Analysis of a Mathematical Model of Malaria Transmission

by

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DECLARATION

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ANALYSIS OF A MATHEMATICAL MODEL OF MALARIA TRANSMISSION

I declare that the above thesis is my own work and that all the sources that I have used or quoted have been indicated and acknowledged by means of complete references.

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Abstract

In this thesis, we analyze a mathematical model for the spread of malaria that consists of ten components. The human host population is divided into two main categories: semi-immune, which included all individuals who were immune to malaria, and non-immune, which included all individuals who were not. However, we further categorized semi-immune people into vulnerable, exposed, infectious, and recovered; non-immune people into vulnerable, exposed, and infectious; and the mosquito population into three classes: susceptible, exposed, and infected. We compute an explicit formula for the reproductive number, which depends on the weight of transmission from non-immune people to mosquitoes and from mosquitoes to non-immune humans, as well as the weight of transmission from semi-immune humans to mosquitoes and from mosquitoes to semi-immune humans. As a result, the square root of the sum of the squares of these weights for the two contact kinds represents the reproductive number for the entire population. The DFE point is GAS if $R_0 \leq 1$, indicating that malaria dies away, and stable if $R_0 > 1$, indicating that malaria persists in the population. The model outcome confirms that the disease-free equilibrium is asymptotically stable when the reproductive number less than one and unstable when the reproductive number greater than one, and we discuss the possibility of a control for malaria transmission throughout a definite sub-group such as non-immune, semi-immune, or mosquitoes.

Keywords: Disease-free, non-immune, and semi-immune equilibria.

Dedication

To my dear mother Tirusew Abete, who passed away in 2015 at the age of 63 when I was studying for my Ph.D., and to my beloved sister Nigist Tirite, who passed away in 1991 at the age of 18 when I was studying for my M.Sc.

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The following published papers are extracts from the thesis.

(1) Gellow, G.T., Munganga, J.M.W.,& Jafari, H. (2023). Analysis of a ten compartmental mathematical model of malaria transmission, *Advanced Mathematical Models & Applications*, 8(2), 140-156.

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List of abbreviations

Abbreviation	Meaning
BBC	Red blood cell
DE	Differential Equation
ODE	Ordinary Differential Equation
IVP	Initial value problem
DFE	Disease Free Equilibrium
EE	Endemic Equilibrium
LAS	Locally Asymptotically Stable
GAS	Globally Asymptotically Stable
LIP	LaSalle's Invariance Principle
ID	Infectous Disease
MMMT	Mathematical Model of Malaria Transmission
WHO	World health organization

Chapter 1

INTRODUCTION

1.1 Background of the study

A disease that is transmitted by a vector is said to be vector-born. A vector is any arthropod, medium, or other agent that allows a pathogenic micro-organism to spread from one infected person to another uninfected person [5, 19]. You can have mechanical or biological vectors. If an agent may infect new hosts directly without first going through a period of multiplication or development in the vector, the vector is said to be a mechanical vector. If an agent multiplies within a vector prior to transmission, the vector is referred to as a biological vector. To transfer the agent to vulnerable hosts, the vector merely carries it by its body parts [14]and the pathogenic agents, which might be bacteria, viruses, or protozoa [102]. The primary cause of sickness in developing nations in Asia and Africa, which are typically found in tropical and subtropical areas, is vector-borne illness [14]. More than half of the world's population is afflicted by vector-borne diseases due to their significant morbidity and mortality rates. According to the table (1.1), each vector-borne disease has a unique pathogen, a vector that serves as a medium of transmission, and a geographic distribution [15]. Infectious agents and their vector organisms are sensitive to variables like temperature, surface water, humidity, wind, soil moisture, and changes in the distribution of forests. Some vector borne diseases are more prevalent in specific

regions due to the vector's capacity to adapt in the particular environment and climate in [1, 66].

In the history of mankind, infectious disease has been significant. The expansion of people and national economies has been impacted by the spread of infectious illnesses. Numerous infectious illnesses, including tetanus, smallpox, and seasonal influenza, are vaccine-preventable. Some illnesses, like HIV, do not have a vaccine to provide immunity [3, 32, 100]and the agent of malaria multiplies in the vector before transmission, as illustrated in Figure (1.1). Malaria is one of the biological vector-borne diseases that is endemic in many regions of the world [6]. It is an old disease with significant social, economic, and health consequences [1]. It is primarily found in tropical and subtropical nations. Despite the fact that the condition has been studied for hundreds of years, it has been declared endemic in 109 countries [100]. There is no effective vaccine in sight, and many of the older antimalarial medications are losing their efficacy due to the parasite developing drug resistance. Malaria affects $300 - 500$ million people annually, and it is estimated that $1.5 - 3$ million people die from it each year, with the majority of these deaths occurring in children under the age of 5 [76]. Most of these deaths are non-immune humans, according to a report [100]. The incidence of malaria in many urban centres of the world is increasing, and almost all areas of high endemicity lie in developing countries where inadequate drainage creates large stagnant water reservoirs that are ideal breeding sites for disease vectors like the Anopheles mosquito [16]. There are no accurate statistics available because the majority of cases occur in rural areas, where a large portion of the population does not have access to hospitals or health care in general and it has the greatest global spread [13]. In India, Plasmodium vivax infections account for about 60% of all infections [13, 16]. Although it rarely results in death or other grave issues, it can nonetheless result in serious sickness. Fatigue, diarrhea, fever, and chills are a few of the Plasmodium vivax symptoms that are frequently seen [5, 13]. The majority of cases of this rarest kind of malaria are in Ghana, Liberia, Nigeria, and the tropical West African region [9]. Because Plasmodium ovale can remain dormant in a patient's liver for a few months to 4 years following an infection with the malaria-causing insect, it occasionally recurs. The patient is most likely to become ill once more if these parasites

recur and invade RBCs [93]. Less than 1% infections of this particular strain of malaria have been reported in the Indian subcontinent, which is a smaller number than that of the other varieties [76]. Its impacts have been felt for a very long time in the tropical and subtropical regions of South and Central America, South East Asia, and Africa [9, 16, 76]. Even though it is not fatal, it nevertheless has a wide range of distributions and is the third most common disease [9, 76].

Table 1.1: Vector-born diseases, Associated vector and the Region of Prevalence

Disease	**Vector**	**Geographical Distribution**
Malaria	Mosquito	Tropics and Sub-tropics
Schistosomiasis	Water snail	Tropics and Sub-tropics
Lymphatic Filariasis	Mosquito	Tropics and Sub-tropics
African Trypanosomiasis	Tsetse fly	Tropical Africa
Drancunculiasis	Crustacean (copepod)	South Asia, Central-West Africa
Leishmaniasis	Phlebotomine sandfly	Asia, Southern Europe, Africa
Onchoerciasis	Blackfly	Africa, Latin America
Dengue	Mosquito	All Tropical Countries
Yellow Fever	Mosquito	Africa

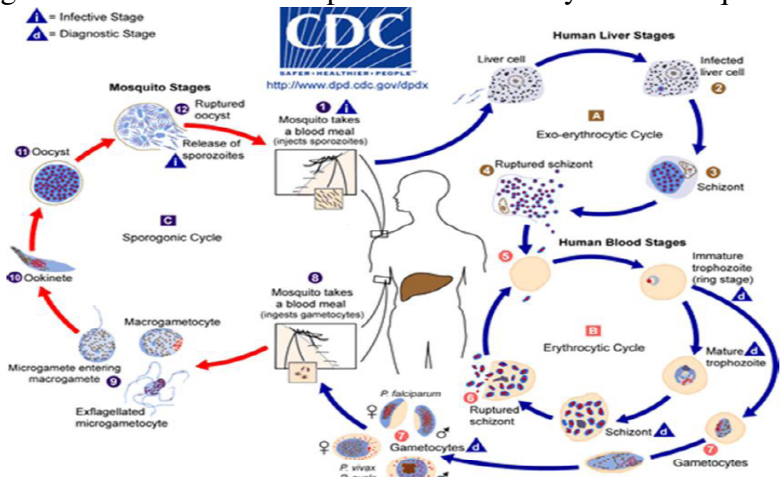
The most dangerous parasite that contributes to the majority of malaria-related infections and fatalities is known to be the plasmodium parasite [5, 22]. South America, Southeast Asia, and Africa are all home to this particular strain of malaria. Fatigue, wooziness, dizziness, abdominal discomfort, aching muscles, a hurting back, joint pain, vomiting, nausea, fever, headache, anemia, and other neurological symptoms are also experienced by the parasite-infected person [76]. Since it is the severest of all the four malaria types, it becomes important that it be checked, diagnosed, and treated on time [62, 76]. This infection also has an adverse effect on brain and the central nervous system. Many times, changes in the levels of consciousness, paralysis, and convulsions can also occur. Of these, Plasmodium falciparum is the most common cause of infection in Africa

and Southeast Asia and is responsible for 80 percent of all malaria cases and 90 percent of deaths [62,76]. The tropics are where it is most prevalent and where it causes the most serious illness. To complete its life cycle, the parasite needs a human and a female Anopheles mosquito as vectors [1]. Being bitten by an infected female Anopheles mosquito, a biological vector for malaria, is the most typical way to contract the disease [96]. Additionally, sharing a needle with an infected person or receiving blood transfused with the disease could spread it. Female Anopheles mosquito bites a person to draw blood and, while doing so, injects sporozoites into the victim's body [96]. This is how malaria infections start. These injected sporozoites quickly make their way to the liver, where they multiply within the liver cells and transform into merozoites. System, where they grow and multiply sexually until the erythrocyte or red blood cell bursts, therefore boosting the number of merozoites and allowing them to attack other red blood cells [93]. Thus, fever and other clinical symptoms are brought on by the cycle's repeat, in which merozoites escape and attack brand-new RBCs. The host's hemoglobin is forced into the parasite's food vacuole, where it is digested, serving as a source of amino acids, during the maturation process of the red blood cell by the parasite, which inserts its lipids and proteins into the RBC's membrane [93]. Male micro-gametocytes and male macro-gametocytes are the two types of gametocytes that are produced when some of the merozoites that enter erythrocytes multiply. These newly generated gametes are then ingested by the female Anopheles mosquito during her blood meal or blood sucking event. This sporogonic stage, during which the parasite breeds sexually, is present in female Anopheles mosquitoes [93]. When micro-gametes enter the macro-gamete stage, zygotes are created in the mosquito's stomach. These zygotes eventually evolve into elongated, motile ookinetes, which pass through the mosquito's midgut wall and turn into oocysts [44, 93]. The oocysts that are created in this way mature and produce thousands of sporozoites inside of them before they ultimately burst and release sporozoites into the mosquito's body [44, 93]. These sporozoites subsequently move on to the salivary glands of the mosquito, which, upon injection or during a blood feeding event, cause the human host to contract malaria, as described in [93]. The main emphasis of this thesis is on the transmission of infection from the bite of infected female Anopheles mosquitoes to humans. Thus, gametocytes are important in the transfer of sporozoites from the mosquito to the

human and malaria from the human to the mosquito. Symptoms of malaria infection in humans include fever, headache, nausea, vomiting, jaundice, an enlarged liver, joint pain, body weakness, dizziness, and a lack of appetite [62, 76]. Figure (1.1) summarizes the complete life cycle of the mosquito, the transmission mechanism as a whole and shows how the symptoms of this condition worsen if medication is not taken to stop the constant destruction of blood cells, which may eventually result in death [44, 93].

A model is a rough approximation of the complicated world, and the construction of a model depends on the processes that are being researched and are intended to be extrapolated. By choosing aspects that appear to be crucial to the subject being investigated in disease development and dynamics, various known biological and clinical facts are integrated in a reduced form in a mathematical model [11, 14]. Finding the most effective ways to stop the spread of a disease or eradicate it requires understanding how infections spread in terms of the number of individuals affected. In order to eradicate the diseases transmitted by vectors, numerous control initiatives were put into place worldwide [25, 34]. Outside of Africa, the majority of these initiatives were successful. The return of vector-borne diseases is caused by a variety of circumstances. Changes in public health policies, insecticide and medication resistance, a shift away from prevention initiatives in favour of emergency preparedness, demographic and societal changes, genetic modifications of pathogens, and changes in public health policy are a few of these factors [42, 59]. These investigations can aid in fitting empirical observations to the questions being asked and can be used to apply theory to situations that are less unknown or known enough to make predictions. The models have been rigorously analysed in order to be accessible to a broad variety of researchers studying the epidemiology, transmission, and other aspects of malaria [62]. This analysis will be helpful in identifying the various between-host models in this field and understanding how they work.

Figure 1.1: Architectural aspects of the Life Cycle of mosquitoes



1.2 The Objective of the study

1.2.1 The general objective of the study

The main goal of this thesis is to develop a mathematical model of malaria transmission in order to better comprehend it. This will be done by developing mathematical models of infectious diseases with and without vaccination inducements, developing various mathematical models of malaria transmission by examining various dimensions (compartments) of infectious disease transmission with and without vaccination inducements, developing mathematical models of malaria in five dimensions, and ultimately developing mathematical models of malaria in ten dimensions (compartments).

1.2.2 The specific objective of the study

Reviewing the main factors considered in earlier research on mathematical modelling of malaria transmission, comprehending how vaccination affects the spread of infectious diseases, analysing the proposed models mathematically and biologically, presenting the mathematical model of infectious disease transmission with and without vaccination, and extending the mathematical model of infectious disease transmission to five-dimensional mathematical models of malaria transmission, and ultimately developing mathematical models of malaria transmission to ten dimensional mathematical models of malaria trans-

mission are the specific objectives of the study.

1.3 The Significant of the study

The results of this study should improve society's understanding of the dynamics of infectious diseases, which will assist in decreasing the effects of infectious diseases in general and malaria transmission in particular, which can be extremely complicated in the absence of immunization. Additionally, they will help society and government agencies decide how to effectively distribute funds for the prevention and management of infectious diseases, and they will help public health organizations and health care facilitators comprehend the procedures and policies that will make it possible for infectious disease prevention and management.

1.4 Preface

In this thesis, the mathematical model of malaria disease transmission is examined. We examine the mosquito life cycle in chapter (1). We offer fundamental definitions, term properties, theorems, and procedures in the chapter (2) because these are necessary to prove the theorems and generate formulas throughout this thesis. In the chapter (3), we plan to go over the key aspects of the mathematical modelling of malaria transmission that have been previously studied. By doing this, we will gain sufficient understanding of the mathematical model of the dynamics of infectious disease spread in general and the mathematical model of the dynamics of malaria spread in particular. In chapter(4), we present and investigate a mathematical model of the spread dynamics of infectious disease by inducing vaccination and without inducing vaccination. In this chapter, we present two models, one by inducing vaccination and the other without inducing vaccination, and finally, we analyse the two models. In chapter(5), we analyse the mathematical modelling of malaria transmission in five compartments; in chapter (6), we extend our scope of compartments from five to ten and analyse this mathematical model of malaria transmission in ten compartments; and in chapter(7), we give the overall conclusion and recommendation of the thesis.

Chapter 2

MATHEMATICAL PRELIMINARIES

This chapter includes definitions, properties of terms, theorems and methods that we used to proof theorems, to formulate mathematical models and to analyse the mathematical models through out this thesis.

2.1 Compound Matrices

Let A be any n by m matrix of real or complex numbers, and let $a_{i_1,....,j_k}$ be the minor of A determined by the rows $(i_1, ..., i_k)$ and the columns $j_1, ..., j_k$, $1 \leq i_1 \leq i_2 < i_k < i_k \leq n$, $1 \leq j_1 \leq j_2 < j_k < j_k \leq m$. The k^{th} multiplicative compound matrix of A^k of A is the $\begin{pmatrix} n \\ k \end{pmatrix}\begin{pmatrix} n \\ k \end{pmatrix}$ matrix whose entries, printed in a lexicographics order are $a_{i_1,....,j_k}$ [36]. When A is a n by m matrix with columns $a_1, a_2, ..., a_k$, A^k is the exterior product $a_1 \bigwedge a_2 \bigwedge ... \bigwedge a_k$. For the case $m = n$, the additive compound matrices are described in the following way. If $A = a_{ij}$ be an n by n matrix, its k^{th} additive compound $A^{[k]}$ of A is $\begin{pmatrix} n \\ k \end{pmatrix}\begin{pmatrix} n \\ k \end{pmatrix}$ matrix by $A^{[k]} = D(I + hA)^{(k)}| = 0$ where D is the differential with respect to h.

For any integer $i = 1, 2, ..., \begin{pmatrix} n \\ k \end{pmatrix}$, let $(i) = (i_1, ..., i_k)$ be the i^{th} member in the lexicographic ordering of all $K-$ tuples of integers of such that $1 \leq i_1 < i_2 < ... < i_k \leq i_n$. In the special

case $k = 1$, $k = n$, we find $A^{[1]} = A, A^{[n]} = Tr(A)$. For $n = 3$, the matrices $A^{[k]}$ are as follows

$$\begin{cases} A^{[1]} = A. \\ A^{[2]} = \begin{pmatrix} a_{11} + a_{22} & a_{23} & -a_{13} \\ a_{32} & a_{11} + a_{33} & a_{12} \\ -a_{31} & a_{21} & a_{22} + a_{33} \end{pmatrix}. \\ A^{[3]} = a_{11} + a_{22} + a_{33}. \end{cases}$$

2.2 Linear space and norm

A linear space: A linear space X over C is a group of members such that for every $x_1, x_2 \in X$ the sum $x_1 + x_2 \in X$ is defined such that $x_1 + x_2 = x_2 + x_1$ and a member $0 \in X$ exists such that $0 + x = x + 0 = x$ for all $x \in X$. Also, for any number $a \in \mathbb{R}$ and any element $x \in X$ the scalar multiplication is defined $ax \in X$ such that $1x = x$, for all $x \in X$,

$$a(bx) = (ab)x = b(ax), \tag{2.1}$$

for all $a, b \in \mathbb{R}$ and all $z \in X$ and $(a + b)x = ax + bx$, for all $a, b \in R$ and all $x \in X$ in [106]. [25] A linear space X is a normed linear space if to each $x \in X$ there matches a non negative real number $\|x\|$ is called the norm of x which assures the next equation (2.2):

$$\|x\| = 0 \Longleftrightarrow x = 0, \ \|x_1 + x_2\| \leq \|x_1\| + \|x_2\| \tag{2.2}$$

for all $a \in \mathbb{R}$ and all $x \in X$ and $\|ax\| = |a|\|x\|$ for the norm on X in [106].

Norm on a linear space: A norm on a linear space X make a metric through the next distance: $\text{dist}(x_1, x_2) = |x_1 - x_2|$, for all $x_1, x_2 \in X$. A normed linear space X able with a metric is said to be a metric space [25]. A norm on $\mathbb{R}_n = \{x = (x_1, x_2, ..., x_n) : x_i \in \mathbb{R}\}$ such that $|x| = \left(\sum_{i=1}^{n} (x_i)^2\right)^{1/2}$ is called Euclidean norm. R_n endowed with a distance function ρ such that $\rho(x, y) = \left(\sum_{i=1}^{n} (x_i - y_i)^2\right)^{1/2}$ is called Euclidean n-space. Let X be a normed linear space and $x \in X$. The open ball about $x_0 \in X$ with radius $\rho > 0$ is the set

$$B_\rho(x_0) := \{x \in X : |x - x_0| < \rho\}. \tag{2.3}$$

The point x_0 is said to be the center of the ball. Let X be a metric space. $O \subset X$ is said to be an open set if for each $x \in O$ there exist $\rho > 0$ such that $x \in B_\rho(x) \subset O$. Let $S \subseteq X$

be a given set. Two points x and y are said to be connected in S if there is a path between x and y lying wholly in S. The whole set S is said to be connected if each pair of points in S is related in S. In $\mathbb{R}_n$, a set S is associated iff it cannot be enclosed in the union of two disjoint open sets [97]. A topological space is compact if each open cover of X has a finite sub-cover. If X is a finite dimensional normed space, then $M \subseteq X$ is compact iff M is closed and bounded [106]. A convex set is a set of members from a vector space such that each the points on the straight line between any two points of the set are also together with this in the set; that is, for any $x, y \in A$ it follows that $tx + (1 - t)y \in A$ for any $t \in [0, 1]$.

2.3 Autonomous dynamical system

An ODE of the form of (2.4), is called an autonomous differential equation all the terms do not depond explicitly on time.

$$\frac{dx}{dt} = f(x) : \tag{2.4}$$

where, $x = x(t) \in \mathbb{R}^n, t \in \mathbb{R}$ and $f : \mathbb{R}^n \to R^n$ is a function which make sure existence of solution to equation (2.4). Usually, supplementary information is needed to decide properties of solutions to the system equation (2.4), and knowing the initial position $x_0 \in \mathbb{R}^n$ is adequate to get its position in all equation [23]. Thus, we believe an IVP associating with equation (2.4):

$$\frac{dx}{dt} = f(x); x(t_0) = x_0 \in \mathbb{R}^n \tag{2.5}$$

Under a set of suitable hypothesis on the function f, the initial value problem (2.5) possesses a unique solution which is defined for all future instants of time. The solution is a continuously differentiable mapping $x(.; t_0, x_0) : R \to \mathbb{R}^n$ with derivative $x^{'}(t) = f(x(t))$ and satisfies $x(t_0; t_0, x_0) = x_0$. The notation $''.; t_0, x_0''$ is used to show the explicit dependence of the solution on the initial value (t_0, x_0) in [23]. So, $x(t; t_0, x_0)$ refers to the position of a particle at time t starting from x_0 at time t_0. Basic properties of the solution mapping are: Evolution of x depends on the elapsed time as a substitute of the initial and final time separately. That is,

$$x(t; t_0, x_0) = x(t - t_0; 0, x_0) \text{ for } t \geq t_0. \tag{2.6}$$

which means that the position of the particle at time $t(\geq t_0)$, initial from the point x_0 at the initial time t_0, is exactly the same as the position of the particle at time $t - t_0$ if it starts from point x_0 at the initial time zero. Because of this property we can always choose the initial time for the IVP (2.5) to be the time instant zero, that is $t_0 = 0$. Initial value property. That is,

$$x(t_0; t_0, x_0) = x_0 \text{ for all } x_0 \in \mathbb{R}_n,\ t_0 \in \mathbb{R} \tag{2.7}$$

That is, we have the following equation (2.8)

$$x(t_2; 0, x(t_1; 0, x_0)) = x(t_1 + t_2; 0, x_0) \tag{2.8}$$

and persistence of solutions with respect to initial values. This property usually referred to as the continuous dependence on initial data, can be insured by some proper hypothesis on the vector field function f in [23]. Therefore, for autonomous ODEs, we can always focus on $t_0 = 0$, and define the solution $\phi(t, x_0) := x(t; 0, x_0)$ and translate the above properties of solutions of the IVP (2.5) into corresponding properties of the mapping $\phi(.,.)$ in [23].

Dynamical system: Let X be a metric space. A dynamical system is a continuous mapping $\phi : \tau x X \to X; \tau \subseteq \mathfrak{R}$ with the following properties: original value property

$$\phi(0, x) = x \text{ for all } x \in X; \tag{2.9}$$

and group property that is we have the following equation (2.10)

$$\phi(t_2; 0, \phi(t_1; 0, x_0)) = \phi(t_1 + t_2; 0, x_0) \text{ for all } t_1, t_2 \in \tau \text{and } x_0 \in X. \tag{2.10}$$

Continuous dependence on the initial data is implied by the continuity of the mapping ϕ. When is $\tau^+ = \{t \in \tau : t \geq 0\}$, then ϕ maps X to itself and forms a semi-group under composition rather than a group; in this case, we call (2.10) a semi-group property [23].

Metric space: Let X be a metric space. A Semi-dynamical system is a continuous mapping $\phi : \tau^+ x X \to X$ with initial value property and semi-group property. When $\tau = Z$, the dynamical system is called a discrete dynamical (semi-dynamical) system, and when $\tau = \mathfrak{R}$, the dynamical (semi-dynamical) system is called a continuous dynamical (semi-dynamical) system. From possessions of solution (2.7)-(2.8) and a solution mapping of

system (2.5) defines an autonomous dynamical system. The system (2.5) is said to be constant if

$$\lim_{t\to\infty} x_i(t) > 0; i = 1, 2, 3, ..., n \tag{2.11}$$

for every trajectory with positive initial conditions. The system equation (2.5) is called uniformly persistent if there is a positive number c such that

$$\liminf_{t\to\infty} x_i(t) > 0; i = 1, 2, 3, ..., n \tag{2.12}$$

for each trajectory with positive initial conditions.

2.4 Existence and Uniqueness of solutions

Consider the initial value problem prearranged in equation (2.5), and let O be an open set in $\Re^n$ holding the origin. Let $x_0 \in O$ and let $\phi(t)$ be the solution to the IVP (2.5) on an interval $J \subset I$. It is called the solution $\phi(t)$ can be continued on the right, if there is an additional solution $\phi(t)$ to the original value problem (2.5) on interval J_1, such that $J \subset J_1$ and sup$J$ belongs to the interior of J_1, can be continued on the left, if there is another solution $\phi(t)$ to original value problem (2.5) on interval J_2, such that $J \subset J_2$ and inf$J$ belongs to the interior of J_2, and is continuous, if it can be continued on the right or on the left, or both. A solution to the initial value problem (2.5) is called a maximal solution if it is not continuous. The function $f(x)$ is said to be locally Lipschitz on an open set O if for each point $z \in O$, there exist a neighbourhood N such that f is Lipschitz on N. i.e, there is $K_N \in \mathbb{R}$ such that

$$|f(x) - f(y)| \leq K_N|x - y| \text{ for } x, y \in N. \tag{2.13}$$

The function $f(x)$ is called globally Lipschitz or simply Lipschitz on O if equation (2.13) holds with a constant K which is independent of z and N [92]. A continuously differentiable function is always locally Lipschitz. In addition, if the domain O is convex, then a continuously differentiable function is globally Lipschitz iff the partial derivatives $\frac{\partial f_i}{\partial x_i},\ i.j = 1, 2, ..., d$ are globally bounded; $f = (f_1, f_2, ..., f_d)$ and $x = (x_1, x_2, ..., x_d)$.

Theorem 2.4.1. *(Existence and uniqueness of a maximal solution)*
Let O be an open subset of $\mathfrak{R}^n$ *and assume that* f *is continuously differentiable on O. Then for any* $t_0 \in \mathfrak{R}$ *and any* $x_0 \in O$ *the original value problem equation* (2.5) *has a unique maximal solution* $\phi(.; t_0, x_0)$ *defined on its maximal open interval* $I_{max} = I_{max}(t_0, x_0)$. *Theorem* (2.4.2) *which follows is the autonomous description of [23] for the global existence of a solution based on the dissipativity condition presented in [23]*

Theorem 2.4.2. *Let* $f : \mathfrak{R}^n \to \mathbb{R}^\varkappa$ *is continuously differentiable, that is its partial derivatives of first order are continuous functions, and there are two constants* α, β *with* $\beta > 0$, *then* $f(x).x \leq \alpha|x|^2 + \beta$. *Then, there exists a unique solution to equation* (2.5) *which is defined globally in time [23].*

2.5 Positive Solution

The presence of unique solutions in a physiologically dynamical system has to be non-negative. Then the existence of a non-negative solution is confirmed in [91] that as: let f in (2.5) has the belongings that solutions of $x(t_0) = x_0 \geq 0$ are unique and, $\forall i, f_i(x) \geq 0$ whenever $x \geq 0$ satisfies $x_i = 0$. Then $x(t) \geq 0, \ \forall t \geq t_0$ for which it is defined, gives $x(t_0) \geq 0$.

2.6 Equilibrium Solutions

[92] A point $\overline{x} \in \mathbb{R}^\varkappa$ is said to be an equilibrium point of equation (2.5) if $f(\overline{x}) = 0$. [92] The equilibrium solution $\overline{x}$ of the dynamical system (2.5) is said to be stable if for any $\epsilon > 0$ there exists $\delta = \delta(\epsilon) > 0$ such that for $x(0) \in R_n$, $||x(0) - \overline{x}|| \leq \delta$ involve the solution $x(t; x_0)$ exists $\forall t \geq 0$ and $||x(t; x_0) - \overline{x}|| \leq \epsilon$ for all $t \geq 0$. The equilibrium solution $\overline{x}$ of the dynamical system (2.5) is asymptotically stable if it is stable and there is a constant $\delta_0 > 0$ such that if $||x(0) - \overline{x}|| \leq \delta_0$, then

$$\lim_{t \to \infty} ||x(t; x_0) - \overline{x}|| = 0. \tag{2.14}$$

The equilibrium solution $\overline{x}$ of (2.5) is GAS if it is stable and

$$\lim_{t \to \infty} ||x(t; x_0) - \overline{x}|| = 0. \tag{2.15}$$

for a given t_0 and $\forall x_0 \in \Omega$. The equilibrium solution $\overline{x}$ of equation (2.5) is unstable if it is not stable. An equilibrium point $\overline{x}$ is stable if the dynamical system can be forced to stay behind in any neighbourhood of $\overline{x}$ by suitable initial condition. It is asymptotically stable if, in addition, any initial solution near the stable state come close to it as $t \to \infty$ [92].

2.7 Basic reproduction number

The basic reproductive number (R_0),Originally created for the demo-graphics revision, it was examined separately and it was separately studied for vector-born illness such as malaria in [73]. For in-host dynamics, R_0 provides the number of recently polluted cells formed by one polluted cell during its life span, pretentious all other cells are vulnerable. From this definition, it is directly clear that when $R_0 < 1$, every polluted individual produces, on average, less than one new polluted individual, and we thus expect that the disease will be empty from the population, or the micro parasite will be empty from the individual. If $R_0 > 1$, the pathogen is able to attack the vulnerable population. This threshold performance is the most significant and useful feature of the R_0 idea. In a widespread infection, we can decide which control actions, and at what size, would be most effective in plummeting $R_0 < 1$, providing important direction for community health initiatives. The degree of R_0 is also used to measure the risk of an epidemic in rising infectious disease. We note, though, that the sensible use of R_0 has been, for the most part, limited to very simple deterministic systems. For contrast with this meadow text in epidemiology, we limit our notice to deterministic, unstructured micro parasite models. There are dissimilar approaches to compute the reproductive number.

Next generation technique is one of the technique which has a loaded history in the literature addresses the origin of R_0, or an a comparable threshold parameter, when more than one class of infectives is concerned in [56] and [89]. In this technique, R_0 is described by means of the next-generation matrix approach explained in [26] and [105]. This approach defines R_0 as the figure of individuals polluted by a solitary polluted individual during his or her entire infectious period, in a population that is completely vulnerable. The dissimilarity is that the primary explanation approximates the total number of pollution within a human group prearranged by one infective human belonging to this group, while the next

one gives the signify figure of new infections per infective in any group per age group anywhere a generation refers to the infection. For a full justification on the configuration of the next generation operative when there are considerably many types see in [32]. Let us suppose that there are n compartments of which m are polluted. We describe the vector $\overline{x} = x_i, i = 1, 2, ..., n$ where x_i denotes the number of persons in the i^{th} section. Let $V_i(\overline{x}) = V_i^- \left(\overline{x}\right) - V_i^+(\overline{x}\right)$ be the rate of form of new infections in section i and let $V_i(\overline{x})$; where V_i is the rate of transfer of individuals into section i by all other means and V_i^- is the rate of transfer of individuals out of the i^{th} compartment. The difference

$$F_i(\overline{x}) - V_i(\overline{x}); \tag{2.16}$$

gives the rate of change of x_i. Note that F_i should include only infections that are newly arising, but does not contain terms which explain the transfer of infectious individuals from one infected section to one more. Assuming that V_i and F_i meet the situation outlined by [105] and [33], we can form the next generation matrix $V^{-1}F$ from matrices of partial derivatives of V_i and F_i. Particularly,

$$V = \frac{\partial V_i(x_0)}{\partial x_j} \quad \text{and} \quad F = \frac{\partial F_i(x_0)}{\partial x_j} \tag{2.17}$$

where $i, j = 1, 2, ..., m$ and where x_0 is the DFE point. The entries of $V^{-1}F$ give the rate at which infected individuals in x_j generate new infections in x_i, times the standard length of time an individual spends in a single stay to partition j. R_0 is prearranged by the ghostly rad by the spectral radius (ρ) of the matrix $V^{-1}F$. As an example, let us consider an susceptible-exposed-infectious-recovery model. Since we are alarmed with the populations that broaden the infection we only need to model contaminated classes (I), and the exposed classes(E). Let us define the model dynamics using the next equations :

$$\frac{dI}{dt} = KE - \gamma I - \mu I \tag{2.18}$$

$$\frac{dE}{dt} = \beta S I - \mu E - KE \tag{2.19}$$

where, γ is the per capita revival rate, K is the rate at which a dormant individual becomes infectious, β is the efficacy of infection of vulnerable individuals S, and μ is the per capita

normal death rate. For this system

$$V = \begin{pmatrix} K+\mu & 0 \\ -K & \mu+\gamma \end{pmatrix} \tag{2.20}$$

$$F = \begin{pmatrix} 0 & \frac{\beta\lambda}{\mu} \\ 0 & 0 \end{pmatrix} \tag{2.21}$$

where λ is the birth rate of vulnerable and thus we have the next

$$R_{0,N} = \frac{K\lambda\beta}{(\mu^2+\gamma\mu)(K+\mu)} \tag{2.22}$$

For the second example, we consider a model of malaria. Let us explain the rate of modify of the contaminated mosquito (M_I) and human (H_I) populations by the next equations:

$$\frac{dM_I}{dt} = \beta_{HM} S_v H_I - \mu_M M_I \tag{2.23}$$

$$\frac{dH_1}{dt} = \beta_{MH} M_I S_h - H_1(\sigma+\alpha+\mu_H) \tag{2.24}$$

Infected humans are formed by the infection of vulnerable humans (S_h), by an infected mosquito with effectiveness β_{MH}. We suppose that they pass away with normal death rate μ_H, die due to disease with rate S and recover from the infection with rate α. Infected mosquitoes are formed when vulnerable mosquitoes (S_v) bite infected humans. We suppose that this procedure has efficacy β_{HM} and suppose that infected mosquitoes can only go away the infected section by dying in nature with rate μ_M. For this system we find that

$$F = \begin{pmatrix} 0 & \beta_{MH} M_S(0) \\ \beta_{HM} H_S(0) & 0 \end{pmatrix}, \tag{2.25}$$

$$V = \begin{pmatrix} \alpha+\sigma+\mu_H & 0 \\ 0 & \mu_H \end{pmatrix}. \tag{2.26}$$

Since V is non-singular we can compute V^{-1}. Thus, we have get the next equation

$$R_0 = \sqrt{\frac{\beta_{HM} M_S(0) \beta_{MH} H_S(0)}{\mu_M(\alpha+\sigma+\mu_H)}} \tag{2.27}$$

This description is still in normal use in epidemiology.

2.8 LAS and GAS points

[105] An n by n matrix A is said to be an M-matrix iff all the diagonal entries are positive and each off-diagonal entry of A is non-positive. [105] Let X^0 is a DFE of the next equation (2.28)

$$x^{'} = F(x,y) - V(x,y),\ y^{'} = g(x,y); \tag{2.28}$$

then the derivatives $\mathrm{DF}(X^0)$ and $DV(X^0)$ are partitioned as

$$\mathrm{DF}(X^0) = \begin{vmatrix} F & 0 \\ 0 & 0 \end{vmatrix} \text{ and } \mathrm{DV}(X^0) = \begin{vmatrix} V & 0 \\ J_3 & J_4 \end{vmatrix} \tag{2.29}$$

where F and V are the $m \times m$ matrices clear by the next equation (2.30)

$$F = \left[\frac{\partial F_i}{\partial x_j}(X^0)\right] \text{ and } F = \left[\frac{\partial V_i}{\partial x_j}(X^0)\right] \tag{2.30}$$

with $1 \leq i, j \leq m$. Further, F is non-negative, V is a non-singular M-matrix and J_3, J_4 are matrices related with the transition conditions of the model, and every one eigenvalues of J_4 have positive real part. An equilibrium solution, X_0, is LAS if the eigenvalues of the matrix the Jacobian matrix $\mathrm{Df}(X^0)$ have negative real parts and uneven if any eigenvalue of $\mathrm{D}(X^0)$ has a positive real part [105]. The eigenvalues of $\mathrm{Df}(X^0)$ can be partitioned keen on two sets analogous to the contaminated and uninfected sections. These two sets are the eigenvalues of $F - V$ and those of $-J_4$. Again the eigenvalues of $-J_4$ all have negative real part, thus the steadiness of the DFE is gritty by the eigenvalues of $F - V$.

Theorem 2.8.1. *[105] Think about the disease transmission model prearranged by equation* (2.28)*. If X_0 is a DFE of the model, then X^0 is LAS if $R_0 < 1$, but unstable if $R_0 > 1$; R_0 is given by the next equation* (2.31)

$$R_0 = \rho(FV^{-1}). \tag{2.31}$$

An equilibrium point $\overline{x}$ of (2.5) is called GAS point if every solutions with dissimilar initial situation converge to it internationally in time. In epidemiology, it is significant to know whether an infectious disease will persevere and wait at a positive level over time, after endemic epidemic and whether this behaviour depends on the original size of the

disease or not. This is addressed mathematically by the GAS of widespread equilibria. For many disease models, the R_0 gives a sharp threshold that totally decides their worldwide dynamics; thus the subsequent property is affirmed [90]. Model equation (2.5) has the pointed threshold property if R_0 given by equation (2.31) such that the DFE P_0 is GAS for $R_0 \leq 1$, and there is a sole EE P^* that is GAS in the interior of the feasible region for $R_0 > 1$. Biologically, the sharp threshold property shows that the disease will finally pass away out if $R_0 \leq 1$, while the disease continues at a positive level if $R_0 > 1$. Though, the rigorous proofs of these global stability consequences are non-trivial for many disease models. In exacting, the global stability of the global equilibrium normally becomes a demanding mathematical problem due to the complexity and high dimension of disease models. Lyapunov functions are used to show stability of systems of odes arising in biology [90]. [106] A continuously differentiable function $V : \mathfrak{R}^n \to \mathfrak{R}^+$ is said to be positive in a region U of $\mathfrak{R}^n$ that contains the origin if $V(0) = 0$ and $V(x) > 0$, for $x \in U$ and $x \neq 0$.

2.9 Lyapunov Function and LIP

[106] Let the system equation (2.5) describe a dynamical system on an open subset $\Omega \subset \mathfrak{R}^n$ and $\overline{x} \in \Omega$ an equilibrium point. A positive specific function $V \in C_1(\Omega, R)$ is called a Lyapunov function of the system equation (2.5) for $\overline{x}$ on a region $B \subset \Omega$ of $\overline{x}$ gives that $V^{'}(\overline{x}) = 0$ and $V^{'}(x) \leq 0,\ \forall x \in B$. where $V^{'}$ is the directional derivative of V in the direction of the vector f.

Theorem 2.9.1. *If there is a positive specific Lyapunov function V of the dynamical system equation* (2.5) *on a neighbourhood B of an equilibrium point $\overline{x}$, then $\overline{x}$ is stable. In adding, if $V^{'}(\overline{x}) < 0 \in B\backslash\overline{x}$, then $\overline{x}$ is asymptotically steady and unsteady if $V_0(\overline{x}) > 0,\ \forall x \in B\backslash\overline{x}$.*

GAS, is determined in conjunction with LIP. Before stating LIP, we initiate the description of $\omega-$ limit set and invariant set under. Let $\phi(t; x_0)$ be the autonomous dynamical system produced by the solutions of (2.5) in [106]. [23] A set $S \subset R_d$ is said to be the $\omega-$ limit set of $\phi(t; x_0)$ if for each $x \in S$, there is a strictly increasing sequence of times t_n, then $\phi(t_n; x_0) \to x$ as $t_n \to \infty$.

It is common to write $S = \omega(x_0)$. In a analogous way, it is distinct the omega limit of a set $A \subset O$, and it is indicated as $\omega(A)$, as the set of points $x \in O$ such that there are two sequences

$$x_n \subset A, t_n \to +\infty \text{ such that } \phi(t_n; x_n) \to x, \text{ as } n \to +\infty. \tag{2.32}$$

[23] A set $M \subset R_d$ is called positively invariant if for all $x \in M$ we have $\phi(t; x) \in M, \forall t \geq 0$. [23] The positive invariance means that as long as a solution passes a point inside M it will stay within M everlastingly.

Theorem 2.9.2. *LaSalle's Invariance Principle(LIP): In [23] Let $K \subset X$ be a compact and positively invariant set, $V : K \subset \mathfrak{R} \to \mathfrak{R}^d$ be continuously differentiable with $V \leq 0$ on K, and let M be the largest invariant set in $E = \{x \in K : V = 0\}$. Then $\phi(t; x_0)$ approaches M as $t \to \infty$ for every $x_0 \in K$.*

LIP requires V to be continuously differentiable but not essentially positive [23]. It is appropriate to any equilibrium set, rather than just a lonely equilibrium point. But when M is just a particular point, it gives extra information about the kind of stability of the equilibrium point. Certainly, when M is just a single point, and we are able to discover a Lyapunov function to make sure that this equilibrium is steady and also convergent as a consequence of LaSalle's principle, and therefore is asymptotically steady. It is often hard to build a Lyapunov functions and no common technique is obtainable. For instance, a common form of Lyapunov functions in the literature of mathematical biology is

$$D = \sum_{i=1}^{n} c_i \left(x_i - x_i^* - x_i^* \ln \frac{x_i}{x_i^*} \right), \tag{2.33}$$

originally from the first integral of a Lotka-Volterra system. When practical to disease models, appropriate coefficients c_i have to be strong-minded such that the derivative of D along solutions of the model is non-positive, and such a and such a determination becomes very difficult for models with high dimension [90]. The next three methods show how to build Lyapunov functions for disease models and therefore set up the GAS of the DFE and EE points. A matrix-theoretic method was introduced in [90] to decide global steadiness of the DFE. Process of the method goes as follows. Consider (2.28) with $\mathcal{F}, \sqsubseteq, F$ and V prearranged above, and set the next

$$f(x, y) := (F - V)x - \mathcal{F}(x, y) + \mathcal{V}(x, y). \tag{2.34}$$

From $x^{'}$ in (2.28) and (2.34), it can be written as follows in equation (2.35)

$$x^{'} = (F - V)x - f(x, y). \tag{2.35}$$

Note that $f(0, y) = 0$. Let $\omega^T \geq 0$ be the left eigenvector of the non negative matrix $V^{-1}F$ equivalent to the eigenvalue $\rho(V^{-1}F) = R_0$.

Theorem 2.9.3. *Let F, V and $f(x, y)$ be clear as in equation* (2.34)*, in that order. If $f(x, y) \geq 0$ in $\Omega \subset \mathfrak{R}^n, F \geq 0, V^{-1} \geq 0$, and $R_0 \leq 1$, then the function $Q = \omega T V^{-1} x$ is a Lyapunov function for model equation* (2.28) *on Ω.*

In applications to infectious disease models, the set Ω in Theorem (2.9.3) is usually selected as a compact subset of $\mathfrak{R}^n_+$ such that $(0, y_0) \in \Omega$ and Ω is positively invariant with admiration to equation (2.28). Hence, the Lyapunov function built in the Theorem (2.9.3) can be used to show not only the worldwide steadiness of the DFE but also stable and therefore set up the survival of an free equilibrium. The next consequence provides in which hypothesis can be expediently checked for disease models.

F, V and $f(x, y)$ be clear as above and let $\Omega \subset \mathfrak{R}^n_+$ be compact such that $(0, y_0) \in \Omega$ and Ω is positively invariant with respect to equation (2.28)*. Let that $f(x, y) \geq 0$ with $f(x, y_0) = 0 \in \Omega$, $F \geq 0$, $V^{-1} \geq 0$, and $V^{-1}F$ is irreducible. Let that the disease-free system $y_0 = g(0, y)$ has a unique equilibrium $y = y_0 > 0$ that is GAS in $\mathfrak{R}^p_+$. Then the next results grasp for equation* (2.28)*: If $R_0 < 1$, then the DFE point P_0 is GAS in Ω and if $R_0 > 1$, then P_0 is unsteady and system equation* (2.28) *is regularly unrelenting and there is at least one free equilibrium.*

A graph-theoretical method was also introduced in [90] to decide worldwide steadiness of the widespread equilibrium. The method was built up on a biased digraph; so, description of some terms of a digraph is obtainable below. The method is clarified using the similar notation as obtainable in [90]. We start by recalling some definitions and consequences from graph theory as stated in [97]. A directed graph (digraph) is an prearranged pair of sets $G = (V, A)$, where V is a set of vertices and A is a set of ordered pairs of vertices of V. The in-degree of a vertex i, denoted as $d^-(i)$, is the number of arcs in G whose terminal vertex is i, and the out-degree $d^+(i)$ is the number of arcs whose initial vertex is i. A subdigraph H of G is spanning if H and G have the same vertex sets. A digraph G is weighted if each arc is assigned a positive weight. The weight $w(H)$ of a subdigraph H is

the manufactured goods of the weights on all its arcs. A tree is a sub-digraph T of G that is a single connected part and in which the in-degree of one vertex, the root, is zero, but each of the residual vertices has in-degree 1. A (directed) path P is a sub-digraph with separate vertices labelled $i_1, i_2, ..., i_m$ so that its arcs are of the form (i_k, i_{k+1}) for $k = 1, 2, ..., m-1$. A (directed) cycle C is the sub-digraph obtained from such a path P by adding the arc (i_m, i_1). If $m = 1$, the cycle consisting of a single vertex i_1 and a single arc (i_1, i_1) is called a loop. A unicyclic graph is a sub-digraph Q consisting of a collection of disjoint rooted trees whose roots are the vertices of a directed cycle. The in-degree of each vertex of such a graph equals 1. Given a biased digraph G with n vertices. Then, the nxn weight matrix is clear by $A = [a_{ij}]$ with entry $a_{ij} > 0$ equal to the weight of arc (j, i) if it exists and 0 otherwise. We indicate such a weighted digraph by (G, A). A digraph G is powerfully linked if for any pair of separate vertices i, j, there is a heading for path from i to j (and also from j to i). A weighted digraph (G, A) is powerfully connected iff the weight matrix A is irreducible. The Laplacian matrix $L = [l_{ij}]$ of (G, A) is clear as next

$$\begin{cases} -a_{ij} & \text{for } i \neq j \\ \sum_{k \neq i} a_{ik} & \text{for } i = j. \end{cases} \tag{2.36}$$

The following gives a graph-theoretic explanation of the cofactors of the diagonal entries of L.

Theorem 2.9.4. *Assume $n \geq 2$ and let c_i be the cofactor of l_{ij} in L. Then we have*

$$c_i = \sum_{\tau \in \tau_i} w(\tau), i = 1, 2, ..., n, \tag{2.37}$$

where τ_i is the set of all spanning trees τ of (G, A) that are rooted at vertex i, and $w(\tau)$ is the weight of T . If (G, A) is strongly connected, then $c_i > 0$ for $1 \leq i \leq n$. The next identity is analogous to the one in [70], following directly from the tree cycle identity [70] when the weighted digraph (G, A) has a certain structure, two new relations among the c_i can be recognized via combinatorial identities.

Theorem 2.9.5. *Let c_i be as given above. If $a_{ij} > 0$ and $d^+(j) = 1$ for some i, j, then we have*

$$c_i a_{ij} = \sum_{k=1} c_j a_{jk} \tag{2.38}$$

Theorem 2.9.6. *If $a_{ij} > 0$ and $d^{-}(i) = 1$ for some i, j, then we have get* (2.39)

$$c_i a_{ij} = \sum_{k=1} c_k a_{ki} \tag{2.39}$$

Theorem 2.9.7. *Let U be an open set in $\Re^m$. Consider a DE system*

$$z_k^{'} = f_k(z_1, z_2, ..., z_m), k = 1, 2, ..., m, \tag{2.40}$$

with $(z_1, z_2, ..., z_m) \in U$. Assume that the next assumptions are satisfied: There is functions $D_i : U \to R, G_{ij} : U \to R$ and constants $a_{ij} \geq 0$ such that for every $1 \leq i \leq n, D_i^{'} \leq \sum_{j=1}^{n} a_{ij} G_{ij}(z)$ for z in u. For $A = [a_{ij}]$, each directed cycle C of (G, A) has

$$\sum_{(s,r)\in\epsilon(c)} G_{rs} \leq 0 \text{ for } z \in U, \tag{2.41}$$

where $E(C)$ denotes the arc set of the directed cycle C. Then, the function

$$D(z) = \sum_{i=1} \sum_{i=1} c_i D_i(z), \text{ with constants } c_i \geq 0 \tag{2.42}$$

as given above, satisfies $D^{'} \leq 0$; that is, D is a Lyapunov function for (2.40).

Theorem (2.9.7) can be used to show the construction of Lyapunov functions for not only models that can be regarded as joined systems on networks but also models that do not have an explicit network structure. In the applications to disease models, the D_i are select from functions usually used in population models. The calculation of D_i follows from the disease model and difficult limits for these derivatives are resolute. The functions G_{ij} and constants a_{ij} are selected so that assumptions (1) and (2) in Theorem (2.9.7) hold concurrently. A weighted digraph is constructed matching to the weight matrix $A = [a_{ij}]$ resolute from assumption (1), depending on the choice of $D_i, i = 1, ..., n$, and estimates of Different numbers and/or types of functions D_i can be used for a particular disease model, giving dissimilar weighted digraphs. The function G_{ij} does not of requirement depend only on z_i and z_j. With information of a state graph structure, the new combinatorial identities (Theorems (2.9.5) can further be practical to derive clearly the coefficients c_i in a constructed Lyapunov function. For the proof of global stability of an equilibrium solution, a new Bendixson criterion for (2.48) was introduced in [68], which is an additional room of the

widespread Dulac situation in [68] and [69]. Before we talk about this method, we give some definitions and properties of norm of a matrix from [85]. Let R denote the he field of real of complex numbers and let $|.|$ denote a norm on the vector space $\mathfrak{R}^n$, where n is a positive integer. Denote by $\updownarrow(\mathfrak{R}^n)$ the normed algebra of all linear functions from $\mathfrak{R}^n$ into $\mathfrak{R}^n$ with the norm $\|.\|$ on $L(\mathfrak{R}^n)$ defined by $\|A\| = \max\{|Ax| : x \in \mathfrak{R}^n,\ |x| \leq 1\}$. Assume that m is a positive integer and $\{p_i : i = 1, ..., m\}$ is a family of supplementary projections on $\updownarrow(\mathfrak{R}^n)$, i.e., $P_i.P_i = P_i; P_i.P_j = 0$ if $i \neq j$, and $\sum_{i=1}^{m} p_i = 1$. Also, it is assumed that $P_i \neq 0$ for any i (hence, $m \leq n$). For each i in $\{1, .., m\}$, define the $[0, \infty]$ valued function $|.|_i$ on $\mathfrak{R}^n$ by the next equation (2.43)

$$|x|_i = |p_i x| \tag{2.43}$$

for each x in $\mathfrak{R}^n$, and define the $[0, \infty]$ valued function $\|.\|$ on $\updownarrow(\mathfrak{R}^n)$ by (2.44)

$$\|A\|_i = \sup\{|Ax|_i,\ x \in \mathfrak{R}^n, 1 = |x|_i > |x|_j \text{ for } i \neq j\} \tag{2.44}$$

for each A in $\updownarrow(\mathfrak{R}^n)$. $|.|$ is a seminorm on $\mathfrak{R}^n$ for each i in $\{1, ..., m\}$. Also, if A is in $\updownarrow(\mathfrak{R}^n)$ and x is in $\mathfrak{R}^n$ with $1 = |x|_i \geq |x|_j$, for $j \neq i$, then so

$$|x| = |\sum_{j=1}^{m} p_j x| \leq |p_i x| + \sum_{j \neq i} |p_j x| \leq m;\ \text{so} \tag{2.45}$$

$$|Ax|_i = |p_i Ax| \leq \|p_i A\||x| \leq m\|p_i A\| \tag{2.46}$$

Hence, $\|A\|_i$ is finite and $\|A\|_i \leq m|p_i A|$. Also, $\|.\|$ is a seminorm on $\updownarrow(\mathfrak{R}^n)$. Furthermore, $\|A\|_i$ is the least number M such that the inequality $\|Ax\|_i \leq m|M|x|_i$ is valid for all $\mathfrak{R}^n$ such that $|x|_i \geq |x|_j$ for $j \neq i$. The inequality $\|Ax\|_i \leq \|A\|i|x|_i$ does not necessarily hold for all $x \in \mathfrak{R}^n$, and the inequality $\|A.B\|_i \leq |A|_i\|B\|_i$ also does not hold in general. However, if $P_i A = AP_i$, then these inequalities are valid. For each $i \in \{1, ..., m\}$ and A in $\mathfrak{R}^n$, define the Lozinskii measure $\mu_i(A)$ of a n by n matrix with respect to the norm $|.|_i$ as

$$\mu_i(A) = \lim_{h \to 0^+} |I + hA|_i - lh. \tag{2.47}$$

Lozinskii measures have been used for judgment of eigenvalues of matrices. They also arise in the stability investigation of linear differential systems when certain vector norm of solutions are used as Lyapunov functions [69]. Now, as presented in [69], we state the

geometric approach using the new Bendixson criterion as follows. Let the map $x \to f(x)$ from an open subset $D \subset \mathfrak{R}^n$ to $\mathfrak{R}^n$ be such that each solution $x(t)$ to the differential equation

$$x_0 = f(x) \tag{2.48}$$

is uniquely resolute by its initial value $x(0) = x_0$, and indicate this solution by $x(t, x_0)$. We state under definitions as given in [69]. Let $\overline{x}$ be an equilibrium point of the system equation (2.48). If $\overline{x}$ is globally steady with respect to D_1, then $\overline{x}$ is necessarily the only equilibrium in D_1 and there exists a compact neighbourhood K of such that every compact subset $F \subset D_1$ satisfies $x(t, F) \subset K$ for adequately large t. Such a K is called fascinating in D_1 for (2.48).

2.10 Bifurcation theory

Dynamics of differential equations system may alter, if at smallest amount one restriction is allowable to vary. For example, equilibrium can become wobbly and furthermore a periodic solution may come into sight or a new stable equilibrium may emerge. Such a qualitative alter in performance is said to be bifurcation, and the value at which these changes occur is called a bifurcation value. Bifurcation investigation is the mathematical revise of changes in the solutions when altering the parameters.The parameter principles where they happen are called bifurcation points. Usually, the classical outbreak models have only one EE point when the $R_0 > 1$, and the DFE point is forever steady when $R_0 < 1$ and unsteady when $R_0 > 1$. So the bifurcation most important from a DFE point to an EE point is onward; in this case, R_0 is the bifurcation parameter and $R_0 = 1$ is the bifurcation value. Though, below some situation in stricture space, for example, when the result of delay for conduct is strong, an outbreak can happen, or a stable EE point can exists even when the doorsill quantity, R_0, of the model being deliberated is less than unity; this occurrence is called backward bifurcation. When an epidemiological model admits manifold non-trivial equilbrium, the model typically shows multifaceted dynamical behavior such as backward bifurcation. In such circumstancess, the decrease of the connected reproduction number under unity is inadequate for illness abolition in the population. Thus, it is significant to recognize backward bifurcations and set up thresholds

for the control of diseases. By analyzing the survival performance of the model in such point's one can get much about the systems properties. To recognize the next section a concise foreword to bifurcation theory might be valued. For space protection reasons this will not be obtainable here, instead we advocate interpretation the basic preface given in [29]. By using bifurcation theory [25] shows that a widespread equilibrium point exists for all $R_0 > 1$ with a transcritical bifurcation at $R_0 = 1$.

Chapter 3

LITERATURE REVIEW

In order to forecast the occurrence of infectious disease epidemics and to direct current research for the eradication of malaria, epidemiologists frequently employ mathematical models [4, 62]. In order to eradicate and regulate [62], it is thought that a combination of many approaches, as opposed to a single style of modeling, may be more effective in the long run. Recent years have seen a boom in activity as a result of international eradication and control efforts, [62]. This has resulted in several studies and publications. Within host models take into account the interaction of the parasite with the immune cells in a specific host in order to analyze the infection phenomena inside the individual host. Population genetic models examine the evolution and spread of the parasite in a complicated environment with varied levels of host immunity, host death, medication availability, and mosquito abundance. In [87], the man who won the Nobel Prize for his work, was the first to begin mathematical modeling of malaria. The association between the prevalence of malaria in humans and the number of mosquitoes was explained by his extremely straightforward model, which has since been substantially expanded. His model did not consider the latency period of the parasite in mosquitoes and their survival during that period. Starting from the basic model in [87] many transmission models of malaria have been developed by considering regulation of the passage of the human host and mosquito vector through these epidemiological compartments as a function of the host and parasite specific factors, their interactions, and external environmental variables. Here, an effort

has been made to expound on the development of these models by taking into account a few exemplary mathematical models that take the complicated interactions between host, vector, and parasite into account. The model in [87] is a highly significant improvement with a focus on application in mosquito eradication. This is because the word hierarchy of models is based on the undeniable fact that the mathematical model of malaria and the beginning of the tree both used the word pathometry to mean the quantitative study of a disease either in the individual or in the community.

In addition to models based on differential equations, other modeling approaches have also been used. Few examples are, integrated models in [62], habitat-based models in [82], climate change in [62], individual-based models in [62], spatial and genetic heterogeneity of host and parasite [62], acquired immunity [4,6,8], age-related model [4,62], and the latent period of infection in mosquitoes and human [4, 62]. When it comes to humans, the burden of malaria varies with age and gender. The majority of malaria deaths in African children happen before the age of 5. Older Africans are less likely to contract the disease due to prolonged exposure and the capacity to build some immunity. The disease load persists throughout adulthood outside of Africa, where there is no ongoing exposure. The spread of malaria in a community is therefore known to be significantly influenced by age and immunity, two interrelated elements. The significance of including immunity in malaria models is discussed in [66]. Including immunity in malaria models is significant for two reasons. The first problem is that unrealistic forecasts result from immunity neglect. Immunity can be added to models to help them become more lifelike. Second, modeling immunity, and specifically the impact of vaccinations, can aid in forecasting the results of vaccination campaigns. Numerous epidemiological studies have concentrated on this crucial issue by modeling immunity and the age structure of the human population(See [4,6,8]). In this case, the illness spreads differently over time and within various age groups depending on each group's immunological capacity. By taking into account the human population density in the infectious class as a function of age and time, age structure was added to the straightforward Ross model, as noted by [4]. In this case, the illness spreads differently over time and within various age groups. But the relationship between age and immunity needs to be more precisely described because the reliance, as

anticipated by this model, did not fit well with the actual trend in prevalence with age. By taking into account a distinct immune class in people and by adding an Immunity function to existing models, immunity can be included in a model in two different ways.

A distinct immune class has been included in some models in [79], whereas complex immunity functions have been included in some models in [42]. Assuming that malaria immunity is not permanent, in [31] first proposed a model including seven compartments in humans. In this concept, a person may either recover from the infected class and directly return to the susceptible class or become re-infected through a temporary immune class. In addition, several mathematical studies have been performed to simulate the effect of environmental variability in the abundance of mosquito populations, such as random fluctuation in the form of color noise in infected mosquito dynamics of the Ross model [88], periodic or noisy form of the force of infection [4, 6]. With the aim of creating accurate and verified malaria modeling frameworks that are able to pinpoint the critical connections between pathogen transmission mechanisms and climatic conditions, numerous studies have also taken the impact of environmental changes into account in a variety of ways, as noted by [83]. In a recent work, [83] devised a model to analyze the dynamics of the mosquito population while taking the simultaneous impacts of temperature and rainfall into account. There are three compartments in the model for humans with a set latency duration, and there are three compartments for mosquitoes. Through parameters relating to mosquitoes, several environmental elements are introduced in this model. While mosquito mortality, biting, sporogonic cycle length, and the likelihood that infected mosquitoes will survive the parasite's incubation period are thought to be dependent on temperature variation, the birth rate of adult mosquitoes is thought to be a function of rainfall and temperature.

The main conclusion of this model is that variations in rainfall patterns substantially influence the endemicity, invasion, and extinction of malaria as well as the abundance of vectors. The temperature, on the other hand, affects the pathogen life cycle and has a bigger impact on the rate at which diseases spread when there is enough rainfall to sup-

port vector development and survival. The strength of the relationship between the two points to a close connection between malaria and poverty. Variations in social and economic factors are generally regarded as being much more significant in malaria-endemic areas than temperature variations [107]. [107] demonstrated through the use of mathematics how local social and economic factors, as well as global warming, affect the R_0 of malaria transmission. Three temperature zones have also been created for each of the three economic circumstances in this model, which takes into account good, moderate, and poor economic conditions among human communities. According to this model, a variety of variables, including endemicity, resistance, endemicity, economic conditions, and the sensitivity of mosquito growth to temperature, regulate disease transmission rates. With three varied temperature zones and diverse socio economic frameworks, they result in various reproduction numbers. In order to prevent disease transmission, these modeling results highlight the necessity of appropriate environmental management practices in addition to an effective healthcare system.

The efficiency of malaria control through various types of intervention strategies can have differential protection, with the former being more protective, according to a mosquito-based model that illustrates how field study design can be approached. When a pathogen enters a population of hosts, it divides the inhabitants into groups based on the amount of parasites they contain and the type of infection they have. After the ground breaking work of in [62], these compartments are denoted by the common notation $SEIR$. To put it simply, they are as follows: the first group is made up of the portion of the host population that is susceptible (S) to infection (I); next is the exposed (E) class, which is made up of the portion of the population whose members are infected by the pathogen but are unable to spread the infection to others during the time between the point of infection and the start of the state of infectiousness, during which the members of the exposed (E) class remain infected. The second category is contagious people, who spread infection to additional people by coming into contact with Susceptibles. The R class, on the other hand, is made up of people who recover from the virus. Depending on the condition, there could be differences in the compartment structure. For instance, the I class of people might not recover at all and pass away; the R class could be made up of those who recover

with temporary or permanent immunity, further splitting the epidemiological compartments. These notations make it feasible to create eight types of compartmental models: $SI, SIS, SEI, SEIS, SIR, SIRS, SEIR$, and $SEIRS$, to use [55] terminology.

For instance, in a $SEIRS$ model, some of the susceptible population is exposed to infection, and some of that population later develops the ability to spread infection. Some members of the infectious class recover from the illness and join the R class with temporary immunity. When immunity is gone, they are once again vulnerable to pathogen attack and move into the S class. Thus, both human and vector compartments have been used in malaria modeling. Epidemiological compartments for a $SEIRS$ model that distinguish between various stages of infection and parasite densities in the host population. Different stages of infection are crucial to the dynamics of transmission. The degree of infectious agent that replicates inside a host may rise from small inoculums to a higher level, and later decline and/or cease altogether as it goes through them. In many cases of infection, the period from the site of infection to the development of symptoms of sickness and the period from the point of infection to the beginning of the state of infectiousness are not the same [4]. The appearance of symptoms is significant for case diagnosis and treatment. The state of the clinical markers presence by + and absence indicated for diagnosis of each compartment is designated by Sero-conversion and Cellular immunity [60,81,94]. Latency of infection in humans was introduced in [4] making an additional Exposed class in humans in [74]. Researchers have modified the basic model in [88] to explain the effect of the age structure of prevalence [4], migration, and visitation of people [94]. Several models were also put forward following the model in [74] by incorporating additional complexities of human immunity, parasite diversity, and resistance to explain enormous quantities of epidemiological data collected in Africa and other areas of the world [12].

The main benefit of these early models was to offer an appropriate control strategy through the transmission threshold criterion, which is based on the parasite's ability to reproduce and is known as the basic reproductive number. Although the term threshold was first used by [88], [43] is where the term first appeared in relation to a parasite's reproductive

value. In every study on the population biology of a parasite, [74], the idea of the fundamental reproductive number has been extensively debated from the start. By estimating R_0, it is also possible to describe the fundamental outcomes of all these models. The Exposed class was added to the mosquitoes according to in [74] after taking this latency interval into account. Therefore, in this model, the mosquito population is divided into three compartments(SEI), and the model studies the time evolution of the exposed class and infected classes in mosquito. The R_0 for this model is consequently scaled down with increasing latency period. In a natural extension to the Ross, the Macdonald model in [74], and Anderson and May considered in [4] the latency period of the parasite in humans, and introduced the Exposed class in human population in their model [4]. Along with the mosquito population, this split the host population into three sections. Thus, this is a $SEIS$ model for the human population, and it consists of four DEs that describe the temporal evolution of the exposed and infected classes of both humans and mosquitoes.

Due to the addition of the human latency period, the fundamental R_0 for this model is further decreased. A comparison of the models used by [4], [74] and [88] to predict the prevalence of infectious diseases. The models reveal that taking into account the latency periods of parasites in humans and mosquitoes not only lowers the long-term prevalence of both infected humans and infected mosquitoes, with the Anderson model having the lowest prevalence and the Ross model having the highest prevalence ([4] and [87], respectively). It also lowers the rates of progression in these final infected populations. These simple models can provide some insight into the impact of various intervention types on the dynamics of disease transmission, even at their smallest level of complexity. The percentage of the population that falls into the exposed and infected classes can be controlled in part by the mosquito density, mosquito bite rate, and mosquito mortality rate. Ross developed the first deterministic DE model of malaria by compartmentalizing the human population into susceptible and infectious human groups, with the infected class reverting to the susceptible class once more to produce the SIS structure. The mosquito population likewise only has two compartments: susceptible and infectious mosquitoes, but due to their short lifespan, they do not recover from infection and hence adhere to the susceptible-infectious structure. Using two DEs, one for the human

and one for the mosquito, the time evolution of the population's proportion in the classes of infectious humans and mosquitoes is investigated. It is obvious that the human biting rate, the proportion of bites that result in human infection, the proportion of bites by which one susceptible mosquito becomes infected, and the ratio of female mosquito numbers to bites that contribute to the increase of the R_0 in this model are related to humans and mosquitoes, and any change in them can have a big impact on malaria transmission. The R_0 can be decreased by raising mosquito mortality and decreasing mosquito biting rates. The Ross model explains the fundamental characteristics of malaria transmission and places the majority of the burden of transmission on mosquito-specific characteristics, opening the door for mosquito-based malaria control programs. Knowing how changes in these parameters affect transmission intensity, which is measured by the R_0, is crucial for any epidemiologist. It is obvious that the reliance on the biting rate suggests that having the biting rate is more efficient given the expressions of the reproduction number in all three models. Thus, lowering the biting rate through the use of bed nets or any other technique will be an efficient way to control the transmission. But not all parameters make this evident. Due to the exponential function of the adult mosquito mortality rate present in these models, for instance, the relative effect of lowering the adult mosquito mortality rate in contrast to the biting rate is different. The $R_0 = 0$ surface demonstrates that the commencement of an epidemic occurs at higher parameter values in the [87] model than in the [4] model.

These findings suggest that, under the model of [4] and [74], reducing the lifespan of adult mosquitoes is more successful at reducing malaria cases than reducing the biting rate. As was previously indicated, these model results gave justification for controlling malaria transmission by mosquitoes using pesticides and insecticide-impregnated bed nets since they alter mosquito density biting rate and mosquito mortality rate. Therefore, even at this modest level of complexity, these models were successful in describing the elements that affect the disease's transmission, which were helpful in the control and eradication of malaria in many nations. Environmental effect [97, 107] has been used in some of the most recent publications on the mathematical modeling of malaria. [97, 107] offers a compartmental model in which people behave in a way similar to the SEIRS pattern

and mosquitoes behave similarly to the SEI pattern. In addition, the temperature now affects some of the metrics relating to insects. There are two of these: the time it takes for mosquito eggs to hatch into adults and the amount of time it takes for a mosquito to swallow Plasmodium gametocytes before they mature into sporozoites and move to the salivary glands.

[97, 107] Use the model to study the effect global warming. Using the estimated increase in temperature of 10 to 3.5 degree centigrade by the year 2100, they show that it is possible in some areas of the world for the $R_0 > 0$ to increase above one; for areas to change from a stable DFE point to one with low levels of endemicity and for other areas to change from low levels of endemicity to high levels. They do, however, conclude by saying that economic and social effect are still more important than temperature effect and a good health care system with good malaria control techniques can overcome the negative effect of an increase in temperature. People go through various stages of the $SEIR$, and a history of earlier infections is retained in the model from [97] derives. The mosquito population is subdivided into juveniles and adults in a submodel included in the study. They incorporate into their model for malaria transmission the steady state value from this submodel for the adult mosquito population. In the mosquito population sub-model, they introduce the dependency of the parameters on an environmental parameter and compute the dependence of the R_0, for the whole malaria model, on this environmental parameter. The spread of the drug-resistant Plasmodium [66] parasite and the development of immunity [66] have both been considered in more current models.

Discuss a model that incorporates a disease strain that is resistant to treatment. Start with the Ross-Macdonald model and work your way up to more intricate models. As a result of their findings, it can be seen that even in the most basic of their models, there is a threshold below which drug resistance does not exist and above which it does. In their investigation of a host-parasite evolution model of malaria, [66] found that the parasite makes investments in its capacity to elude the host's immune response while the host makes gradual improvements to its immune system. While mosquitoes follow an SEI

pattern similar to that described in [107] and humans follow a $SEIRS$-like pattern, [80] describes only one immune class for humans. When in contact with an infected mosquito, humans shift from the susceptible to the exposed class with a certain probability before moving to the infectious class, just like in traditional $SEIRS$ models. Infected individuals can then recover with or without a boost in immunity, returning to the vulnerable class or moving to the recovered class. A novel aspect of this model is that even though people in the recovered class are thought to be immune in the sense that they do not experience severe illness or develop clinical malaria, they still have low levels of Plasmodium in their bloodstream and can transmit the infection to mosquitoes that are susceptible. These rehabilitated people eventually join the susceptible group. When susceptible mosquitoes come into contact with either infectious or recovered humans, they may become infected and switch over to the exposed class. They then move on to the class with the infectious disease. A density-dependent natural death rate causes both people and mosquitoes to abandon the population. The model may now take changing human and mosquito populations into account. Constant population models do not take into consideration the fact that mosquito population fluctuations are essential to the dynamics of malaria. The model also takes into account disease-related human deaths because malaria mortality, particularly in newborns, can be significant in locations with high transmission rates.

[79]Use a linear per capita mortality rate assumption to analyze this model. A R_0 is defined in these new variables when the system is transformed into dimensionless quantities. They demonstrate that an EE point exists when $R_0 > 0$ and that this EE is distinct if there are no diseases that cause death. They demonstrate through linear analysis that the DFE is LAS when the $R_0 < 0$and the unique EE are both $R_0 > 0$, and that both are LAS when either is present. In order to prove their point that the EE is stable for $R_0 > 0$, they conclude by utilizing numerical simulations. Many of the topics covered in [6] be revisited in [4] later evaluation. Additionally, [6] may assemble a variety of data sets for parameter values, such as information on the latent period in humans and mosquitoes, the rate of recovery for humans, the anticipated adult lifetime of mosquitoes, and data on the frequency of malaria across human age distributions. In addition, [4] and [6] investigate the impact of including age structure in the fundamental [88] to [74]. Finally, they address

the implications of a vaccine and the decline in transmission rates on the age-prevalence of malaria as they examine various control measures. Nedelman surveys examines multiple data sets to statistically approximate parameters including inoculation rates, rates of recovery and loss of immunity in people, human-biting rates of mosquitoes, and infectivity and susceptibility of humans and mosquitoes. [64] Also starts with the citeRos15 to [74] paradigm with an additional latent stage for the mosquitoes. The impact of parameter variability is then studied, and an infection-rate-dependent duration of immunity is included.

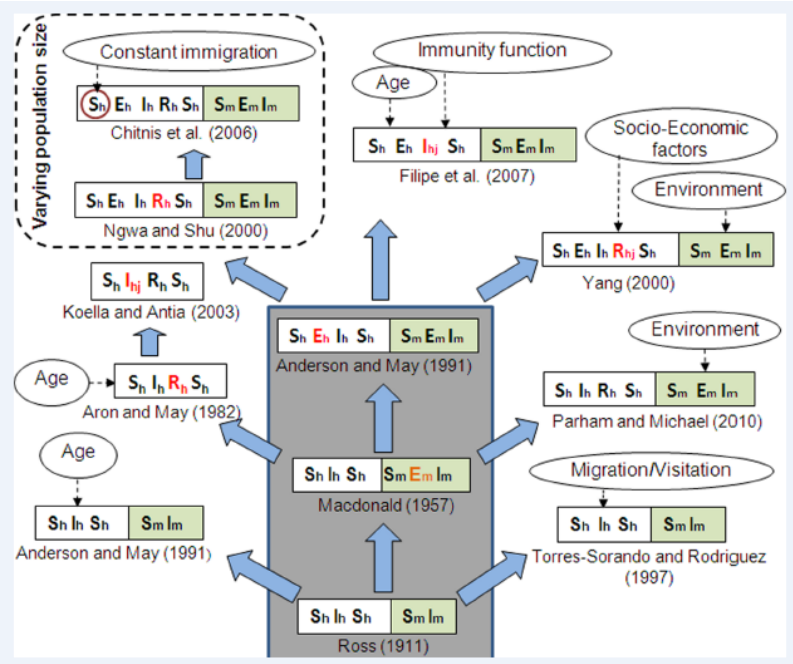
[64] Investigates the effects of vaccines, contrasting those that work on asexual blood stages and those that prevent transmission, to demonstrate that the asexual blood stage vaccines are more effective. [64] Uses this model of immunity to study the effects of vaccines. In the typical SIRS or SEIRS model, a good review of common epidemiological models can be found in the constant parameter [25] of immunity decline. However, ongoing reinfection is necessary for prolonged immunity against malaria; as a result, immunity is quickly lost in the absence of reinfection, whereas protection is long-lasting in the presence of a high infection rate. By relating the rate of immunity loss to the rate of immunization, it is possible to model this non-constant time of immunity. Unlike other models, the [25] and [26] model takes into account continuous human immigration. Once they have recovered, the contagious people join the class of recovered people. Due to this in [25, 26] divided the human population into four classes: susceptible, exposed, infectious, and immune, and divided the mosquito population into three classes: ”susceptible, exposed, infectious, and immune.” The recovered humans have some immunity to the disease and do not get clinically ill, but they still harbor low levels of parasites in their blood stream and can transmit the infection to mosquitoes. After some time, they lose their immunity and return to the susceptible class.

The first time, [25, 26] model described the mathematical model contained the specification of a domain where the model is mathematically and epidemiologically well-posed and defined the R_0 and the DFE as LAS when the $R_0 < 0$ and unstable when the $R_0 > 0$.

show the existence and stability of a DFE point, the existence of at least one EE point, and the description of the existence and stability of the EE point(s) for all the $R_0 > 0$. Numerical simulations demonstrate that for higher values of the disease-induced death rate, a subcritical bifurcation is conceivable at $R_0 = 1$ and that the transcritical bifurcation at $R_0 = 0$ is supercritical in the absence of disease-induced death. Furthermore, the need for a thorough examination of this modeling approach and the development of the models used up to this point is highlighted by the current attention given to the significance of the predictive power of mathematical models in understanding the transmission of infectious diseases. The incorporation of acquired immunity in the model provided by [33] represented a significant advancement for the mathematical modeling of malaria. One class of persons has no immunity to malaria, whereas the other has some immunity, according to a model put forth by [33]. Some people recover with immunity as the non-immune class gets sick. The immunological class has the ability to contract an infection but cannot become clinically unwell or spread disease. The super-infection phenomenon, which is typically connected with macro-parasites, was also incorporated into the model by [33]. As also stated in [4], which is cited.

[11] Also provides a description of Dietz's super-infection paradigm. The temporary nature of acquired immunity is another significant characteristic of malaria. Reviews of the compartmental and continuous models of transient immunity in humans are provided by [6]. In the review of the literature, we try to include some of the more significant aspects of this epidemiology while still keeping it mathematically tractable. The architectural structure of the review of mathematical modeling of malaria is shown in Figure (3.1), where the subscripts h and m stand for human and mosquito, respectively. Human classes susceptible (S_h), exposed (E_h), infectious (I_h) and recovery (R_h) are in the left fold, while mosquito classes susceptible (S_m), exposed (E_m), and infectious (I_m) are in the right fold. Generally speaking, the human classes for malaria infection terminate with the susceptible class left (S_h), but the mosquito populations die from infection, so it can only progress up to the infected class left (I_m). Dotted arrows represent the effects of several complicated components in various models or particular compartments (red), such as age, immunity, environment, and socio economics. Red indicates the first time a new compart-

Figure 3.1: Architectural Structure Of Mathematical Modeling Of Malaria



ment has been added. The subscript $j = 1, 2, 3$ denotes that the relevant compartment has been further subdivided. Dotted arrows indicate the inclusion of complex components in various models or a given compartment. With so many models available, it is not easy to deduce the essential characteristics of the illness and gain a thorough understanding of how the interactions between the vector, parasite, and host led to the formation of the models.

Chapter 4

ANALYSIS OF MATHEMATICAL MODEL OF INFECTIOUS DISEASE

Those who are prone to pollution and are in good health are susceptible. The person has the option to withdraw from the tainted group. People who have the disease and are infectious are said to be infectious. The affected individual has the ability to recover from the disease and leave the contaminated group. People who have recovered from an infection are immune since they have already been exposed to it. When someone has recovered, they encounter resistance. Age, sex, social standing, and competitiveness have little bearing on the likelihood of contracting the infection. There isn't any inherited resistance. The populace interacts with one another in equal measure and mixes regularly. Normal birth and mortality rates are taken into account. All babies fall into the susceptible category. Members of all three classes die at the same rate. In order to maintain a stable population, it is assumed that the birth and death rates are equal. α, β, ρ, μ and γ are all positive, making all the parameters positive.

Table 4.1: State and parameter variable descriptions

Variables	An explanation of the variables
$S(t)$	Vulnerable population at time t
$I(t)$	Infected population at the moment t
$R(t)$	Recovered population at a time t
$V(t)$	Vaccinated population at time t
β	Infection rate per capita
γ	Recovery rate
α	The birth rate of the population
μ	Rate of deaths per capita
ρ	Proportion of those successively vaccinated

4.1 Analysis of the Model without Vaccination

4.1.1 Model Formulation

This model divides people in a population into at-risk, infectious, and well-again categories. On the other hand, in this concept, a person may change from the susceptible group to the infective group when they come into contact with an infected person. For instance, the contact for COVID-19 could be someone who is a few feet away from an infected individual who has just coughed. Individuals who are infectious spread the disease to others who are susceptible and remain in the infectious group for a while (the infectious period) before entering the pool of people who have recovered. As a result, we arrive at the system of first-order non-linear differential equations for our model as follows:

$$\frac{dS}{dt} = \alpha N - \frac{\beta IS}{N} - \mu S \tag{4.1}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I - \mu I \tag{4.2}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{4.3}$$

Since N constant, $N = S(t) + I(t) + R(t)$. With the initial conditions $S(0) \geq 0, I(0) \geq 0$, and $R(0) \geq 0$, we get the expression $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$. For the sake of simplicity, let's

redefine the terms $s = \frac{S}{N}, i = \frac{I}{N}$ and $r = \frac{R}{N}$, which is the proportions. We arrived at(4.4) from (4.1)and $s = \frac{S}{N}$.

$$\frac{ds}{dt} = \frac{d}{dt}\left(\frac{S}{N}\right) = \frac{1}{N}\frac{dS}{dt} - \frac{S}{N^2}\frac{dN}{dt} \tag{4.4}$$

$$= \frac{1}{N}\left(\alpha N - \frac{\beta IS}{N} - \mu S\right) - \frac{S}{N^2}.0 \tag{4.5}$$

$$= \alpha - \frac{\beta IS}{N^2} - \mu\frac{S}{N} = \alpha - \beta is - \mu s. \tag{4.6}$$

From equation (4.2) and $i = \frac{I}{N}$, we obtained the following equation (4.7)

$$\frac{ds}{dt} = \frac{d}{dt}\left(\frac{I}{N}\right) = \frac{1}{N}\frac{dI}{dt} - \frac{I}{N^2}\frac{dN}{dt} \tag{4.7}$$

$$= \frac{1}{N}\left(\frac{\beta IS}{N} - \gamma I - \mu I\right) - \frac{I}{N^2}.0 \tag{4.8}$$

$$= \frac{\beta IS}{N^2} - \gamma\frac{I}{N} - \mu\frac{I}{N} = \beta is - \gamma i - \mu i. \tag{4.9}$$

The following equation was derived from equations (4.3) and $r = \frac{R}{N}$

$$\frac{dr}{dt} = \frac{d}{dt}\left(\frac{R}{N}\right) = \frac{1}{N}\frac{dR}{dt} - \frac{R}{N^2}\frac{dN}{dt} \tag{4.10}$$

$$= \frac{1}{N}(\gamma I - \mu R) - \frac{R}{N^2}.0 \tag{4.11}$$

$$= \gamma\frac{I}{N} - \mu\frac{R}{N} = \gamma i - \mu r. \tag{4.12}$$

The following system equation was created by substituting these new variables into equations (4.1), (4.2) and (4.3), which were derived from (4.13)- (4.15).

$$\frac{ds}{dt} = \alpha - \beta is - \mu s \tag{4.13}$$

$$\frac{di}{dt} = \beta is - \gamma i - \mu i \tag{4.14}$$

$$\frac{dr}{dt} = \gamma i - \mu r \tag{4.15}$$

We arrived at the following equation using the overall population density:

$$s(t) + i(t) + r(t) = 1 \Rightarrow r(t) = 1 - s(t) - i(t). \tag{4.16}$$

To analyze the model equation from (4.1)-(4.3), it is sufficient to take into account equations (4.13) and (4.14).

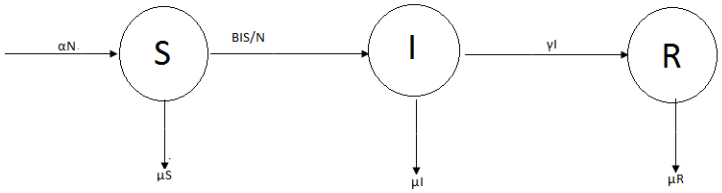


Figure 4.1: Model of infectous disease with out inducing vaccination

4.1.2 Feasible solution

Theorem 4.1.1. *The region where the system's equations' solutions have biological and mathematical significance is indicated by the viable solution. The system of* (4.1)-(4.3) *has a set of feasible solutions that is positively invariant, and it is given by the formula:* $\Omega = (S, I, R) \in R_+^3 : S + I + R = N > 0$. *It will be demonstrated that the region is positively invariant using the system.*

Proof. The total population is given by the equation $N = S + I + R$, which is derived from the system of equations (4.1)-(4.3). As a result, when the DEs (4.1) and (4.3) are added, the results become

$$\frac{dN}{dt} = \frac{dN}{dt} + \frac{dI}{dt} + \frac{dR}{dt} \tag{4.17}$$

$$= \alpha N - \mu S - \mu I - \mu R \tag{4.18}$$

$$= \alpha N - \mu(S + I + R) = \alpha N - \mu N = 0. \tag{4.19}$$

As a result, the differential equation $\frac{dN}{dt} = 0$ is of first order. Calculate this now by integrating both sides of the equation. The outcomes are as follows: $N(t) = N_0 e^{0t}$. Over a lengthy period of time, the population approaches the size of N_0 since at $t = 0, N(0) = N_0$.As a result, over a considerable amount of time, the total number of people approaches $N = N_0$ as $t \to \infty$ means that $N(t)$ approaches N_0. It is implied that $N = N_0$. As a result, boundedness is Ω.

4.1.3 Positivity of Solutions

The positivity of the solutions is the non-negativity of the solutions of the system.

Theorem 4.1.2. *The solution set of the system of equations* (4.1)-(4.3) *is positive if the initial data set is* $(S(0), I(0), R(0)) \geq 0$ *in* Ω.

Proof. The fact that all state variables are positive must be demonstrated. S(t), I(t), and R(t) are state variables, and their values must be for all $t \geq 0$. When considering equation (4.1), we were able to determine the Positivity of S and arrive at the value $S(t) \geq S(0)e^{-\mu t}$. Due to the fact that $\mu > 0$ and $S(0) \geq 0$. After that, all t must equal zero ($S(t) > 0$). The result of Equation (4.2) is $I(t) \geq I(0)e^{-(\gamma+\mu)t)} \geq 0$. The fact that $(\gamma + \mu) > 0$ and $I(0) \geq 0$ means that $I(t) \geq 0$, for all $t \geq 0$. We obtain $R(t) \geq R(0)e^{-\mu t} \geq 0$, followed by $R(t) \geq 0$, for all $t \geq 0$, from (4.1)-(4.3). This means that every variable is positive (for all $t \geq 0$). We have therefore demonstrated the non-negative nature of all variables in the model equations. As a result, the term positivity of solutions refers to the absence of negativity in system solutions.

4.1.4 The Basic Reproduction Number (R_0)

In terms of mathematics, the value of R_0 relates to the peak and final size of an epidemic and is a threshold for the stability of a disease-free equilibrium. The reproductive number can shed light on a disease's dynamics of transmission and help inform prevention tactics. In our model, the key factor controlling the dynamics of disease is the reproductive ratio. Consequently, we get the outcomes listed below. If $R_0 < 1$, then each person who contracts the disease will infect fewer than one person before recovering or passing away, which means the epidemic will spread in the host population and eradication is feasible. If $R_0 > 1$, then each person who contracts the disease will infect more than one person, which means the disease will peter out and eradication is not possible. As a result, $S = N$ and $\frac{di}{dt} > 0$, which are equal to $\beta is - \gamma i - \mu i > 0$, are used to determine the system's fundamental reproduction number, which is $\beta s > \gamma + \mu$. As a result, $R_0 = \frac{\beta s}{\gamma+\mu} > 1$ is obtained from the equation $\frac{\beta s}{\gamma+\mu} > \frac{\gamma+\mu}{\gamma+\mu} = 1$. As a result, R_0 is referred to as the fundamental reproduction number that dictates the model's stability analysis. Another way to think of reproduction numbers is as the number of secondary infections that result from original infections.

4.1.5 Disease free and endemic equilibrium points

By equating the rate of change to zero, which is expressed as $\frac{ds}{dt} = \frac{di}{dt} = \frac{dr}{dt} = 0$, the equilibrium points of the system can be found. The EE and DFE points of the equation system (4.1)-(4.3) are then discussed. In the model discussed above, there are two equilibrium locations. $E_0 = (s = 1, i = 0)$ is the location of the DFE point. By resolving the system equations, it is possible to determine the DFE point $E_0 = (1, 0)$ and the EE point $E_1 = (s, i)$.

$$\beta si - i\gamma - \mu i = 0 \text{ and } \mu - \beta si - \mu s = 0. \tag{4.20}$$

Then, we get $s = \frac{\gamma+\mu}{\beta}$ and $i = \frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)}$. Therefore, we obtained EE point

$$E_1 = \left(\frac{\gamma+\mu}{\beta}, \frac{\mu(\beta-\gamma-\mu)}{\beta(\gamma+\mu)}\right). \tag{4.21}$$

The EE point can only be reached when $\beta > \gamma + \mu$, which means that either $R_0 > 1$ or the infection rate must be higher than the mortality rate of infected people.

4.1.6 Locally stability analysis on DFE and EE points

If you place a system close to an equilibrium point, it will occasionally shift itself there due to the equilibrium point's local stability. The Eigenvalues of the Jacobian matrix that were computed at equilibrium define the local stability of the equilibria. All Eigenvalues of the Jacobian must have negative real parts in order for equilibrium to be LAS, which is a necessary and sufficient condition.

Theorem 4.1.3. *The DFE point E_0 is LAS in the case of $R_0 < 1$, while the EE point E_1 is LAS in the case of $R_0 > 1$.*

Proof. In order to ascertain the stability of the DFE point E_0, we look at the Jacobian matrix of the system assessed at the DFE point. Equation (4.22) provides the Jacobian matrix at the DFE point.

$$J(s,i) = \begin{pmatrix} \frac{d}{ds}(\alpha - \beta is - \mu s) & \frac{d}{di}(\alpha - \beta is - \mu s) \\ \frac{d}{ds}(\beta is - \gamma i - \mu s) & \frac{d}{di}(\beta is - \gamma i - \mu s) \end{pmatrix} \tag{4.22}$$

$$= \begin{pmatrix} -\beta i - \mu & -\beta s \\ \beta i & \beta s - \mu - \gamma \end{pmatrix} \tag{4.23}$$

Using (4.24), one may obtain the Jacobian matrix evaluated at the DFE point E_0.

$$J(1,0) = \begin{pmatrix} -\mu & -\beta \\ 0 & \beta-\mu-\gamma \end{pmatrix} \tag{4.24}$$

If $\beta-\mu-\gamma < 0$ and we obtain $\frac{\beta}{\gamma+\mu} = R_0 < 1$, then the eigenvalues of(4.24) are $\lambda_1 = -\mu < 0$ and $\lambda_2 = \beta-\mu-\gamma < 0$. Due to the fact that both Eigenvalues are negative, the DFE point E_0 is then LAS. One of the most crucial issues with any infectious disease is its capacity to spread throughout a population. A threshold parameter called R_0 can be used to describe this. The average number of infected individuals that the infected individual will produce during its whole period of infective is less than one, if $R_0 < 1$. The system is LAS in the DFE point example. This demonstrates that the disease's prevalence will decrease among the populace. Additionally, a group is infected only when $\beta > \mu + \gamma$.If $\beta-\mu-\gamma > 0$ or $\frac{\beta}{\gamma+\mu} > 1$, the DFE point is unstable. Given that $R_0 > 1$, each infected person who comes into contact with a susceptible person during the course of their whole infective period will result in the infection of multiple people, which will allow the disease to spread to the susceptible population and cause the DFE point to become unstable. It is given that the Jacobian matrix evaluated at the EE point E_1 looks

$$J(E_1) = \begin{pmatrix} \frac{\beta+(1-\gamma)\mu+\mu(1-\mu))}{\gamma+\mu} & -\gamma-\mu \\ \frac{\mu(\beta-\mu-\gamma)}{\gamma+\mu} & 0 \end{pmatrix} \tag{4.25}$$

The equivalent characteristic equation for the EE point E_1 is

$$\begin{vmatrix} \frac{\beta+(1-\gamma)\mu+\mu(1-\mu))}{\gamma+\mu} & -\gamma-\mu \\ \frac{\mu(\beta-\mu-\gamma)}{\gamma+\mu} & 0 \end{vmatrix} = 0 \tag{4.26}$$

In other words, $\lambda^2 + \frac{\mu\beta}{\gamma+\mu}\lambda + \mu(\beta-\gamma-\mu) = 0$. Be aware that both the positive coefficients $\frac{\mu\beta}{\gamma+\mu}$ and $\mu(\beta-\gamma-\mu)$ exist. And these are the Eigen values:

$$\begin{aligned} \lambda &= \frac{-\beta\mu}{2(\mu+\gamma)} \pm \frac{1}{2}\sqrt{\left(\frac{\beta\mu}{(\mu+\gamma)}\right)^2 - 4\mu(\beta-\gamma-\mu)} \\ &= \left(\frac{-\mu R_0}{2}\right) \pm \frac{1}{2}\sqrt{(\mu R_0)^2 - 4\mu(\beta-\gamma-\mu)} \end{aligned} \tag{4.27}$$

Given that $\mu(\beta-\gamma)$ is positive, the quantity under the square root is either less than or higher than $\mu^2 R_0^2$. If this is the case, the Eigen values are complicated by the negative real

portion $-\mu R_0$ and the beta-gamma-mu function. In the event that $\mu^2 R_0^2 < 4\mu(\beta-\gamma-\mu)$, the quantity beneath the square root must be smaller in absolute value than $\mu^2 R_0^2$, yet the real part is still negative. In any case, we get the conclusion that the EE point is stable because both Eigen values' real components are negative. It demonstrates that the EE point is stable since, in both scenarios, the susceptible and infected populations will live and the trajectories will eventually approach the EE point. The linear stability of the equilibrium points leads to the conclusion that the DFE and EE points cannot coexist. The DFE point is stable if $R_0 < 1$, while the EE point is stable if $R_0 > 1$. As an illustration, let's say that after determining the linear stability of both points, it is determined that the reproduction number is $1.5 > 0$ and the Eigen values of the DFE point are $\lambda_1 = -0.5, \lambda_2 = 0.5$. Consequently, it supports our finding that when $R_0 > 1$, trajectories cannot approach the DFE point, and the characteristic equation of the EE point is given by $\lambda^2+0.75\lambda+0.25 = 0$. Furthermore, the Eigen values are $\lambda = -0.3750 \pm 0.3307i$. Since both of the Eigen values' real components are negative, the EE point is stable, supporting our theoretical finding that the EE point is linearly stable when $R_0 > 1$.

4.1.7 Global stability analysis on DFE and EE points

To determine the stability requirement for this equilibrium point, we now investigate the characteristics of the EE points. Building a Lyapunov function demonstrates the world-wide asymptotic stability of the DFE and EE points.

Theorem 4.1.4. *In the event where $R_0 \leq 1$, the DFE point E_0 and EE point E_1 are both GAS on Ω.*

Proof. The following Lyapunov function is created in order to demonstrate the overall stability of the DFE point: $V : \Omega \to R, V(s,i) = i(t)$. Consequently, V's time derivative is

$$\begin{aligned} V(s,i) &= i(t)\beta i s - (\gamma+\mu)i \\ &= (\gamma+\mu)\, i\left(\frac{\beta s}{\gamma+\mu} - 1\right) \\ &= i(t)\,(R_0 s - 1)\,. \end{aligned}$$

Since $s = 1$ in the equilibrium of a free disease, $V(s,i) \leq 0$ for $R_0 < 1$. Additionally, $V(s,i) = 0$ if $i(t) = 0$ or $s(t) = 1$ and $R_0 = 1$. The biggest invariant set in the set

$L = \{s, i \in \Omega / V(s, i) = 0\}$ is therefore reduced to the disease-free equilibrium point. The LaSalle invariance principle states that the DFE point is GAS in Ω since we are in a compact invariant collection. Unlike Lyapunov theorems, LaSalle's principle does not require the function $V(x)$ to be positive and definite. If the biggest invariant set M, contained in the set E of points where V disappears, is reduced to the equilibrium point, i.e., if $M = x_0$, LaSalle's principle allows us to deduce that the equilibrium is attractive. But a shortcoming of LaSalle;s principle, when relevant, is that it demonstrates just the attractiveness of the equilibrium point. It is generally known that in a nonlinear scenario, attractiveness does not imply stability. However, it is necessary to demonstrate Lyapunov stability when the function V is not positive and definite. LaSalle's principle is frequently misquoted because of this. In order to determine asymptotic stability using LaSalle's principle, some additional conditions are required. Additional effort is required in order to derive stability from LaSalle's premise. LaSalle has achieved the most comprehensive results in the direction of his principle to verify asymptotic stability. For the global stability of the EE point E_1 we create the Lyapunov function $L : \Omega_+ \rightarrow R$, where $\Omega_+ = S, I \in \Omega : S > 0, I > 0$ given by the following equation (4.28)

$$L(S, I) = W_1 \left(S - S^* \ln \left(\frac{S}{S^*} \right) \right) + W_2 \left(I - I^* \ln \left(\frac{I}{I^*} \right) \right) \tag{4.28}$$

where W_1 and W_2 are positive constants. Take the derivative of the above function

$$\begin{aligned}
\frac{dL}{dt} &= \frac{dL}{dS}\frac{dS}{dt} + \frac{dL}{dI}\frac{dI}{dt} \\
&= W_1 \left[\frac{dS}{dt} - S^* \left(\frac{S^*}{S} \right) \left(\frac{1}{S^*} \right) \frac{dS}{dt} \right] + W_2 \left[\frac{dI}{dt} - I^* \left(\frac{I^*}{I} \right) \left(\frac{1}{I^*} \right) \frac{dI}{dt} \right] \\
&= W_1 \left[\frac{dS}{dt} - \left(\frac{S^*}{S} \right) \frac{dS}{dt} \right] + W_2 \left[\frac{dI}{dt} - \left(\frac{I^*}{I} \right) \frac{dI}{dt} \right] \\
&= W_1 \left[\left(\frac{S - S^*}{S} \right) \frac{dS}{dt} \right] + W_2 \left[\left(\frac{I - I^*}{I} \right) \frac{dI}{dt} \right] \\
&= W_1 \left[\left(\frac{S - S^*}{S} \right) (-\beta S I + \mu - \mu S) \right] + W_2 \left[\left(\frac{I - I^*}{I} \right) (\beta S I - \gamma I - \mu I) \right].
\end{aligned}$$

Considering the endemic equilibrium point, we have $-\beta S I = -\mu + \mu S^*$ and $\beta S I - \gamma I = \mu I^*$,

then we have

$$\begin{aligned}\frac{dL}{dt} &= W_1\left[\left(\frac{S-S^*}{S}\right)(-\mu+\mu S^*+\mu-\mu S)\right]+W_2\left[\left(\frac{I-I^*}{I}\right)(\gamma I+\mu I^*-\gamma I-\mu I)\right]\\ &= W_1\left[\left(\frac{S-S^*}{S}\right)(\mu S^*-\mu S)\right]+W_2\left[\left(\frac{I-I^*}{I}\right)(\mu I^*-\mu I)\right]\\ &= W_1\left[\left(\frac{S-S^*}{S}\right)\mu(S^*-S)\right]+W_2\left[\left(\frac{I-I^*}{I}\right)\mu(I^*-I))\right].\end{aligned}$$

Thus, we get the following equation

$$\frac{dL}{dt} = -W_1\frac{1}{S}(S-S^*)^2\mu - W_2\frac{1}{I}(I-I^*)^2\mu \leq 0$$

For $W_1 = W_2 = 1$, $\frac{dL}{dt} = -(S-S^*)^2\mu \leq 0$. Also, if $S = S^*$ then $\frac{dL}{dt} = 0$. Hence, by LaSalle variance principle, the EE point is GAS in the interior of Ω.

4.2 Analysis of the Model with vaccination

4.2.1 Model Formulation

Now, we describe our second model in which we have induced vaccination. This is useful to compare spreading of disease in absence of vaccine with in vaccine, know the pace of disease transmission without and with vaccine and the influence of vaccination on disease. However, the suggested model is as follows:

$$\frac{dS}{dt} = \alpha N - \frac{\beta IS}{N} - \mu S - \alpha\rho N \tag{4.29}$$

$$\frac{dI}{dt} = \frac{\beta IS}{N} - \gamma I - \mu I \tag{4.30}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{4.31}$$

$$\frac{dV}{dt} = \alpha\rho N - \mu V \tag{4.32}$$

And $N = S(t) + I(t) + R(t) + V(t)$ is constant. With the initial conditions $S(0) \geq 0, I(0) \geq 0, R(0) \geq 0, V(0) \geq 0$ and we have $\frac{dN}{dt} = \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} = 0$. For simplicity, we can consider the prevalence that is the proportions by redefining using, $s = \frac{S}{N}, i = \frac{I}{N}, r = \frac{R}{N}$

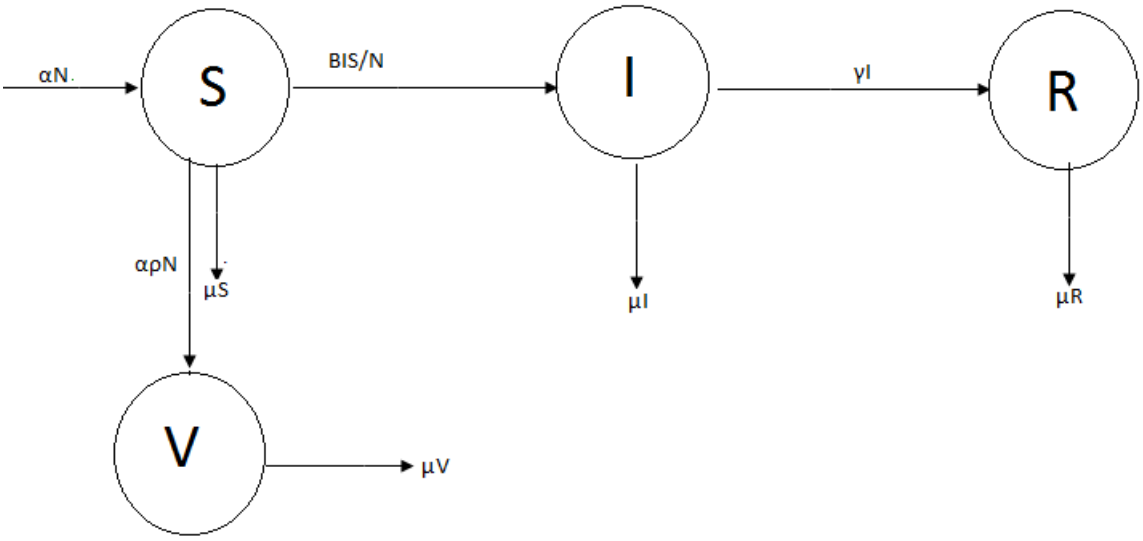


Figure 4.2: Model of infectous disease with inducing vaccination

and $v = \frac{V}{N}$. From equation (4.29) and $s = \frac{S}{N}$ we get

$$\frac{ds}{dt} = \frac{d}{dt}\left(\frac{S}{N}\right) = \frac{1}{N}\frac{dS}{dt} - \frac{S}{N^2}\frac{dN}{dt} \tag{4.33}$$

$$= \frac{1}{N}\left(\alpha N - \frac{\beta IS}{N} - \mu S - \alpha\rho N\right) - \frac{S}{N^2}.0 \tag{4.34}$$

$$= (1-\rho)\mu - \beta is - \mu s \tag{4.35}$$

From equation (4.32) and $v = \frac{V}{N}$, we get

$$\frac{dv}{dt} = \frac{d}{dt}\left(\frac{V}{N}\right) = \frac{1}{N}\frac{dV}{dt} - \frac{V}{N^2}\frac{dN}{dt} \tag{4.36}$$

$$= \frac{1}{N}(\alpha\rho N - \mu V) - \frac{V}{N^2}.0 \tag{4.37}$$

$$= \rho\alpha - \mu v. \tag{4.38}$$

then we get the following equation

$$\frac{ds}{dt} = (1-\rho)\alpha - \beta is - \mu s \tag{4.39}$$

$$\frac{di}{dt} = \beta is - \gamma i - \mu i \tag{4.40}$$

$$\frac{dv}{dt} = \alpha\rho - \mu v \tag{4.41}$$

$$\frac{dr}{dt} = \gamma i - \mu r \tag{4.42}$$

By considering the total population density, we have

$$s(t) + i(t) + r(t) + v(t) = 1 \Rightarrow r(t) = 1 - s(t) - i(t) - v(t). \tag{4.43}$$

Therefore it is enough to consider (4.39) and (4.41) to analysis from (4.29)-(4.32).

4.2.2 Feasible solution

The region where the system's equations' solutions have biological and mathematical significance is indicated by the viable solution.

Theorem 4.2.1. *The system of* (4.29)-(4.32) *has a set of viable solutions that is positively invariant, as shown by the formula:* $\Omega_1 = \{(S, I, R, V) \in R_+^4 : S + I + R + V = N > 0\}$. *The region will be demonstrated to be positively invariant using the system of* (4.29)-(4.32).

Proof. The total population is calculated using the system (4.29)-(4.32) as follows:

$$N = S + I + R + V. \tag{4.44}$$

As a result, when the DE (4.29) and (4.32) are added, the results are

$$\begin{aligned} \frac{dN}{dt} &= \frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} + \frac{dV}{dt} && (4.45)\\ &= \alpha N - \mu(S + I + R + V) && (4.46)\\ &= \alpha N - \mu N = 0 && (4.47) \end{aligned}$$

Therefore, $\frac{dN}{dt} = 0$ consequently, $N(t) = N_0 e^{0t}$ if is a first order differential equation. Over a lengthy period of time, the population approaches the size N_0 since at $t = 0, N(0) = N_0$. As a result, over a considerable amount of time, the total number of people approaches $N = N_0$ as $t \to \infty$ means that $N(t)$ approaches to N_0. It is implied that $N = N_0$. As a result, Ω_1 is bound.

4.2.3 Positivity of Solutions

Theorem 4.2.2. *If the initial data set is* $S(0) \geq 0, I(0) \geq 0, R(0) \geq 0, V(0) \geq 0 \in \Omega_1$, *then the solution set of the system of* (4.29)-(4.32) *is positive* $\forall t \geq 0$.

Proof. We can observe from the examination of the (4.1)-(4.3) above that $S(t), I(t)$, and $R(t)$ are all solutions that are positive solutions, $\forall t \geq 0$. Equation (4.32) yields $\frac{dV}{dt} \geq -\mu V$, and when the two sides of this inequality are integrated, we get $V(t) \geq V(0)e^{-\mu t}$. Since $\mu > 0$ and $V(0) > 0$, $V(t) > 0$, and all $t > 0$. As a result, each and every state variable is positive ($\forall t \geq 0$). We have thus demonstrated the non-negative nature of all state variables. In light of this, $S(t), I(t), R(t)$ and $V(t)$ are all positive solutions $\forall t \geq 0$.

4.2.4 Reproduction rate, EE points and DFE points

You may find the EE point $E_{1v} = (s, i, v)$ and the DFE point $E_{01} = (s, i, v)$ by solving the system of equations below.

$$(1-\rho)\alpha - \beta is - \mu s = 0 \tag{4.48}$$

$$\beta is - \gamma i - \mu i = 0 \tag{4.49}$$

$$\alpha\rho - \mu v = 0 \tag{4.50}$$

Next, we obtain the DFE point $E_{01} = (1-\rho, 0, \rho)$ and the EE point $E_{1v} = \left(\frac{\gamma+\mu}{\beta}, \frac{\mu(\beta(1-\rho)-\gamma-\mu)}{\beta(\gamma+\mu)}, \rho\right)$. We look to the Jacobian matrix of the system assessed at the point E_{01} to determine the stability of the DFE point E_{01}. At equilibrium, the Jacobean matrix is (s, i, v)

$$J(s,i,v) = \begin{pmatrix} -\beta i - \mu & -\beta s & 0 \\ \beta i & \beta s - \gamma - \mu & 0 \\ 0 & 0 & -\mu \end{pmatrix} \tag{4.51}$$

The Jacobean matrix evaluated at DFE point E_{01} is

$$\begin{pmatrix} -\mu & -\beta s & 0 \\ 0 & \beta(1-\rho) - \gamma - \mu & 0 \\ 0 & 0 & -\mu \end{pmatrix} \tag{4.52}$$

At DFE point E_{01}, the characteristic equation is

$$\begin{vmatrix} -\mu - \lambda & -\beta s & 0 \\ 0 & \beta(1-\rho) - \gamma - \mu - \lambda & 0 \\ 0 & 0 & -\mu - \lambda \end{vmatrix} = 0 \tag{4.53}$$

then $\lambda_1 = -\mu = \lambda_2 < 0$ and $\lambda_3 = \beta(1-\rho) - \mu - \gamma$. are the eigenvalues of (4.53). If $\lambda_3 > 1$, which indicates that $\beta(1-\rho) > \mu + \gamma$, then we have $\frac{\beta(1-\rho)}{\gamma+\mu} > 1$, leading to either $R_0\beta(1-\rho) > 1$ or $R_v > 1$. As a result of all Eigenvalues being negative, the DFE point E_{01} is no longer LAS and will start to oscillate. If $\lambda_3 < 1$, which equals $\beta(1-\rho) < \mu + \gamma$, is true, then $\frac{\beta(1-\rho)}{\gamma+\mu} < 1$ is obtained, leading to $R_0(1-\rho) < 1 \Rightarrow R_v < 1$. Due to the fact that all of the Eigenvalues are negative, the DFE point point E_{01} is thus LAS. After the introduction of vaccination in the model, the new reproduction number is $R_v = R_0(1-\rho)$. Only if $R_v > 1$ will the EE point be present.

4.2.5 Local and Global stability analysis

We shall now investigate the DFE and EE point's linear stability. As an example, the reproduction number $R_v = 0.45 < 1$ indicates that the DFE point is steady. $\lambda_1 = -0.5, \lambda_2 = -0.5$ and $\lambda_3 = -0.55$ are the Eigenvalues that correlate to the DFE point. It is hence linearly stable. So, it is clear that when vaccination is used in the SIR model, the infected population, which was at 0.3470, drops to 0.1833 at the infection rate $\beta = 1.5$ as a result of the effect of vaccination. The equivalent characteristic equation for the EE points, E_{1v} is

$$\begin{vmatrix} \frac{-\mu\beta(1-\rho)}{\gamma+\mu} - \lambda & -(\gamma+\mu) & 0 \\ \frac{\mu(\beta(1-\rho)-\mu-\gamma)}{\gamma+\mu} & -\lambda & 0 \\ 0 & 0 & -\mu-\lambda \end{vmatrix} = 0 \tag{4.54}$$

Which is identical to $(\mu+\lambda)\left(\lambda^2 + \frac{\mu(\beta(1-\rho)}{\gamma+\mu}\lambda + \mu(\beta(1-\rho) - \gamma + \mu)\right) = 0$. You should take note of the fact that both the coefficients $\frac{\mu\beta(1-\rho)}{\gamma+\mu}$ and $\mu(\beta(1-\rho) - \gamma - \mu)$ are positive. The following Eigenvalues are obtained by solving the equation above: λ_1 and

$$\lambda_2 = -\frac{\mu\beta(1-\rho)}{\gamma+\mu} \pm \sqrt{\frac{\mu^2\beta^2(1-\rho)^2}{(\gamma+\mu)^2} - 4\mu(\beta(1-\rho) - \gamma - \mu)} \tag{4.55}$$

$$= -\mu R_v \pm \sqrt{\mu^2 R_v^2 - 4\mu(\gamma+\mu)(R_v - 1)}. \tag{4.56}$$

Due to the fact that $\mu(\beta(1-\rho) - \gamma - \mu)$ is positive, the quantity under the square root is either less than or higher than $\mu^2 R_v^2$. If this is the case, $\mu^2 R_0^2 < 4\mu(\beta - \gamma - \mu)$, then the Eigenvalues have a complex real part ($\frac{\mu\beta(1-\rho)}{\gamma+\mu}$, which is negative), and this is why the

Eigenvalues are negative. If not, the square root's absolute value must be less than $\mu^2 R_v^2$, although the real part of the Eigenvalue would still be negative. In any case, since both of the real components of the Eigenvalues are negative as well as λ_1, we draw the conclusion that the EE point is stable. It demonstrates that the EE point is LAS, which means that in either scenario, both the susceptible and infected population would survive. It is also evident that the vaccination parameter has helped to lower the infection rate. Building a Lyapunov function allows one to demonstrate the GAS of the EE point and DFE point. We build the Lyapunov function $V : \Omega \to R, V(s,i,v) = +v(t)s(t) + i(t)$ to demonstrate the DFE point's overall stability. The time derivative of the Lyapunov function V is then supplied.

$$\begin{aligned}
V(s,i,v) &= s(t) + i(t) + v(t) = (1-\rho)\mu - \mu s - (\mu+\gamma)i. \\
&= (\mu+\gamma)\left(\frac{(1-\rho)\mu}{\gamma+\mu} - \frac{\mu s}{\gamma+\mu} - i\right) && (4.57)\\
&= (\mu+\gamma)\left(\frac{\beta(1-\rho)\mu}{\beta(\gamma+\mu)} - \frac{\beta\mu s}{\beta(\gamma+\mu)} - i\right) && (4.58)\\
&= (\mu+\gamma)\left(\frac{R_v\mu}{\beta} - \frac{R_0\mu s}{\beta} - i\right) && (4.59)\\
&= \left(\frac{\mu+\gamma}{\beta}\right)(R_v\mu - R_0\mu s - \beta i) && (4.60)
\end{aligned}$$

Accordingly, if $R_v < 1$, then $V(s,i,v) < 0$, and the DFE point is GAS, at

$$(1-\rho, 0, v), V(s,i,v) = 0. \tag{4.61}$$

So, according to LIP, GAS is the DFE point. We create the Lyapunov function $L : \Omega_+ \to R$, where $\Omega_+ = s,i,v \in \Omega : S > 0, I > 0, v > 0$ and is supplied by

$$L(s,i,v) = W_1\left(s - s^* \ln\left(\frac{s}{s^*}\right)\right) + W_2\left(i - i^* \ln\left(\frac{i}{i^*}\right)\right) + W_3\left(v - v^* \ln\left(\frac{v}{v^*}\right)\right)$$

where W_1, W_2 and W_3 are positive constants to be chosen letters. Then

$$\begin{aligned}
\frac{dL}{dt} &= \frac{dL}{ds}\frac{ds}{dt} + \frac{dL}{di}\frac{di}{dt} + \frac{dL}{dv}\frac{dv}{dt} \\
&= W_1\left(\frac{ds}{dt} - s^*\left(\frac{s^*}{s}\right)\left(\frac{1}{s}\right)\frac{ds}{dt}\right) + W_2\left(\frac{di}{dt} - i^*\left(\frac{i^*}{i}\right)\left(\frac{1}{i}\right)\frac{di}{dt}\right) + W_3\left(\frac{dv}{dt} - v^*\left(\frac{v^*}{v}\right)\left(\frac{1}{v}\right)\frac{dv}{dt}\right) \\
&= W_1\left(\frac{s-s^*}{s}\frac{ds}{dt}\right) + W_2\left(\frac{i-i^*}{i}\frac{di}{dt}\right) + W_3\left(\frac{v-v^*}{v}\frac{dv}{dt}\right) \\
&= W_1(s-s^*)\left(\frac{(1-\rho)\mu}{s} - \beta i - \mu\right) + W_2(i-i^*)(\beta s - \mu - \gamma) + W_3(v-v^*)\left(\frac{\rho\mu}{v} - \mu\right)
\end{aligned}$$

Considering the equilibrium point, we have get the following result

$$\beta i^* = \gamma + \mu \text{ and } v^* = \rho \tag{4.62}$$

and putting the values equation (4.62) in the above equation, we obtain

$$\frac{dL}{dt} = -\mu W_1(1-\rho)\frac{(s-s^*)^2}{ss^*} + \beta(W_2 - w_1)(i-i^*)(s-s^*) - w_3\mu(v-v^*)^2$$

For $W_1 = W_2 = W_3 = 1$ then $\frac{dL}{dt} = -\mu(1-\rho)\frac{(s-s^*)^2}{ss^*} - \mu(v-v^*)^2 \leq 0$ and if $s = s^*$ and $v = v^*$ then $\frac{dL}{dt} = 0$. Hence, by LIP, the EE point is GAS in the interior of Ω_1.

4.3 Numerical Simulation and Discussion

In our simulation, with time measured in days, the susceptible individual (S) is represented by the color blue, the infected person (I) by the color green, and the recovered individual (R) by the color red. We select the following parameter values: We used $\mu = 0.5, \beta = 1.5, \gamma = 0.5$, and the EE point is $(0.6667, 0.1667)$ in fig. (4.3). The infection rate ($\beta = 1.5$) in Figure (4.7) has the effect of decreasing the suscibtable population to a lower level. We gradually raised the infection rate ($\beta = 2$) and observed a drop to a lower level in the susceptible population. The EE point in Fig.(4.4) is at $(0.5000, 0.2500)$. In Figure (4.5), the EE point that corresponds to beta = 2.5 is $(0.4000, 0.3000)$. In Figure e(4.6), the EE point for the value of $\beta = 3$ is shown as $(0.3333, 0.3333)$. The demographic dynamics are depicted in the aforementioned figures. The presence of infection causes the susceptible population to drop to half its previous level, and the infection causes a quick increase in the infected population. The infected population steadily grows while the susceptible population gradually shrinks as the infection rate rises; at $\beta = 3$, the infected population outnumbers the susceptible population. The contact rate has a significant impact on the disease's ability to spread throughout the community, as this graph also shows. As would be assumed logically, if the observed contact rate is high, the rate of infection with the disease will also be high without vaccination. We now choose the parameter values as $\mu = 0.5, \beta = 3$, and $\gamma = 0.5$, and also add the parameter $\rho = 0.67$ as a vaccination rate for the model triggered with vaccine. In the illustration in Fig. (4.6), the EE point corresponding to $\beta = 3$ is $(0.3333, 0.0017, 0.6700)$. According to Fig.(4.7), a vaccination

would be effective then the number of infections to change from increasing to decreasing after the final dosage of the vaccine was provided.

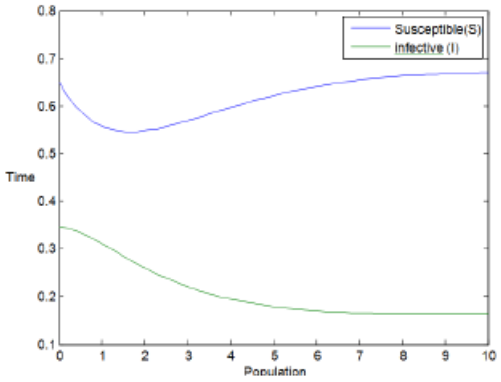


Figure 4.3: SIR model with $\beta = 1.5$

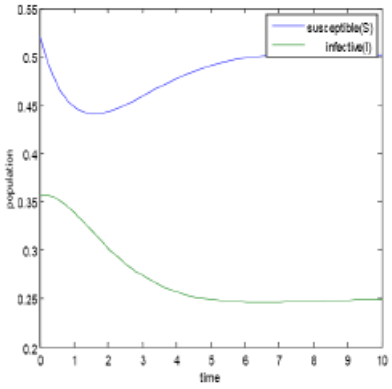


Figure 4.4: SIR model with $\beta = 2$

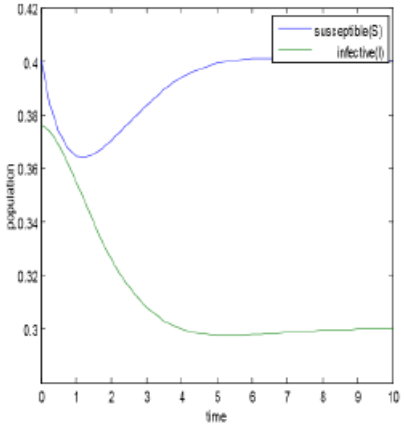


Figure 4.5: SIR model with $\beta = 2.5$

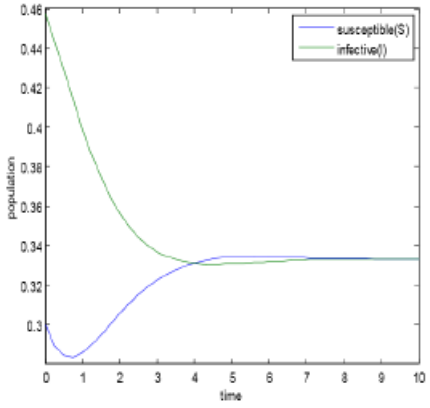


Figure 4.6: SIR model with $\beta = 3$

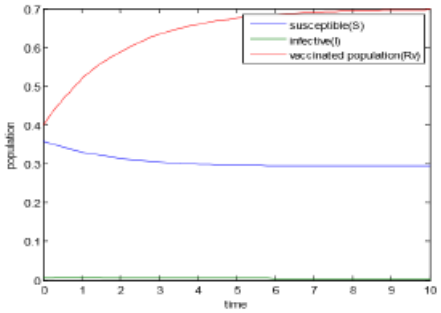


Figure 4.7: SIRV model with $\beta = 2.5$

4.4 Conclusion

Due to vaccination, the susceptible population declines to a lesser extent. The graph above shows that the initial effect of the vaccine is a considerable reduction in the peak number of infections, which is further evidenced by the fact that the infected population decreases significantly as a result of vaccination and the vaccinated population increases. The model clearly demonstrated that contact rates with sick people within a community play a significant role in how quickly a disease spreads. But the infected population quickly drops to a very low level when we introduce immunization to the susceptible group. Then, the disease exhibits the typical behavior of an endemic model in that it disappears below the threshold and transitions to a singular EE above the threshold.

Therefore, if the disease spread across the community in the absence of a vaccine, it would likewise do so once the vaccination campaign was over. The more serious the epidemic, the more intensive the interventions must be to dramatically lower the number of illnesses and fatalities. Unsurprisingly, if interventions are focused, the doses of vaccine required for control are lower. As a result, we can draw the conclusion that an epidemic can be prevented by vaccination and that the rate of infection and reproduction are crucial factors in its occurrence. As the infection rate rises, the susceptible population steadily declines as the infected population rises. The models we looked at indicated that the values of R_v and R_0 had a significant impact on the viability of controlling an epidemic or pandemic. If $R_0 > 1$, we anticipate that all paths in the domain will lead to the EE point based on

the results for the SIR models. Additionally, the vulnerable and infected population is also affected by the infection rate. As a result, we can draw the conclusion that the rate of infection and the number of reproductions are crucial factors in the emergence of an epidemic, which can be stopped by vaccination. As the infection rate rises, the susceptible population steadily declines as the infected population rises but the infected population quickly drops to a very low level when we introduce immunization to the susceptible group. The disease then exhibits the typical behavior for an endemic model, dying out below the threshold and moving to a singular EE over the threshold. Due to vaccination, the susceptible population declines to a lesser extent. The graph above shows that the peak number of infections has greatly decreased as a direct result of the vaccine, along with a considerable decrease in the infected population owing to vaccination and an increase in the population that has received the vaccine.

According to the concept, a population's contact rates with sick people play a significant role in how quickly a disease spreads. As a result, the disease would spread throughout the community once the vaccination was administered, just as it would have done in the absence of the vaccine. As a result, we can draw the conclusion that the rate of infection and the number of reproductions are crucial factors in the emergence of an epidemic. This epidemic can be stopped by vaccination, and the models discussed above are highly helpful in stopping epidemics in a particular population. To dramatically reduce the number of infections and fatalities, interventions must be more extensive the more serious the epidemic. It should come as no surprise that tailored interventions result in decreased immunization requirements for control. In the study of infectious diseases, epidemic modeling is becoming a more vital tool. Three classes-susceptible, infected, and recovered-are used to categorize the entire population in the SIR model. A state without infection and an endemic state are the two equilibrium states of the model. Numerous mathematical analyses and applications to particular diseases have been made of several models for the spread of infectious diseases in populations.

In underdeveloped nations, there are numerous diseases that exist, including COVID-19,

influenza, HINI, dengue, Ebola, and many others more specifically, the higher the value of R_v or R_0) and inform pupils on the SIR paradigm for preventing infectious diseases. Promote the engagement of the health minister in the use of mathematical modeling to combat infectious diseases.

Chapter 5

ANALYSIS OF MATHEMATICAL MODEL OF MALARIA TRANSMISSION IN FIVE DIMENSIONS

5.1 Formulation of Mathematical Model

In this section of the thesis, we analyze the mathematical model of malaria transmission in five compartments. Populations of people and mosquitoes are categorized into classifications that include vulnerable, incubating, infectious, and immune individuals. Let S_h stands for susceptible humans, I_h for infectious humans, R_h for immune humans, S_v for susceptible mosquitoes, and I_v for infectious mosquitoes, with the entire human population and the total mosquito population, respectively, provided by $N_h(t)$ and $N_v(t)$ at time t. Due to their short life cycle, mosquitoes never recover from infection. The mosquito population has barely recovered in this recovery class. In each of the five classifications, there occurs a natural death. There is no vertical transmission of malaria, and all newborns are vulnerable to infections. In other words, neither from mosquito to mosquito nor

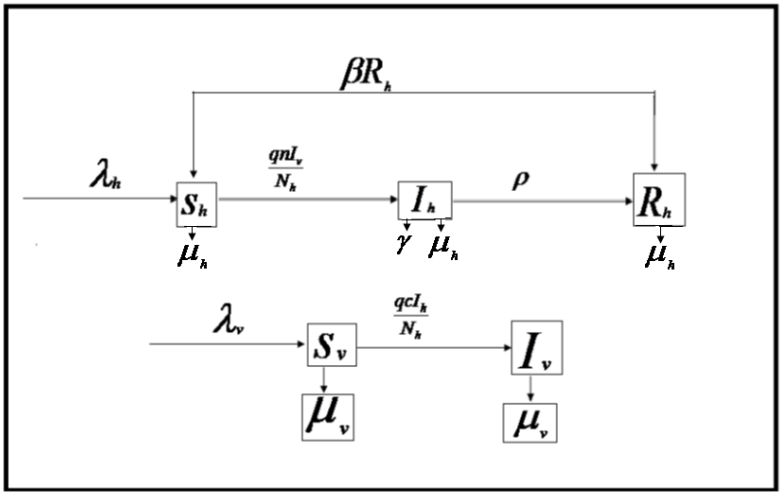
from human to human transmission of malaria exists. Both people and mosquitoes have varying populations overall. The human host that is recovering has a transient immune system that can be compromised and is vulnerable to reinfection. The immunological class is not a part of the model's mosquito component. Regardless of their infection condition, mosquitoes bite human hosts. We disregard the fact that an infected human host is being bitten by an infected female mosquito. When disease-carrying mosquitoes bite their human hosts, malaria is first spread. Let q be the average daily biting rate of a single mosquito on humans, n be the percentage of bites that result in infection, and c be the likelihood that a mosquito will become infected. β represents the per capita rate of immunity loss in human hosts, while ρ represents the rate of immunity acquisition in human hosts. The per capita mortality rate of malaria-infected human hosts is γ, whereas the per capita birth rates of humans and mosquitoes are λ_h and λ_v and the per capita mortality rates of humans and mosquitoes are μ_h and μ_v, respectively. The terms $\frac{qnI_vS_h}{N_h}$ and $\frac{qnI_hS_v}{N_h}$ in the model indicate the rate at which S_h get infected by I_v and $\frac{qnI_hS_v}{N_h}$ indicates the rate at which S_v become infected by I_h, respectively. It is crucial to keep in mind that the amount of N_h accessible per unit of I_v affects the pace at which S_h is infected by I_v. Assume that the μ_h, μ_v, q, n, λ_h, λ_v,β and ρ variables all have positive values. Using the schematic picture (5.1) as a starting point, apply the assumptions, define the state variables, parameters, and terms, and then design the human host-vector host differential equation as shown below to represent the dynamics of malaria transmission in the mosquito and human populations.

$$\begin{aligned}
\frac{dS_h}{dt} &= \lambda_h N_h + \beta R_h - \mu_h N_h - \frac{qnI_vS_h}{N_h} && (5.1)\\
\frac{dI_h}{dt} &= \frac{qnI_vS_h}{N_h} - (\rho + \gamma + \mu_h) I_h. && (5.2)\\
\frac{dR_h}{dt} &= \rho I_h - (\mu_h + \beta) R_h && (5.3)\\
\frac{dS_v}{dt} &= \lambda_v N_v - \mu_v S_v - \frac{cqI_hS_v}{N_h} && (5.4)\\
\frac{dI_v}{dt} &= \frac{qcS_vI_h}{N_h} - \mu_v I_v. && (5.5)
\end{aligned}$$

with positive initial condition

$$\begin{cases} S_h(0) = S_{0h}, I_h(0) = I_{0h}, R_h(0) = R_{0h}, \\ S_v(0) = S_{0v}, I_v(0) = I_{0v}. \end{cases} \tag{5.6}$$

Figure 5.1: The schematic of the mathematical model in five compartment



(5.7) can be used to calculate the overall population sizes N_h and N_v:

$$N_h = S_h + I_h + R_h \text{ and } N_v = S_v + I_v. \tag{5.7}$$

Alternatively from the equation from (5.1)-(5.3), we have the following result.

$$\begin{aligned}
\frac{dN_h}{dt} &= \lambda_h N_h + \beta R_h - \mu_h N_h - \frac{qnI_v S_h}{N_h} + \frac{qnI_v S_h}{N_h} && (5.8)\\
&- (\rho + \gamma + \mu_h) I_h + \rho I_h - (\mu_h + \beta) R_h && (5.9)\\
&= (\lambda_h - \mu_h) N_h - \gamma I_h. && (5.10)
\end{aligned}$$

Now we have derived equation (5.11) from the equation (5.4)-(5.5).

$$\begin{aligned}
\frac{dN_v}{dt} &= \lambda_v N_v - \mu_v S_v - \frac{cqI_h S_v}{N_h} + \frac{qcS_v I_h}{N_h} - \mu_v I_v && (5.11)\\
&= \lambda_v N_v - \mu_v S_v - \mu_v I_v && (5.12)\\
&= \lambda_v N_v - (S_v + I_v)\mu_v && (5.13)\\
&= (\lambda_v - \mu_v) N_v && (5.14)\\
\frac{dN_v}{dt} &= (\lambda_v - \mu_v) N_v. && (5.15)
\end{aligned}$$

Given that $\frac{dN_h}{dt} = (\lambda_h - \mu_h)N_h - \gamma I_h$ and $\frac{dN_v}{dt} = \lambda_v - \mu_v)N_v$, we have get

$$\begin{cases} \frac{dN_h}{dt} = (\lambda_h - \mu_h) N_h - \gamma I_h. \\ \frac{dN_v}{dt} = (\lambda_v - \mu_v) N_v. \end{cases} \tag{5.16}$$

5.2 The existence of the solution

Theorem 5.2.1. *For each $t > 0$, the equations* (5.1) *to* (5.5)*, and* (5.6) *in the feasible domains have positive solutions that remain positive in equation* (5.38)*.*

Proof. The equations for normalized quantities are what we are interested in. In addition, analyzing our model in terms of quantities' proportions rather than population numbers is simpler. This may be accomplished by simplifying the equations from equations (5.18)-(5.30) and scaling the population as in

$$s_h = \frac{S_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, s_v = \frac{S_v}{N_v}, i_v = \frac{I_v}{N_v}, \ell = \frac{N_v}{N_h}. \tag{5.17}$$

$$\begin{aligned}
\frac{ds_h}{dt} &= \frac{d}{dt}\left(\frac{S_h}{N_h}\right) = \frac{1}{N_h}\frac{dS_h}{dt} - \frac{s_h}{N_h}\frac{dN_h}{dt} && (5.18)\\
&= \lambda_h - qn\ell i_v s_h + \beta r_h - \mu_h s_h - s_h\left(\lambda_h - \gamma i_h - \mu_h\right) && (5.19)\\
&= \lambda_h + \beta r_h + i_h\gamma s_h - \left(\lambda_h + qn\ell i_h\right) s_h && (5.20)\\
\frac{di_h}{dt} &= \frac{d}{dt}\left(\frac{I_h}{N_h}\right) = \frac{1}{N_h}\frac{dI_h}{dt} - \frac{i_h}{N_h}\frac{dN_h}{dt} && (5.21)\\
&= \left(\lambda_h + \mu_h\right) i_h + \gamma i_h^2 + nq\ell i_v s_h - \left(\rho + \gamma + \lambda_h\right) + qn\ell i_v s_v && (5.22)\\
&= nq\ell i_v s_h + \gamma i_h^2 - \left(\lambda_h + \gamma + \rho\right) i_h && (5.23)\\
\frac{dr_h}{dt} &= \frac{d}{dt}\left(\frac{R_h}{N_h}\right) = \frac{1}{N_h}\frac{dR_h}{dt} - \frac{r_h}{N_h}\frac{dN_h}{dt} && (5.24)\\
&= \rho i_h + r_h\mu_h + \gamma i_h r_h - \left(\lambda_h + \mu_h\right) r_h && (5.25)\\
&= \rho i_h + \gamma i_h r_h - \left(\beta + \lambda_h\right) r_h && (5.26)\\
\frac{ds_v}{dt} &= \frac{d}{dt}\left(\frac{S_v}{N_v}\right) = \frac{1}{N_v}\frac{dS_v}{dt} - \frac{s_v}{N_v}\frac{dN_v}{dt} && (5.27)\\
&= \lambda_v + s_v\mu_v - s_v\lambda_v - \mu_v s_v - qci_h s_v && (5.28)\\
&= \lambda_v - \left(qci_h + \lambda_v\right) s_v && (5.29)\\
\frac{di_v}{dt} &= \frac{d}{dt}\left(\frac{I_v}{N_v}\right) = \frac{1}{N_v}\frac{dI_v}{dt} - \frac{i_v}{N_v}\frac{dN_v}{dt} && (5.30)\\
&= qcs_v i_v + i_v\mu_v - i_v\lambda_v - \mu_v i_v && (5.31)\\
&= qci_v s_h - \lambda_v i_v && (5.32)
\end{aligned}$$

subject to the restrictions as the following (5.33)

$$\begin{cases} s_h + i_h + r_h = 1 \\ s_v + i_v = 1. \end{cases} \tag{5.33}$$

The system equation does not contain the variables N_h and N_v, as is to be noted. Utilizing the relations

$$\begin{cases} r_h = 1 - s_h + i_h \\ s_v = 1 - i_v \end{cases} \tag{5.34}$$

led to the study of the equation system below.

$$\frac{ds_h}{dt} = \beta + \lambda_h + \gamma i_h s_h - \beta i_h - (\lambda_h + qn\ell i_v + \beta + i_h)\, s_h \tag{5.35}$$

$$\frac{di_h}{dt} = \ell qn i_v + (\gamma i_h - (\gamma + \lambda_h + n))\, i_h \tag{5.36}$$

$$\frac{di_v}{dt} = cqi_h - (cqi_h + \lambda_v)\, i_v \tag{5.37}$$

The model makes epidemiological sense in that region, which is practicable, according to the field

$$\Omega = \left\{(s_h, i_h, i_v) \in R_+^3\right\} \tag{5.38}$$

where $0 \leq s_h \leq 1, 0 \leq i_h \leq 1$, and $0 \leq i_h \leq 1$ are proven to be positive invariant with regard to the (5.35) - (5.37), where R_+^3 includes its lower dimensional faces. We use the symbols $\partial\Omega$ in (5.38), to signify the border and interior of (5.38).

Suppose there exist $t_1 > 0$ such that $S_h(t_1) = 0, S_h^{'}(t_1) \leq 0$ and $S_h, I_h, R_h, S_v, I_v > 0$ for $0 < t < t_1$. Then from system equation (5.1), we have get

$$\frac{dS_h}{dt} = \lambda_h N_h + \beta R_h - \mu_h N_h - \frac{qnI_v S_h}{N_h} \tag{5.39}$$

$$= \lambda_h N_h(t_1) + \beta R_h(t_1) > 0 \tag{5.40}$$

which is an inconsistency. Therefore, $S_h(t) > 0$. System equation (5.2)

$$\Rightarrow \quad \frac{dI_h}{dt} = \frac{qnS_h}{N_h} - (\rho + \gamma + \mu_h)\, I_h \tag{5.41}$$

$$\Rightarrow \quad \frac{dI_h}{I_h} \geq -(\mu_h + \beta + \rho)\, dt \tag{5.42}$$

$$\Rightarrow \quad I_h(t) \geq I_{0h} e^{-(\mu_h + \beta + \rho)t} \tag{5.43}$$

$$\Rightarrow \quad I_h(t) > 0. \tag{5.44}$$

Hence, $I_h(t) > 0$. System equation (5.3)

$$\Rightarrow \quad \frac{dR_h}{dt} = \rho I_h - (\mu_h + \beta) R_h \tag{5.45}$$

$$\Rightarrow \quad \frac{dR_h}{R_h} \geq -(\mu_h + \beta) R_h \tag{5.46}$$

$$\Rightarrow \quad R_h(t) \geq R_{0h} e^{-(\mu_h+\beta)t} \tag{5.47}$$

$$\Rightarrow \quad R_h(t) > 0. \tag{5.48}$$

Therefore, $R_h > 0$. System equation (5.4)

$$\Rightarrow \quad \frac{dS_v}{dt} = \lambda_v N_v - \mu_v S_v - \frac{cqI_h S_v}{N_h} \tag{5.49}$$

$$\Rightarrow \quad \frac{dS_v}{S_v} \geq -(\mu_v + \frac{cqI_h}{N_h})dt \tag{5.50}$$

$$\Rightarrow \quad S_v(t) \geq S_{0v} e^{-(\mu_v + \frac{cqI_h}{N_h})t} \tag{5.51}$$

$$\Rightarrow \quad S_v(t) > 0. \tag{5.52}$$

Hence, $S_v > 0$, and from (5.5) we have get $I_v(t) > 0$. Therefore, the feasible solution set which is positively invariant set of (5.1)-(5.5) is in Ω.

5.3 Equilibrium points and local stability analysis

The model is qualitatively examined in this section to take into account the persistence and stability of its associated equation. Each and every parameter should be non-negative. We solve equations by setting the right sides of equations(5.35) to equation (5.37) to zero. The resulting arrangement is

$$\begin{cases} \beta + \lambda_h + \gamma i_h s_h - \beta i_h - (\lambda_h + qn\ell i_v + \beta + i_h)\, s_h = 0 \\ \ell qn i_v + (\gamma i_h - (\gamma + \lambda_h + n))\, i_h = 0 \\ cqi_h - (cqi_h + \lambda_v)\, i_v = 0. \end{cases} \tag{5.53}$$

In the absence of infection, the model is in a stable state. This state, which we'll refer to as the DFE point E_0 is $(1, 0, 0)$. The Jacobian of (5.53) is determined at E_0 to establish the stability of this equilibrium. On the basis of the Jacobian's eigenvalue's signs, the local steadiness of E_0 is calculated. If all of these eigenvalues' real components are negative,

the equation E_0 is said to be locally steady. The Jacobian matrix is the following when the model is in its stable position:

$$J_E = \begin{pmatrix} -(\lambda_h + \beta + qn\ell i_v - \gamma i_h) & -\beta + \gamma s_h & -qn\ell s_h \\ qn\ell i_v & -G_\Omega + 2\gamma i_h & qn\ell s_h \\ 0 & qc - qci_v & -(qci_h + \lambda_v) \end{pmatrix} \tag{5.54}$$

Calculating (5.54) at the equilibrium point, $(s_h, i_h, i_v) = (1, 0, 0)$, we have

$$J_E = \begin{pmatrix} -(\lambda_h + \beta) & -\beta + \gamma & -qn\ell \\ 0 & -G_\Omega & qn\ell \\ 0 & qc & -\lambda_v \end{pmatrix} \tag{5.55}$$

The eigenvalues of (5.55) are provided by (5.56), where $G_\Omega = \rho + \lambda_h + \gamma$

$$\frac{(\lambda_v + G_\Omega) \pm \sqrt{4G_\Omega\lambda_v R_0 - 4G_\Omega\lambda_v + (\lambda_v + G_\Omega)^2}}{2} \text{ and } -\beta - G_\Omega \tag{5.56}$$

Let's define R_0, also known as the reproductive number of the model equations (5.1) to equation (5.5), as $R_0 = \frac{q^2 n\ell c}{G_\Omega \lambda_v}$. If $R_0 < 1$, then the two eigenvalues have negative values. It aids in the understanding of the malaria infection since it identifies the prerequisite for the development of the disease. In the event when $R_0 < 1$, the DFE point is locally steady. The EE point $E_1 = (s_h, i_v, i_h)$ must satisfy the conditions $i_h > 0, i_v > 0$ and $s_h > 0$ in order to survive and be considered exceptional. Then by adding the system of equations (5.53), then we have get $(\beta + \lambda_h - \gamma i_h)(1 - s_h - i_h) + (qc - \rho)i_h - (qci_h + \lambda_v)\, i_v = 0$. Since $qci_h - (\lambda_v + qci_h)\, i_v = 0$ then we get the following

$$(1 - s_h - i_h)(\beta + \lambda_h - \gamma i_h) = \rho i_h. \tag{5.57}$$

Since $(1 - s_h - i_h) > 0$ and from $\gamma i_h < \lambda_h + \beta$, then we have get $i_h < \frac{\beta + \lambda_h}{\gamma}$. Consequently, an endemic equilibrium point be real, where i_h lies in the interval $\left(0, \min\left\{1, \frac{\beta+\lambda_h}{\gamma}\right\}\right)$ The assumption that $\gamma < \lambda_h + \beta$ is significant important and plays a immense role when malaria persists. It demonstrates that the death rate caused by malaria should be below the point at which the vulnerable human population is replenished as a result of births and the loss of malaria resistance. The preservation of matrices migrate toward the Stein citation in order

to analyze the constancy of the endemic equilibrium. The second additive matrix, which may be calculated from the Jacobian matrix J_E, is represented by the equation (5.58).

$$\begin{pmatrix} -D+3\gamma i_h & qn\ell s_h & qn\ell s_h \\ qc(1-i_v) & -N+\gamma i_h & \gamma s_h-\beta \\ 0 & qn\ell i_v & -Q+2\gamma i_h \end{pmatrix} \text{ where } \begin{cases} N=\beta+qci_h+\lambda_h+qn\ell i_v+\lambda_v \\ Q=G_\Omega+qci_h+\lambda_v \\ D=\lambda_h+G_\Omega+\beta+qcn\ell i_v \end{cases} \tag{5.58}$$

Suppose that N is a 3×3 real matrix. Each and every eigenvalue of N has a negative real component if $tr(N), det\left(N^{[2]}\right)$, and $det(N)$ are all negative.

Proof. We have the following outcome as a result of the Jacobian matrix J_E.

$$\begin{aligned} \mathrm{tr}(J_E) &= 2\gamma i_h - G - qci_h + \gamma i_h - \beta - \lambda_h - qn\ell i_v & (5.59)\\ &= 3\gamma i_h - (G + qci_h + \beta + \lambda_h + qn\ell i_v) < 0. & (5.60) \end{aligned}$$

We have obtained the following from the Jacobian matrix of the system (5.53)

$$\begin{cases} \frac{\beta+(1-\beta)i_h+\lambda_h}{s_h} = \beta+\lambda_h+qn\ell i_v-\gamma i_h \\ \frac{-qn\ell i_v s_h}{i_h} = \gamma i_h - G_\Omega \\ \frac{qci_h(-i_v+1)}{i_v} = \lambda_v \end{cases} \tag{5.61}$$

The equation (5.54) then has the following predetermined determinant.

$$= \begin{vmatrix} \gamma i_h - (qn\ell i_v + \beta + \lambda_h) & -\beta + \gamma s_h & -qn\ell s_h \\ qn\ell i_v & 2\gamma i_h - G_\Omega & qn\ell s_h \\ 0 & qc(-i_v + 1) & -(qci_h + \lambda_v) \end{vmatrix} \tag{5.62}$$

$$= \begin{vmatrix} \beta(-i_h + 1) + \lambda_h + \eta i_h & \gamma s_h - \beta & -qn\ell s_h \\ qn\ell i_v & \frac{\gamma i_h - qn\ell s_h i_v}{i_h} + \gamma i_h & qn\ell s_h \\ 0 & \frac{i_v \lambda_v}{i_h} & \frac{-qci_h}{i_v} \end{vmatrix} \tag{5.63}$$

$$= \left(q^2 n\ell c - \frac{qc\gamma i_h^2}{i_v s_h} - \frac{qn\ell\lambda_v i_v}{i_h} + q^2 n\ell c\right)(\lambda_h + \beta i_h + \beta(1 - i_h)) + \left(\frac{c(-\beta + \gamma s_h)}{s_h} - \frac{n\ell\lambda_v i_v^2}{i_h}\right)$$

$$= -\Psi\left(q^2 n\ell c - \frac{qc\gamma i_h^2}{i_v s_h} - \frac{qn\ell i_v \lambda_v}{i_h}\right) + q^2 n\ell s_h \left(\frac{c(-\beta + \gamma s_h) i_h}{s_h} - qn\ell c(1 - i_v)\right) \tag{5.64}$$

$$= -\Psi\left(q^2 n\ell c - \frac{qc\gamma i_h^2}{i_v s_h} - \frac{qc\ell\lambda_v i_v}{i_h}\right) + q^2 n\ell c s_h \left(\frac{(-\beta + \gamma s_h) i_h}{s_h} - qn\ell(1 - i_v) i_v\right) \tag{5.65}$$

$$= -\Psi\left(\frac{-qc\gamma i_h^2}{i_h s_h} + q^2 n\ell c i_v\right) + q^2 n\ell c s_h \left(\frac{(s_h - 1)(\beta + \lambda_h)}{s_h} + qn\ell i_v^2\right) \tag{5.66}$$

$$= \frac{qc}{i_v s_h}\left(qn\ell i_v^2 s_h - \gamma i_h^2\right) - q^2 n\ell c\left((1 - s_h)(\beta + \lambda_h) - qn\ell i_v^2 s_h\right) \tag{5.67}$$

$$= q^2 n\ell i_v(-\phi + qn\ell i_v s_h) + qc(\Psi\gamma i_h^2 - qn\ell i_v s_h)\frac{(\beta + \lambda_h)(1 - s_h)}{i_v s_h} \tag{5.68}$$

$$= -cq^2 n\ell i_v s_h(\beta + \lambda_h - \gamma i_h) + qc\left(\frac{\Psi\gamma i_h^2 - qni_v s_h(\beta + \lambda_h)(1 - s_h)}{i_v s_h}\right) \tag{5.69}$$

where $\Psi - \eta i_h + \lambda_h + \beta(1 - i_h)$ and since $\gamma < \beta + \lambda_h$ indicate that the determinant ofE_1 is negative. This illustrates how the determinant of the negative value of $J_{E_1}^{[2]}$ can be inferred from the additive matrix. Let *phi* be the diagonal matrix and E_1 be the endemic stability point's (s_h, i_h, i_v) value. Then

$$\phi J_{E_1}^{[2]} \phi^{-1} = \begin{pmatrix} 3\gamma i_h - D & qn\ell i_v s_h & qn\ell i_v \\ qc(1 - i_v)\left(\frac{i_h}{i_v}\right) & -\gamma i_h + D & (\gamma s_h - \beta) i_h \\ 0 & qn\ell\left(\frac{i_v s_h}{i_h}\right) & 2\gamma i_h - Q \end{pmatrix} \tag{5.70}$$

Then the matrix $J_{E_1}^{[2]}$ is stable iff the matrix $\phi J_{E_1}^{[2]} \phi^{-1}$ is steady by examining if the $\phi J_{E_1}^{[2]} \phi^{-1}$ is diagonally leading in rows, because its diagonal element are negative. Represent the

left hands part of $V(t)$ by $H_+(V(t))$, then we have obtained (5.71)

$$\begin{aligned} H_+(|u_1(t)|) &\leq (|u_3(t)| + qn\ell|u_2(t)|) + (-3\gamma i_h(t) + D)|u_1(t)| && (5.71)\\ &\leq \left(|u_3(t)| + \frac{i_h(t)}{i_v(t)}|u_2(t)|\right) qn\ell \frac{i_v(t)s_h(t)}{i_h(t)} + (-3\gamma i_h(t) + \beta)|u_1| && (5.72)\\ H_+(|u_{12}(t)|) &\leq (\gamma s_h(t))|u_2(t)| + (\gamma i_h - N)|u_2(t)| + qc(-i_v + 1)|u_1(t)| && (5.73)\\ H_+(|u_3(t)|) &\leq (2\gamma i_h - Q)|u_3(t)| + qn\ell i_v|u_2(t)| && (5.74) \end{aligned}$$

We also have the subsequent equation (5.75)

$$H_+\left(\frac{i_h}{i_v}|u_2(t)| + |u_2(t)|\right) = \frac{i_h}{i_v}H_+(|u_2(t)| + |u_3(t)|) + \left(\frac{i_h^{'}}{i_h} - \frac{i_v^{'}}{i_v}\right)\frac{i_h}{i_v}(|u_2| + |u_3|). \quad (5.75)$$

By adding equation (5.73) and (5.74), we have obtained equation (5.76)

$$\begin{aligned} H_+(|u_2(t)| + |u_3|) &= qc(1 - i_v)|u_1(t)| + (\gamma i_h + qn\ell i_v - N)|u_2(t)|(\eta - \beta + \gamma s_h + 2\gamma i_h - Q)|u_3(t)|\\ &= qc(1 - \lambda_v)|u_1(t)| - (\lambda_h + \lambda_v + qci_h + \beta - \gamma i_h)|u_2(t)| + \rho(1 - s_h - i_h)|u_3(t)|\\ &- (\lambda_h + \lambda_v + qci_h + \beta - \gamma i_h)\\ &\leq qc(1 - i_v)|u_1(t)| - (\lambda_h + \lambda_v + qci_h + \beta - \gamma i_h)(|u_2(t)| + |u_3(t)|). \quad (5.76) \end{aligned}$$

Substitute (5.76) into (5.75), then we have (5.77)

$$\begin{aligned} H_+\left(\frac{i_h(t)}{i_v(t)}\right)(|u_2(t)| + |u_3(t)|) &\leq \left(\frac{i_h(t)}{i_v(t)}\right)\left(\frac{i_h^{'}(t)}{i_v(t)} - \frac{i_v'(t)}{i_v(t)}\right)(|u_2(t)| + |u_3(t)|) + \frac{i_h(t)}{i_v(t)}\\ &\quad qc(1 - i_v)|u_1(t)| - (\lambda_h + \lambda_v + qci_h + \beta - \gamma i_h)(|u_2(t)| + |u_3(t)|)\\ &\leq qc(1 - i_v)\left(\frac{i_h(t)}{i_v(t)}\right)(|u_1(t)|) + \frac{i_h^{'}(t)}{i_v(t)} - \frac{i_v'(t)}{i_v(t)} - \lambda_h - \lambda_v\\ &- qci_h - \beta + \gamma i_h\frac{i_h(t)}{i_v(t)}(|u_2(t)| + |u_3(t)|). \quad (5.77) \end{aligned}$$

As of equation (5.71) and equation (5.77), we have obtained (5.78)

$$H_+(V(t)) \leq \sup(d_1(t), d_2(t))V(t) \quad (5.78)$$

in which we have the subsequent equation (5.79)

$$\begin{aligned} d_1(t) &= \frac{q\ell ci_v s_h}{i_h} + (3\gamma i_h - D) && (5.79)\\ d_2(t) &= qc(1 - i_v)\frac{i_h}{i_v} + \left(\gamma i_h - \lambda_h - \lambda_v - \beta + \frac{i_h^{'}(t)}{i_v^{'}(t)} - \frac{i_v^{'}(t)}{i_v^{'}(t)}\right). && (5.80) \end{aligned}$$

Using the following expression

$$\begin{cases} \frac{qn\ell i_h s_h}{i_v} = \rho + \lambda_h + \gamma - \gamma i_h + \frac{i_h^{'}(t)}{i_h(t)} \\ qc(1-i_v)\frac{i_h^{'}(t)}{i_h(t)} = \frac{i_v^{'}(t)}{i_v(t)} + \lambda_v \end{cases} \tag{5.81}$$

Equation (5.79) and equation (5.81) make simpler to the subsequent result

$$\begin{aligned} d_1(t) &= \frac{qn\ell i_v s_h}{i_h} - (G_\Omega + \lambda_h + qn\ell i_v + \beta - 3\gamma i_h) && (5.82)\\ &= \frac{i_h^{'}(t)}{i_h(t)} + G_\Omega - \gamma i_h - (G_\Omega + \lambda_h + qn\ell i_v + \beta) && (5.83)\\ &= (2\gamma i_h - \lambda_h - qn\ell i_v + \beta) + \frac{i_h^{'}(t)}{i_h(t)} \quad \text{and} && (5.84)\\ d_2(t) &= \frac{i_h^{'}(t)}{i_h(t)} - \frac{i_v^{'}(t)}{i_v(t)} - \lambda_h - \lambda_v + \gamma i_h - qci_h \\ &= \gamma i_h - \lambda_h - qci_h - \beta + \frac{i_h^{'}(t)}{i_h(t)} \ \text{ so that} && (5.85)\\ & \text{Sup}\{d_1(t), d_2(t)\} \leq \frac{i_h^{'}(t)}{i_h(t)} - \gamma. && (5.86) \end{aligned}$$

From equation (5.86), we have obtained the subsequent

$$\int_0^\infty \text{Sup}\{d_1(t), d_2(t)\}dt \leq [\ln(i_h(t))]_0^\infty - \gamma\omega < 0. \tag{5.87}$$

It is clear from this why the periodic solution(s_h, i_h, i_v) is asymptotically stable. As a result, it is proven that the disease's EE point is steady everywhere.

5.4 Global stablity annalysis

Theorem 5.4.1. *The disease free equilbrium(DFE) point is equal to* $(1, 0, 0)$*. If* $R_0 > 1$ *and the disease free equilbrium(DFE) point* $E_0 = (1, 0, 0)$ *is unstable. If* $R_0 \leq 1$*, then is e disease free equilbrium(DFE) point is equal to* $(1, 0, 0)$ *is globally asyptotically stable(GAS) in* Ω*.*

Proof. Consider the following Lyapunov function (5.88)

$$F = G_\Omega i_v + qci_h \text{ where } G_\Omega = \lambda_h + n + \gamma. \tag{5.88}$$

Its derivatives along the solution of equation (5.35) to equation (5.37) is

$$\begin{aligned} F^{'} &= qci_v\left(qn\ell s_h - G_\Omega i_h\right) + qci_h\left(\gamma i_h - G_\Omega\right) - G_\Omega(cqi_h + \lambda_v i_v) && (5.89)\\ &= qci_v(qn\ell s_h - i_h G_\Omega) + qc\gamma^2 i_h^2 - i_v\lambda_v G_\Omega && (5.90)\\ &= \lambda_v i_v G_\Omega\left(\frac{q^2 n\ell c s_h - G_\Omega\lambda_v}{\lambda_v G_\Omega}\right) + qci_h(\gamma i_h - i_v G_\Omega) && (5.91)\\ &= i_v\lambda_v G_\Omega(R_0 s_h - 1) - qci_h(i_v G_\Omega - \gamma i_h) && (5.92)\\ &\leq i_v\lambda_v G_\Omega(R_0 s_h - 1) \leq 0 \text{ if } R_0 \leq 1. && (5.93) \end{aligned}$$

It is demonstrated that $F^{'} \leq 0$ if $R_0 \leq 1$ and that $F' = 0$ when $R_0 = 1$ and $i_h = i_v = 0$. If $R_0 > 1$, then $F' > 0$ if s_h is sufficiently close to one except when $i_h = i_v = 0$. It is shown that $F^{'} \leq 0$ if $R_0 \leq 1$ and the fairness $F^{'} = 0$ when $R_0 = 1$ and $i_h = i_v = 0$. If $R_0 > 1$, then $F^{'} > 0$ when s_h is adequately close up to one excluding when $i_h = i_v = 0$. According to the Layapunov-Lasalle's theorem, which is cited by [52], this implies that all directions in G_Ω move toward the primary positive invariant subset of the set where we get the following

$$G_\Omega^{'} = 0 \text{ is } \{(s_h, i_h, i_v) \in G_\Omega / G_\Omega^{'} = 0\} \tag{5.94}$$

on the boundary of G_Ω where i_h and i_v are zero that means in s_h- axis, $s_h^{'} = (\lambda_h)(1 - s_h)$ so that $s_h = \left(1 + e^{-(\lambda_h)t}\right) \to 1$ as $t \to \infty$. The disease-free equilibrium point $(1, 0, 0)$ will be approached by all paths found in the G_Ω solution space. As a result, the equilibrium point that is free of infection is GAS, which makes the theorem complete. It is widely known that the reproductive number depends on the product of the spread coefficients $qn\ell$ and qc, the standard residence time of the infective group $(\rho + \lambda_h + \gamma)^{-1}$, and the standard lifespan of the mosquito λ_v^{-1}. Being rid of the resistance loss rate, R_0, is an important point to remember. The concern of an infection can, however, be raised by greater values of ℓ and q. This suggests that even in cases when malaria does not cause disease resistance and there isn't a vaccine yet, the available tools can be effectively employed to control the disease. In the event that $R_0 \leq 1$, the DFE point E_0 is GAS. That is how the infected mosquito, humans, and infection ultimately vanish.

5.5 Sensitivity analysis and simulation

We applied our model to simulate malaria cases, and the results are shown in Fig. eqref11, which indicates that the reported malaria case cost less than 2000. In 2016, there were over 15 million instances reported in [24], starting in the years 2000 – 2006. Table (5.1), lists all the parameter values for our model. According to these parameter values, we carried out numerical simulations of our model and obtained a suitable fitting between the infected human of model (5.1)-(5.5) and the malaria reported cases of WHO, from 2007 – 2016, as shown in Figures (5.5) (a) and (5.5)(b). The parameter settings in Table (5.1) were used to simulate the model compartments in Figure (5.5)(a). In addition, Figure (5.5)(b) shows how the initial size of mosquitoes that are sensitive affects the frequency of human malaria cases. er of human malaria cases in Figure (5.5)(b). The disease is endemic, and the estimated basic reproduction number is 4.5589, according to the information given. With parameter values from Table (5.1), Figures (5.5)(a) and (5.5)(b) demonstrate the solution of the model (5.1)-(5.5). We utilized sensitivity analysis to evaluate the effects of the model parameter values used. This study offers information on the model parameters that have a substantial impact on the theoretical model of malaria transmission in terms of the basic reproduction rate. The normalized forward sensitivity index of a variable to a parameter is what we utilize to conduct this study. A variable's normalized forward sensitivity index, which measures how differently a variable r depends on a parameter s, is defined as follows:

$$\gamma_r^s = \frac{\partial r}{\partial s}.\frac{s}{r}. \tag{5.95}$$

In Table (5.2), the sensitivity indices based on the computed are listed in detail. The parameters are arranged so that the largest sensitive parameter is at the top of the list, followed by the lowest. The most sensitive parameters in Table (5.2) are the mosquito biting rate, natural death rate of humans, loss of immunity rate for humans, recovery rate of humans, transmission rate in humans, transmission rate in mosquitoes, and natural death rate of mosquitoes$\left(n, \mu_h, \rho, \mu_v, \frac{qnI_hS_h}{N_h}, \frac{qnI_hS_v}{N_h}\right)$. The least sensitive parameter is ℓ. At the EE for models (5.1)-(5.5). If the value of n is reduced to 0.087 or less while maintaining the same values for the other variables, then $R_0 < 1(0.9916)$ holds true. If we changed ρ value from 3.5×10^{-5} to 7.9×10^{-5} then $R_0 < 1$, or R_0, would be reduced from 4.5589 – 0.9978.

If the value of $\frac{qnI_hS_h}{N_h}$ is set to 0.023, but the other parameters remain the same, then $R_0 < 1$ will be the result. If 0.023 is used as the value for $\frac{qnI_hS_h}{N_h}$ and all other parameters remain the same, then $R_0 < 1$.

Table 5.1: State variables for the model in five compartements

Variables	Description	Values	Reference
μ_h	per capita normal passing away speed of human being	4.7×10^{-5}	[103]
μ_v	per capita normal passing away speed of mosquitoes	0.1	[24]
β	The speed of defeat of resistance	2.74×10^{-3}	[25]
γ	The death rate of human induced by the disease	9.74×10^{-3}	[25]
ρ	The recovery rate of human	3.5×10^{-3}	[24]
$\frac{qnI_hS_h}{N_h}$	The transmission rate in human	0.048	[25]
$\frac{qnI_hS_v}{N_h}$	The transmission rate in mosquitoes	0.48	[25]

Table 5.2: Sensitivity analysis

Parameter	sensitive index
μ_h	-0.75
μ_v	-0.5
n	1
ρ	0.59
$\frac{qnI_hS_h}{N_h}$	0.5
$\frac{qnI_hS_v}{N_h}$	0.5
ℓ	0.5

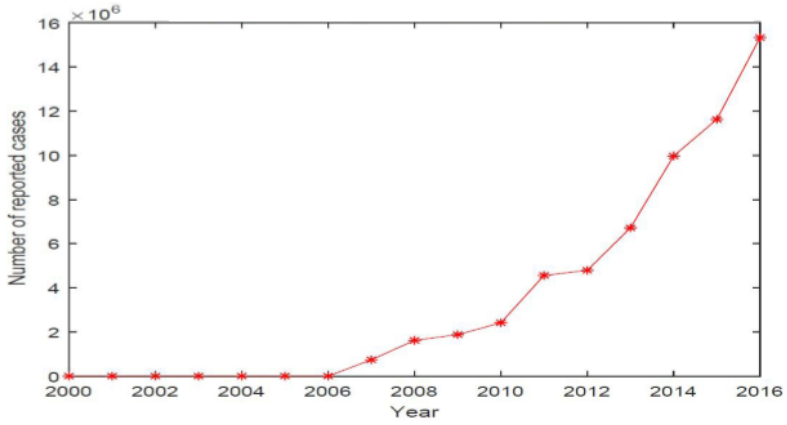


Figure 5.2: Description suitcases of malaria from WHO

5.6 Discussion and Conclusion

We examined a three-dimensional, two-dimensional model that included $S_hI_hR_h$ in a human host and S_vI_v.The typical incidence for the dynamics of malaria in people and mosquitoes, in which immunity declines to the disease refills the reservoir of the susceptible humans. After adding the appropriate inhabitants, the model was revised. The model variables are used to identify the reproductive number. The rate of immunity has no bearing on the reproductive number. The illness-free equilibrium point is unstable if $R_0 > 1$, and it is globally unstable if $R_0 \leq 1$; in contrast, the equilibrium point for the existence of the disease emerges as a singular position where reinvention is always feasible and the sickness never goes away. Since there are currently no effective vaccines against malaria, the methods at hand can be utilized to control it as malaria-induced protection gradually wears off over time. These could be depending on the porch quantity R_0 specifications. The intervention techniques must concentrate on treatment and lowering the content between mosquito and human in order to lower the reproduction number to less than one. Thus, there is a need for effective insecticides and bed nets that have been drug-treated to cut down on mosquito populations. Even if a person is immune to malaria, the illness can still be eradicated because malaria-induced immunity is not permanent.

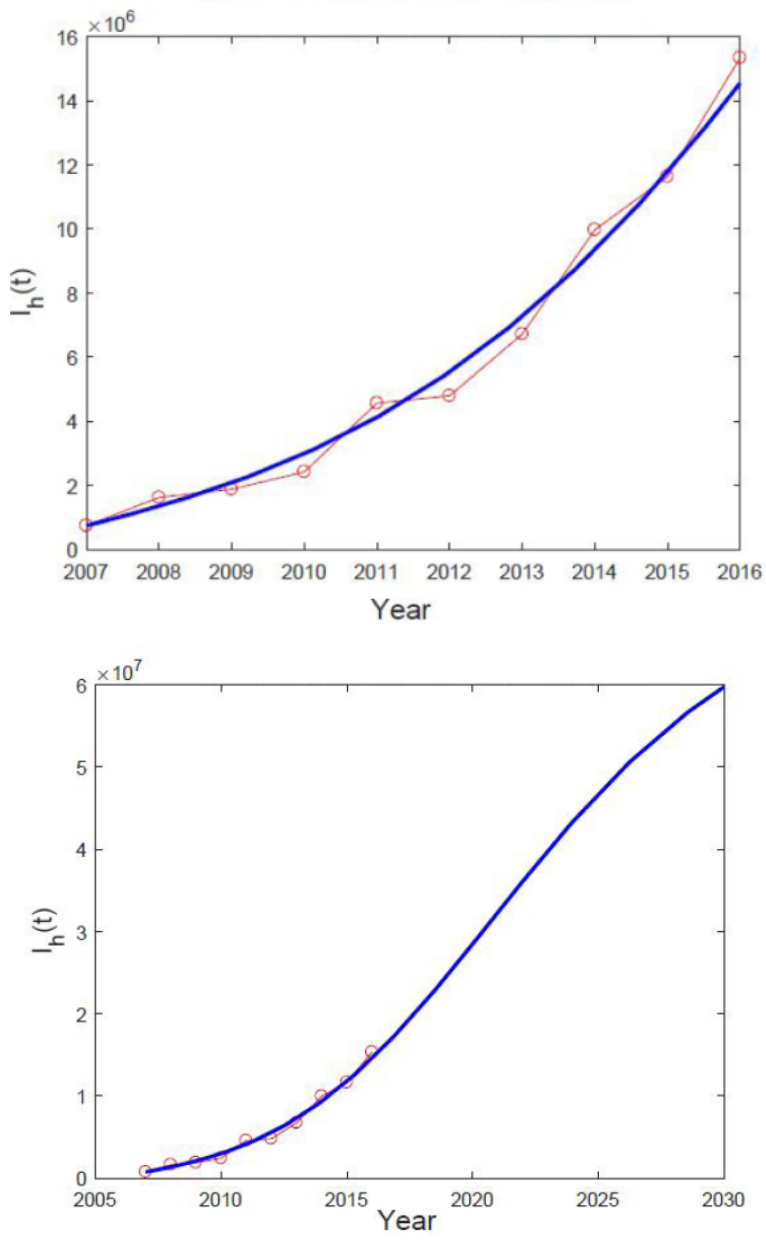


Figure 5.3: Contrast of the malaria suitcases from WHO and the solution of transmittable persons $I_h(t)$ for (5.1)-(5.5), Fig. (5.5)a: Reproduction of malaria suitcases in WHO as of 2007 to 2016, Fig. (5.5)b: Forecast of malaria suitcases for WHO 2007 to 2030.

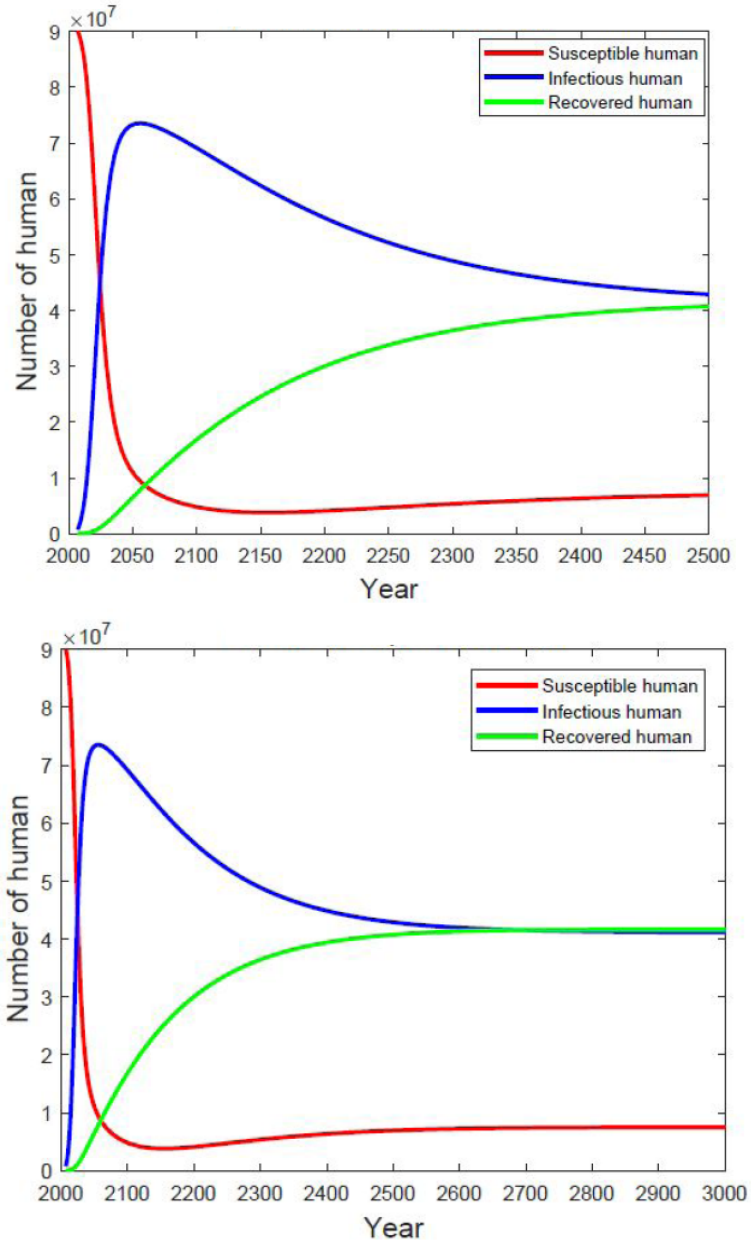


Figure 5.4: Solution of (5.1) to (5.5) with constraint for WHO, Fig. (5.5) (a) replication the number of person as of 2007 to 2500, Fig. (5.5)(b) the number of human from 2007 to 3000

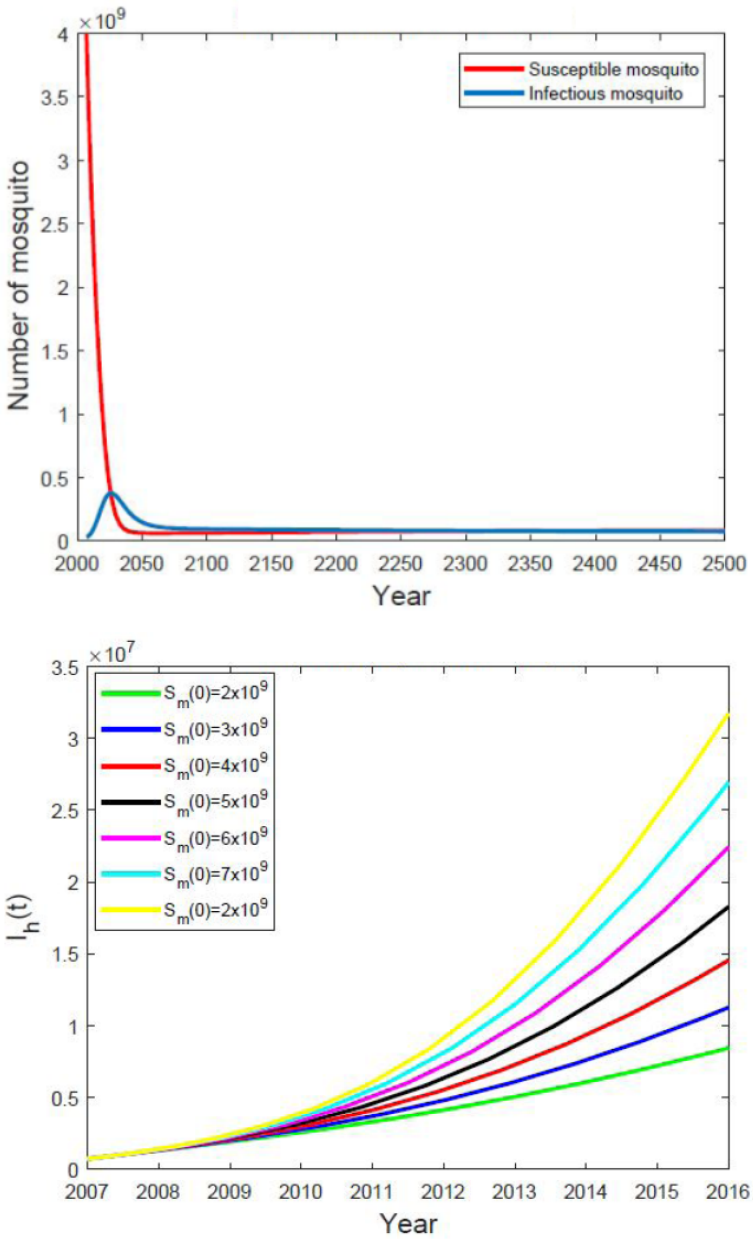


Figure 5.5: Solution of (5.1) to (5.5) with constraints for WHO with the number of mosquito from 2007 to 2500 fig.(5.5)(b): The pressure of original magnitude of vulnerable mosquito on the number of person malaria in WHO

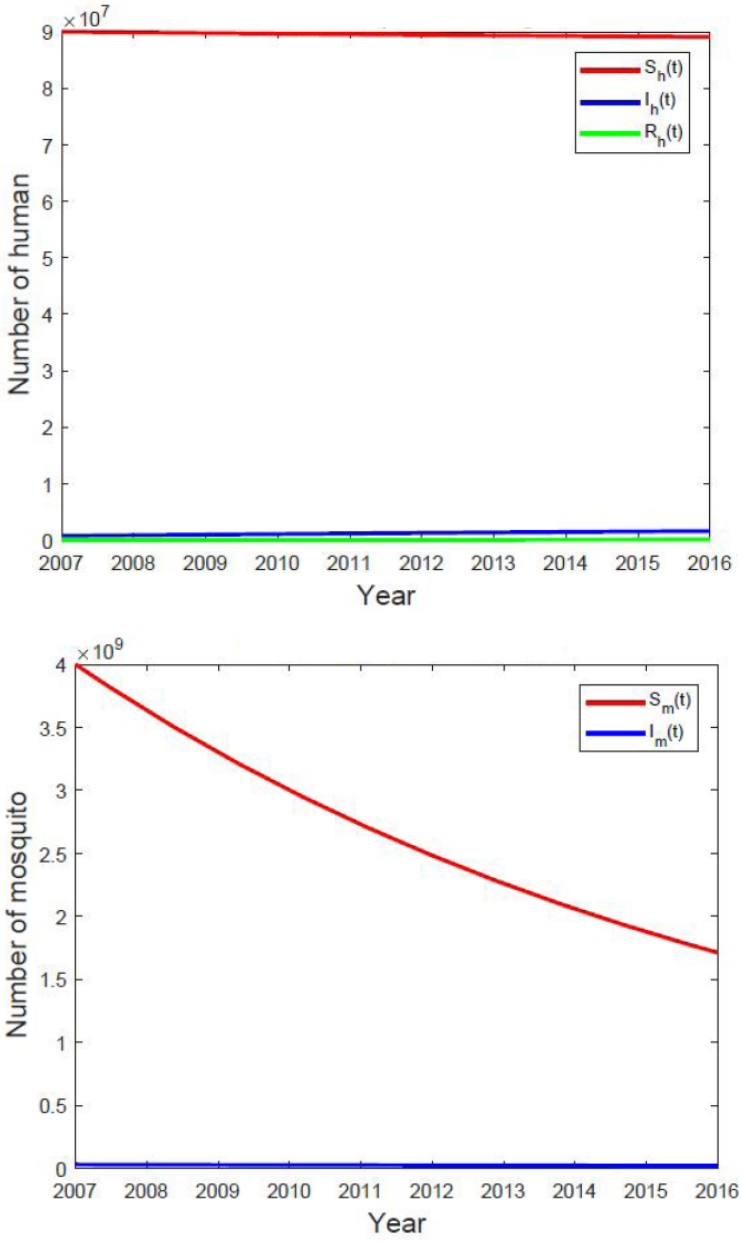


Figure 5.6: Solution of (5.1) to (5.5) with constraint for WHO with the number of mosquito as of 2007 to 2500 fig. (5.5) (b): The pressure of original amount of vulnerable mosquito on the number of person malaria in WHO

Chapter 6

ANALYSIS OF MATHEMATICAL MODEL OF MALARIA TRANSMISSION IN TEN DIMENSIONS

6.1 Formulation of the Model

In order to analyze the ten compartmental mathematical models of malaria transmission, we separated the human population into two categories. All people who have never developed malaria resistance are considered to be members of the non-immune human species, which is the first human type. The term "semi-immune human" refers to a second category of people who, even if they lose their immunity, have at least gained it at some point in their lives. The second group is believed to be less vulnerable since the idea of natural immunity is based on memory. We assume that, the human population is sub-divided into susceptible non-immune (S_e), exposed non-immune (E_e), infectious non-immune (I_e), susceptible semi-immune (S_a), exposed semi-immune (E_a), infectious semi-immune (I_a), recovery semi-immune (R_a). Thus, the total human popu-

lation $N_h(t) = S_e + E_e + I_e + S_a + E_a + I_a + R_a$. We sub-divide the mosquito population into three subclasses: susceptible mosquitoes S_v, exposed mosquitoes E_v and infectious mosquitoes I_v. The mosquitoes stay infectious for life and do not recover. Thus, the total mosquitoes population $N_v(t) = S_v + E_v + I_v$. We assume that non-immune people who have been exposed to the infection develop resistance and join the group of those who have recovered. Malaria cannot be transmitted from mosquito to mosquito or directly from person to person. Every single parasite, weak human, and non-resistant human is born with some level of resistance. Assume there are no deaths from malaria. The rates of birth and natural death are both taken into consideration. The assumption is that the birth and death rates are equal in order to fix the population as a whole. There are infection transmissions from I_v to S_e, from I_v to S_a, from I_e to S_v, from I_a to S_v. In this section,

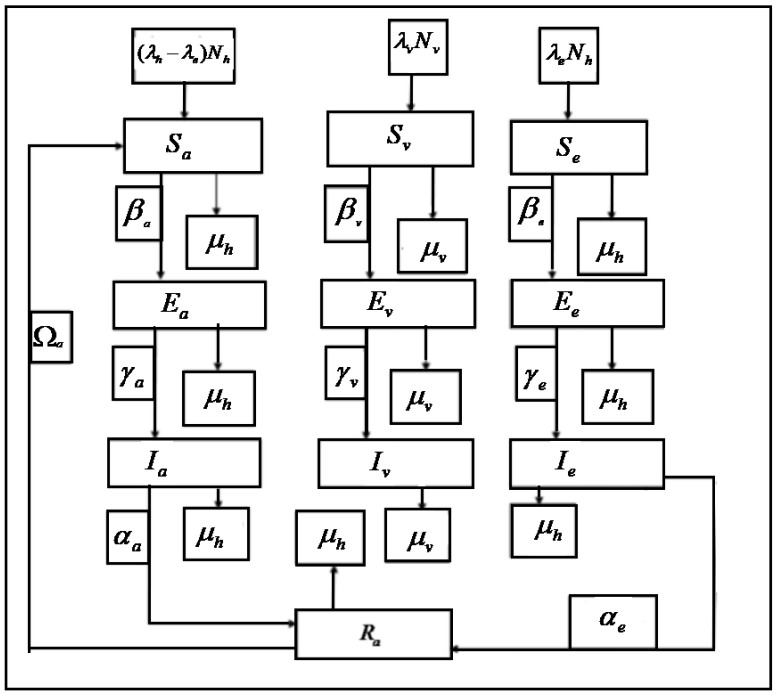


Figure 6.1: The Schematic of the Mathematical Model in Ten compartmental

we refer to the non-immune human population as e, the semi-immune human population as a, and the mosquito population as v. When a susceptible mosquito bites an infectious human who is non-immune to the infection and an infectious human who is semi-immune to the infection, the mosquito moves from the susceptible to the exposed mosquito group.

When an infectious mosquito bites a susceptible human who is non-resistant to the infection and an immune human, the parasite enters the human and the human moves to their own exposed group. The non-immune human leaves the class S_e at the rates of β_e and μ_h and enters the non-immune human class through birth at the rate of λ_e. Humans who are not immune enter the E_e class at a rate of β_e and exit the class at a rate of γ_e and μ_h. The population enters the I_e class with a γ_e rate and exits the I_e class with a α_e and μ_h rate. The susceptible semi-immune human class is entered by birth or human recovery at the rate of Ω_a, and the susceptible semi-immune human class is exited at the rates of β_a and μ_h. Humans with some degree of resistance enter the E_a class at a rate of β_a and exit the class at a rate of γ_a and μ_h. The human population enters the I_a class at a rate of γ_a and exits at a rate of α_a and μ_h. The human population enters the R_a class at a rate of α_a and α_e and exits the class at a rate of μ_h and Ω_a. Mosquitoes enter the susceptible group at birth at a λ_v per capita birth rate and exit the class S_v with β_v and μ_v. The human population enters the class E_v with a β_v rate and leaves it with a γ_v and μ_v rate. The mosquito population enters the infected class at a rate of γ_v and leaves the infectious class at a rate of μ_v. Assume that all the variables are positive. Tables (6.1) and (6.2), respectively. Utilizing the same standard incidence as in the model [80]. Infection occurrences are what we categorize and report as follows: $\beta_e = \Upsilon\varphi_{ve}I_v$ is the infection incidences from mosquitoes to non-immune humans, $\beta_a = \Upsilon\varphi_{va}I_v$ is the infection incidences from mosquitoes to semi-immune humans and $\beta_v = (\varphi_{ev}I_e + \varphi_{av}I_a)\,\Upsilon$ is the disease occurrence from semi-immune humans or non-immune humans to mosquitoes, then β_v is given by the amount of the power of disease from I_a and I_e. In light of this, the compartmental representation in Figure (6.1) can be represented on paper as a set of differential equations

Table 6.1: The explanation of state variables for malaria model of ten dimensional

Variables	The explanation of the state variables
S_e	Susceptible non-immune humans .
E_e	Exposed non-immune humans.
I_e	Infectious non-immune humans.
S_a	Susceptible semi-immune humans.
E_a	Exposed semi-immune humans.
I_a	Infectious semi-immune humans.
R_a	Recovery of humans.
S_v	Susceptible mosquitoes.
E_v	Exposed mosquitoes.
I_v	Infectious mosquitoes.

generated by the following equation, which goes from equation (6.1) to equation (6.10).

$$\frac{dS_e}{dt} = \lambda_e N_h - S_e\left(\Upsilon\varphi_{ve} I_v + \mu_h\right). \tag{6.1}$$

$$\frac{dE_e}{dt} = \Upsilon I_v \varphi_{ve} S_e - E_e\left(\gamma_e + \mu_h\right). \tag{6.2}$$

$$\frac{dI_e}{dt} = \gamma_e E_e - I_e\left(\alpha_e + \mu_h\right). \tag{6.3}$$

$$\frac{dS_a}{dt} = \left(\lambda_h - \lambda_e\right) N_h + \Omega_a R_a - S_a\left(\Upsilon\varphi_{va} I_v + \mu_h\right). \tag{6.4}$$

$$\frac{dE_a}{dt} = S_a \Upsilon\varphi_{va} I_v - E_a\left(\gamma_a + \mu_h\right). \tag{6.5}$$

$$\frac{dI_a}{dt} = \gamma_a E_a - I_a\left(\mu_h + \alpha_a\right). \tag{6.6}$$

$$\frac{dR_a}{dt} = \left(\alpha_a I_a + \alpha_e I_e\right) - R_a\left(\Omega_a + \mu_h\right). \tag{6.7}$$

$$\frac{dS_v}{dt} = \lambda_v N_v - S_v \varphi_{ev} I_e \Upsilon - S_v \mu_v - \varphi_{av} S_v \Upsilon I_a. \tag{6.8}$$

$$\frac{dE_v}{dt} = \left(\varphi_{ev} I_e + \varphi_{av} I_a\right) \Upsilon S_v - E_v\left(\gamma_v + \mu_v\right). \tag{6.9}$$

$$\frac{dI_v}{dt} = \gamma_v E_v - I_v \mu_v. \tag{6.10}$$

Table 6.2: The explanation of parameters for malaria model of ten dimensional

Parameter	The explanation of the parameter
α_e	The rate at which non-immune human progress to recovery.
λ_h	A per capita birth rate of human.
γ_e	The rate at which non-immune human progress to infective.
λ_e	A per capita birth rate of non-immune human.
λ_v	A per capita birth rate of mosquitoes.
α_a	The rate of the infective non-immune human progress to recovery.
γ_a	The rate at which semi-immune human progress to infective.
γ_v	The rate at which mosquito progress to infective.
λ_h	A per capita birth rate of human.
Ω_a	The rate at which recovered humans progress to susceptible.
Υ	The number of bites
μ_h	The death rate of humans.
μ_v	The death rate of of mosquitoes.
φ_{av}	The possibility of an infectious disease spreading from I_a to S_v.
φ_{ev}	The possibility of an infectious disease spreading from I_e to S_v.
φ_{va}	The possibility of an infectious disease spreading from I_v to S_a .
φ_{ve}	The possibility of an infectious disease spreading from I_v to S_e.

with the following affirmative original situation

$$S_{e0}, E_{e0}, I_{e0}, S_{a0}, E_{a0}, I_{a0}, R_{a0}, S_{v0}, E_{v0}, I_{v0} \tag{6.11}$$

6.2 Uniqueness and Existence of the solution

Theorem 6.2.1. *In the domain* $\Omega = \Omega_1 \times \Omega_2$ *for all time* $t \geq 0$*, the malaria model* (6.1) -(6.10) *has a single globally specified solution, where*

$$\Omega_1 = \left\{ \left(\frac{S_e}{N_h}, \frac{E_e}{N_h}, \frac{I_e}{N_h}, \frac{S_a}{N_h}, \frac{E_a}{N_h}, \frac{I_a}{N_h}, \frac{R_a}{N_h}, \frac{S_v}{N_v}, \frac{E_v}{N_v}, \frac{I_v}{N_v} \right) \in [0,1]^{10} \right\} \tag{6.12}$$

such that $0 \leq \frac{S_v}{N_v} + \frac{E_v}{N_v} + \frac{I_v}{N_v} \leq 1$ *and* $0 \leq \frac{S_a}{N_h} + \frac{E_a}{N_h} + \frac{I_a}{N_h} + \frac{R_a}{N_h} + \frac{S_e}{N_h} + \frac{E_e}{N_h} + \frac{I_e}{N_h} \leq 1$ *and*

$$\Omega_2 = \left\{(N_h, N_v) \in R^2\right\} / 0 < N_h \leq \frac{\lambda_h - \mu_h + \sqrt{(\lambda_h - \mu_h)^2 + 4\mu_h}}{\mu_h} \text{ and } 0 < N_v \leq \frac{\lambda_v - \mu_v}{\mu_v} \leq 1$$

Proof. The local existence of the solution follows from the regularity of the function $g = (g_1, g_2, .., g_{10})$ which is of the class continuous differentiable in the domain Ω. We first show that Ω_1 is forward-invariant for all $(N_h, N_v) \in \Omega_2$. It is easy to see that if $x_i = 0$ then $\frac{dx_i}{dt} = g_i(t) \geq 0, i = 1, 2, ..., 10$. It follows that if

$$\frac{S_v}{N_v} + \frac{E_v}{N_v} + \frac{I_v}{N_v} = 0 \Rightarrow \frac{d}{dt}\left(\frac{S_v}{N_v}\right) + \frac{d}{dt}\left(\frac{E_v}{N_v}\right) + \frac{d}{dt}\left(\frac{I_v}{N_v}\right) \geq 0 \tag{6.13}$$

and if $\frac{S_a}{N_h} + \frac{E_a}{N_h} + \frac{I_a}{N_h} + \frac{R_a}{N_h} + \frac{S_e}{N_h} + \frac{E_e}{N_h} + \frac{I_e}{N_h} = 0$ then $\frac{S_a}{N_h} + \frac{E_a}{N_h} + \frac{I_a}{N_h} + \frac{R_a}{N_h} + \frac{S_e}{N_h} + \frac{E_e}{N_h} + \frac{I_e}{N_h} \geq 0$. Moreover, if $\frac{S_v}{N_v} + \frac{E_v}{N_v} + \frac{I_v}{N_v} = 1$ then $\frac{d}{dt}\left(\frac{S_v}{N_v}\right) + \frac{d}{dt}\left(\frac{E_v}{N_v}\right) + \frac{d}{dt}\left(\frac{I_v}{N_v}\right) = -\lambda_v < 0$ and if $\frac{S_a}{N_h} + \frac{E_a}{N_h} + \frac{I_a}{N_h} + \frac{R_a}{N_h} + \frac{S_e}{N_h} + \frac{E_e}{N_h} + \frac{I_e}{N_h} = 1$ then

$$\frac{d}{dt}\left(\frac{S_a}{N_h}\right) + \frac{d}{dt}\left(\frac{E_a}{N_h}\right) + \frac{d}{dt}\left(\frac{I_a}{N_h}\right) + \frac{d}{dt}\left(\frac{R_a}{N_h}\right) + \frac{d}{dt}\left(\frac{S_e}{N_h}\right) + \frac{d}{dt}\left(\frac{E_e}{N_h}\right) + \frac{d}{dt}\left(\frac{I_e}{N_h}\right) = -\frac{\beta_a R_a}{N_h} < 0.$$

Now, we show that Ω_2 is forward invariant for all

$$\left(\frac{S_a}{N_h}, \frac{E_a}{N_h}, \frac{I_a}{N_h}, \frac{R_a}{N_h}, \frac{S_e}{N_h}, \frac{E_e}{N_h}, \frac{I_e}{N_h}, \frac{S_v}{N_v}, \frac{E_v}{N_v}, \frac{I_v}{N_v}\right) \in \Omega_1, \tag{6.14}$$

then $\frac{dN_h}{dt} > 0$ if $\lambda_h > \mu_h$ and $\frac{dN_v}{dt} > 0$ if $\lambda_v > \mu_v$. It is easy to see that

$$\limsup_{t\to\infty} N_v(t) \leq \frac{\lambda_v - \mu_v}{\mu_v} \text{ and } \limsup_{t\to\infty} N_h(t) \leq \frac{\lambda_h - \mu_h + \sqrt{(\lambda_h - \mu_h)^2 + 4\mu_h}}{\mu_h}$$

We get to the conclusion that if the solutions of (6.1)-(6.10) exist worldwide in the domain Ω, then it is mathematically and epidemiologically well-posed. Let $X(t) = (S_e(t), E_e(t), I_e(t), S_a(t), E_a(t), I_a$ and

$$\phi : \Gamma \to \Psi \text{ and } X :\mapsto X' \tag{6.15}$$

such that $\phi = (\phi_1, \phi_2, \phi_3, \phi_4, \phi_5, \phi_6, \phi_7, \phi_8, \phi_9, \phi_{10})$, where

$$\phi_1 = \frac{dS_e}{dt} = \lambda_e N_h - S_e\left(\Upsilon\varphi_{ve} I_v + \mu_h\right). \tag{6.16}$$

$$\phi_2 = \frac{dE_e}{dt} = \Upsilon I_v \varphi_{ve} S_e - E_e\left(\gamma_e + \mu_h\right). \tag{6.17}$$

$$\phi_3 = \frac{dI_e}{dt} = \gamma_e E_e - I_e\left(\alpha_e + \mu_h\right). \tag{6.18}$$

$$\phi_4 = \frac{dS_a}{dt} = \left(\lambda_h - \lambda_e\right) N_h + \Omega_a R_a - S_a\left(\Upsilon\varphi_{va} I_v + \mu_h\right). \tag{6.19}$$

$$\phi_5 = \frac{dE_a}{dt} = S_a \Upsilon\varphi_{va} I_v - E_a\left(\gamma_a + \mu_h\right). \tag{6.20}$$

$$\phi_6 = \frac{dI_a}{dt} = \gamma_a E_a - I_a\left(\mu_h + \alpha_a\right). \tag{6.21}$$

$$\phi_7 = \frac{dR_a}{dt} = \left(\alpha_a I_a + \alpha_e I_e\right) - R_a\left(\Omega_a + \mu_h\right). \tag{6.22}$$

$$\phi_8 = \frac{dS_v}{dt} = \lambda_v N_v - S_v\left(\left(\varphi_{ev} I_e + \varphi_{av} I_a\right)\Upsilon + \mu_v\right). \tag{6.23}$$

$$\phi_9 = \frac{dE_v}{dt} = \left(\varphi_{ev} I_e + \varphi_{av} I_a\right)\Upsilon S_v - E_v\left(\gamma_v + \mu_v\right). \tag{6.24}$$

$$\phi_{10} = \frac{dI_v}{dt} = \gamma_v E_v - I_v \mu_v. \tag{6.25}$$

Then, (6.16)-(6.25) can be written in the form of the following (6.26)

$$X'(t) = \phi(X(t)) : X(0) = (S_{e0}, E_{e0}, I_{e0}, S_{a0}, E_{a0}, R_{a0}, S_{v0}, E_{v0}, I_{v0}) \in \Gamma \tag{6.26}$$

We will perform the confirmation follow by [25]. Suppose that there exists t_1 and t^* with $t_1 < t^*$ such that $S_e(t_1) = 0, \frac{dS_e(t)}{dt} < 0$ in (t_1, t^*) where all the ten compartments are positives. Then from (6.1), we have

$$\frac{dS_e(t)}{dt} = \lambda_e N_h - S_e(t)\,\Upsilon I_v(t)\,\varphi_{ev} - S_e(t)\,\mu_h > 0 \tag{6.27}$$

which is contradiction. Hence, $S_e(t) > 0$ for all $t \geq 0$. Suppose that there exist

$$t_1 = \mathrm{Sup}\left\{t > 0 : S_a, I_a, E_a, R_a, S_e, I_e, R_e, , S_v, E_v, I_v > 0\right\}. \tag{6.28}$$

Then from equation (6.2), we have get the following equation (6.29)

$$\frac{d}{dt}\left(E_e(t)e^{(\gamma_e+\mu_h)t}\right) = \left(\Upsilon I_v(t) S_e(t)\right) e^{(\gamma_e+\mu_h)t}. \tag{6.29}$$

Integrating equation (6.29) from 0 to t_1, we have get equation (6.30)

$$E_e(t)e^{(\gamma_e+\mu_h)t} = E_{e0} + \int_0^{t_1} \left(\Upsilon I_v(\theta) S_e(\theta)\varphi_{ve}\right) e^{(\gamma_e+\mu_h)\theta} d\theta. \tag{6.30}$$

Multiply both sides of (6.30) by $e^{-(\gamma_e+\mu_h)t_1}$, then we have get the following (6.31)

$$E_e(t)(t_1) = (E_{e0})\, e^{-(\gamma_e+\mu_h)t_1} + e^{-(\gamma_e+\mu_h)t_1} \int_0^{t_1} (\Upsilon I_v(\theta) S_e(\theta)\varphi_{ve})\, e^{(\gamma_e+\mu_h)\theta} d\theta > 0. \tag{6.31}$$

Since $I_e(t) > 0$ for all $t \geq 0$, then equation (6.3)

$$\Rightarrow \quad \frac{dI_e(t)}{dt} \geq -(\alpha_e + \mu_e)\, I_e \tag{6.32}$$

$$\Rightarrow \quad \frac{dI_e(t)}{I_e} \geq -(\alpha_e + \mu_e)\, dt \tag{6.33}$$

$$\Rightarrow \quad I_e(t) \geq e^{-(\alpha_e+\mu_e)t} > 0. \tag{6.34}$$

It is simple to observe $S_a(t) > 0$ for all $t \geq 0$. Suppose that there exists t_1 and t^* with $t_1 < t^*$ such that $S_a(t_1) = 0$, $\frac{dS_a(t)}{dt} < 0$ and every the ten compartments are positives that is $S_e(t), E_e(t), I_e(t), S_a(t), I_a(t), E_a(t), R_a(t), S_v(t), I_v(t), E_v(t), > 0$ for $t_1 < t < t^*$. Then from equation (6.4), we have obtained the subsequent

$$\frac{dS_a(t)}{dt} = (\lambda_e - \lambda_h)\, N_h + \Omega_a R_a(t) - S_a \Upsilon \varphi_{va} I_v(t) - S_a(t)\mu_h > 0.$$

which is contradiction. Hence, $S_a(t) > 0, \forall t \geq 0$. As of (6.5) we have obtained

$$\frac{d}{dt}\left(E_a(t)e^{(\gamma_a+\mu_h)t}\right) = (S_a(t)\Upsilon I_v(t)\varphi_{va})\, e^{(\gamma_a+\mu_h)t}. \tag{6.35}$$

Integrating equation (6.35) from 0 to t_1, we have get equation (6.36)

$$\left(E_a(t_1)e^{(\gamma_a+\mu_h)t_1}\right) = -E_{a0} + \int_0^{t_1} (S_a(t)\Upsilon I_v(\theta)\varphi_{va})\, e^{(\gamma_a+\mu_h)\theta} d\theta. \tag{6.36}$$

Multiply both sides of equation (6.36) by $e^{(\gamma_a+\mu_h)t_1}$,then we have get

$$E_a(t_1) = (E_{a0})\, e^{(\gamma_a+\mu_h)t_1} + e^{(\gamma_a+\mu_h)t_1} \int_0^{t_1} (S_a(t)\Upsilon I_v(\theta)\varphi_{va})\, e^{(\gamma_a+\mu_h)\theta} d\theta > 0.$$

Hence, $E_a(t) > 0$ for all $t \geq 0$. Since $E_a(t) > 0$ for all $t \geq 0$ and from (6.6)

$$\Rightarrow \quad \frac{dI_a(t)}{dt} \geq -I_a\,(\alpha_a + \mu_h) \tag{6.37}$$

$$\Rightarrow \quad \frac{dI_a(t)}{I_a} \geq -(\alpha_a + \mu_h)\, dt \tag{6.38}$$

$$\Rightarrow \quad I_a(t) \geq (I_{a0})e^{-(\alpha_a+\mu_h)t} > 0 \tag{6.39}$$

Hence, $I_a(t) > 0$ for all $t \geq 0$. Since $I_a(t) > 0, \forall t \geq 0$ and from equation (6.7)

$$\Rightarrow \quad \frac{dR_a(t)}{dt} \geq -R_a\left(\Omega_a + \mu_h\right) \tag{6.40}$$

$$\Rightarrow \quad \frac{dR_a(t)}{R_a} \geq -\left(\Omega_a + \mu_h\right) dt \tag{6.41}$$

$$\Rightarrow \quad R_a(t) \geq (R_{a0}) e^{-(\Omega_a + \mu_h)t} > 0. \tag{6.42}$$

It is simple observe that $S_v(t) > 0$ for all $t \geq 0$. Suppose that there exists t_1 and t^* with $t_1 < t^*$ such that $S_v(t_1) = 0$, $\frac{dS_v(t)}{dt} < 0$ and every the ten compartments are affirmative that is $S_e(t), E_e(t), I_e(t), S_a(t), E_a(t), I_a(t), R_a(t), S_v(t), E_v(t), I_v(t) > 0$ for $t_1 < t < t^*$. Then from equation (6.8), we have obtained the subsequent

$$\frac{dS_v(t)}{dt} \quad = \quad \lambda_v N_v - S_v(t)\varphi_{ev} I_e(t) - \mu_v S_v(t) - \Upsilon \varphi_{av} S_v(t) I_a(t) > 0 \tag{6.43}$$

which is contradiction, hence $S_v(t) > 0, I_e > 0, I_a > 0, S_v > 0, \forall t \geq 0$ then

$$\Rightarrow \quad \frac{dE_v(t)}{dt} \geq -E_v(t)\left(\gamma_v + \mu_v\right) \tag{6.44}$$

$$\Rightarrow \quad \frac{dE_v(t)}{E_v} \geq -\left(\gamma_v + \mu_v\right) dt \tag{6.45}$$

$$\Rightarrow \quad E_v(t) \geq (E_{v0}) e^{-(\gamma_v + \mu_v)t} > 0 \tag{6.46}$$

Hence, $E_v(t) > 0$ for all $t \geq 0$. Since $E_v(t) > 0$ for all $t \geq 0$ then equation (6.10)

$$\Rightarrow \quad \frac{dI_v(t)}{dt} \geq -I_v(t)\mu_v \tag{6.47}$$

$$\Rightarrow \quad \frac{dI_v(t)}{I_v} \geq -\mu_v dt \tag{6.48}$$

$$\Rightarrow \quad I_v(t) \geq (I_{v0}) e^{-\mu_v t} > 0 \tag{6.49}$$

Hence, $I_v(t) > 0, \forall t \geq 0$. Therefore, the solution of the system equation (6.1) to equation (6.10) is positive. Since the total number of humans population $N_v(t)$ is the sum of $S_e(t)$, $E_e(t)$, $I_e(t)$, $S_a(t)$, $E_a(t)$, $I_a(t)$ and $R_a(t)$, and the total number of mosquito population $N_v(t)$ is the sum of $S_v(t)$, $E_v(t)$ and $I_v(t)$, Since $S_e(t)+E_e(t)+I_e(t)+S_a(t)+E_a(t)+I_a(t)+R_a(t) = N_h$ and $S_v(t) + E_v(t) + I_v(t) = N_v$, then $S_e(t) \leq N_h, E_e(t) \leq N_h, I_e(t) \leq N_h, S_a(t) \leq N_h, E_a(t) \leq N_h, I_a(t) \leq N_h, R_a(t) \leq N_h$, and $S_v(t) \leq N_v, E_v(t) \leq N_v, I_v(t) \leq N_v, \forall t \geq 0$. Thus X is bounded. As a result, there is only one solution that is non-negative and bounded for the equations (6.1) to equation (6.10). As a result, the evidence is now complete.

6.3 Equilibria points

DFE points are equivalent to steady-state solutions in which all residents are totally at risk, i.e., there are no transferable residents and all residents are zero. In EE points, the sickness persists in the population and there is a stable condition

Theorem 6.3.1. *DFE and EE points are at least two of the equilibrium points in the model equations* (6.1) *to equation* (6.10)*.*

Proof. Equations must be solved in order to arrive get the solution.

$$\frac{dS_e}{dt} = \frac{dE_e}{dt} = \frac{dI_e}{dt} = \frac{dS_a}{dt} = \frac{dE_a}{dt} = \frac{dI_a}{dt} = \frac{dR_a}{dt} = \frac{dS_v}{dt} = \frac{dE_v}{dt} = \frac{dI_v}{dt} = 0. \tag{6.50}$$

Therefore, we set the system equation (6.1)-(6.10) equal to zero, then

$$\lambda_e N_h - S_e(\Upsilon\varphi_{ve} I_v + \mu_h) = 0. \tag{6.51}$$

$$\Upsilon S_e \varphi_{ve} I_v - E_e(\gamma_e + \mu_h) = 0. \tag{6.52}$$

$$\gamma_e E_e - I_e(\alpha_e + \mu_h) = 0. \tag{6.53}$$

$$(\lambda_h - \lambda_e) N_h + \Omega_a R_a - S_a(\Upsilon\varphi_{va} I_v + \mu_h) = 0. \tag{6.54}$$

$$S_a \Upsilon\varphi_{va} I_v - E_a(\gamma_a + \mu_h) = 0. \tag{6.55}$$

$$\gamma_a E_a - I_a(\mu_h + \alpha_a) = 0. \tag{6.56}$$

$$(\alpha_a I_a + \alpha_e I_e) - R_a(\Omega_a) = 0. \tag{6.57}$$

$$\lambda_v N_v - S_v \Upsilon(\varphi_{ev} I_e + \varphi_{av} I_a) = 0. \tag{6.58}$$

$$(\varphi_{ev} I_e + \varphi_{av} I_a) \Upsilon S_v - E_v(\gamma_v + \mu_v) = 0. \tag{6.59}$$

$$\gamma_v E_v - I_v \mu_v = 0. \tag{6.60}$$

We were able to derive equation (6.61) from equation (6.51).

$$S_e = \frac{\lambda_e N_h}{\Upsilon\varphi_{ve} I_v + \mu_h}. \tag{6.61}$$

We have arrived at the following conclusion from equations (6.52) and (6.61).

$$E_e = \left(\frac{\Upsilon\varphi_{ve}}{\gamma_e + \mu_h}\right)\left(\frac{\lambda_e N_h}{\Upsilon\varphi_{ve} I_v + \mu_h}\right) I_v \tag{6.62}$$

The following is the outcome we obtained using the equation (6.57)

$$R_a = \left(\frac{\alpha_a + \alpha_e}{\Omega_a}\right) I_a. \tag{6.63}$$

The outcome is as follows when equation (6.63) is substituted for (6.54).

$$S_a = \left(\frac{\lambda_h - \lambda_e}{\Upsilon\varphi_{va}I_v + \mu_h}\right)N_h + \left(\frac{\alpha_a + \alpha_e}{\Upsilon\varphi_{va}I_v + \mu_h}\right)I_a. \tag{6.64}$$

As a result of equation (6.56), we have the following outcome.

$$E_a = \frac{(\alpha_a + \mu_h)I_a}{\gamma_a}. \tag{6.65}$$

The following conclusion was derived from equation (6.58)

$$S_v = \frac{\lambda_v N_v}{\Upsilon\varphi_{ev}I_e + \mu_v + \varphi_{av}I_e\Upsilon} \tag{6.66}$$

The following is the outcome we obtain from the equation (6.60)

$$E_v = \frac{\mu_v I_v}{\gamma_v}. \tag{6.67}$$

In [80], the DFE point is present if the infectious zero, which is $I_e = I_a = I_v = 0$. Then, we obtained (6.68) from (6.61).

$$S_e^* = \frac{\lambda_e N_h}{\mu_h}, \tag{6.68}$$

The following equation, (6.69) , can be obtained from equation (6.64).

$$S_a^* = \left(\frac{\lambda_h - \lambda_e}{\mu_h}\right)N_h, \tag{6.69}$$

Thus we have deduced the following equation, (6.70), from equation (6.66).

$$S_v^* = \frac{\lambda_v N_v}{\mu_v} \tag{6.70}$$

and the values for (6.62), (6.65), (6.63) and (6.67) are all zero, we reached the following disease free equilibrum (DFE)point.

$$X_{dfe} = (S_e^*, 0, 0, S_a^*, 0, 0, 0, S_v^*, 0, 0) \tag{6.71}$$

where S_e*, $S*_a*$, and S_v* are defined in (6.68), (6.69) and (6.70), respectively, there is a DFE point for (6.51) to (6.60), and to get the EE point for (6.51) to (6.60), we have to take the next (6.72)

$$E_v^{**} = \frac{\lambda_v N_v}{\gamma_v + \mu_v}. \tag{6.72}$$

Equation (6.73) is the result of changing equation (6.72) into equation (6.60).

$$I_v^{**} = \frac{\gamma_v \lambda_v N_v}{\mu_v (\gamma_v + \mu_v)}. \tag{6.73}$$

By changing (6.73) into (6.51), we were able to create (6.74).

$$S_e^{**} = \left(\frac{\lambda_e N_h}{\Upsilon \varphi_{ve} \gamma_v}\right)\left(\frac{\mu_v (\gamma_v + \mu_v)}{\lambda_v N_v}\right). \tag{6.74}$$

We have obtained (6.75) by changing (6.74) into (6.52).

$$E_e^{**} = \frac{N_h \lambda_e}{\mu_h + \gamma_e}. \tag{6.75}$$

Substituting (6.74) into (6.53), we have obtained (6.76)

$$I_e^{**} = \left(\frac{\gamma_e \lambda_e}{\alpha_e + \mu_h}\right)\left(\frac{N_h}{\gamma_e + \mu_h}\right). \tag{6.76}$$

We have obtained the next equation from (6.57),

$$I_a = \left(\frac{\Omega_a + \mu_h}{\alpha_a + \alpha_e}\right) R_a. \tag{6.77}$$

We have obtained the following (6.78) if we replace (6.77) into (6.56).

$$E_a = \left(\frac{\mu_h + \alpha_a}{\gamma_a}\right)\left(\frac{\mu_h + \alpha_a}{\gamma_a}\right)\left(\frac{\Omega_a + \mu_h}{\alpha_a + \alpha_e}\right) R_a. \tag{6.78}$$

By substituting (6.78) for (6.56), we obtain eqrefc.

$$S_a = \left(\frac{\gamma_a + \mu_h}{\gamma_a}\right)\left(\frac{\Omega_a + \mu_h}{\alpha_a + \alpha_e}\right) R_a. \tag{6.79}$$

We can get (6.80) if we replace (6.79) into (6.54).

$$R_a^{**} = \frac{(\alpha_a + \alpha_e)(\lambda_e - \lambda_h) N_h}{\Omega_a (\alpha_a + \alpha_e) - (\gamma_a + \mu_h)(\mu_h + \alpha_a)(\Omega_a + \mu_h)}. \tag{6.80}$$

We were able to get (6.81)by changing (6.80) into (6.57).

$$I_a^{**} = \frac{(\Omega_a + \mu_h)(\lambda_e - \lambda_h) N_h}{\Omega_a (\lambda_e + \lambda_a) - (\lambda_a + \mu_h)(\mu_h + \alpha_a)(\Omega_a + \mu_h)}. \tag{6.81}$$

We have obtained (6.82) by changing (6.81) into (6.56).

$$E_a^{**} = \frac{(\mu_h + \alpha_a)(\Omega_a + \mu_h)(\lambda_e - \lambda_h) N_h}{\gamma_a ((\alpha_a + \alpha_e) - (\gamma_a + \mu_h)(\mu_h + \alpha_a)(\Omega_a + \mu_h))}. \tag{6.82}$$

We have obtained (6.83) by changing (6.82) into (6.55).

$$S_a^{**} = \left(\frac{(\mu_h + \alpha_e)(\Omega_a + \mu_h)(\lambda_e - \lambda_h) N_h}{\Omega_a(\alpha_e + \alpha_a) - (\gamma_a + \mu_h)(\mu_h + \alpha a)(\Omega_a + \mu_h)}\right)\left(\frac{\mu_v(\gamma_v + \mu_h)(\gamma_a + \mu_h)}{\gamma_v \lambda_v N_v \Upsilon \varphi_{va} \gamma_a}\right). \quad (6.83)$$

By changing (6.80) into (6.7), we were able to obtain (6.84).

$$S_v^{**} = \frac{\lambda_v N_v((\Omega_a \alpha_a + \Omega_a \alpha_e - (\gamma_a + \mu_h)(\mu_h + \alpha_e)(\Omega_a + \mu_h)))((\alpha_e + \mu_h)(\gamma_e + \mu_h))}{\varphi_{ev}((\Omega_a + \mu_h)(\lambda_e - \lambda_h)(\alpha_e + \mu_h)(\gamma_e + \mu_h) + (\gamma_e \lambda_e N_h)(\Omega_a(\alpha_e + \alpha_e) - (\gamma_a + \mu_h)(\mu_h + \alpha_a)))}$$

As a result, the EE point of the equation (6.1) to (6.10) is

$$(E_v^{**}, I_v^{**}, S_e^{**}, E_e^{**}, I_e^{**}, R_a^{**}, I_a^{**}, E_a^{**}, S_a^{**}, S_v^{**}), \quad (6.84)$$

where $S_e^{**}, E_e^{**}, I_e^{**}, S_a^{**}, E_a^{**}, I_a^{**}, R_a^{**}, S_v^{**}, E_v^{**}$ and I_v^{**} are defined in equation (6.72), (6.73), (6.74), (6.75), (6.76), (6.80), (6.81), (6.82), (6.83) and equation (6.84) respectively. The malaria model has an EE point between equations (6.51) to (6.60). So, given the equation (6.51) to (6.60) of the malaria model system, there is the DFE point and the EE point.

6.4 Reproductive Number

Let us denote the rate of the disease spread from e to e by β_{ee}, from a to a by β_{aa}, from v to v by β_{vv}, from a to e by β_{ae}, from e to a by β_{ea}, from e to v by β_{ev}, from v to e by β_{ve}, from v to a by β_{va} and from v to a by β_{va}. We use the next-generation operator approach outlined by [106]to define the reproductive number as the number of secondary diseases that one transferable individual would cause above the period of the transferable period, given that each is vulnerable and the next-generation matrix beta can be attained by incorporating [71]:

$$\beta = \begin{pmatrix} \beta_{ee} & \beta_{ae} & \beta_{ve} \\ \beta_{ea} & \beta_{aa} & \beta_{va} \\ \beta_{ev} & \beta_{av} & \beta_{vv} \end{pmatrix} \quad (6.85)$$

When each component of β_{fg} characterizes the predictable number of secondary suitcases in the host indexed by g produced by a distinctive primary case in the crowd indexed by f in a totally sensitive population, where g and f can be a, e, and v. Therefore, based on

our theory, the non-diseases are disseminated as follows: $\beta_{ee}, \beta_{aa}, \beta_{vv}, \beta_{ea}$ and β_{ae}. Next, we obtained

$$\beta_{ee} = \beta_{aa} = \beta_{vv} = \beta_{ea} = \beta_{ae} = 0. \tag{6.86}$$

These are the diseases that spread and are also referred to as $\beta_{ev}, \beta_{ea}, \beta_{av}$ and β_{va}. When it took place, we had

$$\beta_{ev} \neq 0, \beta_{ve} \neq 0, \beta_{av} \neq 0, \beta_{va} \neq 0. \tag{6.87}$$

As a result, when we combine (6.86), (6.87) and(6.85), we get below.

$$\beta = \begin{pmatrix} 0 & 0 & \beta_{ve} \\ 0 & 0 & \beta_{va} \\ \beta_{ev} & \beta_{av} & 0 \end{pmatrix}. \tag{6.88}$$

Similar to how β_{fg} has the concept of reproductive number, it can be obtained by adding the average time for the transferable life span, the probability of transmission per contact, the possibility of continued existence up until the transferable state, and the contact number per unit of time in [58]. The elements of β that are $\beta_{ev}, \beta_{av}, \beta_{ve}$ and β_{va} of β are gained. When a disease is recently introduced in a population by one polluted person, R_0 defines as the typical number of secondary cases produced by that pollutant during his full infectious period. In the case of our model, a new pollutant can start in the classes S_v or S_e or S_a. We place a single freshly polluted mosquito at the DFE site and define β_{va} as the anticipated number of susceptible semi-immune humans that this insect will contaminate. From this, we can calculate the equivalent number of (6.89).

$$\beta_{va} = \left(\frac{\gamma_v}{\mu_v + \gamma_v}\right)\left(\frac{\Upsilon S_a}{N_h}\right)\left(\frac{\varphi_{va}}{\mu_v}\right) \tag{6.89}$$

We gained (6.90) by acquiring β_{ve}, where β_{ve} is the predicted number of susceptible non-immune humans that this mosquito will contaminate.

$$\beta_{ve} = \left(\frac{\gamma_v}{\mu_h + \gamma_v}\right)\left(\frac{\Upsilon S_e}{N_h}\right)\left(\frac{\varphi_{ve}}{\mu_v}\right) \tag{6.90}$$

When a disease first manifests itself in a population due to a semi-immune person who has been exposed to pollution at the DFE point, we have (6.91).

$$\beta_{av} = \left(\frac{\gamma_a}{\mu_h + \gamma_a}\right)\left(\frac{\Upsilon S_v}{N_h}\right)\left(\frac{\varphi_{av}}{\mu_h + \alpha_a}\right) \tag{6.91}$$

At the DFE point, we first introduce a single freshly polluted non-immune human to the population after which we have acquired the following equation.

$$\beta_{ev} = \left(\frac{\gamma_e}{\mu_h + \gamma_e}\right)\left(\frac{\Upsilon S_v}{N_h}\right)\left(\frac{\varphi_{ev}}{\mu_h + \alpha_e}\right) \tag{6.92}$$

Let's define the reproductive number, R_0, for the malaria model with (6.1) to (6.10) precisely as the spectral radius of β in [33], followed by the acquired reproductive number, (6.93).

$$(R_0)^2 = (\beta_{ev})(\beta_{ve}) + (\beta_{av})(\beta_{va}) \tag{6.93}$$

where the variables $\beta_{va}, \beta_{ve}, \beta_{av}$ and β_{ev} are specified in the corresponding equations (6.89), equation (6.90), equation (6.91) and equation (6.92), respectively. Let's assume that a person lives at the DFE point without any semi-immune humans, in which case we get the equation (6.94), which states that either all susceptible semi-immune humans are protected by vaccination, there are no semi-immune humans at the disease-free equilibrium, or there are other control measures in place. Consequently, we have

$$S_a = 0 \text{ and } S_e = N_h. \tag{6.94}$$

Moreover, let's assume that there are no non-immune individuals in the human population at the DFE point, as shown by our acquisition of the equation (6.95).

$$S_e = 0 \text{ and } S_a = N_h. \tag{6.95}$$

then we obtain (6.96) from(6.90), (6.92) and (6.95).

$$\beta_{ev} = 0 \quad \text{and} \quad \beta_{ve} = 0. \tag{6.96}$$

Equation (6.96) was put into (6.93), and from there we obtained equation (6.100).

$$R_0 = \sqrt{(\beta_{va})(\beta_{av})}. \tag{6.97}$$

As a result of (6.89), (6.91) and (6.94), we have obtained the subsequent (6.98), and the spread from semi-immune people to mosquitoes is zero.

$$\beta_{av} = 0 \text{ and } \beta_{va} = 0. \tag{6.98}$$

Equation (6.98) was inserted into (6.93), and from there we obtained.

$$R_0 = \sqrt{(\beta_{ve})\,(\beta_{ev})}. \tag{6.99}$$

If R_1 is the reproductive number for an infection caused by β_{ev} or β_{ve}, then equation (6.93) becomes the corresponding equation (6.100)

$$R_1 = \sqrt{(\beta_{ve})\,(\beta_{ev})}. \tag{6.100}$$

and assuming that R_2 represents the reproductive number for pollution caused by either β_{av} or β_{va}, the equation (6.93) becomes the following equation (6.101).

$$R_2 = \sqrt{(\beta_{va})\,(\beta_{av})}. \tag{6.101}$$

We define the reproductive number, R_0, as in (6.102).

$$R_0 = \sqrt{R_1^2 + R_2^2} \tag{6.102}$$

where R_1 and R_2 are defined in equations (6.100) and (6.101), respectively.

6.5 Stability of DFE and EE point

We present a fundamentally crucial justification for the persistence of super and sub-threshold common equilibrium for R_0 close to unity. We make use of the bifurcation finding, which is demonstrated in Appendix 2 of the cited work by [38]. Prior to configuring these outcomes, we first modify the stability equations for equations (6.1) through (6.10) in two scopes. We can rephrase equation (6.1) to equation (6.10) in the compact form $\frac{dx_i}{dt} = f_i(x), i = 1, ..., 10$. The stationary solution is obtained by resolve $f(x) = 0$, anywhere $f = (f_1, ..., f_{10})$.

Theorem 6.5.1. *The disease free stability point is unstable if the reproductive number R_0 is greater than one and it is GAS in ψ if the reproductive number R_0 less than or equal to one, where $\psi = \left\{(S_e, E_e, I_e, S_a, E_a, I_a, R_a, S_v, E_v, I_v) \in R_+^{10}\right\}$ such that, $S_e \geq 0$, $E_e \geq 0$, $I_e \geq 0$, $S_a \geq 0$, $E_a \geq 0$, $I_a \geq 0$, $R_a \geq 0$,$S_v \geq 0$, $E_v \geq 0$, $I_v \geq 0$, the sum of S_e, E_e, I_e, S_a, E_a, I_a and R_a is less than or equal to the total number of people, and the sum of S_v, E_v, and I_v is less than or equal to the total number of mosquitoes.*

Proof: The Proof follows from [106]. We start to rephrase equation (6.1) in the form of $\frac{dS}{dt} = \psi_1(S, I)$ and $\frac{dI}{dt} = \psi_2(S, I)$ wherever $S = (S_e, S_a, S_v)$ and $I = (E_e, I_e, E_a, I_a, R_a, E_v, I_v)$. Suppose B be the Jacobean matrix of $\psi = (\psi_1, \psi_2)$ calculate at the DEF $(S, 0)$. Then we obtained

$$\mathbf{B} = \begin{pmatrix} B_1 - B_2 & 0 \\ B_1 + B_2 & B_3 \end{pmatrix} \qquad \text{wherever} \tag{6.103}$$

$$\mathbf{B_1} = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & M_{ve} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & M_{va} \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & M_{ev} & 0 & M_{av} & 0 & 0 \end{pmatrix} \tag{6.104}$$

$$\mathbf{B_2} = \begin{pmatrix} K_1 & 0 & 0 & 0 & 0 & 0 \\ -\nu_e & K_3 & 0 & 0 & 0 & 0 \\ 0 & 0 & K_2 & 0 & 0 & 0 \\ 0 & 0 & -\nu_v & K_4 & 0 & 0 \\ 0 & -\alpha_e & 0 & -\alpha_a & 0 & 0 \\ 0 & 0 & 0 & 0 & -\nu_v & \lambda_v \end{pmatrix} \tag{6.105}$$

$$\mathbf{B_3} = \begin{pmatrix} \widehat{B_3} & 0 \\ 0 & \lambda_v S_v - \mu_v \end{pmatrix} \tag{6.106}$$

$$\widehat{\mathbf{B_3}} = \begin{pmatrix} \lambda_h - \mu_h S_e - \mu_h & \lambda_h - \mu_h S_e \\ -\mu_h S_a & -\mu_h S_a - \mu_h \end{pmatrix} \tag{6.107}$$

wherever, $K_1 = \nu_e + \mu_h, K_2 = \nu_a + \mu_h, K_3 = \mu_h + \alpha_e, K_4 = \alpha_a + \mu_h$, $M_{ev} = \Upsilon\varphi_{ev}\frac{S_v}{N_h}, M_{av} = \Upsilon\varphi_{av}\frac{S_v}{N_h}, M_{ve} = \Upsilon\varphi_{ve}\frac{S_e}{N_h}, M_{va} = \Upsilon\varphi_{va}\frac{S_a}{N_h}$. If at least one of B's eigenvalues has a positive real component, the DEF point is unstable, and if all of its eigenvalues have negative real components, it is asymptotically stable close by. The eigenvalues of B are therefore $-S_v\mu_v < 0$, as well as those of $\widehat{B_3}$ and $B_1 - B_2$. Numerous statistical analyses demonstrate

that

$$\mathrm{Tr}\left(\widehat{B_3}\right) = \frac{3\sqrt{4\mu_h + (\lambda_h - \mu_h)^2} + \mu_h + \lambda_h}{2} < 0 \text{ and} \tag{6.108}$$

$$\det\left(\widehat{B_3}\right) = \sqrt{(\mu_h - \lambda_h)^2 + \mu_h} > 0 \tag{6.109}$$

As a result, all of $\widehat{B_3}$'s eigenvalues have only strictly negative real components. We came to the conclusion that the eigenvalues of $B_1 - B_2$ are what determine the stability of the DEF point. Observe that B_2 has a positive column sum and a negative off-diagonal way in. It follows that B_2 is a non-singular M-matrix, according to [18]. Additionally, since B_1 is a non-negative matrix as of [106], the following result was discovered: $s(B_1 - B_2) < 0 \Leftrightarrow \rho\left(B_1 B_2^{-1}\right) < 1$ or $s(B_1 - B_2) > 0 \Leftrightarrow \rho\left(B_1 B_2^{-1}\right) > 1$, where $s(Q)$ is the sum of all the real components of the eigenvalues of the matrix Q. For the reason that

$$\mathbf{B_2^{-1}B_1} = \begin{pmatrix} 0 & 0 & 0 & 0 & \beta_{ve} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \beta_{va} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \beta_{ev} & 0 & \beta_{av} & 0 & 0 & 0 \end{pmatrix}$$

wherever β_{ve} is defined in equation (6.90) , β_{va} is defined in equation (6.89) , β_{av} is defined in equation (6.91) and β_{ev} is defined in equation (6.92) in that case $R_0 = \rho\left(B_2^{-1}B_1\right)$. As a result, the generation of disease in mosquitoes is included in our explanation of R_0. Due to the fact that R_0 is positive, $R_0 < 1$ is equivalent to $R_0^2 < 1$; $R_0 = 1$ is equivalent to $R_0^2 = 1$, and $R_0 > 1$ is equivalent to $R_0^2 > 1$. As a result, if $R_0 \leq 1$, the disease free equilibrium point is globally asymptotically stable, and as a result, mosquitoes vanish, whereas if $R_0 > 1$, the disease free equilibrium point is unstable, and as a result, mosquitoes endure.

Theorem 6.5.2. *The stationary equations* (6.1) *to equation* (6.10) *can be summary to a two dimensional one:*

$$F(u) = 0, u = (I_a, I_e) \in U_c \subset R^2 \tag{6.110}$$

anywhere u in U is a release region of $0 \in R^2$ *and F is a number of function of the group* C^∞ *on U. Furthermore for any* $\delta > 0$ *sufficiently small, all solution* $u \in U_c^+ := U_c \cap (0, \delta)^2$

of the equation $F(u) = 0$ *communicate to a exceptional solution* $x = x(u) \in \psi/\{x_{dfe}\}$ *from equation* (6.1) *to equation* (6.10).

A number of bifurcation studies are eliminated with this dimensional reduction. Prior to describing an example of application, we first state a frequent conclusion. Rewrite Equation (6.110) in the form of an equation after that.

$$F(u, \kappa) = 0, \tag{6.111}$$

Whenever there is a bifurcation control with the symbol κ in R. This control can originate from a precise model coefficient or from a large number of models that are all parametrized by κ. For the sake of simplicity, let's consider κ to be one exacting control that occurs in the model. We will take for granted that: (B_1): $\kappa \in V \subset R$, wherever V is a number of region of $\kappa = 0$, (B_2): Function F is distinct on some district UxV of $0 \in R^3$ and is of the group C^2 on UxV, (B_3): $F(0, \kappa) = 0, \forall \kappa V$, furthermore, observance in mind that κ is more or less included in a few control of the model, this permit us to clear a map $\kappa \to R_0(\kappa)$ that is suppose to assure, (B_4): When $\kappa = 0$ we get $R_0(0) = 1$, (B_5): The map $\kappa \to R_0(\kappa)$ is derivable at $\kappa = 0$ and $\frac{dR_0}{d\kappa}|_\kappa \neq 0$, and $B_5^{'}$: The map $\kappa \to R_0(\Theta)$ is derivable at $\kappa = 0$ and $\frac{dR_0}{d\kappa}|_\kappa > 0$. After that, by means of theorem (6.5.2) there is a only one of its kind infection free equilibrium point; therefore the point $u = 0 \in R^2$ match to x_{dfe}. After that, (u_{dfe}, κ), according to B_3, is a one-parameter solution of (6.111) that connects to the original system's disease-free equilibrium point. Currently, we have a collection of $u_{dfe}(I_a, I_e) = (0, 0)$. It will be shown as a result that a transcritical bifurcation may occur when κ crosses $\kappa = 0$, and the symbol for this bifurcation will be revealed. Because of this, we focus on the following situation.

Theorem 6.5.3. *Assume that* B_1 *through* B_4 *are true. The matrix* $B(\kappa) = D_u(0, \kappa)$ *then has two simple eigenvalues,* $\sigma_1(\kappa)$ *and* $\sigma_2(\kappa)$*, which depend continuously on kappa and have values of* $\sigma_1(0) = 0$ *and* $\sigma_2(0) < 0$*, respectively, up to a decrease in the magnitude of* V*. Additionally, if* B_5 *is unspecified, the map* κ *to* $\sigma_1(\kappa) = 0$ *is valid up to a decrease in* V*.Succeed in satisfying* $\sigma_1(\kappa) \neq 0$ *and* $\forall \kappa \in v/\{0\}$.

Suppose v and v^{**} be positive right and left eigenvectors of $B(0)$ equivalent to the null eigenvalue $\sigma_1(0)$ and regularize by $v^T v = v^{**} v = 1$. If we set $\chi = v^{**} D_u^2 F(u_{dfe}, 0)\langle v, v\rangle$ the

subsequent grasp where $D_u^2 F(u_{dfe}, 0)$ is defined in [38].

Theorem 6.5.4. *Assuming that B_1 through B_5 are true. The answer to the equation* (6.111) *is $u(\kappa) \in U(0,1)^2$ iff $\chi\sigma_1(\kappa) < 0$, which means that if $\chi \neq 0$, there is a neighbourhood of $u \subset U$ of $u = 0$ and a neighbourhood of $v \subset V$ of $\kappa = 0$.*

The proof of this result can be found in [38]. Now that we know how the bifurcating answer $u(\kappa)$ works, we can look into it.

Theorem 6.5.5. *Assume that B_1 through B_4 and B_5' are true. Then, if $\eta > 0$, there is widespread equilibrium $x \in \Omega$ close to the infection free equation x_{dfe} for $1 - \eta < R_0 < 1$ and if $\chi > 0$, there is endemic stability $x \in \Omega$ close to the infection free equation x_{dfe} for $1 < R_0 < 1 + \eta$.*

Note that when $\chi 0$, making R_0 somewhat more than one by a little modification in the control, offer increase to a positive branch of stability, in order to provide some strictly relevant analysis of the aforementioned result. However, there isn't an ordinary stable state if we drop R_0 to a little below one. Frequently referred to as a forward bifurcation, this type of bifurcation. For the time being, when $\chi > 0$, we obtain a positive branch of equilibrium when R_0 is just below one. Also known as a backward bifurcation or a sub-critical bifurcation, this type of bifurcation has two branches. To sum up, if we apply the amount R_0 directly to manage the malaria, we must lower R_0 beneath one to prevent it when $\chi > 0$. But in order to prevent malaria when $\chi > 0, R_0$ must be less than the amount suggested by ξ. For some $\eta > 0$, we can observe that $\xi \leq 1 - \eta$. This is according to the theory (6.5.5). We should not forget that the bifurcation was prone to occur at $R_0 = 1$ in the analysis of common epidemic models. In recent times, some authors have developed epidemic models that are crucial to the sub-critical bifurcation at $R_0 = 1$ and have emphasized their importance for the transmission of communicable diseases. For a known control situation, numerous stable states might undoubtedly persist even if $R_0 < 1$. The stability performance may change significantly with only little changes to the underlying concepts of these controls.

6.6 Effort required to control malaria

[52] By connecting the type-reproduction number ω for each host kind, the reproductive number (R_0) is a common signal that clarifies the required control effort for a particular host kind and offers an acceptable reproductive number. We examined the potential for controlling malaria through one of the three host types. The reproductive factor is the projected number of cases in individuals of type l, caused by one infected individual of kind l in a completely susceptible population, either directly or indirectly. We developed it separately for each variety of host. In [85], it is defined as the number of cases in individuals of kind l, directly or indirectly. The three host types that our model considers are mosquitoes, semi-immune hosts, and non-immune hosts. As was shown in the previous part, if we directly apply R_0 to control malaria, we must lower R_0 to less than one to avoid malaria while $\chi < 0$, or we must lower R_0 to less than xi to prevent malaria while $\chi > 0$. If we use the human population as the type host l, it is evident that the original definition of the malaria reproductive number accords with the type reproduction number ω_l. We must send the control to each subgroup in each situation in order to drop R_0 below one or ξ. Given how difficult and expensive it is to control each sub-group in order to minimize malaria, we pose the following question: Is it possible to eradicate malaria by using a particular subgroup of mosquitoes, such as non-immune or semi-immune insects? For each host type non-immune, semi–immune, and mosquito, we calculate the type reproductive numbers $\omega_e, \omega_a, \omega_v$ using the method outlined in [85]. The symbol $\rho(Q)$ is used to represent the spectral radius of the matrix Q, which is the transpose of the vector I, and the matrix Q, which is the 3×3 identity matrix. According to Roberts' citation, $\omega_I = \nu_I^{'} \nu_I \, (I(1-\beta) - \beta\ell_I)^{-1}$ for every $l = e$, a, and v.

$$\begin{cases} \nu_e = (1 \quad 0 \quad 0) \\ \nu_a = (0 \quad 1 \quad 0) \\ \nu_v = (0 \quad 0 \quad 1) \end{cases}, \ell_{\mathbf{e}} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \ell_{\mathbf{a}} = \begin{pmatrix} 0 & 1 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}, \ell_{\mathbf{v}} = \begin{pmatrix} 0 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

and the next-generation matrix indicated by Equation (6.85) is β. The author demonstrates in [85] that if the host kind β_l cannot sustain an epidemic on their own, then ω_l is defined. It is demonstrated logically that $\rho((I - \ell_I)\beta) < 1$ is positive if ω_l is correctly defined. The truth is that if ω_l is defined, a decrease of ω_l below one is sufficient to lower R_0 below 1

by limiting a control to the particular host l. Their theory is appropriate when the model is unable to exhibit the $\chi < 0$ backward bifurcation that is specified by Theorem (6.5.3). But when $\chi > 0$, we reinstate the condition $\rho((I - \ell_I)\beta) < 1$ by $\rho((I - \ell_I)\beta) < \xi < 1$. The following results are obtained for ω_e, ω_a and ω_v.

$$\begin{cases} \omega_e = \frac{R_1^2}{I - R_2^2} \text{ and } R_2 = \beta\rho(I - \ell_e) \\ \omega_a = \frac{R_2^2}{I - R_1^2} \text{ and } R_1 = \beta\rho(I - \ell_a) \\ \omega_v = R_0^2 \text{ and } \quad \beta\rho(I - \ell_v) = 0 \end{cases} \tag{6.112}$$

Assume $\chi > 0$ is true. The same reasoning can be applied if χ is greater than 0 by putting $\xi = 1$. ω_e and ω_a are clearly well defined if $R_1 < \xi$ and $\rho\beta(I - \ell_v) = 0 < 1$ are equal to 0, and ω_v is always well defined regardless of whether the substance is semi-resistant or not. As a result, the following can be said:

1. In regions with $R_1 < \xi$ and $R_2 < \xi$, such as $1 < R_0 < \sqrt{2}\xi$ or $1 < \omega_v < 2\xi^2$, malaria can be completely eliminated by targeting a control to one of the three host types.

2. To eradicate malaria in places where $R_1 < \xi$ and $R_2 > \xi$ exist, it is sufficient to target a control to semi-resistant or mosquito host types.

3. In locations where $R_1 > \xi$ and $R_2 < \xi$ are present, it is sufficient to target a control towards non-resistant mosquito host types.

4. Either we need to simultaneously target semi-resistant and non-resistant host types, or we need to focus on mosquito control in locations where $R_1 > \xi$ and $R_2 > \xi$.

Considering that the aim of the malaria control program is to reduce the proportion of susceptible people in a specific host type $l, l = a, e, v$ after one of the conditions (1) – (4), Keep in mind that the next-generation matrix coefficients, denoted by β_{jl}, represent the expected number of hosts of type l that would contract an infection from a single infectious host of type j. To totally eradicate malaria in the three populations in question, a fraction of $s_l > 1 - \frac{\xi^2}{\omega_l}$ of susceptible host type l needs to be safeguarded (by the control). When $\xi = 1$, see [52, 85]. This is presuming that β_{jl} is linearly affected by the aforementioned controls. The use of bed nets sprayed with insecticide, sporadic preventative care, or a vaccine for those who are not yet resistant can all be used to implement

this control strategy. As a method of vector control for mosquitoes, residual insecticide spraying inside is an option, as are insecticide-treated nets. It is sufficient to eradicate a percentage of mosquitoes greater than $1 - \frac{\xi^2}{\omega_a}$, a percentage of non-resistant mosquitoes greater than $1 - \frac{\xi^2}{\omega_e}$, or a percentage of semi-resistant mosquitoes in areas where condition (1) is satisfied. It is sufficient to destroy a percentage of mosquitoes greater than $1 - \frac{\xi^2}{\omega_v}$ in places where condition (2) is met, or to permanently protect a section of semi-resistant plants more than $1 - \frac{\xi^2}{\omega_a}$. It is sufficient to permanently protect a portion of non-resistant organisms greater than $1 - \frac{\xi^2}{\omega_e}$ or destroy a portion of mosquitoes greater than $1 - \frac{\xi^2}{\omega_v}$ in places where condition (3) is satisfied. For malaria to be completely eradicated or to concurrently protect the non-resistant and the semi-resistant, it is sufficient to permanently remove a part of mosquitoes more than$1 - \frac{\xi^2}{\omega_v}$ at birth in locations where condition (4) is met.

Since the non-immune are the most vulnerable, we must begin the control process with them. This has led to a decline in morbidity and mortality. Effective control may also contribute to the eventual eradication of malaria because requirement (3) is frequently satisfied. A forward bifurcation of endemic steady states in the malaria model is possible, according to simulations with realistic parameter settings. Because of this, eliminating malaria may not always be feasible when R_0 is less than 1. Even if malaria has been completely eradicated in the region in question, a slight disturbance, such as ecological changes, could still result in its reappearance in the three categories (mosquitoes, non-resistant people, and semi-resistant people). In an area with low or moderate malaria transmission, our model suggests that it is sufficient to target a control at a specific host type to eradicate malaria. In a larger area where the birth rate of semi-resistant people is much higher than the birth rate of non-resistant humans, malaria can always be kept under control among the non-resistant population. Malaria can always be maintained under control among the semi-resistant in a populated area where the birth rate of non-resistant people is fairly high, followed by the birth rate of semi-resistant people. With the use of vaccines, malaria can be fully eradicated in some regions where there is a low number of human births. Based on the results of our investigation, we draw the conclusion that if a vaccine or other straightforward preventive measure were to become available, it would

be required to research the particular host type in order to entirely eradicate malaria. In regions where we are unable to target a control toward either non-resistant or semi-resistant host species to prevent the transmission of malaria, our model shows that malaria can be entirely eradicated by controlling mosquitoes. Similar to this, malaria can always be managed by employing non-resistant people in an area where the disease is endemic and there is a high rate of births per person. Epidemiological outbreaks can occasionally occur in regions of the world where the spread of malaria is unpredictable and varies greatly from year to year. Our analysis leads us to the conclusion that we need to pinpoint the exact host type to focus on if we want to eradicate malaria. Even if a simple vaccine or preventive measure were to become available, this would still be the case. Our model shows that, even in environments where we are unable to direct a control toward either the non-resistant human host type or the semi-resistant human host type, malaria can always be entirely eradicated by controlling mosquitoes.

Even if doing so has a well-known result, it is frequently easier said than done. This is because it is impossible to entirely eradicate mosquitoes in places where there is a significant mosquito population. Even if these steps are feasible, they are very expensive. On the other hand, by reducing the mosquito population in locations where malaria transmission is comparatively weak, malaria can be successfully eradicated in areas with a low mosquito population. Consider a region with a very low human birthrate per person, which makes it possible for it to be disregarded, as in the scenario where condition (2) is met. The semi-immune are the only ones who support the human population. Therefore, we must target the semi-immune with the control in order to stop the sickness. In light of this, if a vaccine were available, it would be sufficient to immunize any susceptible semi-immune, and if condition (3) were satisfied, R_2 might naturally be lower than one in accordance with the theory known as transmission-blocking immunity, which considers that immunity reduces the transmission of parasites from semi-immune to mosquito). As a result, the possibility of transmission from a person who is partially immune to a mosquito is discounted. We must concentrate the control on non-immune people in order to stop the disease from spreading since semi-immune people have a built-in immune memory and there is less chance that an infected semi-immune will transmit the disease

to a mosquito. Consequently, if a vaccine were to become available, it would be sufficient to immunize every susceptible, non-immune person.

6.7 Numerical Simulation

Table (6.3) is plotted with a constraint worth mentioning in region two of the charitable figure (6.2): $R_1 = 2.62339 > 1$, $R_2 = 1.4225 > 1$ and $R_0 = 2.97458 > 1$, respectively. Figure (6.3)is achieved with constraint ideals that are evident in Table (6.3) in region one charitable $R_1 = 0.445567 < 1$, $R_2 = 0.36789 < 1$, $R_0 = 0.73795 < 1$, $\omega_e = 1.6876$, $\omega_a = 17.29$ and $\omega_v = 1.3937$ with original situation: $E_e = 0.000$, $E_a = 0.000$, $I_e = 2.0000$, $I_a = 1.00$, $R_a = 29.000$, $E_v = 18.0000$, $I_v = 13.00$, $N_h = 395.00$ and $N_v = 13,000.0000$. with the original situation. An example in mathematics is $R_0 = 2.9838, R_1 = 2.6449$ and $R_2 = 1.4245$ with the following primary situation: $E_e = 0.000, E_a = 0.000, I_e = 2.00, I_a = 1.0000, R_a = 29.0000, E_v = 19.0000, I_v = 11.0000, N_v = 396$ and $N_v = 13,000$ are plotted with constraint worth defined in Table (6.3) region one are specified in Figure (6.2). When using the restrictions in Table (6.3), on region two, we were able to see the broad stability values for the number of transferable non-resistant individuals in Figure (6.4).

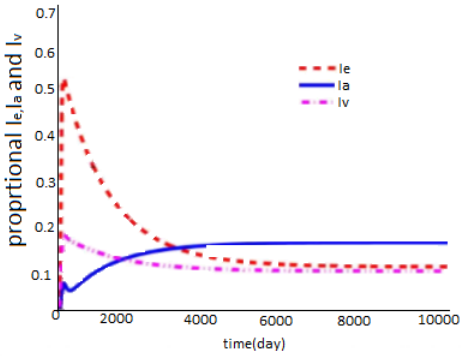


Figure 6.2: Infectous and semi-infectious class: $R_1 > 1$ and $R_2 > 1$

Table 6.3: The Base Line principles and variety for ten dimensional malaria model

No	parameter (constraint)	region one	region two	low	high
1	λ_v	0.23	0.23	0.4	0.39
2	φ_{ve}	0.0430	0.092	0.033	0.45
3	φ_{va}	0.044	0.044	0.03	0.49
4	φ_{ev}	0.33	0.66	0.078	0.96
5	φ_{av}	0.09	0.6600	0.083	0.93
7	γ_e	0.3	0.3	0.087	0.45
8	γ_a	0.09	0.09	0.088	0.04
9	γ_v	0.091	0.094	0.094	0.33
10	α_a	0.03	0.03	0.0025	0.035
11	α_e	0.007	0.006	0.0066	0.087
12	μ_v	0.055	0.066	0.008	0.9
13	Υ	0.48	0.49	0.55	0.77
14	Ω_a	0.88×10^{-5}	0.45×10^{-4}	0.33×10^{-3}	0.77×10^{-6}

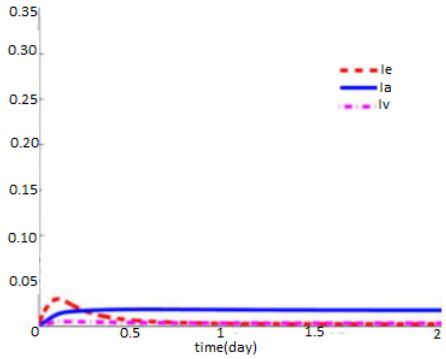


Figure 6.3: Infectous and semi-infectious class: $R_1 < 1$ and $R_2 < 1$

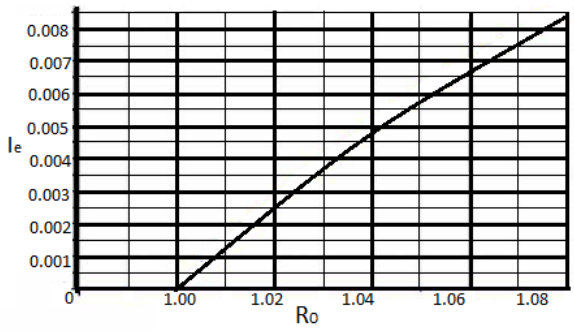


Figure 6.4: Forward birfication

6.8 Conclusion

In this section of the thesis, we examined a 10-compartmental mathematical model for the transmission of malaria. We divided the human host into two major groups: the first group, called non-immune, included all individuals who are not immune to malaria, and the second group, called semi-immune, included those who are somewhat immune to malaria. On the other hand, we divided non-immune persons into vulnerable, exposed, and infectious groups as well as semi-immune people into vulnerable, exposed, and infectious categories. Additionally, we separated the mosquito population into three categories: vulnerable, exposed, and infectious. We provide an explicit formula for the reproductive number that depends on the weights of transmission from non-immune humans to mosquito and from non-immune humans to mosquito, as well as the weights of transmission from semi-immune humans to mosquito and from mosquito to semi-immune humans. As a result, the reproductive number for the entire population is equal to the square root of the sum of the squares of these weights for the two types of interaction. The DFE point is stable if $R_0 > 1$, which indicates that the population is still infected with malaria, and the DFE point is GAS if $R_0 \leq 1$, which indicates that the malaria dies off. We discuss the potential for a control for malaria transmission throughout a specific sub-group such as non-immune or semi-immune mosquitoes. The model's results confirm that the disease free equilibrium is asymptotically stable at the reproductive number less than one and unstable at the reproductive number greater than one. To present the findings and investigate potential outcomes of the developed model, simulations are run. Our model has a singular, globally defined solution that stays in this area for all non-negative moments, and

we have cleared this area of that solution. By using the local stability of the DFE point, we were able to obtain an explicit formula for the reproductive number,R_0. We discussed R_1, which is the weight of the transmission from semi-immune to mosquito and -semi-immune and R_2, which is the weight of the transmission from semi-resistant mosquito to semi-resistant mosquito. When we attempted to evaluate the mathematical modeling of malaria transmission in ten dimensions like we did the other mathematical modeling of malaria transmission, it was challenging or we could not analyze some aspects due to the number of dimensions.

Chapter 7

CONCLUSION AND RECOMMENDATION

Smallpox, tetanus, and seasonal influenza are just a few of the illnesses that can be avoided with vaccination. For some diseases, such as HIV, there is no vaccine against resistance. According to one study, malaria is an infectious illness that passes between people through mosquito bites and claims the lives of almost two million people every year. The prevention of these diseases requires a multi-system approach, which includes the use of vaccines that can be purchased. The spread of communicable diseases has a negative influence on the economics and population growth of non-vaccination countries, even when vaccination campaigns are ineffectual. In this thesis, we look at the analysis of a SIR model with reproduction number R_0 and the analysis of a $SIRV$ model with a new reproduction number R_v. Along with the relationship between the two models SIR and $SIRV$ with regard to the existence of the DFE and EE points, the viability of the solution, the positivity of the solution, the reproductive number, and the analysis of the linear stability and the global stability of both the models SIR and $SIRV$ are all argued. In this thesis, we extend the derivation and analysis to a five-compartmental mathematical model, with three human factors and two insect factors, for better acceptance of the transmission of malaria infection. This mathematical model with five compartments is analyzed by exam-

ining the reproductive number, reproductive viability, equilibrium points, linear stability, and global stability of the solution.

In order to better understand the transmission of malaria infection, we further expand the derivation and analysis in this thesis to a ten-compartmental mathematical model with four variables for semi-immune humans, three variables for non-immune humans, and three variables for mosquitoes. The analysis of the reproductive number, equilibrium points, linear stability, and global stability, as well as the viability and positivity of the solution, are all included in this ten-compartment mathematical model's investigation. It progresses from straightforward analysis to intricate analysis, as we observed in our study of the three, four, five, and ten-compartmental models. The ten-compartmental model in particular was more challenging to assess and less clear-cut than the three, four, and five compartmental models. Although it is advantageous to develop a ten-compartment mathematical model to better understand malaria transmission, we suggested that it would be better to study a model with fewer compartments. It is common knowledge that Ethiopia is one of the underdeveloped countries lacking adequate resources. We suggested to those nations including Ethiopia that they lacked the resources necessary to comprehend the life cycle of mosquitoes, how malaria is spread, and how to create a mathematical model of malaria transmission in order to completely remove the disease from their populations. When we studied the mathematical modeling of malaria transmission in ten compartments like we did with the other mathematical modeling of malaria transmission, it was challenging or we couldn't investigate some points because of the numbers of the dimensions.

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