UNIVERSITY OF CAPE COAST

A MATHEMATICAL MODEL FOR EFFECTIVE CONTROL AND

POSSIBLE ERADICATION OF MALARIA

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A MATHEMATICAL MODEL FOR EFFECTIVE CONTROL AND

POSSIBLE ERADICATION OF MALARIA

BY

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DECLARATION

Candidate's Declaration I hereby declare that this thesis is the result of my

own original research and that no part of it has been presented for another degree

in this university or elsewhere.

Candidate's Signature ....   Date ....
Name: AGNES DONKOR

Supervisors' Declaration

We hereby declare that the preparation and presentation of the thesis were supervised in accordance with the guidelines on supervision of thesis laid down by the University of Cape Coast.

Principal Supervisor's Signature ....   Date ....
Name: PROF. FRANCIS BENYAH

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ABSTRACT

In this study, a novel deterministic mathematical model for the transmission and control of malaria is formulated. The main innovation in the model is that, in addition to the natural death rate of the vector (mosquito) population, a proportion of the *prevention effort* also contributes to a reduction of the vector population. The model assumed that a proportion $c\alpha$, $0 \leq c \leq 1$ of the prevention effort α contributes to the death rate of the vector population. The study showed that there exists a domain where the model is epidemiologically and mathematically well-posed. The study showed that the model has a unique disease free and an endemic equilibrium points. It was established that the disease free equilibrium is locally and globally asymptotically stable when $\mathcal{R}_0 < 1$ and the endemic equilibrium is locally and globally asymptotically stable when $\mathcal{R}_0 > 1$. Parameters of the model were estimated from monthly confirmed malaria cases obtained from the Central Region of Ghana. A sensitivity analysis was carried out to determine the effects of each parameter on the basic reproduction number, $\mathcal{R}_0$. The result from the sensitivity analysis showed that the two most sensitive parameters in the reduction of $\mathcal{R}_0$ are *prevention* and *treatment*. Based on the result from the sensitivity analysis, numerical simulations were performed using various combinations of treatment and prevention to determine an optimal combination that reduces the incidence rate fastest. The result of the simulations showed that, with about 40% of effective prevention coupled with about 40% of treatment, will considerably reduce both the infected human and vector populations. The higher the prevention effort, the higher the reduction in the infected vector population. If the prevention efforts are implemented by all contiguous communities in the region, acting in concert, then a marked reduction should be seen in the infected vector population leading to a complete eradication of malaria in the region, by implication, through out Ghana.

KEY WORDS

Gershgorin circle

Malaria

Parameters

Prevention rate

Stability Analysis

Treatment rate

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DEDICATION

To my family

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CHAPTER ONE

INTRODUCTION

In this chapter, we look at some background information of the study, the statement of the problem, the purpose of this study, the significance of the study and how the chapters of study are organized.

Background of the Study

Since the late 1950s, controlling and elimination of the organisms responsible for infectious diseases has been one of the main focuses of Public health officials. The effectiveness in the improvement in sanitation, enhanced antibiotics and prevention strategies brought hope in the elimination of infectious diseases in the 1960s. Studies have shown that infectious disease agents adapt and evolve over time, and as a result, new infectious diseases come forth and some existing diseases also resurface (Hethcote, 2000). But, resistance to medicine by the microorganisms, demographic evolution, increased urbanization and increased travelling, facilitates the emergence of new infectious diseases and the resurface of existing diseases. According to Hethcote (2000), diseases such as Lyme disease discovered in 1975, Legionnaires disease discovered in 1976, Toxic shock syndrome discovered in 1978, Hepatitis C discovered in 1989, Hepatitis E discovered in 1990, and Hantavirus discovered in 1993 are newly identified diseases. The emergence of Human Immunodeficiency Virus infection and Acquired Immune Deficiency syndrome (HIV/AIDS) in 1981 suddenly gained prominence in the world as a growing public health issue.

Antibiotic-resistant strains of tuberculosis, pneumonia and gonorrhea have evolved and these diseases are reemerging. Malaria, dengue, and yellow fever have also reemerged and are spreading into new regions because of climate change. Diseases such as plague and cholera continue to erupt occasionally.

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Most recently, the reemergence of Ebola virus disease (EVD) in 2013 has perplexed the world. Reemergence continues to be serious medical burden for the world because it is estimated that every year 15 million death are directly related to reoccurrence of infectious diseases (Hethcote, 2000).

According to WHO (2016), each year, about sixteen percent of all deaths all around the world are caused by infectious diseases with most of these deaths in low and middle-income countries and are attributable to preventable or treatable diseases such as diarrhea, lower respiratory infections, HIV/AIDS, tuberculosis, and malaria. Even though significant advances have been made in strategies toward prevention and treatment of most of these diseases, those strategies are often unavailable to the populations most in need (WHO, 2016). Eradication of most infectious diseases could have been made possible if in the course of the epidemic, adequate and timely steps such as prevention strategies, treatment, educational and enlightenment campaigns are done. However, due to lack of adequate policies and timely interventions to mitigate the spread of the diseases many of these diseases finally become endemic in our society. Therefore, proactive steps are needed towards controlling the spread of infectious diseases. Since, it is cheaper to prevent the occurrence of a disease than to cure it.

Statement of the Problem

Malaria is a serious and sometimes fatal epidemic affecting nearly half of the world's population. In 2016, there were 217 million cases, but there were 219 million cases of malaria in 2017 (WHO, 2019). The estimated number of death due to malaria deaths stood at 435,000 (WHO, 2019). World-wide, malaria is the 5th leading cause of death from infectious diseases. But in Africa, it is the 2nd leading cause of death. In 2017, children under five years of age accounted for $61\%(266,000)$ of all malaria deaths worldwide. The Africa Re-

gion is seen as the home to 92% of malaria cases and 93% of malaria deaths in 2017 (WHO, 2019). Malaria is hyper endemic in all parts of Ghana. Ghana's entire population is at risk of malaria, but transmission rates are lower in the urban areas (Naandam, Essel, Nortey, & Soderbacka, 2013). It contributes to over a third of all outpatient cases in Ghana. Malaria contributed to 20% to 30% of death in children under five years of age and 11% of maternal mortality (JSI Research & Training Institute, 2013).

After the work of Ross (1911) many researcher have modelled malaria focusing on different strategies. N. R. Chitnis (2005) modelled malaria as a 7-staged state Ordinary Differential Equations (ODE's) to compare intervention strategies for malaria control for two representative areas of high and low transmission focusing on the most effective prevention strategies.

Objectives of the Study

A number of studies have been carried out to combat vector-borne diseases, and in most cases, they focus on vector-control. In this study, we formulate malaria model considering preventive (α) and treatment (γ) parameters since there is the need to look for best approach or strategies to eliminate malaria from our societies, regions, countries and the world as a whole.
The main objectives of this study were:

(a) To develop mathematical models for the transmission of malaria

   (i) incorporating prevention and treatment as the main control strategies.

   (ii) showing that a certain proportion of the prevention strategies increases the death rate of the mosquitoes.

(b) To estimate the unknown parameters of the model using monthly malaria prevalence data from the Central Regional Health Directorate of the Ghana

Health Service from the year 2013 to 2017 and carry-out sensitivity analysis of the parameters that make-up the basic reproduction number.

(c) To preform several simulations of the model to determine an optimal combination of *prevention and treatment* that reduces the prevalence, and possibly eliminate the disease.

Significance of the study

(a) This study will provide Health care authorities the implementation of the appropriate strategies needed for effective control of malaria.

(b) It will help in the reduction of the number of malaria infection translates to a marked decrease in outpatient malaria cases in our hospitals, thus easing the congestion in our hospitals.

(c) It will help reduce morbidity and mortality due to malaria.

Organization of the Thesis

The study is organized in seven chapters. Chapter One of the thesis deals with the background of the study, the objective of the study and the significance of the study. Chapter Two deals with literature review (Review of Previous Studies on malaria transmission and control). Chapter Three looks at some mathematical concepts necessary for the study. In Chapter Four, we analyze local stability of some selected epidemic models using a corollary of Gershgorin's circle theorem. In Chapter Five, we formulate a mathematical model for malaria transmission incorporating prevention and treatment as the main control

strategies that will help in the reduction and possible eradication malaria by incorporating the effect of prevention on the vector populations.we perform local stability analysis using a corollary of Gershgorin's circle theorem, the global stability of the disease free equilibrium is also done. In chapter Six, we use data to validate the malaria model and perform simulation to determine the combination of controls (prevention/treatment strategies) that will help in the reduction of infected human and vectors populations and hopefully to contribute towards eradication of the infectious diseases. Chapter Seven summarizes the work and salient observations from the study are presented. Some of the observations are discussed and appropriate conclusions drawn based on the result of the study.

Chapter Summary

Several researchers and scientists have proposed different mathematical models for infectious diseases. Mathematical modelling holds great promise in providing new, counter-intuitive insights into the dynamical processes intrinsic to mechanism and control of infectious diseases. This chapter looked at the background of infectious diseases and the implication of mathematics in the control of infectious diseases. A brief statement of the problem was given and the objectives and the significance of the study were stated in this chapter.

CHAPTER TWO

LITERATURE REVIEW

Introduction

Mathematical models for Infectious diseases is the representation of the dynamic transmission cycle, involving interactions between infected and susceptible hosts that are generally expressed as a set of ordinary differential equations (ODEs) (Wu, Dhingra, Gambhir, & Remais, 2013).

Mathematical modelling plays an important role in epidemiology by providing better understanding of the underlying mechanisms for the spread of occurrence and reoccurrence of infectious diseases and suggesting effective control strategies (Hethcote, 2000).

It is an important tool that helps to understand the dynamics of infectious diseases and to support the development of control strategies (Ullah, Zaman, & Islam, 2013).

Review of Previous Studies

The mathematical modelling of malaria transmission started with the work of Ross (1911) and Macdonald (1956) and was continued by (Anderson & May, 1992). Over a century, Mathematical models have been used to produce an explicit framework for understanding malaria transmission dynamics in human population. Sir Ronald Ross is seen as the originator of modern mathematical epidemiology. In his pioneering work on malaria, he observed that it is transmitted from humans and mosquitoes and vice versa while working at the Indian Medical Service in 1911. Ross (1915) formulated a simple model, which is called the classical "Ross model". This model explained the relationship between the number of mosquitoes and incidence of malaria in humans. Different researchers Like Pampana (1969), Anderson and May (1992), Yang and

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Ferreira (2000) and others have formulated different models from the Ross's model. They incorporate different factors such as latent or exposed classes in mosquitoes and humans, age-related differential susceptibility to malaria in human population, acquired immunity and genetic heterogeneity of host and parasite, In Ross first mathematical model of malaria, he used the word "pathometry" to mean "quantitative study of a disease either in the individual or in the community". Ross (1911) received the Nobel Prize in 1902 for his work done on malaria. Ross's major concentration was on prevention of malaria. Despite his contributions, he was unable to convince his contemporaries that malaria could be eradicated through the reduction of the number of mosquitoes. His main advantage was his ability to provide a suitable control strategy through the transmission threshold criterion which is based on the reproductive capacity of the parasite, that is, basic reproductive number $(\mathcal{R}_0)$ as used in the second edition of his book "The Prevention of Malaria", published in 1911.

The idea of threshold could be traced from Fisher's "net reproductive value" for a parasite, ((Fisher, 1999) and (Mandal, Sarkar, & Sinha, 2011)), even though Ross (1911) was the first to use it. George Macdonald in the 1950s, after about 40 years reasserted the value of mathematical epidemiology based on 20 years of fieldwork. He modified Ross (1911) model by incorporating latent period in the mosquito due to malaria parasite development, and considered the survivorship of adult female mosquito as the weakest element in the malaria cycle. His work brought about the basis for a massive World Health Organization (WHO) coordinated campaign. The insecticide dichlorodiphenyltrichloroethane (DDT) was used to kill mosquitoes and this resulted in the elimination of malaria transmission among 500 million people in Africa, ((Macdonald, 1956) and (Pampana, 1969)). In (Macdonald, 1956) model the mosquito population is divided into three compartments (SEI), and the time evolution of the exposed and infected classes in mosquito were studied.

Anderson and May (1992) estimated parameter values from compiled data including the exposed period in mosquitoes and humans, the recovery rate for humans, the life expectancy of adult mosquitoes and malaria prevalence data across age distributions for humans. They discussed the effect of age structure to the basic Ross (1911) model. This was suggested by Anderson and May in the simple Ross (1911) model in which they consider the human population density. Finally, they considered different control strategies, discussing the effects of a vaccine and the reduction of transmission rates on the malaria age-prevalence profile of the human population. Yang and Ferreira (2000) showed that the basic reproductive number of malaria transmission changes with global warming and local social and economic conditions. In their book, the good, intermediate and poor model, economic conditions among human community were considered and each condition was further divided into three temperature zones. A host of factors controlling disease transmission rates in his model are differential immunity, endemicity, resistance, economic conditions and temperature dependence of mosquito development. These modelling results propose the requirement of proper management of the surrounding environment, along with good health care system, in disease transmission. According to N. Chitnis, Hyman, and Cushing (2008), mathematical modelling of malaria can play an important role in comparing the effects of control strategies used individually or in packages. Comparison was done by determining the relative importance of model parameters in malaria transmission and prevalence levels in their work. They compiled two sets of baseline parameter values: one for areas of high transmission and one for low transmission. They computed sensitivity indices of the reproductive number and the endemic equilibrium point to the parameters at the baseline values. They found that in areas of low transmission, the reproductive number and the equilibrium proportion of infectious humans are most sensitive to the mosquito biting rate. In areas of high transmission, the reproductive number is

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again most sensitive to the mosquito biting rate, but the equilibrium proportion of infectious humans is most sensitive to the human recovery rate.

According to Mandal et al. (2011), for all malaria model which were formulated before Ngwa and Shu (2000) model, the total population sizes were considered to be constant. In Ngwa and Shu (2000), they proposed an immunity model in which disease related death rate is considered to be significantly high and the total population not constant. TheNgwa and Shu (2000) model comprises of four compartments in humans namely; Susceptible (S_h) , Exposed (E_h), Infected (I_h) and Immune (R_h) and three compartments in mosquitoes namely; Susceptible (S_m) , Exposed (E_m) and Infected (I_m). In the analysis of their model, they proved that the Basic Reproductive Number, $(\mathcal{R}_0)$, can describe the malaria transmission dynamics of the disease and a globally stable disease-free state exists if $\mathcal{R}_0 < 1$, while for $\mathcal{R}_0 > 1$, the endemic equilibrium becomes globally stable. This model explicitly shows the role of inclusion of demographic effects (net population growth) in predicting the number of fatalities that may arise as a result of the disease.

Also, N. R. Chitnis (2005) and N. Chitnis, Cushing, and Hyman (2006) included constant immigration of susceptible human population in their model. Considering immigration of people and excluding direct human recovery from the infectious to susceptible class as considered in Ngwa and Shu (2000) model and other models. They showed that the population approaches the locally asymptotically stable endemic equilibrium point, or stable disease-free equilibrium point, depending on the initial size of the susceptible class.

Yang and Ferreira (2000) divided the immune class in human population into immune, partially immune and non-immune but with immunologic memory, with each class having differential immunity. The mathematical analysis of Yang's model shows that the effects of these three types of immune responses lead to delay in the reappearance of the individuals, who already had expe-

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rienced malaria, to the susceptible population. Hence the community under high threat of malaria (high) shows low prevalence of individuals with asexual blood-stage infection and without infectious gametocytes, whereas, the same community is relatively free of severe infection due to the increase in immunity by re-infection. Due to lack of confirmed markers of immunological protection, different processes that determine the immunity acquisition to clinical disease and to asymptomatic carriage of malaria parasites are poorly understood.

Filipe, Riley, Darkeley, Sutherland, and Ghani (2007) recommended an insightful approach which is three age-specific "immunity-functions" in their SEI model for the human host. The infected humans are divided into three classes - infected with severe disease, asymptomatic patent infection, and infected with undetectable parasite density. The effect of mosquito density was incorporated through the force of infection. Reducing the susceptibility to clinical disease, speeding up of the clearance of detectable parasites, and increasing tolerance to sub-patent infections are the three immunity functions introduced in the Filipe model. These functions depend on age and disease transmission intensity in a complex manner. They base their model assumptions on the fact that the rates at which both types of immunity - clinical and anti - parasite - develop are different. All these processes have widely varied time scales, which make the disease transmission in this age-structured population complex. The first two types of immune functions reproduced the epidemiological age-prevalence curves seen in empirical data better. The third one i.e. the tolerance to sub-patent infections, is not required to explain the empirical data.

Several mathematical models have been developed with pathogen population structure and heterogeneous host population to explain variable antigenic response, immune selection, pathogen strain structure, (Gupta and Galvani (1999), Gupta and Anderson (1999) and Recker et al. (2004)). Addition of evolution of drug resistance, along with other factors, in the models

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can assist in the design of rational strategies for the control of drug resistance, ((Hastings, 1997), (Dye & Williams, 1997) and (Mackinnon, 2005)). A number of resistant-strain models have been developed based on evolution of drug resistance through host immunity and by considering the practical implications of the Artemisinin combination therapy (ACT) drug policies adopted by a lot of countries. Population genetic considerations of the cost of resistance are also included in this type of models. More recent work elaborates the complexity of the process of drug resistance by considering the interaction of several environmental, pharmacological and genetic factors, (Antao & Hastings, 2011). In general, these resistant-Strain models divide the infected host population into two compartments, i.e., infected by drug-sensitive strain and drug-resistant strain of the parasite. The model proposed by Koella and Antia (2003), further divides the host population infected by drug-sensitive strain into two compartments are treated and untreated. So this model consists of five compartments of human: susceptible, sensitive, infected and treated, sensitive, infected and untreated, infected with the resistant strain, and the recovered . The role of mosquito vector is included through inoculation rates of sensitive and resistant parasites. The main prediction of this model indicates that there is a threshold proportion of people among the infected and treated classes, below which resistance cannot spread, and above which resistance will eventually become fixed in the population. The model also shows that, in the absence of drug or treatment, the fitness of resistant parasite reduces with respect to sensitive parasite; otherwise both the parasites have identical properties. In this case, sensitive and resistant parasites cannot co-exist.

The basic reproductive numbers for the early models depend crucially on the parameters related to mosquito density. Environmental factors, such as temperature, humidity, rainfall and wind patterns have great impact on mosquito reproduction, development and longevity and the parasite survival in its life cycle

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in mosquito. It is known that mosquito breeding is influenced by temperature - a change in temperature from 12^0C to 31^0C reduces the number of days required for breeding from 65 days to 7.3 days. The sporogony of the parasites in vector is completed in 55 days at 16^0C, which reduces to 7 days at 28^0C, (Martens et al, 1995). Influence of temperature and humidity change on the rate of transformation from juveniles to adults in the susceptible class of adult mosquitoes has been modelled, (Li et al., 2002). Malaria typically is found in warmer regions of the world - in tropical and subtropical countries yet malaria does not occur in all warm climates. For example, malaria has been eliminated in some countries with warm climates, while a few other countries have no malaria because Anopheles mosquitoes are not found there.

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 colour noise in infected mosquito dynamics of Ross (1911) model, Chattopadhyay, Sarkar, Chaki, and Bhattacharya (2004), periodic or noisy form of the force of infection, (Anderson & May, 1992). Several studies have also included the effect of environmental fluctuations in ways with the goal to develop realistic and validated malaria modelling frameworks that are able to identify the crucial linkages between pathogen transmission processes and climactic factors(Yang & Ferreira, 2000). Parham and Michael (2010), studied the dynamics of the mosquito population by considering simultaneous effects of rainfall and temperature. The model consists of three compartments in humans with fixed duration of latency, and three compartments in mosquitoes. Different environmental factors are introduced in this model through parameters related to mosquitoes. The birth rate of adult mosquito is considered to be a function of rainfall and temperature, whereas, mosquito mortality rate, biting rate, duration of sporogonic cycle and survival probability of infected mosquitoes over the incubation period of the parasite are considered

to be dependent on temperature variation. The major finding of this model is that changes in rainfall patterns not only influence vector abundance, but also strongly govern malaria endemicity, invasion and extinction. However, when sufficient rainfall exists to sustain vector development and survival, then the temperature affects the pathogen life cycle, and has stronger influence on the rate of disease spread (Azu-Tungmah, 2012).

The Global Malaria Control Strategy is a concerted effort meant to bring about changes in the way malaria problem is addressed. As a result, this strategy stresses the selective use of preventive measures wherever they can lead to sustainable results. The measures are aimed at halting the deteriorating effects of the malaria situation, minimizing the wasteful use of resources and contributing appropriately to the development of health services, intersectoral cooperation and community participation. Malaria affects the health and wealth of nations and individuals alike. In Africa today, malaria is understood to be both a disease of poverty and a cause of poverty (Greenwood & Mutabingwa, 2002) and (Sachs & Malaney, 2002). Malaria is said to have significant measurable direct and indirect costs, and has been proven to be a main constraint to economic development (Sachs & Malaney, 2002). This means the gap in prosperity between countries with malaria and countries without malaria has become wider every single year. Gallup and Sachs (2001) showed that where malaria has been eliminated, economic growth has increased substantially. Hence we need to find cost effectiveness of the intervention strategies.

In this study, we formulate malaria model similar to that of (N. R. Chitnis, 2005). We incorporate prevention strategies that move people directly from the susceptible class to the recovered class. We also assume that a certain proportion of the prevention strategies α increases the death rate of the mosquitoes, that is, $c\alpha$ where $0 \leq c \leq 1$. and perform numerical simulations to come up with the combination of levels of treatment and prevention strategies needed to reduce or

eradicate malaria.

Treatment and Preventive Strategies

It is important to combine strategies if treatment and prevention of malaria it breaking the "host-vector" contact cycle of transmission and curing the infected individuals is our main goal. The control of malaria involves vector control, education and control of parasites in man. The breaking of "man-vector" contact cycle of transmission is the most efficient control measure. Internationally and nationally, the Roll Back Malaria (RBM) Initiative instigated by WHO's Director General in 1998 has integrated malaria into other health programmes and partnerships. There has been an increased campaign in the global awareness of malaria and the Global Fund to Fight AIDS, Tuberculosis and Malaria (GFATM) started operations in 2002. By mid-2004, the GFATM allocated about 2 billion US dollars for malaria control over a five-year period. There have a massive reduction in preventable mortality in low- and middle income countries, as evidenced by the 50% reduction in childhood death, 25% reduction in malaria cases and the World Health Organization(WHO) certification of four countries as malaria-free. "world free of malaria" is the main goal of the World Health Assembly in 2015 which recently endorsed WHO's Global Technical Strategy for Malaria and the Roll Back Malaria Partnership's Action and investment to defeat Malaria (AIM). Their agenda is to reduce malaria case incidence and mortality rates globally by at least 90% by 2030.

Larviciding and Environmental management: It is the destruction of the larval stage of the mosquito by the spraying pesticide and the destruction of breeding sites with the goal of reducing the number of mosquitoes.

spraying (Space and Indoor residual spraying (IRS)): IRS is seen as the most cost effective control method in seasonal transmission zone. It helps in increasing the mosquito death rate and reduces the number of mosquitoes.

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Insecticide-treated bed nets (ITN): The use of INTs is most cost effective method for endemic and Holoendemic zones. According to N. R. Chitnis (2005), ITN's have had a significant impact on disease prevalence and mortality. Man-vector contacts is reduced with an increased number of bed nets and also increases the mosquito death rates.

Insecticide-treated livestock: As stated in N. R. Chitnis (2005), studies are underway in regions that have zoophilic mosquitoes to treat cattle and other livestock close to homesteads with insecticides. There similarities in the effect of Insecticide-treated livestock to IRS, treating livestock with insecticide has been shown to be more cost effective in areas where the mosquitoes are mostly zoophilic. Insecticide-treated livestock is also an effective strategy like IRS.

Intermittent prophylactic treatment (IPT): This is the administration of antimalarial drugs at regular intervals, including those who are not sick, to reduce parasitemia load. It is similar to the treatment taken by travellers from malaria-free regions when visiting malaria-endemic countries.This involves administering malarial medicine to pregnant women, regardless of whether or not they have show symptoms of malaria and that is, Intermittent prophylactic treatment in pregnancy (IPTp). There are Intermittent prophylactic treatment for infants (IPTi).All the controls stated above together with house screening, repellents, fumigants and long sleeved clothing are ways of reducing "man-vector" contact. However, to detect and respond are still serious operational challenges in resource-constrained settings together with low health and information system and uncertain funding streams. There is the meed to intensify the campaign of existing intervention, which includes the early diagnose and treatment of malaria cases with Artemisinin-based Combination Therapy (ACTs).

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Chapter Summary

Infectious diseases impose a huge economic burden to individuals, societies and political systems across the world. Mathematical modeling and analysis of infectious diseases have been central to infectious disease epidemiology (Yusuf & Benyah, 2012). It is an important approach that helps to understand the dynamics of infectious disease and to develop the best control strategies (Ullah et al., 2013).

For malaria, a number of studies have been carried out to combat vector-borne diseases, and in most cases, they focus on vector-control. In this study, we formulate malaria models that incorporate treatment prevention strategies as the controls. We also assume that a certain proportion of the prevention strategies α increases the death rate of the mosquitoes, that is, $c\alpha$ where $0 \leq c \leq 1$.

CHAPTER THREE

MATHEMATICAL BACKGROUND

Introduction

In this chapter some basic definitions and theorems in Mathematical modelling are provided.

Definitions and Theorems

Stability analysis of nonlinear systems have significant differences that complicate them. As opposed to linear systems, nonlinear systems

(a) may have many equilibrium points;

(b) rarely have closed-form solutions;

(c) stability is often only a local result (e.g., valid within some neighborhood of the equilibrium point);

(d) phenomena like *orbits*, *limit cycles* and *bifurcations* can be exhibited by nonlinear system.

We consider an autonomous system of differential equations of the form

$$\frac{d\mathbf{x}}{dt} = \mathbf{f}(\mathbf{x}), \tag{3.1}$$

where $\mathbf{x} = (x_1, \ldots, x_n)^T$, $\mathbf{f}(\mathbf{x}) = (f_1(x_1, \ldots, x_n), \ldots, f_n(x_1, \ldots, x_n))^T$,

The following theorem gives sufficient conditions on the vector function $\mathbf{f}$ for existence and uniqueness of solutions to initial value problems.

Theorem 3.1. Suppose $\mathbf{f}$ and $\dfrac{\partial \mathbf{f}}{\partial x_i}$ for $i = 1, \ldots, n$ are continuous functions of $(x_1, \ldots, x_n)$ on $\mathbb{R}^n$. Then a unique solution exists to the initial value problem

$$\frac{d\mathbf{x}}{dt} = \mathbf{f}(\mathbf{x}), \quad \mathbf{x}(t_0) = \mathbf{x}_0$$

for any initial value $\mathbf{x}_0 \in \mathbb{R}^n$.

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The solution to (3.1), $\mathbf{x}(t) = (x_1(t), x_2(t), \ldots, x_n(t))$ describes parametrically a curve lying in $\mathbb{R}^n$, called a *trajectory* (*orbit* or *path*) of the system. The region $\mathbb{R}^n$ where the solution is graphed, is called *phase space* when $n = 3$, *phase plane* when $n = 2$, and *phase line* when $n = 1$.

Definition 3.1 (Equilibrium Points). A point $\mathbf{x}^* \in \mathbb{R}^n$ is an *equilibrium point* of (3.1) if

$$\mathbf{f}(\mathbf{x}^*) = 0.$$

Example 3.1. Let $n = 2$ and $\mathbf{x} = (x_1(t), x_2(t))^T$. The following system

$$
\begin{aligned}
\frac{dx_1}{dt} &= 30x_1 - 5x_1^2 - 3x_1x_2 \\
\frac{dx_2}{dt} &= 8x_2 - x_2^2 - x_1x_2
\end{aligned}
\tag{3.2}
$$

has equilibrium points $x_1^* = (0, 0)$, $x_2^* = (0, 8)$, $x_3^* = (6, 0)$, and $x_4^* = (3, 5)$.

Local stability

Intuitively, we say an equilibrium point $\mathbf{x}^*$, is *locally stable* if all solutions which start near $\mathbf{x}^*$ (meaning that all initial points in a neighborhood of $\mathbf{x}_*$) remain close to $\mathbf{x}^*$ for all time.

Definition 3.2 (Stability in the sense of Lyapunov). A critical point $\mathbf{x}_*$, of the first-order system in (3.1) is said to be *locally stable* provided that, if the initial values x_0 is sufficiently close to $\mathbf{x}_*$, then $\mathbf{x}(t)$ remains close to $\mathbf{x}^*$ for all $t \geq 0$.

More precisely, the critical point $\mathbf{x}^*$ is *stable* if, for each $\varepsilon > 0$ there exists a $\delta > 0$ such that

$$\|\mathbf{x}_0 - \mathbf{x}^*\| < \delta \implies \|\mathbf{x}(t) - \mathbf{x}^*\| < \varepsilon.$$

The equilibrium point $\mathbf{x} = \mathbf{x}^*$ is called *unstable* if it is not stable.

Definition 3.3 (Asymptotic Stability)**.** The equilibrium point $\mathbf{x}^*$ is said to be *locally asymptotically stable* if $\mathbf{x}^*$ is locally stable and furthermore, all solutions starting near $\mathbf{x}^*$ tend towards $\mathbf{x}^*$ as $t \to \infty$.

That is, there exists $\delta > 0$ such that

$$\|\mathbf{x}_0 - \mathbf{x}^*\| \quad < \quad \delta \quad \Rightarrow \quad \lim_{t \to \infty} \mathbf{x}(t) = \mathbf{x}^* \tag{3.3}$$

For many nonlinear systems, explicit solutions for $\mathbf{x}(t)$ are rarely available. Lyapunov (1892) recognized this difficulty and developed two methods (*indirect* and *direct* methods) for assessing definitions (3.2) and (3.3).

Lyapunov's Indirect Method

Lyapunov's indirect method involves linearizing $\mathbf{f}$ at $\mathbf{x}^*$, and using the eigenvalues of the Jacobian matrix to determine the stability of the equilibrium point $\mathbf{x}_*$.

Theorem 3.2 (Lyapunov's indirect method)**.** Let $\mathbf{x}^*$ be an equilibrium point of the system of differential equations

$$\frac{dx}{dt} = \mathbf{f}(\mathbf{x}), \quad \mathbf{x}(0) = \mathbf{x}_0$$

and let $D \subset \mathbb{R}^n$ be a set containing $\mathbf{x}^*$.
Let

$$\mathbf{A} = \left. \frac{\partial \mathbf{f}}{\partial \mathbf{x}} \right|_{\mathbf{x} = \mathbf{x}^*}$$

such that the linearized system is

$$\frac{d\mathbf{u}}{dt} = \mathbf{A}\mathbf{u}, \quad \mathbf{u} = \mathbf{x} - \mathbf{x}^*,$$

then

(a) $\mathbf{x}^*$ is asymptotically stable if $\operatorname{Re}\lambda_i(\mathbf{A}) < 0$ for $i = 1, \cdots, n,$

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(b) $\mathbf{x}^*$ is unstable if $\text{Re}\lambda_i(\mathbf{A}) > 0$ for at least one i,

where $\text{Re}\lambda_i(\mathbf{A})$ designates the real part of the i-th eigenvalue of $\mathbf{A}$. Since $\mathbf{A}$ is only defined at $\mathbf{x}^*$, stability determined by the indirect method is restricted to small neighborhoods of $\mathbf{x}^*$.

The Routh-Hurwitz Conditions

Routh-Hurwitz conditions enables us to determine the stability of a equilibruim point without finding the eigenvalues of the Jacobian matrix, as stated in Theorem 3.2. The Routh-Hurwitz conditions give necessary and sufficient conditions for all roots of the characteristics polynomial to be negative or have negative real parts thus, implying asymptotic stability.

Theorem 3.3. Given the polynomial,

$$P(\lambda) = \lambda^n + a_1\lambda^{n-1} + \cdots + a_{n-1}\lambda + a_n$$

where the coefficients a_i, $i = 1,\ldots,n$, are real constants, define the n Hurwitz matrices using the coefficients a_i of the characteristics polynomial:

$$H_1 = (a_1), \ H_2 = \begin{bmatrix} a_1 & 1 \\ a_3 & a_2 \end{bmatrix}, \ H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ a_5 & a_4 & a_3 \end{bmatrix}$$

and

$$H_n = \begin{bmatrix} a_1 & 1 & 0 & 0 & \cdots & 0 \\ a_3 & a_2 & a_1 & 1 & \cdots & 0 \\ a_5 & a_4 & a_3 & a_2 & \cdots & 0 \\ \vdots & \vdots & \vdots & \vdots & \cdots & \vdots \\ 0 & 0 & 0 & & \cdots & a_n \end{bmatrix}$$

where $a_j = 0$ if $j > n$. All of the roots of the polynomial $P(\lambda)$ are negative or have negative real part if and only if the determinants of all Hurwitz matrices

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are positive;

$$detH_j > 0, \ j = i, 2, \ldots, n.$$

For example, for $n = 2$, the characteristic equation is

$$\lambda^2 + a_1\lambda + a_2 = 0$$

and the corresponding Hurwitz matrix is

$$H_= \begin{bmatrix} a_1 & 1 \\ 0 & a_2 \end{bmatrix}, detH_2 = (a_1a_2 - 0) > 0.$$

The Routh- Hurwitz criteria implies that $a_1a_2 > 0$.

For example, for $n = 3$, the characteristic equation is

$$\lambda^3 + a_1\lambda^2 + a_2\lambda + a_3 = 0$$

and the corresponding Hurwitz matrix is

$$H_3 = \begin{bmatrix} a_1 & 1 & 0 \\ a_3 & a_2 & a_1 \\ 0 & 0 & a_3 \end{bmatrix}, detH_3 = a_3(a_1a_2 - a_3) > 0.$$

The Routh- Hurwitz criteria implies that $a_3 > 0$, $a_1a_2 > a_3$.

For example, for $n = 4$, the characteristic equation is

$$\lambda^4 + a_1\lambda^2 + a_2\lambda^2 + a_3\lambda^2 + a_4 = 0$$

and the corresponding Hurwitz matrix is

$$H_4 = \begin{bmatrix} a_1 & 1 & 0 & 0 \\ a_3 & a_2 & a_1 & 1 \\ 0 & a_4 & a_3 & a_2 \\ 0 & 0 & 0 & a_4 \end{bmatrix}, detH_4 = a_4[a_1(a_3a_2 - a_4a_1) - a_3a_3] > 0.$$

The Routh- Hurwitz criteria implies that $a_3 > 0$, $a_1a_2 > a_3$.

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Gershgorin's Theorem

When the zero equilibrium is an isolated equilibrium for the system $\frac{dX}{dt} = AX$, then all solutions converge to the origin if and only if the eigenvalues of A are negative or have negative real part (lie in the left half of the complex plane). From the Lyapunov's indirect method, an equilibrium point is locally asymptotically stable if the eigenvalues of the matrix (A) are negative or have negative real part (lie in the left half of the complex plane). Since the characteristic equation for an $n-$ dimension system is a polynomial equation of degree n for which it may be difficult or impossible to find all roots explicitly, the Routh-Hurwitz criterion is widely used in analyzing the stability of the equilibrium point. The Routh Hurwitz criteria gives necessary and sufficient conditions for the eigenvalues to lie in the left half of the complex plane. The Routh-Hurwitz condition also becomes intractable when the number of states exceed 3.

The Gershgorin's Theorem provides sufficient conditions for the eigenvalues to lie in the left half of the complex (Allen, 2007). The Gerschgorin circle theorem is a theorem which may be used to bound the size of the eigenvalues of a square matrix. It was first published by Belorussian mathematician Semyon Aranovich Gerschgorin in 1931. Informally, the theorem says that if the off-diagonal entries of a square matrix over the complex numbers have small norms, then its eigenvalues are similar in norm to the diagonal entries of the matrix. This theorem is a very useful tool in numerical analysis, particularly in perturbation theory (Gómez, 2006).

Theorem 3.4. *(Gershgorin's Theorem). Let A be an $n \times n$ matrix. Let D_i be the disk in the complex plane with center at a_{ii}, and radius*

$$r_i = \sum_{j=1, j \neq i}^{n} |a_{ij}|.$$

Then all eigenvalues of the matrix A lie in the union of the disks $D_i, i = 1, 2, ..., n,$

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$\bigcup_i^n D_i$. *In particular, if λ is an eigenvalue of A, then for some $i = 1, 2, ..., n$,*

$$a_{ii} < -r_i.$$

Corollary 3.1. *(Corollary of Gershgorin Circle Theorem)*

Let **A** be an $n \times n$ matrix with real entries. If the diagonal elements of **A** satisfy

$$a_{ii} < -r_i$$

where

$$r_i = \sum_{j=1, j \neq i}^{n} |a_{ij}|$$

for $i = 1, ..., n$, then the eigenvalues of **A** are negative or have negative real parts (Allen, 2007).

Lyapunov's Direct Method

    Lyapunov direct method is toused to determine global stability of an equilibrium point of a non-linear dynamical system by studying how carefully selected scalar functions of the state behave as the system state evolves. It involves constructing a differentiable scalar Lyapunov function $V(\mathbf{x})$ with an origin at $\mathbf{x}^* = \mathbf{O}$ such that:

(a) $V(\mathbf{x}) > 0, \quad V(\mathbf{O}) = 0, \quad V(\mathbf{x}) > 0$ for all $\mathbf{x}$, and

(b) $\dfrac{\partial V}{\partial \mathbf{x}} \cdot \mathbf{f}(\mathbf{x}, \mathbf{O}) \leq 0$ for all $\mathbf{x}$,

Definition 3.4. *(Positive definite functions)*

(a) A continuously differentiable function $V : \mathbb{R}^n \longrightarrow \mathbb{R}_+$ is said to be *positive definite* in a region U of $\mathbb{R}^n$ that contains the origin if

    (i) $V(0) = 0$, and

    (ii) $V(\mathbf{x}) > 0$,

for $\mathbf{x} \in U$, and $\mathbf{x} \neq 0$.

(b) $V(\mathbf{x})$ is said to be *positive semi-definite* if $V(\mathbf{x}) \geq 0$ for $\mathbf{x} \in U$.

(c) Conversely, $V(\mathbf{x})$ is said to be *negative definite* if $V(\mathbf{x}) < 0$, and

(d) $V(\mathbf{x})$ is said to be *negative semi-definite* if $V(\mathbf{x}) \leq 0$.

Definition 3.5. *(Continuous differentiability)* A function $f(\mathbf{x};t)$ where $f : U \times [a;b] \longrightarrow \mathbb{R}^m$ for a domain $U \times \mathbb{R}^n$ is said to be continuously differentiable over on $U \times [a;b]$ if both $f(\mathbf{x},t)$ and $[\frac{df}{dt}](x,t)$ are continuous on $U \times [a;b]$. Let

$$\dot{\mathbf{x}} = f(\mathbf{x}), \quad \mathbf{x} \in \mathbb{R}^n, \tag{3.4}$$

where $\mathbf{x} \in \mathbb{R}^n$ represents the physical state of the system. If $V(\mathbf{x})$ is a locally positive definite function and $\dot{V}(\mathbf{x})$ is its derivative with respect to time along the trajectories of system (3.4), if $\dot{V}(\mathbf{x})$ is locally negative semi-definite then $V(\mathbf{x})$ is called a *Lyapunov function* of system (3.4).

Unless otherwise stated, we shall restrict ourselves to $V(\mathbf{x})$ that have continuous first partial derivatives. We shall denote the derivative of such a $V(\mathbf{x})$ with respect to time along a trajectory of system (3.4) by $\dot{V}(\mathbf{x}(t))$. This derivative is given by:

$$\dot{V}(\mathbf{x}) = \frac{\partial V}{\partial \mathbf{x}} \cdot f(\mathbf{x})$$

Theorem 3.5. Let $\mathbf{x}_* = 0$ be an equilibrium point for a system described by:

$$\dot{\mathbf{x}} = \mathbf{f}(\mathbf{x})$$

where $\mathbf{f} : U \to \mathbb{R}^n$ is a locally Lipschitz and $U \subset \mathbb{R}^n$ a domain that contains the origin. Let $V : U \to \mathbb{R}$ be a continuously differentiable, positive definite function in U.

(a) If $\dot{V}(\mathbf{x}) = \dfrac{\partial V}{\partial \mathbf{x}} \cdot \mathbf{f} \leq 0$, then $\mathbf{x}_* = 0$ is globally stable.

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(b) If $\dot{V}(\mathbf{x}) = \dfrac{\partial V}{\partial \mathbf{x}} \cdot \mathbf{f} < 0$, then $\mathbf{x}_* = 0$ is globally asymptotically stable.

In both cases above, V is called a Lyapunov function. Moreover, if the conditions hold for all $\mathbf{x} \in \mathbb{R}^n$ and $\|\mathbf{x}\| \to \infty$ implies that $V(\mathbf{x}) \to \infty$, then $\mathbf{x} = 0$ is globally stable in case (a) and globally asymptotically stable in case (b).

Any function that satisfies the conditions of the Lyapunov stability theorem is called a Lyapunov function. Although no general method for constructing Lyapunov functions is known, the following functions or variants of them, are commonly used as Lyapunov function candidates.

(1) Quadratic Lyapunov functions, $V(x) = (x_1 - x_1^*)^2 + (x_2 - x_2^*)^2 + \cdots, + (x_n - x_n^*)^2, \cdots$, where the equilibrium points are given by $x_1^*, x_2^*, \ldots, x_n^*$

(2) Logarithmic Lyapunov function, $V(x) = (x_1 - x_1^* - x_1^* ln(\frac{x_1}{x_1^*})) + (x_2 - x_2^* - x_2^* ln(\frac{x_2}{x_2^*})) + ... + (x_n - x_n^* - x_n^* ln(\frac{x_n}{x_n^*})) + \cdots$

Basic Reproduction Number $\mathcal{R}_0$

The basic reproduction number $\mathcal{R}_0$ is an important concept in mathematical epidemiology as it serves as a threshold parameter that governs the spread of infectious diseases in a population. $\mathcal{R}_0$ determines whether a pathogen can become established in an area where it is introduced (Cianci et al., 2013).

Definition 3.6. The basic reproduction number $\mathcal{R}_0$ is defined as the secondary expected infectives produced from just one infected individual in a susceptible population.

For any infectious disease, one of the most important concerns is its ability to invade a population. If $\mathcal{R}_0 < 1$, then each infected individual in its entire period of infectivity, will produce less than one infected individual on average. In Disease Free Equilibrium (DFE) case, the system is locally asymptotically

stable, which shows that the disease will be wiped out of the population. If $\mathcal{R}_0 > 1$, then each infected individual in its entire infective period having contact with susceptible individuals will produce more than one infected individual, which will then lead to the disease invading the susceptible population, meaning the Endemic Equilibrium (EE) is stable and the DFE is unstable (Ullah et al., 2013).

The Basic Reproduction Number $\mathcal{R}_0$ and Next Generation Matrix

There is hardly a paper on dynamic epidemiological models in the literature where $\mathcal{R}_0$ does not play a role (Diekmann, Heesterbeek, & Roberts, 2009). This metric is useful because it helps determine whether or not an infectious disease will spread through a population.

It has been shown that $\mathcal{R}_0$ is mathematically characterized by regarding infection transmission as a 'demographic process', where producing offspring is not seen as giving birth in the demographic sense, but as causing a new infection through transmission which is referred to as an *'epidemiological birth'*). In a natural way this leads to viewing the infection process in terms of consecutive 'generations of infected individuals', in complete analogy to demographic generations. Subsequent generations growing in size then indicate a growing population (i.e. an epidemic), and the growth factor per generation indicates the potential for growth. Consider a population of individuals (or species) subdivided into n compartments, of which m are infected. Let x_i represent the proportion of the population in the *ith* compartment and let the vector of the proportions in all the compartments be x. In order to compute $\mathcal{R}_0$, it is important to distinguish new infections from all other changes in population. Let

- $F_i(\mathbf{x})$ be the rate of appearance of new infections in compartment i,

- $V_i^+(\mathbf{x})$ be the rate of transfer of individuals into compartment i by all

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means,

- $V_i^-(\mathbf{x})$ be the rate of transfer of individuals out of compartment i.

It is assumed that each function is continuously differentiable at least twice in each variable. The disease transmission model consists of nonnegative initial conditions together with the following system of equations:

$$x_i = f_i(\mathbf{x}) = F_i(\mathbf{x}) - V_i(\mathbf{x}); \quad i = 1....n,$$

where $V_i = V_i^- - V_i^+$. Since each function represents a directed transfer of individuals, they are all nonnegative. We can now define the matrices,

$$F = \left[\frac{\partial F_i}{\partial x_j(\mathbf{x}_0)} \right] \tag{3.5}$$

and

$$V = \left[\frac{\partial V_i}{\partial x_j(\mathbf{x}_0)} \right] \tag{3.6}$$

where x_0 denotes the disease-free equilibrium and the indices $i, j = 1, ..., m$. The entries of the matrix

$$K = FV^{-1}$$

give the rate at which infected individuals of state j generate new infections of type i: The matrix K is called the next generation matrix (Diekmann & Heesterbeek, 2000). $\mathcal{R}_0$ is the spectral radius of the matrix $K = FV^{-1}$: That is

$$\mathcal{R}_0 = \rho(FV^{-1})$$

Investigating Local Stability of Some Selected Epidemic Models

In the subsequent section, a corollary of Gershgorin's circle theorem (3.1) in the previous section will be used to establish the local stability of some selected epidemic models including SEIR model, SEIRS model, HIV/AIDS and tuberculosis transmission models.

The SEIR Model

The SEIR model consists of four compartments, which are the susceptible, *S*, exposed, *E*, infectious, *I* and removed, *R*.
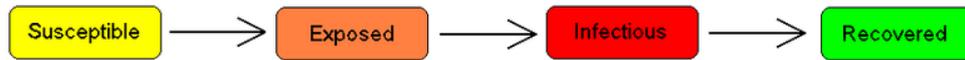
Figure 1: Transition Diagram for SEIR Model

After an initial infection, the individual moves into a latent period for some time, before becoming infectious. An infected host may die from the disease or recover with immunity against re-infection. Let *S* be the proportion of susceptible individuals, *E*, be the proportion of exposed individuals, (infected but are not yet infectious), *I*, be the proportion of infectious individuals, and *R*, is the proportion of recovered individuals, (with immunity). Furthermore, let the contact rate be given by β, μ, is the birth rate (equal to the natural death rate), κ, be the progression rate from *E* to *I* and γ, the recovery rate and δ is the additional rate of disease-induced mortality. Then, using a mass action incidence, leads to the following system of equations.

$$
\begin{aligned}
\dot{S} &= \Lambda - \beta IS - \mu S \\
\dot{E} &= \beta IS - (\kappa + \mu)E \\
\dot{I} &= \kappa E - (\mu + \gamma + \delta)I \\
\dot{R} &= \gamma I - \mu R
\end{aligned}
\tag{3.7}
$$

with

$$
N = S + I + E + R,
$$

Adding the four equations of equation(3.7) gives

$$
\begin{aligned}
\dot{N} &= \dot{S} + \dot{I} + \dot{E} + \dot{R} \\
&= \Lambda - N\mu - \delta I
\end{aligned}
$$

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In the absence of the disease induced death, that is, $\delta = 0$, we have

$$\dot{N}_h = \Lambda - \mu N$$

$$\dot{N} + \mu N = \Lambda \tag{3.8}$$

Solving equation (3.8) we obtain,

$$N(t)e^{\mu t} = \frac{\Lambda e^{\mu t}}{\mu} + C,$$

where C is the constant of integration. Thus,

$$N(t) = \left(\frac{\Lambda e^{\mu t}}{\mu} \times \frac{1}{e^{\mu t}}\right) + Ce^{-\mu_h t}$$

$$= \frac{\Lambda}{\mu} + Ce^{-\mu}$$

Using the initial conditions, $N(0) = N_0$:

$$N_0 = \frac{\Lambda}{\mu} + C$$

$$\text{it follows that} \quad C = N_0 - \frac{\Lambda}{\mu}.$$

so,

$$N(t) + \left(\frac{\Lambda}{\mu t} - N_0\right)e^{-\mu t} = \frac{\Lambda}{\mu} \tag{3.9}$$

This means that,

$$N_h(t) \leq \frac{\Lambda}{\mu}, \quad \text{provided} \quad N(0) \leq \frac{\Lambda}{\mu} \quad \text{for} \quad t \geq 0. \tag{3.10}$$

For positivity of solutions, we apply the following theorem that follows

Theorem 3.6. Let the initial data be $\{S(0) > 0, (E(0), I(0), R(0)) \geq 0\} \in P$.

Then the solution set $\{S, E, I, R\}$ of the system (3.7) is positive for all $t > 0$.

Proof. From the first equation in the model (3.7), we have

$$\frac{dS}{dt} = \Lambda - \beta SI - \mu S$$

$$\geq -\beta SI - \mu S$$

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Using separation of variables and integrating both sides gives

$$\int \frac{dS}{S} \geq \int (-\beta I - \mu_h)dt$$

$$\int \frac{dS}{S} \geq \int (-\beta I dt - \int \mu dt$$

$$\ln S \geq -\int (\beta I)dt + (-\mu)t + C$$

$$\Rightarrow S \geq e^{-\int (\beta I)dt} \times e^{-(\mu_h)}t \times e^C$$

$$\geq (e^{-\int (\beta I)dt} \times e^{-(\mu)t}) \times e^C$$

$$\geq (e^{-\int (\beta I)dt} \times e^{-(\mu)t}) \times M$$

$$\geq M(e^{(-\int (\beta I)dt - (\mu)t)})$$

using the initial conditions: $t = 0, \quad S(0) \geq M$

$$\Rightarrow S \geq S(0)(e^{(-\int (\beta I)dt - (\mu)t)}) \geq 0$$

Therefore,

$$S \geq S(0)(e^{(-\int (\beta I)dt - (\mu)t)}) \geq 0$$

From the second equation we have

$$\frac{dE}{dt} = \beta SI - (\kappa + \mu)E$$

$$\geq -(\kappa + \mu)E$$

$$\frac{dE}{dt} \geq -(\kappa + \mu)E$$

Using separation of variables and integrating both sides gives

$$\int \frac{dE}{E} \geq \int -(\kappa + \mu)dt$$

$$\ln E \geq -(\kappa + \mu)t + c$$

$$\Rightarrow E \geq e^{-(\kappa + \mu)t + c}$$

$$\geq Qe^{-(\kappa + \mu)t}$$

$$\geq E(0)e^{-(\kappa + \mu)t}$$

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where $Q = E(0)$

$$E \geq E(0)e^{-(\kappa+\mu)t} \geq 0$$

similarly, it can be shown that the remaining equations of the system (3.7) are positive for all $t > 0$, because $\eta > 0$ for all $\eta \in R$. $\qquad\qquad\square$

Here, it is important to note that in the absence of the disease, $N(t) \to \dfrac{\Lambda}{\mu}$. Moreover, under the dynamics described by (3.7), the region

$$\Phi = \left\{ (S(t), E(t), I(t), R(t)) \in R_+^4, S(t) + E(t) + I(t) + R(t) \leq 1 \right\}$$

is positively invariant. Thus, the system is both mathematically and epidemiologically well-posed. Therefore, for an initial starting point $x \in \mathbb{R}_+^4$; the trajectory lies in Φ. Hence, our analysis can be restricted to the region Φ.

Stability Analysis of SEIR Model

The system (3.7) has a disease free and an endemic equilibrium points given respectively by

(i) $P^0 = \{S_*^0, E_*^0, I_*^0, R_*^0\} = \{\dfrac{\Lambda}{\mu}, 0, 0, 0\}$

and

(ii) $P * 0 = \{S^*, E^*, I^*, R^*\}$

where
$$S^* = \frac{\mu^2 + (\kappa + \delta + \gamma)\mu + (\delta + \gamma)\kappa}{\beta\kappa},$$
$$E^* = -\frac{\mu^3 + (\kappa + \delta + \gamma)\mu^2 + (\delta + \gamma)\kappa\mu - \beta\kappa\Lambda}{\beta\kappa\mu + \beta\kappa^2},$$
$$I^* = -\frac{\mu^3 + (\kappa + \delta + \gamma)\mu^2 + (\delta + \gamma)\kappa\mu - \beta\kappa\Lambda}{\beta\mu^2 + (\beta\kappa + \beta\delta + \beta\gamma)\mu + (\beta\delta + \beta\gamma)\kappa},$$
$$R^* = -\frac{\gamma\mu^3 + (\gamma\kappa + (\gamma\delta + \gamma^2))\mu^2 + (\gamma\delta + \gamma^2)\kappa\mu - \gamma\beta\kappa\Lambda}{\beta\mu^3 + (\beta\kappa + \beta\delta + \beta\gamma)\mu^2 + (\beta\delta + \beta\gamma)\kappa\mu}.$$

Computation of $\mathcal{R}_0$ for SEIR Model

We compute the basic reproduction number of the SEIR model (3.7). The model has two infected states, E, and I given as

$$
\begin{aligned}
\dot{E} &= \quad \beta IS - (\kappa + \mu)E \\
\dot{I} &= \quad \kappa E - (\mu + \gamma + \delta)I
\end{aligned}
\tag{3.11}
$$

and two uninfected states, S and R. At the infection-free steady state $E_*^0 = I_*^0 = R_*^0 = 0$, and $S_*^0 = (\dfrac{\Lambda}{\mu})$. We will refer to the system (3.11) as the infection subsystem, as it only describes the production of new infections and changes in the states of the already existing infecteds. We use the next-generation matrix approach to compute the basic reproduction number $\mathcal{R}_0$. The vectors F_i and V_i as defined in equation (3.5) and (3.6) are given respectively by

$$
F_i = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix}
$$

and

$$
V_i = V_i^- - V_i^+ = \begin{bmatrix} (\mu + \kappa)E \\ (\mu + \delta + \gamma)I - \kappa E \end{bmatrix}
$$

The matrices $\mathbf{F}$ and $\mathbf{V}$ are given respectively by

$$
\mathbf{F} = \begin{bmatrix} 0 & \beta S_0 \\ 0 & 0 \end{bmatrix}
$$

and

$$
\mathbf{V} = \begin{bmatrix} (\mu + \kappa) & 0 \\ -\kappa & (\gamma + \mu + \delta), \end{bmatrix}
$$

thus,

$$
\mathbf{V}^{-1} = \begin{bmatrix} \dfrac{1}{\kappa + \mu} & 0 \\ \dfrac{\kappa}{(\kappa + \mu)(\gamma + \mu + \delta)} & \dfrac{1}{\gamma + \mu + \delta} \end{bmatrix}
$$

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The Next Generation Matrix given by

$$
\begin{aligned}
K &= FV^{-1} \\
&= \begin{bmatrix} 0 & \beta S_0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{\kappa+\mu} & 0 \\ \dfrac{\kappa}{(\kappa+\mu)(\gamma+\mu+\delta)} & \dfrac{1}{\gamma+\mu+\delta} \end{bmatrix} \\
&= \begin{bmatrix} \dfrac{\beta S_0 \kappa}{(\kappa+\mu)(\gamma+\mu+\delta)} & \dfrac{\beta S_0}{\gamma+\mu+\delta} \\ 0 & 0 \end{bmatrix}
\end{aligned}
$$

The eigenvalues of K are $\lambda_1 = \dfrac{\beta S_0 \kappa}{(\kappa+\mu)(\gamma+\mu+\delta)}$ and $\lambda_2 = 0$ The basic reproduction number $\mathcal{R}_0$ is the positive real eigenvalue of K which is at least as large in modulus as all eigenvalues of K.

$$
\mathcal{R}_0 = \frac{\beta S_0 \kappa}{(\kappa+\mu)(\gamma+\mu+\delta)}.
$$

But $S_0 = \dfrac{\Lambda}{\mu}$, which implies that

$$
\mathcal{R}_0 = \frac{\beta \Lambda \kappa}{\mu(\kappa+\mu)(\gamma+\mu+\delta)}.
$$

The endemic equilibrium can be expressed in terms of the reproduction number $\mathcal{R}_0$ as follows;

$$
P^* = (S^*, E^*, I^*, R^*) = \left(\frac{\Lambda}{\mu \mathcal{R}_0}, \frac{\mu(\mu+\delta+\gamma)}{\beta \kappa}(\mathcal{R}_0 - 1), \frac{\mu}{\beta}(\mathcal{R}_0 - 1), \frac{\gamma}{\beta}(\mathcal{R}_0 - 1) \right)
$$

Local Stability of the Equilibria

We analyse the local stability of the disease free and endemic equilibrium points of the system (3.7).

Theorem 3.7. The disease free equilibrium is locally asymptotically stable if $\mathcal{R}_0 < 1$.

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Proof. The Jacobian matrix J of the system (3.7) is

$$J = \begin{bmatrix} -\beta I - \mu & 0 & -\beta S & 0 \\ \beta I & -(\kappa + \mu) & \beta S & 0 \\ 0 & \kappa & -(\gamma + \mu + \delta) & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix} \qquad (3.12)$$

Evaluating the matrix J at the disease free equilibrium gives

$$J_0 = \begin{bmatrix} -\mu & 0 & -\dfrac{\beta \Lambda}{\mu} & 0 \\ 0 & -(\kappa + \mu) & \dfrac{\beta \Lambda}{\mu} & 0 \\ 0 & \kappa & -(\gamma + \mu + \delta) & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix} \qquad (3.13)$$

The disease free equilibrium point will be asymptotically stable if the eigenvalues of the Jacobian matrix are negative or have negative real parts. The matrix J_0 has a repeated eigenvalue $-\mu$ which are negative.

Next, we consider the sub-matrix

$$J_s = \begin{bmatrix} -(\kappa + \mu) & \dfrac{\beta \Lambda}{\mu} \\ \kappa & -(\gamma + \mu + \delta) \end{bmatrix}.$$

According to the corollary of Gersgorn's circle theorem, the matrix (J_s) will have negative eigenvalues if the following inequalities are satisfied

(i)
$$(\kappa + \mu) > \frac{\beta \Lambda}{\mu}$$

(ii)
$$(\gamma + \mu + \delta) > \kappa$$

From (i) we have

$$1 > \frac{\beta \Lambda}{\mu(\kappa + \mu)}, \qquad (3.14)$$

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and from (ii) we have

$$\frac{(\gamma+\mu+\delta)}{\kappa} > 1. \qquad (3.15)$$

It follows from inequalities (3.14) and (3.15) that

$$\frac{(\gamma+\mu+\delta)}{\kappa} > 1 > \frac{\beta\Lambda}{\mu(\kappa+\mu)}.$$

This implies that

$$\frac{(\gamma+\mu+\delta)}{\kappa} > \frac{\beta\Lambda}{\mu(\kappa+\mu)}.$$

Hence,

$$1 > \frac{\beta\Lambda\kappa}{\mu(\kappa+\mu)(\gamma+\mu+\delta)} \qquad (3.16)$$

but $\dfrac{\beta\Lambda\kappa}{\mu(\kappa+\mu)(\gamma+\mu+\delta)}$ is the Basic Reproduction Number $\mathcal{R}_0$, so from (3.16), we conclude that $\mathcal{R}_0 < 1$. Therefore, the disease free equilibrium is locally asymptotically stable since $\mathcal{R}_0 < 1$. $\qquad\qquad\square$

Next, we use the following theorem to determine the local stability of the endemic equilibrium point.

Theorem 3.8. The Endemic equilibrium is locally asymptotically stable if $\mathcal{R}_0 > 1$.

Proof. The Jacobian matrix J evaluated at the endemic equilibrium gives

$$J_1 = \begin{bmatrix} a-\mu & 0 & -\dfrac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa} & 0 \\ -a & -(\kappa+\mu) & \dfrac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa} & 0 \\ 0 & \kappa & -(\gamma+\mu+\delta) & 0 \\ 0 & 0 & \gamma & -\mu \end{bmatrix} \qquad (3.17)$$

where
$$a = \frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}.$$

One of the eigenvalues is $-\mu$ which is negative so we apply a corollay of the

Gersgorin's circle theorem to the sub-matrix J_e to prove that the endemic equilibrium is locally asymptotically stable if all the eigenvalues of J_1 have negative real part or if $\mathcal{R}_0 > 1$.

The sub-matrix is given by

$$
J_e = \begin{bmatrix} a-\mu & 0 & -\dfrac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa} \\[2ex] -a & -(\kappa+\mu) & \dfrac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa} \\[2ex] 0 & \kappa & -(\mu+\delta+\gamma) \end{bmatrix}
$$

According to the corollary of Gershgorin's circle theorem, the matrix (J_e) will have negative eigenvalues if the following inequalities are satisfied

(i)

$$
-\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}-\mu < \\
-\frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa},
$$

(ii)

$$
-(\kappa+\mu) < \\
-\Big(\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa} \\
+\frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa}\Big),
$$

(iii)

$$
-(\mu+\delta+\gamma) < -\kappa.
$$

The inequalities (i) to(iii) are respectively

(i^*)

$$
\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}+\mu > \\
\frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa}
$$

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(ii^*)

$$(\kappa+\mu) \ > \ \Big(\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}$$
$$+\frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa}\Big)$$

(iii^*)

$$(\mu+\delta+\gamma) > \kappa$$

From (i^*) we have

$$\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}+\mu > \frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa}.$$

This implies that

$$\frac{\mu(\mu+\kappa)(\mu+\gamma+\delta)}{(\mu+\kappa)(\mu+\delta+\delta)} - \frac{\Lambda\beta\kappa}{(\mu+\kappa)(\mu+\delta+\delta)}+\mu > \frac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}.$$

Thus,

$$\mu - \mathcal{R}_0\mu+\mu > \frac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}.$$

It follows that

$$-\mathcal{R}_0\mu > \frac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}$$

Hence,

$$\mathcal{R}_0 < \frac{(\mu+\kappa)(\mu+\gamma+\delta)}{\mu\kappa}.$$

Moreover, from (ii^*)

$$(\kappa+\mu) \ > \ \Big(\frac{\mu^3+\mu^2\delta+\mu\gamma+\mu^2\kappa+\mu\delta\kappa+\mu\gamma\kappa-\Lambda\beta\kappa}{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}$$
$$+\frac{\mu^2+\mu\delta+\mu\gamma+\mu\kappa+\delta\kappa+\gamma\kappa}{\kappa}\Big).$$

This implies that

$$(\mu+\kappa) > \frac{\mu(\mu+\kappa)(\mu+\gamma+\delta)}{(\mu+\kappa)(\mu+\delta+\delta)} - \frac{\Lambda\beta\kappa}{(\mu+\kappa)(\mu+\delta+\delta)} + \frac{(\mu+\kappa)(\mu+\delta+\delta)}{\kappa}.$$

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Dividing through by $(\mu + \kappa)$ gives

$$1 > \frac{\mu}{\mu + \kappa} - \frac{\beta \kappa \Lambda}{(\mu + \kappa)(\mu + \kappa)(\mu + \delta + \gamma)} + \frac{(\mu + \delta + \kappa)}{\kappa}.$$

This is the same as

$$> \frac{\mu}{\mu + \kappa} - \frac{\mu \beta \kappa \Lambda}{\mu(\mu + \kappa)(\mu + \kappa)(\mu + \delta + \gamma)} + \frac{(\mu + \delta + \kappa)}{\kappa}.$$

$$> \frac{\mu}{\mu + \kappa} - \frac{\mu \mathcal{R}_0}{(\mu + \kappa)} + \frac{(\mu + \delta + \kappa)}{\kappa}.$$

$$> \frac{\mu(1 - \mathcal{R}_0)}{\mu + \kappa} + \frac{(\mu + \delta + \kappa)}{\kappa}.$$

And from (iii^*)

$$\frac{(\mu + \delta + \gamma)}{\kappa} > 1. \tag{3.18}$$

Combining inequalities give

$$\frac{(\mu + \delta + \gamma)}{\kappa} > 1 > \frac{\mu(1 - \mathcal{R}_0)}{\mu + \kappa} + \frac{(\mu + \delta + \kappa)}{\kappa}$$

This implies that

$$\frac{(\mu + \delta + \gamma)}{\kappa} > \frac{\mu(1 - \mathcal{R}_0)}{\mu + \kappa} + \frac{(\mu + \delta + \kappa)}{\kappa}$$

$$1 > \frac{\kappa \mu(1 - \mathcal{R}_0)}{(\mu + \kappa)(\mu + \gamma + \delta)} + 1$$

$$0 > \frac{\kappa \mu(1 - \mathcal{R}_0)}{(\mu + \kappa)(\mu + \gamma + \delta)}$$

$$0 > \kappa \mu(1 - \mathcal{R}_0),$$

holds if

$$\mathcal{R}_0 > 1 \tag{3.19}$$

We conclude from (3.19) that the Endemic equilibrium is locally asymptotically stable if $\mathcal{R}_0 > 1$.

$\square$

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Stability Analysis of SEIRS Model

The SEIRS model consists of four compartments, but the individual looses immunity after some time and moves back into the *S* class (that is, the individual becomes susceptible again).
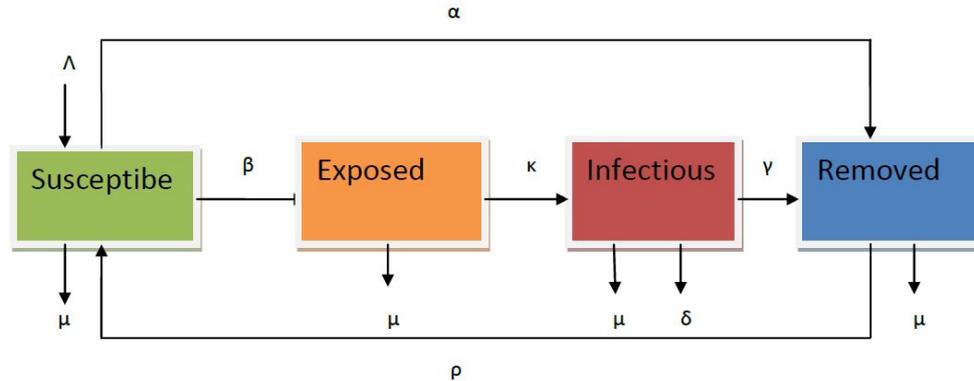
Figure 2: Transition Diagram for SEIRS Model

Let *S* be the proportion of susceptible individuals, *E*, be the proportion of exposed individuals, (infected but are not yet infectious), *I*, be the proportion of infectious individuals, and *R*, is the proportion of recovered individuals, (with temporary immunity). Furthermore, let the contact rate be given by β, Λ is the recruitment rate, *μ* is the birth rate (equal to the natural death rate), κ be the progression rate from *E* to *I*, γ the recovery rate, δ is the additional rate of disease-induced mortality, ρ is the rate of lost of immunity, α is the vaccination rate and *N* is the total population.

The SEIRS model with standard incidence is given as

$$\dot{S} = \Lambda - \frac{\beta I S}{N} - (\mu + \alpha)S + \rho R \qquad (3.20)$$
$$\dot{E} = \frac{\beta I S}{N} - (\kappa + \mu)E$$
$$\dot{I} = \kappa E - (\mu + \gamma + \delta)I$$
$$\dot{R} = \gamma I - (\mu + \rho)R + \alpha S$$

The system (3.20) has two equilibrium points;

(i) a disease freee equilibrium point P^0, given by $P^0 = (S^0, E^0, I^0, R^0)$
$$= \left(\frac{\Lambda(\mu+\rho)}{\mu(\alpha+\mu+\rho)}, 0, 0, \frac{\Lambda\alpha}{\mu(\alpha+\mu+\rho)}\right)$$
and

(ii) and endemic equilibrium point $P^* = (S^*, E^*, I^*, R^*)$, where
$$S^* = \frac{(\delta\kappa+\delta\mu+\gamma\kappa+\gamma\mu+\kappa\mu+\mu^2)}{(\beta\kappa)},$$

$E^* = (\mu+\gamma+\delta)(\Lambda\beta\kappa\mu+\Lambda\beta\kappa\rho-\alpha\delta\kappa\mu-\alpha\delta\mu^2-\alpha\gamma\kappa\mu-\alpha\gamma\mu^2-\alpha\kappa\mu^2-$

$\alpha\mu^3-\delta\kappa\mu^2-\delta\kappa\mu\rho-\delta\mu^3-\delta\mu^2\rho-\gamma\kappa\mu^2-\gamma\kappa\mu\rho-\gamma\mu^3-\gamma\mu^2\rho-\kappa\mu^3-\kappa\mu^2\rho-$

$\mu^4-\mu^3\rho)/(\beta(\delta\kappa\mu+\delta\kappa\rho+\delta\mu^2+\delta\mu\rho+\gamma\kappa\mu+\gamma\mu^2+\gamma\mu\rho+\kappa\mu^2+\kappa\mu\rho+\mu^3+$

$\mu^2\rho)\kappa)$,

$I^* = (\Lambda\beta\kappa\mu+\Lambda\beta\kappa\rho-\alpha\delta\kappa\mu-\alpha\delta\mu^2-\alpha\gamma\kappa\mu-\alpha\gamma\mu^2-\alpha\kappa\mu^2-\alpha\mu^3-\delta\kappa\mu^2-$

$\delta\kappa\mu\rho-\delta\mu^3-\delta\mu^2\rho-\gamma\kappa\mu^2-\gamma\kappa\mu\rho-\gamma\mu^3-\gamma\mu^2\rho-\kappa\mu^3-\kappa\mu^2\rho-\mu^4-\mu^3\rho)/$

$(\beta(\delta\kappa\mu+\delta\kappa\rho+\delta\mu^2+\delta\mu\rho+\gamma\kappa\mu+\gamma\mu^2+\gamma\mu\rho+\kappa\mu^2+\kappa\mu\rho+\mu^3+\mu^2\rho))$,

and

$R^* = (\Lambda\beta\gamma\kappa^2+\alpha\delta^2\kappa^2+2\alpha\delta^2\kappa\mu+\alpha\delta^2\mu^2+\alpha\delta\gamma\kappa^2+3\alpha\delta\gamma\kappa\mu+2\alpha\delta\gamma\mu^2+$

$2\alpha\delta\kappa^2\mu+4\alpha\delta\kappa\mu^2+2\alpha\delta\mu^3+\alpha\gamma^2\kappa\mu+\alpha\gamma^2\mu^2+\alpha\gamma\kappa^2\mu+3\alpha\gamma\kappa\mu^2+2\alpha\gamma\mu^3+$

$\alpha\kappa^2\mu^2+2\alpha\kappa\mu^3+\alpha\mu^4-\delta\gamma\kappa^2\mu-\delta\gamma\kappa\mu^2-\gamma^2\kappa^2\mu-\gamma^2\kappa\mu^2-\gamma\kappa^2\mu^2-\gamma\kappa\mu^3)/$

$(\beta\kappa(\delta\kappa\mu+\delta\kappa\rho+\delta\mu^2+\delta\mu\rho+\gamma\kappa\mu+\gamma\mu^2+\gamma\mu\rho+\kappa\mu^2+\kappa\mu\rho+\mu^3+\mu^2\rho))$.

E_0 and E_1 are the disease free and endemic equilibrium points respectively.

Computation of $\mathcal{R}_0$ for SEIRS Model

The SEIRS has two infected states

$$\dot{E} = \beta I S - (\kappa+\mu)E \tag{3.21}$$

$$\dot{I} = \kappa E - (\mu+\gamma+\delta)I$$

and two uninfected states. At the infection-free steady state $E^0 = I^0 = 0$, hence
$S^0 = \left(\frac{\Lambda(\mu+\rho)}{(\alpha+\mu+\rho)}\right)$, and $R^0 = \frac{\Lambda\alpha}{\mu(\alpha+\mu+\rho)}$ The vectors F_i and V_i are given

respectively by

$$F_i = \begin{bmatrix} \beta SI \\ 0 \end{bmatrix}$$

and

$$V_i = \begin{bmatrix} (\mu + \kappa)E \\ (\mu + \delta + \gamma)I - \kappa E \end{bmatrix}$$

The matrices $\mathbf{F}$ and $\mathbf{V}$ are given respectively by

$$\mathbf{F} = \begin{bmatrix} 0 & \beta S \\ 0 & 0 \end{bmatrix}$$

and

$$\mathbf{V} = \begin{bmatrix} (\mu + \kappa) & 0 \\ -\kappa & (\gamma + \mu + \delta) \end{bmatrix}$$

Thus,

$$V^{-1} = \begin{bmatrix} \dfrac{1}{\kappa + \mu} & 0 \\ \dfrac{\kappa}{(\kappa + \mu)(\gamma + \mu + \delta)} & \dfrac{1}{\gamma + \mu + \delta} \end{bmatrix}$$

The Next Generation Matrix evaluated at P^0, is given by

$$
\begin{aligned}
K &= FV^{-1} \\
&= \begin{bmatrix} 0 & \beta S_0 \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{\kappa + \mu} & 0 \\ \dfrac{\kappa}{(\kappa + \mu)(\gamma + \mu + \delta)} & \dfrac{1}{\gamma + \mu + \delta} \end{bmatrix} \\
&= \begin{bmatrix} \dfrac{\beta S_0 \kappa}{(\kappa + \mu)(\gamma + \mu + \delta)} & \dfrac{\beta S_0}{\gamma + \mu + \delta} \\ 0 & 0 \end{bmatrix}.
\end{aligned}
$$

The eigenvalues of K are $\lambda_1 = \dfrac{\beta S_0 \kappa}{(\kappa + \mu)(\gamma + \mu + \delta)}$ and $\lambda_2 = 0$ The basic reproduction number $\mathcal{R}_0$ is the positive real eigenvalue of K which is at least as large in modulus as all eigenvalues of K.

$$\mathcal{R}_0 = \dfrac{\beta S_0 \kappa}{(\kappa + \mu)(\gamma + \mu + \delta)}$$

But $S_0 = \dfrac{\Lambda(\mu+\rho)}{\mu(\alpha+\mu+\rho)}$, which implies

$$\mathcal{R}_0(\alpha) = \frac{\Lambda}{\mu}\frac{\kappa}{(\kappa+\mu)}\frac{(\mu+\rho)}{(\alpha+\mu+\rho)}\frac{\beta}{(\gamma+\mu+\delta)}.$$

$\mathcal{R}_0(\alpha)$ is the basic reproduction number with effective prevention strategy. The basic reproduction number without effective prevention strategy is

$$\mathcal{R}_0(0) = \frac{\Lambda}{\mu}\frac{\kappa}{(\kappa+\mu)}\frac{\beta}{(\gamma+\mu+\delta)}.$$

It is obvious that,

$$\frac{\Lambda}{\mu}\frac{\kappa}{(\kappa+\mu)}\frac{(\mu+\rho)}{(\alpha+\mu+\rho)}\frac{\beta}{(\gamma+\mu+\delta)} \leq \frac{\Lambda}{\mu}\frac{\kappa}{(\kappa+\mu)}\frac{\beta}{(\gamma+\mu+\delta)},$$

that is,

$$\mathcal{R}_0(\alpha) \leq \mathcal{R}_0(0)$$

We now express the endemic equilibrium point in terms of $\mathcal{R}_0$ as

$$S^* = \frac{\Lambda(\mu+\rho)}{\mathcal{R}_0(\alpha)\mu(\alpha+\mu+\rho)},$$

$$E^* = \frac{(\mu+\gamma+\delta)(\mathcal{R}_0-1)\mu[(\mu+\kappa)(\alpha+\mu+\rho)(\gamma+\mu+\delta)]}{\alpha\kappa(\delta+\mu)+\mu((\alpha+\mu+\rho)(\gamma+\mu+\delta))},$$

$$I^* = \frac{(\mathcal{R}_0-1)\mu[(\mu+\kappa)(\alpha+\mu+\rho)(\gamma+\mu+\delta)]}{\alpha\kappa(\delta+\mu)+\mu((\alpha+\mu+\rho)(\gamma+\mu+\delta))},$$

and

$$
\begin{aligned}
R^* = {} & [\mu\mathcal{R}_0\kappa\gamma(\alpha+\mu+\rho)-(-\delta\kappa\rho-\delta\mu\rho+\gamma\kappa\mu-\gamma\mu\rho-\kappa\mu\rho-\mu^2\rho)]\mu(\mu+\kappa) \\
& (\alpha+\mu+\rho)(\gamma+\mu+\delta)/\mu(\alpha+\mu+\rho)[\alpha\kappa(\delta+\mu)+\mu((\alpha+\mu+\rho) \\
& (\gamma+\mu+\delta))].
\end{aligned}
$$

Local Stability Analysis for the Disease Free Equilibrium Point

The following theorem gives conditions for the disease free equilibrium point to belocally asymptotically stable.

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Theorem 3.9. The disease free equilibrium point (P^0) is locally asymptotically stable if $\mathcal{R}_0 < 1$.

Proof. The Jacobian matrix J for the system (3.20) is

$$
J = \begin{bmatrix}
-\beta I - (\mu + \alpha) & 0 & -\beta S & \rho \\
\beta I & -(\kappa + \mu) & \beta S & 0 \\
0 & \kappa & -(\gamma + \mu + \delta) & 0 \\
\alpha & 0 & \gamma & -(\mu + \rho)
\end{bmatrix}
\tag{3.22}
$$

Evaluating the matrix J at the disease free equilibrium gives

$$
J_0 = \begin{bmatrix}
-(\mu + \alpha) & 0 & -\dfrac{\beta \Lambda (\mu + \rho)}{\mu(\alpha + \mu + \rho)} & \rho \\
0 & -(\kappa + \mu) & \dfrac{\beta \Lambda (\mu + \rho)}{\mu(\alpha + \mu + \rho)} & 0 \\
0 & \kappa & -(\gamma + \mu + \delta) & 0 \\
\alpha & 0 & \gamma & -(\mu + \rho)
\end{bmatrix}
\tag{3.23}
$$

According to the corollary of Gershgorin's circle theorem, the matrix (J_0) will have negative eigenvalues if the following inequalities are satisfied

(i)
$$
(\mu + \alpha) > \frac{\beta \Lambda (\mu + \rho)}{\mu(\alpha + \mu + \rho)} + \rho,
$$

(ii)
$$
(\kappa + \mu) > \frac{\beta \Lambda (\mu + \rho)}{\mu(\alpha + \mu + \rho)},
$$

(iii)
$$
(\gamma + \mu + \delta) > \kappa,
$$

(iv)
$$
(\mu + \rho) > (\alpha + \gamma).
$$

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Combining (ii) and (iii) gives

$$1 > \frac{\beta\Lambda(\mu+\rho)}{\mu(\alpha+\mu+\rho)(\mu+\kappa)}, \tag{3.24}$$

and

$$\frac{(\gamma+\mu+\delta)}{\kappa} > 1, \tag{3.25}$$

From (4.21) and (3.25) we have,

$$\frac{(\gamma+\mu+\delta)}{\kappa} > 1 > \frac{\beta\Lambda(\mu+\rho)}{\mu(\alpha+\mu+\rho)(\mu+\kappa)}$$

which implies that

$$\frac{(\gamma+\mu+\delta)}{\kappa} > \frac{\beta\Lambda(\mu+\rho)}{\mu(\alpha+\mu+\rho)(\mu+\kappa)}.$$

It follows that

$$1 > \frac{\beta\Lambda(\mu+\rho)\kappa}{\mu(\alpha+\mu+\rho)(\mu+\kappa)(\gamma+\mu+\delta)} = \mathcal{R}_0.$$

$\square$

Local Stability Analysis for the Endemic Equilibrium

Theorem 3.10. The Endemic equilibrium (P^*) is locally asymptotically stable if $\mathcal{R}_0 > 1$.

Proof. The Jacobian matrix J evaluated at the endemic equilibrium gives

$$J_1 = \begin{bmatrix} b-(\alpha+\mu) & 0 & -\dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa} & \rho \\ -b & -(\kappa+\mu) & \dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa} & 0 \\ 0 & \kappa & -(\gamma+\mu+\delta) & 0 \\ \alpha & 0 & \gamma & -(\mu+\rho) \end{bmatrix} \tag{3.26}$$

where $b = \dfrac{(\alpha+\mu+\rho)(\mu(\mu+\kappa))(\mu+\gamma+\delta)(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}$

According to the corollary of Gershgorin's circle theorem, the matrix (J_0) will have negative eigenvalues if the following inequalities are satisfied

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(i) $-\dfrac{(\alpha+\mu+\rho)(\mu(\mu+\kappa))(\mu+\gamma+\delta)(\mathcal{R}_0-1)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}-(\alpha+\mu)$
$< -\left(\dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}+\rho\right)$

(ii) $-(\kappa+\mu) < -\left(\dfrac{(\alpha+\mu+\rho)(\mu(\mu+\kappa))(\mu+\gamma+\delta)(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+\right.$
$\left.\dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}\right)$

(iii) $-(\mu+\delta+\gamma) < -\kappa$

(iv) $-(\mu+\rho) < -(\alpha+\gamma)$

The inequalities (i) to (iv) can be rewritten as

(i^*) $\dfrac{(\alpha+\mu+\rho)(\mu(\mu+\kappa))(\mu+\gamma+\delta)(\mathcal{R}_0-1)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+(\alpha+\mu) >$
$\dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}+\rho$

(ii^*) $(\kappa+\mu) > \dfrac{(\alpha+\mu+\rho)(\mu(\mu+\kappa))(\mu+\gamma+\delta)(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+$
$\dfrac{(\mu+\kappa)(\mu+\gamma+\delta)}{\kappa}$

(iii^*) $(\mu+\delta+\gamma) > \kappa$

(iv^*) $(\mu+\rho) > \alpha+\gamma$

Dividing (ii^*) through by $(\kappa+\mu)$ gives

$$1 > \dfrac{(\alpha+\mu+\rho)(\mu)(\mu+\gamma+\delta)(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+\dfrac{(\mu+\gamma+\delta)}{\kappa} \quad (3.27)$$

and dividing (iii^*) through by κ gives

$$\dfrac{(\mu+\delta+\gamma)}{\kappa} > 1 \quad (3.28)$$

From inequalities (3.27) and (3.28)

$\dfrac{(\mu+\delta+\gamma)}{\kappa} > 1 > \dfrac{(\alpha+\mu+\rho)(\mu)(\mu+\gamma+\delta)(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+$
$\dfrac{(\mu+\gamma+\delta)}{\kappa}.$

This implies that

$$1 > \dfrac{(\alpha+\mu+\rho)(\mu)\kappa(1-\mathcal{R}_0)}{\mu(\mu+\kappa)(\mu+\gamma+\delta)+\rho(\mu(\mu+\gamma+\delta)+\kappa(\mu+\delta))}+1.$$

It follows that

$$0 > \frac{(\alpha + \mu + \rho)(\mu)\kappa(1 - \mathcal{R}_0)}{\mu(\mu + \kappa)(\mu + \gamma + \delta) + \rho(\mu(\mu + \gamma + \delta) + \kappa(\mu + \delta))}.$$

The above inequality holds if

$$0 > 1 - \mathcal{R}_0.$$

that is, if

$$\mathcal{R}_0 > 1.$$

$\square$

Remark 3.1. Thus, the disease free equilibrium point is locallyasymptotically stable if $\mathcal{R}_0 < 1$, it is unstable if $\mathcal{R}_0 > 1$ leading to the endemic equilibrium point being stable if $\mathcal{R}_0 > 1$.

Local Stability Analysis of an HIV/AIDS Model

We consider a sexually active population $N(t)$, divided into six compartments: $S(t)$, $I_1(t)$, $I_2(t)$, $I_3(t)$, $A(t)$, and $T(t)$. $S(t)$ represents the number of susceptible individuals; $I_1(t)$ represents the number of HIV-positive individuals in the asymptomatic stage of HIV infection; $I_2(t)$ represents the number of HIV-positive individuals in the pre-AIDS stage but not receiving antiretroviral (ARV) treatment, $I_3(t)$, $A(t)$ represents the number of individuals with full-blown AIDS but not receiving ARV treatment; $T(t)$ represents the number of individuals who are receiving ARV treatment. The population dynamics is given by the following equations:

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$$
\begin{aligned}
\dot{S} &= \Lambda - \left(\frac{\beta_1 I_1}{N} + \frac{\beta_2 I_2}{N} + \frac{\beta_3 I_3}{N}\right)S - (\mu + \rho)S \\
\dot{I_1} &= \left(\frac{\beta_1 I_1}{N} + \frac{\beta_2 I_2}{N} + \frac{\beta_3 I_3}{N}\right)S - (\mu + \alpha_1)I_1 \\
\dot{I_2} &= \alpha_1 I_1 - (\mu + \alpha_2 + \gamma_2)I_2 \\
\dot{I_3} &= \alpha_2 I_2 - (\mu + \alpha_3 + \gamma_3)I_3 \\
\dot{A} &= \alpha_3 I_3 - (\mu + \delta + \gamma_A)A \\
\dot{T} &= \gamma_2 I_2 + \gamma_3 I_3 + \gamma_A A
\end{aligned}
\tag{3.29}
$$

where $\beta_i = cp_i, \quad i = 1,2,3$, is the product of the average number of sexual partners (c) and the probability (p_i) of the infection per partner with an infected individual in I_1, I_2 and I_3 respectively. The total population, $N(t)$ is given by

$$
N = S(t) + I_1(t) + I_2(t) + I_3(t) + A(t) + T(t),
\tag{3.30}
$$

and satisfies

$$
\dot{N} = \Lambda - \mu N - \rho S - \delta A.
\tag{3.31}
$$

Table 1: Variable and Parameters Definition for HIV/AIDS

Parameters	Description
β_1	infection rate of primary infectious individual
β_2	infection rate of asymptomatic infectious individual
β_3	infection rate of symptomatic infectious individual
Λ	Recruitment rate
μ	Natural death rate
α_1	Progression rate from the I_1 to I_2
α_2	Progression rate from the I_2 to I_3
α_3	Progression rate from the I_3 to A
δ	Disease-induced death rate
ρ	Rate of removal of susceptible
α_2	Treatment rate of asymptomatic infectious individual
α_3	Treatment rate of symptomatic infectious individual
α_A	Treatment rate for advance AIDS individual

The dynamics described in (3.29) will be studied in the region Ω, defined by $\Omega = \left\{ (S, I_1, I_2, I_3, A, T) \in R_+^6 \mid S + I_1 + I_2 + I_3 + A + T \leq \dfrac{\Lambda}{\mu} \right\}$ Which is positively invariant.

Equilibrium Points of the Model

The model has two equilibrium points; disease free equilibrium point and endemic equilibrium point given respectively as

$$(S^0, I_1^0, I_2^0, I_3^0, A^0, T^0 = 0) = \left(\frac{\Lambda}{\mu + \rho}, 0, 0, 0, 0, 0 \right)$$

and

$$S^* = \frac{\Lambda}{\lambda + \mu + \rho} \tag{3.32}$$

$$I_1^* = \frac{\lambda}{\mu + \alpha_1} S^* \tag{3.33}$$

$$I_2^* = \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} I_1^* \tag{3.34}$$

$$I_3^* = \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} \frac{\alpha_2}{(\mu + \alpha_3 + \gamma_3)} I_1^* \tag{3.35}$$

$$A^* = \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} \frac{\alpha_2}{(\mu + \alpha_3 + \gamma_3)} \frac{\alpha_3}{(\mu + \delta + \gamma_A)} I_1^* \tag{3.36}$$

$$T^* = \left[\frac{\gamma_2}{\mu} \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} + \frac{\gamma_3}{\mu} \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} \frac{\alpha_2}{(\mu + \alpha_3 + \gamma_3)} \right.$$
$$\left. + \frac{\gamma_A}{\mu} \frac{\alpha_1}{(\mu + \alpha_2 + \gamma_2)} \frac{\alpha_2}{(\mu + \alpha_3 + \gamma_3)} \frac{\alpha_3}{(\mu + \delta + \gamma_A)} \right] \tag{3.37}$$

where $\lambda = \frac{\beta_1 I_1}{N} + \frac{\beta_2 I_2}{N} + \frac{\beta_3 I_3}{N}$

Computation of $\mathcal{R}_0$ using Next Generation Matrix Approach

This model consists of five infection compartments namely; the primary compartments I_1, the asymptomatic compartment I_2, the symptomatic compartment I_3, the advance AIDS compartment A and the treated compartment T. Compartment A and T are assumed not to contribute to the infection transmission because the individuals in compartment A are consider to be generally very weak and hence, could not partake in any sexual act, while those in compartment T are assumed to adhere to the counselling instructions that are provided to them. Although, we do not expect total compliance for abstinence, we assume that the transmission rate of those individuals that fail to comply are negligible.

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The vectors F_i and V_i are given respectively by

$$F_i = \begin{bmatrix} (\dfrac{\beta_1 I_1}{N} + \dfrac{\beta_2 I_2}{N} + \dfrac{\beta_3 I_3}{N})S \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \end{bmatrix},$$

$$V_i^- - V_i^+ = V = \begin{bmatrix} (\mu + \alpha_1)I_1 \\ -\alpha_1 I_1 + (\mu + \alpha + \gamma)I_2 \\ -\alpha_2 I_2 + (\mu + \alpha_3 + \gamma_3)I_3 \\ -\alpha_3 I_3 + (\mu + \delta + \gamma_A)A \\ -\alpha_2 I_2 - \alpha_3 I_3 - \alpha_A A + \mu T \end{bmatrix}$$

By evaluating the Jacobian matrix at the disease free equilibrium of F and V, we obtain

$$F = \begin{bmatrix} \dfrac{\beta_1 I_1}{N} & \dfrac{\beta_2 I_2}{N} & \dfrac{\beta_3 I_3}{N} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \qquad (3.38)$$

and

$$V = \begin{bmatrix} \dfrac{\beta_1 I_1}{N} & \dfrac{\beta_2 I_2}{N} & \dfrac{\beta_3 I_3}{N} & 0 & 0 \\ (\mu + \alpha_1) & 0 & 0 & 0 & 0 \\ -\alpha_1 & (\mu + \alpha_2) & 0 & 0 & 0 \\ 0 & -\alpha_2 & (\mu + \alpha_3 + \gamma_3) & 0 & 0 \\ 0 & 0 & -\alpha_3 & (\mu + \delta + \gamma_A) & 0 \\ 0 & \gamma_2 & \gamma_3 & \gamma_A & \mu \end{bmatrix} \qquad (3.39)$$

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The Next Generation Matrix is given by

$$K = FV^{-1}$$

$$= \begin{bmatrix} M_{11} & M_{12} & M_{13} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix} \qquad (3.40)$$

where

$$M_{11} = \frac{\beta_1 \mu}{(\mu+\rho)(\mu+\alpha_1)} + \frac{\alpha_1 \beta_2 \mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)} \qquad (3.41)$$
$$+ \frac{\alpha_1 \alpha_2 \beta_3 \mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)},$$

$$M_{12} = \frac{\beta_2 \mu}{(\mu+\rho)(\mu+\alpha_2+\gamma_2)} + \frac{\alpha_2 \beta_2 \mu}{(\mu+\rho)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)},$$

$$(3.42)$$

and

$$M_{13} = \frac{\beta_3 \mu}{(\mu+\rho)(\mu+\alpha_3+\gamma_3)} \qquad (3.43)$$

$\mathcal{R}_0(\rho,\gamma)$ is given as

$$= \frac{\beta_1 \mu}{(\mu+\rho)(\mu+\alpha_1)} + \frac{\alpha_1 \beta_2 \mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)}$$
$$+ \frac{\alpha_1 \alpha_2 \beta_3 \mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)}$$

The basic reproduction number for the model is given by

$$\mathcal{R}_0 = \frac{\beta_1}{(\mu+\alpha_1)} + \frac{\alpha_1 \beta_2}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)} + \frac{\alpha_1 \alpha_2 \beta_3}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)}$$

where

(i) $\dfrac{\beta_1}{(\mu+\alpha_1)}$ is the probability of an infective that progresses from I_1 to I_2.

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(ii) $\dfrac{\beta_2}{(\mu+\alpha_2+\gamma_2)}$ is the probability of an infective that progresses from I_3 to I_3.

(iii) $\dfrac{\beta_3}{(\mu+\alpha_3+\gamma_3)}$ is the probability of an infective that progresses from I_3 to A.

From (3.33) we have

$$
\begin{aligned}
\frac{I_1^*}{S^*} &= \frac{\lambda}{(\mu+\alpha_1)} \\
\frac{I_1^*}{S^*} &= \frac{1}{(\mu+\alpha_1)}\frac{\beta_1 I_1+\beta_2 I_2+\beta_3 I_3}{N} \\
\frac{N^*}{S^*} &= \frac{1}{(\mu+\alpha_1)}\left(\beta_1+\frac{\beta_2 I_2}{I_1^*}+\frac{\beta_3 I_3}{I_1^*}\right) \\
\frac{N^*}{S^*} &= \frac{1}{(\mu+\alpha_1)}\left(\beta_1+\frac{\alpha_1\beta_2}{(\mu+\alpha_2+\gamma_2)}+\frac{\alpha_1\alpha_2\beta_3}{(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)}\right) \\
&= \mathcal{R}_0.
\end{aligned}
$$

Thus,

$$
\begin{aligned}
\mathcal{R}_0 &= \frac{N^*}{S^*} \\
&= \frac{S^*+I_1^*+I_2^*+I_3^*+A^*+T^*}{S^*} \\
&= 1+\lambda\frac{1}{(\mu+\alpha_1)}+\lambda\frac{\alpha_1}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)}+ \\
&\quad \lambda\frac{\alpha_1\alpha_2}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)}+ \\
&\quad \lambda\frac{\alpha_1\alpha_2\alpha_3}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)}+ \\
&\quad \lambda\frac{\alpha_1}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)}\left[\frac{\gamma_A}{\mu}+\frac{\alpha_2\gamma_3}{\mu(\mu+\alpha_3+\gamma_3)}+\right. \\
&\quad \left.\frac{\alpha_2\alpha_3\gamma_A}{\mu(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)}\right].
\end{aligned}
$$

This implies that

$$
\begin{aligned}
\mathcal{R}_0-1 &= \lambda\pi \\
\lambda &= \frac{(\mathcal{R}_0-1)}{\pi}
\end{aligned}
$$

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where π is the mean infective period given by

$$\pi = \frac{1}{(\mu+\alpha_1)} + \frac{\alpha_1}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)} + \frac{\alpha_1\alpha_2}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)}$$

$$+ \frac{\alpha_1\alpha_2\alpha_3}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)} +$$
$$+ \frac{\alpha_1}{(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)} \left[\frac{\gamma_A}{\mu} + \frac{\alpha_2\gamma_3}{\mu(\mu+\alpha_3+\gamma_3)} + \right.$$
$$\left. \frac{\alpha_2\alpha_3\gamma_A}{\mu(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)} \right].$$

By substituting λ into the endemic equilibrium point expressed in (3.33)-(3.37), we will obtain the endemic equilibrium in terms of $\mathcal{R}_0$ to be

$$S^* = \left[\frac{\Lambda\pi}{(\mathcal{R}_0-1)+\mu+\rho} \right],$$

$$I_1^* = \left[\frac{(\mathcal{R}_0-1)}{\pi(\mu+\alpha_1)} \right] S^*,$$

$$I_2^* = \left[\frac{\alpha_1}{\pi(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)} \right] (\mathcal{R}_0-1)S^*,$$

$$I_3^* = \left[\frac{\alpha_1\alpha_2}{\pi(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)} \right] (\mathcal{R}_0-1)S^*,$$

$$A^* = \left[\frac{\alpha_1\alpha_2\alpha_3}{\pi(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)} \right] (\mathcal{R}_0-1)S^*,$$

and

$$T^* = \frac{\alpha_1}{\pi(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)}$$
$$\left[\frac{\gamma_2}{\mu} + \frac{\alpha_2\gamma_3}{\mu(\mu+\alpha_3+\gamma_3)} + \frac{\alpha_2\alpha_3\gamma_A}{\mu(\mu+\alpha_3+\gamma_3)(\mu+\delta+\gamma_A)} \right] (\mathcal{R}_0-1)S^*.$$

The Jacobian matrix of the system (3.29) is given by

$$J = \begin{pmatrix} n^* & -\frac{\beta_1}{N}S & -\frac{\beta_2}{N}S & -\frac{\beta_3}{N}S & 0 & 0 \\ m^* & q^* & \frac{\beta_2}{N}S & \frac{\beta_3}{N}S & 0 & 0 \\ 0 & \alpha_1 & p^* & 0 & 0 & 0 \\ 0 & 0 & \alpha_2 & -(\alpha_3+\gamma_3+\mu) & 0 & 0 \\ 0 & 0 & 0 & \alpha_3 & -(\mu+\delta+\gamma_A) & 0 \\ 0 & 0 & \gamma_2 & \gamma_3 & \gamma_A & -\mu \end{pmatrix} \quad (3.44)$$

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where $n^* = -\dfrac{\beta_1 I_1}{N} - \dfrac{\beta_2 I_2}{N} - \dfrac{\beta_3 I_3}{N} - (\mu + \rho)$, $m^* = \dfrac{\beta_1 I_1}{N} + \dfrac{\beta_2 I_2}{N} + \dfrac{\beta_3 I_3}{N}$,

$q^* = \dfrac{\beta_1}{N} S - (\alpha_1 + \mu)$ and $p^* = -(\alpha_2 + \gamma_2 + \mu)$

Local Stability Analysis at the Disease Free Equilibrium Pint

In this section, we investigate the local stability of the disease free equilibrium.

Theorem 3.11. The disease free equilibrium point is locally asymptotically stable if $\mathcal{R}_0 < 1$.

Proof. The Jacobian matrix J evaluated at the disease free equilibrium point is given as

$$
J_0 =
\begin{pmatrix}
-(\mu+\rho) & -\dfrac{\beta_1 \mu}{(\mu+\rho)} & -\dfrac{\beta_2 \mu}{(\mu+\rho)} & -\dfrac{\beta_3 \mu}{(\mu+\rho)} & 0 & 0 \\
0 & p^* & \dfrac{\beta_2 \mu}{(\mu+\rho)} & \dfrac{\beta_3 \mu}{(\mu+\rho)} & 0 & 0 \\
0 & \alpha_1 & t^{**} & 0 & 0 & 0 \\
0 & 0 & \alpha_2 & -(\alpha_3+\gamma_3+\mu) & 0 & 0 \\
0 & 0 & 0 & \alpha_3 & q^{**} & 0 \\
0 & 0 & \gamma_2 & \gamma_3 & \gamma_A & -\mu
\end{pmatrix}
\tag{3.45}
$$

where $p^{**} = \dfrac{\beta_1 \mu}{(\mu+\rho)} - (\alpha_1 + \mu)$, $q^{**} = -(\mu + \delta + \gamma_A)$, $t^{**} = -(\alpha_2 + \gamma_2 + \mu)$

The matrix J_0 has three negative eigenvalue, $\lambda_1 = \mu$, $\lambda_2 = (\mu + \rho)$, $\lambda_3 = (\mu + \delta + \gamma_A)$. The sub-matrix is given as

$$
J_0^s =
\begin{pmatrix}
\dfrac{\beta_1 \mu}{(\mu+\rho)} - (\alpha_1 + \mu) & \dfrac{\beta_2 \mu}{(\mu+\rho)} & \dfrac{\beta_3 \mu}{(\mu+\rho)} \\
\alpha_1 & -(\alpha_2+\gamma_2+\mu) & 0 \\
0 & \alpha_2 & -(\alpha_3+\gamma_3+\mu)
\end{pmatrix}
\tag{3.46}
$$

We now determine the eigenvalue of the sub-matrix J_0^s. According to the corollary of Gershgorin's circle theorem, the matrix (J_0^s) will have negative eigenval-

ues if the following inequalities are satisfied:

$$row1: \quad 1 > \frac{\beta_1\mu}{(\mu+\rho)(\alpha_1+\mu)} + \frac{\beta_2\mu}{(\mu+\rho)(\alpha_1+\mu)} + \frac{\beta_3\mu}{(\mu+\rho)(\alpha_1+\mu)}$$

$$row2: \quad 1 > \frac{\alpha_1}{(\alpha_2+\gamma_2+\mu)}$$

$$row3: \quad 1 > \frac{\alpha_2}{(\alpha_3+\gamma_3+\mu)}$$

where $R_i, \quad i = 1,2,3$ stands for the rows in the matrix.

By multiplying the second term of the right hand side of row 1 by the term obtained in the right hand side of row 2 and also by multiplying the third term of right hand side of row 1 by the terms obtained in right hand side of row 1 and row 3 gives

$$1 > \frac{\beta_1\mu}{(\mu+\rho)(\mu+\alpha_1)} + \frac{\alpha_1\beta_2\mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)}$$
$$+ \frac{\alpha_1\alpha_2\beta_3\mu}{(\mu+\rho)(\mu+\alpha_1)(\mu+\alpha_2+\gamma_2)(\mu+\alpha_3+\gamma_3)},$$

which implies $\mathcal{R}_0(\rho) < 1$. Hence the disease free equilibrium point is locally asymptotically stable.

$\square$

Local Stability Analysis at the Endemic Equilibrium Pint

We now investigate the local stability of the endemic equilibrium point.

Theorem 3.12. The Endemic equilibrium (E_1) is locally asymptotically stable if $\mathcal{R}_0(\alpha) > 1$.

Proof. The Jacobian matrix evaluated at the endemic equilibrium gives

$$J_E = \begin{pmatrix} \lambda^* - (\mu + \rho) & -\dfrac{\beta_1}{\mathcal{R}_0} & -\dfrac{\beta_2}{\mathcal{R}_0} & -\dfrac{\beta_3}{\mathcal{R}_0} & 0 & 0 \\[2mm] \lambda^* & b^* & \dfrac{\beta_2}{\mathcal{R}_0} & \dfrac{\beta_3}{\mathcal{R}_0} & 0 & 0 \\[2mm] 0 & \alpha_1 & u^* & 0 & 0 & 0 \\[2mm] 0 & 0 & \alpha_2 & c^* & 0 & 0 \\[2mm] 0 & 0 & 0 & \alpha_3 & v^* & 0 \\[2mm] 0 & 0 & \gamma_2 & \gamma_3 & \gamma_A & -\mu \end{pmatrix}$$

where $\lambda^* = \dfrac{\beta_1 I_1}{N} + \dfrac{\beta_2 I_2}{N} + \dfrac{\beta_3 I_3}{N}$, $b^* = \dfrac{\beta_1}{\mathcal{R}_0} - (\alpha_1 + \mu)$,

$c^* = -(\alpha_3 + \gamma_3 + \mu)$, $v^* = -(\mu + \delta + \gamma_A)$, $u^* = -(\alpha_2 + \gamma_2 + \mu)$ and $\mathcal{R}_0 = \dfrac{N^*}{S^*}$.

Two of the eigenvalues of J_E are $-\mu$ and $= -(\delta + \gamma_A + \mu)$ which are negative.

The remaining matrix is given by

$$J_E^s = \begin{pmatrix} -\lambda^* - (\mu + \rho) & -\dfrac{\beta_1}{\mathcal{R}_0} & -\dfrac{\beta_2}{\mathcal{R}_0} & -\dfrac{\beta_3}{\mathcal{R}_0} \\[2mm] \lambda^* & \dfrac{\beta_1}{\mathcal{R}_0} - (\alpha_1 + \mu) & \dfrac{\beta_2}{\mathcal{R}_0} & \dfrac{\beta_3}{\mathcal{R}_0} \\[2mm] 0 & \alpha_1 & -(\alpha_2 + \gamma_2 + \mu) & 0 \\[2mm] 0 & 0 & \alpha_2 & -(\alpha_3 + \gamma_3 + \mu) \end{pmatrix}$$

According to the corollary of Gershgorin's circle theorem, the matrix (J_E^s) will have negative eigenvalues if the following inequalities are satisfied

$$\begin{aligned} row1 \quad &: \quad \lambda^* + (\mu + \rho) > \frac{\beta_1 + \beta_2 + \beta_3}{\mathcal{R}_0}, \\[2mm] row2 \quad &: \quad -\lambda^* + (\alpha_1 + \mu) > \frac{\beta_1 + \beta_2 + \beta_3}{\mathcal{R}_0}, \\[2mm] row3 \quad &: \quad 1 > \frac{\alpha_1}{(\alpha_2 + \gamma_2 + \mu)}, \\[2mm] row4 \quad &: \quad 1 > \frac{\alpha_2}{(\alpha_3 + \gamma_3 + \mu)}. \end{aligned}$$

Adding inequalities A_1 and A_2 gives

$$(\mu + \rho) + (\alpha_1 + \mu) > \frac{2(\beta_1 + \beta_2 + \beta_3)}{\mathcal{R}_0}$$

Dividing through by $(\mu + \rho)(\alpha_1 + \mu)$ gives

$$\frac{1}{(\alpha_1 + \mu)} + \frac{1}{(\mu + \rho)} > \frac{2}{\mathcal{R}_0} \left[\frac{\beta_1}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_2}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_3}{(\mu + \rho)(\alpha_1 + \mu)} \right]$$

Multiplying the above inequality by μ gives

$$\frac{\mu}{(\alpha_1 + \mu)} + \frac{\mu}{(\mu + \rho)} > \frac{2}{\mathcal{R}_0} \left[\frac{\beta_1 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_2 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_3 \mu}{(\mu + \rho)(\alpha_1 + \mu)} \right].$$

Dividing through by 2 gives

$$
\begin{aligned}
1 \quad &> \quad \frac{1}{2} \left(\frac{\mu}{(\alpha_1 + \mu)} + \frac{\mu}{(\mu + \rho)} \right) \\
&> \quad \frac{1}{\mathcal{R}_0} \left[\frac{\beta_1 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_2 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_3 \mu}{(\mu + \rho)(\alpha_1 + \mu)} \right]
\end{aligned}
$$

Thus,

$$1 > \frac{1}{\mathcal{R}_0} \left[\frac{\beta_1 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_2 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_3 \mu}{(\mu + \rho)(\alpha_1 + \mu)} \right]. \qquad (3.47)$$

From the inequalities A_3 and A_4, it is obvious that

$$\mathcal{R}_0 > \left[\frac{\beta_1 \mu}{(\mu + \rho)(\alpha_1 + \mu)} + \frac{\beta_2 \mu}{(\mu + \rho)(\alpha_1 + \mu)} * A_3 + \frac{\beta_3 \mu}{(\mu + \rho)(\alpha_1 + \mu)} * (A_3 * A_4) \right].$$

Hence, (3.47) holds provided $\mathcal{R}_0 > 1$. $\qquad \square$

Local Stability Analysis of a Tuberculosis Model

The population of interest is partitioned into three epidemiological classes: susceptible S, latent or exposed E, and infectious I. The incidence rate given by βSI (using the mass action law). A portion $p\beta SI$ gives rise to immediate active cases (fast progression), while the rest $(1-p)\beta SI$ gives rise to latent-TB cases with a low risk of progressing to active TB (slow progression) (Castillo-Chavez & Song, 2004). The progression rate from latent TB to active TB is assumed to be proportional to the number of latent-TB cases, that is, it is given by κE. The total incidence rate is $p\beta SI + \kappa E$. The model is given by the following system:

$$
\begin{aligned}
\dot{S} &= \Lambda - \beta SI - \mu S \\
\dot{E} &= (1-p)\beta SI - \kappa E - \mu E \\
\dot{I} &= p\beta SI + \kappa E - \mu I - \delta I
\end{aligned}
\qquad (3.48)
$$

Table 2: The State Variables for the Tuberculosis Model

Parameters	Description
S	Susceptible individuals
E	Latently infected individuals or exposed individuals
I	Infectious individuals

Table 3: Model Parameters and Their Interpretations for the Tuberculosis Model

Parameters	Discription
Λ	Recruitment rate of susceptible individuals
μ	Natural death rate
β	Transmission rate of active TB
κ	The progression rate from latent TB to active TB (Rate of slow progression)
δ	Death rate due to TB infection
p	Rate of fast progression
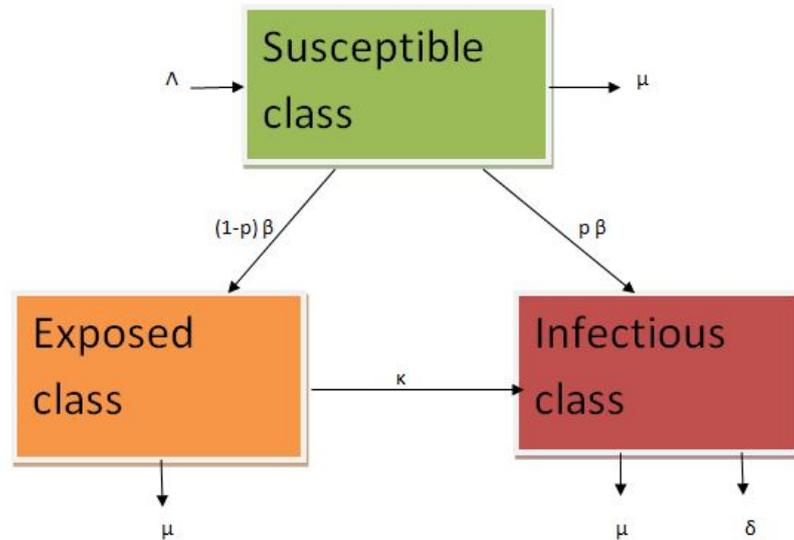
Figure 3: Transition Diagram for Tuberculosis

The Equilibrium Points

The equilibruim points of model (3.48) are

1. Disease free equilibrium point (P^0) given as

$$\left(S^0, E^0, I^0\right) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$$

2. Endemic equilibrium point (P^*) given as

$$\left(S^*, E^*, I^*\right) = \Big(\frac{(\delta\kappa + \delta\mu + \kappa\mu + \mu^2)}{(\beta(\mu p + \kappa))},$$
$$-\frac{(p-1)(\Lambda\beta\mu p + \Lambda\beta\kappa - \delta\kappa\mu - \delta\mu^2 - \kappa\mu^2 - \mu^3)}{((\mu p + \kappa)(\mu + \kappa)\beta)},$$
$$\frac{(\Lambda\beta\mu p + \Lambda\beta\kappa - \delta\kappa\mu - \delta\mu^2 - \kappa\mu^2 - \mu^3)}{(\beta(\delta\kappa + \delta\mu + \kappa\mu + \mu^2))}\Big)$$

Computation of $\mathcal{R}_0$ of a Tuberculosis Model

The system (3.48) has two disease states, E, and I given by

$$\dot{E} = (1-p)\beta SI - \kappa E - \mu E \qquad (3.49)$$
$$\dot{I} = p\beta SI + \kappa E - \mu I - \delta I$$

and one uninfected state, S. At the infection-free steady state $E^0 = I^0 = 0$, and $S^0 = \left(\frac{\Lambda}{\mu}\right)$.

We use the next-generation approach to compute the basic reproduction number $\mathcal{R}_0$. The vectors $\mathbf{F}_i$ and $\mathbf{V}_i$ are given respectively by

$$\mathbf{F}_i = \begin{bmatrix} (1-p)\beta S \\ p\beta S \end{bmatrix},$$

and

$$\mathbf{V}_i = \mathbf{V}_i^- - \mathbf{V}_i^+ = \begin{bmatrix} (\mu+\kappa)E \\ (\mu+\delta)I - \kappa E \end{bmatrix}$$

The matrices $\mathbf{F}$ and $\mathbf{V}$ are given respectively by

$$\mathbf{F} = \begin{bmatrix} 0 & (1-p)\beta S \\ 0 & p\beta S \end{bmatrix},$$

and

$$\mathbf{V} = \begin{bmatrix} (\mu+\kappa) & 0 \\ -\kappa & (\mu+\delta) \end{bmatrix}.$$

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Thus

$$\mathbf{V}^{-1} = \begin{bmatrix} \dfrac{1}{\kappa+\mu} & 0 \\ \dfrac{\kappa}{(\kappa+\mu)(\mu+\delta)} & \dfrac{1}{\mu+\delta} \end{bmatrix}$$

The Next Generation Matrix is given by

$$
\begin{aligned}
K &= \mathbf{F}\mathbf{V}^{-1} \\
&= \begin{bmatrix} 0 & (1-p)\beta S_0 \\ 0 & p\beta S_0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{\kappa+\mu} & 0 \\ \dfrac{\kappa}{(\kappa+\mu)(\mu+\delta)} & \dfrac{1}{\mu+\delta} \end{bmatrix} \\
&= \begin{bmatrix} \dfrac{(1-p)\beta S_0 \kappa}{(\kappa+\mu)(\mu+\delta)} & \dfrac{(1-p)\beta S_0}{\mu+\delta} \\ \dfrac{p\beta S_0 \kappa}{(\kappa+\mu)(\mu+\delta)} & \dfrac{p\beta S_0}{\mu+\delta} \end{bmatrix}
\end{aligned}
$$

The Basic reproduction number $\mathcal{R}_0$ is the positive real eigenvalue of K which is at least as large in modulus as all eigenvalues of K.

$$\mathcal{R}_0 = \frac{\beta S_0(\kappa+\mu p)}{(\kappa+\mu)(\mu+\delta)}$$

But

$$S_0 = \frac{\Lambda}{\mu}$$

this implies

$$\mathcal{R}_0 = \frac{\beta\Lambda(\kappa+\mu p)}{\mu(\kappa+\mu)(\gamma+\mu+\delta)}$$

The endemic equilibrium point (P^*) can now be expressed in terms of $\mathcal{R}_0$ as

$$(P^*) = (S^*, E^*, I^*) = \left(\frac{\Lambda}{\mu\mathcal{R}_0}, -\frac{(p-1)(\mathcal{R}_0-1)\mu(\mu+\delta)}{(\mu p+\kappa)\beta}, \frac{(\mathcal{R}_0-1)\mu}{\beta} \right)$$

Local Stability Analysis of the Disease Free Equilibrium

We analyze the local stability of the disease free Equilibrium by applying the theorem which follows.

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Theorem 3.13. The disease free equilibrium is locally asymptotically stable if $\mathcal{R}_0 < 1$.

Proof. The Jacobian matrix J of the system (3.48) is

$$J = \begin{bmatrix} -\beta I - \mu & 0 & -\beta S \\ (1-p)\beta I & -(\kappa+\mu) & (1-p)\beta S \\ p\beta I & \kappa & p\beta S - \delta - \mu \end{bmatrix} \quad (3.50)$$

Evaluating the matrix (3.50) at the disease free equilibrium gives

$$J_0 = \begin{bmatrix} -\mu & 0 & -\dfrac{\beta\Lambda}{\mu} \\ 0 & -(\kappa+\mu) & \dfrac{(1-p)\beta\Lambda}{\mu} \\ 0 & \kappa & \dfrac{p\beta\Lambda}{\mu} - (\mu+\delta) \end{bmatrix} \quad (3.51)$$

The disease free equilibrium point will be locally asymptotically stable if the eigenvalues of the Jacobian matrix are negative or have negative real parts. The matrix J_0 has one eigenvalue $-\mu$ which is negative. The remaining submatrix is given by

$$J_r = \begin{bmatrix} -(\kappa+\mu) & \dfrac{(1-p)\beta\Lambda}{\mu} \\ \kappa & \dfrac{p\beta\Lambda}{\mu} - (\mu+\delta) \end{bmatrix}$$

According to the corollary of Gershgorin's circle theorem, the matrix (J_r) will have negative eigenvalues if the following inequalities are satisfied:

$$(\kappa+\mu) > \frac{(1-p)\beta\Lambda}{\mu} \quad (3.52a)$$

$$-\frac{p\beta\Lambda}{\mu} + (\mu+\delta) > \kappa \quad (3.52b)$$

Dividing (3.52a) through by $(\kappa+\delta)$ yields

$$1 > \frac{(1-p)\beta\Lambda}{\mu(\kappa+\mu)} \quad (3.53)$$

Also dividing (3.52b) through by κ yields

$$-\frac{p\beta\Lambda}{\mu\kappa} + \frac{(\mu+\delta)}{\kappa} > 1$$

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$$\frac{-p\beta\Lambda + \mu(\mu + \delta)}{\mu\kappa} > 1 \qquad (3.54)$$

From (3.53) and (3.54) we have,

$$\frac{-p\beta\Lambda + \mu(\mu + \delta)}{\mu\kappa} \quad > \quad 1 > \frac{(1-p)\beta\Lambda}{\mu(\kappa + \mu)}$$

$$\Rightarrow -p\beta\Lambda + \mu(\mu + \delta) \quad > \quad \frac{\mu\kappa\beta\Lambda - p\mu\kappa\beta\Lambda}{\mu(\kappa + \mu)}$$

$$\Rightarrow \Big(-p\beta\Lambda + \mu(\mu + \delta)\Big)\mu(\kappa + \mu) \quad > \quad \mu\kappa\beta\Lambda - p\mu\kappa\beta\Lambda$$

$$\Rightarrow -p\kappa\mu\beta\Lambda - p\beta\Lambda\mu^2 + \mu(\mu + \delta)\mu(\kappa + \mu) \quad > \quad \mu\kappa\beta\Lambda - p\mu\kappa\beta\Lambda$$

$$\Rightarrow \mu(\mu + \delta)\mu(\kappa + \mu) \quad > \quad \mu\kappa\beta\Lambda + p\beta\Lambda\mu^2$$

$$\Rightarrow 1 \quad > \quad \frac{\mu(\kappa + \mu p)\beta\Lambda}{\mu(\delta + \mu)\mu(\kappa + \mu)}$$

$$\Rightarrow 1 \quad > \quad \frac{(\kappa + \mu p)\beta\Lambda}{\mu(\delta + \mu)(\kappa + \mu)}$$

$$\Rightarrow 1 \quad > \quad \mathcal{R}_0$$

$$\mathcal{R}_0 \quad < \quad 1$$

Epidemiologically, if $\mathcal{R}_0 < 1$, the epidemic is expected to be eliminated and should persist if $\mathcal{R}_0 > 1$. Therefore, we conclude that from the above proof the disease free equilibrium (E_0) is locally asymptotically stable. $\qquad \square$

Local Stability Analysis of the Endemic Equilibrium Point

We now investigate the local stability of the endemic equilibrium Point.

Theorem 3.14. The endemic equilibrium is locally asymptotically stable if $\mathcal{R}_0 > 1$.

Proof. Evaluating the matrix (3.50) at the endemic equilibrium gives

$$J_e^s = \begin{bmatrix} -(\mathcal{R}_0 - 1)\mu - \mu & 0 & -\dfrac{\beta\Lambda}{\mathcal{R}_0\mu} \\ -(1-p)(1-\mathcal{R}_0)\mu & -(\kappa + \mu) & \dfrac{(1-p)\beta\Lambda}{\mathcal{R}_0\mu} \\ -p(1-\mathcal{R}_0)\mu & \kappa & \dfrac{p\beta\Lambda}{\mathcal{R}_0\mu} - (\mu + \delta) \end{bmatrix} \qquad (3.55)$$

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According to equation the corollary of Gershgorin's circle theorem, the matrix (J_e^s) will have negative eigenvalues if the following inequalities are satisfied:

$$(\mathcal{R}_0 - 1)\mu + \mu > \frac{\beta\Lambda}{\mathcal{R}_0\mu} \tag{3.56a}$$

$$(\kappa + \mu) > (1-p)(1-\mathcal{R}_0)\mu + \frac{(1-p)\beta\Lambda}{\mathcal{R}_0\mu} \tag{3.56b}$$

$$-\frac{p\beta\Lambda}{\mathcal{R}_0\mu} + (\mu+\delta) - p(1-\mathcal{R}_0)\mu > \kappa \tag{3.56c}$$

Dividing (3.56b) through by $(\kappa + \mu)$ gives

$$1 > \frac{(1-p)(1-\mathcal{R}_0)\mu}{(\kappa+\mu)} + \frac{(1-p)\beta\Lambda}{\mathcal{R}_0\mu(\kappa+\mu)}.$$

Thus,

$$1 > \frac{(1-p)\mathcal{R}_0\mu(1-\mathcal{R}_0)\mu + (1-p)\beta\Lambda}{\mathcal{R}_0\mu(\kappa+\mu)} \tag{3.57}$$

Dividing (3.56c) through by κ gives

$$-\frac{p\beta\Lambda}{\mathcal{R}_0\mu\kappa} + \frac{(\mu+\delta)}{\kappa} - \frac{p(1-\mathcal{R}_0)\mu}{\kappa} > 1.$$

Thus,

$$\frac{-p\beta\Lambda + (\mu+\delta)\mathcal{R}_0\mu - p\mathcal{R}_0\mu(1-\mathcal{R}_0)\mu}{\mathcal{R}_0\mu\kappa} > 1 \tag{3.58}$$

From (3.57) and (3.58)

$$\frac{-p\beta\Lambda + (\mu+\delta)\mathcal{R}_0\mu - p\mathcal{R}_0\mu(1-\mathcal{R}_0)\mu}{\mathcal{R}_0\mu\kappa} > 1 > \frac{(1-p)\mathcal{R}_0\mu(1-\mathcal{R}_0)\mu + (1-p)\beta\Lambda}{\mathcal{R}_0\mu(\kappa+\mu)}$$
$$\tag{3.59}$$

Expanding and simplifying (3.59) gives

$$-p\beta\Lambda\mathcal{R}_0\mu\kappa - p\beta\Lambda\mathcal{R}_0\mu^2 - p\mathcal{R}_0^2\mu^3(1-\mathcal{R}_0)\kappa - p\mathcal{R}_0^2\mu^4(1-\mathcal{R}_0) +$$

$$(\mu+\delta)(\kappa+\mu)\mathcal{R}_0^2\mu^2 > \beta\Lambda\mathcal{R}_0\mu\kappa - p\beta\Lambda\mathcal{R}_0\mu\kappa +$$

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$$\mathcal{R}_0^2 \mu^3 (1 - \mathcal{R}_0)\kappa - p\mathcal{R}_0^2 \mu^3 (1 - \mathcal{R}_0)\kappa$$

$$-p\beta\Lambda\mu - p\mathcal{R}_0\mu^3(1 - \mathcal{R}_0) + (\mu + \delta)(\kappa + \mu)\mathcal{R}_0\mu \; > \; \beta\Lambda\kappa + \mathcal{R}_0\mu^2(1 - \mathcal{R}_0)\kappa$$

$$\Rightarrow -p\beta\Lambda\mu - \beta\Lambda\kappa + (\mu + \delta)(\kappa + \mu)\mathcal{R}_0\mu \; > \; \mathcal{R}_0\mu^2(1 - \mathcal{R}_0)\kappa +$$

$$p\mathcal{R}_0\mu^3(1 - \mathcal{R}_0)$$

$$-\beta\Lambda(\mu p + \kappa) + \mathcal{R}_0\mu(\mu + \delta)(\kappa + \mu) \; > \; \mathcal{R}_0\mu^2(1 - \mathcal{R}_0)(\mu p + \kappa)$$

$$-\frac{\beta\Lambda(\mu p + \kappa)}{\mathcal{R}_0\mu(\mu + \delta)(\kappa + \mu)} + \frac{(\mathcal{R}_0\mu(\mu + \delta)(\kappa + \mu))}{(\mathcal{R}_0\mu(\mu + \delta)(\kappa + \mu))} \; > \; \frac{\mathcal{R}_0\mu^2(1 - \mathcal{R}_0)(\mu p + \kappa)}{\mathcal{R}_0\mu(\mu + \delta)(\kappa + \mu)}$$

$$-1 + 1 \; > \; \frac{\mu(1 - \mathcal{R}_0)(\mu p + \kappa)}{(\mu + \delta)(\kappa + \mu)}$$

$$0 \; > \; \mu(1 - \mathcal{R}_0)(\mu p + \kappa)$$

$$\mathcal{R}_0 \; > \; 1$$

This shows that the Endemic Equilibrium point is locally asymptotically stable if $\mathcal{R}_0 > 1$. $\qquad\qquad\square$

Chapter Summary

In the earlier part of the chapter, we looked at some definitions, theorem and methods that will be needed for the study. We investigated the local stability of both the disease free and endemic equilibria of SEIR, SEIRS, an HIV/AIDS and a Tuberculosis models in the latter part of chapter. It was observed that no matter the state or the dimension of the system or matrix this corollary can be used to analyse the local stability for both disease free and endemic equilibrium, by establishing that if $\mathcal{R}_0 < 1$, this means that the Jacobian matrix will have negative or negative real part eigenvalues. Thus, disease free equilibrium is stable but if $\mathcal{R}_0 > 1$, the endemic equilibrium is stable.

CHAPTER FOUR

MODEL FORMULATION

Introduction

In this chapter, we formulate a deterministic mathematical model for the transmission and control of malaria. The motivation for our models comes from the fact that, in a closed environment, an optimal combination of prevention and treatment can reduce both the number of infected humans and infected mosquitoes, and eventually eliminate the disease from the community. The main innovation in our model is that, in addition to the natural death rate of the vector (mosquito), a proportion of the *prevention effort* also contributes to a reduction of the mosquito population.

There are many infectious diseases for which there is a cure, yet they remain endemic in many communities around the world. Malaria is one of such infectious disease. In spite of the fact that there is not yet a vaccine for malaria, there a number of preventive measures which, when properly administered, can play the role of "vaccination", by reducing considerably, the size of the susceptible class. The key to eradicating any infectious disease lies in effective treatment for the infected population, plus a rapid reduction in the susceptible class below a certain threshold.

Malaria Transmission

Malaria is an infectious disease mainly found in tropical areas such as Sub-Saharan Africa, Central and South America, the Indian subcontinent, South East Asia and the Pacific islands which are called malaria regions. Malaria is caused by parasites called the genus Plasmodium - a protozoan parasite transmitted by an infectious female Anopheles mosquito that are transmitted to people through the bites of infected mosquitoes. There are five parasite species

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that cause malaria in human; P. falciparum, P. vivax, P. malarie, P. ovale and P. knowlesi (WHO, 2019). It is possible to get infected with more than one type of Plasmodium parasite. Each parasite causes a slightly different type of illness. Malaria parasites spread by infecting successively two types of hosts: humans and the female Anopheles mosquito.

In human, the parasites grow and multiply first in the liver cells where they under go multiple asexual fission [schizogony] and then in the red cells of the blood where successive broods parasites grow and destroy them, releasing daughter parasites ("merozoties") that continue the cycle by invading other red cells. After being released from the liver cells, apart from the P. falciparum, the merozoites either infect other liver cells, thus continuing the pre-erythrocytic state, or attach to erythrocytes and penetrate these cells (Agyepong, 2008). Inside the erythrocyte, the plasmodium begins to enlarge as uninucleate cell called trophozoite. The trophozoite's nucleus then divides asexually to produce a schizont that has 6-24 nuclei. The schizont divides and produces mononucleated merozoites (Aikawa & Seed, 1998). This erythrocytic stage is cyclic and repeats itself approximately every 48 to 72 hours or longer, depending on the species of plasmodium involved. Occasionally merozoites differentiate into macro and micro gametocytes, which do not rapture the erythrocyte. The symptoms of malaria are cause by the blood stage parasites (gametocytes, which occur in male and female forms).

In mosquito, when certain forms of blood parasites are ingested during blood feeding by a female Anopheles mosquito. In the mosquito's gut, the infected erythrocytes lyse and gametes fuse to form a diploid zygote known as ookinete (Aikawa & Seed, 1998). The ookinete migrates to the mosquito's gut wall, penetrates and forms an oocyst on its outer surface. In the process called sporogony, the oocyst undergoes meiosis and forms a form of the parasite called a sporozoite that migrate to the mosquito's salivary glands after about 10-18

days (CDC, 2019). When the Anopheles mosquito bites another human for blood meal, it inject anticoagulant saliva together with sporozoite which migrate to the liver, thereby beginning the new cycle. Thus the infected mosquito carries the disease from one human to another (acting as a 'vector'), while infected humans transmit the parasite to the mosquito, in contrast to the human host, the mosquito vector does not suffer from the presence of the parasites.

The common first symptoms of malaria are a headache, aching muscles, tummy ache and weakness or lack of energy. A day or so later, the body temperature may rise (up to 40 degrees Celsius) and the patient may have: a fever, shivers, mild chills, severe headache, vomiting, diarrhoea, and loss of appetite (Adiku, 2013). However, it takes at least six days for symptoms to appear. The time it takes symptoms to appear can vary with the type of parasite that the mosquito was carrying.

A Malaria Transmission Model Without Exposed Compartment

We formulate a malaria transmission model as an *SIRS* for the host population and *SI* for the vector population. The total human population $N_h(t)$ is divided into the susceptible $S_h(t)$, the infectious $I_h(t)$ and the recovered $R_h(t)$. The total vector population $N_v(t)$ is split into susceptible $S_v(t)$ and infectious $I_v(t)$. It is assumed that, a susceptible host becomes infectious after a bite by an infected mosquito and the susceptible mosquito becomes infectious after it bites an infected host. The key to controlling the spread of any infectious disease lies in effective treatment (if one is available) and effective prevention (if a vaccine is available). In the case of malaria, there are a variety of treatment available. Even though there is no vaccine for malaria, implementation of effective treatment strategies can be used to effectively control the transmission. We denote the prevention rate by α, then $c\alpha$ is the proportion of the prevention effort, that contribute to the reduction of the vector populations. The human population

decreases through a density-dependent per capita emigration and natural death rate, and through a per capita disease-induced death rate.

Figure 4 shows the transition diagram for a malaria transmission model without exposed compartment.
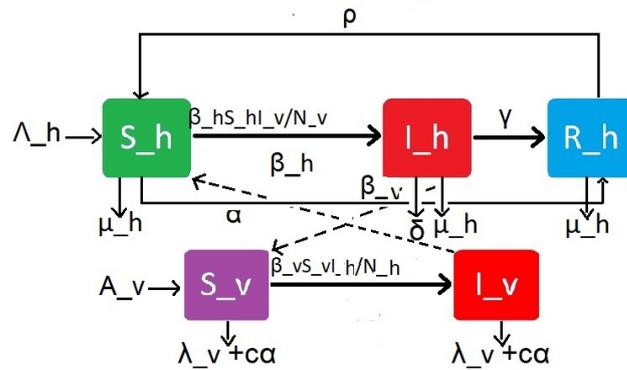
Figure 4: A Flow Chart of a 5-Staged States Malaria Model

Table 4: The State Variables for a 5-Staged State Malaria Transmission Model

Populations	Description
S_h	Number of susceptible human
I_h	Number of infectious human
R_h	Number of Recovered human
S_v	Number of Susceptible vector
I_v	Number of infectious vector
N_h	Total human population
N_v	Total vector population

Table 5: Model Parameters and Their Interpretations

Parameters	Description
Λ_h	Humans recruitment birth rate
μ_h	Humans death rate
γ	recovery rate of human
α	Prevention rate
β_h	Transmission rate of host
	(product of biting rate and probability of transmission of disease)
δ	Disease-induced death rate for humans
ρ	Rate of loss of immunity for humans
λ_v	Vector birth rate = vector death rate
$c\alpha$	proportion of prevention effort that
	contributes to vector death rate $0 \leq c \leq 1$
β_v	Transmission rate of vector
	(product of biting rate and probability of transmission of disease)

Assumptions

The following assumptions are made in order to formulate the equations of the model:

- The development of malaria starts when the infectious female mosquito bites the human host.

- The infective human population recovers with temporary immunity with clinical treatment.

- Mosquitoes do not die from the infection.

- There is no super infection of the disease.

- All new borns are susceptible.

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- Certain proportion of the prevention strategies contribute to the death rate of the mosquitoes.

Applying the assumptions, definitions of state variables and parameters above, the system of non-linear differential equations which describe the dynamics of a malaria model without exposed compartment are formulated as:

$$
\begin{aligned}
\frac{d\bar{S}_h}{dt} &= \Lambda_h - \beta_h \bar{S}_h \frac{\bar{I}_v}{N_v} + \rho \bar{R}_h - \mu_h \bar{S}_h - \alpha \bar{S}_h \\
\frac{d\bar{I}_h}{dt} &= \beta_h \bar{S}_h \frac{\bar{I}_v}{N_v} - \gamma \bar{I}_h - \mu_h \bar{I}_h - \delta \bar{I}_h \\
\frac{d\bar{R}_h}{dt} &= \gamma \bar{I}_h - \mu_h \rho \bar{R}_h + \alpha \bar{S}_h \\
\frac{d\bar{S}_v}{dt} &= A_v - \beta_v \bar{S}_v \frac{\bar{I}_h}{N_h} - (\lambda_v + c\alpha) \bar{S}_v \\
\frac{d\bar{I}_v}{dt} &= \beta_v \bar{S}_v \frac{\bar{I}_h}{N_h} - (\lambda_v + c\alpha) \bar{I}_v
\end{aligned}
\tag{4.1}
$$

with total human and vector populations given respectively by

$$
\bar{N}_h = \bar{S}_h + \bar{I}_h + \bar{R}_h,
$$

and

$$
\bar{N}_v = \bar{S}_v + \bar{I}_v.
$$

Adding the first three equations of equation(4.1) gives

$$
\begin{aligned}
\frac{d\bar{N}_h}{dt} &= \frac{d\bar{S}_h}{dt} + \frac{d\bar{I}_h}{dt} + \frac{d\bar{R}_h}{dt} \\
&= \Lambda_h - N_h \mu - \delta I_h
\end{aligned}
$$

In the absence of the disease induced death, that is, $\delta = 0$, we have

$$
\begin{aligned}
\frac{d\bar{N}_h}{dt} &= \Lambda_h - \mu_h \bar{N}_h \\
\frac{d\bar{N}_h}{dt} + \mu_h \bar{N}_h &= \Lambda_h
\end{aligned}
\tag{4.2}
$$

Solving equation (4.2) we obtain,

$$
\bar{N}_h(t) e^{\mu_h t} = \frac{\Lambda_h e^{\mu_h t}}{\mu_h} + C,
$$

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where C is the constant of integration. Thus,

$$
\begin{aligned}
\bar{N}_h(t) &= \left(\frac{\Lambda_h e^{\mu_h t}}{\mu_h} \times \frac{1}{e^{\mu_h t}}\right) + Ce^{-\mu_h t} \\
&= \frac{\Lambda_h}{\mu_h} + Ce^{-\mu_h}
\end{aligned}
$$

Using the initial conditions, $\bar{N}_h(0) = \bar{N}_{h0}$:

$$
\bar{N}_{h0} = \frac{\Lambda_h}{\mu_h} + C
$$

$$
\text{it follows that} \quad C = \bar{N}_{h0} - \frac{\Lambda_h}{\mu_h}.
$$

so,

$$
\bar{N}_h(t) + \left(\frac{\Lambda_h}{\mu_h t} - \bar{N}_{h0}\right)e^{-\mu_h t} = \frac{\Lambda_h}{\mu_h} \tag{4.3}
$$

This means that,

$$
\bar{N}_h(t) \leq \frac{\Lambda_h}{\mu_h}, \quad \text{provided} \quad \bar{N}_h(0) \leq \frac{\Lambda_h}{\mu_h} \quad \text{for} \quad t \geq 0. \tag{4.4}
$$

Similarly, adding the last two equations of equation(4.1) gives

$$
\begin{aligned}
\frac{d\bar{N}_v}{dt} &= \frac{d\bar{S}_v}{dt} + \frac{d\bar{I}_v}{dt} \\
&= A_v - N_v(\lambda_v + c\alpha) \tag{4.5}
\end{aligned}
$$

Solving equation (4.5) we have,

$$
\bar{N}_h(t)e^{(\lambda_v + c\alpha)t} = \frac{A_v e^{(\lambda_v + c\alpha)t}}{(\lambda_v + c\alpha)} + M
$$

where M is the constant of integration

$$
\begin{aligned}
\bar{N}_v(t) &= \left(\frac{A_v e^{(\lambda_v + c\alpha)t}}{(\lambda_v + c\alpha)} \times \frac{1}{e^{(\lambda_v + c\alpha)t}}\right) + Me^{-(\lambda_v + c\alpha)t} \\
&= \frac{A_v}{(\lambda_v + c\alpha)} + Me^{-(\lambda_v + c\alpha)t}
\end{aligned}
$$

Using the initial condition $\bar{N}_v(0) = \bar{N}_{v0}$ we obtain

$$
\bar{N}_{v0} = \frac{A_v}{(\lambda_v + c\alpha)} + C
$$

$$
\text{it follows that} \quad M = \bar{N}_{v0} - \frac{A_v}{(\lambda_v + c\alpha)}.
$$

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Thus,

$$\bar{N}_v(t) + \left(\frac{A_v}{(\lambda_v + c\alpha)t} - \bar{N}_{v0}\right)e^{-(\lambda_v + c\alpha)t} = \frac{A_v}{(\lambda_v + c\alpha)t} \tag{4.6}$$

This implies that,

$$\bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)}, \quad \text{provided} \quad \bar{N}_v(0) \leq \frac{A_v}{(\lambda_v + c\alpha)} \text{for} \quad t \geq 0. \tag{4.7}$$

For positivity of solutions, we apply the theorem that follows

Theorem 4.1. Let the initial data be $\{(S_h(0), S_v(0)) > 0, (I_h(0), R_h(0), I_v(0)) \geq 0\} \in \Omega)$. Then the solution set $\{S_h, I_h, R_h, S_v, I_v\}$ of the system (4.1) is positive for all $t > 0$.

Proof. From the first equation in the model (4.1), we have

$$\frac{dS_h}{dt} = \Lambda_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h$$

$$\geq -\beta_h S_h I_v - \alpha S_h - \mu_h S_h$$

Using separation of variables and integrating both sides gives

$$\int \frac{dS_h}{S_h} \geq \int (-\beta_h I_v - \alpha - \mu_h)dt$$

$$\int \frac{dS_h}{S_h} \geq \int (-\beta_h I_v dt - \int \alpha + \mu_h)dt$$

$$\ln S_h \geq -\int (\beta_h I_v)dt + (-\alpha - \mu_h)t + C$$

$$\Rightarrow S_h \geq e^{-\int(\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t} \times e^C$$

$$\geq (e^{-\int(\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t}) \times e^C$$

$$\geq (e^{-\int(\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t}) \times M$$

$$\geq M(e^{(-\int(\beta_h I_v)dt - (\alpha + \mu_h)t)})$$

using the initial conditions: $t = 0, \quad S_h(0) \geq M$

$$\Rightarrow S_h \geq S_h(0)(e^{(-\int(\beta_h I_v)dt - (\alpha + \mu_h)t)}) \geq 0$$

Therefore,

$$S_h \geq S_h(0)(e^{(-\int(\beta_h I_v)dt - (\alpha + \mu_h)t)}) \geq 0$$

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From the second equation we have

$$\begin{aligned}
\frac{dI_h}{dt} &= \beta_h S_h I_v - (\gamma + \mu + \delta)I_h \\
&\geq -(\gamma + \mu + \delta)I_h \\
\frac{dI_h}{dt} &\geq -(\gamma + \mu + \delta)I_h
\end{aligned}$$

Using separation of variables and integrating both sides gives

$$\begin{aligned}
\int \frac{dI_h}{I_h} &\geq \int -(\gamma + \mu + \delta)dt \\
\ln I_h &\geq -(\gamma + \mu + \delta)t + c \\
\Rightarrow I_h &\geq e^{-(\gamma + \mu + \delta)t + c} \\
&\geq P e^{-(\gamma + \mu + \delta)t} \\
&\geq I_h(0)e^{-(\gamma + \mu + \delta)t}
\end{aligned}$$

where $P = I_h(0)$

$$I_h \geq I_h(0)e^{-(\gamma + \mu + \delta)t} \geq 0$$

similarly, it can be shown that the remaining equations of the system (4.1) are positive for all $t > 0$. $\square$

Positive Invariant Region

The positive invariant region is obtained in the following theorem.

Theorem 4.2. The solutions of the system (4.1) are feasible for all $t > 0$ if they enter the invariant region $\Omega = \Omega_h \times \Omega_v$

Proof. Let $\Omega = (\bar{S}_h, \bar{I}_h, \bar{R}_h, \bar{S}_v, \bar{I}_v) \in R_+^5$ be any solution of system (4.1) with non-negative initial conditions.

From (4.4) all feasible solutions set of the human population of the model (4.1) enters the region.

$$\Omega_h = \left\{ (S_h, I_h, R_h) \in R_+^3 : S_h > 0, I_h \geq 0, R_h \geq 0, N_h(t) \leq \frac{\Lambda_h}{\mu_h} \right\}.$$

Similarly, from (4.7) the feasible solutions set of the mosquito enters the region

$$\Omega_v = \left\{ (S_v, I_v) \in R_+^2 : S_h > 0, I_h \geq 0, \bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)} \right\}.$$

Therefore, the feasible solutions set for the model (4.28) is given by

$$\Omega = \left\{ (S_h, I_h, R_h, S_v, I_v) \in R_+^5 : (S_h, S_v) > 0, (I_h, R_h, I_v) \geq 0; \right.$$
$$\left. \bar{N}_h(t) \leq \frac{\Lambda_h}{\mu_h}; \bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)} \right\}.$$

Therefore, the region Ω is positively-invariant (i.e. solutions remain positive for all times, (t) and the model (4.1) is biologically, epidemiologically meaningful and mathematically well-posed in the domain Ω. $\square$

Now, let $S_h = \dfrac{\bar{S}_h}{\Lambda_h/\mu_h}, I_h = \dfrac{\bar{I}_h}{\Lambda_h/\mu_h}, R_h = \dfrac{\bar{R}_h}{\Lambda_h/\mu_h},$

Similarly, let $S_v = \dfrac{\bar{S}_v}{A_v/(\lambda_v + c\alpha)}, I_v = \dfrac{\bar{I}_v}{A_v/(\lambda_v + c\alpha)}.$

System (4.1) can be written as the equivalent form:

$$\begin{aligned}
\dot{S}_h &= \mu_h - \beta_h S_h I_v + \rho R_h - \mu_h S_h - \alpha S_h \\
\dot{I}_h &= \beta_h S_h I_v - \gamma I_h - \mu_h I_h - \delta I_h \\
\dot{R}_h &= \gamma I_h - \mu_h R_h - \rho R_h + \alpha S_h \\
\dot{S}_v &= (\lambda_v + c\alpha) - \beta_v S_v I_h - (\lambda_v + c\alpha) S_v \\
\dot{I}_v &= \beta_v S_v I_h - (\lambda_v + c\alpha) I_v.
\end{aligned} \tag{4.8}$$

Let $\mu_c = (\lambda_v + c\alpha)$, then equation (4.8) becomes

$$\begin{aligned}
\dot{S}_h &= \mu_h - \beta_h S_h I_v + \rho R_h - \mu_h S_h - \alpha S_h \\
\dot{I}_h &= \beta_h S_h I_v - \gamma I_h - \mu_h I_h - \delta I_h \\
\dot{R}_h &= \gamma I_h - \mu_h R_h - \rho R_h + \alpha S_h \\
\dot{S}_v &= \mu_c - \beta_v S_v I_h - \mu_c S_v \\
\dot{I}_v &= \beta_v S_v I_h - \mu_c I_v.
\end{aligned} \tag{4.9}$$

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Equilibrium Pints of the Model

The two equilibrium points of the system (4.9) are

(a) Disease Free equilibrium $(S_h^0, I_h^0, R_h^0, S_v^0, I_v^0)$

$$= \left(\frac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}, 0, \frac{\alpha}{(\alpha + \rho + \mu_h)}, 1, 0 \right)$$

(b) Endemic equilibrium $(E_1) = ((S_h^*, I_h^*, R_h^*, S_v^*, I_v^*))$ $S_h^* = \mu_c(\gamma + \mu_h + \delta)(\delta\rho\mu_c +$

$\delta\mu_c\mu_h + \gamma\mu_c\mu_h + \rho\beta_v\mu_h + \rho\mu_c\mu_h + \beta_v\mu_h\mu_h + \mu_c\mu_h^2)/$

$((\alpha\delta\mu_h\mu_c + \alpha\gamma\mu_h\mu_c + \alpha\mu_h^2\mu_c + \delta\rho\beta_h\mu_c + \delta\rho\mu_h\mu_c + \delta\beta_h\mu_h\mu_c + \delta\mu_h^2\mu_c + \gamma\rho\mu_h\mu_c +$

$\gamma\beta_h\mu_h^2 + \gamma\mu_h^2\mu_c + \rho\beta_h\mu_h\mu_c + \rho\mu_h^2\mu_c + \beta_h\mu_h^2\mu_c + \mu_c\mu_h^3)\beta_v),$

$I_h^* = -(\alpha\delta(\mu_c)^2\mu_h + \alpha\gamma(\mu_c)^2\mu_h + \alpha(\mu_c)^2\mu_h^2 + \delta\rho(\mu_c)^2\mu_h + \gamma\rho(\mu_c)^2\mu_h + \gamma(\mu_c)^2\mu_h^2 -$

$\rho\beta_h\beta_v\mu_h\mu_c + \delta(\mu_c)^2\mu_h^2 + \rho(\mu_c)^2\mu_h^2 - \beta_h\beta_v\mu_h\mu_h\mu_c + (\mu_c)^2\mu_h^3)/$

$\beta_v(\alpha\delta\mu_h\mu_c + \alpha\gamma\mu_h\mu_c + \alpha\mu_h^2 + \delta\rho\beta_h\mu_c + \delta\rho\mu_h\mu_c + \delta\beta_h\mu_h\mu_c + \delta\mu_h^2\mu_c + \gamma\rho\mu_h\mu_c +$

$\gamma\beta_h\mu_h\mu_c + \gamma\mu_h^2\mu_c + \rho\beta_h\mu_h\mu_c + \rho\mu_h^2\mu_c + \beta_h\mu_h^2\mu_c + \mu_h^3\mu_c),$

$R_h^* = -(-\alpha\delta^2(\mu_c)^2 - \alpha\delta\gamma(\mu_c)^2 - \alpha\delta\beta_v\mu_h(\mu_c)^2 - 2\alpha\delta(\mu_c)^2\mu_h - \alpha\gamma\beta_v\mu_h\mu_c -$

$\alpha\gamma\mu_c\mu_h - \alpha\beta_v\mu_h\mu_h\mu_c - \alpha(\mu_c)^2\mu_h^2 +$

$\delta\gamma(\mu_c)^2\mu_h + \gamma^2(\mu_c)^2\mu_h - \gamma\beta_h\beta_v\mu_c\mu_c + \gamma(\mu_c)^2\mu_h^2)/$

$\beta_v(\alpha\delta\mu_h\mu_c + \alpha\gamma\mu_h\mu_c + \alpha\mu_h^2\mu_c + \delta\rho\beta_h\mu_c + \delta\rho\mu_h\mu_c + \delta\beta_h\mu_h\mu_c + \delta\mu_h^2\mu_c + \gamma\rho\mu_h\mu_c +$

$\gamma\beta_h\mu_h\mu_c + \gamma\mu_h^2\mu_c + \rho\beta_h\mu_h\mu_c + \rho\mu_h^2\mu_c + \beta_h\mu_h^2\mu_c + \mu_h^3\mu_c),$

$S_v^* = \mu_c(\alpha\delta\mu_h\mu_c + \alpha\gamma\mu_h\mu_c + \alpha\mu_h^2\mu_c + \delta\rho\beta_h\mu_c + \delta\rho\mu_h\mu_c + \mu_c\delta\beta_h\mu_h + \delta\mu_h^2\mu_c +$

$\gamma\rho\mu_h\mu_c + \gamma\beta_h\mu_h\mu_c + \gamma\mu_h^2\mu_c + \rho\beta_h\mu_h\mu_c + \rho\mu_h^2\mu_c + \beta_h\mu_h^2\mu_c + \mu_h^3\mu_c)/$

$(\beta_h[\delta\rho\mu_c + \delta\mu_c\mu_h + \gamma\mu_c\mu_h + \rho\beta_v\mu_c + \rho\mu_c\mu_h + \mu_c\beta_v\mu_h + \mu_c\mu_h^2]),$

$I_v^* = -(\alpha\delta(\mu_c)^2\mu_h + \alpha\gamma(\mu_c)^2\mu_h + \alpha(\mu_c)^2\mu_h^2 + \delta\rho(\mu_c)^2\mu_h +$

$\delta(\mu_c)^2\mu_h^2 + \gamma\rho(\mu_c)^2\mu_h + \gamma(\mu_c)^2\mu_h^2 - \rho\beta_h\beta_v\mu_c\mu_h + \rho(\mu_c)^2\mu_h^2 - \mu_c\mu_h\beta_h\beta_v\mu_h +$

$(\mu_c)^2\mu_h^3)/(\delta\rho\mu_c + \delta\mu_c\mu_h + \gamma\mu_c\mu_h + \rho\beta_v\mu_c + \rho\mu_c\mu_h + \mu_h\beta_v\mu_h + \mu_c\mu_h^2)\beta_h\mu_c)$

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Computation of $\mathcal{R}_0$ using Next Generation Matrix Approach

This system (4.8) has two infectious states, I_h, and I_v given by

$$\dot{I}_h = \beta_h S_h I_v - \gamma I_h - \mu_h I_h - \delta I_h \tag{4.10}$$

$$\dot{I}_v = \beta_v S_v I_h - \mu_c I_v$$

and three uninfected states, S_h, R_h and S_v. At the infection-free steady state $I_h^0 = I_v^0 = 0$,

$$S_h^0 = \frac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)},$$
$$R_h^0 = \frac{\alpha}{(\alpha + \rho + \mu_h)}$$

and

$$S_v^0 = 1.$$

Recall from Chapter three that F_i is the rate of appearance of new infections in compartment i, $V_i^+(\mathbf{x})$ is the rate of transfer of individuals into compartment i by all means, $V_i^-(\mathbf{x})$ is the rate of transfer of individuals out of compartment i and $V_i = V_i^- - V_i^+$.

The vectors F_i and V_i are given respectively by

$$F_i = \begin{bmatrix} \beta_h S_h I_v \\ \beta_v S_v I_h \end{bmatrix} \tag{4.11}$$

and

$$V_i = V_i^- - V_i^+ = \begin{bmatrix} (\gamma + \mu_h + \delta)I_h \\ \mu_c I_v \end{bmatrix} \tag{4.12}$$

We now define the matrices,

$$\mathbf{F} = \left[\frac{\partial F_i}{\partial x_j} \right]_{x_j = \mathbf{x}_0} \tag{4.13}$$

and

$$\mathbf{V} = \left[\frac{\partial V_i}{\partial x_j(\mathbf{x}_0)} \right]_{x_j = \mathbf{x}_0} \tag{4.14}$$

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where $x_j = (S_h, I_h, R_h, S_v, I_v)$ and $x_0 = (S_h^0, I_h^0, R_h^0, S_v^0, I_v^0)$ denotes the disease-free equilibrium and the indices $i, j = 1, ..., m$. The entries of the matrix.

From equation (4.10), we obtain

$$\mathbf{F} = \begin{bmatrix} 0 & \beta_h S_h^0 \\ \beta_v S_v^0 & 0 \end{bmatrix},$$

$$\mathbf{V} = \begin{bmatrix} (\gamma + \mu_h + \delta) & 0 \\ 0 & \mu_c \end{bmatrix}$$

and

$$\mathbf{V}^{-1} = \begin{bmatrix} \dfrac{1}{\gamma + \mu_h + \delta} & 0 \\ 0 & \dfrac{1}{\mu_c} \end{bmatrix}$$

The Next Generation Matrix K is two-dimensional and given by

$$
\begin{aligned}
K &= FV^{-1} \\
&= \begin{bmatrix} 0 & \beta_h S_h^0 \\ \beta_v S_v^0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{(\gamma + \mu_h + \delta)} & 0 \\ 0 & \dfrac{1}{\mu_c} \end{bmatrix} \\
&= \begin{bmatrix} 0 & \dfrac{\beta_h S_h^0}{\mu_c} \\ \dfrac{\beta_v S_v^0}{(\gamma + \mu_h + \delta)} & 0 \end{bmatrix}
\end{aligned}
$$

The eigenvalues of K are given by

$$\lambda_1 = \sqrt{\frac{\beta_h \beta_v S_h^0 S_v^0}{\mu_c (\mu_h + \gamma + \delta)}} \text{ and } \lambda_2 = -\sqrt{\frac{\beta_h \beta_v S_h^0 S_v^0}{\mu_c (\mu_h + \gamma + \delta)}}.$$

The basic reproduction number $\mathcal{R}_0(\alpha)$ is the spectral radius of K given as

$$= \sqrt{\frac{\beta_h \beta_v}{\mu_c (\mu_h + \gamma + \delta)} \cdot \frac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}},$$

since $S_h^0 = \dfrac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}$ and $S_v^0 = 1$.

But $\dfrac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)} \leq 1$. It is obvious that

$$\mathcal{R}_0^2(\alpha) = \frac{\beta_h \beta_v (\mu_h + \rho)}{\mu_c (\mu_h + \gamma + \delta)(\alpha + \mu_h + \rho)} \leq \frac{\beta_h \beta_v}{\mu_c (\mu_h + \gamma + \delta)} = \mathcal{R}_0^2(0)$$

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The inequality above indicate that the basic reproduction number with prevention is less than the basic reproduction without prevention.

The Endemic equilibrium (E_1) can be expressed in terms of the basic reproduction number $(\mathcal{R}_0^2)$ as

$$(E_1) = (S_h^*, I_h^*, R_h^*, S_v^*, I_v^*) \tag{4.15}$$

given $(S_h^*, I_h^*, R_h^*, S_v^*, I_v^*)$ by

$$S_h^* = \frac{\mu_c \beta_v \mu_h (\mu_h + \rho) + \mu_c (\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)(\gamma + \mu_h + \delta)}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

$$I_h^* = \frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

$$R_h^* = -\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

$$S_v^* = \frac{\mu_c[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}$$

$$I_v^* = \frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)}$$

Local Stability Analysis of the Equilibrium Points

We investigate the local stability of the equilibrium points. The jacobian matrix for the system (4.9) is given as

$$J = \begin{bmatrix} -\beta_h I_v - \alpha - \mu_h & 0 & \rho & 0 & -\beta_h S_h \\ \beta_h I_v & -(\mu_h + \gamma + \delta) & 0 & 0 & \beta_h S_h \\ 0 & \gamma & -(\mu_h + \rho) & 0 & 0 \\ 0 & -\beta_v S_v & 0 & -I_h\beta_v - \mu_c & 0 \\ 0 & \beta_v S_v & 0 & I_h\beta_v & -\mu_c \end{bmatrix} \tag{4.16}$$

Local Stability Analysis at the Disease Free Equilibrium

We now investigate the local stability of the disease free equilibrium.

Theorem 4.3. The disease free equilibrium point is locally asymptotically stable if $\mathcal{R}_0(0) < 1$.

Evaluating the Jacobian matrix at the disease free equilibrium point (E_0) with $\alpha = 0$ gives

$$J_0 = \begin{bmatrix} -\mu_h & 0 & \rho & 0 & -\beta_h \\ 0 & -(\mu_h+\gamma+\delta) & 0 & 0 & \beta_h \\ 0 & \gamma & -(\mu_h+\rho) & 0 & 0 \\ 0 & -\beta_v & 0 & -\mu_c & 0 \\ 0 & \beta_v & 0 & 0 & -\mu_c \end{bmatrix} \tag{4.17}$$

From columns $1, 3$ and 4, we obtain these three eigenvalues $\lambda_1 = -\mu_h, \lambda_2 = -(\mu_h + \rho)$ and $\lambda_3 = \mu_c$.

The remaining matrix is given as

$$J_r = \begin{bmatrix} -(\mu_h+\gamma+\delta) & \beta_h \\ \beta_v & -\mu_c \end{bmatrix} \tag{4.18}$$

From the Routh-Hurwitz criterion,

$$det(J_r) > 0$$

This implies,

$$(\mu_h+\gamma+\delta)\mu_c - \beta_h\beta_v \;>\; 0$$

$$(\mu_h+\gamma+\delta)\mu_c \;>\; \beta_h\beta_v$$

$$1 > \frac{\beta_h\beta_v}{(\mu_h+\gamma+\delta)\mu_c}$$

but

$$\frac{\beta_h\beta_v}{\mu_c(\mu_h+\gamma+\delta)} = \mathcal{R}_0^2(0),$$

this implies that

$$\mathcal{R}_0(0) < 1.$$

we conclude that the disease free equilibrium is locally stable.

Local Stability Analysis at the Endemic Equilibrium Point

We investigate the local stability of the endemic equilibrium point.

Theorem 4.4. The Endemic equilibrium (E_1) is locally asymptotically stable if $\mathcal{R}_0(\alpha) > 1$.

Proof. Evaluating the Jacobian matrix at the endemic equilibrium gives

$$J_1 = \begin{bmatrix} a - \alpha - \mu_h & 0 & -\rho & -b & \\ -a & -(\mu_h + \gamma + \delta) & 0 & 0 & b \\ \alpha & \gamma & -(\mu_h + \rho) & 0 & 0 \\ 0 & -c & 0 & d - \mu_c & 0 \\ 0 & c & 0 & -d & -\mu_c \end{bmatrix} \quad (4.19)$$

Using the corollary of Gershgorin's circle theorem, the matrix (J_1) will have negative eigenvalues if the following inequalities are satisfied. Thus,

$$a_{ii} < -\sum_{j=1, j \neq i}^{n} |a_{ij}|.$$

So,

(i) From row 1

$$\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)} - \alpha - \mu_h <$$
$$- \frac{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)](\gamma + \mu_h + \delta)}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

(ii) From row 2

$$-(\mu_h + \gamma + \delta) < -\Big(\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho)\mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)}$$
$$+ \frac{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)](\gamma + \mu_h + \delta)}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}\Big)$$

(iii) From row 3

$$-(\rho + \mu_h) < -(\alpha + \gamma)$$

(iv) From row 4

$$\left(\frac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}-\mu_c\right)<$$

$$-\frac{\mu_c\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)]}$$

(v) From row 5

$$-\mu_c<-\left(\frac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}+\right.$$

$$\left.\frac{\mu_c\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)]}\right)$$

Rearranging (i)- (v) give

(i*) $\alpha+\mu_h>\dfrac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)}$

$$+\frac{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)](\gamma+\mu_h+\delta)}{\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}$$

(ii*) $(\mu_h+\gamma+\delta)>\dfrac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)}$

$$+\frac{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)](\gamma+\mu_h+\delta)}{\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}$$

(iii*) $(\rho+\mu_h)>(\alpha+\gamma)$

(iv*) $\mu_c>\dfrac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}+$

$$\frac{\mu_c\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)]}$$

(v*) $\mu_c>-\dfrac{(1-\mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)}{[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}+$

$$\frac{\mu_c\beta_v[\beta_h(\delta\rho+\delta\mu_h+\gamma\mu_h+\rho\mu_h+\mu_h^2)+\mu_h(\gamma+\mu_h+\delta)(\alpha+\mu_h+\rho)]}{\beta_h[\beta_v\mu_h(\mu_h+\rho)+\mu_c(\delta\rho+\delta\mu_h+\gamma\mu_h+\mu_h^2+\rho\mu_h)]}$$

Dividing the left hand terms by the right hand terms each from (i^*) - (v^*), we

obtain

$$1 > \left(\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)} + \right.$$
$$\left. \frac{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)](\gamma + \mu_h + \delta)}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]} \frac{1}{(\alpha + \mu_h)} \right)$$
$$\times \frac{1}{(\alpha + \mu_h)} \tag{4.20a}$$

$$1 > \frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)} \tag{4.20b}$$
$$+ \frac{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

$$1 > \frac{(\alpha + \gamma)}{(\rho + \mu_h)} \tag{4.20c}$$

$$1 > \frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]} \tag{4.20d}$$
$$+ \frac{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}$$

$$1 > -\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)}{[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]} \tag{4.20e}$$
$$+ \frac{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}$$

From equation (4.20b) let

$$U = \frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)}$$

and

$$V = \frac{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}$$

so that

$$\frac{1}{V} = \frac{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]}$$

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Equation (4.20b) becomes

$$1 > U + V \tag{4.21}$$

Adding (4.20d) and (4.20e) gives

$$1 > \frac{\beta_v[\beta_h(\delta\rho + \delta\mu_h + \gamma\mu_h + \rho\mu_h + \mu_h^2) + \mu_h(\gamma + \mu_h + \delta)(\alpha + \mu_h + \rho)]}{\beta_h[\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)]} \tag{4.22}$$

which can be rewritten as

$$1 > \frac{1}{V} \tag{4.23}$$

or

$$-1 > -V \tag{4.24}$$

Adding equation (4.21) and (4.24) gives

$$0 > U \tag{4.25}$$

That is,

$$0 > \left(\frac{(1 - \mathcal{R}_0^2(\alpha))\mu_h\mu_c(\alpha + \mu_h + \rho)}{\beta_v\mu_h(\mu_h + \rho) + \mu_c(\delta\rho + \delta\mu_h + \gamma\mu_h + \mu_h^2 + \rho\mu_h)}\right) \tag{4.26}$$

Equation (4.26) holds $\Leftrightarrow$

$$\mathcal{R}_0^2(\alpha) > 1 \tag{4.27}$$

$\square$

In the next section, we formulate a 7-staged states malaria model with exposed compartment

A Malaria Transmission Model With Exposed Compartment

In the previous section, we formulated a malaria transmission model without the exposed classes. In this section, we formulate and analyze a malaria model with exposed class as an *SEIRS* for the host population and *SEI* for the vector population similar to that of (N. R. Chitnis, 2005) by combining biting

rate and transmission rate as β_h for host and β_v for vector, describing the transmission of malaria. It is also assumed that a certain proportion of the prevention strategies contribute to the death rate of the mosquito. The human population is divided into: susceptible, $S_h(t)$, exposed or latent, $L_h(t)$, infectious, $I_h(t)$, and recovered (immune), $R_h(t)$ classes. People are born (at a constant per capita rate) or immigration (at a constant rate) into the susceptible class. When an infectious mosquito bites a susceptible human, symptoms usually appear 10-15 days after the bite (WHO, 2019). This period is called the incubation or exposed period before the person becomes clinically ill and it is termed a exposed compartment or class. Progress to the infectious class from the exposed class at a rate that is the reciprocal of the duration of the latent period. About seven days of proper treatment, the infectious humans recover and move to the recovered class. The recovered humans have some immunity to the disease and do not get clinically ill. After some months, they lose their immunity and return to the susceptible class. The prevention strategies also remove people directly from the susceptible class to the removed class. The human population decreases through a density-dependent per capita emigration and natural death rate, and through a per capita disease-induced death rate.

The mosquito population is divided into: susceptible, $S_v(t)$, exposed or latent, $L_v(t)$, and infectious, $I_v(t)$ classes. Female mosquitoes (we do not include male mosquitoes in our model because only female mosquitoes bite animals for blood meals) are born or migrate to the susceptible class through birth. The parasite, with some probability, when the mosquito bites an infectious human or a recovered human (the probability of transmission of infection from a recovered human is much lower than that from an infectious human), the mosquito moves from the susceptible to the exposed class. After some period of time, dependent on the ambient temperature and humidity, the parasite develops into sporozoites and enters the mosquito's salivary glands; and the mosquito moves from the

exposed class to the infectious class. The mosquito remains infectious for life. Mosquitoes leave the population through a per capita density-dependent natural death rate and an effect of prevention effort.
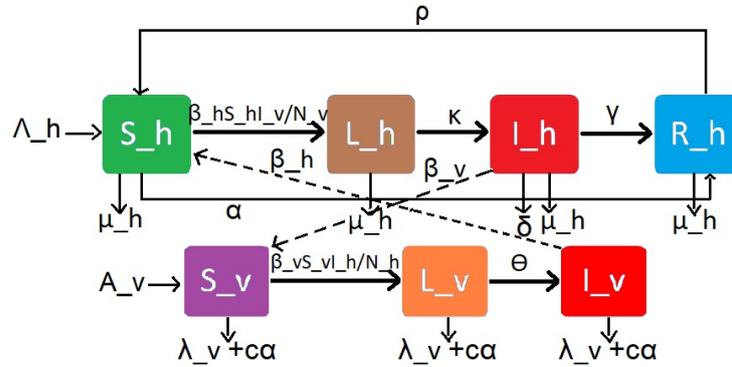
Figure 5: Transition Diagram for a Malaria Transmission Model With Exposed
   Compartment

Table 6: The State Variables for a 7-Staged State Malaria Transmission Model

Populations	Description
I_h	Number of infectious human
S_h	Number of susceptible human
L_h	Number of exposed or latent humans
R_h	Number of Recovered human
I_v	Number of infectious vector
S_v	Number of Susceptible vector
L_v	Number of exposed mosquito
N_h	Total human population
N_v	Total mosquito population

Table 7: Model Parameters and Their Interpretations

Parameters	Description
Λ_h	Humans recruitment birth rate
μ_h	Humans death rate
κ	Progression rate for humans exposed class to infectious class at time t
γ	recovery rate of human
α	Prevention rate
β_h	Transmission rate of host (product of biting rate and probability of transmission of disease)
δ	Disease-induced death rate for humans
ρ	Rate of loss of immunity for humans
λ_v	Vector birth rate = vector death rate
$c\alpha$	proportion of prevention effort that contributes to vector death rate $0 \leq c \leq 1$
θ	Progression rate for vector
β_v	Transmission rate of vector (product biting rate and probability of transmission of disease)

We model the effect of preventive strategies on the vector population and apply the same assumptions used in previous section, the system of non-linear differential equations which describe the dynamics of a malaria model with ex-

posed compartment as:

$$\frac{d\bar{S}_h}{dt} = \Lambda_h - \beta_h \bar{S}_h \frac{\bar{I}_v}{N_v} - \alpha \bar{S}_h + \rho \bar{R}_h - \mu_h \bar{S}_h$$

$$\frac{d\bar{L}_h}{dt} = \beta_h \bar{S}_h \frac{\bar{I}_v}{N_v} - (\kappa + \mu_h)\bar{L}_h$$

$$\frac{d\bar{I}_h}{dt} = \kappa \bar{L}_h - (\gamma + \mu_h + \delta)\bar{I}_h$$

$$\frac{d\bar{R}_h}{dt} = \gamma \bar{I}_h - \mu_h \bar{R}_h + \alpha \bar{S}_h - \rho \bar{R}_h \qquad (4.28)$$

$$\frac{d\bar{S}_v}{dt} = A_v - \beta_v \bar{S}_v \frac{\bar{I}_h}{N_h} - (c\alpha + \lambda_v)\bar{S}_v$$

$$\frac{d\bar{L}_v}{dt} = \beta_v \bar{S}_v \frac{\bar{I}_h}{N_h} - (\theta + \lambda_v + c\alpha)\bar{L}_v$$

$$\frac{d\bar{I}_v}{dt} = \theta \bar{L}_v - (c\alpha + \lambda_v)\bar{I}_v$$

with

$$\bar{N}_h = \bar{S}_h + \bar{L}_h + \bar{I}_h + \bar{R}_h,$$

and

$$\bar{N}_v = \bar{S}_v + \bar{L}_v + \bar{I}_v.$$

The total human population can be determined from

$$\frac{d\bar{N}_h}{dt} = \frac{d\bar{S}_h}{dt} + \frac{d\bar{L}_h}{dt} + \frac{d\bar{I}_h}{dt} + \frac{d\bar{R}_h}{dt}$$

$$= \Lambda_h - N_h \mu - \delta I_h$$

In the absence of the disease induced death, that is, $\delta = 0$, we have

$$\frac{d\bar{N}_h}{dt} = \Lambda_h - \mu_h \bar{N}_h$$

$$\frac{d\bar{N}_h}{dt} + \mu_h \bar{N}_h = \Lambda_h \qquad (4.29)$$

Solving equation (4.29) we obtain,

$$\bar{N}_h(t)e^{\mu_h t} = \frac{\Lambda_h e^{\mu_h t}}{\mu_h} + C$$

where C is the constant of integration

$$\bar{N}_h(t) = \left(\frac{\Lambda_h e^{\mu_h t}}{\mu_h} \times \frac{1}{e^{\mu_h t}}\right) + Ce^{-\mu_h t}$$

$$= \frac{\Lambda_h}{\mu_h} + Ce^{-\mu_h}$$

Using the initial conditions, $\bar{N}_h(0) = \bar{N}_{h0}$:

$$\bar{N}_{h0} = \frac{\Lambda_h}{\mu_h} + C$$

$$\Rightarrow C = \bar{N}_{h0} - \frac{\Lambda_h}{\mu_h}.$$

so,

$$\bar{N}_h(t) + \left(\frac{\Lambda_h}{\mu_h t} - \bar{N}_{h0}\right)e^{-\mu_h t} = \frac{\Lambda_h}{\mu_h} \tag{4.30}$$

This means that,

$$\bar{N}_h(t) \le \frac{\Lambda_h}{\mu_h}, \quad \text{provided} \quad \bar{N}_h(0) \le \frac{\Lambda_h}{\mu_h} \quad \text{for} \quad t \ge 0. \tag{4.31}$$

Similarly, the total vector population can be determined from

$$\frac{d\bar{N}_v}{dt} = \frac{d\bar{S}_v}{dt} + \frac{d\bar{L}_v}{dt} + \frac{d\bar{I}_v}{dt}$$

$$= A_v - N_v(\lambda_v + c\alpha) \tag{4.32}$$

Solving equation (4.32) we obtain,

$$\bar{N}_h(t)e^{(\lambda_v + c\alpha)t} = \frac{A_v e^{(\lambda_v + c\alpha)t}}{(\lambda_v + c\alpha)} + M$$

where M is the constant of integration

$$\bar{N}_v(t) = \left(\frac{A_v e^{(\lambda_v + c\alpha)t}}{(\lambda_v + c\alpha)} \times \frac{1}{e^{(\lambda_v + c\alpha)t}}\right) + Ce^{-(\lambda_v + c\alpha)t}$$

$$= \frac{A_v}{(\lambda_v + c\alpha)} + Me^{-(\lambda_v + c\alpha)t}$$

Using the initial conditions, $\bar{N}_v(0) = \bar{N}_{v0}$:

$$\bar{N}_{v0} = \frac{A_v}{(\lambda_v + c\alpha)} + M$$

$$\Rightarrow M = \bar{N}_{v0} - \frac{A_v}{(\lambda_v + c\alpha)}.$$

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Thus,

$$\bar{N}_v(t) + \left(\frac{A_v}{(\lambda_v + c\alpha)t} - \bar{N}_{v0}\right)e^{-(\lambda_v + c\alpha)t} = \frac{A_v}{(\lambda_v + c\alpha)t} \qquad (4.33)$$

This implies that,

$$\bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)}, \quad \text{provided} \quad \bar{N}_v(0) \leq \frac{A_v}{(\lambda_v + c\alpha)} \quad \text{for} \quad t \geq 0. \qquad (4.34)$$

For positivity of solutions, we apply the theorem that follows.

Theorem 4.5. Let the initial data be

$$\{(S_h(0), S_v(0)) > 0, (L_h(0), I_h(0), R_h(0), L_v(0), I_v(0)) \geq 0\} \in D).$$

Then the solution set $\{S_h, L_h, I_h, R_h, S_v, L_v I_v\}$ of the system (4.28) is positive for all $t > 0$.

Proof. From the first equation in the model (4.28), we have

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h \\
&\geq -\beta_h S_h I_v - \alpha S_h - \mu_h S_h
\end{aligned}$$

Using separation of variables and integrating both sides gives

$$\begin{aligned}
\int \frac{dS_h}{S_h} &\geq \int (-\beta_h I_v - \alpha - \mu_h)dt \\
\int \frac{dS_h}{S_h} &\geq \int (-\beta_h I_v)dt - \int (\alpha + \mu_h)dt \\
\ln S_h &\geq -\int (\beta_h I_v)dt + (-\alpha - \mu_h)t + C \\
\Rightarrow S_h &\geq e^{-\int (\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t} \times e^C \\
&\geq (e^{-\int (\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t}) \times e^C \\
&\geq (e^{-\int (\beta_h I_v)dt} \times e^{-(\alpha + \mu_h)t}) \times N \\
&\geq N(e^{(-\int (\beta_h I_v)dt - (\alpha + \mu_h)t)})
\end{aligned}$$

using the initial conditions: $t = 0, \quad S_h(0) \geq N$

$$\Rightarrow S_h \geq S_h(0)(e^{(-\int (\beta_h I_v)dt - (\alpha + \mu_h)t)}) \geq 0$$

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Therefore,

$$S_h \geq S_h(0)(e^{(-\int (\beta_h I_v)dt - (\alpha + \mu_h)t)}) \geq 0$$

From the second equation we have,

$$
\begin{aligned}
\frac{dL_h}{dt} &= \beta_h S_h I_v - (\kappa + \mu_h)L_h \\
&\geq -(\kappa + \mu_h)L_h \\
\frac{dL_h}{dt} &\geq -(\kappa + \mu_h)L_h
\end{aligned}
$$

Using separation of variables and integrating both sides gives

$$
\begin{aligned}
\int \frac{dL_h}{L_h} &\geq \int -(\kappa + \mu_h)dt \\
\ln L_h &\geq -(\kappa + \mu_h)t + c \\
\Rightarrow L_h &\geq e^{-(\kappa + \mu_h)t + c} \\
&\geq H e^{-(\kappa + \mu_h)t} \\
&\geq I_h(0)e^{-(\kappa + \mu_h)t}
\end{aligned}
$$

where $H = L_h(0)$

$$I_h \geq L_h(0)e^{-(\gamma + \mu_h)t} \geq 0$$

similarly, it can be shown that for all $t > 0$, the remaining equations of the system (4.28) are positive. $\qquad \square$

Positive Invariant Region

The positive invariant region is obtained in the following theorem.

Theorem 4.6. The solutions of the system (4.28) are feasible for all $t > 0$ if they enter the invariant region $D = D_h \times D_v$

Proof. Let $D = (\bar{S}_h, \bar{L}_h, \bar{I}_h, \bar{R}_h, \bar{S}_v, \bar{L}_v, \bar{I}_v) \in R_+^7$ be any solution of system (4.28) with non-negative initial conditions.

From (4.31) all feasible solutions set of the human population of the model

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(4.28) enters the region.

$$D_h = \left\{ (S_h, L_h, I_h, R_h) \in R_+^4 : S_h > 0, L_h \geq 0, I_h \geq 0, R_h \geq 0, N_h(t) \leq \frac{\Lambda_h}{\mu_h} \right\}.$$

Similarly, from (4.34) the feasible solutions set of the mosquito enters the region

$$D_v = \left\{ (S_v, L_v, I_v) \in R_+^3 : S_v > 0, L_v \geq 0, I_v \geq 0, \bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)} \right\}.$$

The feasible solutions set for the model (4.28) is given by

$$
\begin{aligned}
D \;=\; & \left\{ (S_h, L_h, I_h, R_h, S_v, L_v, I_v) \in R_+^7 : (S_h, S_v) > 0, (L_h, I_h, R_h, L_v, I_v) \geq 0; \right. \\
& \left. \bar{N}_h(t) \leq \frac{\Lambda_h}{\mu_h}; \bar{N}_v(t) \leq \frac{A_v}{(\lambda_v + c\alpha)} \right\}.
\end{aligned}
$$

Therefore, the region D is positively-invariant (i.e. solutions remain positive for all times, (t) and the model (4.1) is biologically, epidemiologically meaningful and mathematically well-posed in the domain D.

$\square$

Let $S_h = \dfrac{\bar{S}_h}{\Lambda_h/\mu_h}, L_h = \dfrac{\bar{L}_h}{\Lambda_h/\mu_h},\, I_h = \dfrac{\bar{I}_h}{\Lambda_h/\mu_h}, R_h = \dfrac{\bar{R}_h}{\Lambda_h/\mu_h},$

Similarly, Let $S_v = \dfrac{\bar{S}_v}{A_v/(\lambda_v + c\alpha)}, L_v = \dfrac{\bar{L}_v}{A_v/(\lambda_v + c\alpha)}, I_v = \dfrac{\bar{I}_v}{A_v/(\lambda_v + c\alpha)}.$

system (4.28) in the invariant space D can be written as the equivalent seven-dimensional non-linear system of ODEs:

$$
\begin{aligned}
\dot{S}_h &= \mu_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h \\
\dot{L}_h &= \beta_h S_h I_v - (\kappa + \mu_h) L_h \\
\dot{I}_h &= \kappa L_h - (\gamma + \mu_h + \delta) I_h \\
\dot{R}_h &= \gamma I_h - \mu_h R_h + \alpha S_h - \rho R_h \\
\dot{S}_v &= (\lambda_v + c\alpha) - \beta_v S_v I_h - (\lambda_v + c\alpha) S_v \\
\dot{L}_v &= \beta_v S_v I_h - \theta L_v - (\lambda_v + c\alpha) L_v \\
\dot{I}_v &= \theta L_v - (\lambda_v + c\alpha) I_v
\end{aligned}
\tag{4.35}
$$

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Let $\mu_c = (\lambda_v + c\alpha)$, now, the model becomes

$$\dot{S}_h = \mu_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h$$

$$\dot{L}_h = \beta_h S_h I_v - (\kappa + \mu_h) L_h$$

$$\dot{I}_h = \kappa L_h - (\gamma + \mu_h + \delta) I_h$$

$$\dot{R}_h = \gamma I_h - \mu_h R_h + \alpha S_h - \rho R_h \qquad (4.36)$$

$$\dot{S}_v = \mu_c - \beta_v S_v I_h - \mu_c S_v$$

$$\dot{L}_v = \beta_v S_v I_h - \theta L_v - \mu_c L_v$$

$$\dot{I}_v = \theta L_v - \mu_c I_v$$

the feasible solutions set for the model (4.64)is given by

$$\Omega = \Big\{ (S_h, L_h, I_h, R_h, S_v, L_v, I_v) \in R_+^7 : (S_h, S_v) > 0, (L_h, I_h, R_h, L_v, I_v) \geq 0;$$
$$\bar{N}_h(t) \leq 1; \bar{N}_v(t) \leq 1 \Big\}.$$

Equilibrium Points of the Model

The system (4.35) has two equilibrium points namely;

(a) Disease Free equilibrium $p^* = (S_h^0, L_h^0, I_h^0, R_h^0, S_v^0, L_v^0, I_v^0)$
$$= \Big(\frac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}, 0, 0, \frac{\alpha}{(\alpha + \rho + \mu_h)}, 1, 0, 0 \Big)$$

(b) Endemic equilibrium $(p^*) = $ see equation (12)

Computation of $\mathcal{R}_0$ using Next Generation Approach

This system (4.35) has four infected states, L_h, I_h, L_v, and I_v given by

$$\dot{L}_h = \beta_h S_h I_v - (\kappa + \mu_h) L_h$$

$$\dot{I}_h = \kappa L_h - (\gamma + \mu_h + \delta) I_h$$

$$\dot{L}_v = \beta_v S_v I_h - \theta L_v - \mu_c L_v \qquad (4.37)$$

$$\dot{I}_v = \theta L_v - \mu_c I_v$$

and Three uninfected state, S_h. At the infection-free steady state $L_h^0 = I_h^0 = L_v^0 = I_v^0 = 0$ and $S_h^0 = \dfrac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}$.

The vectors F_i and V_i are given respectively by

$$F_i = \begin{bmatrix} \beta_h S_h I_v \\ 0 \\ \beta_v S_v I_h \\ 0 \end{bmatrix}, \tag{4.38}$$

and

$$V_i = \begin{bmatrix} (\kappa + \mu_h) L_h \\ -\kappa L_h + (\gamma + \mu_h + \delta) I_h \\ \theta L_v + \mu_c L_v \\ -\theta L_h + \mu_c I_v \end{bmatrix} \tag{4.39}$$

The partial derivatives of (4.38) with respect to (L_h, I_h, L_v, I_v) and the Jacobian matrix of F_i is given as

$$F = \begin{bmatrix} 0 & 0 & 0 & \beta_h S_h \\ 0 & 0 & 0 & 0 \\ 0 & \beta_v S_v & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix},$$

Similarly, the partial derivatives of (4.39) with respect to (L_h, I_h, L_v, I_v) and the Jacobian matrix of V at the disease-free equilibrium point E_0 is given as

$$V = \begin{bmatrix} (\kappa + \mu_h) & 0 & 0 & 0 \\ -\kappa & (\gamma + \mu_h + \delta) & 0 & 0 \\ 0 & 0 & (\theta + \mu_c) & 0 \\ 0 & 0 & -\theta & \mu_c \end{bmatrix}$$

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The inverse of the matrix V is given as:

$$V^{-1} = \begin{bmatrix} \dfrac{1}{(\kappa+\mu_h)} & 0 & 0 & 0 \\[2ex] \dfrac{\kappa}{(\kappa+\mu_h)(\gamma+\mu_h+\delta)} & \dfrac{1}{(\gamma+\mu_h+\delta)} & 0 & 0 \\[2ex] 0 & 0 & \dfrac{1}{(\theta+\mu_c)} & 0 \\[2ex] 0 & 0 & \dfrac{\theta}{(\theta+\mu_c)\mu_c} & \dfrac{1}{\mu_c} \end{bmatrix}$$

The Next Generation Matrix K is given by

$$
\begin{aligned}
K &= FV^{-1} \\[2ex]
&= \begin{bmatrix} 0 & 0 & 0 & \beta_h S_h^0 \\ 0 & 0 & 0 & 0 \\ 0 & \beta_v S_v^0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \begin{bmatrix} \dfrac{1}{(\kappa+\mu_h)} & 0 & 0 & 0 \\[1.5ex] a^{***} & b^{***} & 0 & 0 \\[1ex] 0 & 0 & c^{***} & 0 \\[1ex] 0 & 0 & d^{***} & \dfrac{1}{\mu_c} \end{bmatrix} \\[3ex]
&= \begin{bmatrix} 0 & 0 & \dfrac{\beta_h S_h^0 \theta}{(\theta+\mu_c)\mu_c} & \dfrac{\beta_h S_h^0}{\mu_c} \\[2ex] 0 & 0 & 0 & 0 \\[2ex] \dfrac{\kappa\beta_v S_v^0}{(\kappa+\mu_h)(\gamma+\mu_h+\delta)} & \dfrac{\kappa\beta_v S_v^0}{(\gamma+\mu_h+\delta)} & 0 & 0 \\[2ex] 0 & 0 & 0 & 0 \end{bmatrix}
\end{aligned}
$$

where $a^{***} = \dfrac{\kappa}{(\kappa+\mu_h)(\gamma+\mu_h+\delta)}$, $b^{***} = \dfrac{1}{(\gamma+\mu_h+\delta)}$,

$c^{***} = \dfrac{\theta}{(\theta+\mu_c)\mu_c}$ and $d^{***} = \dfrac{1}{(\theta+\mu_c)}$

The eigenvalues of K are given by

$\lambda_1 = 0, \lambda_2 = 0, \lambda_3 = -\sqrt{\dfrac{\beta_h\beta_v S_v S_h^0 \theta\kappa}{\mu_c(\kappa+\mu_h)(\mu_h+\gamma+\delta)(\theta+\mu_c)}}$,

and $\lambda_4 = \sqrt{\dfrac{\beta_h\beta_v S_v S_h^0 \theta\kappa}{\mu_c(\kappa+\mu_h)(\mu_h+\gamma+\delta)(\theta+\mu_c)}}$

The basic reproduction number $\mathcal{R}_0$ is the positive real eigenvalue of K which is at least as large in modulus as all eigenvalues of K.

$$\mathcal{R}_0 = \sqrt{\dfrac{\beta_h\beta_v S_v S_h^0 \theta\kappa}{\mu_c(\kappa+\mu_h)(\mu_h+\gamma+\delta)(\theta+\mu_c)}}$$

$$= \sqrt{\frac{\beta_h \beta_v \theta \kappa}{\mu_c(\kappa+\mu_h)(\mu_h+\gamma+\delta)(\theta+\mu_c)} \cdot \frac{(\mu_h+\rho)}{(\alpha+\mu_h+\rho)}}$$

$$= \sqrt{\frac{\beta_h \beta_v \theta(\mu_h+\rho)\kappa}{\mu_c(\kappa+\mu_h)(\mu_h+\gamma+\delta)(\theta+\mu_c)(\alpha+\mu_h+\rho)}}$$

Since at the infection-free steady state $S_v^0 = 1$ and $S_h^0 = \dfrac{(\mu_h+\rho)}{(\alpha+\mu_h+\rho)}$.

The Endemic equilibrium (p^*) can be expressed in terms of the basic Reproduction number $(\mathcal{R}_0^2)$ and simplified as

$$(p^*) = (S_h^*, L_h^*, I_h^*, R_h^*, S_v^*, L_v^*, I_v^*) \tag{4.40}$$

given $(S_h^*, L_h^*, I_h^*, R_h^*, S_v^*, L_v^*, I_v^*)$ by

$S_h^* = \dfrac{a}{b}$

$a = (\mu_h+\kappa)(\mu_c+\theta)(\gamma+\mu_h+\delta)\Big(\kappa\beta_v(\rho+\mu_h) + \mu_c(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$b = \kappa\beta_v\Big(\mu_h(\mu_h+\kappa)(\mu_h+\alpha+\rho)\theta(\gamma+\mu_h+\delta) + \beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$L_h^* = \dfrac{-c}{d}$

$-c = \Big((\mathcal{R}_0^2(\alpha) - 1)\mu_c\mu_h(\mu_h+\kappa)(\mu_c+\theta)(\gamma+\mu_h+\delta)(\mu_h+\alpha+\rho)\Big)(\gamma+\mu_h+\delta)$

$d = \kappa\beta_v\Big(\mu_c\mu_h(\mu_h+\kappa)(\mu_h+\alpha+\rho)(\mu_c+\theta)(\gamma+\mu_h+\delta) + \mu_c\beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$I_h^* = \dfrac{-e}{f}$

$-e = (\mathcal{R}_0^2(\alpha) - 1)\mu_c(\mu_h+\kappa)(\mu_c+\theta)(\gamma+\mu_h+\delta)(\mu_h+\alpha+\rho)$

$f = \kappa\beta_v\Big(\mu_h(\mu_h+\kappa)(\mu_h+\alpha+\rho)(\mu_c+\theta)(\gamma+\mu_h+\delta) + \mu_c\beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$R_h^* = \dfrac{k}{t}$

$k = -(\mathcal{R}_0^2(\alpha) - 1)\mu_c\mu_h(\mu_h+\kappa)(\mu_c+\theta)(\gamma+\mu_h+\delta)(\mu_h+\alpha+\rho)$

$t = \kappa\beta_v\Big(\mu_h(\mu_h+\kappa)(\mu_h+\alpha+\rho)(\mu_c+\theta)(\gamma+\mu_h+\delta) + \mu_c\beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$S_v^* = \dfrac{g}{h}$

$$g = \mu_c \Big((\mu_h(\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho) + \beta_h \theta (\delta \kappa \rho + \delta \kappa \mu_h + \delta \rho \mu_h +$$
$$\delta \mu_h^2 + \gamma \kappa \mu_h + \gamma \rho \mu_h + \gamma \mu_h^2 + \kappa \rho \mu_h + \kappa \mu_h^2 + \rho \mu_h^2 + \mu_h^3) \Big)$$
$$h = \beta_h \theta \Big(\kappa \beta_v (\rho + \mu_h) + \mu_c (\delta \kappa \rho + \delta \kappa \mu_h + \delta \rho \mu_h + \delta \mu_h^2 + \gamma \kappa \mu_h + \gamma \rho \mu_h + \gamma \mu_h^2 + \kappa \rho \mu_h +$$
$$\kappa \mu_h^2 + \rho \mu_h^2 + \mu_h^3) \Big)$$
$$L_v = \frac{-n}{m}$$
$$-n = \mu_c (\mathcal{R}_0^2(\alpha) - 1) \mu_c \mu_h (\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho)$$
$$m = \beta_h (\theta + \mu_c) \Big(\kappa \beta_v (\rho + \mu_h) + \mu_c (\delta \kappa \rho + \delta \kappa \mu_h + \delta \rho \mu_h + \delta \mu_h^2 + \gamma \kappa \mu_h + \gamma \rho \mu_h +$$
$$\gamma \mu_h^2 + \kappa \rho \mu_h + \kappa \mu_h^2 + \rho \mu_h^2 + \mu_h^3) \theta \Big)$$

$$I_v = \frac{-q}{r}$$
$$-q = (\mathcal{R}_0^2(\alpha) - 1) \mu_c \mu_h (\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho)$$
$$r = \beta_h (\theta + \mu_c) \Big(\kappa \beta_v (\rho + \mu_h) + \mu_c (\delta \kappa \rho + \delta \kappa \mu_h + \delta \rho \mu_h + \delta \mu_h^2 + \gamma \kappa \mu_h + \gamma \rho \mu_h + \gamma \mu_h^2 +$$
$$\kappa \rho \mu_h + \kappa \mu_h^2 + \rho \mu_h^2 + \mu_h^3) \Big)$$

Local Stability Analysis of the Equilibrium Points

We investigate the local stability of the equilibrium points. The jacobian matrix for the system (4.35) is given as

$$J = \begin{bmatrix} n^* & 0 & 0 & \rho & 0 & 0 & -\beta_h S_h \\ \beta_h I_v & -m^* & 0 & 0 & 0 & 0 & \beta_h S_h \\ 0 & \kappa & -(\mu_h + \gamma + \delta) & 0 & 0 & 0 & 0 \\ \alpha & 0 & \gamma & -p^* & 0 & 0 & 0 \\ 0 & 0 & -\beta_v S_v & 0 & -t^* & 0 & 0 \\ 0 & 0 & \beta_v S_v & 0 & \beta_v I_h & -q^* & 0 \\ 0 & 0 & 0 & 0 & 0 & \theta & -\mu_c \end{bmatrix} \qquad (4.41)$$

where $n^* = \beta_h I_v - (\alpha + \mu_h)$, $m^* = (\kappa + \mu_h)$, $p^* = (\mu_h + \rho)$, $q^* = (\theta + \mu_c)$ and $t^* = \beta_v I_h - \mu_c$.

Local Stability Analysis of the Disease Free Equilibrium Point

Now, we investigate the local stability of the disease free equilibrium point with $\alpha = 0$, since $\mathcal{R}_0(\alpha) < \mathcal{R}_0(0)$

Theorem 4.7. The disease free equilibrium (E_0) with $\alpha = 0$ is locally asymptotically stable if $\mathcal{R}_0^2(\alpha) < \mathcal{R}_0^2(0) < 1$.

Proof.

$$
J_0 = \begin{bmatrix}
-\mu_h & 0 & 0 & \rho & 0 & 0 & -p^* \\
0 & -m^* & 0 & 0 & 0 & 0 & p^* \\
0 & \kappa & -(\mu_h+\gamma+\delta) & 0 & 0 & 0 & 0 \\
0 & 0 & \gamma & -p^* & 0 & 0 & 0 \\
0 & 0 & -\beta_v & 0 & -\mu_c & 0 & 0 \\
0 & 0 & \beta_v & 0 & 0 & -q^* & 0 \\
0 & 0 & 0 & 0 & 0 & \theta & -\mu_c
\end{bmatrix} \tag{4.42}
$$

where $p^* = -\beta_h$, $m^* = (\kappa+\mu_h)$, $p^* = (\mu_h+\rho)$, $q^* = (\theta+\mu_c)$

From rows $1, 4$ and 5, we get three of the eigenvalues $\lambda_1 = -\mu_h, \lambda_2 = -(\mu_h+\rho)$ and $\lambda_3 = -\lambda_v$ which are negatives. We have the remaining matrix as

$$
J_s = \begin{bmatrix}
-(\kappa+\mu_h) & 0 & 0 & p^* \\
\kappa & -(\mu_h+\gamma+\delta) & 0 & 0 \\
0 & \beta_v & -(\theta+\mu_c) & 0 \\
0 & 0 & \theta & -\mu_c
\end{bmatrix} \tag{4.43}
$$

Using the corollary of Gershgorin's circle theorem, the matrix (J_0) will have negative eigenvalues if the following inequalities are satisfied. Thus,

$$
a_{ii} < - \sum_{j=1, j \neq i}^{n} | a_{ij} | .
$$

Therefore,

From row 1

$$
-(\kappa+\mu_h) < -\beta_h \tag{4.44a}
$$

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From row 2

$$-(\mu_h + \gamma + \delta) < -\kappa \tag{4.44b}$$

From row 3

$$-(\theta + \mu_c) < -\beta_v \tag{4.44c}$$

From row 4

$$-\mu_c < -\theta \tag{4.44d}$$

Which is the same as

$$(\kappa + \mu_h) > \beta_h \tag{4.45a}$$

$$(\mu_h + \gamma + \delta) > \kappa \tag{4.45b}$$

$$\theta + \mu_c > \beta_v \tag{4.45c}$$

$$\mu_c > \theta \tag{4.45d}$$

from (4.45a) we have,

$$1 > \frac{\beta_h}{(\kappa + \mu_h)}. \tag{4.46}$$

And from (4.45b) we obtain,

$$\frac{\mu_h + \gamma + \delta}{\kappa} > 1. \tag{4.47}$$

It can be seen from (4.46) and (4.47) that

$$\frac{\mu_h + \gamma + \delta}{\kappa} > 1 > \frac{\beta_h}{(\kappa + \mu_h)}$$

$$\Rightarrow \frac{\mu_h + \gamma + \delta}{\kappa} > \frac{\beta_h}{(\kappa + \mu_h)}$$

$$1 > \frac{\kappa \beta_h}{(\kappa + \mu_h)(\mu_h + \gamma + \delta)} \tag{4.48}$$

Also from (4.45c) and (4.45d) we obtain,

$$1 > \frac{\beta_v}{\theta + \mu_c} \tag{4.49}$$

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and

$$\frac{\mu_c}{\theta} > 1 \tag{4.50}$$

It can be seen from (4.49) and (4.50) that,

$$\frac{\mu_c}{\theta} > 1 > \frac{\beta_v}{\theta + \mu_v}.$$

This implies

$$\frac{\mu_c}{\theta} > \frac{\beta_v}{\theta + \mu_c},$$

thus

$$\frac{\mu_c(\theta + \mu_c)}{\theta \beta_v} > 1 \tag{4.51}$$

From (4.48) and (4.51) we get,

$$\frac{\mu_c(\theta + \mu_c)}{\theta \beta_v} > 1 > \frac{\kappa \beta_h}{(\kappa + \mu_h)(\mu_h + \gamma + \delta)} \tag{4.52}$$

This implies

$$\frac{\mu_c(\theta + \mu_c)}{\theta \beta_v} > \frac{\kappa \beta_h}{(\kappa + \mu_h)(\mu_h + \gamma + \delta)}.$$

This is the same as

$$1 > \frac{\kappa \beta_h \theta \beta_v}{\mu_c(\theta + \mu_c)(\kappa + \mu_h)(\mu_h + \gamma + \delta)}$$

Hence

$$\mathcal{R}_0^2(0) < 1$$

$$\implies \mathcal{R}_0(0) < 1$$

$\square$

Local Stability Analysis of Endemic Equilibrium Point

Theorem 4.8. The Endemic equilibrium (E_1) is locally asymptotically stable if $\mathcal{R}_0(\alpha) > 1$.

Proof. The Jacobian matrix evaluating at the Endemic equilibrium (E_0) gives

$$
J_e =
\begin{bmatrix}
a^* - \alpha - \mu_h & 0 & 0 & \rho & 0 & 0 & -b^* \\
-a^* & x^* & 0 & 0 & 0 & 0 & b^* \\
0 & \kappa & u^* & 0 & 0 & 0 & 0 \\
\alpha & 0 & \gamma & v^* & 0 & 0 & 0 \\
0 & 0 & -c^* & 0 & d^* - \mu_c & 0 & 0 \\
0 & 0 & c^* & 0 & -d^* & w^* & 0 \\
0 & 0 & 0 & 0 & 0 & \theta & -\mu_c
\end{bmatrix}
\tag{4.53}
$$

$u^* = -(\mu_h + \gamma + \delta), \, x^* = -(\kappa + \mu_h), \, v^* = -(\mu_h + \rho), \, w^* = -\theta - \mu_c,$

$a^* = \dfrac{a_1}{b_1}$

$a_1 = (1 - \mathcal{R}_0^2(\alpha))\mu_c\mu_h(\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho)$

$b_1 = \beta_h(\theta + \mu_c)\Big(\kappa\beta_v(\rho + \mu_h) + \mu_c(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h +$

$\gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$b^* = \dfrac{a_2}{b_2}$

$a_2 = \beta_h(\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)\Big(\kappa\beta_v(\rho + \mu_h) + \mu_c(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h +$

$\delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$b_2 = \kappa\beta_v\Big(\mu_h(\mu_h + \kappa)(\mu_h + \alpha + \rho)(\mu_c + \theta)(\gamma + \mu_h + \delta) + \beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h +$

$\delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$c^* = \dfrac{a_3}{b_3}$

$a_3 = \beta_v\mu_c\Big((\mu_h(\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho) + \beta_h\theta(\delta\kappa\rho + \delta\kappa\mu_h +$

$\delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$b_3 = \beta_h\theta\Big(\kappa\beta_v(\rho + \mu_h) + \mu_c(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 +$

$\kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

$d^* = \dfrac{a_4}{b_4}$

$a_4 = (1 - \mathcal{R}_0^2(\alpha))\mu_c(\mu_h + \kappa)(\mu_c + \theta)(\gamma + \mu_h + \delta)(\mu_h + \alpha + \rho)$

$b_4 = \Big(\kappa\beta_v(\rho + \mu_h) + (\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h + \gamma\mu_h^2 + \kappa\rho\mu_h +$

$\kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3)\Big)$

Using the corollary of Gershgorin's circle theorem, the matrix (J_e) will have

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negative eigenvalues if the following inequalities are satisfied. Thus,

$$a_{ii} < -\sum_{j=1,j\neq i}^{n} |a_{ij}|.$$

Therefore, J_e we obtain the following.

From row 1

$$(a^* - \mu_h - \alpha) < -(\rho + b^*) \tag{4.54a}$$

From row 2

$$\mu_h + \kappa < -(a^* + b^*) \tag{4.54b}$$

From row 3

$$-(\delta + \mu_h + \gamma) < -\kappa \tag{4.54c}$$

From row 4

$$-(\mu_h + \rho) < -(\alpha + \gamma) \tag{4.54d}$$

From row 5

$$-\mu_c < -(d^* - c^*) \tag{4.54e}$$

From row 6

$$-(\theta + \mu_c) < (-d^* + c^*) \tag{4.54f}$$

From row 7

$$-\mu_c < -\theta. \tag{4.54g}$$

The (4.55a) to (4.55g) can be rewritten as

$$\mu_h + \alpha > \rho + a^* + b^* \tag{4.55a}$$

$$1 > \frac{a^*}{\mu_h + \kappa} + \frac{b^*}{\mu_h + \kappa} \tag{4.55b}$$

$$\frac{\delta + \mu_h + \gamma}{\kappa} > 1 \tag{4.55c}$$

$$\frac{\alpha + \gamma}{\mu_h + \rho} > 1 \tag{4.55d}$$

$$\mu_c > d^* + c^* \tag{4.55e}$$

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$$\theta + \mu_c > -d^* + c^* \tag{4.55f}$$

$$\mu_c > \theta \tag{4.55g}$$

From (4.55b) and (4.55c) we get

$$\frac{\delta + \mu_h + \gamma}{\kappa} \quad > \quad 1 > \frac{a^*}{\mu_h + \kappa} + \frac{b^*}{\mu_h + \kappa}$$

$$\frac{\delta + \mu_h + \gamma}{\kappa} \quad > \quad \frac{a^*}{\mu_h + \kappa} + \frac{b^*}{\mu_h + \kappa}$$

$$1 \quad > \quad \frac{a^* \kappa}{(\mu_h + \kappa)(\delta + \mu_h + \gamma)} + \frac{b^* \kappa}{(\mu_h + \kappa)(\delta + \mu_h + \gamma)} \tag{4.56}$$

Let $a^{**} = \dfrac{a_1 \kappa}{(\mu_h + \kappa)(\delta + \mu_h + \gamma)}$ and $b^{**} = \dfrac{b_1 \kappa}{(\mu_h + \kappa)(\delta + \mu_h + \gamma)}$
Then (4.56) becomes

$$1 > a^{**} + b^{**} \tag{4.57}$$

Adding (4.55e) and (4.55f) yields

$$\theta + 2\mu_c > 2c^* \tag{4.58}$$

If

$$\theta + 2\mu_c > 2c^*$$

then

$$2\theta + 2\mu_c > 2c^*$$

so

$$2(\theta + \mu_c) > \qquad 2c^*$$

$$\theta + \mu_c > \qquad c^* \tag{4.59}$$

$$1 > \quad \frac{c^*}{\theta + \mu_c}$$

also from (4.55g) we get

$$\frac{\mu_c}{\theta} > 1 \tag{4.60}$$

From (4.59) and (4.60) we have

$$\frac{\mu_c}{\theta} > 1 > \frac{c^*}{\theta + \mu_c},$$

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this implies

$$1 > \frac{c^*\theta}{(\theta+\mu_c)\mu_c}.$$

But

$$\frac{c_1^*\theta}{(\theta+\mu_c)\mu_c} = \frac{1}{b^{**}}$$

This implies (4.60) becomes

$$\begin{aligned}
1 &> \frac{1}{b^{**}} \\
b^{**} &> 1 \\
-1 &> -b^{**} \qquad (4.61)
\end{aligned}$$

Adding (4.57) and (4.61) gives

$$a^{**} = \frac{a_{11}}{b_{11}}$$

$$a_{11} = \kappa(1 - \mathcal{R}_0^2(\alpha))\mu_c\mu_h(\mu_h + \kappa)\theta(\gamma+\mu_h+\delta)(\mu_h+\alpha+\rho)$$

$$b_{11} = \beta_h(\theta+\lambda_v)\Big(\kappa\beta_v(\rho+\mu_h) + \mu_c(\delta\kappa\rho + \delta\kappa\mu_h + \delta\rho\mu_h + \delta\mu_h^2 + \gamma\kappa\mu_h + \gamma\rho\mu_h +$$
$$\gamma\mu_h^2 + \kappa\rho\mu_h + \kappa\mu_h^2 + \rho\mu_h^2 + \mu_h^3\Big)(\mu_h+\kappa)(\delta+\mu_h+\gamma))$$

$$\begin{aligned}
0 &> a^{**} \\
0 &> (1 - \mathcal{R}_0^2(\alpha)) \\
\mathcal{R}_0^2(\alpha) &> 1 \qquad (4.62) \\
\implies \mathcal{R}_0(\alpha) &> 1 \qquad (4.63)
\end{aligned}$$

This implies that,

$$\mathcal{R}_0^2(0) > \mathcal{R}_0^2(\alpha) > 1.$$

$$\square$$

This shows that, if adequate and timely steps such as prevention, treatment, educational and enlightenment campaign, etc. are taken in the course of the epidemic, vector-host diseases such as malaria could be reduced or possibly eradicated from our communities.

Global Stability Analysis of the Malaria Model With Exposed Class

For a nonlinear population models, the eigenvalues of the linearized system are normally used to establish their stability. These methods only establish the infinitesimal perturbations (local stability) of the initial state but the real world populations are subjected to large perturbations, therefore it is very important for a model to be stable relative to large perturbations in the initial state. In this section, we deal with global properties of the malaria model with exposed compartment using the approach given in Castillo-Chavez, Feng, and Huang (2002) for the Disease Free Equilibrium.

Global stability conditions for the Disease Free Equilibrium

We have established that the disease-free equilibrium is locally asymptotic stable (l.a.s) whenever $\mathcal{R}_0 < 1$ and unstabl when $\mathcal{R}_0 > 1$. Now, we want to establish the global stability of the disease-free equilibrium. According the Castillo-Chavez et al. (2002), for the system

$$
\begin{aligned}
\dot{S_h} &= \mu_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h \\
\dot{L_h} &= \beta_h S_h I_v - (\kappa + \mu_h) L_h \\
\dot{I_h} &= \kappa L_h - (\gamma + \mu_h + \delta) I_h \\
\dot{R_h} &= \gamma I_h - \mu_h R_h + \alpha S_h - \rho R_h \\
\dot{S_v} &= \mu_c - \beta_v S_v I_h - \mu_c S_v \\
\dot{L_v} &= \beta_v S_v I_h - \theta L_v - \mu_c L_v \\
\dot{I_v} &= \theta L_v - \mu_c I_v
\end{aligned}
\tag{4.64}
$$

with disease-free equilibrium $\mathbf{E}_0 : (S_h^0, L_h^0, I_h^0, R_h^0, S_v^0, L_v^0, I_v^0) =$
$\left(\dfrac{(\mu_h + \rho)}{(\alpha + \mu_h + \rho)}, 0, 0, \dfrac{\alpha}{(\alpha + \rho + \mu_h)}, 1, 0, 0 \right)$.
The two conditions that follow must be met in order to guarantee the global asymptotic stability of the disease-free state. First, System (4.64) must be writ-

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ten in the form:

$$\dot{x} = F(\mathbf{x}, \mathbf{I}) \tag{4.65}$$

$$\dot{E} = G(\mathbf{x}, \mathbf{I}) \quad G(\mathbf{x}, 0) = 0$$

where $\mathbf{x} \in \mathbb{R}^3$ denotes (its components) the number of susceptible human, susceptible vector and recovered human(that is, uninfected individuals) and $\mathbf{I} \in \mathbb{R}^4$ denotes (its components) the number of latent human, infectious human, latent vector and infectious vector (that is, infected individuals including latent and infectious) $\mathbf{E}_0 = (S_h^0, L_h^0, I_h^0, R_h^0, S_v^0, L_v^0, I_v^0)$ denotes the disease-free equilibrium of this system. And the conditions (1) and (2) below must be met to guarantee global asymptotic stability.

1. For $\dfrac{dx}{dt} = F(\mathbf{x}, 0),$ $\mathbf{x}^*$ is the globally asymptotic stable (g.a.s)

2. $G(\mathbf{x}, \mathbf{I}) = \mathbf{A}\mathbf{I} - \hat{G}(\mathbf{x}, \mathbf{I}),$ $\hat{G}(\mathbf{X}, \mathbf{I}) \geq 0$ for $(\mathbf{x}, \mathbf{I}) \in D,$

where $\mathbf{A} = \mathbf{D}_1 \mathbf{G}(\mathbf{x}^*, 0)$ is an M-matrix (the off diagonal elements of A are non-negative) and D is the region where the model makes biological sense. If System (4.65) satisfies the above two conditions then the following theorem holds:

Theorem 4.9. The equilibrium point $\mathbf{E}_0$ is a globally asymptotic stable (g.a.s.) equilibrium of (4.65) provided that $\mathcal{R}_0 < 1$ (l.a.s.) and that assumptions (l) and (2) are satisfied.

Considering the system (4.64),

$F(\mathbf{x}, 0) = ((\rho + \mu_h) - S_h((\alpha + \rho + \mu_h)), \alpha - R_h((\alpha + \rho + \mu_h)), 1, 0, 0, 0)$

$G(\mathbf{x}, \mathbf{I}) = \mathbf{A}\mathbf{I} - \hat{G}(\mathbf{x}, \mathbf{I})$

$$\mathbf{A} = \begin{pmatrix} -(\kappa + \mu_h) & 0 & 0 & \beta_h \\ \kappa & -(\gamma + \mu_h + \delta & 0 & 0 \\ 0 & \beta_v & -(\theta + \lambda_v) & 0 \\ 0 & 0 & \theta & -\lambda_v \end{pmatrix}$$

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$$\hat{G}(\mathbf{x} = \begin{pmatrix} \mathbf{g_1(x)} \\ \mathbf{g_2(x)} \\ \mathbf{g_3(x)} \\ \mathbf{g_4(x)} \end{pmatrix} = \begin{pmatrix} \beta_h I_v(1 - S_h) \\ 0 \\ \beta_v I_h(1 - S_v) \\ 0 \end{pmatrix}$$

Since $0 \leq S_h \leq 1$, and $0 \leq S_v \leq 1$, it is clear that $\hat{G}(\mathbf{x}) \geq 0$.

It is also clear that, $\mathbf{x}^* = \left(\dfrac{(\rho + \mu_h)}{((\alpha + \rho + \mu_h))}, \dfrac{\alpha}{((\alpha + \rho + \mu_h))}, 1, 0, 0, 0, 0 \right)$ is a g.a.s

equilibrium of $\dfrac{d(\mathbf{x})}{dt} = \mathbf{F}(\mathbf{x}, \mathbf{0})$. Hence, by the above theorem $\mathbf{E}_0$ is g.a.s.

Chapter Summary

We analysed the systems of five and seven non-linear differential equations which described the dynamics of malaria models with 3 variables for humans and 2 variables for mosquitoes and 4 variables for humans and 3 variables for mosquitoes respectively. We demonstrated that there exists a domain where the models are epidemiologically and mathematically well-posed.

We perform local stability analysis of the model. The next generation method is used to derive the basic reproduction number, $\mathcal{R}_0$, a threshold quantity that determines whether a disease be eradicated or not. We investigated that if $\mathcal{R}_0 < 1$ then the disease-free equilibrium is stable and the disease can be eradicated from the population by applying a corollary of Gershgorin's circle theorem. We have proved that the disease-free equilibrium is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable when $\mathcal{R}_0 > 1$. And the endemic equilibrium point which is locally asymptotically stable when $\mathcal{R}_0 > 1$. We used the (Castillo-Chavez et al., 2002) approach for the global stability analysis.

CHAPTER FIVE

PARAMETER ESTIMATIONS AND SIMULATIONS

Introduction

In this chapter, the malaria model with exposed compartment proposed in Chapter Four is used to estimate parameters, perform sensitivity analysis and carry out numerical simulations with data on confirmed malaria cases obtained from the Central Regional Health Directorate of the Ghana Health Service. A sensitivity analysis is carried out to determine the effect of each parameter on the basic reproduction number $\mathcal{R}_0$. Numerical simulations are performed to determine an optimal combination of treatment and prevention needed to effectively control malaria.

Estimating the Parameters for the Model

After formulating a model, one of the most important steps is to compare the model with data or perform what is often referred to as validation. Model validation is the process of determining the degree to which a mathematical model is an accurate representation of the real-world data. It is very important to link our models to data as this helps us to gain more confidence in the model formulated and to obtain realistic estimates of the parameters. One of the biggest challenge in epidemic modelling is the estimation of parameters in the model validation process. There are different methods of estimating parameters. Commonly used methods are; Method of moments, Method of maximum likelihood, Method of minimum χ^2, Method of least squares and others.

A suitable curve for the model is obtained using the data by applying Least Squares Estimation method. The method of least squares is about estimating parameters by minimizing the squared discrepancies between observed data and their expected values. It is a form of mathematical regression analysis

that finds the line of best fit for the data set, providing a visual demonstration of the relationship between the data points. Its aim is to create a straight line that minimizes the sum of squares of the errors generated by the results of the associated equations, such as the square residual values and the values anticipated based on the model. Non-linear least squares is a form of least square analysis used to fit a set of m observations with a model that is non-linear in n unknown parameters.

Consider the system of ODEs,

$$\frac{d\mathbf{y}}{dt} = \mathbf{f}(t,\mathbf{y};\mathbf{p}), \quad \mathbf{y}(0) = \mathbf{y}_0, \tag{5.1}$$

where $\mathbf{y} \in R^n$, $\mathbf{f} \in R^n$, and $\mathbf{p} = (p_1, p_2, \cdots, p_m) \in R^m$, is the vector of unknown parameters. Suppose, we have a collection of k data points: $(t_1, Y_1), (t_2, Y_2), \cdots (t_k, Y_k)$. The *least squares method* determines the optimal parameters, by minimizing the sum of the squares of the residuals

$$E(\mathbf{p}) = \sum_{i=1}^{k} \|\mathbf{y}(t_i;\mathbf{p}) - \mathbf{Y}_i\|_2^2, \tag{5.2}$$

where $\mathbf{y}(t_i;\mathbf{p})$ is the parameter-dependent solution of (5.1) evaluated at the time points t_i, and $\mathbf{Y}_i$ is the vector of observed values at times t_i. In this notation, the model (4.64) can be written in the form $\mathbf{y}(t;\mathbf{p}) = \begin{pmatrix} S_h(t,\mathbf{p}) \\ E_h(t,\mathbf{p}) \\ I_h(t,\mathbf{p}) \\ R_h(t,\mathbf{p}) \\ S_v(t,\mathbf{p}) \\ E_v(t,\mathbf{p}) \\ I_v(t,\mathbf{p}) \end{pmatrix}$,

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which is the state vector, and $\mathbf{p} = \begin{pmatrix} \Lambda_h \\ \beta_h \\ \vdots \\ \vdots \\ c \end{pmatrix} \in R^m$, is the parameter vector.

The nonlinear least-squares (nonlinear data-fitting) problem given in Equation (5.2) is implemented in a number of routines in MATLAB's Optimization Toolbox, including namely; *lsqcurvefit, lsqnonlin, fminsearch* and *nlinfit*. We estimated the parameters of our model using *lsqcurvefit*.

Demographic Parameters

Most demographic parameters are well-known for a given population. In the following, the parameters in the model (4.64) were estimated using data on confirmed malaria cases from the Central Regional Health Directorate of the Ghana Health Service from the year 2013 to 2017 (see appendix1A) and demographic statistics of Ghana. The population of the central region is 2,201,863 according to the 2010 population census (Service, 2013). With a growth rate of 3.1% per annum (www.indexmundi (2017 est) accessed 23/07/2018), it is estimated that the population of the central region for year 2017 is 2,567,369. The mean population from 2009 to 2017 is 2,567,369.

The mean of the data on confirmed malaria cases is given as; 58745,56029, 55069,55819, 58773,67299, 67621,60664, 51910,58955,57289, 57501
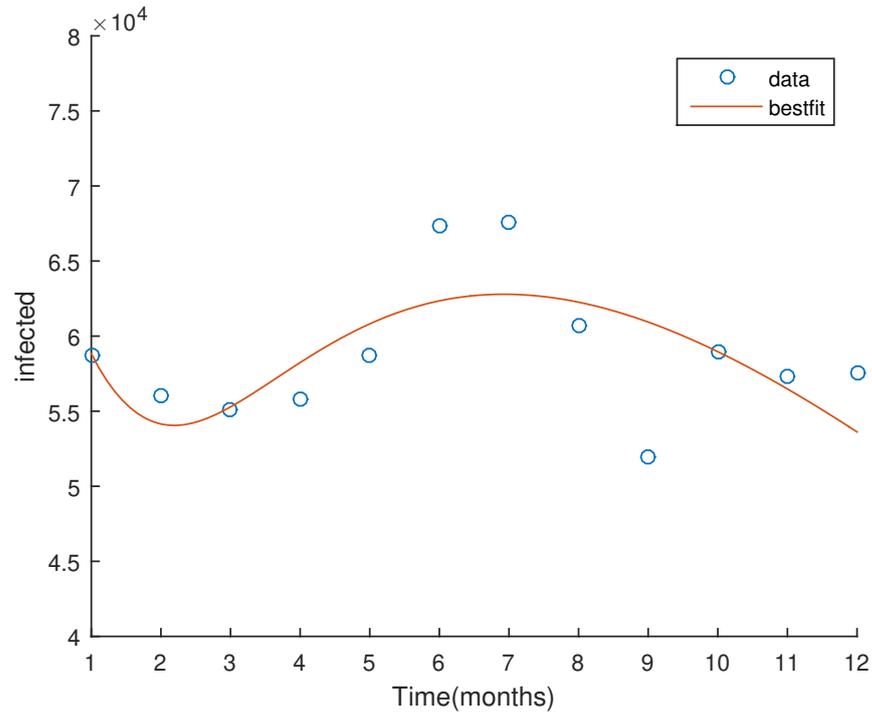Figure 6 shows the plot of the mean of the data on confirmed malaria cases in months.

Figure 6: A Plot of the Mean of the Data on Confirmed Malaria Cases.

A fourth order Runge-Kutta numerical scheme is used to perform numerical simulations in Matlab

The natural mortality for human μ : The natural mortality is postulated to be equal to the inverse of the life expectancy at birth, Life expectancy at birth in Ghana for the year 2018 is 63.5 (WHO 2018 accessed 07/10/2018), that is $\mu = \dfrac{1}{(63.5)(365.25)}$ per day.

Recovery rate γ : It is assumed that it will take 7 days for humans to recover from malaria infection through proper treatment process, that is, $\gamma = \dfrac{1}{7}$ per day.

Lost of immunity ρ : It is also assumed that a person who has completely recovered from malaria will lose his/her malaria acquired immunity after 6 months based on information received from medical malaria researchers in Ghana, so $\rho = \dfrac{1}{180}$ per day.

The natural mortality for mosquito λ_v : The life expectancy of an adult anopheles mosquito is assumed to be 25 days (N. R. Chitnis, 2005), which means

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$\lambda_v = \dfrac{1}{25}$ per day.

Finally, the mosquitoes population is taken to be five times that of the human population. Therefore, $N_h = 2,567,369$ and $N_v = 12,836,845$.

Table 8 shows the estimated parameters and their sources for model (4.64). The rates are given per day.

Table 8: Model Parameters and Values

Parameters	Value	Unit	Source
μ_h	0.0000431	day^{-1}	WHO2018 accessed 07/10/2018
κ	0.140705	day^{-1}	Estimated
γ	$\dfrac{1}{7}$	day^{-1}	Estimated
β_h	0.837773	day^{-1}	Estimated
α	0.5	day^{-1}	Estimated
δ	0.000008	day^{-1}	Estimated
ρ	0.0056	day^{-1}	Calculated
λ_v	0.033	day^{-1}	Calculated
θ	0.291499	day^{-1}	Estimated
β_v	0.729255	day^{-1}	Estimated

Sensitivity Analysis

The assessment of the changes associated with model outcomes as the model parameters are varied is the main goal of sensitivity analysis. This method is very important because it helps us to identify the weak points in the model.These can then be strengthened by experimentation, or simply noted and caution taken in any application. For a simple model, it is done by differentiate the outcome with respect to each parameter in turn. The derivatives give the exact rate of

change of predictions with respect to the parameters.

To know how best to reduce or eradicate an infectious disease such as malaria, and to minimize it mortality, it is essential to know the relative importance of different factors responsible for its transmission and prevalence. Since errors normally occur in data collection and presumed estimation parameter and initial condition values used for fitting is often subject to variation, we determine the relative importance of the model on parameter disease transmission by performing the sensitivity analysis. Moreover, because, the prefixed parameters are selected from a range, the fitted parameters may also vary in a range. Hence, a variation in the parameters varies the output of the model, but the question lies in determining the parameters which has the most significant impact on the output. There are several ways in which one can perform sensitivity analysis, either by performing it on a dynamical system or on static quantities such as the reproduction number or equilibrial prevalence. In order to perform sensitivity analysis of a dynamical system, we assume that there is a dependence of a parameter say p by the differential equations, such that:

$$z_i'(t) = f_i(z_1, ..., z_n, t, p), \quad i = 1, ..., n.$$

The parameter p represents one of the coefficients in the system or in the initial conditions. Thus, the solution of the initial value problem takes into account the function of both the time variable t and the parameter $p : z_i(t, p), \quad i = 1, ..., n.$

Initial disease transmission is directly related to $\mathcal{R}_0$, and disease prevalence is directly related to the endemic equilibrium point, specifically the sizes of E_h, I_h, R_h, E_v and I_v. These sizes represent the individuals (humans and mosquitoes) who have some life stage of Plasmodium in their bodies. The fraction of infectious humans, I_h, is especially important because it represents the people that suffer the most and is directly related to the total number of malaria deaths. We

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calculate the sensitivity indices of the reproductive number, $\mathcal{R}_0$, to the different parameters in the model. These indices tell us how crucial each parameter is to disease transmission and prevalence. In conducting the sensitivity analysis, we use methods described by (N. Chitnis et al., 2008). The normalized forward sensitivity index of a variable to a parameter is the ratio of the relative change in the variable to the relative change in the parameter. When the variable is a differentiable function of the parameter, the sensitivity index may be alternatively defined using partial derivatives.

Definition 5.1. A parameter is said to be sensitive if small change in the parameter value produce a large changes in the solution of the differential equations. The derivative of the solution for the parameter is used to examine a change in the solution of the model with respect to the particular parameter. The partial derivatives may be used to define the sensitivity index.

Definition 5.2. The normalized forward sensitivity index of a variable, u, that depends continuously on a parameter, p, is defined as:

$$\Upsilon_p^u = \frac{\partial u}{\partial p} \cdot \frac{p}{u}$$

The sensitivity indices of the model 5.3 and model 4.64 are computed for each parameter involved in our $\mathcal{R}_0$. The numerical values obtained after solving the respective partial derivative for the parameters in our $\mathcal{R}_0$.

Table 9: $\mathcal{R}_0(\alpha)$ Values With Respect to Model Parameters for (4.64) and (5.3)

Parameters	sign	Value of $\mathcal{R}_0$ with $c\alpha$	Value of $\mathcal{R}_0$ with $c = 0$
c	-	0.4547	0
μ_h	-	0.0071	0.9240
κ	+	0.2044	0.8985
γ	-	0.9996	0.9990
α	-	1.4437	0.9890
δ	-	0.000056	0.000056
ρ	+	0.9813	0.000051
λ_v	-	0.7276	1.3640
θ	-	0.1823	0.6983
β_h	+	1	1
β_v	+	1	1

The dynamics of these parameters by the use of box plots are shown below:
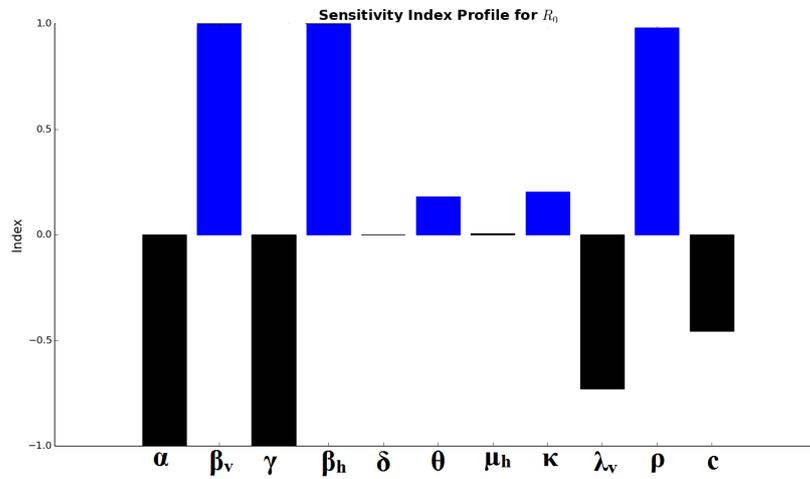
Figure 7: The Box Plot for the Parameters With Their Influence on The $\mathcal{R}_0$ For Malaria Model With $c\alpha$.
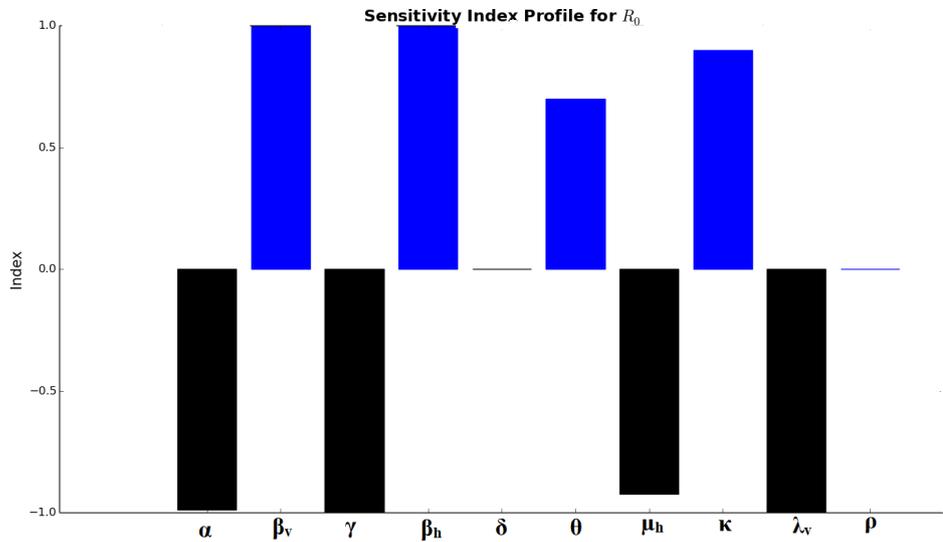
Figure 8: The Box Plot for the Parameters With Their Influence on The $\mathcal{R}_0$ for Malaria Model Without $c\alpha$.

The sensitivity index with negative signs indicates that, for an increase in

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the corresponding parameters there is a decrease in the value of the reproduction number $\mathcal{R}_0$ while parameters with positive signs implies that the value of the reproduction number increases when the corresponding parameters are increased. It is noted that the sensitivity index of $\mathcal{R}_0$ with respect to β_v and β_h do not depend on the values of the parameters because $\Upsilon_{\beta_v}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \beta_v} \cdot \frac{\beta_v}{\mathcal{R}_0}$ and $\Upsilon_{\beta_h}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \beta_h} \cdot \frac{\beta_h}{\mathcal{R}_0}$ are always exactly equal to 1.

For the model (4.64), the most sensitive parameter is the prevention rate α which is $\left(\Upsilon_{\alpha}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \alpha} \cdot \frac{\alpha}{\mathcal{R}_0} = -1.4437 \right)$, the basic number $\mathcal{R}_0$ decreases as prevention rate increases which support the claim that prevention rate has effect on both human and vector populations. The second sensitive parameter is treatment rate γ that is, $\left(\Upsilon_{\gamma}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \gamma} \cdot \frac{\gamma}{\mathcal{R}_0} = -0.9996 \right)$, the basic reproduction number $\mathcal{R}_0$, decreases as treatment increase. For the model (5.3), the most sensitive parameter is the mosquito birth rate λ_v which is $\left(\Upsilon_{\lambda_v}^{\mathcal{R}_0} = \frac{\partial \mathcal{R}_0}{\partial \lambda_v} \cdot \frac{\lambda_v}{\mathcal{R}_0} = -1.3640 \right)$, the basic reproduction number decreases as the mosquito birth rate increases. We would expect $\mathcal{R}_0$ to increase because increasing λ_v increases the number of mosquitoes. However, the mosquito birth rate is density dependent. As the birth rate increases and the number of mosquitoes increases, the death rate also increases because the environment can only support a certain number of mosquitoes. Therefore, the average lifespan of the mosquito also decreases. Mathematically, at equilibrium population size, the per capita birth rate, λ_v , is equal to the per capita death rate. Thus, at equilibrium, λ_v is also the per capita death rate; and with an exponential distribution for the death rate, $\frac{1}{\lambda_v}$ is the expected lifespan of the mosquitoes. As the latent period of Plasmodium in mosquitoes is of the same order as the lifespan of the mosquitoes, shortening the lifespan of the mosquito reduces the reproductive number. Thus any changes in λ_v have two opposite effects. Increasing λ_v increases the mosquitoes population which tends to increase $\mathcal{R}_0$, and also decreases the mosquito lifespan which tends to reduce $\mathcal{R}_0$. The second sensitive parameter is treatment rate γ that

is, $\left(\Upsilon_\gamma^{\mathcal{R}_0} = \dfrac{\partial \mathcal{R}_0}{\partial \gamma} \cdot \dfrac{\gamma}{\mathcal{R}_0} = -0.9990 \right)$, the basic reproduction number $\mathcal{R}_0$, decreases as treatment increase. This means that, as more infected humans are treated the disease reduces.

The sensitivity index of $\mathcal{R}_0$ with respect to the control parameter α is, $\left(\Upsilon_\alpha^{\mathcal{R}_0} = \dfrac{\partial \mathcal{R}_0}{\partial \alpha} \cdot \dfrac{\alpha}{\mathcal{R}_0} = -0.9890 \right)$, which means alpha has a great impact on the reduction of the disease malaria as expected. For almost all parameters, the sign of the sensitivity indices of $\mathcal{R}_0$ (i.e., whether $\mathcal{R}_0$ increases or decreases when a parameter increases) corresponds with an intuitive expectation.

Basic Reproduction Number, $\mathcal{R}_0(\alpha)$

The basic reproduction number with $\alpha = 0.5$, $\gamma = \dfrac{1}{7}$ and other parameter values taking from Table 8 is

$$\mathcal{R}_0(\alpha) = 0.7746$$

The Relationship Between $\mathcal{R}_0(\alpha)$ and $\mathcal{R}_0(0)$

From Chapter Four, we have

$$\mathcal{R}_0^2(\alpha) = 0.8221 < \mathcal{R}_0^2(0) = 10.3366$$

and it true because from the calculation, This shows that if there is no prevention strategy in place, the communities as well as the regions and the country will be endemic but if proper prevention strategies (α) are adopted and we get the estimated number of people needed to stick to the prevention strategies, the infectious disease malaria could be eradicated from our communities.

Numerical Simulations

In this section, we present the numerical analysis of the model. A numerical simulation of the model is conducted to find out the dynamics of the disease

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in the human and vector populations. The simulations were conducted using MATLAB's ode45.

The initial conditions used are proportions of the total humans and mosquito populations given as $S_h = 0.7961, \quad E_h = 0, \quad I_h = 0.2039, \quad R_h = 0, \quad S_v = 0.89, \quad E_v = 0, \quad I_v = 0.11.$

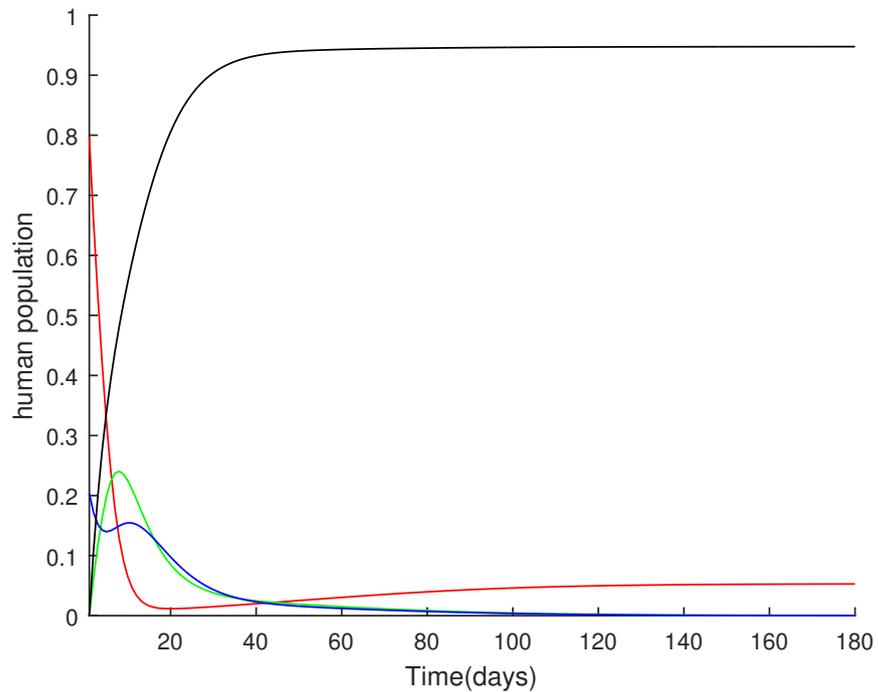The plots tells us the impact of the current interventions we are practicing in the country.

Figure 9: A Plot Illustrating the Changes in the Four State Variables of the Malaria Model Showing the Dynamics With Time, of Susceptible Humans, Exposed Humans, Infected Humans and Shows the Dynamics of Recovered Humans.
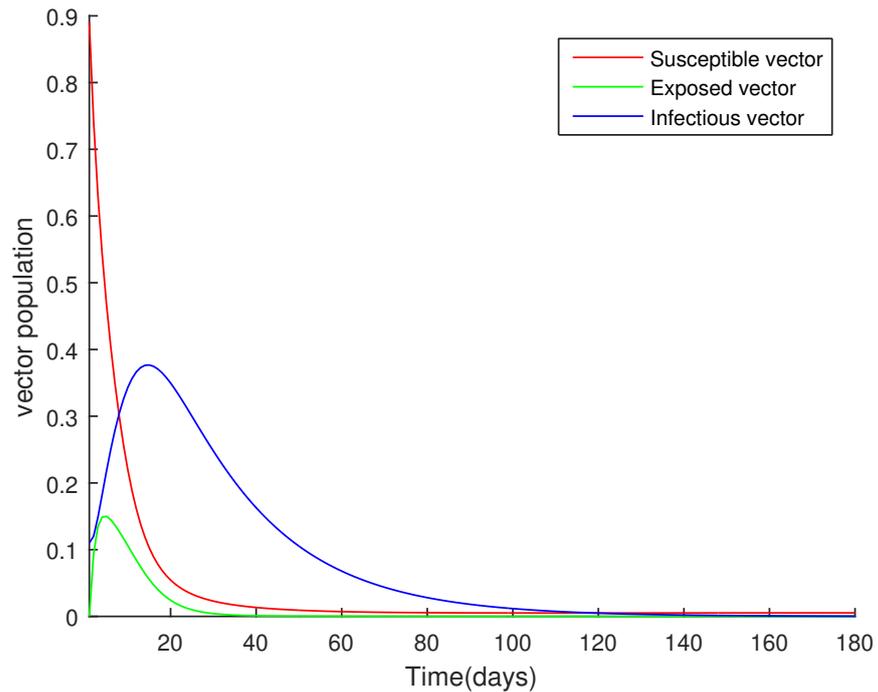
Figure 10: A Plot Illustrating the Changes in the Three State Variables of the Malaria Model Showing the Dynamics With Time, of Susceptible, Exposed and Infectious Mosquitoes.

In Figure 9 and Figure 10, the curves of the two disease classes of the human population and the three vector classes are decreasing as time increases, which is positive for the current interventions in the human population, but there is still more work to be done in the human population. Therefore, we will consider the effects of varying the main parameters responsible for malaria control after considering malaria prevalence rate in the population now.

Prevalence in the Malaria Model

Prevalence is defined as the ratio of the number of cases of a disease in a population and with the number of individuals in a population at a given time.
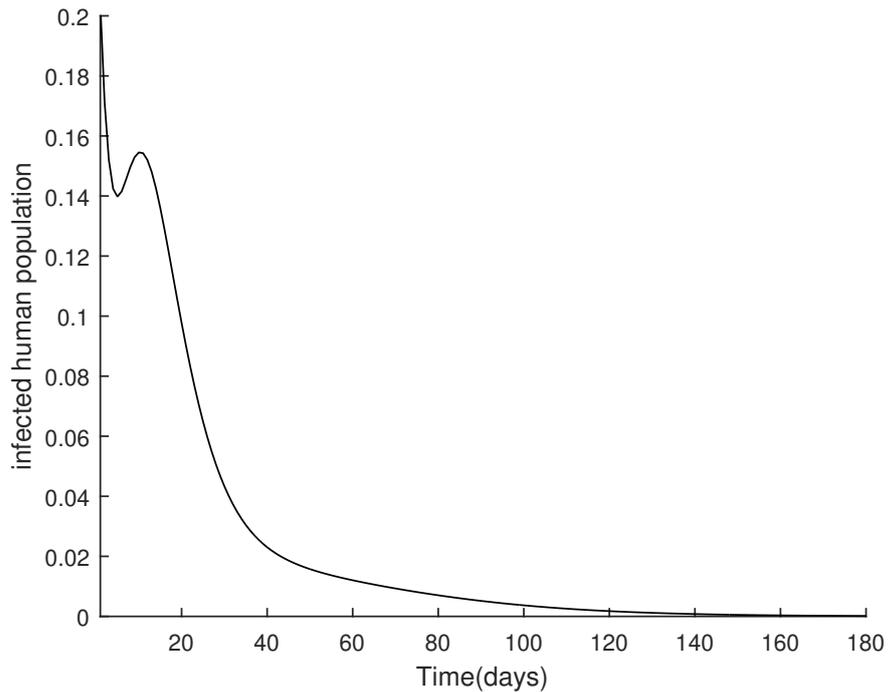
Figure 11: A Plot Illustrating changes of Prevalence with Time.

Figure 11 shows that the prevalence rate as of now is high which confirms that there is more work to be done if we want to achieve malaria free society.

The main strategy that will be considered for controlling malaria is to find the right combinations of preventative measures and treatment needed to reduce or eradicate malaria by considering:

1. The percentage of people needed to carry out the preventative strategies in order to eradicate malaria.

2. The percentage of infected people needed to seek proper treatment to help eradicate malaria.

Our simulations examine the effect of different combinations of treatment and preventative measures on the transmission of the disease.

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Effect of Treatment on the Infected Human and Vector Populations (4.64)

In this section, we examine the effect of treatment on the infected human and vector populations . The analysis of the effect of increasing the treatment rate at some levels of "prevention" is done by keeping prevention rate constant and varying treatment rate. This gives different values of $\mathcal{R}_0$ for fixed values of alpha (prevention) and varying values of gamma (treatment). Specifically, gamma assumed the values $0.1, 0.2, 0.4, 0.6, 0.8$ for each fixed value of alpha.

Table 10: $\mathcal{R}_0(\alpha)$ values for Fixed α and Varying γ for (4.64)

alpha values	gamma values	$\mathcal{R}_0(\alpha)$ with $c = 0.05$
0.1	0.1	2.5055
0.1	0.2	1.7718
0.1	0.4	1.2530
0.1	0.6	1.0231
0.1	0.8	**0.8860**
0.2	0.1	1.6911
0.2	0.2	1.1959
0.2	0.4	**0.8457**
0.2	0.6	**0.6905**
0.2	0.8	**0.5980**
0.4	0.1	1.0834
0.4	0.2	**0.7662**
0.4	0.4	**0.5418**
0.4	0.6	**0.4424**
0.4	0.8	**0.3831**
0.6	0.1	**0.8095**
0.6	0.2	**0.5724**
0.6	0.4	**0.4048**
0.6	0.6	**0.3305**
0.6	0.8	**0.2863**
0.8	0.1	**0.6476**
0.8	0.2	**0.4580**
0.8	0.4	**0.3239**
0.8	0.6	**0.2644**
0.8	0.8	**0.2290**

From Table 10, it can be observed that some $\mathcal{R}_0(\alpha)$ values are less than 1, which imply that if we have those levels of prevention and treatment, there is the possibility of reducing or eradicating this infectious disease.

Plots showing the effect of keeping prevention rate constant and varying treatment rate on the infected human population.
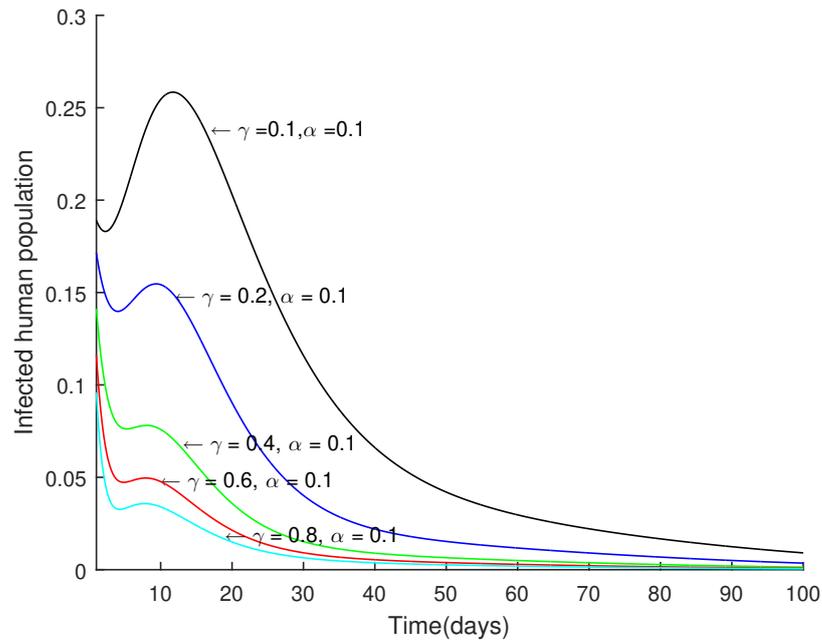
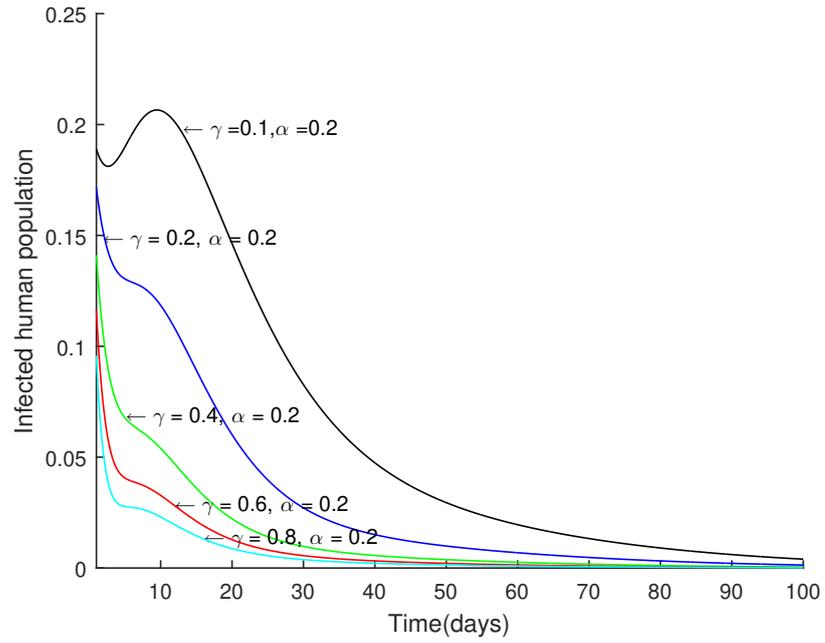Figure 12: Plot of Infected Human Population Against Time With $\alpha = 0.1$.

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Figure 13: Plot of Infected Human Population Against Time With $\alpha = 0.2$.
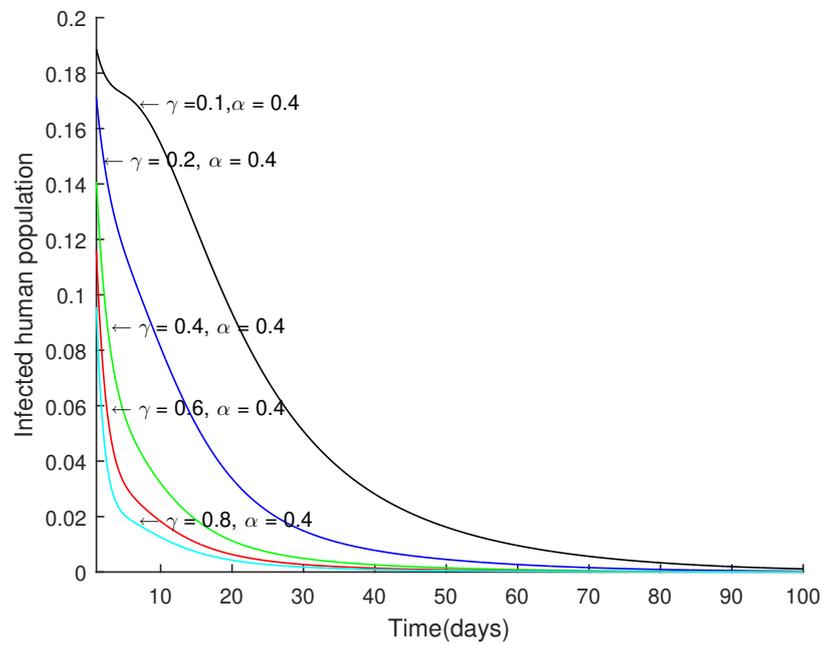
Figure 14: Plot of Infected Human Population Against Time With $\alpha = 0.4$.

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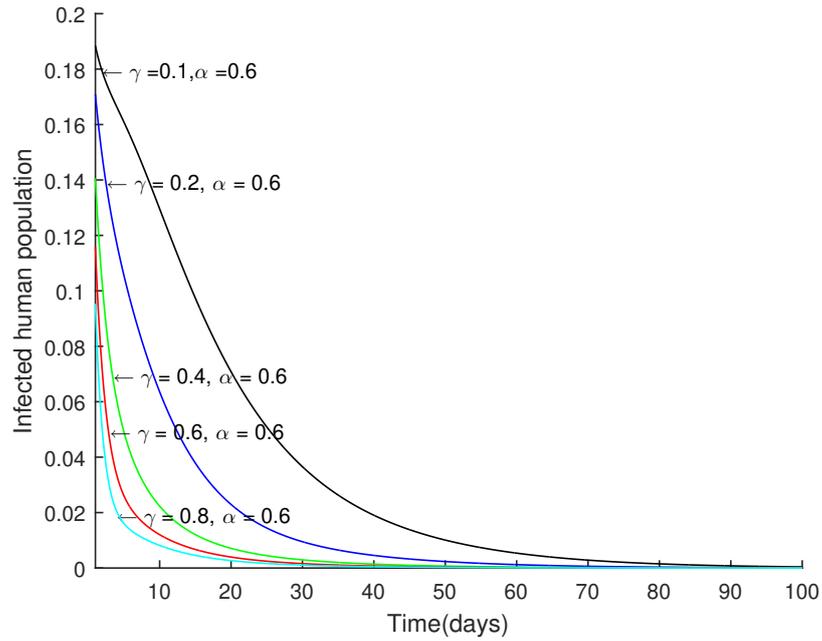
Figure 15: Plot of Infected Human Population Against Time With $\alpha = 0.6$.
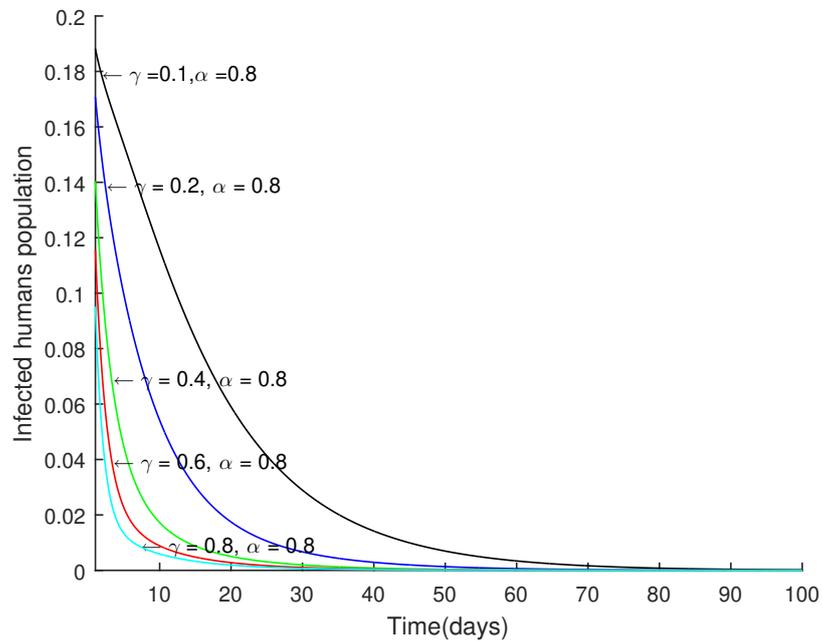
Figure 16: Plot of Infected Human Population Against Time With $\alpha = 0.8$.

From Figure 12 to 16, it can be observed that, holding the prevention rate constant and increasing treatment rate from 0.1 through to 0.8, for each constant

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prevention rate, the number of infected humans increases to a maximum and then decreases to a certain minimum. For instance, with $\alpha = 0.1$ and $\gamma = 0.1$, the proportion of infected human population increases to 0.27 and then decreases to about 0.01. The $\mathcal{R}_0(\alpha)$ values for $\gamma = 0.1, 0.2, 0.4, 0.6$ are all greater than 1 except $\gamma = 0.8$. This means they will all converge to the endemic equilibrium except $\gamma = 0.8$ which converges to the disease free equilibrium.

Also, with $\alpha = 0.2$ and $\gamma = 0.1$ and 0.2 the infected human population converge to the endemic equilibrium but for $\gamma > 0.4$ the infected human population converge to the disease free equilibrium.

For $\alpha = 0.4$ the infected human population converge to the disease free equilibrium accept for $\gamma \geq 0.2$. and $\gamma = 0.1$ which converge to the endemic equilibrium. But for $\alpha = 0.6$ and 0.8, the infected human population converge to the disease free equilibrium for all levels of γ. That is all curves converges to disease free equilibrium. The Figure 17 to Figure 21 shows the effect of keeping prevention rate constant and varying treatment rate on the infected vector population
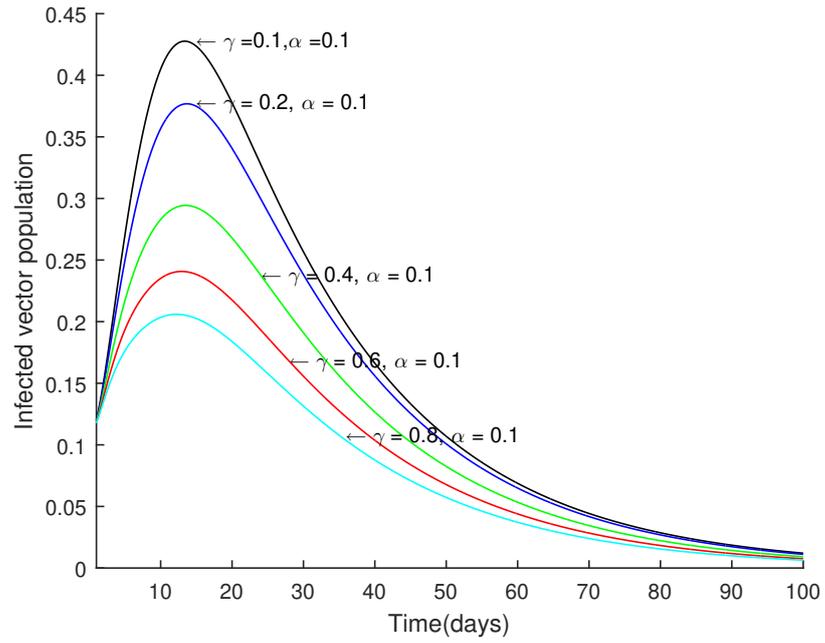
Figure 17: Plot of Infected Vector Population Against Time With $\alpha = 0.1$.
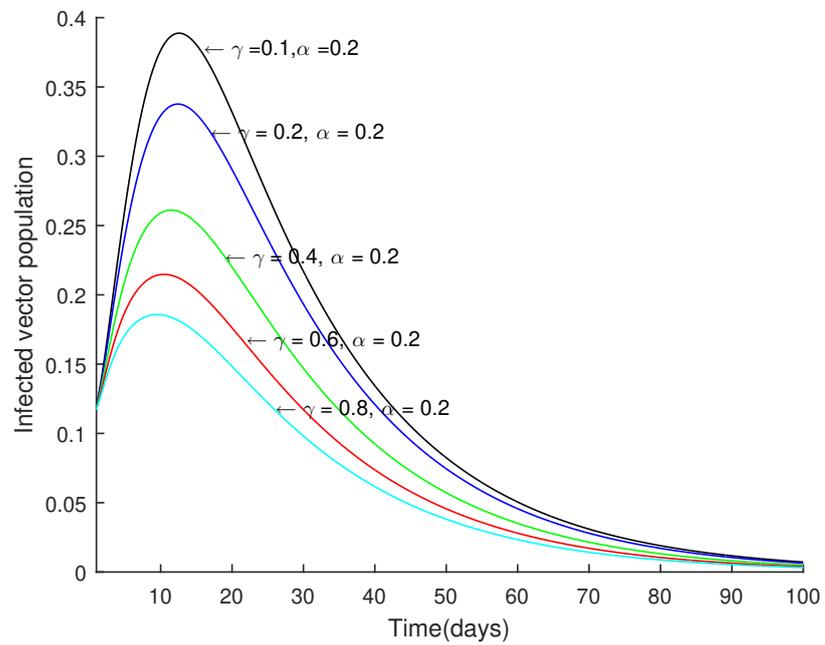

Figure 18: Plot of Infected Vector Population Against Time With $\alpha = 0.2$.
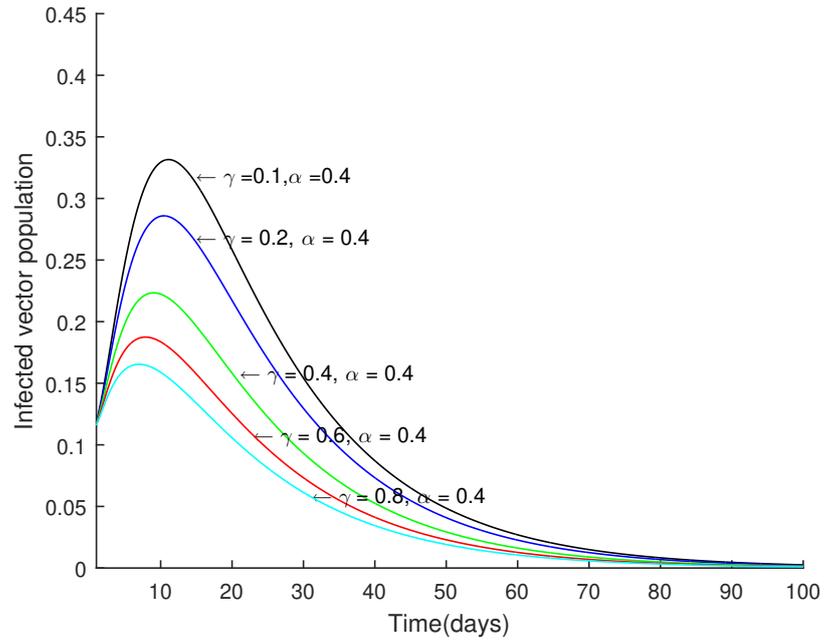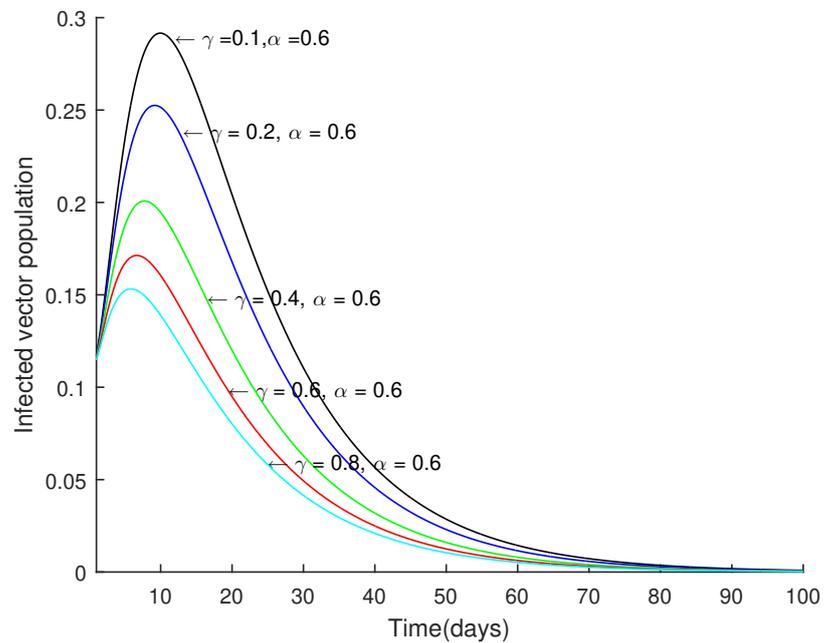
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Figure 19: Plot of Infected Vector Population Against Time With α = 0.4.

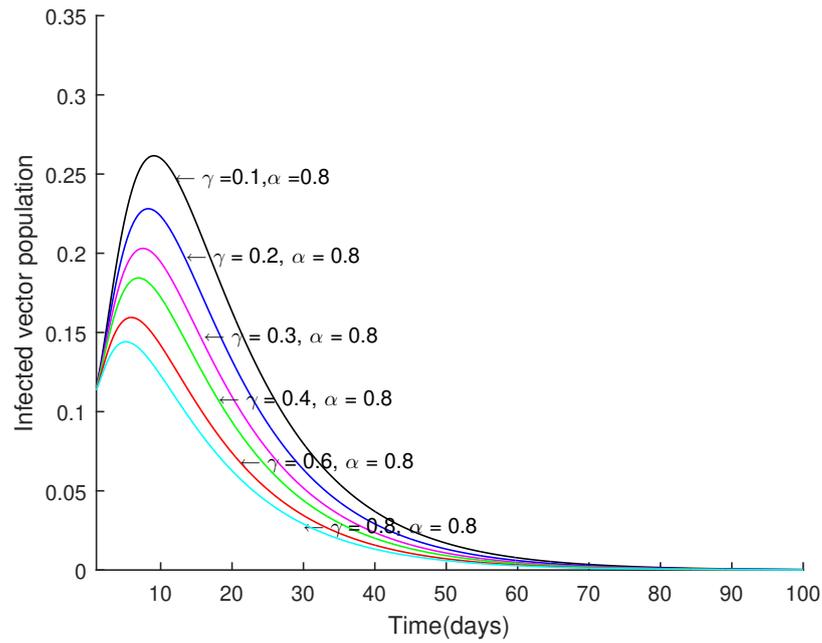Figure 20: Plot of Infected Vector Population Against Time With α = 0.6.

Figure 21: Plot of Infected Vector Population Against Time With $\alpha = 0.8$.

From figures 17 to 21, we display the effect of various rates of treatment of the infected human on the infected mosquito population. The figures show that increasing the rate of treatment decreases the infected mosquito population. Fix prevention rates and varying values of treatment rate from 0.1 to 0.8 for each fix prevention rate yield significant drop in the proportion of infected mosquitoes number. This means that there will be less infected mosquitoes and less susceptible humans to propagate the disease.

Effect of a Prevention on the Infected Human and Vector Populations for Model (4.64)

We examine the effect of prevention on the infected populations by keeping treatment constant and varying prevention rate ($\alpha = 0.1, 0.2, 0.4, 0.6, 0.8$). The table and diagrams below, show the effect of increasing the prevention rate at some constant levels of "treatments". Thus, it gives different values of $\mathcal{R}_0$ as gamma (treatment) is fixed and alpha (prevention) varied.

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Table 11: $\mathcal{R}_0(\alpha)$ Values for Fixed γ and Varying α for (4.64)

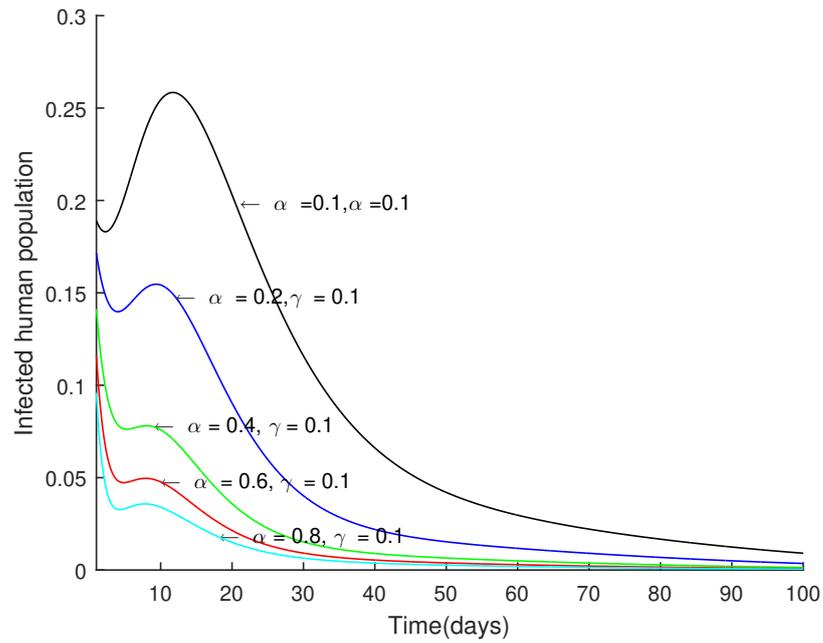| gamma values	alpha values	$\mathcal{R}_0(\alpha)$ with $c = 0.05$
0.1	0.1	2.5055
0.1	0.2	1.6911
0.1	0.4	1.0834
0.1	0.6	**0.8095**
0.1	0.8	**0.6476**
0.2	0.1	1.7718
0.2	0.2	1.1959
0.2	0.4	0.7662
0.2	0.6	**0.5724**
0.2	0.8	**0.4580**
0.4	0.1	1.2530
0.4	0.2	**0.8457**
0.4	0.4	**0.5418**
0.4	0.6	**0.4048**
0.4	0.8	**0.3239**
0.6	0.1	1.0231
0.6	0.2	**0.6905**
0.6	0.4	**0.4424**
0.6	0.6	**0.3305**
0.6	0.8	**0.2644**
0.8	0.1	**0.8860**
0.8	0.2	**0.5980**
0.8	0.4	**0.3831**
0.8	0.6	**0.2863**
0.8	0.8	**0.2290**

Figure 22: Plot of Infected Human Population Against Time With $\gamma = 0.1$.
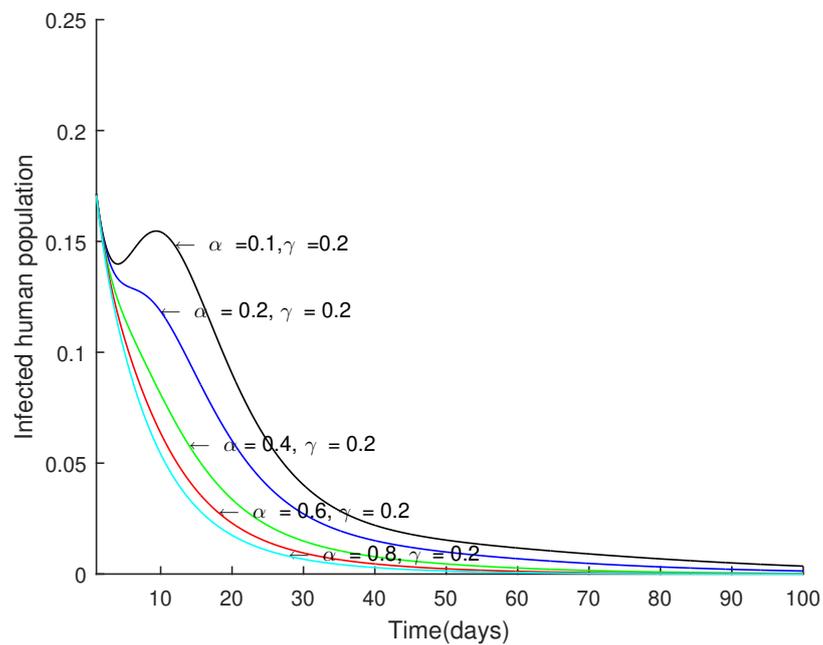
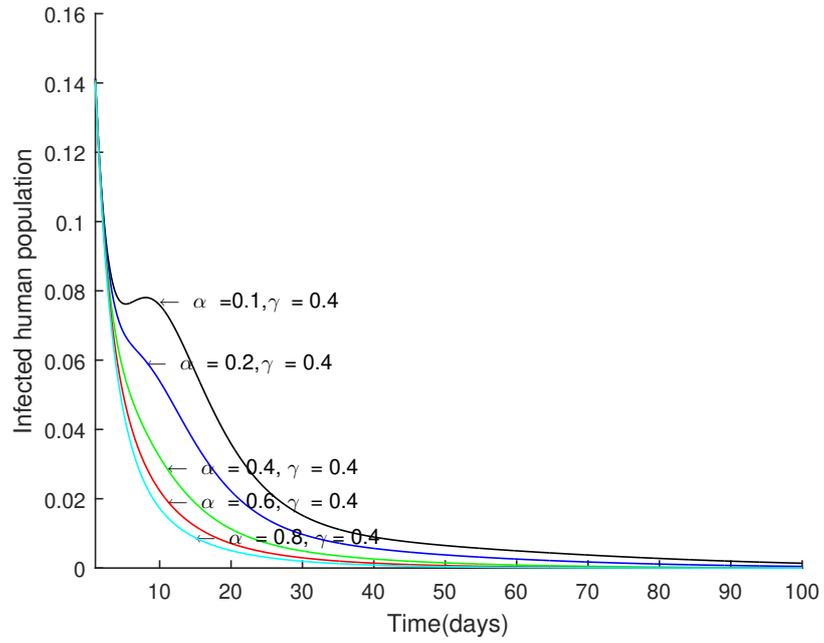Figure 23: Plot of Infected Human Population Against Time With $\gamma = 0.2$.

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Figure 24: Plot of Infected Human Population Against Time With $\gamma = 0.4$.

Figure 25: Plot of Infected Human Population Against Time With $\gamma = 0.6$.
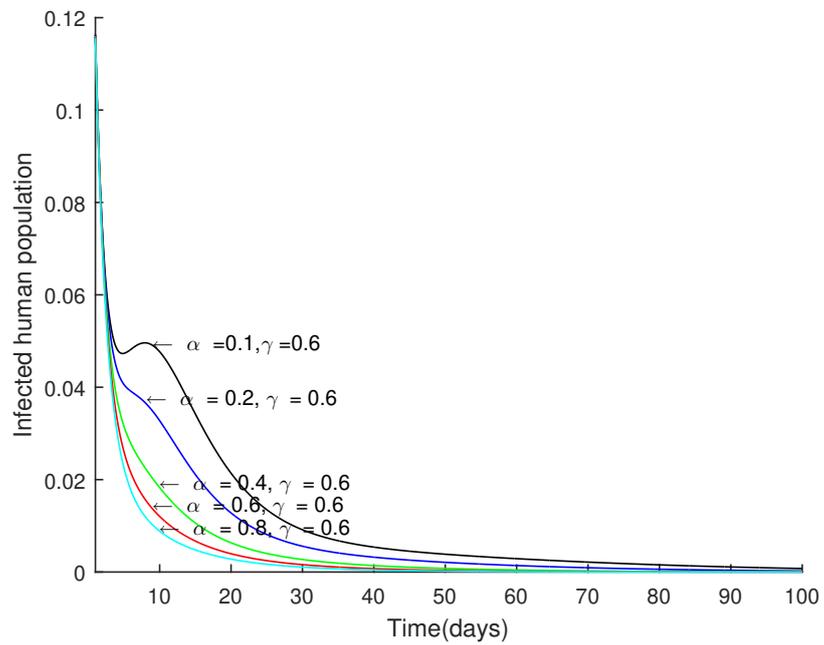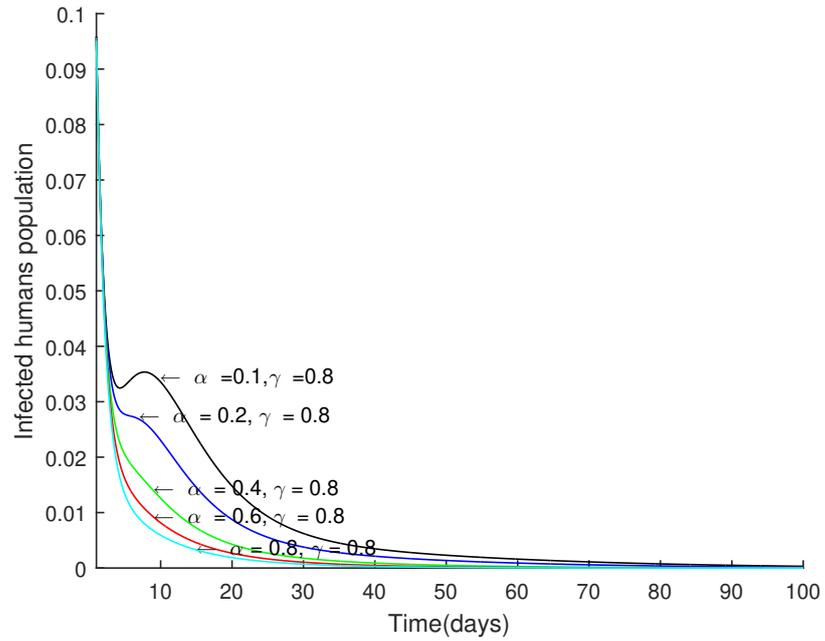
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Figure 26: Plot of Infected Human Population Against Time With $\gamma = 0.8$.

Figures 22 to 26, show the effect of "prevention" on the infected human population. Holding treatment rate at fixed values and varying the prevention from 0.1 to 0.8, the infected humans population dropped. The plot of vector population against time by keeping gamma constant and varying alpha.
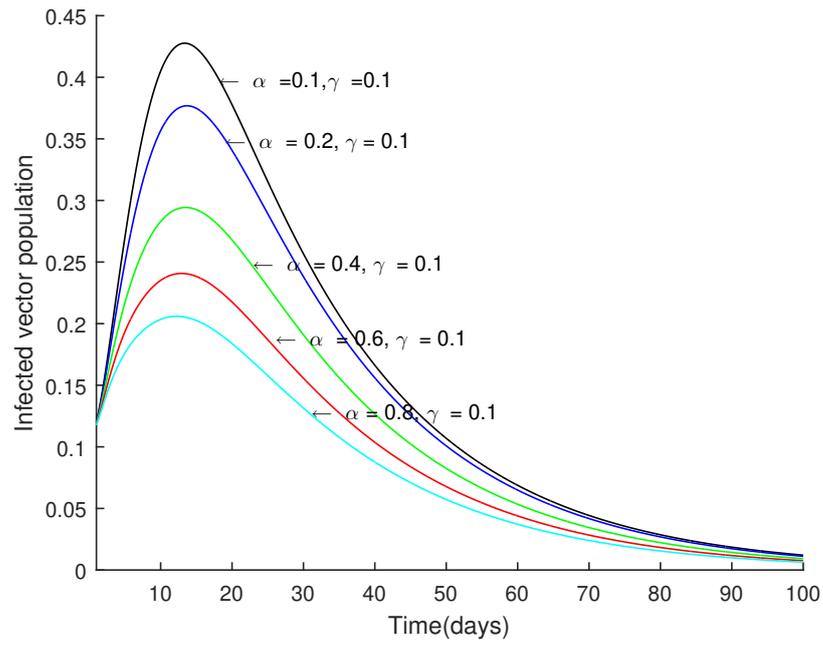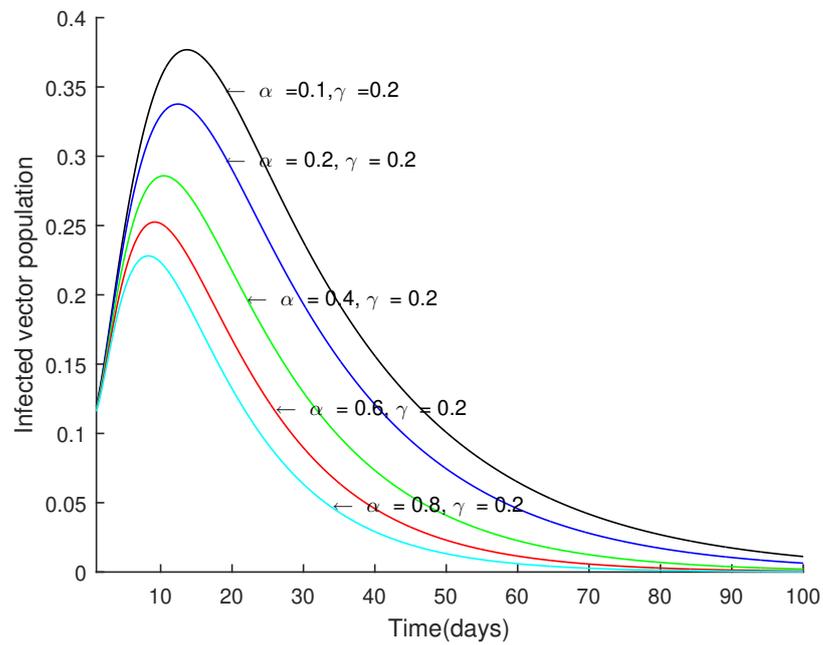
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Figure 27: Plot of Infected Vector Population Against Time With $\gamma = 0.1$.

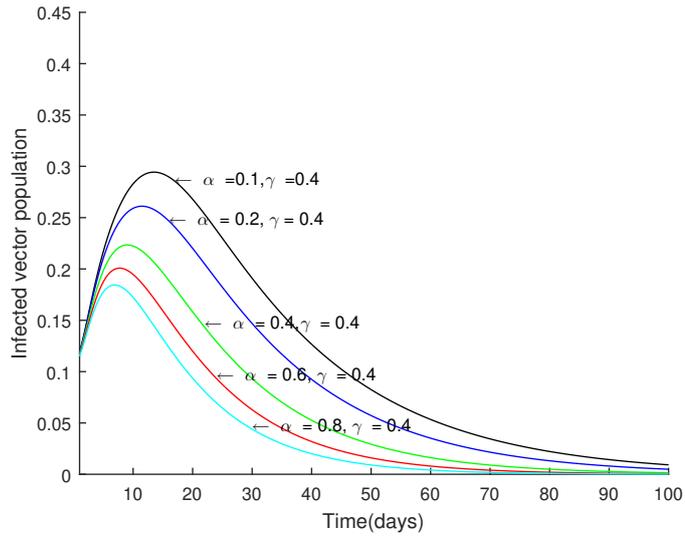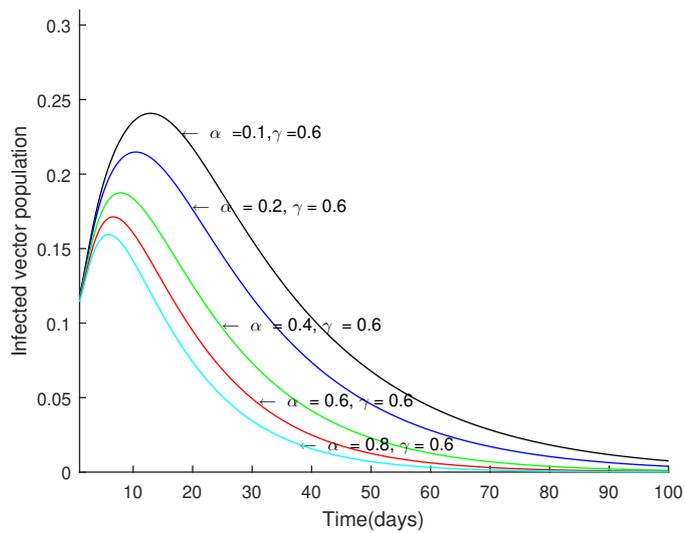Figure 28: Plot of Infected Vector Population Against Time With $\gamma = 0.2$.

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Figure 29: Plot of Infected Vector Population Against Time With γ = 0.4.

Figure 30: Plot of Infected Vector Population Against Time With γ = 0.6.
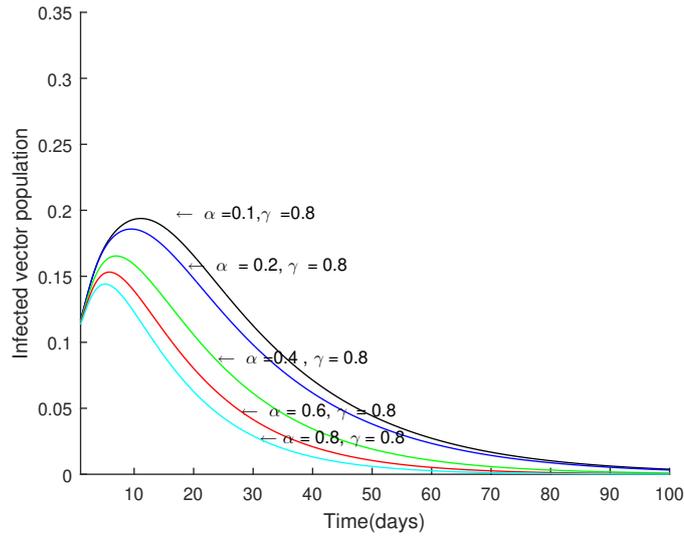
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Figure 31: Plot of Infected Vector Population Against Time With $\gamma = 0.8$.

In Figures 27 to 31, we examine the effect of increasing the prevention rate of the infected human on the infected mosquito population, I_v . It can be observed that, holding the "treatment rate" constant at some fixed values and increasing prevention rate from 0.1 through to 0.8 decreases the number of infected mosquito. The implication is that, the susceptible mosquitoes find it difficult to find an infected human to bite and the prevention rate also contribute to the death of mosquitoes in all the class. If the cycle continues, it will decreasing their population in the long run and the end result will be a malaria-free society.

Effect of Treatment With Constant Alpha and Increasing Values Of c

In this section, the value of c is increased form 0 to 0.25 with constant alpha value of 0.4 and varying gamma values $0.1, 0.2, 0.4, 0.6, 0.8$. The value of $\mathcal{R}_0(\alpha)$ for each c is computed and the graph for each c value draw.

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Table 12: Table Showing the Value of $\mathcal{R}_0(\alpha)$ for Each c Values With Fixed α

Values and Varying γ for Model (4.64)

alpha values	0.1	0.2	0.4	0.6	0.8
gamma values	0.4	0.4	0.4	0.4	0.4
$\mathcal{R}_0(\alpha)$ for $c = 0.1$	0.9127	0.6454	0.4564	0.3726	0.3227
$\mathcal{R}_0(\alpha)$ for $c = 0.15$	0.7952	0.5623	0.3976	0.3247	0.2812
$\mathcal{R}_0(\alpha)$ for $c = 0.2$	0.7080	0.5007	0.3541	0.2891	0.2504
$\mathcal{R}_0(\alpha)$ for $c = 0.2$	0.6401	0.4527	0.3201	0.2614	0.2264

Figure 32: Plot of Infected Human Population Against Time With $\alpha = 0.4$.

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Figure 33: Plot of Infected Vector Population Against Time With $c = 0.1$.

Figure 34: Plot of Infected Vector Population Against Time With $c = 0.15$.

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Figure 35: Plot of Infected Vector Population Against Time With $c = 0.2$.

Figure 36: Plot of Infected Vector Population Against Time With $c = 0.25$.

From Figure 33 to Figure 36 it can be seen that as the value of c increases the infected vector population decreases to zero faster. For instance, from Figure

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33, it takes about 70 days before the infected vector population decreases to zero whiles in Figure 36 it takes just 42 days for the infected vector to decrease to zero. Also, from Table 12, the value of $\mathcal{R}_0(\alpha)$ decreases as the value of c increases, which confirms that $c\alpha$ contribute to the death rate of mosquitoes.

Effect of Varying $c\alpha$ with Fixed gamma

We examine the effect of increasing prevention rate while keeping treatment constant. The Table 13 show the corresponding $\mathcal{R}_0(\alpha)$ values of c as c increase form 0 to 0.25 with constant gamma value of 0.4 and varying alpha values $0.1, 0.15, 0.2, 0.25$. and the graph for each c value draw .

Table 13: $\mathcal{R}_0(\alpha)$ Values for Different c With $\gamma = 0.4$ and Varying α for (4.64)

alpha values	0.4	0.4	0.4	0.4	0.4
gamma values	0.1	0.2	0.4	0.6	0.8
$\mathcal{R}_0(\alpha)$ for $c = 0.1$	0.89436	0.64103	0.45641	0.37353	0.32386
$\mathcal{R}_0(\alpha)$ for $c = 0.15$	0.779241	0.55851	0.397667	0.32544	0.282176
$\mathcal{R}_0(\alpha)$ for $c = 0.2$	0.69384	0.497308	0.354087	0.28978	0.251253
$\mathcal{R}_0(\alpha)$ for $c = 0.25$	0.627311	0.44962	0.320134	0.261996	0.22716

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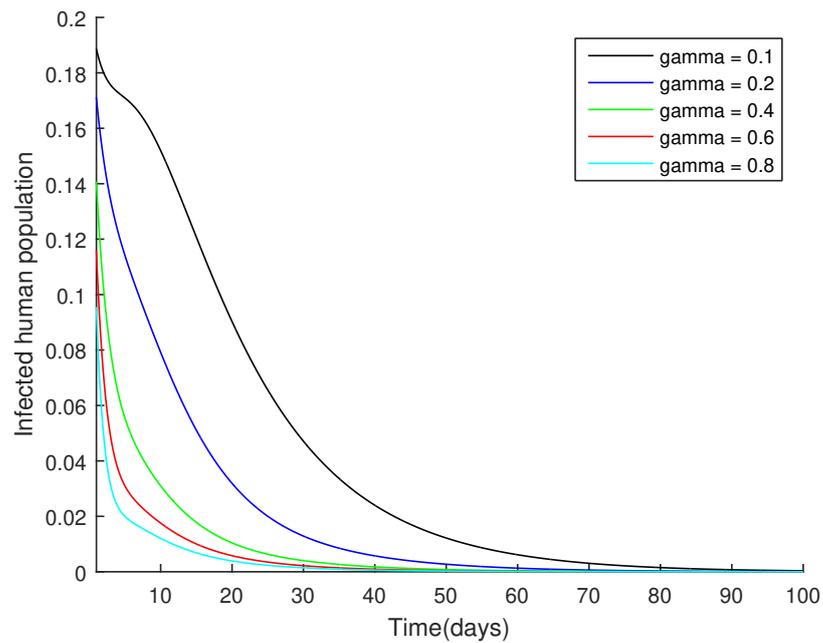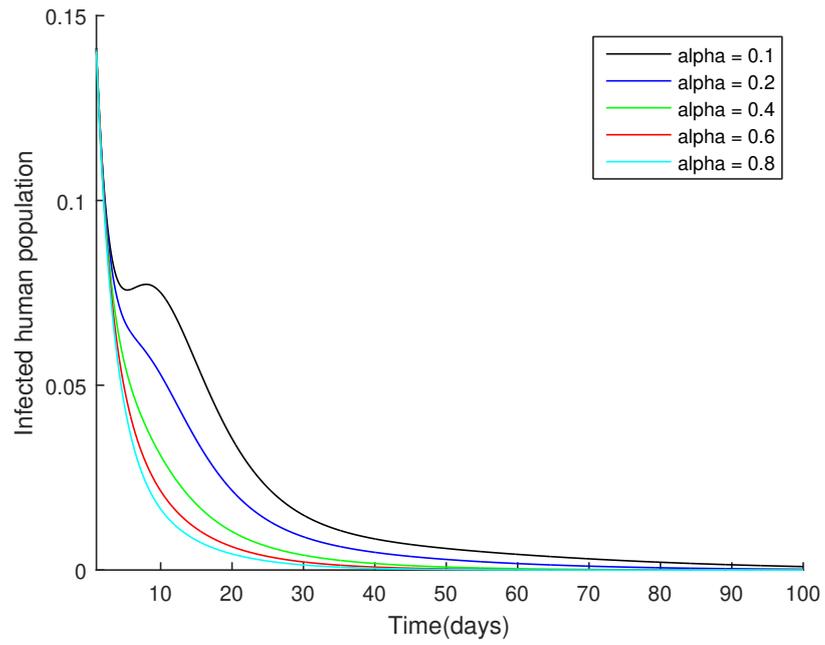
Figure 37: Plot of Infected Human Population Against Time With $c = 0.1$.
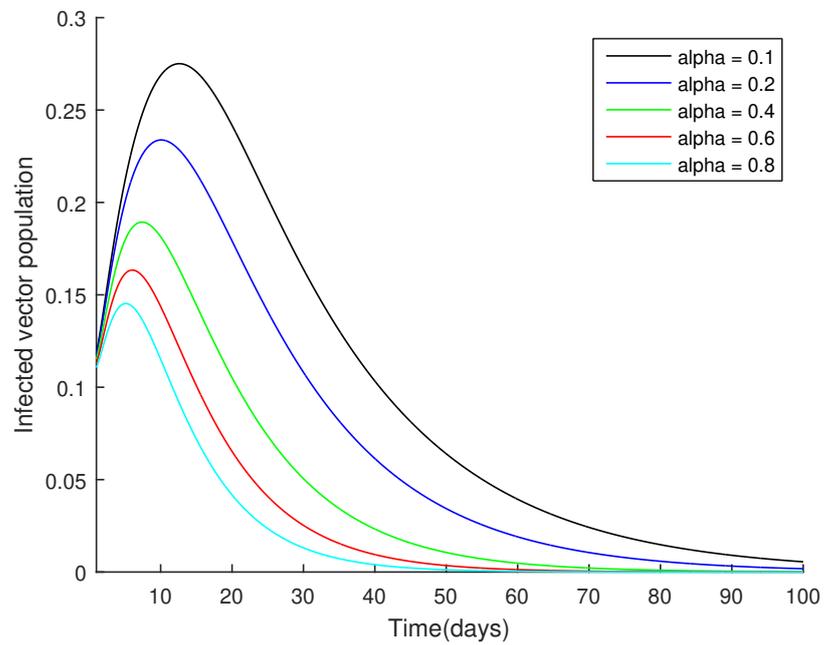
Figure 38: Plot of Infected Vector Population Against Time With $c = 0.1$.
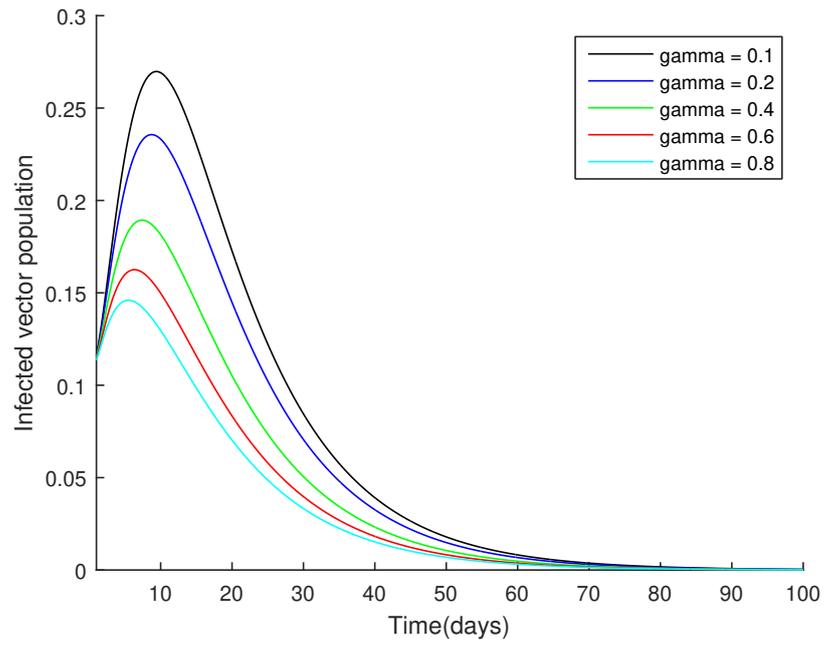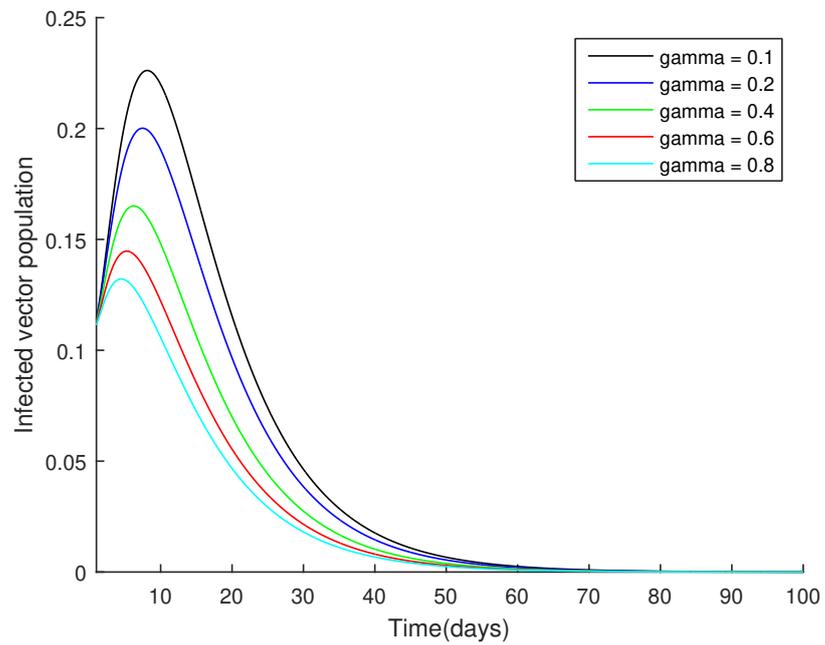
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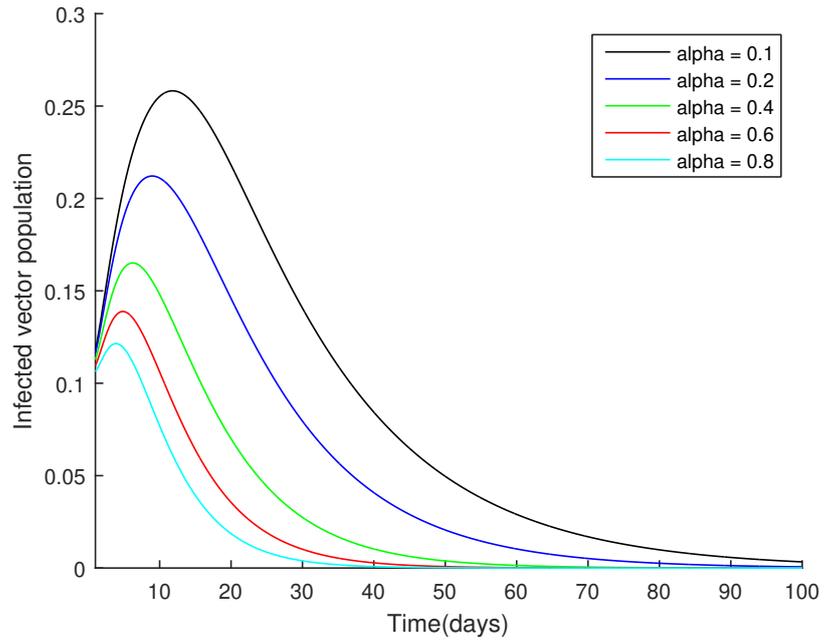
Figure 39: Plot of Infected Vector Population Against Time With $c = 0.15$.

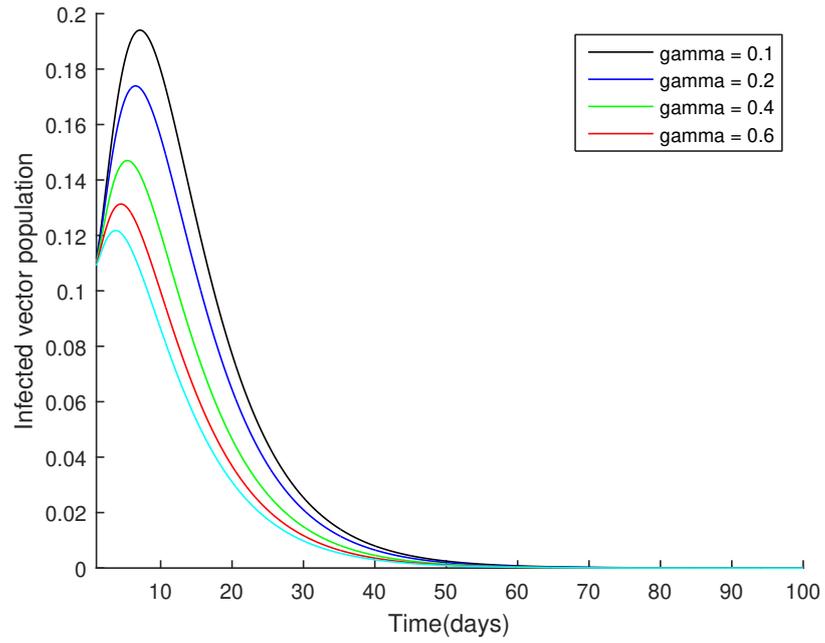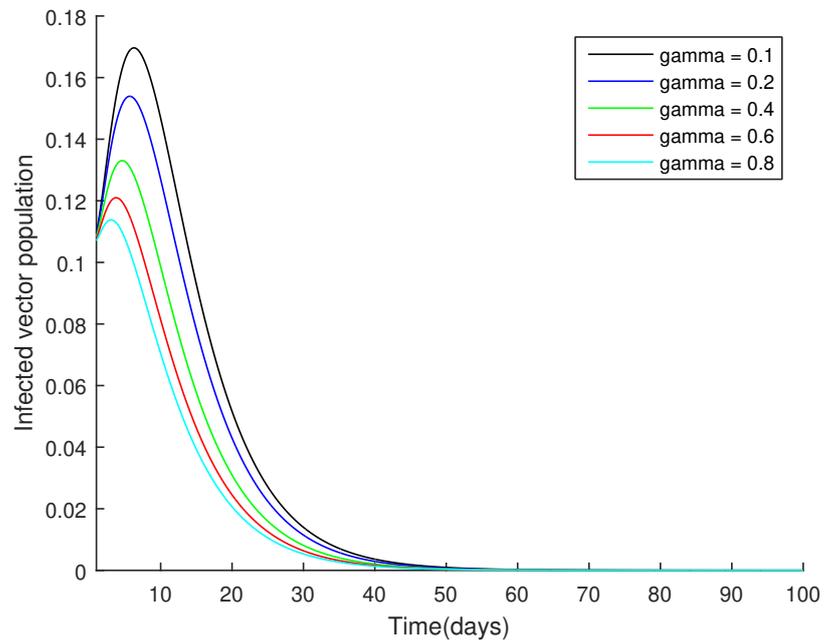Figure 40: Plot of Infected Vector Population Against Time With $c = 0.2$.

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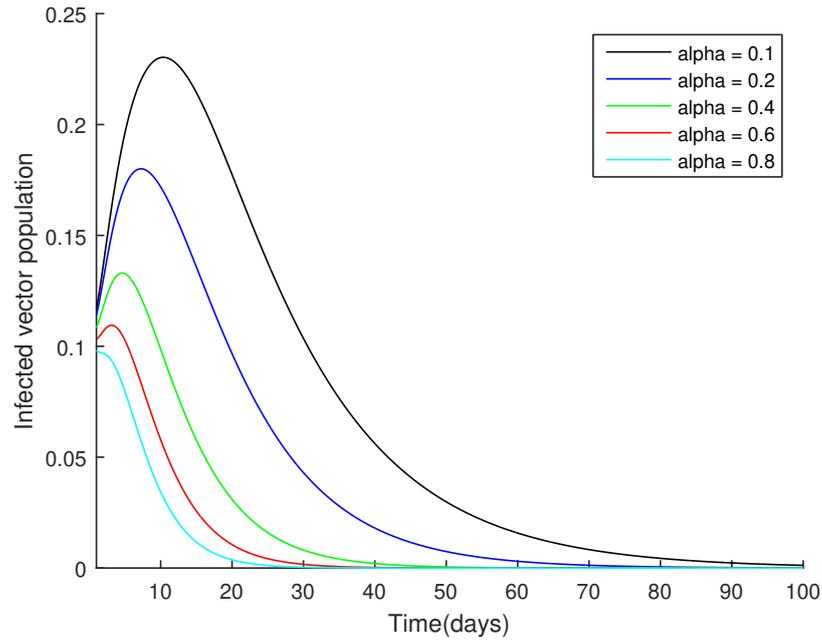
Figure 41: Plot of Infected Vector Population Against Time With $c = 0.25$.

From Figure 38 to Figure 41, it can be observed that as c increases the infected vector population decreases to zero. And, from Table 13, the value of $\mathcal{R}_0(\alpha)$ decreases as the value of c increases, which indicate that $c\alpha$ has effect on the death rate of mosquitoes.

Analysis of Model Without Effect of Prevention Effort on Vector Population

In the previous section, we looked at the graphs and basic reproduction numbers on the effect of prevention and treatment on a malaria model with effect of prevention strategies on the vector population. In this section, we compare the graphs and basic reproduction numbers on the effect of prevention strategies and treatment of the malaria model with $c = 0$ of equation (4.64). If $c = 0$, then

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the model (4.64) becomes;

$$\dot{S}_h = \mu_h - \beta_h S_h I_v - \alpha S_h + \rho R_h - \mu_h S_h$$

$$\dot{L}_h = \beta_h S_h I_v - (\kappa + \mu_h)L_h$$

$$\dot{I}_h = \kappa L_h - (\gamma + \mu_h + \delta)I_h$$

$$\dot{R}_h = \gamma I_h - \mu_h R_h + \alpha S_h - \rho R_h \qquad (5.3)$$

$$\dot{S}_v = \lambda_v - \beta_v S_v I_h - \lambda_v S_v$$

$$\dot{L}_v = \beta_v S_v I_h - (\theta + \lambda_v)L_v$$

$$\dot{I}_v = \theta L_v - \lambda_v I_v$$

Effect of Treatment on the Infected Human and Vector Populations for Model (5.3)

The effect of prevention on the infected human and vector populations is determine for model (5.3). Different values of $\mathcal{R}_0$ for fixed values of alpha (prevention) whiles the values of gamma (treatment) are varied. Specifically, gamma assumed the values $0.1, 0.2, 0.4, 0.6, 0.8$ for each fixed value of alpha are shown the Table 14.

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Table 14: $\mathcal{R}_0(\alpha)$ Values for Fixed α and Varying γ for (5.3)

alpha values	gamma values	$\mathcal{R}_0(\alpha)$ with $c = 0.05$
0.1	0.1	2.6774
0.1	0.2	1.8934
0.1	0.4	1.3390
0.1	0.6	1.0933
0.1	0.8	**0.9468**
0.2	0.1	1.9190
0.2	0.2	1.3571
0.2	0.4	**0.9597**
0.2	0.6	**0.7836**
0.2	0.8	**0.6786**
0.4	0.1	1.3663
0.4	0.2	**0.9663**
0.4	0.4	**0.6833**
0.4	0.6	**0.5579**
0.4	0.8	**0.4832**
0.6	0.1	**1.1182**
0.6	0.2	**0.7908**
0.6	0.4	**0.5592**
0.6	0.6	**0.4566**
0.6	0.8	**0.3954**
0.8	0.1	**0.9695**
0.8	0.2	**0.6857**
0.8	0.4	**0.4849**
0.8	0.6	**0.3959**
0.8	0.8	**0.3429**

Figure 42: Plot of Infected Human Population Against Time With $\alpha = 0.1$.

Figure 43: Plot of Infected Human Population Against Time With $\alpha = 0.2$.

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Figure 44: Plot of Infected Human Population against Time with α = 0.4.
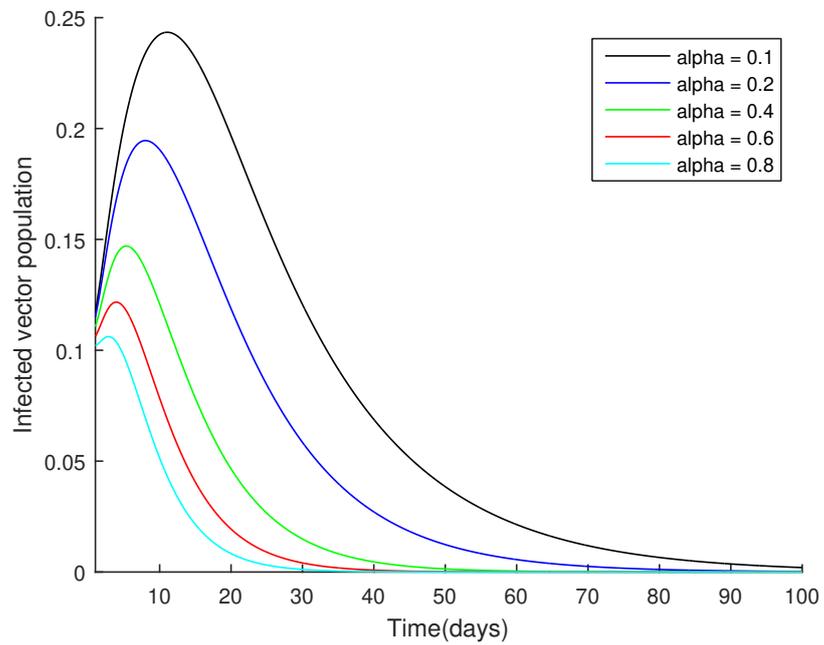

Figure 45: Plot of Infected Human Population Against Time With α = 0.6.

Figure 46: Plot of Infected Human Population Against Time With $\alpha = 0.8$.

The Figures 47 to Figure 51 show the effect of keeping prevention rate fixed and varying treatment rate on the infected vector population.

Figure 47: Plot of Infected Vector Population Against Time With $\alpha = 0.1$.

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Figure 48: Plot of Infected Vector Population Against Time With α = 0.2.

Figure 49: Plot of Infected Vector Population Against Time With α = 0.4.

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Figure 50: Plot of Infected Vector Population Against Time With α = 0.6.

Figure 51: Plot of Infected Vector Population Against Time With α = 0.8.

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Effect of Prevention on the Infected Human and Vector Populations for Model (5.3)

We determine the effect of treatment on the infected populations. The Table 15 and diagrams that follow, analyze the effect on increasing the prevention rate at some fixed levels of "treatments". Table 15 shows different values of $\mathcal{R}_0$ as gamma (treatment) is fixed for some values and alpha (prevention) varied.

Table 15: $\mathcal{R}_0(\alpha)$ Values for Fixed γ and Varying α For (5.3)

gamma values	alpha values	$\mathcal{R}_0(\alpha)$ with $c = 0.05$
0.1	0.1	2.6774
0.1	0.2	1.9190
0.1	0.4	1.3663
0.1	0.6	1.1182
0.1	0.8	**0.9695**
0.2	0.1	1.8934
0.2	0.2	1.3571
0.2	0.4	0.9663
0.2	0.6	**0.7908**
0.2	0.8	**0.6857**
0.4	0.1	1.3390
0.4	0.2	**0.9597**
0.4	0.4	**0.6833**
0.4	0.6	**0.5592**
0.4	0.8	**0.4849**
0.6	0.1	1.0933
0.6	0.2	**0.7836**
0.6	0.4	**0.5579**
0.6	0.6	**0.4566**
0.6	0.8	**0.3959**
0.8	0.1	**0.9468**
0.8	0.2	**0.6786**
0.8	0.4	**0.4832**
0.8	0.6	**0.3954**
0.8	0.8	**0.3429**

It can be observed that, the values for $\mathcal{R}_0$ in Table 10 and Table 11 are less than the $\mathcal{R}_0$ values for Table 14 and Table 15. This means that $c\alpha$ has an impart on the value of $\mathcal{R}_0$.
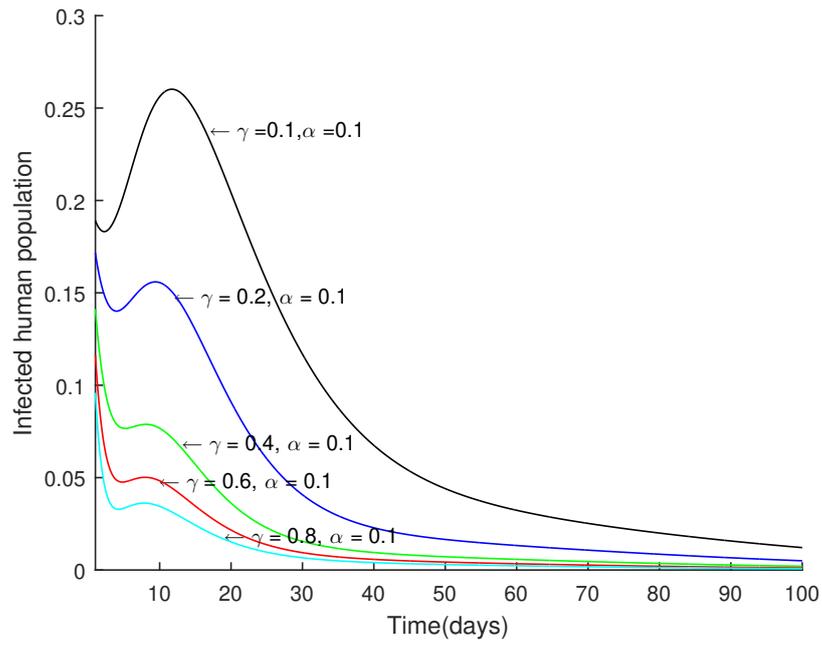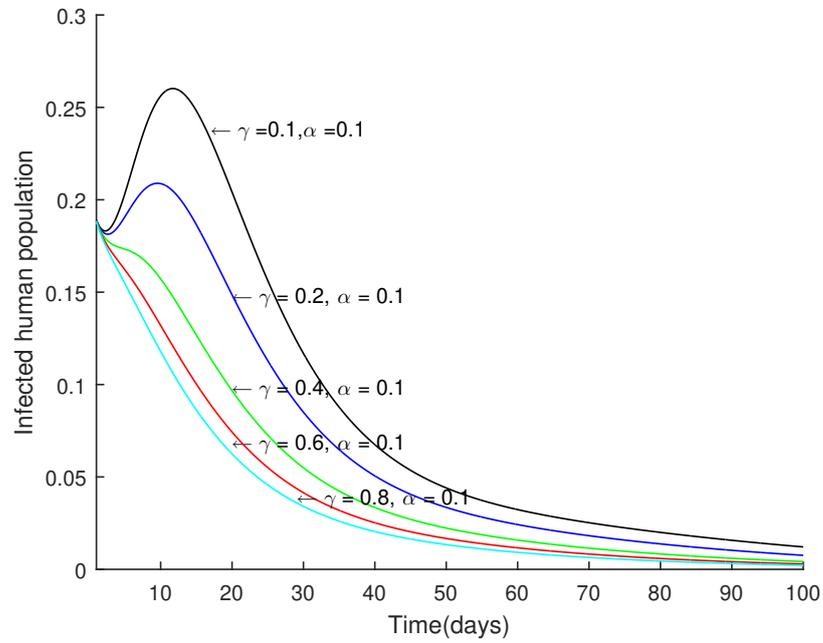

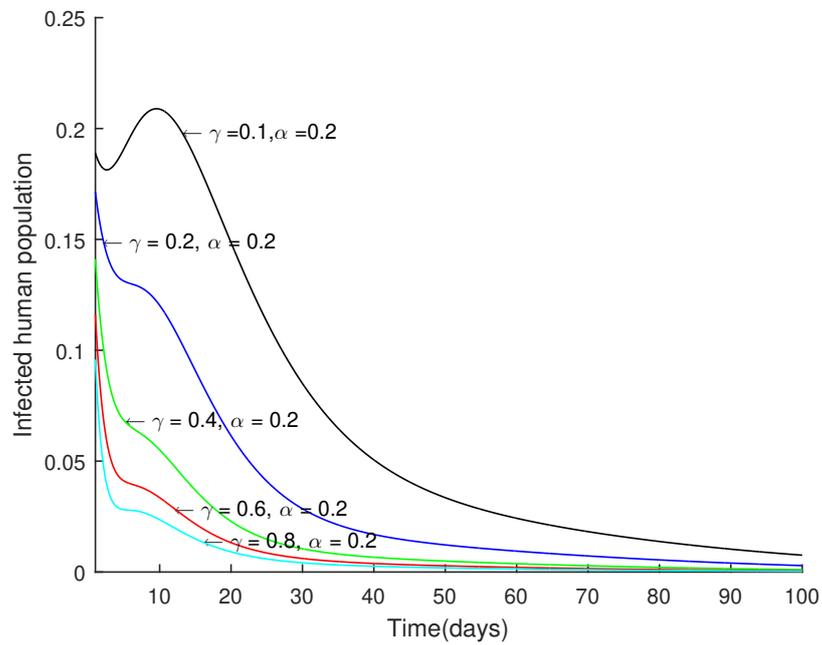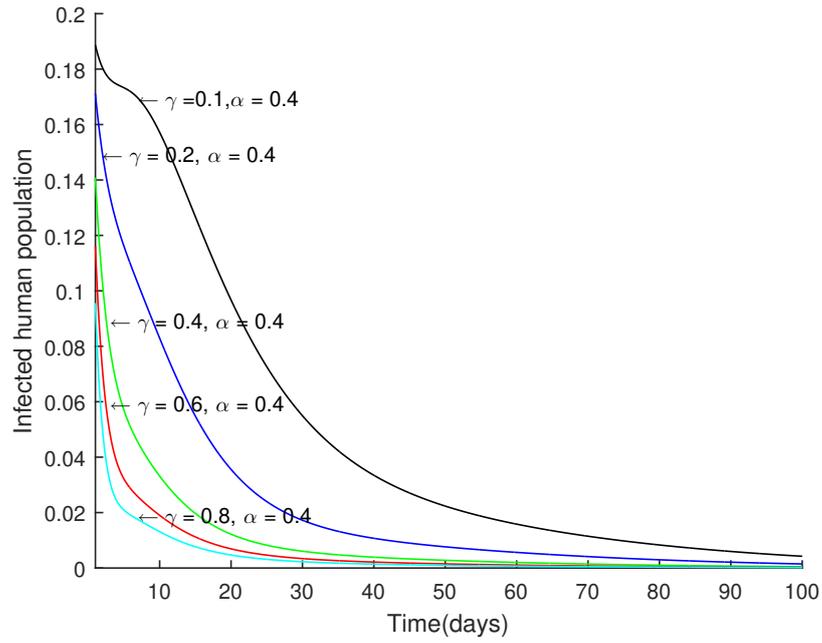Figure 52: Plot of Infected Human Population Against Time With $\gamma = 0.1$.

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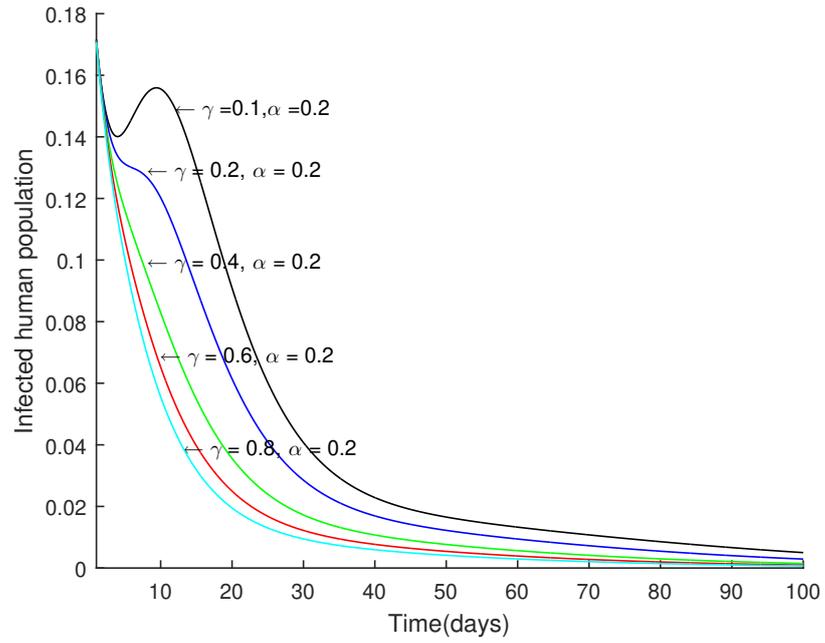
Figure 53: Plot of Infected Human Population Against Time With $\gamma = 0.2$.
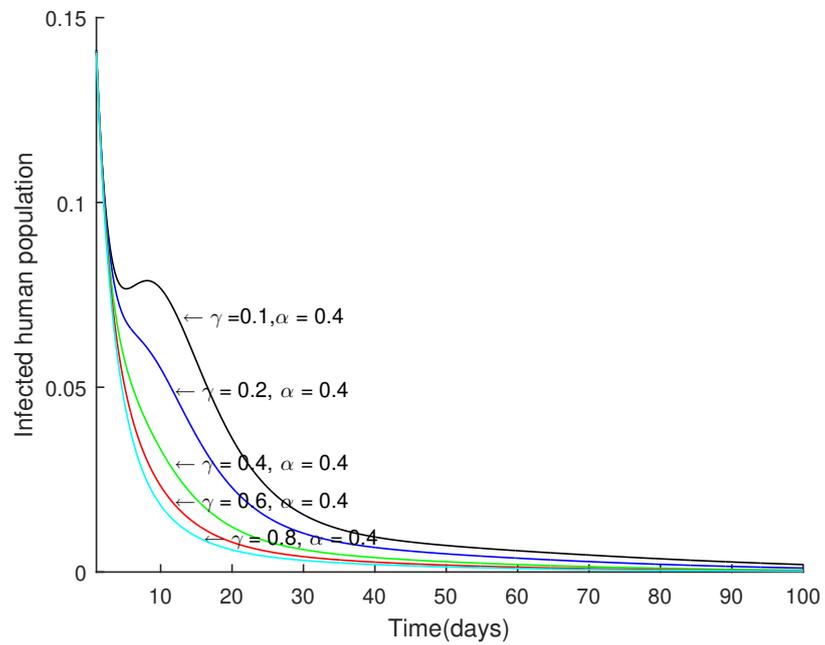
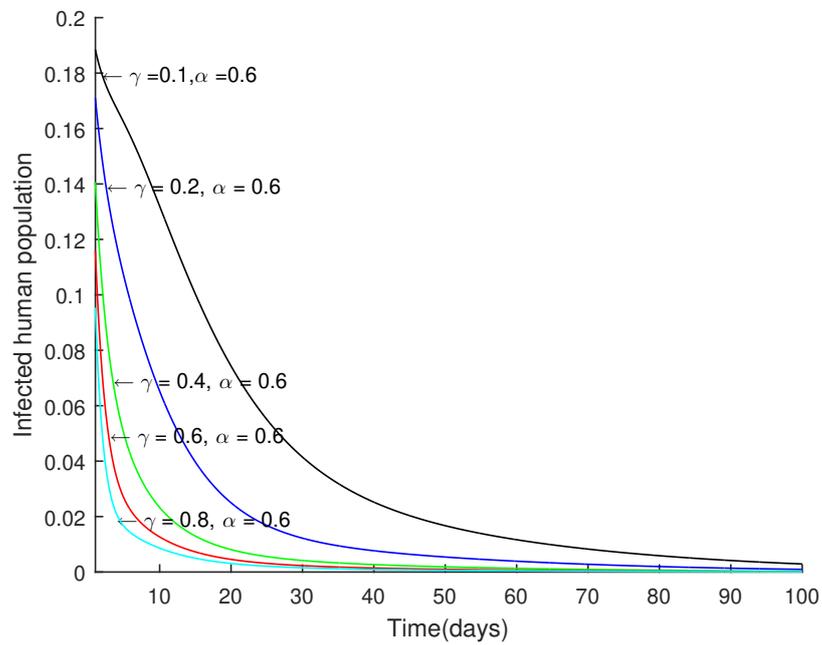Figure 54: Plot of Infected Human Population Against Time With $\gamma = 0.4$.

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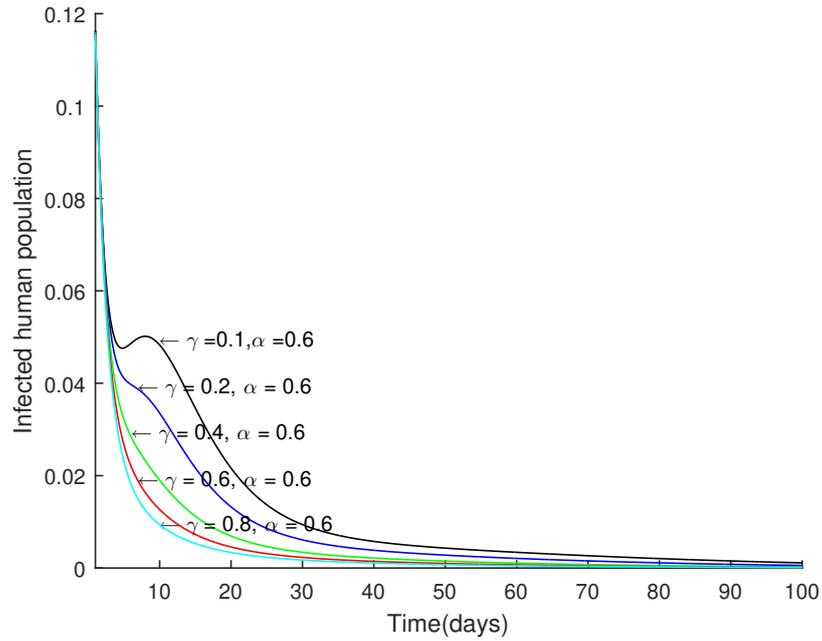
Figure 55: Plot of Infected Human Population Against Time With $\gamma = 0.6$.
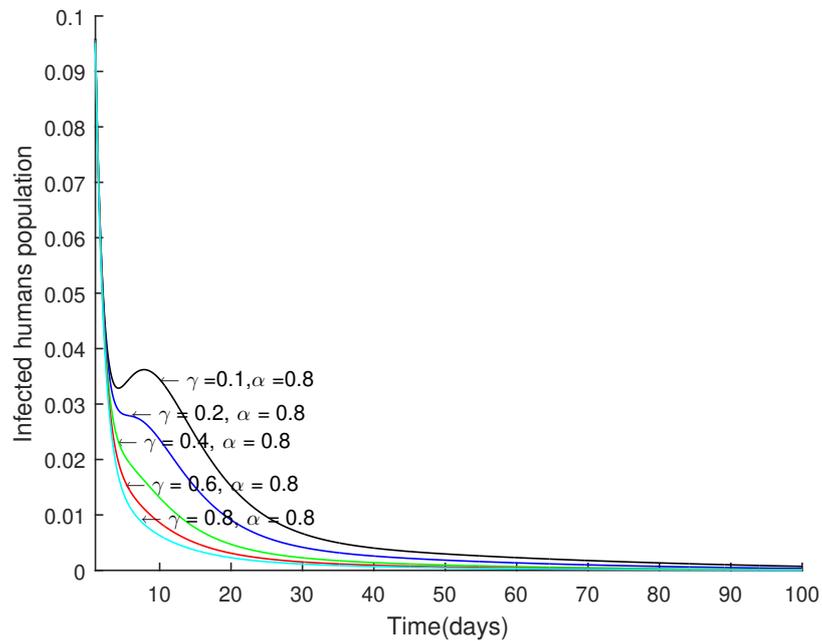
Figure 56: Plot of Infected Human Population Against Time With $\gamma = 0.8$.
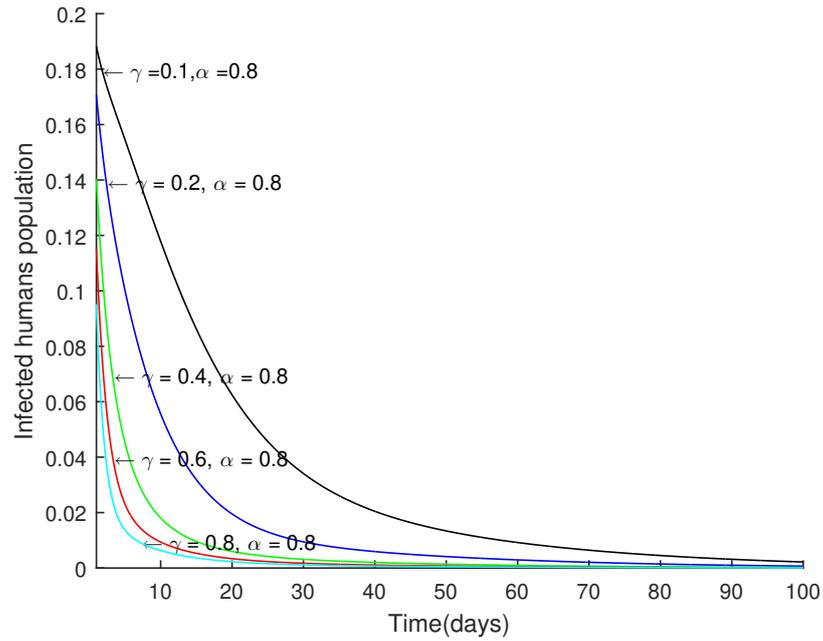
Figure 52 to Figure 56, show the effect of "prevention" on the infected human population. Holding treatment rate constant at 0.1, 0.2, 0.4, 0.6, and

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0.8, and varying the prevention from 0.1 to 0.8 for each fix gamma, the infected humans population dropped.
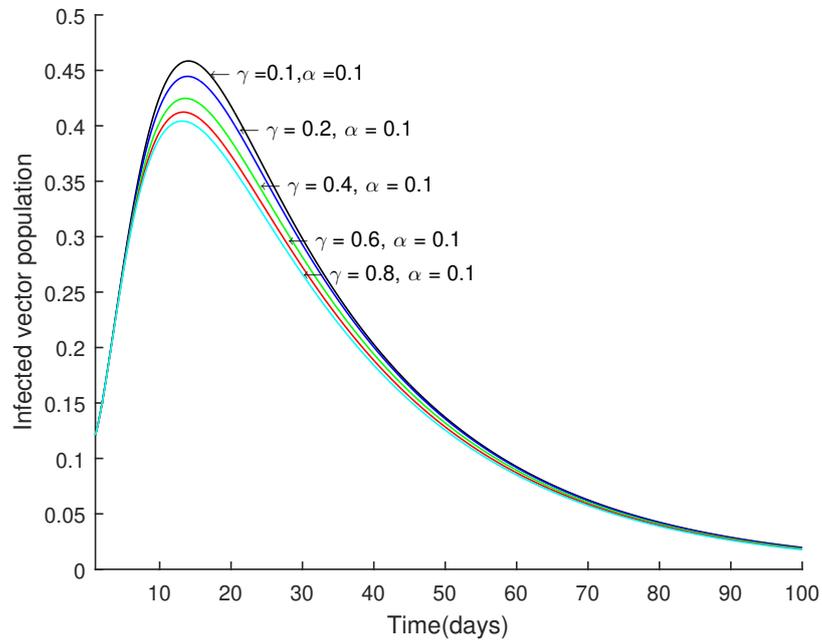
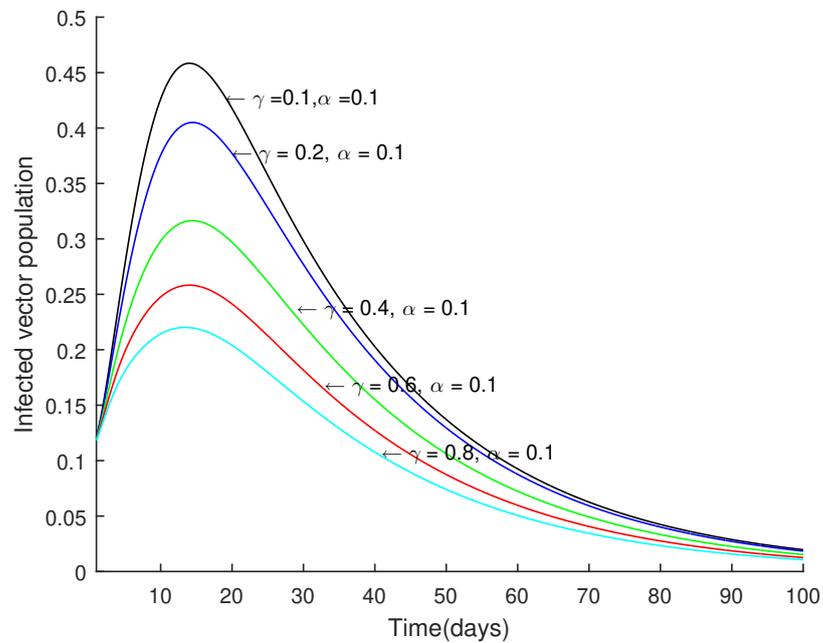Figure 57: Plot of Infected Vector Population Against Time With $\gamma = 0.1$.
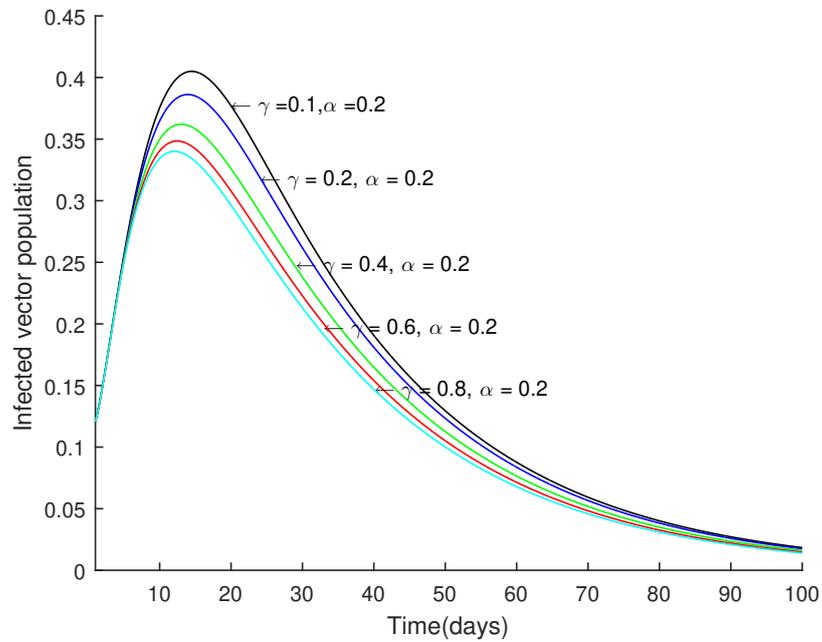
Figure 58: Plot of Infected Vector Population Against Time With $\gamma = 0.2$.

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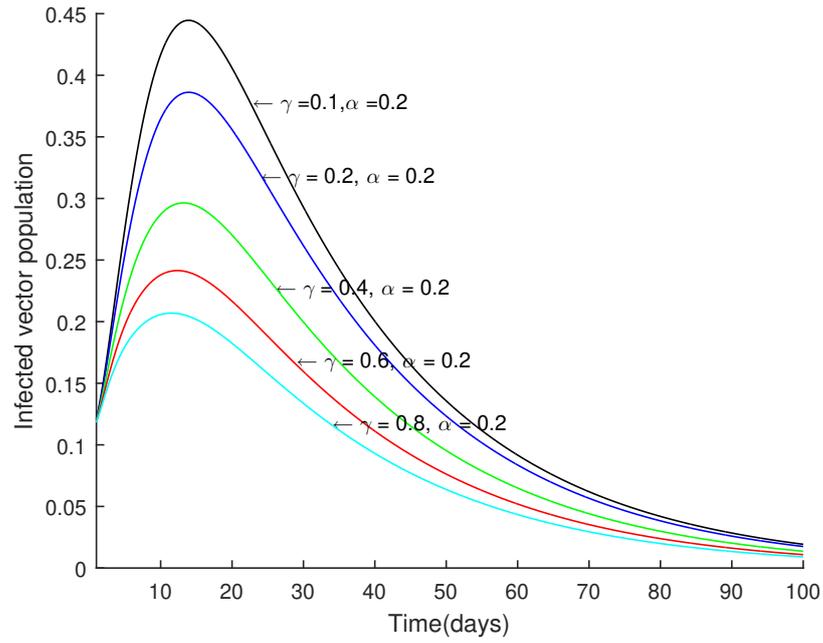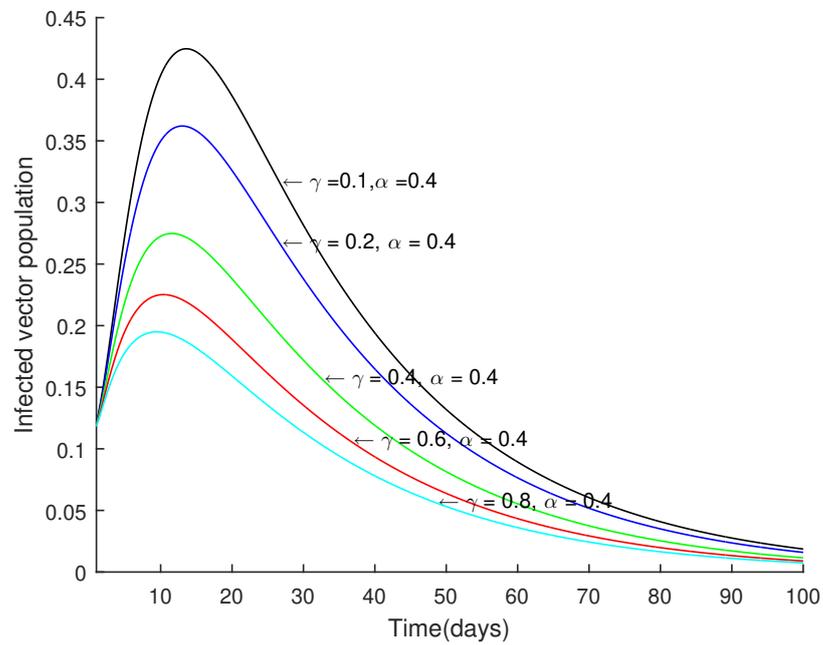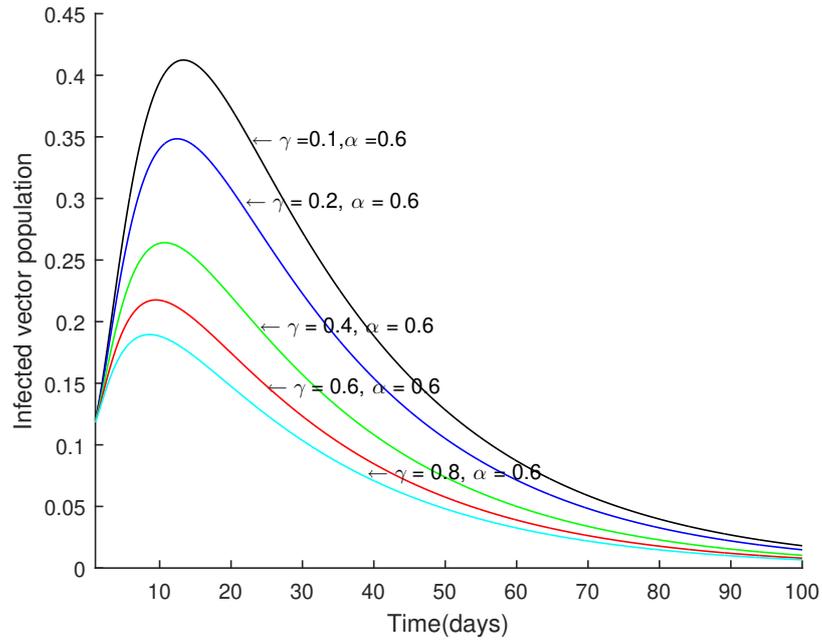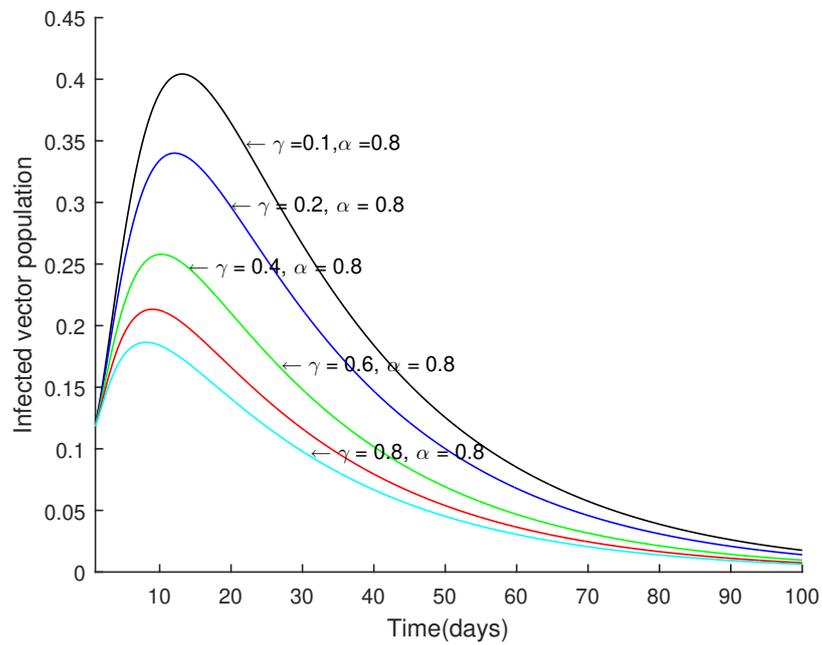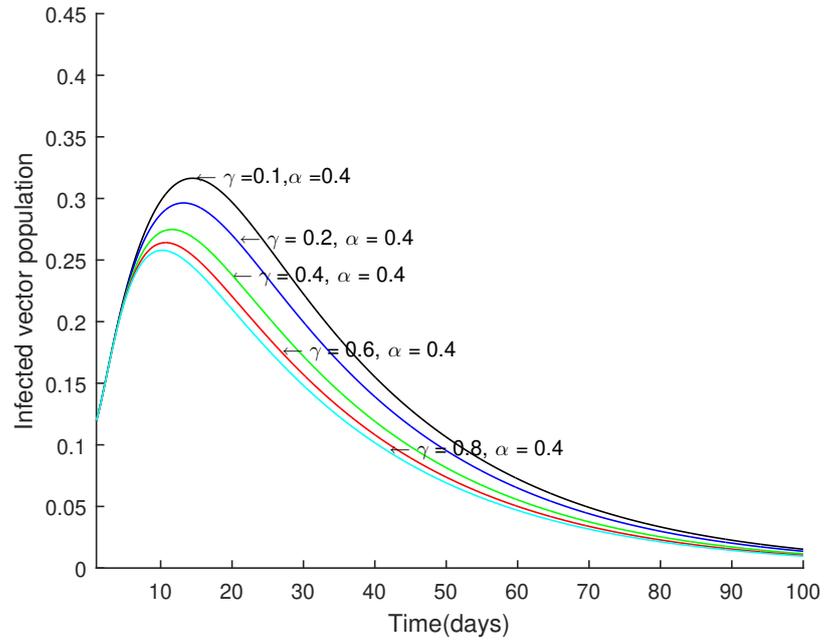
Figure 59: Plot of Infected Vector Population Against Time With γ = 0.4.
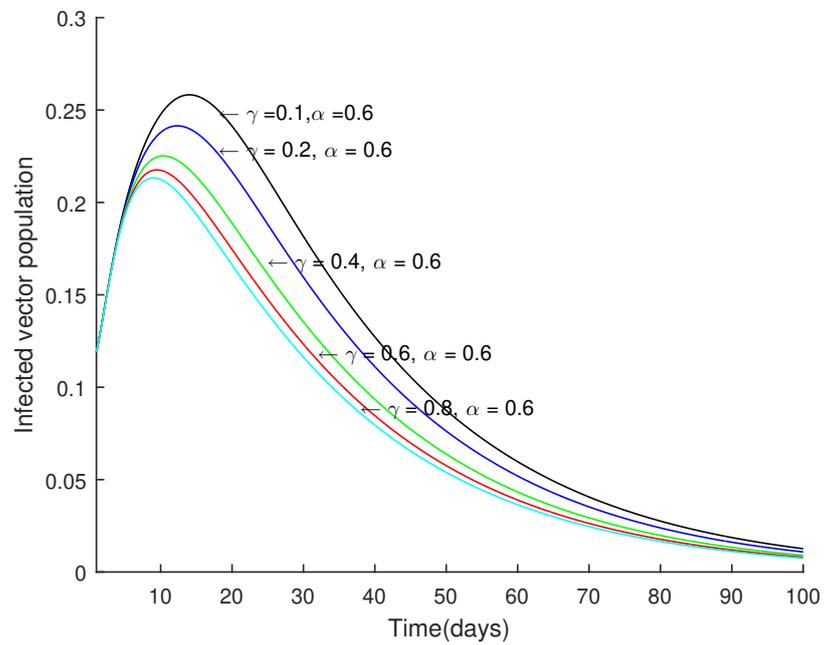
Figure 60: Plot of Infected Vector Population Against Time With γ = 0.6.

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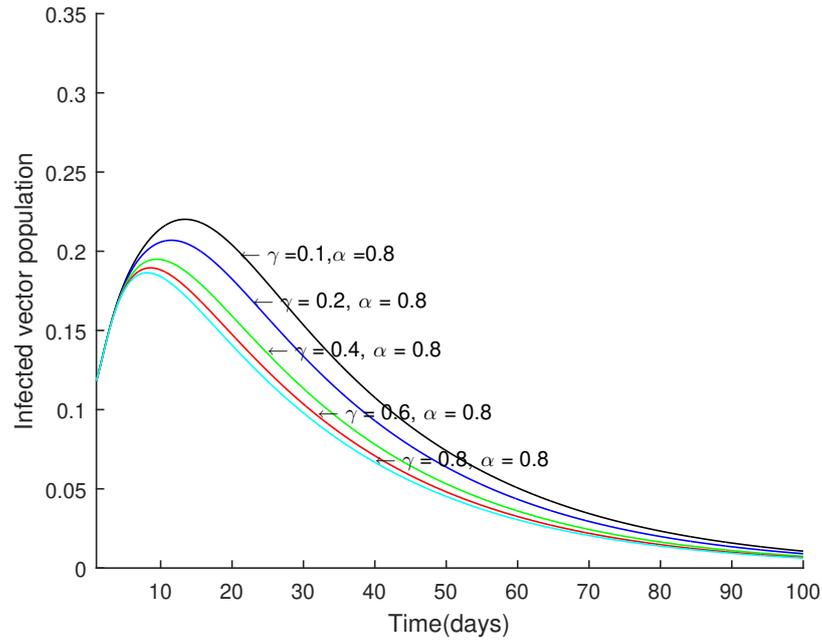
Figure 61: Plot of Infected Vector Population Against Time With γ = 0.8.

It can be observed that, $\mathcal{R}_0$ values for model (4.64) are less all the $\mathcal{R}_0$ values for model (5.3), this confirms that the model (4.64) which is malaria model with effect of prevention α with effect on the vector population gives a better result than model (5.3). Comparing Figures (17-21) to Figures (47-51) show the impact of prevention rate α on the vector population. It can be seen that for the graphs of the model (4.64, the infected population get to zero faster than the graphs of model (sevens). This means that through a concerted effort with treatment level of about 40% (that is ,if about 40% of the infected human seek proper treatment) and about 50% and above prevention rate (which is if 50% or more of the population adhere to the prevention strategies) it will help to reduce or eradicate malaria in the small neighbourhood which is the communities and country as whole.

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Chapter Summary

The parameters for the model (4.64) were estimated and the estimated parameters were used to compute for the basic reproduction and for numerical simulation. Graphs were plotted and comparisons were done between the graph of malaria model with the effect of prevention parameter on the vector to malaria model without the effect of prevention parameter on the vector. Sensitivity analysis was also done for the models considered in this thesis and the results discussed.

CHAPTER SIX

SUMMARY, CONCLUSIONS AND RECOMMENDATIONS

Overview

In this chapter, the summary and conclusion of the study is presented. Some recommendations based on the work done is also presented.

Summary

The main objective of this thesis was to formulate mathematical models of some selected infectious disease and analyse the behaviour of these models at their equilibrium point (i.e Local and Global stability analysis). A mathematical model for effective control of a vector host (malaria model) with exposed compartment was also formulated.

The main method used to analyse the local stability of the equilibrium points of epidemic models is the **Lyapunov's indirect method,** that is, to determine whether the eigenvalues of the Jacobian matrix evaluated at the equilibrium points of the system are negative or have negative real part (that is, lie in the left half of the complex plane).

Since the characteristic equation for an $n-$ dimensional system is a polynomial equation of degree n for which it may be difficult or impossible to find all roots explicitly, the Routh-Hurwitz criterion is widely used in analyzing the stability of the equilibrium point. The Routh Hurwitz criterion gives necessary and sufficient conditions for the eigenvalues to lie in the left half of the complex plane. While the Routh-Hurwitz criterion may be useful on occasion (ie small system or system of low order), it is complicated to apply in problem of many dimensions (Brauer & Castillo-Chaves, 2000). The Routh-Hurwitz condition also becomes intractable especially when the number of states exceed 3.

In this study, a corollary of Gershgorin's circle theorem (3.1) was used to establish the local stability of some selected epidemic models.

The second part of Chapter Three was devoted to investigating local stability of some general epidemic models (SIR, SEIR and SEIRS models) using a Corollary of Gershgorin's Circle Theorem. The investigation of local stability of some selected infectious diseases (an HIV/AIDS model and a Tuberculosis model) using a corollary of Gershgorin's circle theorem was also done in the latter part of the chapter. In the Chapter Four, formulation and analysis of a mathematical model to better understand the transmission and spread of a vector-host model (malaria) was done. Mathematically, malaria model without exposed compartment is formulated (that is, *SIRS* for the host population and *SI* for the vector population) and malaria model similar to that of (N. R. Chitnis, 2005) with exposed compartment (that is, *SEIRS* for the host population and *SEI* for the vector population) but there is an effect of prevention rate to the vector population were modelled. It was shown that there exists a domain where the model is epidemiologically and mathematically well-posed.

A basic reproductive number, ($\mathcal{R}_0$) was defined, which is epidemiologically accurate in that it provides the expected number of new infections (in mosquitoes or humans) from one infectious individual (human or mosquito) over the duration of the infectious period given that all other members of the population are susceptible. The basic reproduction numbers $\mathcal{R}_0(0)$ of the vector-host models without α was compared to basic reproduction numbers with α ($\mathcal{R}_0(\alpha)$). A corollary of Gershgorin's circle theorem was used to established that the disease free equilibrium is locally asymptotical stable if $\mathcal{R}_0 < 1$, which means the disease can not persist and the endemic equilibrium is also locally asymptotical stable if $\mathcal{R}_0 > 1$, which implies the disease can persist.

The conditions used by (Castillo-Chavez et al., 2002) was used to established that the disease free equilibrium is globally asymptotically stable if

$\mathcal{R}_0 < 0$. From the data on confirmed malaria cases from the Central Regional Directorate of Ghana Health Service, the unknown Parameters in the malaria model with exposed compartment were estimated. The estimated values and known values from literature for the parameters were used to perform numerical simulations using MATLAB's ode45 and sensitivity analysis of the model was also performed. Sensitivity analysis of the parameters to the basic reproduction number to known how sensitive each of the parameter in the formula for the $\mathcal{R}_0$ towards the eradication of the malaria was carried out. Conclusions were drawn based on the values of the control parameters. The values of $\mathcal{R}_0(\alpha)$ and $\mathcal{R}_0(0)$ were calculated and the two results were compared. The result showed that if proper prevention strategy (α) are adopted, the infectious disease malaria could be eradicated from our communities.

Some ways of reducing man-vector contact and treatment were looked at, that is, the right combinations of the levels of "the preventive measures program" and "treatment rate" needed to reduce or possibly eradicate the malaria.

Conclusions

A corollary of the Gershgorin's circle theorem was used to establish the local stability of different epidemic models. It was observed that no matter the state or the dimension of the system or matrix this corollary can be used to analyse local stability for both disease free and endemic equilibrium, by establishing that if $\mathcal{R}_0 < 1$, the Jacobian matrix will have negative or negative real part eigenvalues. Thus, disease free equilibrium is stable but if $\mathcal{R}_0 > 1$, the Jacobian matrix will have negative or negative real part eigenvalues making the endemic equilibrium is stable.

The comparison of the basic reproduction numbers ($\mathcal{R}_0$) of the malaria models without α to the model with α was done. It was observed that, the basic reproduction number $\mathcal{R}_0(\alpha)$ was less than $\mathcal{R}_0(0)$. This means that if the

prevention strategy stated in chapter two is followed properly, malaria will go on extinction in our communities and the country as a whole. Because from the value of $\mathcal{R}_0(0)$ if there is no prevention strategy in place, the communities as well as the regions and the country will be endemic but if right levels of prevention strategies (α) are adopted and if the estimated number of people stick to the prevention strategies, then malaria could be eradicated from our communities.

From the sensitivity analysis, for the model (4.64), the most sensitive parameter is the prevention rate $\alpha = -1.4437$, the basic number $\mathcal{R}_0$ decreases as prevention rate increases which support the claim that prevention rate has effect on both human and vector populations. The second sensitive parameter is treatment rate $\gamma = -0.9996$, the basic reproduction number $\mathcal{R}_0$, decreases as treatment increase. For the model (5.3), the most sensitive parameter is the mosquito birth rate $\lambda_v = -1.3640$, the basic reproduction number decreases as the mosquito birth rate increases. We would expect $\mathcal{R}_0$ to increase because increasing λ_v increases the number of mosquitoes. However, the mosquito birth rate is density dependent. As the birth rate increases and the number of mosquitoes increases, the death rate also increases because the environment can only support a certain number of mosquitoes. Therefore, the average lifespan of the mosquito also decreases. Mathematically, at equilibrium population size, the per capita birth rate, λ_v, is equal to the per capita death rate. Thus, at equilibrium, λ_v is also the per capita death rate; and with an exponential distribution for the death rate, $\dfrac{1}{\lambda_v}$ is the expected lifespan of the mosquitoes. As the latent period of Plasmodium in mosquitoes is of the same order as the lifespan of the mosquitoes, shortening the lifespan of the mosquito reduces the reproductive number. Thus any changes in λ_v have two opposite effects. Increasing λ_v increases the mosquitoes population which tends to increase $\mathcal{R}_0$, and also decreases the mosquito lifespan which tends to reduce $\mathcal{R}_0$. The second sensitive

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parameter is treatment rate $\gamma = -0.9990$, the basic reproduction number $\mathcal{R}_0$, decreases as treatment increase. This means that, as more infected humans are treated the disease reduces.

The sensitivity index of $\mathcal{R}_0$ with respect to the control parameter $\alpha = -0.9890$, which means alpha has a great impact on the reduction of malaria as expected. For almost all the parameters, the sign of the sensitivity indices of $\mathcal{R}_0$ (i.e., whether $\mathcal{R}_0$ increases or decreases when a parameter increases) corresponds with an intuitive expectation.

Some ways of reducing man-vector contact and treatment were carried out. It was observed that, if all "the preventive measures programme" stated are carried out properly to cover at least 40% of the entire population and around 50% or more of the infected population are diagnosed and treated early, malaria cases in these sets of closed neighbourhoods (is, the communities) and the entire region (Central Region) as well as the whole country will be brought to the barest minimum. Because from Figure 22, the infected human populations increase and it takes a longer time before it decreases, but with Figures 14 and 24, the infected human populations decrease and approach zero within the shortest possible time. For instance, from Figure 12, for $\gamma = 0.1$ and $\alpha = 0.1$, the infected human populations increase to about 0.27 before it decreases to 0.01 in more than 100 days and it still converges to the endemic equilibrium, while in Figure 16, for $\gamma = 0.8$ and $\alpha = 0.8$, the infected human populations decrease to 0 in just about 25 days. This means for $\gamma = 0.8$ and $\alpha = 0.8$, there will be no infectious humans available for susceptible mosquitoes to become infectious after 25 days of applying the stated control strategies properly.

Also, in Figure 17 for $\gamma = 0.1$ and $\alpha = 0.1$, it takes more than 100 days for the infected vector population to reduces to 0.01 whiles form Figure 16 for $\gamma = 0.8$ and $\alpha = 0.8$, it takes about 65 days for the infected vector population to reduces to 0 which is the disease free equilibrium but Figure 17 with $\gamma = 0.1$

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and $\alpha = 0.1$, converges to the endemic equilibrium. This means for $\gamma = 0.8$ and $\alpha = 0.8$, there will be no infectious vector available for susceptible human to become infected. Similarly, in Figure 27 for $\gamma = 0.1$ and $\alpha = 0.1$, it takes a longer time for the infected vector population reduces to 0.01 while it takes a shorter time in Figure 31 for $\gamma = 0.8$ and $\alpha = 0.8$, to get to 0.

Thus, the existence of mosquitoes will not necessarily increase the rate of malaria infection. Humans and mosquitoes can co-exist in the communities without malaria because mosquitoes are also needed in the food chain and may have some economical importance to human.

Different values of c were picked with fixed α value of 0.4, varying values of gamma from 0.1 to 0.8 and c from 0.1 to 0.25 and fixed gamma value of 0.4, varying values of alpha from 0.1 to 0.8 with the same c values, it was observed that, as c increases the infected vector population decreases to zero faster. For instance, from Figure 33 to Figure 36 and Figure 38 to Figure 41, as the value of c increases the vector population decreases to zero faster. Looking at Figure 33, it takes about 70 days before the vector population decreases to zero whiles in Figure 36 it takes just 42 days for the vector to decrease to zero. Similarly, in Figure 38 it takes about 45 days for the infected vector population to decrease to zero but in Figure 41 it take just 25 for the infected vector population to decrease to zero. Also, from Table 12 and Table 13, the values of $\mathcal{R}_0(\alpha)$ decreases as the value of c increases, which confirms that $c\alpha$ contribute to the death rate of mosquitoes.

Since $c\alpha$ is the proportion of preventive measure that contribute to the death rate of the vector population, it is suggested that if by concerted effort about 40% and above of the people in the closed neighbourhood (that is, the communities) apply due diligence to the preventive measures states in Chapter three and about 40% and above of the infected human are treated well, there will be no infected human to infect the mosquitoes. Also, since the mosquito's life

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expectancy is just 30, all the infected mosquitoes will die out and this will help humans and mosquitoes to co-exist in the communities without malaria. There are many places in the world such as Cape Town in South Africa and Maryland in USA where mosquitoes abound but has not yet recorded malaria cases.

Furthermore, it can seen From Figure 17 to Figure 21 and Figure 27 to Figure 31 that it takes a shorter time for the infected vector population to decrease to zero or the minimum value while from Figure 47 to Figure 51 and Figure 57 to Figure 61 it takes longer time for the infected vector population to decrease to the zero or the minimum value. These graphs show the impact of prevention rate α on the vector population.

Recommendations

From the results of this work, it is recommended that, the corollary of Gershgorin's circle theorem that gives a necessary condition for the eigenvalues to lie in the left half of the complex plane (that is, the eigenvalues of the matrix (A) are negative or have negative real part) provides a simple way out in local stability analysis. Since it does not matter the state or the dimension of the system or matrix it can be used to investigate epidemic models without struggle. Because the characteristic equation for an $n-$ dimension system is a polynomial equation of degree n for which it may be difficult or impossible to find all roots explicitly, and the Routh-Hurwitz condition also becomes intractable especially when the number of states exceed 3.

Also, Malaria eradication continues to pose a big challenge to National Malaria Control Programme in most developing countries, hence there is the need to strengthen the control strategies at hand as well as looking for some new ones, because observations from Figures 24 to 26 show that increasing clinical treatment rate has positive impact on controlling the disease because increasing

treatment rate reduces the basic reproduction. Prompt and effective diagnosis and treatment of infected individuals can avoid severe or complicated malaria and reduce malaria related deaths. Intermittent prophylactic treatment should be encouraged during pregnancy and for infants.

The prevention measures campaign should be intensified, because from Figures 14 to 16, it can be seen that increasing prevention rate also has positive impact on controlling the disease.

The prevention strategies stated in chapter two and the treatment should go hand in hand in the eradication process.

Future Work

The model will be eventually validated by applying it to malaria data of the entire country (Ghana). Bifurcation analysis to model applied to the data for the entire country will also be studied. Furthermore, application of optimal control method to obtain cost effective combinations of prevention and treatment levels is needed to control the disease that can drastically reduce the disease and possibly eradicate it.

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APPENDICES

APPENDIX A : Data and code for the Plot of Curve of Best Fit

Period Total Malaria Cases

January February March April May   June   July   August September Oct. Nov.   December

2013 82680 73049 66203 66874 77111 91850 99551 86145 74224 95954 87150 83686

2014 61574 71532 63776 51730 57725 65101 53835 52198 43329 44244 42266 42836

2015 46936 42645 51483 57158 47945 61312 71619 57932 49113 50718 51645 56601

2016 53604 46633 45839 57347 53266 59300 53888 54201 48209 56671 53185 46943

2017 48933 46285 48044 45988 57817 58930 59213 52844 44674 47190 52201 57438

Mean 58745 5602 55069 55819 58773 67299 67621 60664 51910 58955 57289 57501

function sevenODE˙lsqcurvefitFB2

clear all

function Y = Bigode(p, t)

%% y0=[2508655;0;58745;0;12540120;3780;293000];

y0=[1267369;0;58836;0;12740000;6120;90725;];

 %Initial states

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```
[T,Yv]=ode45(@sevenfun,t,y0);

%


function dY = sevenfun(t,y)

f1=p(1);

f2=p(2);


% Daily Parameters estimates

%% a1=0.000215;a2=0.007;b1=(1/17);b2=(1/18);g=0.05;


%% d1=0.0000548;d2=(1/30);e1=(0.001);e2=(1/200);r=0.2;

%

% Monthly parameter Estimates

%a1=0.00645;a2=0.21;b1=30/17;b2=30/18;g=0.05;

%d1=0.001644;d2=1;e1=0.065;e2=30/200;r=0.2;


%a1=0.00152;a2=0.21;b1=30/11;b2=30/18;g=0.04;

%d1=0.001284;e2=30/200;r=0.3;e1=0.0594;%d2=30/25;


a1=0.00152;a2=0.21;b1=30/14;b2=30/11;g=0.1;

d1=0.00128;e1=0.0594;e2=30/200;r=0.25;%d2=30/25;



N=2567700;

M=12836900;


%% N =2567369;

%% M= 2332390;
```

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```
Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);

c=0.05;

dydt = zeros (size(y));

dydt(1) = a1- f1*Sh*(Im/M) - (d1 +r)*Sh + e2*Rh;

dydt(2) = f1*Sh*(Im/M) - (b1 + d1)*Eh;

dydt(3) = b1*Eh - (g + d1 + e1)*Ih;

dydt(4) = g*Ih - (e2 +d1)*Rh +r*Sh;

dydt(5) = a2 - f2*Sm*(Ih/N) - (a2+c*r)*Sm;

dydt(6) = f2*Sm*(Ih/N) - (b2 + a2+c*r)*Em;

dydt(7) = b2*Em -( a2+c*r)*Im;

dY = dydt;

%dydt = [dydt(1); dydt(2); dydt(3);""

 dydt(4); dydt(5); dydt(6); dydt(7)];


end

Tpts=T;

Y=Yv(:,3);

sizeYv=size(Yv)

  Y˙v=Yv

end

t=[1 2 3 4 5 6 7 8 9 10 11 12]';
```

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y= [58745,56029,55069,55819, 58773,67299,''''

 67621,60664, 51910,58955,57289, 57501]';

p0=[0.8 0.5]';

[p,Rsdnrm,Rsd,ExFlg,OptmInfo,Lmda,Jmat]=''''

lsqcurvefit(@Bigode,p0,t,y);

fprintf(1,'''t''Rate Constants:''n')

for k1 = 1:length(p)

   fprintf(1, '''t''t''p(%d) = %8.5f''n', k1, p(k1))

end

P=p

normRsd=Rsdnrm

tv = linspace(min(t), max(t));

Yfit = Bigode(P, tv);

sizeYfit=size(Yfit);

Yfit˙data = Bigode(P, t)

err = Yfit˙data - y

figure(1)

plot(t, y, 'o')

hold on

hlp = plot(tv, Yfit);

hold off

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%grid

xlim([1,12])

ylim([40000,80000])

title('plot of mean of monthly data')

xlabel('Time(months)')

ylabel('infected human')

%legend(hlp, 'Y˙1(t)', 'Location','N')

legend('data','bestfit ')

figure(2)

plot(t,Yv(:,1),'r',t,Yv(:,2),'g',t,Yv(:,3),'b',t,

Yv(:,4),'y')

title('Plot of human population against time')

xlim([1,12])

xlabel('Time(years)')

ylabel('Number of People')

legend('Susceptible ','Exposed ','Infectious ',

'Recovered ',2)

figure(3)

plot(t,Yv(:,5),'r',t,Yv(:,6),'g',t,Yv(:,7),'b')

title('Plot of vector population against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of vectors')

legend('Susceptible vector ','Exposed vector',

'Infectious vector',2)

```
figure(4)

plot(t,Yv(:,1),'r')

title('Plot of susceptible human population

against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of humans')


figure(5)

plot(t,Yv(:,2),'b')

title('Plot of exposed human population

against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of humans')



figure(6)

plot(t,Yv(:,3),'y')

title('Plot of infected human population

 against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of humans')


figure(7)

plot(t,Yv(:,4),'g')

title('Plot of recovered human population
```

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against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of humans')

figure(8)

plot(t,Yv(:,5),'b')

title('Plot of susceptible vector population

 against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of vectors')

figure(9)

plot(t,Yv(:,6),'g')

title('Plot of exposed vector population

against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of vectors')

figure(10)

plot(t,Yv(:,7),'r')

title('Plot of infected vector population

 against time')

xlim([1,12])

xlabel('Time(months)')

ylabel('Number of vectors')

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%R0 = sqrt(((d1+e2)*f2*f1*a1*b2*b1)/((r+d1+e2)*""

(b1+d1)*(g+d1+e1)*(b2+a2)*a2))

end

APPENDIX B: Matlab code for Parameter Estimation

```
function sevenALL˙lsqcurvefitFBopt2


function t2c


clear all
%% format long
function Y = Bigode(p, t)
y0=p(10:16);
%% y0=[2507000;1655;58745;0;12740120;3780;93000];
%y0=[204;0;53;0;1019;3;262;];
%% y0=[1200000;800000;523565;0;11188475;1617825;
 30600];
% y0=[1750000;250000;523565;0;12188475;648425; 0];
%% y0=[1544135;500000;523565;0;10030600;2188475;
617825;];
 %%y0=[2567369;0;58836;0;12740000;6120;90725;]; ""
  %Initial states
[T,Yv]=ode45(@sevenfun,t,y0);
%


function dY = sevenfun(t,y)
%% b˙h=p(1);    Transmission rate for humans
%% b˙v=p(2);    Transmission rate for mosquitoes
%% a1=p(3);     Recruitment rate for humans
%% a2=p(4);     Recruitment rate for mosquitoes
%% b1=p(5);     Progression rate for humnas
```

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%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

N=1;

M=1;

%

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);

%

p(3)= 0.000047467;

%% p(3)=0.0217/(360);

%%indexmundi(2017 est) 29/03/2019

p(4)=0.04;

p12=0.0002373;

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

p10=1/(180);

p11=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

% p(4)=1/30;

c=0.05;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p11 +p(7))*Sh + p10*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p11)*Eh;

dydt(3) = p(5)*Eh - (p(8) + p11 + p(9))*Ih;

dydt(4) = p(8)*Ih - (p10+p11)*Rh +p(7)*Sh;

%%dydt(5) = p(4)*M- p(2)*Sm*(Ih/N) - p(4)*Sm;

dydt(5) = p12 - p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em - (p(4)+c*p(7))*Im;

dY = dydt;

end

Tpts=T;

Y=Yv(:,3);

sizeYv=size(Yv)

  Y˙v=Yv

end

y=(1.0e+05/2567700) *[5.2356 5.5507 5.8657 6.286295 6.70685 ""

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7.127405 7.54796 7.831035...

   8.1141 8.466846 8.819582 9.172318 9.525054 9.87779 ""

   8.9960 9.201738...

   8.525686 7.849634 7.173582 6.49755 6.3853 6.2731 6.2785...

   6.2838 6.2307 6.1776]';

% Initial parameter guesses

% [p(1) P(2) p(3) p(4) p(5) p(6) p(7) p(8) p(9) p(10) p(11) p(12)];

% [b˙h b˙v a1   a2   b1   b2   c   r   e1   e2   d1   d2]

%

%format long

%y0=[1750000 250000 523565 0 12188475 648425 0];

pt0 = [p0 y0]';

%lb=[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0]';

%ub=[1 1 1 1 1 1 1 1 1 2.6*10^6 10^6 10^6 10^6 13*10^6

 10^6 10^6]';

lb=[0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0]';

ub=[1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1]';

[p,Rsdnrm,Rsd,ExFlg,OptmInfo,Lmda,Jmat]=lsqcurvefit""

(@Bigode,pt0,t,y,lb,ub);

P=p

fprintf(1,'"tRate Constants:"n')

for k1 = 1:length(P)

```
    fprintf(1, '"t"tP(%d) = %8.6f'n', k1, P(k1))
end
sizeRsd = size(Rsd)

Residual=Rsd
tv = linspace(min(t), max(t));
Yfit = Bigode(P, tv);
size˙tv= size(tv)
size˙Yfit=size(Yfit)
Yfit˙data = Bigode(P, t)
err = Yfit˙data - y
normRsd=Rsdnrm

figure(1)
plot(t, y, 'o')
hold on
hlp = plot(tv, Yfit);
hold off
%grid
xlim([1,26])
%ylim([50000,68000])
title('plot of mean of monthly data')
xlabel('Time(months)')
ylabel('infected')
%legend(hlp, 'Y˙1(t)', 'Location','N')
legend('data','bestfit ')

figure(2)
```

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% plot(tv,Yfit(:,1),'r',tv,Yfit(:,2),'g',tv,Yfit(:,3),'''

'b',tv,Yfit(:,4),'k')

plot(t,Yv(:,1),'r',t,Yv(:,2),'g',t,Yv(:,3),'b',

t,Yv(:,4),'y')

title('Plot of human populations against time')

xlim([1,26])

%ylim([40000,3000000])

xlabel('Time(years)')

ylabel('Humna Populations')

legend('Susceptible ','Exposed ','Infectious ',

'Recovered ',2)

figure(3)

%% plot(tv,Yfit(:,5),'r',tv,Yfit(:,6),'g',

tv,Yfit(:,7),'b')

plot(t,Yv(:,5),'r',t,Yv(:,6),'g',t,Yv(:,7),'b')

title('Plot of vector population against time')

xlim([1,26])

%ylim([40000,13000000])

xlabel('Time(months)')

ylabel('Vector Populations')

legend('Susceptible vector ','Exposed vector','''

'Infectious vector',2)

figure(4)

plot(t,Yv(:,1),'r')

title('Plot of susceptible human population

against time')

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xlim([1,26])

xlabel('Time(months)')

ylabel('Number of humans')

figure(5)

plot(t,Yv(:,2),'b')

title('Plot of exposed human population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of humans')

figure(6)

plot(t,Yv(:,3),'g')

title('Plot of infected human population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of humans')

figure(7)

plot(t,Yv(:,4),'k')

title('Plot of recovered human population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of humans')

figure(8)

plot(t,Yv(:,5),'b')

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title('Plot of susceptible vector population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of vectors')

figure(9)

plot(t,Yv(:,6),'m')

title('Plot of exposed vector population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of vectors')

figure(10)

plot(t,Yv(:,7),'g')

title('Plot of infected vector population against time')

xlim([1,26])

xlabel('Time(months)')

ylabel('Number of vectors')

% Calculate R˙0

P(10)=1/(200);

P(11)=1/(63.5*365);

P(12)=1/30;

b˙h=P(1); b˙v=P(2); a1=P(3); a2=P(4); b1=P(5); b2=P(6);

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c=P(7); r=P(8); e1=P(9); e2=P(10); d1=P(11); d2=P(12);

R0 = sqrt((((d1+e2)*b˙h*b˙v*a1*b2*b1)/((r+d1+e2)*““

(b1+d1)*(c+d1+e1)*(b2+a2)*a2))

end

190

APPENDIX C: Simulations

format long

tspan =1:180;

%%y0=[1200000;800000;523565;0;9648380;""

1617825;1570695];

%y0=[2414793;172179;515271;1000000;12999030;""

1504;233168;];

%y0=[0.709817;0.265597;0.206593;0.405566;0.966447;""

0.089243;0.000113;];

%y0=[0.989062;0.187707;0.207499;0.346842;0.998910;""

0.000079;0.067232;];

%y0=[0.709817;0.265597;0.206593;0.405566;0.966447;""

0.089243;0.000113;];

%y0=[0.95;0;0.05;0;0.98;0;0.02;];

y0=[0.7961 0 0.2039 0 0.89 0 0.11];

% Integrate the ODEs with the optimal parameter values

[t,y] = ode45(@cg514,tspan,y0,[])

%lsqcurvefit

%loading data

%y=[523565 586574 754796 811411 987779 649753 627307

 628384 617765];

%I=x(2:end,3) - data';

%p(7) = 0.1;

%p(8) = 0.1;

tspan = (0:.1:180);

t˙vals = (1:180);

191

```
figure(1)

plot(t,y(:,1),'r',t,y(:,2),'g',t,y(:,3),'b',t,y(:,4),'k')

%title('Plot of human population against time')

xlim([1,180])

%xlim([1,365])

%ylim(0,1])

xlabel('Time(days)')

ylabel('human populations')

legend('Susceptible ','Exposed ','Infectious ','Recovered ',2)


figure(2)

plot(t,y(:,5),'r',t,y(:,6),'g',t,y(:,7),'b')

%title('Plot of vector population against time')

xlim([1,180])

%ylim(0,1])

%xlim([1,365])

%ylim([40000,13000000])

xlabel('Time(days)')

ylabel('vector population')

legend('Susceptible vector ','Exposed vector','Infectious vector',2)


figure(3)

plot(t,y(:,1),'r')

%title('Plot of susceptible human""

 population against time')

%xlim([1,365])

xlim([1,180])
```

192

%ylim([0,1])

xlabel('Time(days)')

ylabel('susceptible human population')

figure(4)

plot(t,y(:,2),'b')

%title('Plot of exposed human population against time')

%xlim([1,365])

xlim([1,180])

%ylim([0,1])

xlabel('Time(days)')

ylabel('exposed human population')

figure(5)

plot(t,y(:,3),'k')

%title('Plot of infected human ""

population against time')

%xlim([1,365])

xlim([1,180])

%ylim([0,1])

%ylim([0,0.35])

xlabel('Time(days)')

ylabel('infected human population')

figure(6)

plot(t,y(:,4),'g')

```
%title('Plot of recovered human ""

population against time')

%xlim([1,365])

xlim([1,180])

xlabel('Time(days)')

ylabel('recovered human population')


figure(7)

plot(t,y(:,5),'b')

%title('Plot of susceptible vector ""

population against time')

%xlim([1,365])

xlim([1,180])

xlabel('Time(days)')

ylabel('susceptible vector population')


figure(8)

plot(t,y(:,6),'g')

%title('Plot of exposed vector ""

population against time')

%xlim([1,365])

xlim([1,180])

xlabel('Time(days)')

ylabel('exposed vector population')


figure(9)

plot(t,y(:,7),'r')

%title('Plot of infected vector ""
```

194

population against time')

xlim([1,180])

%xlim([1,365])

xlabel('Time(days)')

ylabel('infected vector population')

figure(10)

plot(t,y(:,1),'r',t,y(:,2),'g',t,y(:,3),'''

'b',t,y(:,4),'k',t,y(:,5),'y',t,y(:,6),'m',t,y(:,7),'c')

%title('Plot of all solutions')

%xlim([1,365])

xlim([1,180])

%ylim([40000,3000000])

xlabel('Time(days)')

ylabel('all populations')

legend('Susceptible host ','Exposed host','''

'Infectious host','Recovered host', 'Susceptible vector''''

','Exposed vector ','Infectious vector',2)

195

APPENDIX D: Matlab code for the Plot of fixed alpha and varying gamma

Matlab code for the plot of infected human""

and vector population against time with""

fixed values of alpha and varying gamma values""

format long

tspan =1:360;

%y0=[0.722376;0.269204;0.204495;0.277203;...

0.962685;0.151393;0.003099;];

%y0=[2177829;160723;516646;1000000;12579547;

0;333719;];

%y0=[2414793;172179;515271;1000000;12999030;

1504;233168;];

%y0=[0.709817;0.265597;0.206593;0.405566;

0.966447;0.089243;0.000113;];

%y0=[0.7961 0 0.2039 0 0.89 0 0.11];

%y0=[0.95;0;0.05;0;0.98;0;0.02;];

y0=[0.7961 0 0.2039 0 0.89 0 0.11];

% Integrate the ODEs with the optimal

parameter values

tspan = (0:.1:100);

t˙vals = (1:100);

figure(1)

[t,y] = ode45(@c11,tspan,y0,[])

196

```
plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.1';

%txt = '"leftarrow gamma = 1';

text(17,0.24,txt)

%title('infected human population

against time with varying gamma and constant

 alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected human population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c12,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(12,0.15,txt)

%m(1).color='red';

plot(t,y(:,3),'b')


%hold on

%[t,y] = ode45(@c13,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

%text(12,0.1,txt)
```

197

```
%m(1).color='red';

%plot(t,y(:,3),'m')



hold on

[t,y] = ode45(@c14,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(13,0.07,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c16,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(10,0.05,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)



hold on

[t,y] = ode45(@c18,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(19,0.02,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off
```

```
figure(2)

[t,y] = ode45(@c11,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.1';

%txt = '"leftarrow gamma = 1';

text(15,0.43,txt)

%title('infected human population

against time with varying gamma and constant

alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c12,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(15,0.38,txt)

%m(1).color='red';

plot(t,y(:,7),'b')


%hold on

%[t,y] = ode45(@c13,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.1';
```

```
%txt = '"leftarrow gamma = 1';

%text(18,0.32,txt)

%m(1).color='red';

%plot(t,y(:,7),'m')




hold on

[t,y] = ode45(@c14,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(24,0.24,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c16,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(28,0.17,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)



hold on

[t,y] = ode45(@c18,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(36,0.11,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)
```

200

figure(3)

[t,y] = ode45(@c21,tspan,y0,[])

plot(t,y(:,3),'k')

txt='''leftarrow ''gamma =0.1,''alpha =0.2';

%txt = '''leftarrow gamma = 1';

text(13,0.2,txt)

%title('infected human population

against time with varying gamma and constant

alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.25])

xlabel('Time(days)')

ylabel('Infected human population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@c22,tspan,y0,[])

txt='''leftarrow ''gamma = 0.2, ''alpha = 0.2';

%txt = '''leftarrow gamma = 1';

text(2,0.15,txt)

%m(1).color='red';

plot(t,y(:,3),'b')

201

```
%hold on

%[t,y] = ode45(@c23,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

%text(4,0.1,txt)

%m(1).color='red';

%plot(t,y(:,3),'m')




hold on

[t,y] = ode45(@c24,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(5,0.07,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c26,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(12,0.03,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)




hold on

[t,y] = ode45(@c28,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';
```

```
text(16,0.015,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off


figure(4)

[t,y] = ode45(@c21,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.2';

%txt = '"leftarrow gamma = 1';

text(16,0.38,txt)

%title('infected human population

against time with varying gamma and constant

alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

%ylim([0,0.5])

xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c22,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(17,0.32,txt)
```

```
%m(1).color='red';

plot(t,y(:,7),'b')


%hold on

%[t,y] = ode45(@c23,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

%text(18,0.27,txt)

%m(1).color='red';

%plot(t,y(:,7),'m')



hold on

[t,y] = ode45(@c24,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(19,0.23,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c26,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(22,0.17,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on
```

```
[t,y] = ode45(@c28,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(26,0.12,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)



%figure(5)

%[t,y] = ode45(@c31,tspan,y0,[])

%plot(t,y(:,3),'k')

%txt='"leftarrow "gamma =0.1,"alpha =0.3';

%txt = '"leftarrow gamma = 1';

%text(9,0.18,txt)

%title('infected human population

 against time with varying gamma and constant

 alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

%xlim([1,100])

%xlabel('Time(days)')

%ylabel('Infected human population')


%legend('v=0.1',2)

%hold on

%[t,y] = ode45(@c32,tspan,y0,[])

%txt='"leftarrow "gamma = 0.2, "alpha = 0.3';
```

```
%txt = '"leftarrow gamma = 1';

%text(2,0.15,txt)

%m(1).color='red';

%plot(t,y(:,3),'b')


%hold on

%[t,y] = ode45(@c33,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(2,0.12,txt)

%m(1).color='red';

%plot(t,y(:,3),'m')



%hold on

%[t,y] = ode45(@c34,tspan,y0,[])

%txt='"leftarrow "gamma = 0.4, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(6,0.06,txt)

%plot(t,y(:,3),'g')

%legend('v=0.3',2)

%hold on

%[t,y] = ode45(@c36,tspan,y0,[])

%txt='"leftarrow "gamma = 0.6, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(4,0.04,txt)

%plot(t,y(:,3),'r')

%legend('v=0.4',2)
```

206

```
%hold on

%[t,y] = ode45(@c38,tspan,y0,[])

%txt='"leftarrow "gamma = 0.8, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(9,0.02,txt)

%plot(t,y(:,3),'c')

%legend('v=0.4',2)

%hold off


%figure(6)

%[t,y] = ode45(@c31,tspan,y0,[])

%plot(t,y(:,7),'k')

%txt='"leftarrow "gamma =0.1,"alpha =0.3';

%txt = '"leftarrow gamma = 1';

%text(15,0.35,txt)

%title('infected human population against time

with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

%xlim([1,100])

%xlabel('Time(days)')

%ylim([0,0.5])

%ylabel('Infected vector population')


%legend('v=0.1',2)

%hold on
```

207

```
%[t,y] = ode45(@c32,tspan,y0,[])

%txt='"leftarrow "gamma = 0.2, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(16,0.29,txt)

%m(1).color='red';

%plot(t,y(:,7),'b')


%hold on

%[t,y] = ode45(@c33,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(17,0.24,txt)

%m(1).color='red';

%plot(t,y(:,7),'m')



%hold on

%[t,y] = ode45(@c34,tspan,y0,[])

%txt='"leftarrow "gamma = 0.4, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(19,0.2,txt)

%plot(t,y(:,7),'g')

%legend('v=0.3',2)

%hold on

%[t,y] = ode45(@c36,tspan,y0,[])

%txt='"leftarrow "gamma = 0.6, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(22,0.14,txt)
```

208

```
%plot(t,y(:,7),'r')

%legend('v=0.4',2)


%hold on

%[t,y] = ode45(@c38,tspan,y0,[])

%txt='"leftarrow "gamma = 0.8, "alpha = 0.3';

%txt = '"leftarrow gamma = 1';

%text(26,0.1,txt)

%plot(t,y(:,7),'c')

%legend('v=0.4',2)



figure(5)

[t,y] = ode45(@c41,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(7,0.17,txt)

%title('infected human population

 against time with varying gamma and

 constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected human population')
```

209

```
%legend('v=0.1',2)

hold on

[t,y] = ode45(@c42,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(2,0.15,txt)

%m(1)8olor='red';

plot(t,y(:,3),'b')


%hold on

%[t,y] = ode45(@c43,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

%text(2,0.12,txt)

%m(1).color='red';

%plot(t,y(:,3),'m')



hold on

[t,y] = ode45(@c44,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(3,0.09,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c46,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.4';
```

210

```
%txt = '"leftarrow gamma = 1';

text(3,0.06,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@c48,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(7,0.02,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off


figure(6)

[t,y] = ode45(@c41,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.4';

%txt = '"leftarrow gamma = 1';

text(15,0.32,txt)

%title('infected human population

against time with varying gamma and

constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.45])
```

211

```
xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c42,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(15,0.27,txt)

%m(1).color='red';

plot(t,y(:,7),'b')


%hold on

%[t,y] = ode45(@c43,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

%text(17,0.21,txt)

%m(1).color='red';

%plot(t,y(:,7),'m')



hold on

[t,y] = ode45(@c44,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(21,0.16,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)
```

212

```
hold on

[t,y] = ode45(@c46,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(23,0.11,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@c48,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(31,0.06,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)


figure(7)

[t,y] = ode45(@c61,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.6';

%txt = '"leftarrow gamma = 1';

text(2,0.18,txt)

%title('infected human population

against time with varying gamma and

constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;
```

213

```
xlim([1,100])

xlabel('Time(days)')

ylabel('Infected human population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c62,tspan,y0,[])

txt='''leftarrow "gamma = 0.2, "alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(2.5,0.14,txt)

%m(1).color='red';

plot(t,y(:,3),'b')


%hold on

%[t,y] = ode45(@c63,tspan,y0,[])

%txt='''leftarrow "gamma = 0.3, "alpha = 0.6';

%%txt = '''leftarrow gamma = 1';

%text(3,0.1,txt)

%%m(1).color='red';

%plot(t,y(:,3),'m')



hold on

[t,y] = ode45(@c64,tspan,y0,[])

txt='''leftarrow "gamma = 0.4, "alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(3.5,0.07,txt)

plot(t,y(:,3),'g')
```

214

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c66,tspan,y0,[])

txt='''leftarrow ''gamma = 0.6, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(3,0.05,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@c68,tspan,y0,[])

txt='''leftarrow ''gamma = 0.8, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(4,0.02,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off

figure(8)

[t,y] = ode45(@c61,tspan,y0,[])

plot(t,y(:,7),'k')

txt='''leftarrow ''gamma =0.1,''alpha =0.6';

%txt = '''leftarrow gamma = 1';

text(12,0.29,txt)

%title('infected human population

 against time with varying gamma and

 constant alpha = 0.1')

%xlim([1,365])

215

```
%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@c62,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(13,0.24,txt)

%m(1).color='red';

plot(t,y(:,7),'b')


%hold on

%[t,y] = ode45(@c63,tspan,y0,[])

%txt='"leftarrow "gamma = 0.3, "alpha = 0.6';

%%txt = '"leftarrow gamma = 1';

%text(14,0.20,txt)

%%m(1).color='red';

%plot(t,y(:,7),'m')



hold on

[t,y] = ode45(@c64,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';
```

216

```
text(16.5,0.15,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c66,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(19.5,0.1,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@c68,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(25,0.06,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)




figure(9)

[t,y] = ode45(@c81,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.8';

%txt = '"leftarrow gamma = 1';

text(2,0.18,txt)

%title('infected human population against
```

217

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected humans population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@c82,tspan,y0,[])

txt='''leftarrow "gamma = 0.2, "alpha = 0.8';

%txt = '''leftarrow gamma = 1';

text(2.5,0.14,txt)

%m(1).color='red';

plot(t,y(:,3),'b')

%hold on

%[t,y] = ode45(@c83,tspan,y0,[])

%txt='''leftarrow "gamma = 0.3, "alpha = 0.8';

%%txt = '''leftarrow gamma = 1';

%text(2.5,0.11,txt)

%%m(1).color='red';

%plot(t,y(:,3),'m')

hold on

[t,y] = ode45(@c84,tspan,y0,[])

218

```
txt='"leftarrow "gamma = 0.4, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(3.5,0.07,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c86,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(3.5,0.04,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@c88,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(7.5,0.01,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off


figure(10)

[t,y] = ode45(@c81,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.8';

%txt = '"leftarrow gamma = 1';

text(12,0.25,txt)
```

219

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.35])

xlabel('Time(days)')

ylabel('Infected vector population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@c82,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(13.5,0.2,txt)

%m(1).color='red';

plot(t,y(:,7),'b')

hold on

[t,y] = ode45(@c83,tspan,y0,[])

txt='"leftarrow "gamma = 0.3, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(16,0.15,txt)

%m(1).color='red';

plot(t,y(:,7),'m')

220

hold on

[t,y] = ode45(@c84,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(18,0.11,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@c86,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(21,0.07,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@c88,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(30,0.03,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)

function dY = c11(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

221

```
%% a1=p(3);      Recruitment rate for humans

%% a2=p(4);      Recruitment rate for mosquitoes

%% b1=p(5);      Progression rate for humnas

%% b2=p(6);      Progression rate for mosquitoes

%% c=p(7);       vaccination rate

%% r=p(8);       Recovery rate

%% e1=p(9);      Disease induced death rate

%% e2=p(10);     Loss of immunity

%% d1=p(11);     Natural death rate for humans

%% d2=p(12);     Natural death rate for mosquitoes


%N=2567700;

%M=12836900;


N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;
```

```
%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);


c=0.05;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;
```

223

p(6) = 0.291499;

p(7) = 0.1;

p(8) = 0.1;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05

 0.2 0.0026 1/200 1/(63.5*365)]';

function dY = c12(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

224

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);

%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

225

```
%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);


c=0.05;


%p(12)=0.03;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;
```

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

p(7) = 0.1;

p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 0.2

 0.0026 1/200 1/(63.5*365)]';

function dY = c14(t,y)

227

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);

%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

228

```
%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);


c=0.05;

p(7) = 0.1;

    p(8)=0.4;

%c=0.01;
```

229

%p(12)=0.03;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

230

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091

0.05 0.2 0.0026 1/200 1/(63.5*365)]';

function dY = c16(t,y)

%% bˑh=p(1);   Transmission rate for humans

%% bˑv=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

```
Em=y(6);

Im=y(7);


%p(3)=3.1./(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

%p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);
```

232

c=0.05;

p(7) = 0.1;

p(8) = 0.6;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 0.2

0.0026 1/200 1/(63.5*365)]';

function dY = c18(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

```
Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);
```

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%p(11)=1/(63.5*365);

c=0.05;

p(7) = 0.1;

p(8) = 0.8;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

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dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 0.2

0.0026 1/200 1/(63.5*365)]';

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APPENDIX E: Matlab code for the Plot of fixed gamma and varying alpha

format long

tspan =1:360;

%y0=[0.722376;0.269204;0.204495;0.277203;0.962685;

0.151393;0.003099;];

%y0=[2177829;160723;516646;1000000;12579547;

0;333719;];

%y0=[2414793;172179;515271;1000000;12999030;

1504;233168;];

%y0=[0.709817;0.265597;0.206593;0.405566;

0.966447;0.089243;0.000113;];

%y0=[0.7961 0 0.2039 0 0.89 0 0.11];

%y0=[0.95;0;0.05;0;0.98;0;0.02;];

y0=[0.7961 0 0.2039 0 0.89 0 0.11];

% Integrate the ODEs with the optimal

parameter values

tspan = (0:.1:100);

t˙vals = (1:100);

figure(1)

[t,y] = ode45(@cg11,tspan,y0,[])

plot(t,y(:,3),'k')

txt='˙"leftarrow "gamma =0.1,"alpha =0.1';

%txt = '˙"leftarrow gamma = 1';

238

text(21,0.2,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected human population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg12,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(12,0.15,txt)

%m(1).color='red';

plot(t,y(:,3),'b')

hold on

[t,y] = ode45(@cg14,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(9,0.08,txt)

plot(t,y(:,3),'g')

239

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg16,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(10,0.05,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@cg18,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(18,0.02,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off

figure(2)

[t,y] = ode45(@cg11,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.1';

%txt = '"leftarrow gamma = 1';

text(18,0.4,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

240

```
%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg12,tspan,y0,[])

txt='''leftarrow ''gamma = 0.2, ''alpha = 0.1';

%txt = '''leftarrow gamma = 1';

text(19,0.35,txt)

%m(1).color='red';

plot(t,y(:,7),'b')




hold on

[t,y] = ode45(@cg14,tspan,y0,[])

txt='''leftarrow ''gamma = 0.4, ''alpha = 0.1';

%txt = '''leftarrow gamma = 1';

text(23,0.25,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg16,tspan,y0,[])

txt='''leftarrow ''gamma = 0.6, ''alpha = 0.1';

%txt = '''leftarrow gamma = 1';

text(26,0.19,txt)
```

241

```
plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg18,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.1';

%txt = '"leftarrow gamma = 1';

text(31,0.13,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)



figure(3)

[t,y] = ode45(@cg21,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.2';

%txt = '"leftarrow gamma = 1';

text(12,0.15,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.25])

xlabel('Time(days)')

ylabel('Infected human population')
```

242

```
%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg22,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(10,0.12,txt)

%m(1).color='red';

plot(t,y(:,3),'b')




hold on

[t,y] = ode45(@cg24,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(14,0.06,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg26,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(18,0.03,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg28,tspan,y0,[])
```

243

txt='"leftarrow "gamma = 0.8, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(28,0.01,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off

figure(4)

[t,y] = ode45(@cg21,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.2';

%txt = '"leftarrow gamma = 1';

text(19,0.35,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

%ylim([0,0.5])

xlabel('Time(days)')

ylabel('Infected vector population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg22,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

244

text(19,0.3,txt)

%m(1).color='red';

plot(t,y(:,7),'b')

hold on

[t,y] = ode45(@cg24,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(22,0.20,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg26,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(26,0.12,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@cg28,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.2';

%txt = '"leftarrow gamma = 1';

text(34,0.05,txt)

plot(t,y(:,7),'c')

245

%legend('v=0.4',2)

figure(5)

[t,y] = ode45(@cg41,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(10,0.078,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.16])

xlabel('Time(days)')

ylabel('Infected human population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg42,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(8,0.06,txt)

%m(1)8olor='red';

246

```
plot(t,y(:,3),'b')



hold on

[t,y] = ode45(@cg44,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(11,0.03,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg46,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(11,0.02,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg48,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(15,0.01,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off
```

247

```
figure(6)

[t,y] = ode45(@cg41,tspan,y0,[])

plot(t,y(:,7),'k')

txt='''leftarrow "gamma =0.1,"alpha =0.4';

%txt = '''leftarrow gamma = 1';

text(17,0.29,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.45])

xlabel('Time(days)')

ylabel('Infected vector population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg42,tspan,y0,[])

txt='''leftarrow "gamma = 0.2, "alpha = 0.4';

%txt = '''leftarrow gamma = 1';

text(16,0.25,txt)

%m(1).color='red';

plot(t,y(:,7),'b')




hold on
```

248

```
[t,y] = ode45(@cg44,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(22,0.15,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg46,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(24,0.1,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg48,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.4';

%txt = '"leftarrow gamma = 1';

text(30,0.05,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)


figure(7)

[t,y] = ode45(@cg61,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.6';

%txt = '"leftarrow gamma = 1';

text(9,0.05,txt)
```

```
%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.12])

xlabel('Time(days)')

ylabel('Infected human population')


%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg62,tspan,y0,[])

txt='''leftarrow ''gamma = 0.2, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(8,0.038,txt)

%m(1).color='red';

plot(t,y(:,3),'b')



hold on

[t,y] = ode45(@cg64,tspan,y0,[])

txt='''leftarrow ''gamma = 0.4, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(10,0.02,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on
```

250

[t,y] = ode45(@cg66,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(9,0.015,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@cg68,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(10,0.01,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off

figure(8)

[t,y] = ode45(@cg61,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.6';

%txt = '"leftarrow gamma = 1';

text(18,0.23,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

251

ylim([0,0.31])

xlabel('Time(days)')

ylabel('Infected vector population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg62,tspan,y0,[])

txt='''leftarrow ''gamma = 0.2, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(20,0.18,txt)

%m(1).color='red';

plot(t,y(:,7),'b')

hold on

[t,y] = ode45(@cg64,tspan,y0,[])

txt='''leftarrow ''gamma = 0.4, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(25,0.1,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg66,tspan,y0,[])

txt='''leftarrow ''gamma = 0.6, ''alpha = 0.6';

%txt = '''leftarrow gamma = 1';

text(31,0.05,txt)

plot(t,y(:,7),'r')

252

```
%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg68,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.6';

%txt = '"leftarrow gamma = 1';

text(38,0.02,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)




figure(9)

[t,y] = ode45(@cg81,tspan,y0,[])

plot(t,y(:,3),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.8';

%txt = '"leftarrow gamma = 1';

text(10,0.035,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

xlabel('Time(days)')

ylabel('Infected humans population')


%legend('v=0.1',2)
```

253

hold on

[t,y] = ode45(@cg82,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(7,0.028,txt)

%m(1).color='red';

plot(t,y(:,3),'b')

hold on

[t,y] = ode45(@cg84,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(9,0.015,txt)

plot(t,y(:,3),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg86,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(9,0.01,txt)

plot(t,y(:,3),'r')

%legend('v=0.4',2)

hold on

[t,y] = ode45(@cg88,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.8';

254

%txt = '"leftarrow gamma = 1';

text(15,0.004,txt)

plot(t,y(:,3),'c')

%legend('v=0.4',2)

hold off

figure(10)

[t,y] = ode45(@cg81,tspan,y0,[])

plot(t,y(:,7),'k')

txt='"leftarrow "gamma =0.1,"alpha =0.8';

%txt = '"leftarrow gamma = 1';

text(17,0.2,txt)

%title('infected human population against

time with varying gamma and constant alpha = 0.1')

%xlim([1,365])

%p(7) = 0.1;

%p(8) = 0.01;

xlim([1,100])

ylim([0,0.35])

xlabel('Time(days)')

ylabel('Infected vector population')

%legend('v=0.1',2)

hold on

[t,y] = ode45(@cg82,tspan,y0,[])

txt='"leftarrow "gamma = 0.2, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(19,0.16,txt)

255

```
%m(1).color='red';

plot(t,y(:,7),'b')




hold on

[t,y] = ode45(@cg84,tspan,y0,[])

txt='"leftarrow "gamma = 0.4, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(24,0.09,txt)

plot(t,y(:,7),'g')

%legend('v=0.3',2)

hold on

[t,y] = ode45(@cg86,tspan,y0,[])

txt='"leftarrow "gamma = 0.6, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(28,0.05,txt)

plot(t,y(:,7),'r')

%legend('v=0.4',2)


hold on

[t,y] = ode45(@cg88,tspan,y0,[])

txt='"leftarrow "gamma = 0.8, "alpha = 0.8';

%txt = '"leftarrow gamma = 1';

text(31,0.03,txt)

plot(t,y(:,7),'c')

%legend('v=0.4',2)
```

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```
function dY = cg11(t,y)

%% b˙h=p(1);     Transmission rate for humans

%% b˙v=p(2);     Transmission rate for mosquitoes

%% a1=p(3);      Recruitment rate for humans

%% a2=p(4);      Recruitment rate for mosquitoes

%% b1=p(5);      Progression rate for humnas

%% b2=p(6);      Progression rate for mosquitoes

%% c=p(7);       vaccination rate

%% r=p(8);       Recovery rate

%% e1=p(9);      Disease induced death rate

%% e2=p(10);     Loss of immunity

%% d1=p(11);     Natural death rate for humans

%% d2=p(12);     Natural death rate for mosquitoes


%N=2567700;

%M=12836900;


N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);
```

```
Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);
```

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c=0.05;

p(7) = 0.1;

p(8) = 0.1;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 0.2''''

 0.0026 1/200 1/(63.5*365)]';

function dY = cg12(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

```
Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;
```

261

```
%p(10)=1/(200);

%p(11)=1/(63.5*365);


c=0.05;

p(7) = 0.1;

p(8) = 0.2;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;



dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;
```

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 ""

0.2 0.0026 1/200 1/(63.5*365)]';

function dY = cg14(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

N=1;

M=1;

```
Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;
```

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%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);

c=0.05;

p(7) = 0.1;

p(8) = 0.4;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05 ""

0.2 0.0026 1/200 1/(63.5*365)]';

function dY = cg16(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

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```
N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1./(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;

%p(4) = 0.033000;
```

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```
%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);


c=0.05;

p(7) = 0.1;

p(8) = 0.6;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;



dydt = zeros (size(y));

dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;
```

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dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365) 0.033 0.1 0.091 0.05''''

 0.2 0.0026 1/200 1/(63.5*365)]';

function dY = cg18(t,y)

%% b˙h=p(1);   Transmission rate for humans

%% b˙v=p(2);   Transmission rate for mosquitoes

%% a1=p(3);   Recruitment rate for humans

%% a2=p(4);   Recruitment rate for mosquitoes

%% b1=p(5);   Progression rate for humnas

%% b2=p(6);   Progression rate for mosquitoes

%% c=p(7);   vaccination rate

%% r=p(8);   Recovery rate

%% e1=p(9);   Disease induced death rate

%% e2=p(10);   Loss of immunity

%% d1=p(11);   Natural death rate for humans

%% d2=p(12);   Natural death rate for mosquitoes

%N=2567700;

%M=12836900;

```
N=1;

M=1;

Sh=y(1);

Eh=y(2);

Ih=y(3);

Rh=y(4);

Sm=y(5);

Em=y(6);

Im=y(7);


%p(3)=3.1/(100*365);

%p(3)=2.18/(100);

%%indexmundi(2017 est) 07/2018

%p(4)=;

%p(5)=0.1;

%p(6)=0.091;

%p(7)=0.02;

%p(8)=0.7;

%p(9)=0.0035%

%p(10)=1/(200);

p(11)=1/(63.5*365);

% p(11)=1/(63.5);

%%WHO2018 07/10/2018

%p(4)=1/30;

%p(1) = 0.015472;

%p(2) = 0.049326;

%p(3) = 0.000085;
```

%p(4) = 0.033000;

%p(5) = 0.360425;

%p(6) = 0.000538;

%p(7) = 0.021030;

%p(8) = 0.120961;

%p(9) = 0.000002;

%p(10)=1/(200);

%p(11)=1/(63.5*365);

c=0.05;

p(7) = 0.1;

p(8) = 0.8;

p(1) = 0.837773;

p(2) = 0.729255;

p(3) = 0.000047;

p(4) = 0.040000;

p(5) = 0.140705;

p(6) = 0.291499;

%p(7) = 0.1;

%p(8) = 0.2;

p(9) = 0.000008;

p(10)=1/(180);

p(11)=1/(63.5*365);

p(12)=0.0002373;

%p(12)=0.03;

dydt = zeros (size(y));

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dydt(1) = p(3)- p(1)*Sh*(Im/M) - (p(11) +p(7))*Sh + p(10)*Rh;

dydt(2) = p(1)*Sh*(Im/M) - (p(5) + p(11))*Eh;

dydt(3) = p(5)*Eh - (p(8) + p(11) + p(9))*Ih;

dydt(4) = p(8)*Ih - (p(10) +p(11))*Rh +p(7)*Sh;

dydt(5) = p(12)- p(2)*Sm*(Ih/N) - (p(4)+c*p(7))*Sm;

%% dydt(5) = d2*M - p(2)*Sm*(Ih/N) - p(12)*Sm;

dydt(6) = p(2)*Sm*(Ih/N) - (p(6) + p(4)+c*p(7))*Em;

dydt(7) = p(6)*Em -(p(4)+c*p(7))*Im;

dY = dydt;

%%p0 = [0.2 0.4 3.1/(100*365)

 %0.033 0.1 0.091 0.05 0.2 0.0026

 % 1/200 1/(63.5*365)]';

APPENDIX F: Maple code for computing equilibrium points and $\mathcal{R}_0$

dS[h] := -S[h]*Y[m]*"beta[h]-"alpha*S[h]+

     "rho*R[h]-S[h]*"mu[h]+"Lambda[h]

dL[h] := "beta[h]*S[h]*Y[m]-("kappa+"mu[h])*L[h]

dY[h] := -"delta*Y[h]-"gamma*Y[h]+"kappa*L[h]-Y[h]*"mu[h]

dR[h] := "alpha*S[h]+"gamma*Y[h]-"rho*R[h]-R[h]*"mu[h]

dS[m] := -S[m]*Y[h]*"beta[m]-S[m]*"lambda[m]+"lambda S[m]

dL[m] := "beta[m]*S[m]*Y[h]-("theta+"lambda[m])*L[m]

dY[m] := "theta*L[m]-Y[m]*"lambda[m]

eqPts := solve(–dL[h], dL[m], dR[h], dS[h], dS[m],

dY[h], dY[m]˝,

    [S[h], L[h], Y[h], R[h], S[m], L[m], Y[m]])

DFE := eqPts[1]

EE := eqPts[2]

with(LinearAlgebra);

with(linalg);

J := jacobian([dS[h], dL[h], dY[h], dR[h], dS[m],

 dL[m], dY[m]],

  [S[h], L[h], Y[h], R[h], S[m], L[m], Y[m]]);

J0 := subs(DFE, op(J))

J1 := subs(EE, op(J))

B := matrix([["kappa+"mu[h], 0, 0, 0],

  [-"kappa, "gamma+"mu[h]+"delta, 0, 0],

  [0, 0, "theta+"lambda[m], 0], [0, 0, -"theta,

  "lambda[m]]])

V := inverse(B)

F := matrix([[0, 0, 0, "beta[h]*("rho+"mu[h])*

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"Lambda[h]

   /(("alpha+"rho+"mu[h])*"mu[h])],

   [0, 0, 0, 0], [0, "beta[m], 0, 0], [0, 0, 0, 0]])

M := multiply(F, V)

eigenvals(M)

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APPENDIX G: Sage code for computing $\mathcal{R}_0$ with respect to parameter

```
(beta˙h, beta˙v, theta, mu˙h, rho,

k,lambda˙v, gamma,

delta, alpha, S˙h, R˙h, I˙v, L˙v,

I˙h, L˙h) = var('beta˙h', 'beta˙v',

'theta', 'mu˙h', 'rho','k','lambda˙v',

 'gamma', 'delta',

'alpha','S˙h', 'R˙h', 'I˙v', 'L˙v', 'I˙h', 'L˙h')


R0=sqrt(beta˙h*beta˙v*theta*(mu˙h+rho)

*k/((lambda˙v+c*alpha)*(k+mu˙h)*

(mu˙h+gamma+delta)*(theta+(lambda˙v+c*alpha))*

(alpha +mu˙h + rho)))

show(R0)


A = diff(R0, beta˙h)*beta˙h/R0

show(A)


B = diff(R0, beta˙v)*beta˙v/R0

show(B)


C = diff(R0,theta)*theta/R0

show(C)


D = diff(R0,mu˙h)*mu˙h/R0

show(D)
```

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E = diff(R0,rho)*rho/R0

show(E)

%F = diff(R0,Lambda˙h)*Lambda˙h/R0

%show(F)

G = diff(R0,k)*k/R0

show(G)

H = diff(R0,lambda˙v)*lambda˙v/R0

show(H)

GAMMA = -gamma/(delta+gamma+mu˙h)

show(GAMMA)

I = diff(R0,gamma)*gamma/R0

show(I)

DELTA = -delta/(delta+gamma+mu˙h)

show(DELTA)

J = diff(R0,delta)*delta/R0

show(J)

ALPHA = -alpha/(alpha+mu˙h+rho)

show(ALPHA)

M = diff(R0,alpha)*alpha/R0

show(M)

APPENDIX H: Python code for sensitivity graphs

%PYTHON CODE FOR SENSITIVITY GRAPHS

#!/usr/bin/python


```python
import matplotlib.pyplot as plt

import numpy as np

import math as m


#objects = ( r'$"alpha$', r'$"beta˙v$',

 '$"gamma$', r'$"beta˙h$', '$"delta$','"

  r'$"theta$',r'$"mu˙h','$"kappa$',

 '"lambda˙v', r'$"rho$')
#y˙pos = np.arange(len(objects))
#performance = [-0.989035258, 1,

 -0.999642077, 1, -0.0000055980,

 0.6983396737, -0.9240220809, 0.8985017125,

  -1.0, 0.0000513152 ]
objects = (r'$"alpha$', r'$"beta˙v$',

 '$"gamma$', r'$"beta˙h$', '$"delta$','"

  r'$"theta$',r'$"mu˙h','$"kappa$',

 '"lambda˙v', r'$"rho$', 'c')
y˙pos = np.arange(len(objects))
performance = [-1, 1, -0.999642077, 1,

 -0.000055980, 0.1823284259, 0.0070905130, "

 0.2043701746,  -0.7275815124, 0.9812896997, "

 -0.4547389852]
```

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```
barlist = plt.bar(y˙pos, performance,

align='center', alpha = 1)

barlist[0].set˙color('black')

barlist[1].set˙color('b')

barlist[2].set˙color('black')

barlist[3].set˙color('b')

barlist[4].set˙color('black')

barlist[5].set˙color('b')

barlist[6].set˙color('black')

barlist[7].set˙color('b')

barlist[8].set˙color('black')

barlist[9].set˙color('b')

barlist[10].set˙color('black')

#plt.setp(y˙pos, xticks=[0.1, 0.5, 0.9],

xticklabels=['$““epsilon˙I$',

'$““sigma˙M$', '$““theta$', '$““mu˙B$', '$““mu˙I$',

 '$““mu˙M$'],yticks=[0.0001, 0.0002, 0.0003])““

plt.xticks(y˙pos, r'objects',““

 fontsize=15, weight = 'bold')

plt.ylabel('Index', fontsize=15)““

plt.title('Sensitivity Index Profile

for $R˙0$', fontsize = 17, weight = 'bold')

plt.show()
```

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