving the characteristic polynomial [27].

Suppose we are given an n^{th} order homogeneous system of differential equations with constant coefficients: $X'(t) = AX(t)$,

$$X(t) = \begin{bmatrix} x_1(t) \\ x_2(t) \\ \vdots \\ x_n(t) \end{bmatrix}$$

$$A = \begin{bmatrix} a_{11} & a_{12} & \vdots & a_{1n} \\ a_{21} & a_{22} & \vdots & a_{2n} \\ \cdots & \cdots & \cdots & \cdots \\ a_{n1} & a_{n2} & \vdots & a_{nn} \end{bmatrix}$$

where $X(t)$ is an n-dimensional vector containing the unknown functions, A is a square matrix of size $n \times n$.

The stability or instability of the equilibrium state is determined by the signs of the real parts of the eigenvalues of A. To find the eigenvalues, it is necessary to solve the characteristic equation $det(A - \lambda I) = 0$, which is reduced to an algebraic equation of the n^{th} degree $a_0\lambda^n + a_1\lambda^{n-1} + a_2\lambda^{n-2} + ... + a_{n-1}\lambda + a_n = 0$

The roots of this equation can be easily calculated in the cases $n = 2$, and in some cases when $n \geq 3$. In such situations, methods allowing to determine whether all roots have negative real parts and establish the stability of the system without solving the characteristic equation itself, are of great importance. One of these methods is Routh-Hurwitz criterion, which provides the necessary and sufficient conditions for the stability of the system.

Consider again the characteristic equation $a_0\lambda^n + a_1\lambda^{n-1} + a_2\lambda^{n-2} + ... + a_{n-1}\lambda + a_n = 0$, describing the dynamic system. Note that the necessary condition for the stability is satisfied if all the coefficients $a_i > 0$. Therefore, we assume that the coefficient $a_0 > 0$. We write the Hurwitz matrix and it is composed as follows. The main diagonal of the matrix contains elements $a_1, a_2, ..., a_n$. The first column contains numbers with odd indices a_1, a_3, a_5.... In each row, the index of each following

number (counting from left to right) is 1 less than the index of its predecessor. All other coefficients a_i with indices greater than n or less than 0 are replaced by zeros. The result is a matrix of this kind:

$$\begin{bmatrix} a_1 & a_0 & 0 & 0 & 0 & 0 & \vdots & 0 \\ a_3 & a_2 & a_1 & a_0 & 0 & 0 & \vdots & 0 \\ a_5 & a_4 & a_3 & a_2 & a_1 & a_0 & \vdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & 0 & 0 & 0 & 0 & \vdots & a_n \end{bmatrix}$$

The principal diagonal minor δ_i of the Hurwitz matrix are given by the formulas:

$\Delta_1 = a_1$

$\Delta_2 =$

$$\begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix}$$

$\Delta_3 =$

$$\begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{vmatrix}$$

$\Delta_n =$

$$\begin{vmatrix} a_1 & a_0 & 0 & \vdots & 0 \\ a_3 & a_2 & a_1 & \vdots & 0 \\ a_5 & a_4 & a_3 & \vdots & 0 \\ \cdots & \cdots & \cdots & \cdots & \cdots \\ 0 & 0 & 0 & \vdots & a_n \end{vmatrix}$$

We now formulate the Routh-Hurwitz stability criterion: The roots of the characteristic equation have negative real parts if and only if all the principal diagonal minors of the Hurwitz matrix are positive provided that $a_0 > 0, \Delta_1 > 0, \Delta_2 > 0, \cdots, \Delta_n > 0$.

$\Delta_n = a_n\Delta_{n-1}$, the last inequality can be written as $a_n > 0$. For the most common systems of the $2nd$, $3rd$ and $4th$ order, we obtain the following stability criteria:

For a second order systems, the condition of the stability is given by: $a_0 > 0$, $\Delta_1 = a_1 > 0$, $\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} = a_1a_2 > 0$.
That is, all coefficients of the quadratic characteristic equation must be positive.

For the $3rd$ order system, the stability criterion is defined by the inequalities: $a_0 > 0$, $\Delta_1 = a_1 > 0$, $\Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} = a_1a_2 - a_0a_3 > 0, \Delta_3 = a_3 > 0$.
For the $4th$ order system, we get the following set of inequalities: $a_0 > 0$

$$\Delta_1 = a_1 > 0, \Delta_2 = \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} = a_1a_2 - a_0a_3 > 0,$$

$$\Delta_3 = \begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ 0 & a_4 & a_2 \end{vmatrix} = a_1a_2a_3 - a_1^2a_4 - a_0a_3^2 > 0,$$

$\Delta_4 = a_4 > 0$.

If all the $n-1$ principal minors of the Hurwitz matrix are positive and the n^{th} order minor is zero: $\Delta_n = 0$, the system is at the boundary of the stability. As $\Delta_n = a_n\Delta_{n-1}$, then there are two options:

1. The coefficient $a_n = 0$. This corresponds to the case when one of the roots of the auxiliary equation is zero. The system is on the boundary of the periodic stability.

2. The determinant $\Delta_{n-1} = 0$. In this case, there are two complex conjugate imaginary roots. The system is on the boundary of the oscillatory stability.

The Routh-Hurwitz stability criterion can be conveniently used to analyze the stability of the low order systems. The computational complexity grows significantly with the

increase of the order [23].

3.3 conclusion

In summary, this chapter has provided a foundational understanding of the mathematical concepts and tools that support our mini thesis. We have established definitions, propositions and theorems that will serve as the building blocks for our subsequent analysis.

Chapter 4

Formulation and Theoretical Analysis of the Model.

In this chapter we will look at the formulation of the model, positivity and boundedness of solutions, equilibrium points (disease-free and endemic equilibrium points), the basic reproduction number (R_0) of the model and stability analysis of the SEIR-SEI model of malaria transmission of disease-free equilibrium point.

4.1 Model Formulation

The model is formulated to describe the spread of malaria in human and mosquito populations with the total population at time t denoted by $N_h(t)$ and $N_m(t)$ respectively. The human population is divided into four compartments, namely: susceptible humans (S_h), exposed humans (E_h), infected humans (I_h) and recovered humans (R_h). After recovery, an individual can lose immunity and therefore move from the recovered

class back to the susceptible class. The mosquito population is divided into three epidemiological classes as follows: susceptible mosquitoes (S_m), exposed mosquitoes (E_m) and infected mosquitoes (I_m). The mosquito population does not have a recovery class as mosquitoes never recover from infection, hence their infected period ends with their death due to their relatively short life cycle. Therefore,

$$N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t) \text{ and}$$

$$N_m(t) = S_m(t) + E_m(t) + I_m(t).$$

The flow chart of the model of malaria parasite transmission between humans and mosquitoes is shown in the diagram below (figure 4.1):

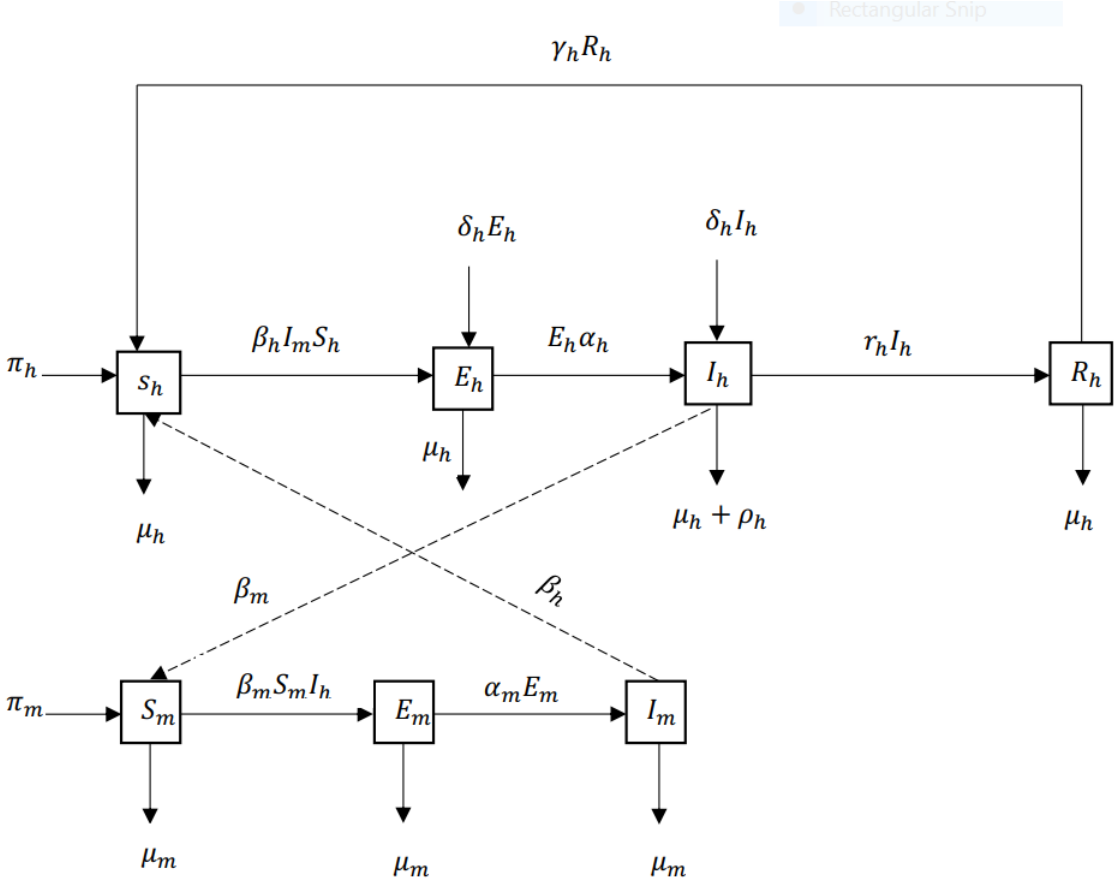

Figure 4.1: The flow chart of the model of malaria parasite transmission

The model was derived based on the following assumptions:

i) The rate of increase of infected humans is directly proportional to the number of infectious and number of susceptible humans.

ii) Humans move from infected compartment to recovery compartment with progression rate of r_h.

iii) A human can die at any stage, either by natural death (rate denoted by μ_h) or if infected, (death rate denoted by ρ_h).

iv) Infected mosquitoes do not recover from malaria.

v) Recovered humans are vulnerable to become infected when bitten by infected mosquitoes.

The model equations are given by:

$$\frac{dS_h}{dt} = \pi_h - \beta_h S_h I_m - \mu_h S_h + \gamma_h R_h \tag{4.1.1}$$

$$\frac{dE_h}{dt} = \beta_h S_h I_m + \delta_h E_h - \alpha_h E_h - \mu_h E_h \tag{4.1.2}$$

$$\frac{dI_h}{dt} = \alpha_h E_h + \delta_h I_h - r_h I_h - (\mu_h + \rho_h) I_h \tag{4.1.3}$$

$$\frac{dR_h}{dt} = r_h I_h - \mu_h R_h - \gamma_h R_h \tag{4.1.4}$$

$$\frac{dS_m}{dt} = \pi_m - \beta_m S_m I_h - \mu_m S_m \tag{4.1.5}$$

$$\frac{dE_m}{dt} = \beta_m S_m I_h - \alpha_m E_m - \mu_m E_m \tag{4.1.6}$$

$$\frac{dI_m}{dt} = \alpha_m E_m - \mu_m I_m \tag{4.1.7}$$

The above equations follow the conditions that $S_h \geq 0; E_h \geq 0; I_h \geq 0; R_h \geq 0; S_m \geq 0; E_m \geq 0$ and $I_m \geq 0$.

Table 4.1: Description of variables

Variables	**Description**
S_h	Number of susceptible humans
E_h	Number of exposed humans
I_h	Number of infected humans
R_h	Number of recovered humans
S_m	Number of susceptible mosquitoes
E_m	Number of exposed mosquitoes
I_m	Number of infected mosquitoes
N_h	Total human population
N_m	Total mosquito population

Table 4.2: Description of parameters

Parameters	**Description**
ρ_h	Human death rate due to Malaria
δ_h	Human infected recruitment due to various reasons such as migration and vertical transmission
γ_h	waning rate of immunity to reinfection
π_h	Recruitment rate of human
π_m	Recruitment rate of mosquitoes
β_h	The human contact rate
β_m	The mosquitoes contact rate
μ_m	Natural death rate for mosquitoes
μ_h	Natural death rate for humans
α_m	incubation rate for mosquitoes
α_h	incubation rate for humans
r_h	recovery rate for humans

4.2 Theoretical Analysis of the Model

4.2.1 Positivity of the Solutions

In order for the model equations $4.1.1-4.1.7$ to be biologically and epidemiologically meaningful and well posed it is appropriate to show that the variables involved in our model are positive. This requirement is stated as a lemma and its proof is provided as follows:

Lemma 4.2.1. *If* $S_h(0)>0; E_h(0)>0; I_h(0)>0; R_h(0)>0; S_m(0)>0; E_m(0)>0$ *and* $I_m(0)>0$*, then the solutions* $\{S_h(t); E_h(t); I_h(t); R_h(t); S_m(t); E_m(t); I_m(t)\}$ *of equations* $4.1.1-4.1.7$ *are positive for all* $t \geq 0$ *[3].*

Proof. From the initial conditions given, we can show that the solutions of equations $(4.1.1)-(4.1.7)$ are positive. We proceed by contradiction by assuming that there exists a time t_1 such that:

$S_h(t_1)=0; S_h'(t_1)\leq 0; E_h(t)\geq 0; I_h(t)\geq 0; R_h(t)\geq 0; S_m(t)\geq 0; E_m(t)\geq 0, I_m(t)\geq 0;$

for $t\in[0,t_1]$.

or there exists a t_2 such that:

$E_h(t_2)=0; E_h'(t_2)\leq 0; S_h(t)\geq 0; I_h(t)\geq 0; R_h(t)\geq 0; S_m(t)\geq 0; E_m(t)\geq 0; I_m(t)\geq 0;$

for $t\in[0,t_2]$.

or there exists a t_3 such that:

$I_h(t_3)=0; I_h'(t_3)\leq 0; S_h(t)\geq 0; E_h(t)\geq 0; R_h(t)\geq 0; S_m(t)\geq 0; E_m(t)\geq 0; I_m(t)\geq 0;$

for $t\in[0,t_3]$.

or there exists a t_4 such that:

$R_h(t_4) = 0; R'_h(t_4) \leq 0; S_h(t) \geq 0; E_h(t) \geq 0; I_h(t) \geq 0; S_m(t) \geq 0; E_m(t) \geq 0; I_m(t) \geq 0;$

for $t \in [0, t_4]$.

or there exists a t_5 such that:

$S_m(t_5) = 0; S'_m(t_5) \leq 0; S_h(t) \geq 0; E_h(t) \geq 0; I_h(t) \geq 0; R_h(t) \geq 0; E_m(t) \geq 0; I_m(t) \geq 0;$

for $t \in [0, t_5]$.

or there exists a t_6 such that:

$E_m(t_6) = 0; E'_m(t_6) \leq 0; S_h(t) \geq 0; E_h(t) \geq 0; I_h(t) \geq 0; R_h(t) \geq 0; S_m(t) \geq 0; I_m(t) \geq 0;$

for $t \in [0, t_6]$.

or there exists a t_7 such that:

$I_m(t_7) = 0; I'_m(t_7) \leq 0; S_h(t) \geq 0; E_h(t) \geq 0; I_h(t) \geq 0; R_h(t) \geq 0; S_m(t) \geq 0; E_m(t) \geq 0;$

for $t \in [0, t_7]$.

From the first case we can say

$$S'_h(t_1) = \pi_h + \gamma_h \times R_h > 0$$

This is a contradiction to $S'_h(t_1) \leq 0$; meaning that $S_h(t_1) > 0$ for $t_1 \geq 0$.

From the second case we can say

$$E'_h(t_2) = \beta_h S_h I_m > 0$$

This is a contradiction to $E'_h(t_2) \leq 0$; meaning that $E_h(t_2) > 0$ for $t_2 \geq 0$.

From the third case we can say

$$I'_h(t_3) = \alpha_h E_h > 0$$

This is a contradiction to $I'_h(t_3) \leq 0$; meaning that $I_h(t_3) > 0$ for $t_3 \geq 0$.

From the fourth case we can say

$$R'_h(t_4) = r_h I_h > 0$$

This is a contradiction to $R_h'(t_4) \leq 0$; meaning that $R_h(t_4) > 0$ for $t_4 \geq 0$.

From the fifth case we can say

$$S_m'(t_5) = \pi_m > 0$$

This is a contradiction to $S_m'(t_5) \leq 0$; meaning that $S_m(t_5) > 0$ for $t_5 \geq 0$.

From the sixth case we can say

$$E_m'(t_6) = \beta_m S_m I_h > 0$$

This is a contradiction to $E_m'(t_6) \leq 0$; meaning that $E_m(t_6) > 0$ for $t_6 \geq 0$.

From the seventh case we can say

$$I_m'(t_7) = \alpha_m E_m > 0$$

This is a contradiction to $I_h'(t_7) \leq 0$; meaning that $I_m(t_7) > 0$ for $t_7 \geq 0$.

Therefore the solutions $S_h(t); E_h(t); I_h(t); R_h(t); S_m(t); E_m(t)$ and $I_m(t)$ of equations $4.1.1 - 4.1.7$ are positive for all $t \geq 0$. □

4.2.2 Boundedness of the Model (Solution Region)

In order for the model equations (4.1.1 - 4.1.7) to be biologically and epidemiologically meaningful and well posed, it is appropriate to show that the variables involved in our model are bounded. This requirement is stated as a theorem and its proof is provided as follows:

Theorem 4.2.1. *If* $S_h(0) > 0; E_h(0) > 0; I_h(0) > 0; R_h(0) > 0; S_m(0) > 0; E_m(0) > 0$ *and* $I_m(0) > 0$*, then the solutions* $\{S_h(t); E_h(t); I_h(t); R_h(t); S_m(t); E_m(t); I_m(t)\}$ *of equations* $4.1.1 - 4.1.7$ *are bounded for all* $t \geq 0$.

Proof. It suffices to prove that the total living population size is bounded for all $t > 0$, According to lemma 4.2.1, all the variables involved in our model remain positive if the initial values are positive.

Boundedness of the total human population:

The rate of change of total human population size $N_h = S_h + E_h + I_h + R_h$ can be obtained as:

$$\frac{dN_h}{dt} = \frac{dS_h}{dt} + \frac{dE_h}{dt} + \frac{dI_h}{dt} + \frac{dR_h}{dt}$$

$$= (\pi_h - \beta_h S_h I_m - \mu_h S_h + \gamma_h R_h) + (\beta_h S_h I_m + \delta_h E_h - \alpha_h E_h - \mu_h E_h) + (\alpha_h E_h + \delta_h I_h -$$

$$r_h I_h - (\mu_h + \rho_h) I_h) + (r_h I_h - \mu_h R_h - \gamma_h R_h)$$

$$= \pi_h - \mu_h (S_h + E_h + I_h + R_h) + \delta_h E_h + \delta_h I_h - \rho_h I_h$$

$$= \pi_h - \mu_h N_h - \rho_h I_h + \delta_h (E_h + I_h).$$

Therefore it is obtained as : $\frac{dN_h}{dt} \geq \pi_h - \mu_h N_h$. The solution of this differential equation is found to be $N_h(t) \geq \frac{\pi_h}{\mu_h} + [N_{h_0} - (\frac{\pi_h}{\mu_h}) e^{-\mu_h(t)}]$ showing that $N_h(t) \to \frac{\pi_h}{\mu_h}$ as t$\to\infty$. The term N_{h_0} denotes the initial total human population and is non-negative. Thus $\frac{\pi_h}{\mu_h}$ is an upper bound of the total human population $N_h(t)$ that is $N_h \geq \frac{\pi_h}{\mu_h}$.

Boundedness of total mosquito population:

Just similar to the above, the rate of change of total mosquito population $N_m = S_m + E_m + I_m$ can be obtained as:

$$\frac{dN_m}{dt} = \frac{dS_m}{dt} + \frac{dE_m}{dt} + \frac{dI_m}{dt} =$$

$$(\pi_m - \beta_m S_m I_h - \mu_m S_m) + (\beta_m S_m I_h - \alpha_m E_m - \mu_m E_m) + (\alpha_m E_m - \mu_m I_m)$$

$$= \pi_m - \mu_m S_m - \mu_m E_m - \mu_m I_m$$

$$= \pi_m - \mu_m (S_m + E_m + I_m) = \pi_m - \mu_m N_m$$

which can be written as: $\frac{dN_m(t)}{dt} = \pi_m - \mu_m N_m$. The solution of this differential equation can be found to be: $N_m(t) = e^{\frac{\pi_m}{N_{mo}}(t) - \mu_m(t)}$. This show that $N_m(t) \to 0$ as t $\to \infty$. zero is a lower bound of the total mosquito population $N_m \geq 0$. □

4.3 Equilibrium Points and Stability

Equilibrium points are the solutions of the model equations satisfying the following condition:

$$\frac{dS_h}{dt} = 0; \frac{dE_h}{dt} = 0; \frac{dI_h}{dt} = 0; \frac{dR_h}{dt} = 0; \frac{dS_m}{dt} = 0; \frac{dE_m}{dt} = 0; \frac{dI_m}{dt} = 0.$$

Taking the conditions above into consideration, the system of differential equations of the model becomes:

$$\pi_h - \beta_h S_h I_m - \mu_h S_h + \gamma_h R_h = 0 \tag{4.3.1}$$

$$\beta_h S_h I_m + \delta_h E_h - \alpha_h E_h - \mu_h E_h = 0 \tag{4.3.2}$$

$$\alpha_h E_h + \delta_h I_h - r_h I_h - (\mu_h + \rho_h) I_h = 0 \tag{4.3.3}$$

$$r_h I_h - \mu_h R_h - \gamma_h R_h = 0 \tag{4.3.4}$$

$$\pi_m - \beta_m S_m I_h - \mu_m S_m = 0 \tag{4.3.5}$$

$$\beta_m S_m I_h - \alpha_m E_m - \mu_m E_m = 0 \tag{4.3.6}$$

$$\alpha_m E_m - \mu_m I_m = 0 \tag{4.3.7}$$

4.3.1 Disease-free Equilibrium (E_0)

Diease-free equilibrium points are steady state solutions where there is no malaria in human population or plasmodium parasite in the mosquitoes population. Disease-free implies that $E_h^* = I_h^* = R_h^* = E_m^* = I_m^* = 0$. Substituting this into $(4.3.1)$ and $(4.3.5)$ gives $S_h^* = \frac{\pi_h}{\mu_h}$ and $S_m^* = \frac{\pi_m}{\mu_m}$

Thus we obtain:

$$E_0 = (S_h^*; E_h^*; I_h^*; R_h^*; S_m^*; E_m^*; I_m^*)$$

$$E_0 = (\frac{\pi_h}{\mu_h}; 0; 0; 0; \frac{\pi_m}{\mu_m}; 0; 0)$$

4.3.2 The Basic Reproduction Number (R_0) of the SEIR-SEI Model of Malaria Transmission

Applying the next generation approach and considering the system of ordinary differential equations (ODEs) of our model below:

$$\begin{aligned}
\frac{dS_h}{dt} &= \pi_h - \beta_h S_h I_m - \mu_h S_h + \gamma_h R_h \\
\frac{dE_h}{dt} &= \beta_h S_h I_m + \delta_h E_h - \alpha_h E_h - \mu_h E_h \\
\frac{dI_h}{dt} &= \alpha_h E_h + \delta_h I_h - r_h I_h - (\mu_h + \rho_h) I_h \\
\frac{dR_h}{dt} &= r_h I_h - \mu_h R_h - \gamma_h R_h \\
\frac{dS_m}{dt} &= \pi_m - \beta_m S_m I_h - \mu_m S_m \\
\frac{dE_m}{dt} &= \beta_m S_m I_h - \alpha_m E_m - \mu_m E_m \\
\frac{dI_m}{dt} &= \alpha_m E_m - \mu_m I_m
\end{aligned}$$

The vectors F and V are defined as:

$$F = \begin{bmatrix} \beta_h S_h I_m \\ 0 \\ \beta_m S_m I_h \\ 0 \end{bmatrix}; V = \begin{bmatrix} (\mu_h + \alpha_h - \delta_h) E_h \\ (\rho_h + \mu_h + r_h - \delta_h) I_h - \alpha_h E_h \\ (\alpha_m + \mu_m) E_m \\ \mu_m I_m - \alpha_m E_m \end{bmatrix}$$

Now, with the partial derivatives of F with respect to (E_h, I_h, E_m, I_m) the jacobian matrix of F is constructed and evaluated at the disease-free equilibrium, and takes the form:

$$\mathbf{F} = \begin{bmatrix} 0 & 0 & 0 & \beta_h S_h \\ 0 & 0 & 0 & 0 \\ 0 & \beta_m S_m & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

Similary, with the partial derivatives of V with respect to (E_h, I_h, E_m, I_m) the jacobian matrix of V is constructed and evaluated at the disease-free equilibrium, and takes the form:

$$\mathbf{V} = \begin{bmatrix} (\mu_h + \alpha_h - \delta_h) & 0 & 0 & 0 \\ -\alpha_h & (\rho_h + \mu_h + r_h - \delta_h) & 0 & 0 \\ 0 & 0 & (\alpha_m + \mu_m) & 0 \\ 0 & 0 & -\alpha_m & \mu_m \end{bmatrix}$$

The inverse of matrix $\mathbf{V}$ is found to be:

$$\mathbf{V}^{-1} = \begin{bmatrix} \frac{1}{(\mu_h + \alpha_h - \delta_h)} & 0 & 0 & 0 \\ \frac{-\alpha_h}{(\mu_h + \alpha_h - \delta_h)(-\rho_h - \mu_h - r_h + \delta_h)} & \frac{-1}{(-\rho_h - \mu_h - r_h + \delta_h)} & 0 & 0 \\ 0 & 0 & \frac{1}{(\alpha_m + \mu_h)} & 0 \\ 0 & 0 & \frac{\alpha_m}{(\alpha_m + \mu_m)\mu_m} & \frac{1}{(\mu_m)} \end{bmatrix}$$

Now computing $\mathbf{FV}^{-1}$, we get:

$$\mathbf{FV}^{-1} = \begin{bmatrix} 0 & 0 & \frac{\beta_h \frac{\pi_h}{\mu_h}\alpha_m}{(\alpha_m+\mu_m)\mu_m} & \frac{\beta_h \frac{\pi_h}{\mu_h}}{\mu_m} \\ 0 & 0 & 0 & 0 \\ \frac{-\beta_m \frac{\pi_m}{\mu_m}\alpha_h}{(\mu_h+\alpha_h-\delta_h)(-\rho_h-\mu_h-r_h+\delta_h)} & \frac{-\beta_m \frac{\pi_m}{\mu_m}}{-\rho_h-\mu_h-r_h+\delta_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

The characteristic equation is computed by $|\mathbf{FV}^{-1} - \lambda I| = 0$, which is:

$$\begin{vmatrix} -\lambda & 0 & \frac{\beta_h \frac{\pi_h}{\mu_h}\alpha_m}{(\alpha_m+\mu_m)\mu_m} & \frac{\beta_h \frac{\pi_h}{\mu_h}}{\mu_m} \\ 0 & -\lambda & 0 & 0 \\ \frac{-\beta_m \frac{\pi_m}{\mu_m}\alpha_h}{(\mu_h+\alpha_h-\delta_h)(-\rho_h-\mu_h-r_h+\delta_h)} & \frac{-\beta_m \frac{\pi_m}{\mu_m}}{-\rho_h-\mu_h-r_h+\delta_h} & -\lambda & 0 \\ 0 & 0 & 0 & -\lambda \end{vmatrix} = 0$$

Therefore the eigenvalues are given by $\lambda = 0$ or $\lambda = \mp = \sqrt{\frac{\pi_m \alpha_h \pi_h \alpha_m \beta_h \beta_m}{\mu_h \mu_m^2 (\alpha_m+\mu_m)(\mu_h+\alpha_h-\delta_h)(\rho_h+\mu_h+r_h-\delta_h)}}$, the factors $(\mu_h + \alpha_h - \delta_h)$ and $(\rho_h + \mu_h + r_h - \delta_h)$ can both be positive or both negative. The two factors can be both positive if, $(\mu_h + \alpha_h > \delta_h)$ and $(\rho_h + \mu_h + r_h > \delta_h)$ or both negative if, $(\mu_h + \alpha_h < \delta_h)$ and $(\rho_h + \mu_h + r_h < \delta_h)$.

The basic reproduction number, $R_0 = \rho(\mathbf{FV}^{-1})$, is the spectral radius of the product $(\mathbf{FV}^{-1})$. Hence:

$$R_0 = \sqrt{\frac{\pi_m \alpha_h \pi_h \alpha_m \beta_h \beta_m}{\mu_h \mu_m^2 (\alpha_m + \mu_m)(\mu_h + \alpha_h - \delta_h)(\rho_h + \mu_h + r_h - \delta_h)}}$$

(4.3.10)

R_0 is the dominant eigenvalue of matrix $\mathbf{FV}^{-1}$.

4.3.3 Stability Analysis of The Disease-free Equilibrium Point

From section (4.3.1) above we found the disease free equilibrium point to be:

$$\begin{aligned} E_0 &= (S_h^*; E_h^*; I_h^*; R_h^*; S_m^*; E_m^*; I_m^*) \\ &= (\frac{\pi_h}{\mu_h}; 0; 0; 0; \frac{\pi_m}{\mu_m}; 0; 0) \end{aligned}$$

Theorem 4.3.1. *The DFE,* (E_0) *of the system* $(4.1.1 - 4.1.7)$ *is locally asymptotically stable if* $R_0 < 1$ *and unstable if* $R_0 > 1$.

Proof. The Jacobian matrix for the system 4.1.1 - 4.1.7 is given by:

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

$$J = \begin{bmatrix} -\beta_h I_m - \mu_h & 0 & 0 & \gamma_h & 0 & 0 & -\beta_h S_h \\ \beta_h I_m & (\delta_h - \alpha_h - \mu_h) & 0 & 0 & 0 & 0 & \beta_h S_h \\ 0 & \alpha_h & (\delta_h - r_h - (\mu_h + \rho_h)) & 0 & 0 & 0 & 0 \\ 0 & 0 & r_h & (-\mu_h - \gamma_h) & 0 & 0 & 0 \\ 0 & 0 & -\beta_m S_m & 0 & (-\beta_m I_h - \mu_m) & 0 & 0 \\ 0 & 0 & \beta_m S_m & 0 & \beta_m I_h & (-\alpha_m - \mu_m) & 0 \\ 0 & 0 & 0 & 0 & 0 & \alpha_m & -\mu_m \end{bmatrix}$$

Therefore the Jacobian matrix of the model at the DFE is:

$$J(E_0) = \begin{bmatrix} -\mu_h & 0 & 0 & \gamma_h & 0 & 0 & -\beta_h \frac{\pi_h}{\mu_h} \\ 0 & (\delta_h - \alpha_h - \mu_h) & 0 & 0 & 0 & 0 & \beta_h \frac{\pi_h}{\mu_h} \\ 0 & \alpha_h & (\delta_h - r_h - \mu_h - \rho_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & r_h & (-\mu_h - \gamma_h) & 0 & 0 & 0 \\ 0 & 0 & -\beta_m \frac{\pi_m}{\mu_m} & 0 & -\mu_m & 0 & 0 \\ 0 & 0 & \beta_m \frac{\pi_m}{\mu_m} & 0 & 0 & (-\alpha_m - \mu_m) & 0 \\ 0 & 0 & 0 & 0 & 0 & \alpha_m & -\mu_m \end{bmatrix}$$

We need to find condition(s) under which all the eigenvalues of $J(E_0)$ have negative real parts. As the first and fifth columns contain only the diagonal terms, we have two trivial negative eigenvalues, $\lambda = -\mu_h$ and $\lambda = -\mu_m$. The other five eigenvalues can be obtained from the sub-matrix $J_s(E_0)$, formed by excluding the first and fifth rows and columns of $J(E_0)$. Therefore we have:

$$J_s(E_0) = \begin{bmatrix} (\delta_h - \alpha_h - \mu_h) & 0 & 0 & 0 & \beta_h \frac{\pi_h}{\mu_h} \\ \alpha_h & (\delta_h - r_h - \mu_h - \rho_h) & 0 & 0 & 0 \\ 0 & r_h & (-\mu_h - \gamma_h) & 0 & 0 \\ 0 & \beta_m \frac{\pi_m}{\mu_m} & 0 & (-\alpha_m - \mu_m) & 0 \\ 0 & 0 & 0 & \alpha_m & -\mu_m \end{bmatrix}$$

In the same way, the third column of $J_s(E_0)$ contains only the diagonal term which

gives a negative eigenvalue, $\lambda = -\mu_h - \gamma_h$. The remaining four eigenvalues are obtained from the sub-matrix $J_{s_1}(E_0)$.

$$J_{s_1}(E_0) = \begin{bmatrix} (\delta_h - \alpha_h - \mu_h) & 0 & 0 & \beta_h \frac{\pi_h}{\mu_h} \\ \alpha_h & (\delta_h - r_h - \mu_h - \rho_h) & 0 & 0 \\ 0 & \beta_m \frac{\pi_m}{\mu_m} & (-\alpha_m - \mu_m) & 0 \\ 0 & 0 & \alpha_m & -\mu_m \end{bmatrix}$$

The eigenvalues of the matrix $J_{s_1}(E_0)$ are the roots of the characteristic equation:

$$(\lambda - \delta_h + \alpha_h + \mu_h)(\lambda - \delta_h + r_h + \mu_h + \rho_h)(\lambda + \alpha_m + \mu_m)(\lambda + \mu_m) - \frac{\alpha_h \alpha_m \beta_m \pi_m \beta_h \pi_h}{\mu_h \mu_m}$$

Let:

$$B_1 = \alpha_h + \mu_h - \delta_h$$

$$B_2 = r_h + \mu_h + \rho_h - \delta_h$$

$$B_3 = \alpha_m + \mu_m$$

$$B_4 = \mu_m$$

Then we have the polynomial equation:

$$A_4\lambda^4 + A_3\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0 = 0$$

where:

$$A_4 = 1$$

$$A_3 = B_1 + B_2 + B_3 + B_4$$

$$A_2 = (B_1 + B_2)(B_3 + B_4) + B_1B_2 + B_3B_4$$

$$A_1 = (B_1 + B_2)B_3B_4 + (B_3 + B_4)B_1B_2$$

$$A_0 = B_1B_2B_3B_4 - \frac{\alpha_h \alpha_m \beta_m \pi_m \beta_h \pi_h}{\mu_h \mu_m}$$

Writing A_0 in terms of the basic reproduction number, R_0, yields:

$$A_0 = B_1B_2B_3B_4(1 - R_0^2).$$

The Routh-Hurwitz criterion states that all roots of the polynomial have negative

real parts if and only if the coefficients A_i are positive and matrices $H_i > 0$, for $i = 0, 1, 2, 3, 4$.

Given that all $B_{i's}$ are positive, we can conclude that $A_1 > 0$, $A_2 > 0$, $A_3 > 0$, $A_4 > 0$. Moreover, if $R_0 < 1$, it follows that $A_0 = B_1B_2B_3B_4(1 - R_0^2) > 0$. Additionally, the Hurwitz matrices for the polynomial $A_4\lambda^4 + A_3\lambda^3 + A_2\lambda^2 + A_1\lambda + A_0 = 0$ are found to be positive.

Define the matrices H_1, H_2, H_3 and H_4 as follows:

$H_1 = A_3 > 0$

$H_2 =$

$$\begin{vmatrix} A_3 & A_4 \\ A_1 & A_2 \end{vmatrix} > 0$$

$H_3 =$

$$\begin{vmatrix} A_3 & A_4 & 0 \\ A_1 & A_2 & A_3 \\ 0 & A_0 & A_1 \end{vmatrix} > 0$$

$H_4 =$

$$\begin{vmatrix} A_3 & A_4 & 0 & 0 \\ A_1 & A_2 & A_3 & A_4 \\ 0 & A_0 & A_1 & A_2 \\ 0 & 0 & 0 & A_0 \end{vmatrix} > 0$$

Therefore, all the eigenvalues of the jacobian matrix $J_{s_1}(E_0)$ have negative real parts when $R_0 < 1$, and the disease-free equilibrium point is locally asymptotically stable. However, when $R_0 > 1$, $A_0 < 0$, and there will be exactly one sign change in either A_4, A_3, A_2, A_1, A_0. As a result, there is one eigenvalues with positive real part, and the disease-free equilibrium point is unstable.

□

4.3.4 Endemic Equilibrium (E_e)

Apart from the disease-free equilibrium point, we shall demonstrate that the model also possesses an endemic equilibrium point denoted as E_e. The endemic equilibrium point is a positive steady state solution where the disease persists in the population, indicating that both I_m and I_h are positive.

From equation (4.3.7), Solving for I_m^{**} and E_m^{**}

$$\alpha_m E_m^{**} - \mu_m I_m^{**} = 0$$

$$\alpha_m E_m^{**} = \mu_m I_m^{**}$$

$$E_m^{**} = \frac{\mu_m I_m^{**}}{\alpha_m}$$

$$\implies I_m^{**} = \frac{\alpha_m E_m^{**}}{\mu_m}$$

If I_m^{**} is positive so is E_m^{**} and vice versa.

Adding $(4.3.5)$ and $(4.3.6)$ to solve for E_m^{**} and S_m^{**} :

$$\pi_m - \beta_m S_m I_h - \mu_m S_m + \beta_m S_m I_h - \alpha_m E_m - \mu_m E_m = 0$$

$$\pi_m - \mu_m S_m - E_m(\alpha_m + \mu_m) = 0$$

$$E_m^{**} = \frac{\pi_m - \mu_m S_m^{**}}{\alpha_m + \mu_m}$$

$$S_m^{**} = \frac{\pi_m - E_m^{**}(\alpha_m + \mu_m)}{\mu_m}$$

E_m^{**} is feasible (positive) only if $\pi_m - \mu_m S_m^{**} > 0$; i.e $S_m^{**} < \frac{\pi_m}{\mu_m}$

Using $(4.3.4)$:

$$r_h I_h - \mu_h R_h - \gamma_h R_h = 0$$

$$r_h I_h - (\mu_h + \gamma_h) R_h = 0$$

$$\frac{r_h I_h}{\mu_h + \gamma_h} = R_h$$
$$R_h^{**} = \frac{r_h I_h^{**}}{\mu_h + \gamma_h}$$
$$\text{Let } a_o = \frac{r_h}{\mu_h + \gamma_h} \text{ then, } R_h^{**} = a_0 I_h^{**}$$

Using (4.3.3):

$$\alpha_h E_h + \delta_h I_h - r_h I_h - \mu_h I_h - \rho_h I_h = 0$$

$$\alpha_h E_h + I_h(\delta_h - r_h - \mu_h - \rho_h) = 0$$

we obtain:

$$E_h^{**} = -\frac{I_h^{**}(\delta_h - r_h - \mu_h - \rho_h)}{\alpha_h}$$
$$\text{Let } a_1 = \frac{(r_h + \mu_h + \rho_h - \delta_h)}{\alpha_h} \text{ then, } E_h^{**} = -a_1 I_h^{**}$$

a_1 is positive only if

$$\delta_h < r_h + \mu_h + \rho_h.$$

Combining (4.3.1) and (4.3.2)

$$\pi_h - \beta_h S_h I_m - \mu_h S_h + \gamma_h R_h + \beta_h S_h I_m + \delta_h E_h - \alpha_h E_h - \mu_h E_h = 0$$

$$\pi_h - \mu_h S_h + \gamma_h R_h + \delta_h E_h - \alpha_h E_h - \mu_h E_h = 0$$

we obtain:

$$S_h^{**} = \frac{\pi_h + \gamma_h R_h^{**} + E_h^{**}(\delta_h - \alpha_h - \mu_h)}{\mu_h}$$

Substituting the above R_h^{**} and E_h^{**} we get:

$$S_h^{**} = \frac{\pi_h + a_2 I_h^{**}}{\mu_h}$$

$$\text{where } a_2 = \gamma_h a_o + (-\delta_h + \alpha_h + \mu_h) a_1$$

S_h^{**} is feasible if $\pi_h + a_2 I_h^{**} > 0$.

Substituting S_h^{**} and E_h^{**} in equation (4.3.2) yields:

$$I_m^{**} = \frac{a_1 \mu_h (\alpha_h + \mu_h - \delta_h) I_h^{**}}{\beta_h (\pi_h + a_2 I_h^{**})}$$

Taking equation (4.3.5)

$$\pi_m - \beta_m I_h S_m + \mu_m S_m = 0$$

Solving for I_h^{**}, we get:

$$I_h^{**} = \frac{\pi_m - \mu_m S_m^{**}}{\beta_m S_m^{**}} \text{ , } I_h > 0 \iff \mu m S_m^{**} < \pi_m$$

Thus we obtain:

$$E_e = (S_h^{**}; E_h^{**}; I_h^{**}; R_h^{**}; S_m^{**}; E_m^{**}; I_m^{**})$$

$$I_m^{**} = \frac{a_1 \mu_h (\alpha_h + \mu_h - \delta_h) I_h^{**}}{\beta_h (\pi_h + a_2 I_h^{**})}$$

$$I_h^{**} = \frac{\pi_m - \mu_m S_m^{**}}{\beta_m S_m^{**}}$$

$$S_h^{**} = \frac{\pi_h + a_2 I_h^{**}}{\mu_h}$$

$$E_h^{**} = -a_1 I_h^{**}$$

$$R_h^{**} = a_0 I_h^{**}$$

$$E_m^{**} = \frac{\pi_m - \mu m S_m^{**}}{\alpha_m + \mu_m}$$

$$S_h^{**} = \frac{\pi_h + a_2 I_h^{**}}{\mu_h}$$

4.4 Conclusion

In summary, this chapter focuses on the formulation and theoretical analysis of the SEIR-SEI model. We begin by establishing the model and proceed to demonstrate the positivity of the solutions, for the model equations $4.1.1 - 4.1.7$. We also investigate the boundedness of the model, find both the disease-free equilibrium (E_0) and Endemic equilibrium (E_e), and find the basic reproduction number (R_0). Finally, we assess the stability of the disease-free equilibrium point.

Chapter 5

Quantitative Analysis of the Model

In this chapter, we conduct sensitivity analysis on the basic reproduction number, perform numerical simulation of the model using MATLAB, and verify whether the outcomes of the quantitative analysis align with those derived from the qualitative analysis. These are carried out to illustrate and understand the behaviour of the model.

5.1 Sensitivity Analysis

In this section, we perform sensitivity analysis of the basic reproduction number (R_0). The sensitivity indices of (R_0) are calculated to determine the importance of each parameter in disease transmission. This analysis helps identify which parameters have the most significant impact on (R_0), allowing for the implementation of targeted intervention strategies in disease control and prevention.

Since the basic reproduction number is a function of some parameters, we can evaluate the relative sensitivity of R_0 to each parameter upon which it depends.

$$\text{sensitivity index}=\frac{\partial R_0}{\partial p_i}.\frac{p_i}{R_0}$$

where:

$$R_0=\sqrt{\frac{\pi_m\alpha_h\pi_h\alpha_m\beta_h\beta_m}{\mu_h\mu_m^2(\alpha_m+\mu_m)(\mu_h+\alpha_h-\delta_h)(\rho_h+\mu_h+r_h-\delta_h)}}$$

and p_i, for $i=1,2,3,4,5,6,7,8,9,10,11$ the variables p_i represents individual parameters in R_0 as follows:

$p_1=\rho_h$, $p_2=\delta_h$,$p_3=\pi_h$, $p_4=\pi_m$, $p_5=\beta_h$, $p_6=\beta_m$, $p_7=\mu_m$,$p_8=\mu_h$, $p_9=\alpha_h$, $p_{10}=\alpha_m$, $p_{11}=r_h$.

Table 5.1: Parameters and values used in the simulations

Parameters	**Values**	**Sources**
ρ_h	0.001	[20]
δ_h	0.05	[14]
γ_h	0.05	[14]
π_h	0.000215	[14]
π_m	0.07	[14]
β_h	0.011	[20]
β_m	0.0051	Assumed
μ_m	0.067	[14]
μ_h	0.0000548	[14]
α_h	0.05	[16]
α_m	0.0043	[16]
r_h	0.143	Assumed

$$\begin{aligned}&\frac{\partial R_0}{\partial \rho_h}.\frac{\rho_h}{R_0}\\ &=\frac{\rho_h}{-2\,\rho_h-2\,\mu_h-2\,r_h+2\,\delta_h}\\ &=-0.002576591\end{aligned}$$

$$\frac{\partial R_0}{\partial \delta_h}.\frac{\delta_h}{R_0}$$

$$= 1/2\,\frac{\delta_h\,(\rho_h + 2\,\mu_h + r_h - 2\,\delta_h + \alpha_h)}{(\rho_h + \mu_h + r_h - \delta_h)\,(\mu_h + \alpha_h - \delta_h)}$$

$$=0.01368784656$$

$$\frac{\partial R_0}{\partial \pi_h}.\frac{\pi_h}{R_0}=0.5$$

$$\frac{\partial R_0}{\partial \pi_m}.\frac{\pi_m}{R_0}=0.5$$

$$\frac{\partial R_0}{\partial \beta_h}.\frac{\beta_h}{R_0}=0.5$$

$$\frac{\partial R_0}{\partial \beta_m}.\frac{\beta m}{R_0}=0.5$$

$$\frac{\partial R_0}{\partial \mu_m}.\frac{\mu_m}{R_0}$$

$$=\frac{-2\,\alpha_m - 3\,\mu_m}{2\,\alpha_m + 2\,\mu_m} = -1.469845722$$

$$\frac{\partial R_0}{\partial \mu_h}.\frac{\mu_h}{R_0}$$

$$=1/2\,\frac{-{\delta_h}^2 + (\alpha_h + 4\,\mu_h + r_h + \rho_h)\,\delta_h - 3\,{\mu_h}^2 + (-2\,r_h - 2\,\rho_h - 2\,\alpha_h)\,\mu_h - \alpha_h\,(r_h + \rho_h)}{(\rho_h + \mu_h + r_h - \delta_h)\,(\mu_h + \alpha_h - \delta_h)}$$

$$=-0.500750122$$

$$\frac{\partial R_0}{\partial \alpha_h}.\frac{\alpha_h}{R_0}$$

$$=\frac{\mu_h - \delta_h}{2\,\mu_h + 2\,\alpha_h - 2\,\delta_h}$$

$$=-0.009634123470$$

$$\frac{\partial R_0}{\partial \alpha_m}.\frac{\alpha_m}{R_0}$$

$$=\frac{\mu_m}{2\,\alpha_m + 2\,\mu_m}$$

$$=0.4698457223$$

$$\frac{\partial R_0}{\partial r_h}.\frac{r_h}{R_0}$$

$$=\frac{r_h}{-2\,\rho_h - 2\,\mu_h - 2\,r_h + 2\,\delta_h}$$

$$=-0.4998084650$$

The sensitivity indices of R_0 are derived above. A positive value in the sensitivity index indicates that increasing the parameter,while keeping all other parameters constant, results in an increase in the value of R_0. Conversely, a negative sensitivity index indicates that increasing the parameter, while keeping all other parameters constant, leads to a decrease in the value of R_0.

Based on our sensitivity analysis, a negative sensitivity index, suggests that: Increasing the values of the parameters ρ_h, μ_h, μ_m, α_h and r_h would lead to a reduction in the value of R_0 thereby reducing the disease prevalence. Only a reduction in parameters' values whose sensitivity indices are positive would be beneficial in disease control, whereas parameters with negative sensitivity indices must be increased for disease control.

A magnitude of sensitivity index, indicates the strength or degree of influence of the parameters on the model's output. A higher magnitude, whether positive or negative suggests that the parameter has a stronger impact on the model's results. Example parameter μ_m, has a high negative magnitude, that shows that it has a strong impact on the model's outcome. Parameters π_h, π_m, β_h, β_m and α_m have a high positive magnitude, so they have a strong and positive impact on the model's outcome. Increasing these parameters could lead to the outbreak of the disease. The remaining parameters with moderate negative or positive magnitude have less impact on the model's outcome, decreasing or increasing these parameters may contribute to the control or enhancement of the disease.

5.2 Simulation of the Model Using MATLAB

To investigate the role played by epidemiological parameters in the model dynamics, simulations of the model are carried out using MATLAB software. The numeric values of the parameters used and corresponding sources are given in Tables 5.2 and 5.3 respectively. Different values of the reproduction number, R_0, i.e., $R_0 < 1$ and $R_0 > 1$ are obtained using the parameter values provided in the tables.

Using parameter values given in Table 5.2, along with initial conditions: $S_{h0} = 120$, $E_{h0} = 60$, $I_{h0} = 20$, $R_{h0} = 18$, $S_{m0} = 160$, $E_{m0} = 80$, $I_{m0} = 50$, a simulation study was conducted. The results, represented as trajectories, are presented in figures 5.1 and 5.2 for each category (humans and mosquitoes) over time. Phase portraits were generated for infectious for each category, with respect to the remaining compartments. These phase portraits are illustrated in Figures 5.3, 5.4, 5.5, and 5.6. Furthermore, using these parameter values the reproduction number was computed, and its value was found to be $R_0 = 0.038403171$. It was observed that $R_0 < 1$, indicating that the disease-free equilibrium point is locally asymptotically stable.

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Table 5.2: Parameter values for which $R_0 < 1$

Parameters	**Values**	**Source/reference**
ρ_h	0.001	[20]
δ_h	0.001	[14]
γ_h	0.001	[14]
π_h	0.000215	[14]
π_m	0.07	[16]
β_h	0.011	[20]
β_m	0.0051	Assumed
μ_m	0.067	[14]
μ_h	0.0000548	[14]
α_h	0.05	[16]
α_m	0.0043	[16]
r_h	0.143	Assumed

Figure 5.1 below shows the trajectories for dynamics of human population versus time in seconds when $R_0 < 1$. Initially, the number of susceptible humans (S_h) increased and then started dropping until it reached 3.92. The number of exposed humans (E_h), infected humans (I_h) and recovered humans (R_h) all remained at zero. These trajectories, confirm the existence of the disease-free equilibrium point denoted as $E_0 = (S_h^*; E_h^*; I_h^*; R_h^*; S_m^*; E_m^*; I_m^*)$,

with values $E_0 = (\frac{\pi_h}{\mu_h}; 0; 0; 0, \frac{\pi_m}{\mu_m}, 0, 0)$.

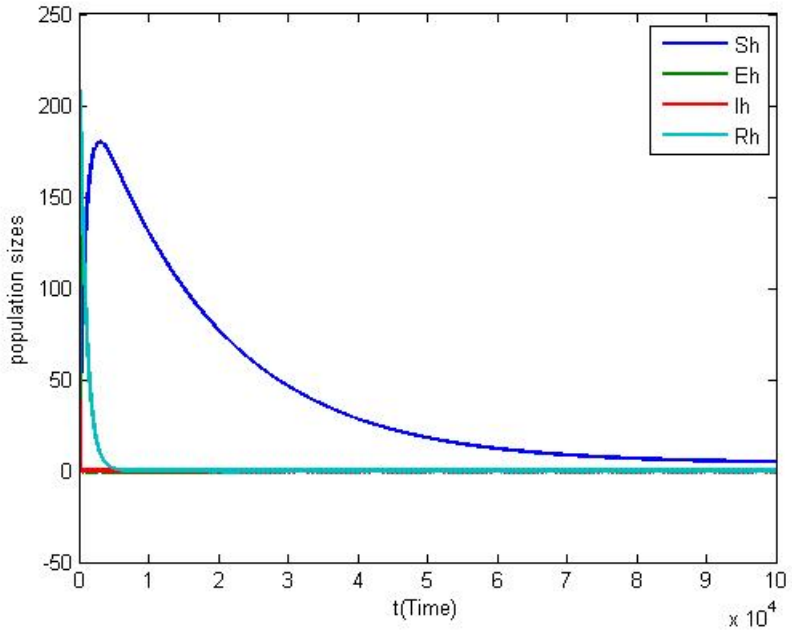

Figure 5.1: Dynamics of human population versus time in seconds, when $R_0 < 1$.

Figure 5.2 below shows the trajectories for dynamics of mosquitoes population versus time in seconds when $R_0 < 1$. The number of susceptible mosquitoes (S_m) initially increased slightly and then starts declining until it reaches 1.045. The number of exposed mosquitoes (E_m) also increases slightly and then starts declining until it reaches zero, where it remains. The number of infected mosquitoes increases and then starts declining until it reaches zero where it remains. These trajectories confirm the existence of the disease-free equilibrium point, denoted as $E_0 = (S_h^*; E_h^*; I_h^*; R_h^*; S_m^*; E_m^*; I_m^*)$, where $E_0 = (\frac{\pi_h}{\mu_h}; 0; 0; 0, \frac{\pi_m}{\mu_m}, 0, 0)$.

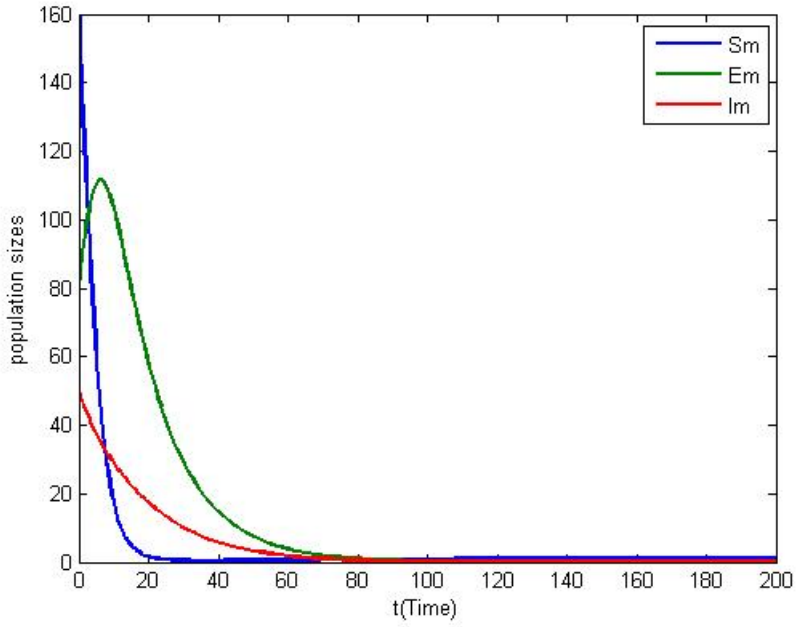

Figure 5.2: Dynamics of mosquito population versus time in seconds, when $R_0 < 1$.

The phase portrait in figure (5.3) below shows the relationship between the number of susceptible humans and the number of infected humans when $R_0 < 1$, considering various initial conditions. The red ball indicates the equilibrium point of the two compartments. According to the equilibrium point, we can conclude that there is no disease in human population.

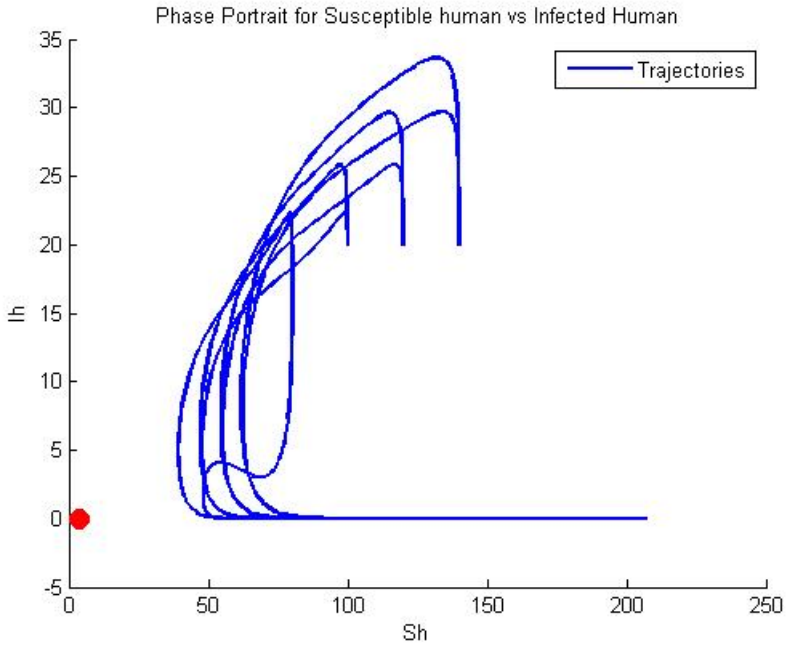

Figure 5.3: Infected humans versus susceptible humans, when $R_0 < 1$.

The phase portrait in figure (5.4) below, illustrate the relationship between the number of exposed humans and the number of infected humans when $R_0 < 1$, considering various initial conditions. The equilibrium point is indicated with the red ball and it is located at zero. This signifies that there is no disease in human population.

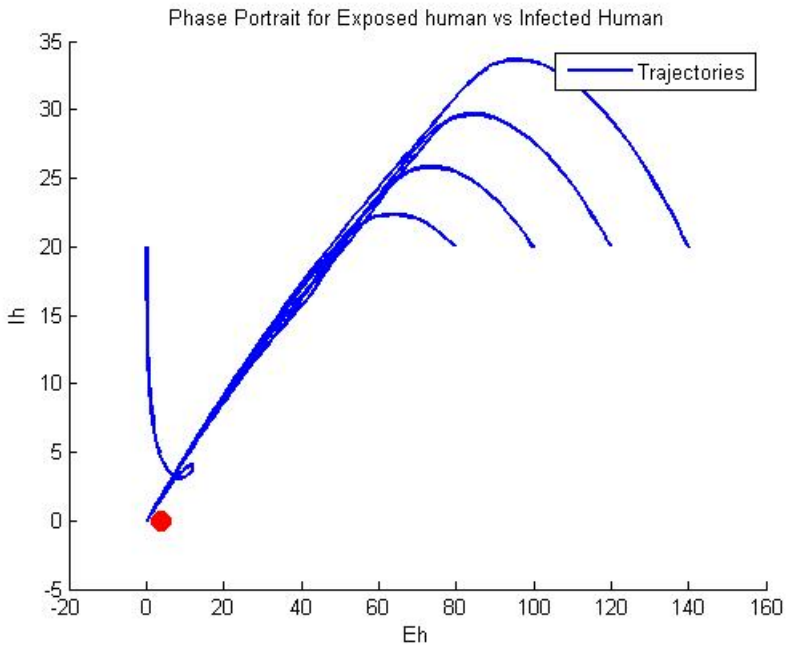

Figure 5.4: Infected humans versus exposed humans, when $R_0 < 1$.

The phase portrait in figure (5.5) below illustrates the relationship between the number of recovered humans and the number of infected humans when $R_0 < 1$, considering various initial conditions. The equilibrium point is indicated with a red ball. We can observe that both recovered and infected human coexist at zero, indicating the absence of the disease in human population.

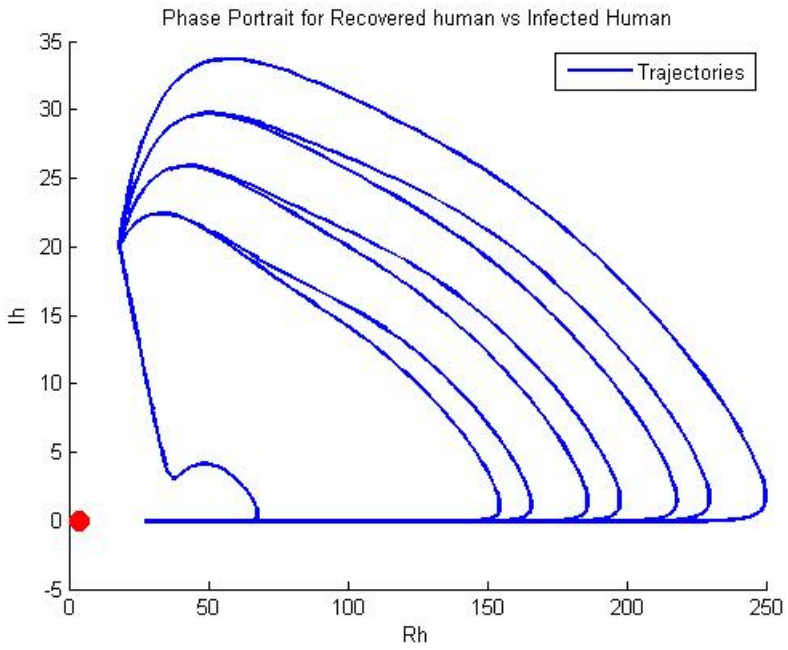

Figure 5.5: Infected humans versus recovered humans, when $R_0 < 1$.

The phase portrait in figure (5.6) below illustrate the relationship between the number of susceptible mosquitoes and the number of infected mosquitoes for $R_0 < 1$, considering various initial conditions. The equilibrium point, indicated in red, inicates that there is no disease in the mosquitoes population.

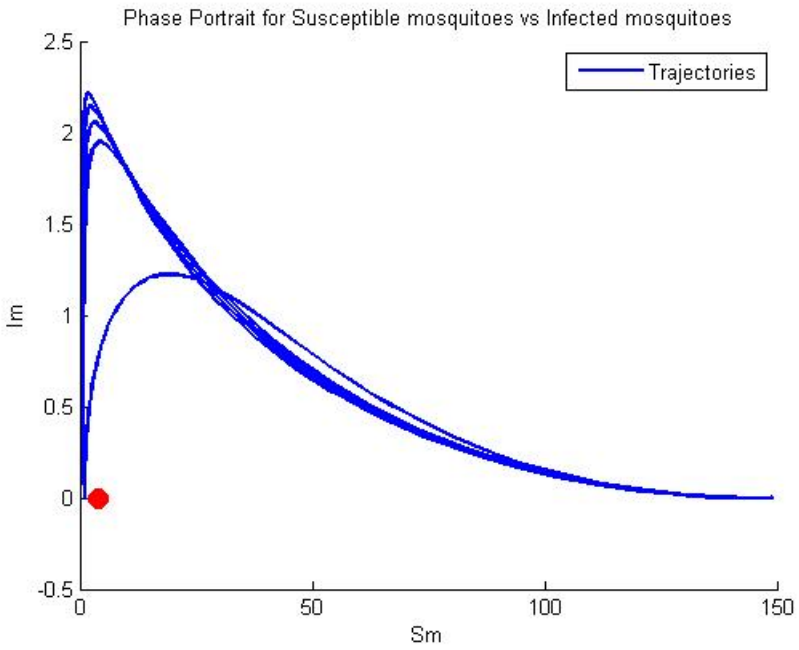

Figure 5.6: Infected mosquitoes versus susceptible mosquitoes, when $R_0 < 1$.

Using the parameter values provided in Table 5.3, along with the initial conditions as follows: $S_{h0} = 120$, $E_{h0} = 60$, $I_{h0} = 20$, $R_{h0} = 18$, $S_{m0} = 160$, $E_{m0} = 80$ and $I_{m0} = 50$, a simulation study was conducted and the results in a form of trajectories, are presented in figures 5.7 and 5.8 for both humans and mosquitoes over time. Additionally, a simulation study was performed to analyse for infectious compartments for each category with respect to the other compartments. The results are given in the phase portraits shown in figure 5.9, 5.10, 5.11, and 5.12. Furthermore, using these parameter values, the reproduction number (R_0) is computed and its value is found to be $R_0 = 110.39$. It's observed that $R_0 > 1$,indicating that the disease-free equilibrium point is locally asymptotically unstable.

Table 5.3: Parameter values for which $R_0 > 1$

Parameters	**Values**	**Source/reference**
ρ_h	0.001	[25]
δ_h	0.001	[9]
γ_h	0.9	[25]
π_h	1.2	[20]
π_m	10	[24]
β_h	0.2	[9]
β_m	0.24	[3]
μ_m	0.067	[9]
μ_h	0.0115	[6]
α_h	0.06	[9]
α_m	1	[24]
r_h	0.04	Assumed

Figure 5.7 below shows the trajectories for dynamics of human population over time when $R_0 > 1$. The number of susceptible humans (S_h) and the number of recovered humans (R_h) remain at the low levels, while the number of infected humans (I_h) as well as the number of exposed human (E_h) are observed at high levels. This pattern confirms the existence of an endemic equilibrium point in human population, denoted

as $E_e = (S_h^{**}; E_h^{**}; I_h^{**}; R_h^{**}; S_m^{**}; E_m^{**}; I_m^{**})$.

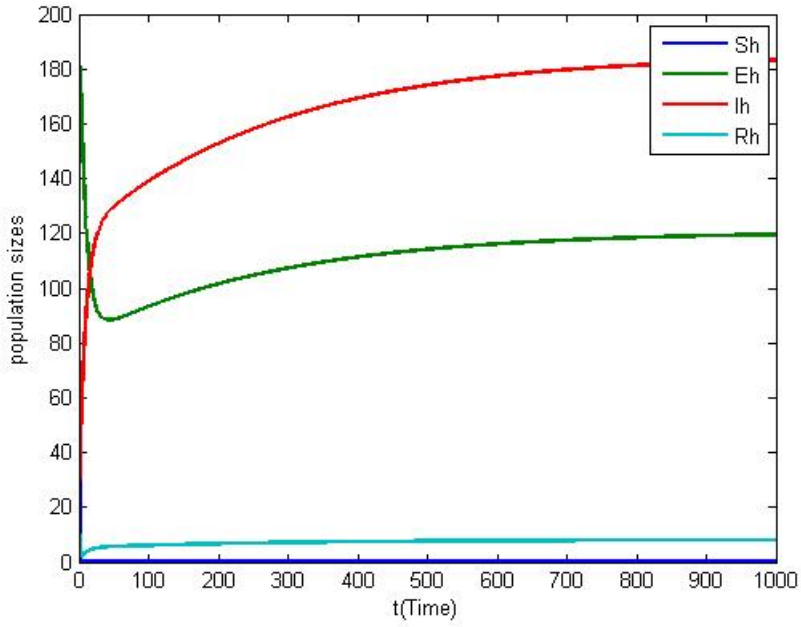

Figure 5.7: Dynamics of human population versus time in seconds, when $R_0 > 1$.

Figure 5.8 below illustrates the trajectories for dynamics of mosquitoes population over time in seconds when $R_0 > 1$. The number of susceptible mosquitoes (S_m) and the number of of recovered mosquitoes (R_m) are observed at the low levels, while the number of infected mosquitoes (I_m) and the number of exposed mosquitoes (E_m) are observed at high levels. These observations confirm the existence of an endemic equilibrium point within the mosquitoes population, denoted as $E_e = (S_h^{**}; E_h^{**}; I_h^{**}; R_h^{**}; S_m^{**}; E_m^{**}; I_m^{**})$.

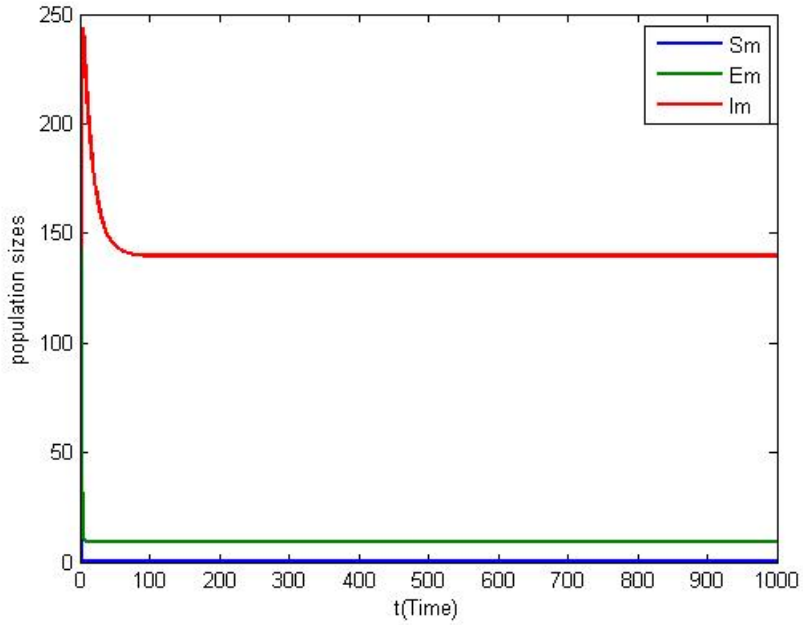

Figure 5.8: Dynamics of mosquito population versus time in seconds, when $R_0 > 1$.

The phase portrait in figure (5.9) below illustrates the relationship between the number of susceptible humans and the number of infected humans for $R_0 > 1$. It is evident from the phase portrait that susceptible and infected human populations coexist at non-zero levels. This observation indicates that the disease can persist within the human population.

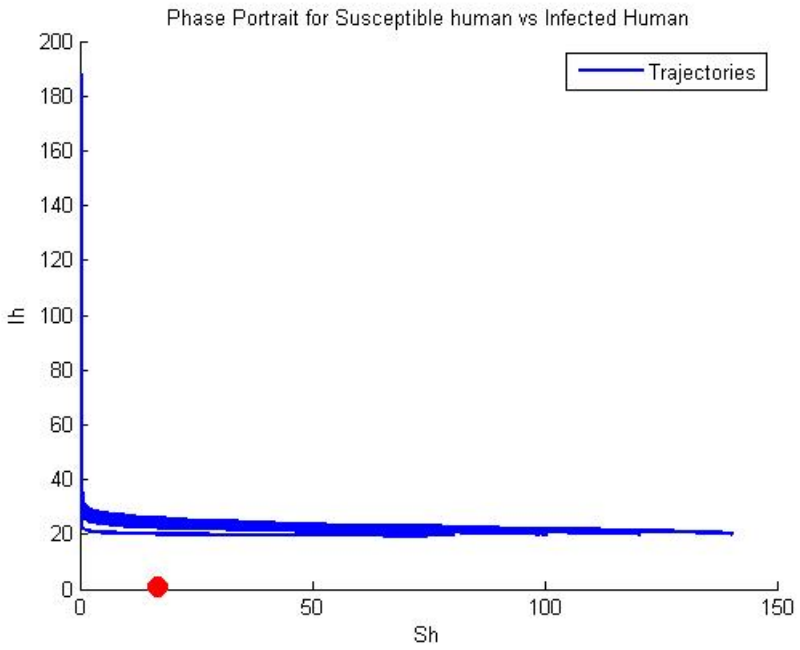

Figure 5.9: Infected humans versus susceptible humans, when $R_0 > 1$.

The phase portrait in figure (5.10) below shows the relationship between the number of exposed humans and the number of infected humans for $R_0 > 1$, with different initial conditions. According to the phase portrait, as well as at the equilibrium point indicated in red we can see that there is a disease in the human population.

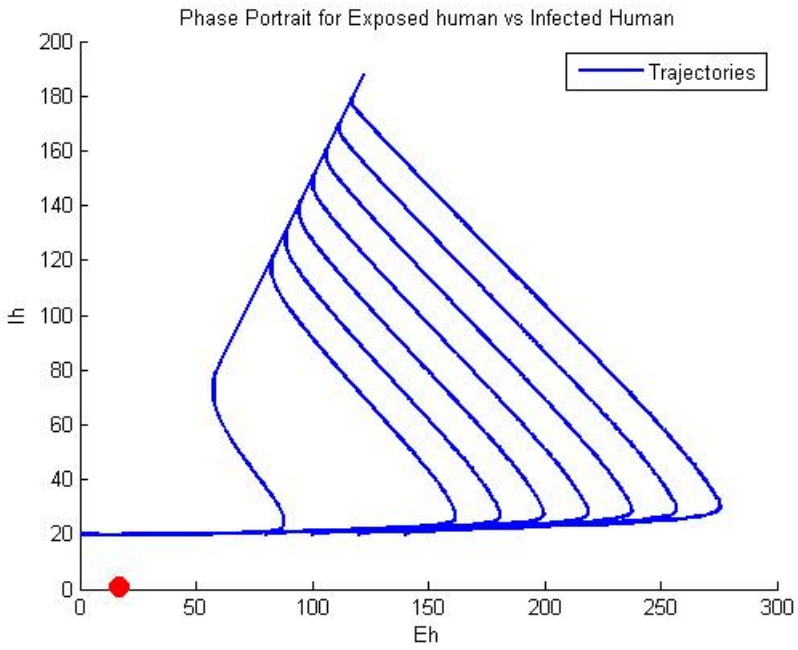

Figure 5.10: Infected humans versus exposed humans, when $R_0 > 1$.

The phase portrait in figure (5.11) below shows the relationship between the number of recovered humans and the number of infected humans for $R_0 > 1$ with different initial conditions. According to the phase portrait, as well as at the equilibrium point indicated in red we can see that there is a disease in the human population.

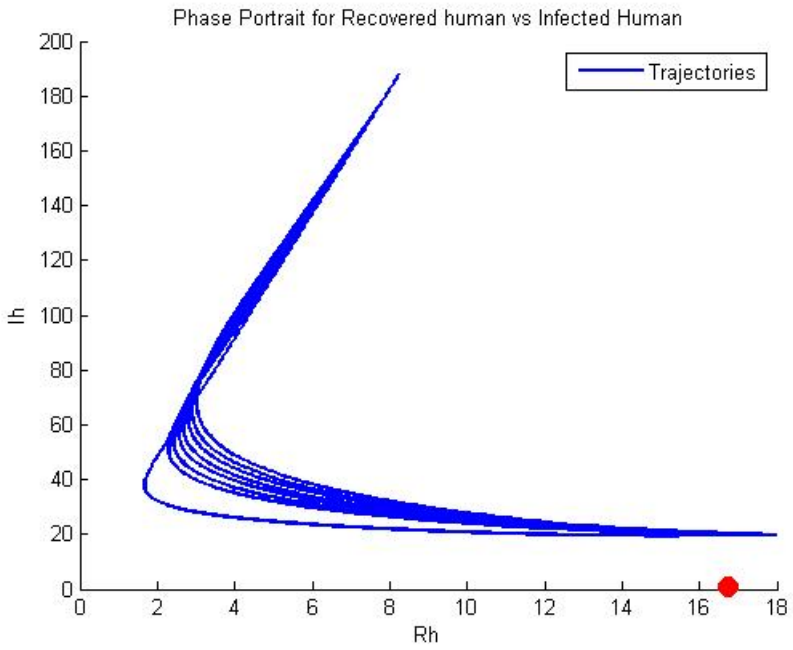

Figure 5.11: Infected humans versus recovered humans, when $R_0 > 1$.

The phase portrait in figure (5.12) below shows the relationship between the number of susceptible mosquitoes and the number of infected mosquitoes for $R_0 > 1$ with different initial conditions. According to the phase portrait, as well as at the equilibrium point indicated in red we can see that there is a disease in the mosquitoes population.

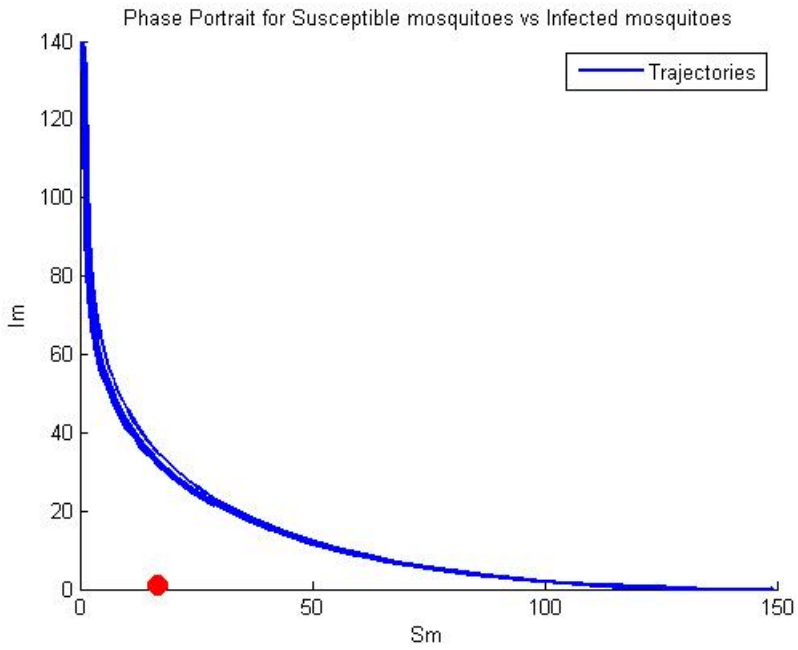

Figure 5.12: Infected mosquitoes versus susceptible mosquitoes, when $R_0 > 1$.

5.3 Conclusion

In conclusion, this chapter focuses on the quantitative analysis of the model. We conducted a sensitivity analysis of the basic reproduction number and performed a simulation of the model in MATLAB using parameter values obtained from the literature. Our results confirm that the findings from the quantitative analysis align with those from the qualitative analysis.

Chapter 6

Conclusion

In this work, we have formulated and analysed a compartmental model for malaria transmission dynamics in human and mosquitoes population. The human population is divided into four compartments: susceptible, exposed, infected and recovered, while the mosquito population is divided into three compartments: susceptible, exposed and infected. Dynamics of mosquito population is studied along with that of human population to determine whether a malaria outbreak will occur or not. Positivity and boundedness of the solution have been studied, hence it is interpreted that the model equations are mathematically and epidemiologically well posed. The disease-free equilibrium is applied to study the stability analysis. In particular the stability is investigated by paying more attention to basic reproduction number.

In this study the infected recruitment, was incorporated in the model, in order to find ways of controlling malaria disease very well. With the help of sensitivity analysis we can say that if the infected recruitments are kept under control, then it has a strong control over the spread of malaria disease. The basic reproduction number R_0 is derived.

Clearly, the numerical simulation study supports that the disease-free equilibrium (DFE) is locally asymptotically stable whenever the reproduction number $R_0 < 1$. With a help of sensitivity analysis and numerical simulation (trajectories) it is also noticed that in order to reduce the basic reproduction number R_0 below one, it's very necessary to give a focus on the human and mosquitoes contact rate.

However the model does not include all possible factors influencing malaria transmission such as climate change. Moreover the model has not been used for stability analysis of endemic equilibrium point. In addition, our model is designed using ordinary differential equations that consider variables that change with time only, and randomness is not considered.

With regards to the aforementioned limitations, possible recommendations for future work are outlined including extension of the model to incorporate all possible factors that aids malaria transmission, the stability analysis of the endemic equilibrium point can be investigated, and when considering random variables, a model containing stochastic equations will be more realistic.

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Appendix A

ETHICAL CLEARANCE CERTIFICATE

Ethical Clearance Reference Number: SOS-0085 Date: 18 July 2022

This Ethical Clearance Certificate is issued by the University of Namibia Ethics Committee (REC) in accordance with the University of Namibia's Research Ethics Policy and Guidelines. Ethical approval is given in respect of undertakings contained in the Research Project outlined below. This Certificate is issued on the recommendations of the ethical evaluation done by the ethics committee.

Title of Project: ANALYSIS OF MALARIA TRANSMISSION DYNAMICS IN HUMAN AND MOSQUITO POPULATIONS

Student: HILMA YVONNE SHAANIKA

Student Number: 200917331

Supervisor(s): DR. MORGAN. M KAMGA PENE
DR. RODRIGUES GNITCHOGNA

Centre for Research Services

Take note of the following:

1. Any significant changes in the conditions or undertakings outlined in the approved Proposal must be communicated to the ethics committee. An application to make amendments may be necessary.
2. Any breaches of ethical undertakings or practices that have an impact on ethical conduct of the research must be reported to the ethics committee
3. The Principal Researcher must report issues of ethical compliance to the ethics committee (through the Chairperson) at the end of the Project or as may be requested by the ethics committee
4. The ethics committee retains the right to:

i) Withdraw or amend this Ethical Clearance if any unethical practices (as outlined in the Research Ethics Policy) have been detected or suspected,

ii) Request for an ethical compliance report at any point during the course of the research.

The ethics committee wishes you the best in your research.

Dr. Zivayi Chiguvare (Chairperson Ethics Committee)

Prof. Davis Mumbengegwi (Head, Multidisciplinary Research)

Appendix B

CENTRE FOR RESEARCH SERVICES
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UNAM
UNIVERSITY OF NAMIBIA

RESEARCH PERMISSION LETTER

Date: 08/08/2022

Student Name: HILMA YVONNE SHAANIKA

Student Number: 200917331

Programme: Master of Science in Applied Mathematics

Approved Research Title: ANALYSIS OF MALARIA TRANSMISSION DYNAMICS IN HUMAN AND MOSQUITO POPULATIONS

TO WHOM IT MAY CONCERN

I hereby confirm that the above-mentioned student is registered at the University of Namibia for the programme indicated. The proposed study met all the requirements as stipulated in the University guidelines and has been approved by the relevant committees.

The proposal adheres to ethical principles as per attached Ethical Clearance Certificate. Permission is hereby granted to carry out the research as described in the approved proposal.

Best Regards

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