MATHEMATICAL MODELING OF THE RECENT SPREAD OF DISEASES IN METAPOPULATION SYSTEMS: The Case of Ebola Virus in West Africa and Zika Virus in South America.

by

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Student number: 6407-178-2 I make the declaration that Mathematical Modeling Of The Recent Spread Of Diseases In Metapopulation Systems: The Case of Ebola Virus in West Africa and Zika Virus in South America. is my own work, approved by my supervisor and college of graduate studies and that all the sources that I have quoted or make mention of have been duly indicated and acknowledged with complete references. I further make declaration that this thesis is new and have not previously been submitted for examination at Unisa or any where else or even part of this work for another qualification or research at any other institution of higher learning.

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I Gabriel Oluwamuyiwa OLUPITAN do certify that this academics research was done in Department of Mathematical Sciences, University of South Africa, Florida science campus, South Africa, from July 2018 to June 2021, under the supervision and mentoring of Research Professor Emile Franc DOUNGMO GOUFO and co-supervison of Dr Tchepmo. Which an original academic exercise of the researcher, no aspect of the result have previously been submitted in any form or for any degree or diploma at any institution of higher education or learning. We acknowledged every authors and owner of other material quoted in this work.

Dedication

I dedicate this thesis to the glory of God almighty, maker of heaven and earth. To the memory of my dad Jonathan Ayodeji Olupitan. I also dedicate this thesis to the entire OLUPITAN Dynasty headed by my Mentor Senator Titus Olajide Olupitan who bankrolled me throughout the course of my studies.

Publications

The following articles are extracts from this thesis.

- A metapopulation model for zika virus disease transmission dynamics between linked communities;Recent Trends on Numerical Methods and Application to Modelling Nature,Physica Scripta,PHYSSCR-114100
- A metapopulation model for Ebola Virus Disease transmission dynamics between linked communities.

Conferences, Symposiums and Webinar

- A Metapopulation Mathematical Analysis of Local Stability of Zika Virus disease transmission dynamics". SANUM,2019, Math. Dept., University of Pretoria, South Africa. (March 2019)
- Mathematical Modelling Skills With Applications Workshop Department of Mathematics, University of Benin, Benin City, Nigeria.(13th–17th July, 2020)
- 43rd South African Symposium of Numerical and Applied Mathematics (SANUM 2019
- Mathematical Modelling Skills With Applications Workshop Department of Mathematics, University of Benin, Benin City, Nigeria.(13th–17th July, 2020)
- Mathematical Computational & Statistical Biology (MCSB) Group Webinar on Optimal Control 3rd-9th August. 2020
- Department of Mathematical Science, University of South Africa (UNISA) Departmental Talk on 2nd June, 2021

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Keywords

- Ebola Virus Disease
- Zika Virus Disease
- Ordinary differential equation
- Initial Value Problem
- Bifurcation Analysis
- Stability Analysis
- Ebola-free Endemic Equilibrium
- Zika-free Endemic Equilibrium
- $\beta-$fractional derivative
- Ebola Virus Dynamics
- Zika Virus Dynamics
- Metapopulation
- Travel Model between patches
- Control measures

Abstract

In this time of global health issues, there are out there many viruses that are shaking the world, including the chikungunya virus, human immunodeficiency virus, corona virus, ebola virus and zika virus.
A metapopulation model describing the spread of Ebola virus disease (EVD) between two patches is developed. Disease susceptible individuals moving from one patch into the other patch, with entries into each of the patch as population grow. Due to migration into the patch and birth, with assumption that birth rate and death rate constant. We also considered movement between the infected individual, amongst patches. Ebola Virus Disease (EVD), is a very contagious and highly infectious disease which spread is determined by the number of secondary contacts of an infectious individual moving from one community to another. We show that the metapopulation model is non-negative, providing condition for stability of the disease at disease free equilibrium (DFE). Which is said to be linearly stable if $\mathbf{R}_0 < 1$ and unstable if $\mathbf{R}_0 > 1$.

We also developed and analyzed a metapopulation mathematical model of Zika Virus disease (ZVD) transmission dynamics in linked communities, with movement parameter related to the two patches. With assumption that Zika infected individuals do not migrate, we express the reproduction number representing the biological parameter involved in rate of secondary infection of Zika Virus Disease (ZVD) in both patches. Stability analysis is performed after which we consider four preventive measures such as personal protective measures, use of indoor residual spray, responsiveness to health guidelines and health awareness and the prevention of movement from one infected community to another. Numerical simulations are performed and show compartment dynamics that concur with the analysis.

Contents

Chapter 1

Introduction

Ebola virus disease (EVD), which ravaged several countries of the world, especially in West Africa, though highly contagious and noted for its high mortality rate since the initial discovery in 1976 by the medical researcher, Dr. Peter Piotin in Zaire now Democratic Republic of Congo (DRC), Africa [Team, 2014] said that Ebola virus disease (EVD) is not a death sentence because it can be treated. So also is Zika virus disease (ZVD), though not as deadly as EVD is a vector borne disease with higher transmission occurrences from infected individual. ZVD in recent years attracted global attention because of its effect among neonates in Brazil, other South American countries and Europe [Ogunbanjo, 2016, **?**].

We focus this study on a mathematical model to study and investigate the effect of metapopulation in the spread of EVD and ZVD noting the impact of movement of individuals from one population to another i.e the effect of metapopulation and optimal control techniques i.e certain control measures on the proliferation dynamics of the disease. This chapter is structured as follows: Background of the study, Relevant questions guiding the research, Aim and objectives of the research, Motivation of the study and Mathematical preliminaries.

1.1 Background of the study.

Mathematical Modelling has been a great tool in the hand of researchers and this tool have been used to make unimaginable impact to the world at large. As such, mathematical modelling techniques have successfully helped to check the rate of change of differences in natural occurrences, taking in mind relevant mathematical principles. Recently the world recorded a great number of casualty as a result of the resurgence of Ebola virus disease (EVD) outbreak in certain part of Africa, especially West Africa. EVD is a deadly disease in humans which have recorded up to 90% rate of fatality. Ebola Virus which was formerly known and called Ebola haemorrhagic fever was first noticed greatly in its appearance in 1976 where two reoccurring outbreaks of the virus occurred in two communities of Nzara in Sudan and Yambuku, Democratic Republic of Congo [Tseng and Chan, 2015]. EVD outbreak was a scary scene in West Africa from 2014 to 2016 and the fatality rate was very high. Zika virus disease is not as deadly as Ebola virus disease, because of its mode of transmission in human is not as rapid as that of EVD. The effect of Zika virus disease (ZVD), caused by a bite from the Aaedes Mosquitoes, was first noticed in the African continent, found in a monkey in 1947 and later found to be prevalent in human in 1952 from some countries. The outbreak of ZVD was reported in 2013 at the island Yap, in South America. EVD and ZVD have taken a whole new dimension in terms of dangerousness, due to the effect of migration to and from prevalent communities. From the data released by World Health Organisation (WHO) as of May 2016 data from respective governments, report about 28,616 suspected cases of Ebola virus disease and 11,310 deaths from infected individuals [Organization et al., 2014,Organization et al., 2016]. While on March 2016, a Zika virus disease outbreak reported 1,263 suspected cases, EW21 and EW30, an estimated average suspected cases of about of 293 individual and confirmed cases of more than 200 ZVD were recorded per week in South America [Duffy et al., 2009]. In the same vain, Javier 2015 reports record of about 1.5 million individual with ZVD in 2014. He also maintained that Brazil has seen more and more new-born cases with microcephaly abnormal, exhibiting severe congenital condition associated with a small head, irregular shaped and incomplete brain development. Consequently, successive governments in Africa and South America have put up different policies to combat the ugly situation. Unfortunately, this had yielded little result. Despite the fact that governments have been firing at full cylinders to put an end to EVD and ZVD, there is a dearth of empirical research on mathematical modeling on the spread of EVD and ZVD in metapopulation system. Against this background, this study will attempt to do a mathematical modeling of the metapopulation dynamics of these hydra-headed diseases. The field of Mathematical Modeling has been a great tool in modeling

natural occurrences whereby mathematical assumptions are taken governed by known mathematical law, and used to build research in the field of mathematical modeling where differential equations and integral equations are used to describe many instances. Principles of stochastic processes have been employed to given results to real life problems, where the probability space is considered Ω variables of the sample space are defined, as well as the time t and the probability density function $f(t)$.

1.2 Problem Statement

The literature on metapopulation modeling of diseases is robust, for instance, Jean Jules Tewa et al [Tewa et al., 2012], examined the mathematical analysis of two patched disease model with reference to a tuberculosis transmission. while, [Gould et al., 1985] examined the analysis of a multi-vector disease model without any reference to a specific disease. In like manner [Hethcote, 1989], investigated the real-time forecast of global epidemic spreading. These and many other studies were concerned with specific diseases other than EVD and ZVD. To the best of our knowledge, research work on the recent spread of diseases in metapopulation systems in Africa and South America has not been extensively explored in literature. The effect of migration, tourism, asylum seekers as well as air and land travel of any kind have made the research on issues bothering the dynamics of spread of disease in metapopulation systems of great research interest. Hence, this work will focus on effect of migration and other travels on transmission dynamics of EVD and ZVD on linked communities. We seek to know the influences of movement to and from different communities with prevalence of EVD and ZVD respectively. This work also seek to formulate a metapopulation model, what are the equilibrium points of the model and how can the possible impact of the key parameters of the model be investigated? Which seek to reduce such transmission with optimal control strategies. Thereby, helping public health experts put up proper and adequate measures. Hence, contribute its own quota to the existing body of knowledge in Mathematical Modeling of diseases in metapopulation systems.

1.3 Research Aim and Objectives

1.3.1 Research aim

Our study is aimed at understanding transmission dynamics of Ebola virus disease (EVD) and Zika virus disease (ZVD) in metapopulation systems, make analysis of the spread of the disease, the system of transmission in linked communities, taking into account the migration of susceptible individual from one location to another, helping to formulate a mathematical model of prediction and formulate adequate control measure in reducing the risk attached to contracting the disease and making recommendation to avoid future occurrences.

1.3.2 Research objectives

To achieve this aim, the following objectives are set:

- Establishing a metapopulation mathematical model suitably representing the attribute of the diseases as they manifest, putting in mind all constraints.
- Establishing metapopulation mathematical models, capable of analysing mode of transmission dynamics of ZVD and EVD in relation to movement in and out of connected communities.
- Using epidemiological models to focus mainly on the transmission dynamics of these infections, so also look at the trait dynamics from one community to the other community: genetic , cultural and addictive characters. Each and every epidemiological units will be looked at to make proper and adequate model assumption. In addition, collection of data will be very important as we will be looking at the irregularities that may arise from wrong data interpretation and data analysis, Ellner et al(1995).
- Making use of results from previous research as a guide to the investigation which will be carried out on the epidemic state and endemic state, to study the extent of the existence of a global equilibrium point for the metapopulation and discuss its stability.
- Developing new numerical schemes, which will serve as tools to predict the movements from small patches

to larger patches of the matapopulation system, effectively, modeling the relationship of the sink and serve sources.

- Formulating an optimal control model for EVD and ZVD respectively.The control variable for the EVD u_1 which is the fraction of susceptible human who do not travel from patch one to patch two adhering to educational campaign at time t,u_2 is the fraction of susceptible human who do not travel from two patch to patch one adhering to educational campaign at time t, u_3 is the controlled treatment, isolation and safe burial of infected individuals as a means of controlling and preventing the spread at time t, and u_4 is the effectiveness of vaccine as well as other treatment at time t. The control variable for the ZVD are $u_1(t)$ which is the personal preventive strategy and measures adopted to protect oneself from contracting ZVD such as insect repellent or mosquito net to reduce the contacts between human, wearing of long sleeve clothing which covers the body properly. Adequate use of insecticide spraying to kill mosquitoes is $u_2(t)$, $u_3(t)$ is the rate of treatment of those infected with ZVD, $u_4(t)$ represents the efforts deployed to reduce the movement of infected people from patch one to patch two through screening and testing. While $u_5(t)$ represent effective health regulations approved by WHO and CDC as means of personal protection against the disease.

- Analyzing the optimal control for EVD and ZVD using Pontryagin's Maximum Principle and Cost-effectiveness Analysis.

1.3.3 Motivation for the study

Zika virus disease (ZVD) is one of health emergencies causing death globally but that can be treated using surgery. Ebola virus disease (EVD) which has terminated human lives in west coast of Africa.

- This research is motivated as a form of search for mathematical solution to spread of diseases from one geographical location to another. because of various type of travels. Finding a way to help reduce the effect of disease transmission from a particular location to another.

- The need for our continuous research and findings on exploring new methods and techniques like those related to the concept of differential equations and applying them specifically to epidemic models of current diseases including Ebola and Zika.

- Another motivation for this thesis is expressed by the necessity of using mathematical models of some real life phenomena like those mentioned above, to establish broader outlooks on their evolution, so as to be able to make wider recommendations and predictions.
- The desire of this research is to bring about a faster ways of predicting the spread of Ebola and Zika Viruses in a metapopulation, to observe the necessary process and formulate new dynamics which will have a great impact and help the concerned government and organisation responsible for health management to formulate policies as a result this accomplishment.
- Another motivation to this work is taken by the need to use numerical models to investigate the rational behind this epidemic, proffer adequate solution and add some new models to the existing ones which have in the past served as tools used to predict and analyze epidemiological issues.

1.4 Mathematical Modeling

Concepts of Mathematical Modeling have been a great tool in the hand of researchers that has been used to make unimaginable impact to the world at large. In the field, we apply mathematical modeling techniques to check the rate of change in natural occurrences translating in appropriate differential equations, obeying relevant mathematical principles. Mathematical modeling is the basic translation of real life and physical situation of real world issues to mathematical equations, expressions and representations for proper mathematical analysis, formulation and prediction which in turn help to give solution and better understanding to real life situations and problems.

Mathematical models are formulated in different ways depending on the set objectives as well as the aim of the model. Mathematical Models are linear or non linear, static or dynamic,deterministic or stochastic as well as discrete or continuous. The nature of the problem will determine the type of model that will be appropriate for use. While,defining all the arguments, prediction, observation and projection the proposed mathematical model is aimed to achieve.

Mathematical models also make use of assumptions in order to avoid ambiguity, redundancy and unrealistic

results because the mathematical models must be realistic and applicable to real life issues. Mathematical modeling is applicable in predicting several sectors of modern technical and scientific world. Mathematical modeling has been used successfully in meteorological sciences, physical sciences, social sciences: especially in mathematics of finance, engineering and biological sciences. In biological sciences, mathematical modeling have been useful in its application to the study of epidemic, spread of diseases, fisheries and aquatic and a whole lot of area of life. [Kapur, 1988] Sates that mathematical models depend on the fact that a mathematical modeler depends on real world factors to formulate a model which tends to predict and formulate a possible solution to the real world problem.

1.5 Epidemiological preliminaries

Spread of diseases in history of humanity is dated as far back as 10BC [Frank MacFarlane Burnet et al., 1972]. Biblical, epidemic outbreak such as the Egyptian plaque which killed several animal as an outcome of unusual large widespread of disease can also be seen as one of such older account. Such unusual deaths are caused by the pathogens which are agents bacterial and virus. The pathogens are carried by the vectors which are capable of transmitting and transferring the agents from one place to another at a particular rate without having any negative or harmful effect in them, such agents are also the vector of such pathogenic substance.

Once the human population have a contact with the vector, the disease is hence transferred and begin to manifest depending on individual systemic immune response. The way individuals react to disease differentiate those who show symptoms symptomatic to those who do not show symptoms yet can transmit the infection asymptomatic. Human are regarded as being susceptible to disease when they are prone to develop the disease but are yet to be infected. The category is denoted by S. Exposed individuals are the collection of individuals who have ingested the pathogen, have been infected but yet to show visible symptoms of such infection or disease. The infected are the number of individuals in a population who are either symptomatic or asymptomatic, they are denoted by I. Those who recovered are denoted by R, those who successfully recover from the infection either naturally thanks to antibodies or by other treatment methods.

In epidemiology, diseases have different periods within which they manifest. That is known as the latent period which is the period when the disease or infection haven't manifested or when the individual infected haven't

become infectious. In measles it is within 10 days while it is 2 days for Influenza. The period is referred to as the incubation period of the disease or infection. The infection period of the disease then comes up when the infectives can transmit infection to either a susceptible host or vector at any contact, either by the bodily fluid, blood contact and otherwise depending on the pathogenic characteristics of the infection at time t. Mean rate of infection, the absolute mean number of persons the initial infected individual is prone to infect is called the basic reproduction rate or standard reproduction number, denoted by R_0.

The standard or basic reproduction number is very important and useful in the study of mathematical modeling of infectious diseases. Generally, in mathematical modeling, it is known that when $R_0 < 1$, the disease will die out i:e the infection can not grow but on the other hand,when $R_0 > 1$, then the infection grows and might lead to an epidemic outbreak.

- Epidemic: An epidemic is a very serious outbreak of a disease. There could be epidemics of most common infections like flu.
- Agent: These are the common pathogens that causes diseases such as Virus, Bacteria
- Vector: Organisms which are very active in the transmission of infectious agent from a host to another.
- Contact Rate: The rate of interactions of a particular community or population.
- Asymptomatic: The individual who does not in anyway show symptoms of the disease
- Susceptible: Those are the group of individuals who can develop the disease but are yet to be infected. They are denoted by S
- Exposed: The class of the population who host the infection but has not yet began to be infectious, denoted as E
- Infected: A member of the population such that having been infected is transmitting the infection to others. Simply denoted as I
- Passive Immune: This is the class or member of the population such as pregnant women if when pregnant, such woman is infected, but have some antibodies across the placenta that gives the baby passive immunity. Denoted as M

- Recovery: Members of the host population who were infected but having gone through some medication, vaccines etc recovered and became normal. Denoted as R
- Models: Mathematical models are either Deterministic; current event depends on the past event as well as the occurrence at a time t. Stochastic: do not depend on previous or future events, random time accounted for at such instance. [Hethcote, 1989] introduced deterministic epidemiological models for infectious diseases of three basic types,which have been extended to numerous mathematical models SI, SIR,SIRS, SIS, SEIR and SEIRS used in the description of epidemiological transfer and transmission of disease dynamics. For the purpose of this thesis, we will be using the SIR, SI and SEIR models to describe the Zika and Ebola disease dynamics.

Basically in determining the mathematical model which will be used to model disease dynamics of a particular disease a mathematical model considers the population size, the susceptible human or vector population, depending of the disease dynamics, movement of individuals and the rate of interaction which determine the spread or otherwise, the infection period, the mode of transmission of the disease, ecological and human effect, Immunity of infected individuals as well as the incubation period of the disease are the very important criteria examined before a mathematical model is used.

1.5.1 SIS model:

This model divides the disease compartment into the susceptible (S) and the infectives (I). The model is common for diseases like malaria where infectives individuals do not have immunity and can return to be susceptible after recovery. Which is the reason why the model is called the SIS model.(For more details check [Shuaib et al., 2014, Nåsell, 1996, Luo and Tay, 2013]).

1.5.2 SIR model:

The SIR model compartment are subdivided as the susceptible (S), Infectives (I) and Recovered (R) class. The model is commonly used for modeling infectious diseases like measles, rubella and mumps where after recovery,

recovered individual are endowed with some sort of permanent immunity.(For more details see [Rachah and Torres, 2015, Weiss, 2013, Kibona and Yang, 2017]).

1.5.3 SEIRS model:

This epidemiological model describes a given disease dynamics with an exposed period where individuals may be symptomatic ar asymptomatic. With total population subdivided into classes namely susceptible (S), Exposed (E), Infectives (I) and Recovered (R). In this case, movement of individuals from each compartment occurs with recovered individuals after losing their immunity returning back to being susceptible with time. (For more details see [Ma, 2009, Melesse and Gumel, 2010, Wang, 2002]).

1.6 Ebola Virus Disease(EVD)

1.6.1 History

Ebola Virus Disease (EVD) is on record to be one of the most serious viral disease which is currently known in the world today. EVD is very severe and fatal sickness known to human with fatality rate of about 90%.

Ebola virus disease became an epidemic and a global public health concern in 2013 when it became prevalent in West Africa. EVD was first discovered in 1976 as a result of a disease in Sudan and in Yambuku, a small village located near Ebola river in Democratic Republic of Congo where the disease name. Ebola virus disease (EVD), was before then called Ebola haemorrhagic fever, which manifest primarily in human and primates. Ebola Virus (EV) comes in six species, with four of the species very dominant in humans, namely: Za$\ddot{i}$re ebolavirus (ZE) Sudan ebolavirus (SE), Tai Forest (TF) which was formerly known as Ebola Ivory Coast(EIC) and Bundibugyo ebolavirus (BE).

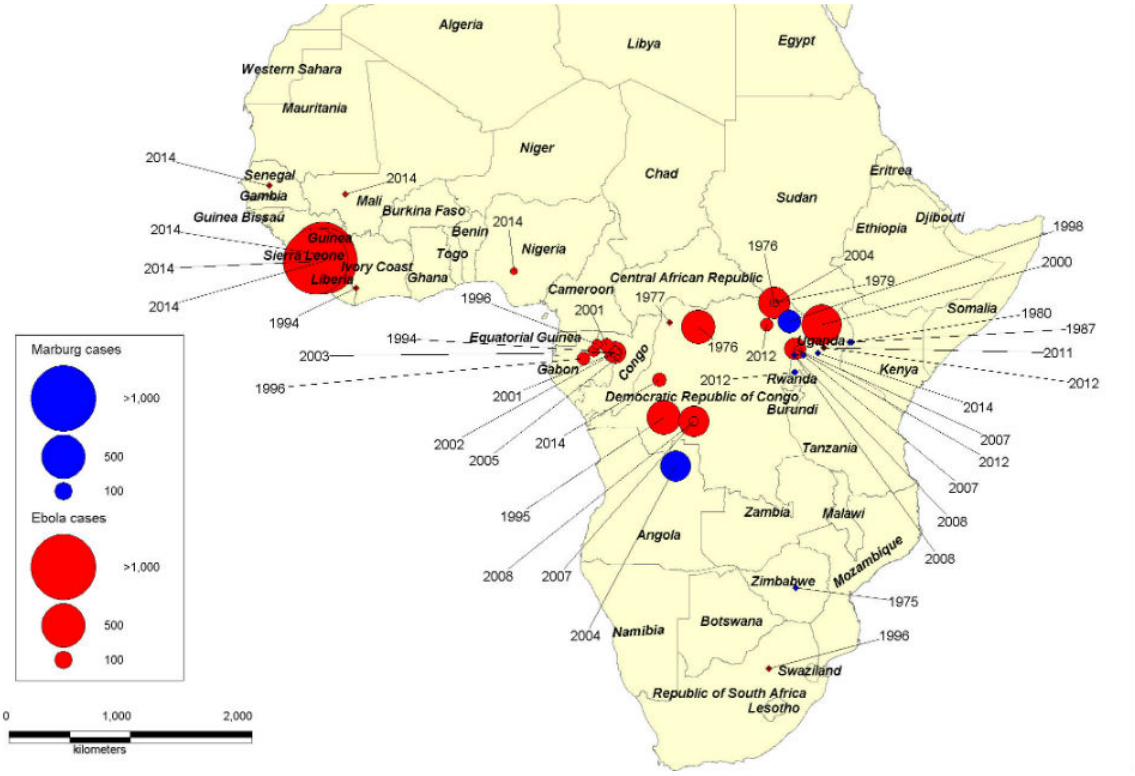


Figure 1.1: Ebola Virus Disease prevalence in Africa

1.6.2 Transmission

Research has shown that EVD transferred to human when in contact with infected primates such as monkey, apes and other wild animals like bats, who are considered as reservoir of the EVD. On the other hand, transfer of EVD from one Human-to- another Human, is either through direct contact of infected persons, contact with bodily fluids, blood, as well as body and organ secretions of an infected individuals. Improper disposal of dead animals and humans play a majour role in the transmission of EVD, and had killed very many health officials treating infected individuals. EVD is a deadly illness that often manifests with symptoms including fever, severe headache, general body pain, muscles pains, soar throats and acute internal weakness. This is followed by several organs damage eventually leading to death in the space of weeks when proper and adequate care are not given. The incubation period of EVD is from 2 to 21 days depending on the individual and body immune system.

1.6.3 Treatment

EVD currently do not have a specific and particular drug health officials usually treat the symptoms as they manifest in the infected individuals, giving fluids and other infusion to manage the infected individuals blood pressure, sugar level, pains and diarrhea. The procedure of treatment begins with the blood sample of an infected individual taken to laboratory for proper diagnosis. No anti retro-viral drug currently has been licensed by the world health organization (WHO) and Centre for Disease Control (CDC). Recently, Recombinant vesicular stomatitis virus–Zaire Ebola virus (rVSV-ZEBOV) vaccine for vaccinating adults was approved for medical use in 2019 by European Union (EU). The vaccine was also subjected to usage in the $\acute{E}$Quateur province of DR Congo in a 2018 [Cnops et al., 2015] and have been extensively used to vaccinate more than 90,000.

1.7 Zika Virus Disease(ZVD)

1.7.1 History

ZVD is of the genus Flavivirus family [Daudens-Vaysse et al., 2016] with about 53 different species [Dick et al., 1952]. ZVD is caused by mosquito that is very close and related phylogenetically to the already existing mosquito-borne flaviviruses known by public health specialist Dengue Virus Disease (DVD), Yellow Fever Virus Disease (YFVD) and West Nile Virus Disease (WNVD) [Gould et al., 1985].The virus which was first discovered in Uganda over 70 years ago while some researcher where working on YFVD in a forest in Uganda, Africa. ZVD was first found in a rhesus monkey but the disease was not reported in human until late 1951 in a study carried out in Africa by Fagbemi a Nigerian Sero-epidemiologist and some other African researchers before the outbreak of ZVD which occured in Yap Island [Fagbami, 1977] , Micronesia. Prior to that outbreak, only few occurrences of ZVD had been recorded in Africa and Asia before the 2007 Yap Island outbreak. With epidemiological surveillance, epidemiological and entomological studies carried out, ZVD is seen as a prevalent in travelers and migrants from tropical countries to non tropical countries. This is a form of metapopulation, the main focus of this thesis. However, the recent spread of ZVD in South America [Daudens-Vaysse et al., 2016] have led to concerns of public health expert as well as mathematical epidemiologists looking at various possible ways to reduce the neonatal problems in neonate born to ZVD infected mother [Chaikham and Sawangtong, 2017].

1.7.2 Transmission

ZVD is an arboviral disease which also manifests like a DVD-like infection is believed to be transmitted by the Aedes mosquito which is the main vector. There are other mode of transmission of ZVD besides the mosquito vector, transplacental transmission between an infected mother and the new born child is presently a global concern on the rate of ZVD infection [Duffy et al., 2009]. ZVD can also be transmitted sexually [Kucharski et al., 2016]. Safety guidelines for prevention of sexually transmission of ZVD by World Health Organization and other public health organization. ZVD can also be transmitted through unscreened blood transfusion [Wagner et al., 2019, Willyard, 2017].

1.7.3 Treatment

Clinical observation shows that ZVD causes acute febrile sickness, about 25% of infected persons develop mild and self-limited illnesses, with flu-like syndromes which occur with some slight fever, rash, headache, myalgia and frequent vomiting [Chikaki and Ishikawa, 2009] . ZVD is an emerging infection, with no specified antiviral drug or vaccine [Dick et al., 1952]. Because the ZVD manifest like DVD, the drugs and procedure used for the treatment of DVD are used [Fauci and Morens, 2016, Chikaki and Ishikawa, 2009]. The prevention of ZVD is a deliberate measure which include prevention of arboviral infection, using mosquito treated nets, wearing long gear covering body. Efforts towards having a vaccine to prevent ZVD are currently ongoing [Barrett, 2018] pregnant women in ZVD prone communities are advised to avoid crowded areas.

1.8 Metapopulation

A metapopulation is a concept that has been a very powerful demographical tool in analysis of ecological processes, spatial processes and temporal processes. metapopulation is a constituent of spatially separated populations of a group of the same species, either animals or organisms interacting at some level. [Vandermeer and Carvajal, 2001] gave a definition of metapopulation as "set of local populations within some larger area, where typically migration from one local population to at least some other patches is possible" Metapopulation is also considered to be a random walk which animals undergo within the range of their home. For the purpose of this thesis, we define a slightly simpler version, as a cohort of local populations between which distributing, spreading of living things or people over a wide area is possible. Especially within their natural habitat in form of a local population, subcommunity or subpopulation. These are groups of such individuals inhabiting a particular habitat or a patch and due to the common boundaries and nearness of some sort, share and interact with each other. The potential population in each of the habitats and patches is very important because features of a metapopulation are the critical habitat, how and where interactions occur within or outside, as events happen from one patch to another. Metapopulation is a concept fondly used in conservation and pest management which is used to explain persistence of species.

Metapopulation models often refereed to as patchy models considers the implicitly characteristics of both

temporal and spatial subpopulations. The concept of metapopulation has been widely explored farther habitats are considered because of various means of transportation, especially in humans [Heino and Hanski, 2001]. Air travels, tourism, migration and so on, have made movement from one habitat to another easy. In these model we are looking at local habitat patches which exist and there are interactions between the each of the communities, what is the effect of such movements and interactions on the spread of diseases.

1.8.1 CoInfection

Coinfection occurs when an infected individual is diagonized simultaneously with multiple pathogen species. In virology, coinfection of infected individuals includes simultaneous effect of a single cell by two or more virus or bacterial particles. The most common coinfection globally is tuberculosis and HIV [Muthuri and Malonza, 2018]. For the purpose of this thesis, we are not considering coinfection of EVD and ZVD. ZVD and Chikungunya virus disease (CVD) are flavivirus and alphavirus respectively, which are infectious RNA arboviruses transmitted to humans by the bite of Aedesspecies mosquitoes [Fleming-Dutra et al., 2016,Sanchez-Vargas et al., 2004]. Making coinfection of both ZVD and CVD possible in human. There is no evidence of coinfection of EVD and ZVD in the literature.

1.9 Mathematical preliminaries

We discuss briefly essential principles of mathematical modeling used in this thesis. The concept of basic reproduction number, stability results for ordinary differential equation, bifurcation analysis, optimal control method, the general optimal control problem, Pontryagin's maximum principle, necessary and sufficient conditions of the optimal control. Kermack-McKendrick, introduced the deterministic model for communicable diseases. Which is a system of two differential equations:

$$S' = -\beta SI$$

$$I' = (\beta S - \alpha)I$$

$$R' = \alpha I$$

the population under study is divided into three compartments: S,I, and R with the key value Threshold governing the evaluation of the epidemic given by:

$$R_0 = \frac{\beta S}{\alpha}$$

R_0 defines the number of secondary infection after an interaction with the infectious case.

- when $R_0 < 1$,in this case,is the rate the disease will decline and eventually die out.
- when $R_0 > 1$,in this case,each existing infection causes more than one new infection. Such that

$$\left(\frac{dI}{dt} > 0\right)$$

extensions allow the model to take in some new parameters like birth, migration and death and some sort of immunity, which is represented as:

$$\frac{dS}{dt} = b_0 + b_S S + b_I I + b_R R - \lambda S - m_S S$$

$$\frac{di}{dt} + \frac{di}{da} = \delta(a)\lambda(S + \sigma R) - \gamma(a)i - \mu(a)i - m_i(a)i$$

$$I(t) = \int_0^\infty i(a,t)da$$

$$\frac{dR}{dt} = \int_0^\infty (\gamma(a)i(a,t)da - \sigma\lambda R - m_R R$$

where b_0 is known as the rate of immigration of the susceptible population, b_j is the birth rate and m_j is the mortality rate in a given state j. with infection pressure

$$\lambda = \int_0^\infty (\beta(a)i(a,t)da).$$

Kermack and McKendrick showed that stationary solution is attainable in an endemic state

Theorem 1.9.1. {*Kermack-McKendrick*} *A general epidemic notation evolves according to the differential equations from initial values* $(S_0, I_0, 0)$*, where* $S_0 + I_0 = N$.

1. *(Survival and Total Size). This is the entire sample scale, which is the population where infection ultimately cases spreading, given a positive number* S_∞ *of susceptible remains uninfected, and the total number* R_∞ *of*

individual which ultimately infected are then removed equals to $S_0 + I_0 - S_\infty$. *Then there exists the unique root of the equation*

$$N - R_\infty = S_0 + I_0 - R_\infty = S_0 e^{-\frac{R_0}{\rho}}$$

where $I_0 < R_\infty < S_0 + I_0, \rho = \frac{\gamma}{\beta}$ *accumulatively are the relative removal rate.*

2. *(Threshold Theorem). In a given population, under which a given state is maintained, a majour outbreak occurs if and only if* $\frac{dI}{dx}(0) > 0$*; this happens only if initial number of* $S - 0 > \varrho$.

3. *(Second Threshold Theorem) If* S_0 *exceeds a given threshold* ϱ *by a small quantity* ν *while the initial number of infectives* I_0 *is small relatives* ν*, then the remaining number of susceptibles left in the population is approximately* $\varrho - \nu$ *the level of susceptibles is to a certain point below the threshold as it originally was above it:*

Proof. Given the rate of transmission of the equations above

$$\frac{1}{S}\frac{dS}{dt} = -\frac{\beta}{\gamma}\frac{dR}{dt} = -\frac{1}{\varrho}\frac{dR}{dt}$$

, from which we get

$$S(t) = S_0 e^{-}\frac{R(t)}{\varrho}$$

where R_0 is equal to 0 as $t \to \infty$

□

Theorem 1.9.2. *Let* $(S(t), I(t))$ *be a solution of the differential equation as defined above. If* $\sigma > 1$ *then* $D = ((S, 0) : 0 < S < 1)$ *is an asymptotic stability region for the equilibrium point* $\left(\frac{1}{\sigma}, \frac{\delta(\sigma-1)}{\lambda}\right)$*, where* $\sigma = \frac{\lambda}{(\gamma+\delta)}$ *If* $\sigma < 1$ D *is an asymptotic stability region.*

Theorem 1.9.3. *Assume that* $P, Q \in R$ *are continuously differentiable in an open connected region* D*, one the solution path of*

$$x'(t) = P(x, y)$$

$$y'(t) = Q(x, y)$$

if there exists a continuous differentiable point in D such that:

$$\frac{\partial}{\partial x}(BP) + \frac{\partial}{\partial y}(BQ)$$

then, there are no closed paths in D

Proof. The Closed paths must contain at least one eliminate possibility, so that if R contains no closed paths in D. Since no path leaves D, R is contained in D, by assumption

$$\frac{\partial}{\partial x}(BP) + \frac{\partial}{\partial y}(BQ)$$

has the same sign throughout D and Green's theorem,

$$0 \neq \int\int_R \left[\frac{\partial}{\partial x}(BP) + \frac{\partial}{\partial y}(BQ)\right] dA = int_\Gamma (BP)dy - BQdx$$

$$= \int_\Gamma B\left(\frac{dx}{dt}\frac{dy}{dt} - \frac{dy}{dt}\frac{dx}{dt}\right) dt = 0$$

which is a contradiction. □

1.9.1 Basic Reproduction Number

The basic reproduction number or basic reproduction ratio denoted by R_0 is as the average number of persons infected by an index infective individual in a population considering that all others are susceptible [[Van den Driessche and Watmough, 2002, Van den Driessche and Watmough, 2008] In this study, the reproduction number is carefully thought out with the peculiarities of EVD and ZVD respectively. The movement within each patch played a critical role in the maximum reproduction number R_{max} which was adopted to represents average number of secondary case resulting from the contact of the index case with susceptible individuals in each of the population. The maximum reproduction number helps in determining whether or not a disease (Ebola and Zika) will spread through in each of their separate metapopulation. The transmission and contagion effect of EVD and ZVD will be reduced to zero as disease will be regarded to have died out of the each metapopulation, if $R_{max} < 1$. Whenever $R_{max} > 1$, meaning each infected individual who is either infected with EVD or ZVD in their respective metapopulation, infects more than one person as the case may be, such that EVD and ZVD disease persists in the population.

In doing this, we explore the non-negative next generation matrix to find the basic reproduction number, which is the spectral radius of the next generation matrix. The next generation matrix technique which was studied by Van dan Driessche and Watmough [van den Driessche and Watmough, 2002, van den Driessche, 2017] is a general method for $Rmax$ in cases where several classes of infections are involved. Basic reproduction number cannot be determined from mathematical models alone considering the heterogeneous population especially with spatial factors to be considered. Different stages of the disease are grouped on n compartments such that $x = (x_1, x_2, x_3, ..., x_n)^t$ for every $x_i \geqslant 0$ indicating the number of individuals in each of the compartment depending on the mathematical model. Let X_d be the set of all disease free state, that is $X_d = x \geqslant 0 : x_i = 0, i = 1, 2, 3, ..., m$ where m is the number of disease free state in each of the population. Let $\mathcal{F}_i(x)$ be the appearance rate of new arrival of infected individual in compartment i, $\mathcal{V}_i^+$ is the rate of transfer of infected individuals into compartment i, by all means considered, V_i^- is the rate of transfer out of compartment i by other means as E_0 and Z_0 is the Ebola free equilibrium and Zika free equilibrium respectively.

Considering a non-negative disease transmission model as state and a continuously differentiable function of the system of equation:

$$\frac{dx_i}{dt} = \mathcal{F}_i - \mathcal{V}_i(x), i = 1, 2, 3, ..., n \tag{1.9.1}$$

where n is the number of compartment in the population considered and $\mathcal{V}_i(x) = \mathcal{V}_i^-(x) - \mathcal{V}_i^+(x)$. If x_0 is the disease free equilibrium point as the derivatives of F and V represented by mxm matrices, then:

F and V matrices are computed such that F= Jacobian Matrix of $\mathcal{F}$ at disease free equilibrium $\left[\frac{\partial \mathcal{F}_i(x_0)}{\partial x_i}\right]$
V= Jacobian Matrix of $\mathcal{V}$ at disease free equilibrium $\left[\frac{\partial \mathcal{V}_i(x_0)}{\partial x_i}\right]$

with $1 \leqslant i \leqslant m$

The matrices F contains trend of new infections while V contains the transfer of infection. The basic reproduction number $R_0 = \rho(FV^{-1})$ of the next generation matrix which is defined as FV^{-1} is the spectral radius or the dominant eigenvalue of the next generation matrix.

1.9.2 Stability Analysis

The stability analysis of any ordinary differential equation is very important as regards mathematical modeling. Stability analysis of a dynamical system play a very important role, the stability and instability of the equilibra determine these roles. Hence, it is very useful to be able to be able to classify equilibrium point based on its stability.

Definition 1.9.1. *A steady state x^* is said to be Lyapunov stable if any trajectory stationary near x^* remains forever. In other words $\forall\ \epsilon > 0$, $\exists\ \delta > 0$ such that if $\|x(0) - x^* < \delta\|$, then $\|x(0) - x^*\| < \epsilon$*

Definition 1.9.2. *A steady state x^* is said to be asymptotically stable if it is Lyapunov stable and all trajectory converges to x^*. In other words $\forall\ \epsilon > 0$, $\exists\ \delta > 0$ such that if $\|x(0) - x^* < \delta\|$, then $\lim_{t\to\infty} \|x(0) - x^*\| = 0$*

Theorem 1. *Given the system $\dot{x} = Ax$, where A is the matrix of the linearized nonlinear system (1.5). Then,*

- *the equilibrium point, $\dot{x}$, is stable if all the eigenvalues of A have only imaginary parts.*
- *the equilibrium point, $\dot{x}$, is asymptotically stable if all the eigenvalues of A have negative real parts.*
- *the equilibrium point is unstable in all other cases.*

Local stability:

Considering a system of an ordinary differential equation below:

$$\frac{dx}{dt} = F(x) \tag{1.9.2}$$

where $x = (x_1, x_2, ..., x_n)^T$ and $F = (F_1, F_2, ..., F_n)^T$ where each F_i for every $i = 1, 2, 3, ..., n$ is a continuous function for $\mathbb{R}^n$ to $\mathbb{R}$.

The equilibrium point for the above system (1.9.2) is found by setting $\frac{dx_i}{dt} = 0$ for $i = 1, 2, 3, ..., n$ which gives

$$F_i(\bar{x_1}, \bar{x_2}, \bar{x_3}, ..., \bar{x_n}) = 0$$

for $i \neq 1, 2, 3, ..., n$ and $\bar{x} = (\bar{x_1}, \bar{x_2}, \bar{x_3}, ..., \bar{x_n})^T$ in $\mathbb{R}^n$.
To determine the steady state solution (local stability) of the equilibrium point, we shift the origin to $\bar{x}$ using transformation;

$$X_i = x_i - \bar{x_i}, i = 1, 2, 3, ..., n$$

neglecting higher order terms with this change of variable in equation (1.9.2) we have a linearized term below;

$$\frac{dX}{dt} = AX.$$

Which is called the Jacobian matrix of the system (1.9.2) such that

$$A = \frac{\partial F_i}{\partial X_i}$$

and

$$X = (X_1, X_2, X_3, ..., X_n)^T$$

and the system (1.9.2) is said to be asymptotically stable for system (1.9.2).

Whenever the eigenvalues of the Jacobian matrix are will negative real parts, to ensure that the dynamic system is linearly asymptotically stable at equilibrium point, the sign of the roots of the characteristics equation corresponding to the Jacobian matrix are useful relying on verifiable mathematical assertions like the Routh Hurwitz Criterion [Afanasiev et al., 2013] of stability. Which gives necessary and sufficient condition for a polynomial to have all its roots negative real parts.

Routh Hurwitiz Criterion:

The Routh- Hurwitz stability criterion is a popular and well used mathematical analysis in control system which gives necessary and sufficient condition to adequate establishment of stability of a linear dynamical system of a differential equation.

The Routh test or Routh array as it is popularly called is an effective and efficient algorithm developed by Edward John Routh in 1876. Edward who is an English mathematician used his array to check if all roots

of a certain characteristics polynomial of a linear system do have negative real parts. While o the other hand, another German Mathematician named Adolf Hurwitz in 1895 proposed after an independent research by arranging coefficients of a polynomial into an array which he named the Hurwitz matrix.

Showing that the polynomial is stable if and only if it is clearly shown that the sequence of the eigenvalues of it's sub-matrices are non-negative. Both Edwards and Adolf's procedures which are equivalent in determining the determinant of a characteristic polynomial is popularly called the Routh-Hurwitz Criterion if and only if all the elements of the first column be nonzero and have the same sign .

In the application of Routh-Hurwitz criterion,two special cases are considered, although they are not likely to occur in applications. The first of this special case occurs when a coefficient in the first column is zero, in calculation of the array. Second special case occurs when all coefficients in a row are zero when calculating the array.

Routh-Hurwitz Theorem

Theorem 2. *A Polynomial* $q(s) = q_0 s^n + q_1 s^{n-1} + ... + q_n$ *where* $(q_1 \in R, q_0 \neq 0)$ *is stable if and only if all* $n+1$ *elements of the first column of the routh table are nonzero and have same sign.*

$$\alpha^n + a_1\alpha^{n-1} + a_2\alpha^{n-2} + ... + a_n = 0 \tag{1.9.3}$$

where $a_1, a_2, a_3, ..., a_n$ be n real numbers whose roots have negative real parts if and only if the values of the determinants of the matrices are positive,

$$M_1 = \begin{pmatrix} u_1 \end{pmatrix}, M_2 = \begin{pmatrix} u_1 & 1 \\ u_3 & u_2 \end{pmatrix}, M_3 = \begin{pmatrix} u_1 & 1 & 0 \\ u_3 & u_2 & u_1 \\ u_5 & u_4 & u_3 \end{pmatrix},$$

$$M_4 = \begin{pmatrix} u_1 & 1 & 0 & 0 \\ u_3 & u_2 & u_1 & 1 \\ u_5 & u_4 & u_3 & u_2 \\ u_7 & u_6 & u_5 & u_4 \end{pmatrix}, M_n = \begin{pmatrix} u_1 & 1 & 0 & 0 & . & 0 \\ u_3 & u_2 & u_1 & 1 & . & 0 \\ u_5 & u_4 & u_3 & u_2 & . & 0 \\ u_7 & u_6 & u_5 & u_4 & . & 0 \\ . & . & . & . & . & . \\ 0 & . & . & . & . & u_n \end{pmatrix}$$

1st Dimension:

$$M_1 = \begin{pmatrix} u_1 \end{pmatrix}$$

, $u_1 > 0$

2nd Dimension:

$q(s) = s^2 + a_1 s + a_0$ which have both roots in the open left plane of the characteristics equation $q(s) = 0$ is stable. if and only if $a_1 i > 0$

3rd Dimension:

A third order polynomial $q(s) = s^3 + a_2 s^2 + a_1 s + a_0$ has all roots in the open left plane if and only if a_2, a_0 are positive and $a_2 a_1 > a_0$

4th Dimension:

Fourth order polynomial $q(s) = S^4 + a_3 s^3 + a_2 s^2 + a_1 s + a_0$ has all roots in the open left plane if and only if $a_3 a_2, a_1$ are positive and $a_3 a_2 a_1 > a_0$

nth Dimension:

Let,

$$q(s) = a_n s^n + a_{n-1}s^{n-1} + a_{n-2}s^{n-2} + ... + a_1 s + a_0$$

$$M_n = \begin{vmatrix} a_n & a_{n-2} & a_{n-4} & a_{n-6} & . & a_0 \\ a_{n-1} & a_{n-3} & a_{n-5} & a_{n-7} & . & 0 \\ b_{n-1} & b_{n-3} & b_{n-5} & b_{n-7} & . & 0 \\ c_{n-1} & c_{n-3} & c_{n-5} & c_{n-7} & . & 0 \\ . & . & . & . & . & . \\ h_{n-1} & . & . & . & . & s_n \end{vmatrix}$$ Number of roots of $q(s)$ with positive real parts is equal to the number of changes in sign of the first column of the Routh array.$-\frac{1}{a_{n-1}} \begin{pmatrix} a_n & a_{n-2} \\ a_{n-1} & a_{n-3} \end{pmatrix}$

(For further reading on Routh-Hurwitz Criterion, check [Khatwani, 1981, Clark, 1992])

Central Manifold Theory:

The Central Manifold theorem is well stated and will be used to prove the local asymptotic stability of the endemic equilibrium point.

Theorem 3. *Consider the following system of ordinary differential equations with parameter* τ

$$\frac{dx}{dt} = f(x, \tau), f : \mathbb{R}^n \times \mathbb{R} \to \mathbb{R} and C^2(\mathbb{R}^n \times \mathbb{R}) \tag{1.9.4}$$

Where 0 is an equilibrium point of the system i:e $f(0, \tau) \equiv 0 \forall \tau$ *and with the assumption that the following holds:*

1. $A = D_x f(0,0) = \frac{\partial f_{x_i}}{\partial x_j(0,0)}$ *is the linearization matrix of the system (1.9.5) around the equilibrium 0 and* τ *evaluated at 0. Zero is a simple eigenvalue of A and the other eigenvalues of A have negative real parts.*

2. *Matrix A has a right eigenvector w and a left eigenvalue v(each corresponding to the zero eigenvalue); let*

f_k be the k^{th} component of f and

$$a = \sum_{i,j,k=1}^{n} w_i w_j v_k \frac{\partial^2 f_k}{\partial x_i \partial x_j}(0,0), b = \sum_{j,k=1}^{n} u_i v_k \frac{\partial^2 f_k}{\partial x_i \partial \tau}(0,0)$$

The local dynamics of the system around 0 is totally determined by the signs of a and b

i : $a > 0, b > 0$ when $\tau \ll 1$, 0 is locally asymptotically stable and $\exists$ a positive unstable equilibrium, when $0 < \tau \ll 1$, 0 is unstable and there exist a negative, locally asymptotically stable equilibrium;

ii : $a < 0, b < 0$ when $\tau < 0$, with $|\tau| \ll 1$, 0 is unstable; when $0 < \tau \ll 1$ is locally asymptotically stable, and $\exists$ a positive unstable equilibrium.

iii $a < 0, b < 0$ when $\tau < 0$ with $|\tau| \ll 1$, 0 is stable and positive unstable equilibrium appears;

iv $a < 0, b > 0$ when τ changes from negative to positive, 0 changes its stability from stable to unstable. Corresponding a negative equilibrium becomes positive and locally asymptotically stable.

(For more details on Central Manifold Theorem, see [Mohammed et al., 2008, Renardy, 1992]).

Global stability:

To ensure the dynamic system is globally asymptotically stable at any region even if it is not close to the origin, the comparison theorem that is the Castillo-Chavez et al [Castillo-Chavez et al., 2002] theorem as well as Lyapunov Functions of the general linear forms have been very useful.

Theorem 4. *The dynamical system of (1.9.2) written in the form $X^{'}(t) = F(X,Y)\ Y^{'}(t) = G(X,Y), G(X,0) = 0$ where $X\mathbb{R}_+^m$ denotes the number of uninfected individuals and $Y\mathbb{R}_+^n$ which denotes the number of infected individuals including all other compartments.*

The disease free equilibrium (DFE) of the mathematical model $M_0 = (X_0, 0)$ such that the following conditions holds such that $For X^{'}(t) = F(X_0, 0)\ X_0$ is globally asymptotically stable

$$G(X,Y) = AY - \hat{G}(X,Y), \hat{G}(X,Y) \geqslant 0$$

for $(X, Y)\mathcal{D}$ where the system (1.9.2) satisfies the given condition if and only if the theorem holds.

Theorem 5. *The fixed point of the DFE $M_0 = (X_0, 0)$ is globally asymptotically stable for the system (1.9.2) given $R_0 < 1$ and the condition above is satisfied.*

(For more details on Global Stability, see [Mei, 2013, Shu et al., 2020]).

1.9.3 Lyapunov Function

Lyapunov function have been a useful mathematical tool in population dynamics which was first constructed by Volterra in 1920 for a predator-prey model. Provided the necessary and sufficient conditions are met the global asymptotic stability follows directly from the LaSalles Invariance Principle [La Salle, 1976]. The dynamical system given on an open set as defined above i.e $\Omega \subset \mathcal{R}$ and $\bar{x} \in \Omega$ an equilibrium point. A function $V \subset C(\Omega, \mathcal{R})$ is called a Lyapunov function provided

$$\dot{V}(x) = \lim_{h \to 0} \frac{V(x + hf(x)V(x))}{h} = \nabla V(x).f(x) \leq 0 \forall x \in \mathcal{D} \tag{1.9.5}$$

where $\dot{V}(x)$ is the divided derivative of V in the direction of F.Additionally, $\dot{V}(\bar{x}) = 0$ and $V(x) > 0 \ \forall x \in D \ \{\bar{x}\}$, then V is a positively define Lyapunov function.

Applying chain rule on $V(x(t))$ given that $x = x(t)$ is a solution of the dynamical function defined above. Hence we have

$$\frac{dV(x(t))}{dt} = \sum_{n=1}^{U} \frac{\partial V(x(t))}{\partial x_n} . \frac{dx_n(t)}{dt} \nabla V.f(x) \dot{V}(x(t)) \tag{1.9.6}$$

The equation reveals the reason why $\dot{V}$ is sometimes called the trajectory inclined derivative, which gives information about V without having prior information about their solutions

Theorem 6. *If we can find a positive Lyapunov function V of the dynamical system differentiable on the neighborhood of D with equilibrium point $\bar{x}$, then $\bar{x}$ can be said to be asymptotically stable if $\dot{V}(x(t)) < 0$, $\forall \ x \in D \ \{\bar{x}\}$ and asymptotically unstable if $\dot{V}(x(t)) > 0$, $\forall \ x \in D \ \{\bar{x}\}$*

Theorem 7 (LaSalle's Invariance Principle)**.** *Let V be a Lyapunov function of the system (1.9.2) defined on $\mathbb{D}$. We define S such that, $S = x \in \bar{\mathbb{D}}\Omega : \dot{V}(x) = 0$. Let G be the largest invariant set in S. Every boundary of trajectory for $t \geqslant 0$ for the system (1.9.2),which remain in $\mathbb{D}$ approaches the set S as $t \to +\infty$*

(For more details on Lyapunov Function, see [Diehl et al., 2010, Rafikov et al., 2008]).

1.9.4 Sensitivity Analysis

Sensitivity Analysis is used to test the effectiveness of some properties on a given quantity of a model.

Definition 1.9.3. *The absolute sensitivity coefficient of a quantity R with respect to a parameter x is defined as the rate of change R with respect to x. It is denoted by $\frac{\partial R}{\partial x}$*

This sensitivity coefficient gives the information of increment or decrement as a parametric variable. The sensitivity coefficient gives the effect of the sensitivity of the variable in the model and the influence of parameter of the quantities R and x respectively.

Definition 1.9.4. *The relative sensitivity coefficient (or normalized forward sensitivity index) of a quantity R with respect to a parameter x is*

$$R_x = \frac{\partial R}{\partial x} \times \frac{x}{R}$$

The sensitivity analysis, is very useful in epidemiological modeling, which is used to investigate the effect of parametric entries as it affects the number of secondary infections. (For more details on Sensitivity Analysis, see [Saltelli, 2002, Christopher Frey and Patil, 2002]).

1.9.5 Bifurcation Analysis

In the study of dynamical system and its analysis, it have been seen that, there are various form of reaction and changes regarding the behaviour of the system and adaptation to such changes. Mathematical examination of such changes in qualitative behaviour of dynamical systems as its parameter passes through a critical value in the system called a bifurcation point. This critical point is also known as Bifurcation Analysis. This changes occur as responses in the behaviour of the dynamical system to for example the stability of an equilibrium point, the appearance of periodic solutions which initially were not present due to changes in initial conditions as well as parameter values in the model. Bifurcation can also occur in a dynamical system when certain parameters

not included initial are added to the model. The parameters which are responsible for these sudden changes in the system are known as bifurcation parameters [Ueta and Chen, 2000]. In mathematical epidemiology, the basic reproduction number have been one of the bifurcation parameters known, when $R_0 = 1$ direction of the bifurcation can be determined either as a supercritical movement or a sub-critical movement. Which is an example of a local bifurcation used in analysing changes in stability of equilibra as a model parameter varies with basic reproduction number R_0 being a key parameter in this regard.

Subcritical Bifurcation which is also called Backward Bifurcation (BB) whenever there is a coexistence between an unstable endemic equilibrium and a stable disease-free equilibrium at R_0 when such coexistence is less than unity near the threshold R0 = 1. Conversely, a supercritical bifurcation also known as Forward Bifurcation (FB) occurs only when a locally asymptotically stable positive equilibrium tends to appear at R_0 slightly above unity. Where Castillo-Chavez and Song [Mathematical Biosciences ..., 2004] proposed a general center manifold theory to determine the existence of forward and backward bifurcations in epidemiological models. (For more details on Bifurcation Theorem, see [Ma, 2009, Melesse and Gumel, 2010, Wang, 2002]).

1.9.6 Optimal Control Analysis

Optimal control theory, a concept derived from the calculus of variation and optimality, is a mathematical technique which has proved very useful in decision making regarding complex biological situations where the behaviour of a dynamical system is described by state variable(s) [Lenhart and Workman, 2007]. With the general knowledge that there are possible ways of modifying and adjusting state variable(s) x when acted upon with suitable controls. Which the dynamic of the system (state x) depends on which usually is the control$u$ [Okosun et al., 2013, Okosun et al., 2017, Oke et al., 2018]. The control dynamics u is to effect either a minimization or maximization of the given objective functional $J(u(t), x(t), t)$ which attains the expected goal and required cost [Fleming and Lions, 2012]. The optimal solution which is desired is said to be achieved when the set goals are met. The functional variables as well depends on the control and the state variables.

The Pontryagin Maximum Principle [Pontryagin et al., 1962] are one of the different methods used in calculating optimal control dedicated to specific models. In its own case, it allows for the calculation of the control strategy model of an ordinary differential system of equation with given constraints. With other powerful control techniques

which are derived using partial differential equation and difference equation. Pontryagin et al., 1962 Optimal control is very useful technique for mathematical epidemiology, it helps in controlling stability of a dynamical system when proper control measure are added to the system. Application of controls in a system changes the dynamical system from one position to a suitable position and controls helps in getting more valuable information of the system and helps more in making better observation.

we consider an optimal control of the form

$$\min_u \{\psi(t_f, x(t_f)) + \int_0^{t_f} g_{0(t,x(t),u(t))dt}\}$$

when

$$f(x(t)) = [x_1(t), x_2(t), ..., x_n(t)]^T \forall \mathbb{R}^n$$

is the control vector given $f(u(t)) = [u_1(t), ..., u_{u_c}(t)]^T \forall \mathbb{R}^m$ is the control vector.

The state and control vectors are governed by the dynamic system described by a set of first order differential equation.

$$\frac{dx}{dt} = f(t, x(t), u(t)); x_0 = x(0), 0 \leqq t \leqq t_f \tag{1.9.7}$$

The function

$$f_{h_0} : T \times \mathbb{R}^n \times \mathbb{R}^m \mathbb{R}^n$$

$$f_{g_0} : T \times \mathbb{R}^n \times \mathbb{R}^m \mathbb{R}^n$$

are continuously differentiable with respect to each component of x and u and piece-wise continuous with respect to t.

1.9.7 Pontrayin's Maximum Principle

The principle converts the maximization and minimization of the objective function J The converstion of maximum and minimum of the objective functional J is carried out basically by Pontrayin Maximum principle, coupled with the state variable into maximising or minimizing pointwisely with respect to the control and the Hamiltonian.

In this thesis, an optimal control problem is formulated with the aim of minimizing the effect of transmission of Zika virus disease and Ebola virus disease in a metapopulation system. We incorporate the model time dependent control measures for preventing intervention of migrating individual to and from both patches . Then we applied optimal control method using Pontrayin's maximum principle to determine the sufficient condition for optimal control of the Ebola virus and Zika virus respectively. Which may lead to further studies that is relevant to more clinical research.

Theorem 8. *If $u^*(t)$ and $x^*(t)$ are optimal problem (Equation) then $\exists$ a piece-wise differential adjoint variable $\theta(t)$ such that*

$$H(t, x(t), u(t), \theta(t)) \leq H(t, x^*(t), u^*(t), \theta(t)) \tag{1.9.8}$$

for all contents of u at each time t, where H is the Hamiltonian and is written as $H = f(t, x(t), u(t)) + \theta(t)g(t, x(t), u(t))$ and

$$\frac{\lambda(t)}{dt} = -\frac{\partial H(t, x^*(t), u^*(t), \theta(t)), \theta(t_f)}{\partial X} = 0$$

Necessary Condition

If $u^*(t)$ and $x^*(t)$ are optimal, then the following condition holds:

$$\frac{\theta(t)}{dt} = -\frac{\partial H(t, x^*(t), u^*(t), \theta(t))}{\partial X}, \tag{1.9.9}$$

$\theta(t_f) = 0$

$$\frac{\partial H(t, x^*(t), u^*(H, \theta(t)))}{\partial U} = 0$$

Sufficient Condition

If $u^*(t)$ and $\theta(t_f)$ satisfies the following conditions:

$$\frac{\theta(t)}{dt} = -\frac{\partial H(t, x^*(t), u^*(t), \theta(t))}{\partial X}, \tag{1.9.10}$$

$\theta(t_f) = 0$

$$\frac{\partial H(t, x^*(t), u^*(H, \theta(t)))}{\partial U} = 0$$

Then $u^*(t)$ and $x^*(t)$ are optimality value, where $\theta(t)$ which denotes the increase of the objective functional and gives the shadow price or co-state variable due to a marginal increase of the state variable. This makes it easy for policy makers and public health organization to generate direct contribution in the objective function and also to control the variable which is represented by the terms $f(t, x(t), u(t))$ in the Hamiltonian. Which also can used for variable change in order to generate some contribution to the objective function in the future as deemed fit by experts. [Pontryagin et al., 1962, Kassa and Hove-Musekwa, 2014, Aweke and Kassa, 2015]

Chapter 2

Literature Review

- Mathematical Epidemiology: Epidemiological models focuses mainly on the movement and the system which the transmission of diseases takes, the dynamics of the transmission and the traits which are transmitted from one place to another, from one community to another, from one state or province to another, from one country to another. the study of epidemic was first carried out as early as in the days of the Prophets, as in the Holy Bible, in the book of Exodus: it described the plague that the Almighty Jehovah God brought unto the people of Egypt through the hands of Moses and the wise men of the land of Egypt where not able to prevent the outbreak of the epidemic, which lead to the death of thousands, both animals and human alike. Aristotle in 384BC gave discussion about some living creature as agent of diseases. Which was developed as a theory in the 16th century. Leeuwenhoek(1723) with the use of enlarging instruments was able to see germs and make physical expression. Physician and Medical laboratory scientist have contributed immensely to the study of mathematical epidemiology. The general mechanism of the rate of spread of infection which are mainly carried by the pathogens such as measles, influenza and Chicken pox. Which mainly are carried by virus are very infectious. While the pathogens such are Gonorrhea, Tuberculosis are transmitted by bacteria and are not viral infectious. The diseases like Malaria are carried vectors and agents who have been infected. This diseases have form part of our daily living, whereby we have epidemic diseases which comes and cause a lot of causality and the endemics diseases which is always present in a given community. Epidemiological models are developed to as to formulate a mathematical model for the spread of the epidemic and are

formulated to analysis the rate of interaction of such epidemic: taking information with relevant technique and then use the information to formulate an hypothesis. Also in some case of Mathematics of Epidemic, data are taken and are used for future prediction, if such case occurs in future. Mathematical modeling of epidemic gives us the underlying facts which contributes and influences the spread of diseases and it also use this same means to possible solutions given then parameters within reach. Kermack and McKenrick in 1927 formulated a straight forward and a simpler model that had similar behaviour to some observed epidemic. McNeil in 1992 [McNeil and Khakee, 1992], modeled the the growth in Britain and China, while Anderson in 1982 [Anderson, 1982], modeled the population dynamics of infectious diseases and mathematical models on sexually transmitted diseases was done by Blythe and Castillo-Chavez in 1990 [Brauer et al., 2012,Blythe and Castillo-Chavez, 1990]. Mathematical Epidemiological models have been developed into ability to model in various ways such as: Models with more compartments, Vertical and Vector Transmission, Non Homogeneous and Age structured populations, Variable infectivity and Macroparasitic infections, and Stochastic Models

- Ebola Virus Disease (EVD); previously called Ebola haemorrhagic fever, causing severe, often fatal illnesses in humans, as the virus which always remain potent, when usually transmitted to human whether living or dead, wild animals alike, the EVD can be spread across human population through human to human transmission. EVD comes with an average case fatality rate around 50%. The rate at which this fatality have varied is between 25% to 90% in previous outbreaks. During the 2014-2016 EVD outbreak in West Africa, which was on record as the largest and most complex Ebola outbreak since the discovery of the virus in 1976 [Team, 2014]. Recording far more cases of death in that single outbreak than all other previous incidence combined. Spreading between countries and territories, starting in Guinea, with movement across land boarders of neighbouring countries like Seria Leone and Liberia [Gire et al., 2014]. The Ebola haemerrhagic fever, belongs to the family of filoviridae which are severe viral and fatal hemorrhagic disease usually coming out with initial symptoms of fever, malaise, bleeding, shock, multi-organ system failure, reduction in sight and neuro systemic pains. This ravaging Ebola Virus is a members of the filoviridae family(Filo Virus) discussed, which is referred to as genus Ebola, together with the genus Marbug Virus and the Genus Gueva Virus. Genus Ebola Virus is itself is subdivided into distinct species, namely: Bundibuggo , Zaire, Sudan, Reston and Taii which are all (EVD). The Ebola virus can also be spread through indirect means of contact with environments contaminated with such fluids. The rate at which the infected zone play a great role in the amount of people affected with the disease when traveling in and out of the infected area is very high [Fulford

et al., 2002]. The first human case of EVD believed to have lead to the current outbreak was the case of a two year old boy who died on 6 December, 2013 in the village of Meliandon in Guinea. Leading to death of family members who had close contact with the deceased, exhibiting symptoms consistent with Ebola infection. Affecting individual who came in direct contact with infected environment, leading to spread of disease to other villages, cities and countries through movement of infected people from one place to another. Example is the case of the Liberian official Late Patrick Swayer [Garrett, 2015, Ambe and Kombe, 2019], who died in Lagos, Nigeria. Which made the virus prevalent in Nigeria because of the first set of people that came in contact with him. Which lead to the death of Dr Stella Emayo Adadavoh. Gire et al [Gire et al., 2014] looked at clinical acts of Ebola virus Disease as it affected human at the Ngaliema Hospital in Zaire. In 1989 Sureau PH et al [Sureau, 1989] conducted medical and clinical observations of haemorrhagic manifestations in Ebola haemorrhagic fever in Zaire. In 1995, EVD due to EBOV-Z reemerged in the DRC [Gulland, 2014] caused an estimated 315 cases and 250 deaths, representing (CFR:81%) of cases that occurred during this large epidemic. While in the 2008 Ebola outbreak, which occurred in Kasai Occidental Province of DRC there were 32 recorded cases with 15 deaths (CFR: 47%) [Gire et al., 2014].

- Zika Virus Disease (ZVD), a viral infection of the family flavivindae (genus flavivirus) mosquito-borne positive stranded RNA, causing massive health emergency, large-scale and unprecedented outbreak in the North and South America [Boorman et al., 1956]. Historically, Zika Virus Disease (ZVD) was discovered in the forest code named Zika forest of Uganda in 1947, ZVD was not prevalent for abut 60 years of the first case found in the equatorial zone of Africa and Asia. ZVD, which often come with symptoms similar to mild form of dengue fever with no specific treatment since the outbreak of ZVD in 2016. Which at that time defiled basic care by medications or vaccines. Making ZVD a global menace to the world health community and the research world. ZVD is usually seen to begin its spread from pregnant women to their babies, leading to acute microcephaly, a severe brain malfunctions, coming with other child birth defects. Zika Virus Disease (ZVD) is primarily spread by female mosquitos as stated by Hayes et al [Hayes, 2009] and the virus is usually transmitted during sexual intercourse or during blood transfusion. During the quarterly report of the Latin America and the Caribbian in 2015, which drew attention on the rapid spread of Zika in countries like Barbados, Brazil, Bolivia, Colombia, The Dominican Republic, Ecuador, El Salvador, Haiti, Honduras, Mexico, Panama, Paraguay, Pueto Rico and Venezuela the most hit. While in 2016, the number of countries with ZVD infection increased to more than 50 countries, all experiencing transmission of ZVD

within their respective local communities. The effect of this prompted the United States in January of 2016 to issue a travel guidance to countries affected with ZVD local transmission of active cases. They also included guideline for pregnant woman, the use of enhanced precautions and considering postponing travel.

The first isolated issue of ZVD was recorded in 1947 after a research on a rhesus macque monkey placed in a cage in the Zika forest of Uganda near the Lake Victoria, by the scientist of yellow fever research institute [Musso et al., 2015]. A second case of isolation from the mosquito was discussed by Oehler E et al in January, 1948 [Oehler et al., 2014]. The first true case of human infection of ZVD was identified by Fauci AS et al [Fauci and Morens, 2016]. Not much of human infection was deducted or investigate for more than 40 years, but in 2007, there were reported cases of 15 confirmed ZVD cases in human from the continent of Africa to southeast Asia, Rasmussen A. B et al [Rasmussen et al., 2016]. In 1954, ZVD was seen to occur in eastern Nigeria where it was seen that the conditions and symptoms showing on three individual who were observed. Where the patients with liver damage and serological studies showed a relationship between jaundice and the development of virus [Rowthorn et al., 2009]. Jan C. et al in 1978 [JAN et al., 1935], looked at the serological studies for arbvirus antibodies. Where they gave an analysis by taking samples of potent serum specimen. They carried out this study on 1.279 human serum specimen collected from adults in south-eastern part of Garbon from June to September 1975 during a multipurpose epidemiological survey. The result of which showed positivity of more than 25% [Krauer et al., 2016]. In 2007, there was a mild outbreak of ZVD characterized by rash on the Yap Island located in the south western pacific Ocean [Sulania et al., 2016]. Which was first time that ZVD was discovered outside the continent of Africa and Asia. This outbreak in April of 2007 was characterised by rash and the likes in Yap Island in the Federated States of Micronesia [Johnson et al., 2005]. Where similar experiment as that which was carried out in Garbon and Nigeria was carried out on random serum samples of selected men investigating RNA of Zika, which is a flavivirus in the family of yellow fever, dengue,West Nie and Japanese encephalitic Virus [Hayes, 2009, Solomon and Mallewa, 2001]. ZVD has spread in the Americas and the Caribbean, following first detection in Brazil in May 2015. The risk of ZVD emergence in Europe increased as imported cases are repeatedly reported. Together with Chikungunya Virus and Dengue Virus. In 2017, Baud D, et al [Baud et al., 2017] showed through a research titled Zika, a new threat to human reproduction, that followed by French Polynesia in 2013 and Brazil in 2015. the ZVD is mainly transmitted through aedes

mosquito bites, but sexual and post-transfusion transmission which most times are not checked, have been reported with symptoms like low grade fever, maculopopular rash, conjuctivitis, myalgia,arthralgia and asthenia. Asymptomatic male-to-female transmission has also been described. Importantly, ZVD RNA can prevent at least 6 months in Semen.

Mathematical modeling in epidemiology is concerned with describing the spread of diseases and its effect on people which cut across discipline like Mathematics, Engineering, Philosophy, Biology, Economics and Sociology. Which are used as tools to formulate and produce a better understood model which explains the spread of infections and ways of controlling them. This have lead to several ground breaking research in mathematical modeling and mathematical biology among them, we count the models of metapopulation and metacommunities. Metapopulation models are defined as system of differential equations generated by discrete spatial models with continuous time metapopulation models have been previously analyzed in numerous articles. This models compare various models of incorporate spatial dynamics by modeling different population and checking their effects to immediate environment. Fulford et al [Fulford et al., 2002], looked at the extreme individuals based models which describe spatial structure within the location of territories The application of mathematics to the study of infectious disease was initiated by Daniel Bernoulli in 1760. Which was necessary at that time because of the public health demand, when there was an outburst of smallpox in his community. He proposed the first deterministic model on pandemic of smallpox by introducing two systems of ordinary differential equations [Bernoulli and Petropolitanae, 1760, Brauer et al., 2001, Brauer et al., 2019]. In 1906 Winchester Hammer postulated that the possible course of an epidemic depends on the rate of contact between susceptible and infectious individuals, which is regarded as secondary infection [Anderson, 1982, Chowell and Nishiura, 2014, Jones, 1884]. A notion which became one of the most important concepts in mathematical epidemiology and mathematical modeling of disease transmission dynamics. Also known as the mass-action principle, which states that the net rate of spread of infection is assumed to be proportional to the product of the density of susceptible individual, multiplied by the density of infectious individuals. Ross in 1911 in his own finding proposed a deterministic model for malaria epidemic, where he showed that reducing the number of anopheles mosquitoes can eradicate malaria disease. In 1926 McKendrick developed a stochastic model for malaria epidemic, where he considered the case of recovery and subdivided the population into compartments: Susceptible-Infected-Removed [Kermack and McKendrick, 1927]. The success of his studies was later in 1927 revisited by McKendrick and Kermack, when they collaborated

and proposed a deterministic model. They proved that the population will be disease free when there is no secondary infection between the infected individuals, and that the disease will invade the population when the number secondary infection is more than one [Kermack and McKendrick, 1927]. An SIR model incorporating births and deaths was formulated in 1929 by Soper [Soper, 1929] which was extended in 1932 by Kermack and McKendrick [Kermack and McKendrick, 1927]. In view of this, very many mathematician took interest in building mathematical models of epidemiology, demonstrating their properties and allowing for possible reduction of the transmission dynamics of diseases. Building on the achievements of Kermack and McKendrick [Kermack and McKendrick, 1927], mathematical modeling have been very useful in curbing spread of infectious diseases in different population, communities around the globe. Helping Government as well as public health agencies make proper health policies using compartmental models which are often described mathematical models. Researchers have extensively studied compartmental models, showing the transmission dynamics and describing mechanism behind the spread of infectious diseases. [Goufo et al., 2014] described a general SIR model with classical derivative and generalized version using the beta-derivative, which enabled detailed study of the endemic equilibrium points. With assumptions that all individuals were initially susceptible such that transmission disease dynamics was governed by bilinear incidence based on mass action law. Also, Vargas-De-Leon (2011) [Vargas-De-León, 2011] examined a SIS epidemic model which analysed stability of the steady states using Lyapunov function and the model also established structure with standard incidence.

In another related work, [Liu, 2013] presented a SEIRS Mathematical model, with incorporation of media coverage with random perturbation. Dealing with stability and boundedness of disease—free as well as endemic equilibria of the deterministic model. Related to the above, Li et al (2006) [Li et al., 2006] also studied an SEIR model with special emphasis on the different rate at which infected individuals are pushed in the latent (exposed), infected and recovered period. With assumptions that individuals move into the susceptible and exposed classes are constant. Castillo-Chavez and Feng [Mathematical Biosciences ..., 2004, Brauer et al., 2019] in their several works on mathematical models in epidemiology, proposed a SEIR model for TBD, establishing global stability of the disease-free equilibrium. Which emphasizes the stability of disease in a broader region and existence of a unique endemic equilibrium (EE) whenever basic reproduction number $R_0 > 1$. Tchepmo Djomegni et al [Tchepmo Djomegni et al., 2019] considered a mathematical model to understand the transmission dynamics of HIV/AIDS in an environment, incorporating isolation of individuals by physical separation. [Adeniyi et al., 2020]

in a SQIRE mathematic model presented a COVID-19 disease dynamics, with empirical data from the Nigeria Centre for Disease Control (NCDC). With compartments for Quarantined humans, Infectious humans, Recovered humans and Education compartment. [Yang and Xiao, 2010] considered a SIRV model including a vaccinated compartment in which the analysis of the model shows that increasing the rate of vaccination aids eradication of the disease. Literature surveyed beforehand involved the transmission dynamics of infectious diseases which are contracted by susceptible individual, which is referred to as in-host. While diseases such as Dengue fever, Malaria fever and Zika Virus always require host and vector compartment in the dynamics of the model. In view of this, our Zika Virus disease model requires two interacting populations of both human host and mosquito vector for the Zika Virus disease (ZVD) transmission dynamics. In May 2015,World Health Organization (WHO) in its report, revealed the first local transmission of ZVD in the north east of Brazil [Daudens-Vaysse et al., 2016]. In which by February 2016, suspected ZVD cases have been reported around 20 countries in and around Americas and Southern America, with Brazilian Ministry of Health reporting an estimated cases of about 500,000 to 1,500,000 suspected ZVD occurrence[[Organization et al., 2016, Daudens-Vaysse et al., 2016, Duffy et al., 2009]]. While Ebola virus disease (EVD), which was declared an epidemic of Public Health Emergency of International Concern (PHEIC) by World Health Organization(WHO) in August, 2014 [Organization et al., 2014] Mathematical models for transmission dynamics of ZVD and EVD are useful in providing better insight into the behaviour of the diseases. Which have great influenced public health awareness, helped in decision making processes regarding the intervention strategies for preventing and adequate control strategies of EVD and ZVD.

Metapopulation represents one of the most recent development in the long- running ecological research on population regulation. The metapopulation concept has been influential in the study of ecology. It assumes that the rate of distribution of many species can be described as a system with a local community such that rate at which the community interacts is checked to turnover a particular result which is checked and evaluated. Matapopulation is also considered as a set of discrete populations of the same species, in the same general geographical area, that may exchange individual through migration, dispersal or human-mediated movement. The metapopulation concepts lends itself to modeling because its core dynamics of population. This model are used to evaluate the condition of species habitat, the habitat management often includes controlling the rate and pattern of habitat. Schtickzelle et al [Schieffelin et al., 2014], used a structured metapopulation model to study effect of grazing on the bog fertility butterfly in south-eastern Belgium. In 2004 Julien Arino et al [Arino

and Van den Driessche, 2003] developed a metapopulation model of the carnivorous land snail to control timber harvest. In another related work, [Fulford et al., 2002] developed a SEIR Metapopulation Dynamics of an Infectious Disease of Tuberculosis. The metapopulation mathematical model presented in this work is motivated from the studies carried out by [Njagarah and Nyabadza, 2014] where they researched the transmission dynamics of a metapopulation mathematics model for cholera between communities linked by migration in conjunction with movement interaction of human in two populations.

Chapter 3

Mathematical Model Formulation and Analysis

This chapter is devoted to the formulation of the two metapopulation cases of Ebola model and Zika model as well as their full descriptions with respect to flow diagrams, parameters and variables involved.

3.1 Ebola Model

Ebola virus disease (EVD) is a severe, often fatal illness in humans which manifest as the Ebola fever disease. A virus which belongs to the family of filoviridae is known to be serious and deadly hemorrhagic disease which shows symptoms of gastrointestinal disorder, excessive fever, bleeding and multiple organ failure [Dowell et al., 1999,**?**]. EVD outbreaks have fatality rate of up to 90% [Dixon and Schafer, 2014]. Ebola first appeared in 1976 in two simultaneous outbreaks,in Nzara, Sudan and in Yambuku, Democratic Republic of Congo [Team et al., 1978]. Sometimes in October of 2014, 244 out of 450 health care personnel died having been infected with Ebola [Rewar and Mirdha, 2014].

The World Health Organisation (WHO) and respective governments reported a total of 28,616 suspected cases

of EVD and 11,310 deaths from infected individuals [Schieffelin et al., 2014].The rate at which the infected zone play a great role in the amount of people affected with the disease when traveling in and out of the infected area is very high [Argueta and Wasem, 2016].

Believed that the first human case of EVD leading to the current outbreak was a two year old boy who died on 6 december, 2013 in the village of Meliandon in Guinea, which lead to death of close members of his family and symptoms consistent with Ebola infection was observed [Rewar and Mirdha, 2014, Heen, 2016]. Which also affected people who came in direct contact with the infected environment and the disease was spread to other villages, cities and countries through movement of infected people from one place to another. Example is the case of the Liberian official late Patrick Swayer [Shuaib et al., 2014, Heen, 2016], who died in Lagos, Nigeria.

Mathematical modeling has been a great too in the hands of researchers in designing measures of prevention and control of infectious diseases [Kermack and McKendrick, 1927, Brauer et al., 2001, Goufo and Maritz, 2015]. Mathematical modeling have been used to better understand the transmission mechanism of infectious diseases. It has been able to predict the features that are dominant in the spread of diseases. The models helps in making predictions with effect to manifestation of the disease, and such are used to formulate control strategies.

Metapopulation concept have served as a great tool in the analysis of dis-aggregated population [Arino and Van den Driessche, 2003]. The models involves movement of individuals between communities which are connected. For example, [Arino and Van den Driessche, 2003, Arino et al., 2005] developed a multi city epidemic model and a multi-species epidemic model, where they check the effect of transmission of epidemic as relation to the patches and several disease. [Wang and Zhao, 2004, Wang and Zhao, 2008] looked at the occurrence of disease transmission in communities connected by migration, hoe disease dynamics in a patchy environment. [Salmani, 2005] [Goufo et al., 2014] presented a fractional SEIR metapopulation model of the spread of measles with restriction to four patches. This paper is motivated by an article on guardian print media published on 1st August, 2019 gave a report that "Rwanda's government briefly closed and then reopened part of a busy land border with the Democratic Republic of the Congo on Thursday, prompting panic and confusion in both countries." The re-emergence of Ebola virus disease in Democratic Republic of Congo (DRC), which prompted other countries who share boarder with the country to close down their boarders. We use a mathematical model to study the effect of movement of people from one population to another with the effect of the Ebola virus disease (EVD) dynamics.

3.2 Ebola Model Formation

We consider a SEIR metapopulation model, we consider two patches representing two communities connected by the movement of individuals through means of transportation. In and Ebola virus disease transmission, which have a latent state of few days, allowing individuals few day of movement before the disease sets to its full capacity in the body system. We assume that it is only the healthy carrier who can move from one place to another, we are looking at the movement between connected cities. In a case where an individual works in the city, but resides outside the city.

The assumption is necessitated because an individual who is susceptible in a population can be infectious in another population due to movement within the two populations. So also an infectious individual can move within populations amidst the infectious class. Movement within the infected class may be more shorter time than the time required for individual to move from one sub population into another. Transmission resulting from individuals movement to and fro each patch is assumed to be very much likely, given the conditions that the bodily fluid of a susceptible individual can be an easy means of how Ebola virus disease is easily spread. Transmission is highly probably at entry points, in case of a migrated who is infected, bodily fluid of an infected person gives a high risk of contamination.

In general transmission dynamics of Ebola heamealogious in humans is complex due to local and long range movements of individuals. It is of note that movement between communities and population depends mainly on the size of the population as well as the distance between these populations Such close contact with bodily fluids, blood contact, contact with body organs of an infected individual or other bodily fluids of infected animals.

The model is formulated with a general population which is considered in two patches with reference to Ebola virus disease transmission and the disease states of individuals in the system at time t. The compartments are divided into classes of individuals in the population who are immunologically naive, they are the susceptible class denoted by S. With the exposed individuals denoted by E, while the infected class is denoted by I and those individuals who have recovered are denoted as R but with temporary immunity, because they are prone to getting infected if they contract the disease again. We assume that the movement within patches are homogenous, we also assume that the Ebola virus disease is highly infectious.

The model explore the possibility of movement of susceptible individuals from one patch to another patch. During which we assume that immigration of susceptible individuals can be the cause of infection because susceptible individual might be infected which makes it possible that susceptible individuals in patch 1 can be infectious in patch 2 at the rate $\omega_1 S_1$ while the susceptible individual can be infectious at the rate $\omega_2 S_2$ in the exposed class of patch 1 moving onward to being infectious in patch 1. The rate at which new susceptible are recruited into the system is at rates A_1 and A_2 for the first and second patch respectively.

Which can be as a means of new birth or immigration of a susceptible individual at time t. The movement of infectious individual within the two patches are the typical individuals who show symptoms which play a very important role in metapopulation model of Ebola virus disease since this class contributes to the transmission of the disease. It is very important to note that the time which the virus will take in each and every individual's body before manifestation of its symptoms differs from an individual to another. The overall dynamics of the population account for by the combined effects of two patches. We assumed that the recovered individuals might die naturally at the rate $\mu_1 R_1$ and $mu_2 R_2$ in the two patches respectively.

As a matter of fact, the effect of the disease would have taken a great toll on the physical well being of the recovered individual, it is very unlikely that there will be movement between the two patches, because the recovered individual will be confined in their patch having just recovered from a disease. The susceptible population is going out following a possibility of natural death at rate $\mu_1 S_1$ and $\mu_2 S_2$ and they move from patch to patch at rate $\omega_1 S_1$ and $\omega_2 S_2$ respectively. The exposed compartment suffer natural death at rates $\mu_1 E$ and $\mu_2 E_1$ respectively with respect to the rate of exposure and differentials in immunity. While infected compartment suffer natural death at rate $\mu_1 I_1$ and $\mu_2 I_2$ respectively. They also suffer death due to the disease at rates $\delta_1 I_1$ and $\delta_2 I_2$ respectively.

So also the rate of transmission of disease within patches from one compartment to another is such that, susceptible individuals becomes exposed at a rate $\beta_i S_i I_i$ where $i = (1, 2)$ for both patches. The exposed individuals becomes infective at rate κ_i where $i = (1, 2)$ for both patches, while the infected individuals recover at rate α_i for both patches where $i = (1, 2)$. Because of the recent resurgence of EVD in DRC and other neighbouring countries, with possibility of EVD in individual who have previously recovered, we then used a as the rate at which recovered individuals lose their assumed immunity and become suceptible again. . The diagram representing the flow of the disease progression is given below :

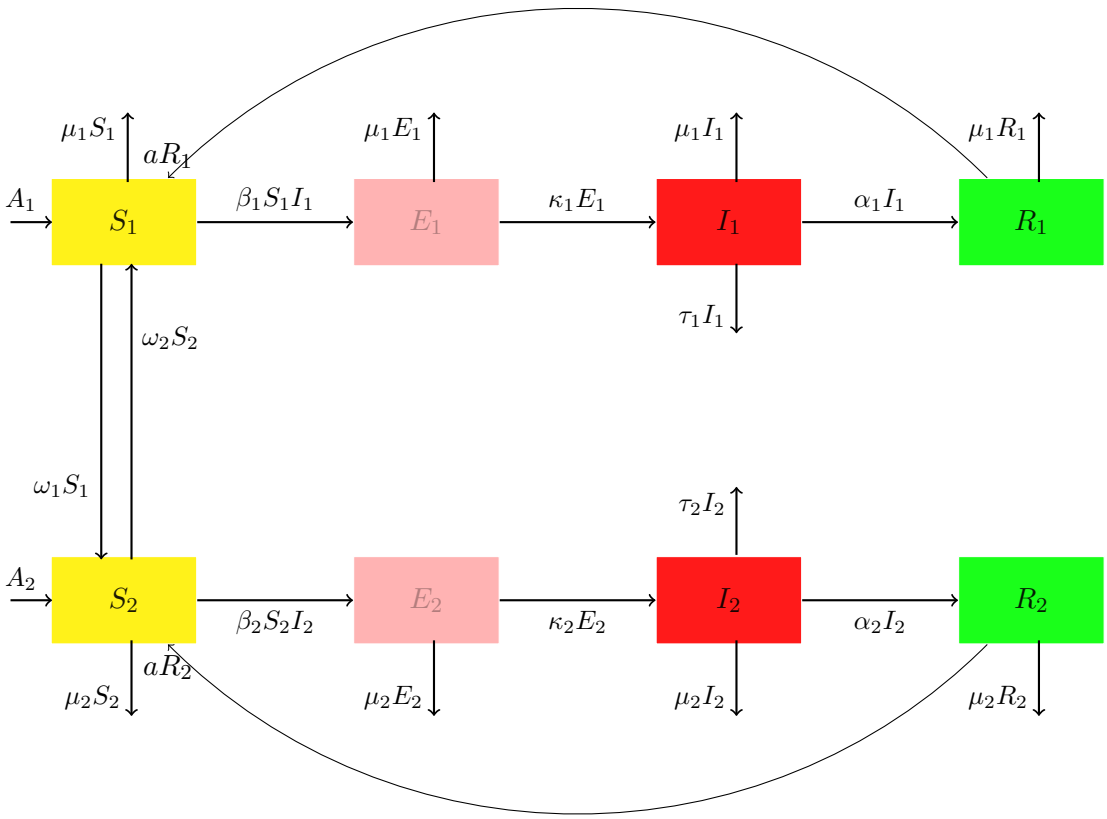


Figure 3.1: Schematic diagram of the disease dynamics

When we assume that the exposed period after the transmission of infection to susceptible individual before transiting the infection is The initial conditions of the model are such that $S_1(0) > 0$, $E_1(0) \geqslant 0$ $I_1(0) \geqslant 0$, $R_1(0) \geqslant 0$ for the first patch and $S_2(0) > 0$, $E_2(0) \geqslant 0$ $I_2(0) \geqslant 0$, $R_2(0) \geqslant 0$ for the second patch.

The sub-population are connected by migration of individuals from first community to the second and back. A key issue of interest is the fact that disease can be in extinction in one sub-population and re-emerge in the other. Which makes the rate of infection different between the subpopulation. The total population of the first patch, namely N_1 is the interaction of the sum of S_1, E_1, I_1 and R_1 in the system of equation(2.1) and the total population of the second patch, namely N_2 evolves around the sum of S_2, E_2, I_2 and R_2 in the system of equation (3.2.1), considering the fact that sub-population are independent of other adjoining communities geographically

because they are not connected,but migration and inter communal interaction allows for some sort of connection then the development of the sub-population is given after showing the total meta-population dynamics.

$$\begin{cases} \frac{dS_1}{dt} &= A_1 - \beta_1 S_1 I_1 - (\mu_1 + \omega_1) S_1 + \omega_2 S_2 + a R_1 \\ \frac{dE_1}{dt} &= \beta_1 S_1 I_1 - (\kappa_1 + \mu_1) E_1 \\ \frac{dI_1}{dt} &= \kappa_1 E_1 - (\alpha_1 + \mu_1 + \tau_1) I_1 \\ \frac{dR_1}{dt} &= \alpha_1 I_1 - \mu_1 R_1 - a R_1 \\ \frac{dS_2}{dt} &= A_2 - \beta_2 S_2 I_2 - (\mu_2 + \omega_2) S_2 + \omega_1 S_1 + a R_2 \\ \frac{dE_2}{dt} &= \beta_2 S_2 I_2 - (\kappa_2 + \mu_2) E_2 \\ \frac{dI_2}{dt} &= \kappa_2 E_2 - (\alpha_2 + \mu_2 + \tau_2) I_2 \\ \frac{dR_2}{dt} &= \alpha_2 I_2 - \mu_2 R_2 - a R_2 \end{cases} \tag{3.2.1}$$

3.2.1 Positivity and Boundedness of Ebola Model Solution

The system of equation (3.2.1) is a vector (multi-variables polynomial) function of class C^{∞} , by the Cauchy-Piccard theorem [Wouk, 1963] there exists a unique (local) solution of the system (3.2.1). Which is on the premise that for the rest of the analysis, we assume that the solution of (3.2.1) is non-negative. Ensuring non-negativity of both populations at all time.

Table 3.1: Description of State Variables and Parameters

State Variables	Description
N_1, N_2	Total human population in patch one and two.
S_1, S_2	Susceptible population in patch one and two.
E_1, E_2	Exposed population in patch one and two.
I_1, I_2	Infected population in patch one and two.
R_1, R_2	Recovered population in patch one and two.
Parameters	Description
A_1, A_2	Recruitment rate of human into patch 1 and patch 2 respectively.
μ_1, μ_2	Natural death rate of respective individuals in both patch 1 and patch 2.
α_1, α_2	Recovery rate for each patch respectively.
ω_1, ω_2	Movement of susceptible human population within both patches respectively.
a	Rate at which Recovered Individuals becomes Susceptible for both patch.
β_1, β_2	Transmission probability of Susceptible Individual becomes infected with the virus.
τ_1, τ_2	Disease induced death rate of respective individuals in both patch 1 and patch 2.
κ_1, κ_2	Exposed individual becomes infected in both patch 1 and patch 2 at this rate.

3.2.2 Boundedness of Solution

Proposition 3.2.1. *The functions $S_1, E_1, I_1, R_1, S_2, E_2, I_2, R_2$ solutions of the system (3.2.1) are bounded.*

Proof. Consider total human population for both patches

$$N_T = N_1 + N_2, \tag{3.2.2}$$

where

$$N_1 = S_1 + E_1 + I_1 + R_1, \quad N_2 = S_2 + E_2 + I_2 + R_2. \tag{3.2.3}$$

Differentiating (3.4.1) with respect to t and taking into account for (3.2.1), we get

$$\begin{aligned}
N' &= N_1^{'} + N_2^{'} \\
&= S_1^{'} + E_1^{'} + I_1^{'} + R_1^{'} + S_2^{'} + E_2^{'} + I_2^{'} + R_2^{'} \\
&= A_1 + A_2 - \mu_1(S_1 + E_1 + I_1 + R_1) - \mu_2(S_2 + E_2 + I_2 + R_2) - \tau_1 I_1 - \tau_2 I_2 \\
&= A_1 + A_2 - \mu_1 N_1 - \mu_2 N_2 - \tau_1 I_1 - \tau_2 I_2 \\
&\leq A_1 + A_2 - \mu_T(N_1 + N_2) - \tau_1 I_1 - \tau_2 I_2 \\
&\leq A_1 + A_2 - \mu_T N_T - \tau_1 I_1 - \tau_2 I_2 \\
&\leq A_1 + A_2 - \mu_T N_T \quad (\text{since } I_1, I_2 \geq 0),
\end{aligned}$$

where $\mu_T \leq min\{\mu_1, \mu_2\}$. Solve the differential inequality, we get

$$N_T(t) \leq \frac{A_1 + A_2}{\mu_T} + \left(N_T(0) - \frac{A_1 + A_2}{\mu_T}\right) e^{-\mu_T t} = N_T(0)e^{-\mu_T t} + (1 - e^{-\mu_T t})\frac{A_1 + A_2}{\mu_T}.$$

If $N_T(0) \leq \frac{A_1+A_2}{\mu_T}$, then $N_T(t) \leq \frac{A_1+A_2}{\mu_T}$ for all $t > 0$. However, if $\frac{A_1+A_2}{\mu_T} < N_T(0)$, then $N_T(t) \leq N_T(0)$ for all $t > 0$. In either cases we always have

$$N_T(t) \leq \max\left(N_T(0), \frac{A_1 + A_2}{\mu_T}\right)$$

for all $t \geq 0$. This shows that the total human population N_T is bounded.

Theorem 9. *Given the model equation (3.2.1) which has a bounded positive solution on the biological feasible region is positively invariant in region Ω defined by*

$$\left\{(S_1, E_1, I_1, R_1, S_2, E_2, I_2, R_2)\epsilon R_+^8 : N \leqslant \frac{A_1 + A_2}{\mu_n}\right\}$$

with initial conditions $S_1(0) > 0, E_1(0) \geqslant 0, I_1(0) \geqslant 0, R_1(0) \geqslant 0$ and $S_2(0) > 0, E_2(0) \geqslant 0 I_2(0) \geqslant 0, R_2(0) \geqslant 0$

Proof. Let the total population for both patches of the model be

$$N_T(t) = N_1(t) + N_2(t) \tag{3.2.4}$$

such that

$$N_1(t) = S_1 + E_1 + I_1 + R_1$$

$$N_2 = (t)S_2 + E_2 + I_2 + R_2$$

Differentiating with respect to t

$$N_T^{'}(t) = N_1^{'}(t) + N_2^{'}(t) \tag{3.2.5}$$

$$N_T^{'}(t) = S_1^{'}(t) + E_1^{'}(t) + I_1^{'}(t) + R_1^{'}(t) + S_2^{'}(t) + E_2^{'}(t) + I_2^{'}(t) + R_2^{'}(t)$$

$$N_T^{'}(t) = A_1 - \beta_1 S_1 I_1 - (\mu_1 + \omega_1)S_1 + \omega_2 S_2 + aR_1 + \beta_1 S_1 I_1 - (\kappa_1 + \mu_1)E_1 + \kappa_1 E_1 - (\alpha_1 + \mu_1 + \tau_1)I_1 + \alpha_1 I_1 - \mu_1 R_1$$

$$-aR_1 + A_2 - \beta_2 S_2 I_2 - (\mu_2 + \omega_2)S_2 + \omega_1 S_1 + aR_2 + \beta_2 S_2 I_2 - (\kappa_2 + \mu_2)E_2 + \kappa_2 E_2 - (\alpha_2 + \mu_2 + \tau_2)I_2 + \alpha_2 I_2 - \mu_2 R_2 - aR_2$$

$$N_T^{'}(t) = A_1 - \mu_1 S_1 - \mu_1 E_1 - \mu_1 I_1 - \mu_1 R_1 + A_2 - \mu_2 S_2 - \mu_2 E_2 - \mu_2 I_2 - \mu_2 R_2 - \tau_1 I_1 - \tau_2 I_2$$

$$N_T^{'}(t) = A_1 - \mu_1(S_1 + E_1 + I_1 + R_1) + A_2 - \mu_2(S_2 + E_2 + I_2 + R_2) - \tau_1 I_1 - \tau_2 I_2$$

$$\therefore = A_1 + A_2 - \mu_1(N_1(t)) - \mu_2(N_2(t)) - \tau_1 I_1 - \tau_2 I_2$$

making assumption that

$$\mu_n = min\{\mu_1, \mu_2\}$$

$$N_T^{'}(t) = A_1 + A_2 - \mu_n(N_1(t) + N_2(t)) - \tau_1 I_1 - \tau_2 I_2 \tag{3.2.6}$$

since $\tau_1 I_1$ and $\tau_2 I_2$ are non-negative reduces to

$$N_T^{'}(t) = A_1 + A_2 - \mu_n N_T(t)$$

$$\therefore \frac{dN_t(t)}{dt} + \mu_n N_T(t) \leq A_1 + A_2$$

$$\frac{d}{dt}(e^{\mu_n(t)} N_T(t)) \leq (A_1 + A_2) e^{\mu_n(t)}$$

Integrating with respect to t yields

$$N_n(t) \leq \frac{(A_1 + A_2)}{\mu_n} + K e^{-\mu_n(t)} \tag{3.2.7}$$

taking the limit as $t \to \infty$

$$\lim_{t \to \infty} N_n(t) \leq \frac{(A_1 + A_2)}{\mu_n}$$

Thus

$$0 \leq N_n(t) \leq N_n(t) \leq \frac{(A_1 + A_2)}{\mu_n}$$

□

Lemma 1. *The space of all possible states of the system of equation(3.2.1) is given by*

$$\Omega := \left\{ (S_1, E_1, I_1, R_1, S_2, E_2, I_2, R_2) \epsilon R_+^8 : N \leqslant \frac{A_1 + A_2}{\mu_n} \right\}$$

where $\mu_n = min\{\mu_1, \mu_2\}$

3.2.3 Equilibrium points

The model has four equilibrium points: Ebola free equilibrium (EFE) E_0 of both patches, endemic free equilibrium in each of the patch E_1 and E_2 which are the boundary endemic equilibria and endemic equilibrium in both patches E_3 referred to as interior equilibrium all in the domain Ω as obtained from the system of equations (3.2.1). With non negative initial conditions.

The equilibrium points of the system (3.2.1) are determined by solving the resulting equations in each patch obtained by equating the derivatives of the system (3.2.1) to zero.

Ebola Free Equilibrium point

E_0 is the Ebola free equilibrium (EFE) which occurs when the both communities which are connected via immigration do not have any case of Ebola Virus infection.

$$E_0 = (S_1^o, 0, 0, 0, S_2^o, 0, 0, 0)\, \epsilon R_+^8. \tag{3.2.8}$$

where

$$S_1^o = \frac{A_1\ \mu_2 + A_1\ \omega_2 + A_2\ \omega_2}{\mu_1\ \mu_2 + \mu_1\ \omega_2 + \mu_2\ \omega_1}, S_2^o = \frac{(\mu_2\omega_1 + \omega_1\omega_2)A_1 + (\omega_1\omega_2 + \mu_1\mu_2 + \mu_2\omega_1 + \mu_1\omega_2)A_2}{\mu_1\ \mu_2^2 + \mu_1\mu_2\ \omega_2 + \mu_2^2\ \omega_1 + \mu_2\omega_1\omega_2 + \mu_1\mu_2\omega_2 + \mu_1\omega_2^2}$$

Ebola Free Endemic Equilibrum points

E_1 is the Ebola free endemic equilibrium which occurs when Ebola is prevalent in the first patch but not present in the second patch, which in turn makes recruitment of healthy individuals almost zero. Susceptible Individuals will not migrate to the community that is Ebola prevalent or migration will be almost zero.

$$E_1 = (S_1^*, E_1^*, I_1^*, R_1^*, S_2^*, 0, 0, 0)\epsilon R_+^8. \tag{3.2.9}$$

where

$$S_1^* = \frac{U_3A_1 + a\alpha_1 I_1^*}{\beta_1 I_1^* \mu_1}, S_2^* = \frac{A_2}{\beta_2 I_2^* \mu_2}$$

$$E_1^* = \frac{\beta_1 I_1^* \left(U_3A_1 + a\alpha_1 I_1^*\right)}{(\beta_1 I_1^* - \mu_1)U_1},$$

$$I_1^* = \frac{\kappa_1\beta_1 I_1^* \left(U_3A_1 + a\alpha_1 I_1^*\right)}{(\beta_1 I_1^* - \mu_1)U_1U_2}$$

$$R_1^* = \frac{\alpha_1 I_1^*}{U_3}$$

$$U_1 = (\kappa_1 + \mu_1), U_2 = (\alpha_1 + \mu_1 + \tau_1), U_3 = (a + \mu_1)$$

E_2 is the Ebola free endemic equilibrium which occurs when Ebola is prevalent in the second patch but not present in the first patch, which in turn makes recruitment of healthy individuals almost zero since susceptible individuals will not migrate to the community that is Ebola prevalent or migration will be almost zero.

$$E_2 = (S_1^*, 0, 0, 0, S_2^*, E_2^*, I_2^*, R_2^*)\epsilon R_+^8. \tag{3.2.10}$$

where

$$S_1^* = \frac{A_1}{\beta_1 I_1^* \mu_1}, S_2^* = \frac{U_3 A_2 + b\alpha_2 I_2^*}{\beta_2 I_2^* \mu_2},$$
$$E_2^* = \frac{\beta_2 I_2^* \left(U_6 A_2 + b\alpha_2 I_2^*\right)}{(\beta_2 I_2^* - \mu_2) U_2},$$

$$I_2^* = \frac{\kappa_2 \beta_2 I_2^* \left(U_6 A_2 + b\alpha_2 I_2^*\right)}{(\beta_2 I_2^* - \mu_2) U_2 U_5}$$

$$R_2^* = \frac{\alpha_2 I_2^*}{U_6}$$

$$U_4 = (\kappa_2 + \mu_2), U_5 = (\alpha_2 + \mu_2 + \tau_2), U_6 = (\mu_2 + b)$$

Ebola Endemic Equilibrum point

E_3 is the Ebola endemic equilibrium (EEE) which occurs when Ebola is prevalent in the both patches, which in turn makes recruitment of healthy individuals almost zero as well since susceptible individuals will not migrate to

and from both communities that is Ebola prevalent and migration will be almost zero.

$$E_3 = (S_1^{**}, E_1^{**}, I_1^{**}, R_1^{**}, S_2^{**}, E_2^{**}, I_2^{**}, R_2^{**}) \epsilon R_+^8. \tag{3.2.11}$$

where

$$S_1^{**} = \frac{U_6U_3A_1U_4 + a\alpha_1 I_1^* U_4U_6 + U_3\omega_2 U_6 A_2 + bU_3\omega_2\alpha_2 I_2^*}{U_0U_3U_4U_6 - U_1U_2U_3U_6}$$

,

$$S_2^{**} = \frac{\begin{array}{r} U_7A_2(U_0U_3U_4U_6 - U_1U_2U_3U_6) + b\alpha_2 I_2^*(U_0U_3U_4U_6 - U_1U_2U_3U_6) \\ + U_7\omega_1(U_3U_4U_6A_1U_4U_6\alpha_1 I_1^* + U_3U_6\omega_2 A_2 + bU_3\omega_2 I_2^*) \end{array}}{U_4U_7(U_0U_3U_4U_6 - U_1U_2U_3U_6)}$$

$$E_1^{**} = \frac{\beta_1 I_1^*(U_6U_3A_1U_4 + a\alpha_1 I_1^* U_4U_6 + U_3\omega_2 U_6A_2 + bU_3\omega_2\alpha_2 I_2^*)}{U_1(U_0U_3U_4U_6 - U_1U_2U_3U_6)}$$

$$E_2^{**} = \frac{\beta_2 I_2^* \begin{pmatrix} U_7A_2(U_0U_3U_4U_6 - U_1U_2U_3U_6) + b\alpha_2 I_2^*(U_0U_3U_4U_6 - U_1U_2U_3U_6) \\ + U_7\omega_1(U_3U_4U_6A_1U_4U_6\alpha_1 I_1^* + U_3U_6\omega_2 A_2 + bU_3\omega_2 I_2^*) \end{pmatrix}}{U_4U_5U_7(U_0U_3U_4U_6 - U_1U_2U_3U_6)}$$

$$I_1^{**} = \frac{\kappa_1\beta_1 I_1^*(U_6U_3A_1U_4 + a\alpha_1 I_1^* U_4U_6 + U_3\omega_2 U_6A_2 + bU_3\omega_2\alpha_2 I_2^*)}{U_1U_2(U_0U_3U_4U_6 - U_1U_2U_3U_6)}$$

$$I_2^{**} = \frac{\kappa_2\beta_2 I_2^* \begin{pmatrix} U_7A_2(U_0U_3U_4U_6 - U_1U_2U_3U_6) + b\alpha_2 I_2^*(U_0U_3U_4U_6 - U_1U_2U_3U_6) \\ + U_7\omega_1(U_3U_4U_6A_1U_4U_6\alpha_1 I_1^* + U_3U_6\omega_2 A_2 + bU_3\omega_2 I_2^*) \end{pmatrix}}{U_4U_5U_6U_7(U_0U_3U_4U_6 - U_1U_2U_3U_6)}$$

$$R_1^{**} = \frac{\alpha_1 I_1^*}{U_3}, R_2^{**} = \frac{\alpha_2 I_2^*}{U_6}$$

For the disease free equilibrium, we assume that in both sub-populations, there are no infected individuals, neither are there any one who is exposed. it is assumed that all the compartment are without the infection. Which reduces the system of equations (3.2.1) to

$$\frac{dS_1}{dt} = A_1 + \omega_2 S_2 - \omega_1 S_1 - \mu_1 S_1 \tag{3.2.12}$$

$$\frac{dS_2}{dt} = A_2 + \omega_1 S_1 - \omega_2 S_2 - \mu_2 S_2 \tag{3.2.13}$$

Setting the right hand side (RHS) of equation (3.2.14) and (3.2.15) to zero and solving for the equilibrium points, we obtain

$$S_1^o = \frac{\omega_2(A_1 + A_2) + \mu_2 A_1}{\omega_1\mu_2 + \mu_1\omega_2 + \mu_1\mu_2}, S_2^o = \frac{(\mu_2\omega_1 + \omega_1\omega_2)A_1 + (\omega_1\omega_2 + \mu_1\mu_2 + \mu_2\omega_1 + \mu_1\omega_2)A_2}{\mu_1\ \mu_2^2 + \mu_1\mu_2\ \omega_2 + \mu_2^2\ \omega_1 + \mu_2\omega_1\omega_2 + \mu_1\mu_2\omega_2 + \mu_1\omega_2^2}$$

Therefore, with non negative initial conditions

$$DFE(S_1^o, E_1, I_1, R_1, S_2^o, E_2, I_2, R_2) = (S_1^o, 0, 0, 0, S_2^o, 0, 0, 0)\,.$$

3.2.4 Basic Reproduction Number

To find R_0 which is the basic reproduction number for this system, we use the next generation matrix described by [Diekmann et al., 1990, Van den Driessche and Watmough, 2002, van den Driessche and Watmough, 2002] to calculate the basic reproduction number of the system of equation (3.2.1) where we define matrices $\mathbb{F}$ and $\mathbb{V}$ the inflow and outflow from the Exposed and Infectious compartments.

$$\mathbb{F} = \begin{bmatrix} 0 & \beta_1 S_1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \beta_2 S_2 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

and

$$\mathbb{V} = \begin{bmatrix} c_0 & 0 & -\delta_2 & 0 \\ -\kappa_1 & c_1 & 0 & 0 \\ -\delta_2 & 0 & c_2 & 0 \\ 0 & 0 & -\kappa_2 & c_3 \end{bmatrix}$$

where

$$c_0 = (\kappa_1 + \mu_1)c_1 = (\tau_1 + \alpha_1 + \mu_1), c_2 = (\kappa_2 + \mu_2), c_3 = \tau_2 + \alpha_2 + \mu_2$$

Where the largest eigenvalue and hence the spectral radius $\rho(FV^{-1})$ is R_0. Since the existence of infection is isolated in respective community which is connected only through movement of individuals or migration, then the communities specific reproduction numbers will be given below,

$$\mathbb{FV}^{-1} = \begin{bmatrix} \frac{\beta_1 S_{10}\kappa_1 c_2}{c_1(c_0c_2-\mu_1\mu_2)} & \frac{\beta_1 S_1}{c_1} & \frac{\beta_1 S_1 \kappa_1 \mu_2}{c_1(c_0c_2-\mu_1\mu_2)} & 0 \\ 0 & 0 & 0 & 0 \\ \frac{\beta_2 S_2 \mu_1 \kappa_2}{c_3(c_0c_2-\mu_1\mu_2)} & 0 & \frac{\beta_2 S_2 c_0 \kappa_2}{c_3(c_0c_2-\mu_1\mu_2)} & \frac{\beta_2 S_2}{c_3} \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

where

$$c_0 = (\kappa_1 + \mu_1), c_1 = (\tau_1 + \alpha_1 + \mu_1), c_2 = (\kappa_2 + \mu_2)\, c_3 = (\tau_2 + \alpha_2 + \mu_2).$$

With corresponding eigenvalues,

$$\frac{1}{2}\frac{S_1\beta_1 c_2 c_3\kappa_1 + S_2\beta_2 c_0 c_1\kappa_2 + \sqrt{\begin{array}{l} {S_1}^2{\beta_1}^2{c_2}^2{c_3}^2{\kappa_1}^2 - 2\,S_1S_2\beta_1\beta_2 c_0c_1c_2c_3\kappa_1\kappa_2 \\ \quad + 4\,S_1S_2\beta_1\beta_2 c_1c_3\mu_1\mu_2\kappa_1\kappa_2 + {S_{20}}^2{\beta_2}^2{c_0}^2{c_1}^2{\kappa_2}^2 \end{array}}}{c_1c_3\left(c_0c_2 - \mu_1\mu_2\right)}$$

,

$$-\frac{1}{2}\frac{S_1\beta_1 c_2 c_3\kappa_1 + S_2\beta_2 c_0 c_1\kappa_2 + \sqrt{\begin{array}{l} {S_{10}}^2{\beta_1}^2{c_2}^2{c_3}^2{\kappa_1}^2 - 2\,S_1S_2\beta_1\beta_2 c_0c_1c_2c_3\kappa_1\kappa_2 \\ \quad + 4\,S_1S_2\beta_1\beta_2 c_1c_3\mu_1\mu_2\kappa_1\kappa_2 + {S_2}^2{\beta_2}^2{c_0}^2{c_1}^2{\kappa_2}^2 \end{array}}}{c_1c_3\left(c_0c_2 - \mu_1\mu_2\right)}$$

0, 0

such that

$$R_0 = \frac{1}{2}\frac{S_1\beta_1 c_2 c_3\kappa_1 + S_2\beta_2 c_0 c_1\kappa_2 + \sqrt{\begin{array}{l} {S_1}^2{\beta_1}^2{c_2}^2{c_3}^2{\kappa_1}^2 - 2\,S_1S_2\beta_1\beta_2 c_0 c_1 c_2 c_3\kappa_1\kappa_2 \\ \quad + 4\,S_1S_2\beta_1\beta_2 c_1 c_3\mu_1\mu_2\kappa_1\kappa_2 + {S_2}^2{\beta_2}^2{c_0}^2{c_1}^2{\kappa_2}^2 \end{array}}}{c_1c_3\left(c_0c_2 - \mu_1\mu_2\right)}$$

is the basic reproduction number for the first and second patch.

3.2.5 Local Stability of the Ebola Free Equilibrium (EFE) E_0

We will establish the local stability of the (EFE) in the theorem below

Theorem 10. *The Ebola free equilibrium, (DFE) of the model system is locally asymptotically stable (LAS) if* $R_0 < 1$

Proof. For the Ebola free equilibrium, the assumption that in both sub-populations, there are no infected individual holds. Such that no one is infected in either of the compartments, reducing (3.2.1) to E_0. We linearize the system of equation (3.2.1), then we derive the Jacobian matrix $J(E_0)$ at E_0, hence obtaining the characteristics equation as follows:

$$J(E_0) = \begin{bmatrix} U_1 & 0 & -\beta_1 S_1 & a & \omega_2 & 0 & 0 & 0 \\ 0 & U_2 & \beta_1 S_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & U_3 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & U_4 & 0 & 0 & 0 & 0 \\ \omega_1 & 0 & 0 & 0 & U_5 & 0 & -\beta_2 S_2 & b \\ 0 & 0 & 0 & 0 & 0 & U_6 & \beta_2 S_{20} & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & U_7 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & U_8 \end{bmatrix}$$

where

$$S_1 = \frac{\omega_2(A_1 + A_2) + \mu_2 A_1}{\omega_1\mu_2 + \mu_1\omega_2 + \mu_1\mu_2}, S_2 = \frac{(\mu_2\omega_1 + \omega_1\omega_2)A_1 + (\omega_1\omega_2 + \mu_1\mu_2 + \mu_2\omega_1 + \mu_1\omega_2)A_2}{\mu_1\ \mu_2^2 + \mu_1\mu_2\ \omega_2 + \mu_2^2\ \omega_1 + \mu_2\omega_1\omega_2 + \mu_1\mu_2\omega_2 + \mu_1\omega_2^2}$$

$$U_1 = -\mu_1 - \omega_1, U_2 = -\kappa_1 - \mu_1$$

$$U_3 = -\alpha_1 - \mu_1 - \tau_1, U_4 = -a - \mu_1, U_5 = -\mu_2 - \omega_2, U_6 = -\kappa_2 - \mu_2, U_7 = -\alpha_2 - \mu_2 - \tau_2, U_8 = -b - \mu_2$$

Then the characteristic equation at E_0 of the linearised system of the model (3.2.1) is given below.

$$|J(E_0)| = \begin{vmatrix} U_1 - \psi & 0 & -\beta_1 S_1 & a & \omega_2 & 0 & 0 & 0 \\ 0 & U_2 - \psi & \beta_1 S_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & U_3 - \psi & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & U_4 - \psi & 0 & 0 & 0 & 0 \\ \omega_1 & 0 & 0 & 0 & U_5 - \psi & 0 & -\beta_2 S_2 & b \\ 0 & 0 & 0 & 0 & 0 & U_6 - \psi & \beta_2 S_2 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & U_7 - \psi & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & U_8 - \psi \end{vmatrix} = 0$$

Thus, the determinant $det(\mathbf{J} - \psi I) = 0$ and the equivalent eigenvalues of the system (3.2.1) at (E_0) is given by

$\psi^{(1)} = -\mu_2 - \omega_2, \psi^{(2)} = -\mu_1 - \omega_1, \psi^{(3)} = -\kappa_2 - \mu_2 \psi^{(4)} = -\kappa_1 - \mu_1, \psi^{(5)} = -\alpha_2 - \mu_2 - \tau_2, \psi^{(6)} = -\alpha_1 - \mu_1 - \tau_1,$ $\psi^{(7)} = -b - \mu_2$ and $\psi^{(8)} = -a - \mu_1$

From the values of all the off-diagonal entries of $|J(E_0)|$ which are non-negative. Therefore, it is a Metzler matrix. Based on the fact that $\Omega \geqslant 0$, then the system (3.2.1), is positively invariant in R_+^8, Implying that any trajectory of the system (3.2.1), from an initial state in the positive orthant R_+^8remains in R_+^8 forever. Clearly from the determinant of E_0 we see that the reproduction number of both patches are seen

Which implies that the system (3.2.1) is said to be locally asymptotically stable(LAS) at (EFE). Which completes the proof. □

The global stability of disease-free equilibrium will now be established.

3.2.6 Global Stability of the Ebola Free Equilibrium (EFE) E_0

we then show that the disease free equilibrium is globally asymptotically stable;

Theorem 11. *The disease free equilibrium (DFE) of the model system is globally asymptotically stable (GAS) if* $R_0 < 1$

Proof. Define a Lyapunov function candidate as follows;

$$V = (E_1, I_1, E_2, I_2) = \frac{A_1}{\mu_1}\beta_1 E_1 + C_0 I_1 + \frac{A_2}{\mu_2}\beta_2 E_2 + C_1 I_2$$

Hence, $\frac{A_1}{\mu_1}\beta_1 > 0, \frac{A_2}{\mu_2}\beta_2 > 0, C_0 > 0, C_1 > 0$ which is positive. it is easy to see the DFE such that the Lyapunov function of the system of equation (3.2.1) is satisfied. By Differentiating with respect to t, we have

$$\dot{V} = \frac{A_1}{\mu_1}\beta_1 E_1' + C_0{}' + \frac{A_2}{\mu_2}\beta_2 E_2' + C_1 I_2'$$

$$\dot{V} = \frac{A_1}{\mu_1}\beta_1 \left[\beta_1 S1 I_1 - (F_0)E_1\right] + C_0 \left[\kappa_1 E_1 - (F_1)I_1\right] + \frac{A_2}{\mu_2}\beta_2 \left[\beta_2 S2 I_2 - (F_2)E_2\right] + C_1 \left[\kappa_2 E_2 - (F_3)I_2\right]$$

where $F_0 = (\kappa_1 + \mu_1), F_1 = (\alpha_1 + \mu_1 + \tau_1), F_2 = (\kappa_2 + \mu_2), F_3 = (\alpha_2 + \mu_2 + \tau_2)$

By expansion and collecting of like terms we have

$$\dot{V} = \left[C_0\kappa_1 - \frac{A_1\beta_1F_0}{\mu_1}\right]E_1 + \left[\frac{A_1\beta_1^2S_1}{\mu_1} - C_0F_1\right]I_1 + \left[C_1\kappa_2 - \frac{A_2\beta_2F_2}{\mu_2}\right]E_2 + \left[\frac{A_2\beta_2^2S_2}{\mu_2} - C_1F_3\right]I_2$$

At Ebola free Equilibrium, where

$$S_1 = \frac{\omega_2(A_1 + A_2) + \mu_2A_1}{\omega_1\mu_2 + \mu_1\omega_2 + \mu_1\mu_2}, S_2 = \frac{(\mu_2\omega_1 + \omega_1\omega_2)A_1 + (\omega_1\omega_2 + \mu_1\mu_2 + \mu_2\omega_1 + \mu_1\omega_2)A_2}{\mu_1\ \mu_2^2 + \mu_1\mu_2\ \omega_2 + \mu_2^2\ \omega_1 + \mu_2\omega_1\omega_2 + \mu_1\mu_2\omega_2 + \mu_1\omega_2^2}$$

let

$$S_1 = \frac{m_1}{m_2}, S_2 = \frac{m_3}{m_4}$$

above

$\therefore$

$$\dot{V} = \left[C_0\kappa_1 - \frac{A_1\beta_1F_0}{\mu_1}\right]E_1 + \left[\frac{A_1\beta_1^2m_1}{\mu_1m_2} - C_0F_1\right]I_1 + \left[C_1\kappa_2 - \frac{A_2\beta_2F_2}{\mu_2}\right]E_2 + \left[\frac{A_2\beta_2^2m_3}{\mu_2m_4} - C_1F_3\right]I_2$$

$$\dot{V} = \left[C_0\kappa_1 - \frac{A_1\beta_1F_0}{\mu_1}\right]E_1 + \left[\frac{A_1\beta_1^2m_1}{\mu_1m_2} - C_0F_1\right]I_1 + \left[C_1\kappa_2 - \frac{A_2\beta_2F_2}{\mu_2}\right]E_2 + \left[\frac{A_2\beta_2^2m_3}{\mu_2m_4} - C_1F_3\right]I_2$$

$\therefore$

$$\dot{V} = C_0\kappa_1\left[1 - \frac{A_1\beta_1F_0}{C_0\kappa_1\mu_1}\right]E_1 + C_0F_1\left[\frac{A_1\beta_1^2m_1}{C_0F_1\mu_1m_2} - 1\right]I_1 + C_1\kappa_2\left[1 - \frac{A_2\beta_2F_2}{C_1\kappa_2\mu_2}\right]E_2 + C_1F_3\left[\frac{A_2\beta_2^2m_3}{C_1F_3\mu_2m_4} - 1\right]I_2$$

rearranging

$$\dot{V} = C_0\kappa_1\left[1 - \frac{A_1\beta_1F_0}{C_0\kappa_1\mu_1}\right]E_1 + C_1\kappa_2\left[1 - \frac{A_2\beta_2F_2}{C_1\kappa_2\mu_2}\right]E_2 + C_0F_1\left[\frac{A_1\beta_1^2m_1}{C_0F_1\mu_1m_2} - 1\right]I_1 + C_1F_3\left[\frac{A_2\beta_2^2m_3}{C_1F_3\mu_2m_4} - 1\right]I_2$$

$$\dot{V} = C_0C_1\kappa_1\kappa_2C_0C_1F_1F_3\left[R_0^2 - 1\right]E_1E_2I_1I_2 \leq 0$$

if $R_0 \leq 1$ Hence the Ebola free equilibrium is globally asymptotically stable for $R0 \leq 1$ $\square$

3.2.7 Local Stability of the Ebola Free Endemic Equilibrium (EFEE) E_1 and E_2

We will establish the local stability of the (EFEE) in the theorems below

Theorem 12. *The Ebola free endemic equilibrium, (EFE) of the model system is locally asymptotically stable (LAS) if* $R_0 < 1$

Proof. For Ebola free endemic equilibrium, we assume that in both sub-populations movement is low, i.e $\omega << 1$. Such that infection is not recorded in the second that because immigration is reduced but not totally canceled i.e $(I_1 = 0, I_2 \neq 0)$. We linearize the system of equation (3.2.1),then we derive the Jacobian matrix $J(E_1)$ at E_1, hence obtaining the characteristics equation as follows:

$$J(E_1) = \begin{bmatrix} a_{11} & 0 & -\beta_1 U3 & a & \omega_2 & 0 & 0 & 0 \\ U2\,\beta_1 & -\kappa_1 - \mu_1 & \beta_1 U3 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a - \mu_1 & 0 & 0 & 0 & 0 \\ \omega_1 & 0 & 0 & 0 & -\mu_2 - \omega_2 & 0 & -\beta_2 U4 & b \\ 0 & 0 & 0 & 0 & 0 & -\kappa_2 - \mu_2 & \beta_2 U4 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -b - \mu_2 \end{bmatrix}$$

where $a_{11} = -U2\,\beta_1 - \mu_1 - \omega_1, a_{33} = -\alpha_1 - \mu_1 - \tau_1, a_{77} = -\alpha_2 - \mu_2 - \tau_2$

$$U2 = \frac{\left(\beta_1\left(\left(A_1 + A_2\right)\omega_2 + A_1\mu_2\right)\kappa_1 - \left(\mu_1 + \kappa_1\right)\left(\alpha_1 + \mu_1 + \tau_1\right)\left(\left(\mu_2 + \omega_2\right)\mu_1 + \mu_2\omega_1\right)\right)\left(a + \mu_1\right)}{\beta_1\left({\mu_1}^3 + \left(a + \tau_1 + \alpha_1 + \kappa_1\right){\mu_1}^2 + \left(\left(a + \tau_1 + \alpha_1\right)\kappa_1 + a\left(\tau_1 + \alpha_1\right)\right)\mu_1 + a\tau_1\kappa_1\right)\left(\mu_2 + \omega_2\right)}$$

$$U3 = \frac{\left(\mu_1 + \kappa_1\right)\left(\alpha_1 + \mu_1 + \tau_1\right)}{\beta_1\kappa_1}, U4 = \frac{\left(\mu_1 + \kappa_1\right)\left(\alpha_1 + \mu_1 + \tau_1\right)\omega_1 + A_2\beta_1\kappa_1}{\beta_1\kappa_1\left(\mu_2 + \omega_2\right)}$$

Using upper triangular matrix principle [Coelho and Milies, 1993] for the upper diagonal, then we have

$$J(E_1) = \begin{bmatrix} a_{11} & 0 & -\beta_1 U3 & a & \omega_2 & 0 & 0 & 0 \\ U2\,\beta_1 & -\kappa_1 - \mu_1 & \beta_1 U3 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a - \mu_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & -\mu_2 - \omega_2 & 0 & -\beta_2 U4 & b \\ 0 & 0 & 0 & 0 & 0 & -\kappa_2 - \mu_2 & \beta_2 U4 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -b - \mu_2 \end{bmatrix}$$

The matrix $J(E_1)$ is an upper triangular matrix. Its eigenvalues are also eigenvalues of the upper triangular matrices. The trace of E_1 is given as: $-U2\,\beta_1 - a - b - \alpha_1 - \alpha_2 - \kappa_1 - \kappa_2 - 4\,\mu_1 - 4\,\mu_2 - \omega_1 - \omega_2 - \tau_1 - \tau_2 \leqslant 0$ As the eigenvalues of the $det(\mathbf{J}(\mathbf{E_1}) - \psi I) = 0$ gives:

$$\psi^{(1)} = -\mu_2 - \omega_2, \lambda^{(2)} = -\kappa_2 - \mu_2, \lambda^{(3)} = -\kappa_1 - \mu_1, \psi^{(4)} = -\alpha_2 - \mu_2 - \tau_2, \psi^{(5)} = -\alpha_1 - \mu_1 - \tau_1$$

$$, \psi^{(6)} = -b - \mu_2, \psi^{(7)} = -a - \mu_1, \psi^{(8)} = -U2\,\beta_1 - \mu_1 - \omega_1$$

Since the values of $\psi^{(1)} < 0$, $\psi^{(2)} < 0$ $\psi^{(3)}$, $\psi^{(4)}$, $\psi^{(5)} < 0$, $\psi^{(6)} < 0$, $\psi^{(7)} < 0$ and $\lambda^{(8)} < 0$ have no positive signs, hence the equilibrium point $R_0 < 1$, then E_1 is asymptotically stable.

Theorem 13. *The Ebola free endemic equilibrium, (EFEE) of the model system is locally asymptotically stable (LAS) if* $R_0 < 1$

Proof. For the Ebola free endemic equilibrium, the assumption that in both sub-populations, there are infected individual in patch one and no infections in second patch holds. Such that no one is infected in second compartment, reducing (3.2.1) to E_2 i.e $(I_1 \neq 0, I_2 = 0)$. We linearize the system of equation (3.2.1),then we derive the Jacobian matrix $J(E_2)$ at E_2, hence obtaining the characteristics equation as follows:

We form the Jacobian matrix of the system as follows

$$J(E_2) = \begin{bmatrix} -\mu_1 - \omega_1 & 0 & -M_0 & a & \omega_2 & 0 & 0 & 0 \\ 0 & -\kappa_1 - \mu_1 & M_0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a - \mu_1 & 0 & 0 & 0 & 0 \\ \omega_1 & 0 & 0 & 0 & a_{55} & 0 & -M_1 & b \\ 0 & 0 & 0 & 0 & U2\,\beta_2 & -\kappa_2 - \mu_2 & M_1 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & -a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -b - \mu_2 \end{bmatrix}$$

where $a_{33} = -\alpha_1 - \mu_1 - \tau_1, a_{55} = -U2\,\beta_2 - \mu_2 - \omega_2, a_{77} = -\alpha_2 - \mu_2 - \tau_2$

$M_1 = \frac{(\kappa_2+\mu_2)(\alpha_2+\mu_2+\tau_2)}{\kappa_2}$, $M_0 = \frac{\beta_1((\kappa_2+\mu_2)(\alpha_2+\mu_2+\tau_2)\omega_2+A_1\beta_2\kappa_2)}{(\mu_1+\omega_1)\beta_2\kappa_2}$

$$U2 = \frac{(\beta_1\,((A_1 + A_2)\,\omega_2 + A_1\mu_2)\,\kappa_1 - (\mu_1 + \kappa_1)\,(\alpha_1 + \mu_1 + \tau_1)\,((\mu_2 + \omega_2)\,\mu_1 + \mu_2\omega_1))\,(a + \mu_1)}{\beta_1\,({\mu_1}^3 + (a + \tau_1 + \alpha_1 + \kappa_1)\,{\mu_1}^2 + ((a + \tau_1 + \alpha_1)\,\kappa_1 + a\,(\tau_1 + \alpha_1))\,\mu_1 + a\tau_1\kappa_1)\,(\mu_2 + \omega_2)}$$

Using upper triangular matrix principle [Coelho and Milies, 1993] for the lower diagonal, then we have

$$J(E_2) = \begin{bmatrix} -\mu_1 - \omega_1 & 0 & -M_0 & a & \omega_2 & 0 & 0 & 0 \\ 0 & -\kappa_1 - \mu_1 & M_0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a - \mu_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_{55} & 0 & -M_1 & b \\ 0 & 0 & 0 & 0 & U2\,\beta_2 & -\kappa_2 - \mu_2 & M_1 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & -a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -b - \mu_2 \end{bmatrix}$$

trace of

$$E_2 - U2\,\beta_2 - a - b - \alpha_1 - \alpha_2 - \kappa_1 - \kappa_2 - 4\,\mu_1 - 4\,\mu_2 - \omega_1 - \omega_2 - \tau_1 - \tau_2 \leqslant 0$$

The determinant

$$det(\mathbf{J}(\mathbf{E_2}) - \lambda I) = 0$$

gives:

$$\psi^{(1)} = -\mu_1 - \omega_1, \psi^{(2)} = -\kappa_2 - \mu_2, \psi^{(3)} = -\kappa_1 - \mu_1 \psi^{(4)} = -\alpha_2 - \mu_2 - \tau_2$$

,

$$\psi^{(5)} = -\alpha_1 - \mu_1 - \tau_1 \psi^{(6)} = -b - \mu_2, \psi^{(7)} = -a - \mu_1$$

and $\psi^{(8)} = -U2\ \beta_2 - \mu_2 - \omega_2$

Since the values of $\psi^{(1)} < 0$, $\psi^{(2)} < 0$ $\psi^{(3)}$, $\psi^{(4)}$, $\psi^{(5)} < 0$, $\psi^{(6)} < 0$, $\psi^{(7)} < 0$ and $\psi^{(8)} < 0$ have no positive signs, hence the equilibrium point $R_0 < 1$, then E_2 is asymptotically stable.

3.2.8 Local Stability of the Ebola Endemic Equilibrium (EEE) E_3

we then show that the disease free equilibrium is globally asymptotically stable;

$$J(E_3) = \begin{bmatrix} a_{11} & 0 & -M_2 & \omega_2 & 0 & 0 & 0 & \\ U4\ \beta_1 & -\kappa_1 - \mu_1 & M_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a - \mu_1 & 0 & 0 & 0 & 0 \\ \omega_1 & 0 & 0 & 0 & a_{55} & 0 & -M_3 & b \\ 0 & 0 & 0 & 0 & \beta_2 U5 & -\kappa_2 - \mu_2 & M_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & \kappa_2 & a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -b - \mu_2 \end{bmatrix}$$

where $a_{11} = -U4\ \beta_1 - \mu_1 - \omega_1, a_{33} = -\alpha_1 - \mu_1 - \tau_1, a_{55} = -U5\ \beta_2 - \mu_2 - \omega_2, a_{77} = -\alpha_2 - \mu_2 - \tau_2$

$$U4 = \frac{\begin{array}{c}(A_1\beta_1\beta_2\kappa_1\kappa_2\left(\left(-\left(\alpha_1+\mu_1+\tau_1\right)\left(\mu_1+\omega_1\right)\beta_2+\omega_2\beta_1\left(\mu_2+\tau_2+\alpha_2\right)\right)\kappa_1\right.\\ \left.-\mu_1\beta_2\left(\alpha_1+\mu_1+\tau_1\right)\left(\mu_1+\omega_1\right)\kappa_2+\omega_2\mu_2\beta_1\kappa_1\left(\mu_2+\tau_2+\alpha_2\right)\left(a+\mu_1\right)\right.\end{array}}{\beta_1\beta_2\kappa_2\left({\mu_1}^3+\left(a+\tau_1+\alpha_1+\kappa_1\right){\mu_1}^2+\left(\left(a+\tau_1+\alpha_1\right)\kappa_1+a\left(\tau_1+\alpha_1\right)\right)\mu_1+a\tau_1\kappa_1\right)}$$

$$U5 = \frac{\begin{array}{c}(A_2\beta_1\beta_2\kappa_1\kappa_2+\alpha_1\beta_2\kappa_1\kappa_2\omega_1+\alpha_1\beta_2\kappa_2\mu_1\omega_1\left(-\left(\mu_2+\kappa_2\right)\left(\mu_2+\tau_2+\alpha_2\right)\right.\\ \left.\left(\mu_2+\omega_2\right)\beta_1+\omega_1\beta_2\kappa_2\left(\mu_1+\tau_1\right)\kappa_1+\mu_1\omega_1\beta_2\kappa_2\left(\mu_1+\tau_1\right)\left(b+\mu_2\right)\right.\end{array}}{\beta_1\beta_2\kappa_1\left({\mu_2}^3+\left(b+\tau_2+\alpha_2+\kappa_2\right){\mu_2}^2+\left(\left(b+\tau_2+\alpha_2\right)\kappa_2+b\left(\tau_2+\alpha_2\right)\right)\mu_2+b\tau_2\kappa_2\right)}$$

$$M_2 = \frac{\left(\mu_1+\kappa_1\right)\left(\alpha_1+\mu_1+\tau_1\right)}{\beta_1\kappa_1}, M_3 = \frac{\left(\mu_2+\kappa_2\right)\left(\mu_2+\tau_2+\alpha_2\right)}{\beta_2\kappa_2}$$

From the values of all the diagonal entries of $|J(E_3)|$ which are non-negative. We use the upper triangular matrix principle [Coelho and Milies, 1993]. Therefore,based on the fact that the determinant $det(\mathbf{J}(\mathbf{E_3}) - \psi I) = 0$ becomes:

$$J(E_3) = \begin{bmatrix} a_{11} & 0 & -M_2 & \omega_2 & 0 & 0 & 0 & \\ U4\,\beta_1 & -\kappa_1-\mu_1 & M_2 & 0 & 0 & 0 & 0 & 0 \\ 0 & \kappa_1 & a_{33} & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & \alpha_1 & -a-\mu_1 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & a_{55} & 0 & -M_3 & b \\ 0 & 0 & 0 & 0 & \beta_2\,U5 & -\kappa_2-\mu_2 & M_3 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & a_{77} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -b-\mu_2 \end{bmatrix}$$

Laving all the entries on the upper diagonal matrix. The trace of $J(E_3)$ is

$$-U4\,\beta_1 - U5\,\beta_2 - a - b - \alpha_1 - \alpha_2 - \kappa_1 - \kappa_2 - 4\,\mu_1 - 4\,\mu_2 - \omega_1 - \omega_2 - \tau_1 - \tau_2 \leq 0$$

Where the eigenvalues of $J(E_3)$ are given as:

$$\psi^{(1)} = -\kappa_2 - \mu_2, \psi^{(2)} = -\kappa_1 - \mu_1, \psi^{(3)} = -\alpha_2 - \mu_2 - \tau_2,$$

$$\psi^{(4)} = -\alpha_1 - \mu_1 - \tau_1, \psi^{(5)} = -b - \mu_2, \psi^{(6)} = -a - \mu_1, \psi^{(7)} = -U5\ \beta_2 - \mu_2 - \omega_2$$

and $\psi^{(8)} = -U4\ \beta_1 - \mu_1 - \omega_1$

such that stability of E_3 is clearly seen from the determinant of E_3. If $R_0 > 1$, then E_3 has positive roots hence E_3 is unstable when $R_0 > 1$. When $R_0 < 1$

which shows that E_3 have negative real parts and by rewriting the determinant of E_3 $\psi^{(1)} < 0, \psi^{(2)} < 0, \psi^{(3)} < 0, \psi^{(4)} < 0, \psi^{(5)} < 0, \psi^{(6)} < 0, \psi^{(7)} < 0$ and $\psi^{(8)} < 0$ are stable since the trace of E_3 is negative and the eigenvalues of E_3 have constant sign. Thus, E_3 is local asymptotically stable.

3.3 Zika Model

Zika Virus Disease (ZVD), a mosquito-borne positive stranded RNA Virus of the family (genus flavivirus) flavivindae [Lindenbach et al., 2007], is now causing an unprecedented large-scale outbreak in th discovered in Uganda in 1947, ZVD was confined for the first 60 years to the equatorial zone of Africa and Asia [Dick et al., 1952].

The first isolated issue of ZVD was recorded in April 1947 from a rhesus macque monkey placed in a case in the Zika forest of Uganda near the Lake Victoria, by the scientist of yellow fever research institute [Dick et al., 1952, Macnamara, 1954]. Zika is primarily spread by female aedes aegyptic mosquitos as by [Hayes, 2009], and is usually transmitted during sexual intercourse or by blood transfusion [Foy et al., 2011]. In 1954, ZVD was seen to occur in eastern Nigeria where it was seen that the conditions with it showing on three patients, one by isolation of the virus and two by a rise in serum antibodies. Where the patients with liver damage and serological studies showed a relationship between jaundice and the development of virus [Adekolu-John and Fagbami, 1983, Macnamara, 1954, Fagbami, 1977].

The first true case of human infection of ZVD was identified by [Fauci and Morens, 2016]. Not much of human infection was deducted or investigate for more than 40 years, but in 2007, there were reported cases of about 13 further confirmed human cases of ZVD from the continent of Africa to southeast Asia, [Fauci and Morens, 2016]. In 2007, ZVD caused an outbreak of relatively mild diseases characterized by rash, arthralgia and conjunctivitis on Yap Island which is located in the south western percific Ocean. Jan C. et al in 1978, looked at the serological studies for arbvirus antibodies. Where they gave an analysis by taking samples of potent serum specimen. They

carried out this study on 1.279 human serum specimen collected from adults in south-eastern part of garbon from June to September 1975 during a multipurpose epidemiological survey. The result of which showed positivity of more than 25%.

Which was first time that ZVD was prevalently discovered outside the continent of Africa and Asia. This outbreak in April, 2007 was characterised by rush, and the likes in Yap Island in the Federated States of Micronesia. Where similar experiment as that which was carried out in Garbon and Nigeria was carried out on serum samples from patients in the acute phase of illness contained RNA of Zika, a flavivirus in the family of yellow fever, dengue,West Nie and Japanese encephalite Virus [Dick et al., 1952]. Following first detection of ZVD in Brazil in May 2015, ZVD has spread in the Americas and the Caribbean, prompting series of health emergencies and travel precautions from global health supervisory agencies and government. The risk of ZVD emergence in Europe increased as imported cases are repeatedly reported, coming also with reports of Chikungunya Virus and Dengue Virus. Which manifest with ZVD similar symptoms.

In 2017, Baud D, et all showed through a research titled Zika, a new threat to human reproduction, that followed by French polynesia in 2013 and Brazil in 2015. the ZVD is mainly transmitted through aedes mosquitoe bites, but sexual and post-transfusion transmission which most times are not checked, have been reported with symptoms like low grade fever, maculopopular rash, conjuctivitis, myalgia,arthralgia and asthenia. Asymptomatic male-to-female transmission has also been described. Importantly, ZVD RNA can prevent at least 6 months in Semen. The need to increase discussion and research to improve understanding of the Zika virus disease dynamics and transmission as well as movement of people from one place to another is very important and to develop effective control and preventive strategies of the outbreak of ZVD

The recent ZVD outbreak in Brazil with close to two million estimated cases from early 2015 to early 2017 was received with global awareness and quick response by world health bodies. Because of the large number of infections, rate of transmission and the sporadic increase in the number of reported case as well as the spread of infection as well as the resultant death recorded. An which became a public health emergency as said raising several governmental travel restriction as well as warning from the World Health Organization(WHO). As such, the ZVD outbreak activated intervention and measures from both government, policy makers and scholars.

Various government through their respective Centre for Disease Control (CDC) and other global public health

advocacy agencies activated series of emergency response by establishing management centres as well as issuing travel guide, creating response teams, exposed individuals contact tracing, case management, public health awareness, infection prevention and ZVD control practices. With very reasonable scholastic approach to the menace from relevant medical research, public health advisory data and statistics as well as complimentary mathematical models which helped in the understanding, modeling and predicting the disease transmission dynamics based on relevant statistics, helping to shape policy makers. Because of the relevance and usefulness of mathematical models, which play very critical roles in prevention and helping with adequate control measures for mitigating infectious and non infectious diseases [Wang et al., 2019]. Kucharski, AJ [Kucharski et al., 2016] developed a transmission dynamics of ZVD in island populations, giving a model analysis.

Also [Gao et al., 2016]in their research, considered the prevention and control of Zika as a mosquito-borne and sexually transmitted disease, with a ZVD mathematical model with human and vector compartments, with SEI for the structure of the mosquitoes and SEIR structure for humans, with an estimated reproduction number. Also [Maxian et al., 2017] analyzed the disparity in cases male and female as well as age and sex structured ZVD spread model. [Wang et al., 2019] considered a ZVD mathematical model, with spread to human from mosquito bites and sexual contacts from human to human. With various protective and preventive control measures such as the use of insecticide treated net, use of condoms, indoor spraying and treatment of infected individuals. With the advocacy of health agencies and other control measures which have reduced sexual transmission of ZVD, but the effect of migration and air travel has caused the transmission of ZVD from certain region to another region. [Momoh and Fügenschuh, 2018] also considered the optimal control of ZVD dynamics, with four control measures. In this paper, we consider the transmission dynamics of ZVD between linked communities, using a metapopulation mathematical model to study the control of ZVD transmission dynamics in two connected population. Studying the optimal control of ZV infection with five preventive measures which include responses to public health instruction and guidelines on movement or migration to and from prevalent region, efforts deployed to reduce on movement or migration of infected individuals to and from prevalent region, use of insecticide to kill mosquitoes and personal hygiene such as wearing of protective gear.

3.3.1 Zika Model Formation

We consider a SIR metapopulation model for human and SI model for mosquito. Two patches representing two communities connected by the movement of individuals through means of transportation are considered, which includes travel rates for the recovered as well. Each patch i is divided into three classes namely Susceptible host S_{hi}, Infected host I_{hi} and Recovered host R_{hi}, $i = 1, 2$. The total population of human at each patch at time t is $N_{h_i} = S_{h_i} + I_{hi} + R_{hi}$. The vector (mosquito) population N_v is a stand alone, assuming that mosquito do not have log travel in the air. It is divided into two classes namely susceptible vector S_v and Infected vector I_v. It is assumed that infected mosquito with Zika Virus are infectious for life. Susceptible mosquito are recruited into the patch i at a constant rate π_{hi} and die naturally at a rate μ_{hi}. Susceptible host S_{hi} becomes infected host at rate $\beta_{vihi} S_{hi} I_{vi}$, where β_{vihi} is the probability of transmission from infectious mosquito to susceptible humans. Humans in both patches die naturally at rate μ_{hi} and those infected recover at rate α_{hi}. Recovered can lose their acquired immunity and become susceptible at rate σ_i. Susceptible mosquito $S_{vi}(t)$ are recruited at constant rate π_{vi} and naturally die at rate μ_{vi}. They can be infected by humans at a rate $\beta_{hivi} S_{vi} I_{hi}$, where β_{hivi} is the probability of transmission from infected human to susceptible mosquito. Infected mosquito die at rate μ_{vi}. We also assume travel between patches at constant rate λ_i, and disease induced death at rate d_i. The mathematical model describing the above scenario is given by the system of ordinary differential equations

$$
\begin{cases}
\frac{dS_{h1}}{dt} = \pi_{h1} - \beta_{v1h1} S_{h1} I_{v1} - \lambda_1 S_{h1} - \mu_{h1} S_{h1} + \lambda_2 S_{h2} + \sigma_1 R_{h1} \\
\frac{dI_{h1}}{dt} = \beta_{v1h1} S_{h1} I_{v1} - (\mu_{h1} + d_1 + \alpha_1) I_{h1} \\
\frac{dR_{h1}}{dt} = \alpha_1 I_{h1} - \mu_{h1} R_{h1} - \sigma_1 R_{h1} \\
\frac{dS_{v1}}{dt} = \pi_{v_1} - \mu_{v_1} S_{v_1} - \beta_{h1v_1} S_{v_1} I_{h1} \\
\frac{dI_{v1}}{dt} = \beta_{h1v_1} S_{v_1} I_h - \mu_{v_1} I_{v_1} \\
\frac{dS_{h2}}{dt} = \pi_{h2} - \beta_{v2h2} S_{h2} I_{v2} - \lambda_2 S_{h2} - \mu_{h2} S_{h2} + \lambda_1 S_{h1} + \sigma_2 R_{h2} \\
\frac{dI_{h2}}{dt} = \beta_{v2h2} S_{h2} I_{v2} - (\mu_{h2} + d_2 + \alpha_2) I_{h2} \\
\frac{dR_{h2}}{dt} = \alpha_2 I_{h2} - \mu_{h2} R_{h2} - \sigma_2 R_{h2} \\
\frac{dS_{v2}}{dt} = \pi_{v_2} - \mu_{v_2} S_{v_2} - \beta_{h_2v_2} S_{v_2} I_{h_2} \\
\frac{dI_{v2}}{dt} = \beta_{h_2v_2} S_{v_2} I_{h_2} - \mu_{v_2} I_{v_2}
\end{cases}
\tag{3.3.1}
$$

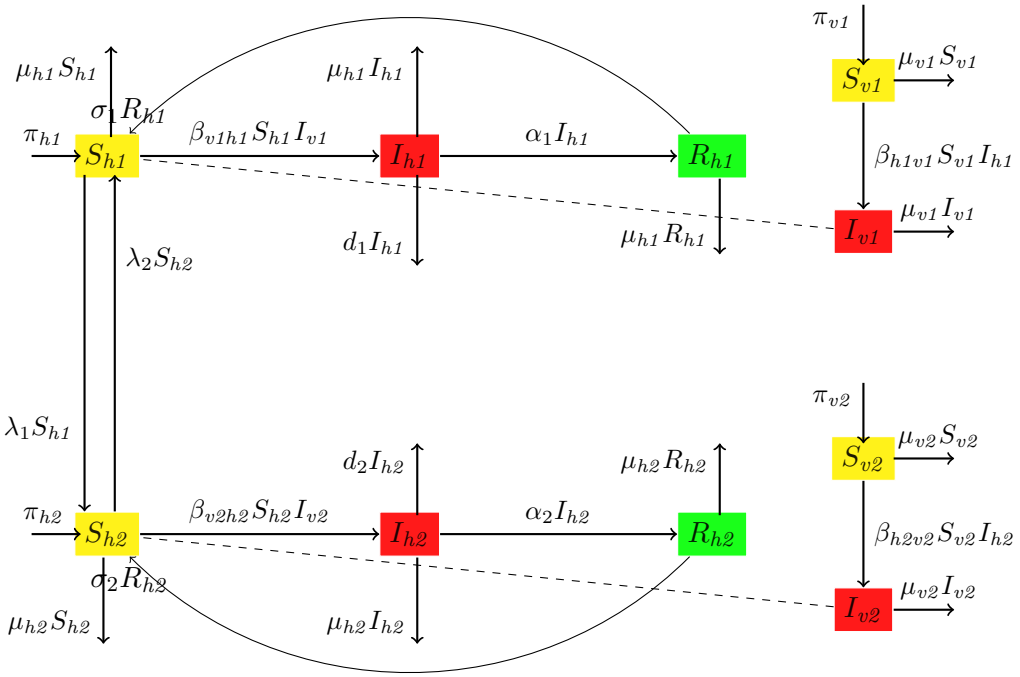


Figure 3.2: Schematic diagram of the disease dynamics

associated with the nonnegative initials conditions

$$S_{hi}(0) = S_{hi}(0), I_{hi}(0) = I_{hi}(0), R_{hi}(0) = R_{hi0}, S_{vi}(0) = S_{hi}(0), I_{vi}(0) = I_{hi}(0), \quad i = 1, 2. \tag{3.3.2}$$

The description of the variables and parameters employed in the above model is given in Table 3.2. In the analysis of the above model, we set

$$c_0 = \mu_{h2} + d_2 + \alpha_2, c_1 = \mu_{h2} + \sigma_2, c_2 = \mu_{h1} + d_1 + \alpha_1, c_3 = \mu_{h1} + \sigma_1.$$

We would like to understand the disease dynamics within the population and investigate the optimal strategies to reduce the spread of infection at low cost.

3.3.2 Positivity and Boundedness of Zika Model Solution

The system of equations (3.3.1) has an initial condition by

Table 3.2: Description of State Variables and Parameters

State Variables	Description
N_{h1}, N_{h2}	Total human population in patch one and two.
S_{h1}, S_{h2}	Susceptible human population in patch one and two.
I_{h1}, I_{h2}	Infected human population in patch one and two.
R_{h1}, R_{h2}	Recovered human population in patch one and two.
N_{v1}, N_{v2}	Total vector population in patch one and two.
S_{v1}, S_{v2}	Susceptible vector population in patch one and two.
I_{v1}, I_{v2}	Infected vector population in patch one and two.
Parameters	Description
π_h, π_v	Recruitment rate of human and vector population respectively.
μ_h, μ_v	Natural death rate of human and vector population respectively.
α	Recovery rate.
λ	Movement of susceptible human population.
σ	Recovery rate of infected human .
β_{hv}	Transmission probability of Susceptible mosquito with infected humans.
β_{vh}	Transmission probability of Susceptible humans with infected mosquito.
d	Possible disease induced death.

Lemma 2. *If* $S_{h_1}(0), I_{h_1}(0), R_{h_1}(0), S_{v_1}(0), I_{v_1}(0), S_{h_2}(0), I_{h_2}(0), R_{h_2}(0),$
$S_{v_2}(0)$ *and* $I_{v_2}(0)$ *are non-negative, all variables* $S_{h_1}(t), I_{h_1}(t), R_{h_1}(t), S_{v_1}(t), I_{v_1}(t), S_{h_2}(t), I_{h_2}(t), R_{h_2}(t),$
$S_{v_2}(t)$ *and* $I_{v_2}(t)$*are non-negative for all* $t > 0$

Lemma 3. *Given a closed set*

$$\Omega = \{(S_{h_1}, I_{h_1}, R_{h_1}, S_{v_1}, I_{v_1}, S_{h_2}, I_{h_2}, R_{h_2}, S_{v_2}, I_{v_2}) \in \boldsymbol{R}_+^{10} : (S_{h_1} + I_{h_1} + R_{h_1} + S_{h_2} + I_{h_2} + R_{h_2}) \leq \frac{\pi_{h1} + \pi_{h2}}{\mu_{human}},$$

$$(S_{v_1} + I_{v_1} + S_{v_2} + I_{v_2}) \leq \frac{\pi_{v_1} + \pi_{v2}}{\mu_{mosquitoes}}\}$$

Proof. Firstly, we prove the positivity of solutions of the Zika Virus model as follows: We note that the positivity

of S_{h1}, R_{h1} and S_{v1} depends on that of I_{h1} in the first patch and the positivity of S_{h2}, R_{h2} and S_{v2} depends on that of I_{h2}. From the second equation of (3.3.1), we have

$$\frac{dI_{h1}}{dt} = \beta_{v1h1} S_{h1} I_{v1} - C_0 I_{h1} \tag{3.3.3}$$

where $C_0 = (\mu_{v_1} + d_1 + \alpha_1)$ The integrating factor of (3.3.3) is $e^{C_0 t}$ which when multiplied by (3.3.3) gives

$$e^{C_0 t}\frac{dI_{h1}}{dt} + C_0 e^{C_0 t} I_{h1} = \beta_{v1h1} S_{h1} I_{v1} e^{C_0 t}$$

$$\frac{d}{dt}(e^{C_0 t}) = \beta_{v1h1} S_{h1} I_{v1} e^{C_0 t}$$

Integrating both sides with respect to t yields

$$e^{C_0 t} I_{h1} = \int \beta_{v1h1} S_{h1} I_{v1} e^{C_0 t} dt + K_1$$

$$I_{h1} = K_1 e^{C_0 t} + e^{C_0 t} \int \beta_{v1h1} e^{C_0 t} dt \geq 0 \tag{3.3.4}$$

as $t \to \infty (t > 0)$ where K_1 is a constant of integration.

From the third equation of (3.3.1) we have that

$$\frac{dR_{h1}}{dt} = C_1 R_{h1} - \alpha_1 I_{h1} \tag{3.3.5}$$

where $C_1 = (\mu_{h1} + \sigma_1)$ Multiplying with the approximate integrating factor I.F $e^{C_1(t)}$ hence we obtain

$$e^{C_1(t)}\frac{dR_{h1}}{dt} + C_1 e^{C_1(t)} R_{h1} = \alpha_1 I_{h1} e^{C_1(t)}$$

$$\therefore \frac{d}{dt}(e^{C_1(t)} R_{h1}) = \alpha_1 I_{h1} e^{C_1(t)}$$

Integrating with respect to t

$$e^{C_1(t)} R_{h1} - \int \alpha_1 I_{h1} e^{C_1(t)} dt + K_2$$

where k_2 is a constant of integration.

$$R_{h1} = K_2 e^{-C_1(t)} + e^{-C_1(t)} \int \alpha_1 I_{h1} e^{C_1(t)} dt \geq 0 for t \geq 0 \tag{3.3.6}$$

Now, for the first equation(3.3.1), I have that

$$\frac{dS_{h1}}{dt} + (C_2 + \beta_{v1h1} I_{v1}) = \sigma_1 R_{h1} + \lambda_2 S_{h2} \tag{3.3.7}$$

which can be expressed as

$$\frac{dS_{h1}}{dt} + f(I_{v1})S_{h1} = \sigma_1 R_{h1} + \lambda_2 S_{h2} \tag{3.3.8}$$

where $f(I_{v1}) = C_2 + \beta_{v1h1} I_{h1}$ and $C_2 = \mu_{h1} + \lambda_1$ Multiplying with the I.F $e^{\int_0^t f(I_{v1})dI_{v1}}$ gives

$$e^{\int_0^t f(I_{v1})dI_{v1}} \frac{dS_{h1}}{dt} + f(I_{v1}) e^{\int_0^t f(I_{v1})dI_{v1}} S_{h1} = (\sigma_1 R_{h1} + \lambda_2 S_{h2}) e^{\int_0^t f(I_{v1})dI_{v1}}$$

$$\therefore \frac{d}{dt}(e^{\int_0^t f(I_{v1})dI_{v1}} S_{h1}) = (\sigma_1 R_{h1} + \lambda_2 S_{h2}) e^{\int_0^t f(I_{v1})dI_{v1}}$$

Integrating with respect to t

$$e^{\int_0^t f(I_{v1})dI_{v1}} S_{h1} = K_3 + \int_0^t (\sigma_1 R_{h1} + \lambda_2 S_{h2}) e^{\int_0^t f(I_{v1})dI_{v1}}$$

$$S_{h1} = K_3 e^{-\int_0^t f(I_{v1})dI_{v1}} + e^{-\int_0^t f(I_{v1})dI_{v1}} \int_0^t (\sigma_1 R_{h1} + \lambda_2 S_{h2}) e^{\int_0^t f(I_{v1})dI_{v1}} \geq 0 \tag{3.3.9}$$

for $t > 0$ Considering the fifth equation of (3.3.1), we have

$$\frac{dI_{v1}}{dt} + \mu_{v1} I_{v1} = \beta_{h1v1} S_{v1} I_{h1} \tag{3.3.10}$$

The Integrating factor I.F is $e^{\mu_{v1}(t)}$ by multiplying through by the I.F results in

$$e^{\mu_{v1}(t)} \frac{dI_{v1}}{dt} + \mu_{v1} e^{\mu_{v1}(t)} I_{v1} = \beta_{v1h1} S_{v1} I_{h1} e^{\mu_{v1}(t)}$$

$$\frac{d}{dt}(e^{\mu_{v1}(t)} I_{v1}) = \beta_{v1h1} S_{v1} I_{h1} e^{\mu_{v1}(t)}$$

Integrating with respect to t

$$e^{\mu_{v1}(t)} I_{v1} = K_3 + \int \beta_{v1h1} S_{v1} I_{h1} e^{\mu_{v1}(t)}$$

Thus,

$$I_{v1} = K_3 e^{-\mu_{v1}(t)} + e^{-\mu_{v1}(t)} \int \beta_{v1h1} S_{v1} I_{h1} e^{\mu_{v1}(t)} dt \geq 0, t \geq 0 \tag{3.3.11}$$

Further, from fourth equation of (3.3.1),

$$\frac{dS_{v1}}{dt} + (\beta_{v1h1} I_{h1} + \mu_{v1}) I_{v1} S_{v1} = \pi_{v1}$$

$$\frac{dS_{v1}}{dt} + f(I_{v1}) S_{v1} = \pi_{v1} \tag{3.3.12}$$

where $f(I_{v1}) = \beta_{v1h1} I_{h1} + \mu_{v1}$ after expanding by the I.F $e^{\int_0^t f(I_{v1})}$

$$\frac{d}{dt}(e^{\int_0^t f(I_{v1})} S_{v1}) = \pi_{v1} e^{\int_0^t f(I_{v1}) dI_{h1}} \tag{3.3.13}$$

Integrating with respect to t

$$e^{\int_0^t f(I_{v1})} S_{v1} = K_4 + \pi_{v1} \int e^{\int_0^t f(I_{v1}) dI_{h1}} dt$$

$$S_{v1} = K_4 e^{-\int_0^t f(I_{v1})} + \pi_{v1} e^{-\int_0^t f(I_{v1})} \Big[\int e^{\int_0^t f(I_{v1}) dI_{h1}} \Big] > 0 \tag{3.3.14}$$

for $t > 0$ From the seventh equation of (1.1), we have

$$\frac{dI_{h2}}{dt} = \beta_{v2h2} S_{h2} I_{v2} - C_3 I_{h2} \tag{3.3.15}$$

where $C_3 = (\mu_{v_2} + d_2 + \alpha_2)$ The integrating factor of (2.5) is $e^{C_3 t}$ which when multiplied by (2.5) gives

$$e^{C_3 t} \frac{dI_{h2}}{dt} + C_3 e^{C_3 t} I_{h2} = \beta_{v2h2} S_{h2} I_{v2} e^{C_3 t}$$

$$\frac{d}{dt}(e^{C_3 t}) = \beta_{v2h2} S_{h2} I_{v2} e^{C_3 t}$$

Integrating both sides with respect to t yields

$$e^{C_3 t} I_{h2} = \int \beta_{v2h2} S_{h2} I_{v2} e^{C_3 t} dt + K_5$$

$$I_{h2} = K_5 e^{C_3 t} + e^{C_3 t} \int \beta_{v2h2} e^{C_3 t} dt \geq 0 \tag{3.3.16}$$

as $t \to \infty (t > 0)$ where K_5 is a constant of integration. From the eighth equation of (3.3.1) we have that

$$\frac{dR_{h2}}{dt} = C_4 R_{h12} - \alpha_2 I_{h2} \tag{3.3.17}$$

where $C_4 = (\mu_{h2} + \sigma_2)$ Multiplying () with the approximate integrating factor I.F $e^{C_4(t)}$ hence we obtain

$$e^{C_4(t)} \frac{dR_{h2}}{dt} + C_4 e^{C_4(t)} R_{h2} = \alpha_2 I_{h2} e^{C_4(t)}$$

$$\therefore \frac{d}{dt}(e^{C_4(t)} R_{h2}) = \alpha_2 I_{h2} e^{C_4(t)}$$

Integrating with respect to t

$$e^{C_4(t)} R_{h2} - \int \alpha_2 I_{h2} e^{C_4(t)} dt + K_6$$

where k_6 is a constant of integration.

$$R_{h2} = K_5 e^{-C_4(t)} + e^{-C_4(t)} \int \alpha_2 I_{h2} e^{C_4(t)} dt \geq 0 for t \geq 0 \tag{3.3.18}$$

Now, for the fifth equation(3.3.1), I have that

$$\frac{dS_{h2}}{dt} + (C_5 + \beta_{v2h2} I_{v2}) = \sigma_2 R_{h2} + \lambda_1 S_{h1} \tag{3.3.19}$$

which can be expressed as

$$\frac{dS_{h2}}{dt} + f(I_{v2}) S_{h2} = \sigma_2 R_{h2} + \lambda_1 S_{h1} \tag{3.3.20}$$

where $f(I_{v2}) = C_5 + \beta_{v2h2} I_{h2}$ and $C_5 = \mu_{h2} + \lambda_2$ Multiplying with the I.F $e^{\int_0^t f(I_{v2}) dI_{v2}}$ gives

$$e^{\int_0^t f(I_{v2}) dI_{v2}} \frac{dS_{h2}}{dt} + f(I_{v2}) e^{\int_0^t f(I_{v2}) dI_{v2}} S_{h2} = (\sigma_2 R_{h2} + \lambda_1 S_{h1}) e^{\int_0^t f(I_{v2}) dI_{v2}}$$

$$\therefore \frac{d}{dt}(e^{\int_0^t f(I_{v2}) dI_{v2}} S_{h2}) = (\sigma_2 R_{h2} + \lambda_1 S_{h1}) e^{\int_0^t f(I_{v2}) dI_{v2}}$$

Integrating with respect to t

$$e^{\int_0^t f(I_{v2}) dI_{v2}} S_{h2} = K_4 + \int_0^t (\sigma_2 R_{h2} + \lambda_1 S_{h1}) e^{\int_0^t f(I_{v2}) dI_{v2}}$$

$$S_{h2} = K_5 e^{-\int_0^t f(I_{v2}) dI_{v2}} + e^{-\int_0^t f(I_{v2}) dI_{v2}} \int_0^t (\sigma_2 R_{h2} + \lambda_1 S_{h1}) e^{\int_0^t f(I_{v2}) dI_{v2}} \geq 0 \tag{3.3.21}$$

for $t > 0$ Considering the tenth equation of (3.3.1), we have

$$\frac{dI_{v2}}{dt} + \mu_{v2} I_{v2} = \beta_{h2v2} S_{v2} I_{h2} \tag{3.3.22}$$

The Integrating factor I.F is $e^{\mu_{v2}(t)}$ by multiplying () through by the I.F results in

$$e^{\mu_{v2}(t)} \frac{dI_{v2}}{dt} + \mu_{v2} e^{\mu_{v2}(t)} I_{v2} = \beta_{v2h2} S_{v2} I_{h2} e^{\mu_{v2}(t)}$$

$$\frac{d}{dt}(e^{\mu_{v2}(t)} I_{v2}) = \beta_{v2h2} S_{v2} I_{h2} e^{\mu_{v2}(t)}$$

Integrating with respect to t

$$e^{\mu_{v2}(t)} I_{v2} = K_5 + \int \beta_{v2h2} S_{v2} I_{h2} e^{\mu_{v2}(t)}$$

Thus,

$$I_{v2} = K_5 e^{-\mu_{v2}(t)} + e^{-\mu_{v2}(t)} \int \beta_{v2h2} S_{v2} I_{h2} e^{\mu_{v2}(t)} dt \geq 0, t \geq 0 \tag{3.3.23}$$

Further, from ninth equation of (3.3.1),

$$\frac{dS_{v2}}{dt} + (\beta_{v2h2} I_{h2} + \mu_{v2}) I_{v2} S_{v2} = \pi_{v2}$$

$$\frac{dS_{v2}}{dt} + g(I_{v2}) S_{v2} = \pi_{v2} \tag{3.3.24}$$

where $f(I_{v2}) = \beta_{v2h2} I_{h2} + \mu_{v2}$ after expanding by the I.F $e^{\int_0^t f(I_{v2})}$

$$\frac{d}{dt}(e^{\int_0^t g(I_{v2})} S_{v2}) = \pi_{v2} e^{\int_0^t f(I_{v2}) dI_{h2}} \tag{3.3.25}$$

Integrating with respect to t

$$e^{\int_0^t g(I_{v2})} S_{v2} = K_6 + \pi_{v2} \int e^{\int_0^t f(I_{v2}) dI_{h2}} dt$$

$$S_{v2} = K_5 e^{-\int_0^t g(I_{v2})} + \pi_{v2} e^{-\int_0^t g(I_{v2})} \Big[\int e^{\int_0^t g(I_{v2}) dI_{h2}} \Big] > 0 \tag{3.3.26}$$

for $t > 0$

Thus, the solution

$$S_{h1}, I_{h1}, R_{h1}, S_{v1} I_{v1}, S_{h2}, I_{h2}, R_{h2} S_{v2}$$

and I_{v2} of the Zika model with initial conditions $S_{h_1}(0) = S^0_{h1} > 0, I_{h_1}(0) = I^0_{h1} \geq 0, R_{h_1}(0) = R^0_{h1} \geq 0, S_{v_1}(0) = S^0_{v1} > 0, I_{v_1}(0) = I^0_{v1} \geq 0, S_{h_2}(0) = S^0_{h2} > 0, I_{h_2}(0) = I^0_{h2} \geq 0, R_{h_2}(0) = R^0_{h2} \geq 0, S_{v_2}(0) = S^0_{v2} > 0, I_{v_2}(0) = I^0_{h1} \geq 0$ are positive for all $t > 0$ Hence the proof. □

Let the total human population for both patches of the model be

$$N_h = N_{h1} + N_{h2} \tag{3.3.27}$$

such that

$$N_{h1} = S_{h1}(t) + I_{h1}(t) + R_{h1}(t) \tag{3.3.28}$$

$$N_{h2} = S_{h2}(t) + I_{h2}(t) + R_{h2}(t) \tag{3.3.29}$$

Differentiating with respect to t

$$N_h^{'} = N_{h1}^{'} + N_{h2}^{'} \tag{3.3.30}$$

$$N_h^{'} = S_{h1}^{'}(t) + I_{h1}^{'}(t) + R_{h1}^{'}(t) + S_{h2}^{'}(t) + I_{h2}^{'}(t)$$

$$N_h^{'} = \pi_{h1} - \beta_{v1h1} S_{h1} I_{v1} - \lambda_1 S_{h1} - \mu_{h1} S_{h1} + \lambda_2 S_{h2}$$

$$+\sigma_1 R_{h1} + \beta_{v1h1} S_{h1} I_{v1} - (\mu_{h1} + d_1 + \alpha_1) I_{h1} + \alpha_1 I_{h1} - \mu_{h1} R_{h1}$$

$$-\sigma_1 R_{h1} + \pi_{h2} - \beta_{v2h2} S_{h2} I_{v2} - \lambda_2 S_{h2} - \mu_{h2} S_{h2} + \lambda_1 S_{h1}$$

$$+\sigma_2 R_{h2} + \beta_{v2h2} S_{h2} I_{v2} - (\mu_{h2} + d_2 + \alpha_2) I_{h2} + \alpha_2 I_{h2} - \mu_{h2} R_{h2} - \sigma_2 R_{h2}$$

$$N_h^{'} = \pi_{h1} + \pi_{h2} - \mu_{h1}(S_{h1} + I_{h1} + R_{h1}) - \mu_{h2}(S_{h2} + I_{h2} + R_{h2} + d_1 I_{h1} + d_2 I_{h2})$$

$$N_h^{'} = \pi_{h1} + \pi_{h2} - \mu_{h1} N_{h1}(t) - \mu_{h2} N_{h2}(t) + d_1 I_{h1} + d_2 I_{h2}$$

With the assumption that, Let

$$\mu_h = min\{\mu_{h1}, \mu_{h2}\}$$

$$N_h^{'}(t) = \pi_{h1} + \pi_{h2} - \mu_h(N_{h1}(t) + N_{h2}(t)) + d_1 I_{h1} + d_2 I_{h2}$$

$$N_h^{'}(t) = \pi_{h1} + \pi_{h2} - \mu_h N_h(t) + d_1 I_{h1} + d_2 I_{h2} \tag{3.3.31}$$

Since $dI_{h1}(t)$ and $dI_{h2}(t)$ are non-negative, then reduces to

$$N_h^{'}(t) \leq \pi_{h1} + \pi_{h2} - \mu_h N_h(t)$$

Therefore,

$$\frac{dN_h(t)}{d(t)} + \mu_h N_h(t) \leq \pi_{h1} + \pi_{h2}$$

Integrating with respect to t

$$N_h(t) \leq \frac{(\pi_{h1} + \pi_{h2})}{\mu_h} + Ke^{-}\mu_h t \tag{3.3.32}$$

Taking the limit as $t \to \infty$

$$\lim_{t\to\infty} N_h(t) \leq \frac{(\pi_{h1} + \pi_{h2})}{\mu_h} \tag{3.3.33}$$

Thus

$$0 \leq N_h(t) \leq \frac{(\pi_{h1} + \pi_{h2})}{\mu_h}$$

Furthermore, let the total mosquito population for both patch be

$$N_v = N_{v1}(t) + N_{v2}(t) \tag{3.3.34}$$

such that

$$N_{v1}(t) = S_{v1}(t) + I_{v1}(t) \tag{3.3.35}$$

$$N_{v2}(t) = S_{v2}(t) + I_{v2}(t) \tag{3.3.36}$$

Differentiating with respect to t

$$N_v^{'} = N_{v1}^{'} + N_{v2}^{'} \tag{3.3.37}$$

$$= S_{v1}^{'}(t) + I_{v1}^{'}(t) + S_{v2}^{'}(t) + I_{v2}^{'}(t)$$

$$= \pi_{v1} - \mu_{v1}S_{v1} - \beta_{h1v1}S_{v1}I_{h1} + \beta_{h1v1}S_{v1}I_{h1} - \mu_{v1}I_{v1} + \pi_{v2} - \mu_{v2}S_{v2}$$
$$-\beta_{h2v2}S_{v2}I_{h2} + \beta_{h2v2}S_{v2}I_{h2} - \mu_{v2}I_{v2}$$

Therefore

$$N_v^{'}(t) = (\pi_{v1} + \pi_{v2}) - \mu_{v1}(S_{v1} + I_{v1}) - \mu_{v2}(S_{v2} + I_{v2})$$

Let,

$$\mu_m = min\{\mu_{v1}, \mu_{v2}\}$$

$$N_v^{'}(t) = (\pi_{v1} + \pi_{v2}) - \mu_m(N_{v1}(t) + N_{v2}(t))$$

$$= (\pi_{v1} + \pi_{v2}) - \mu_m N_v(t)$$

$$\frac{dN_{v1}(t)}{dt} + \mu_m N_v(t) = (\pi_{v1} + \pi_{v2}) \tag{3.3.38}$$

Integrating with respect to t we have,

$$N_v(t) = \frac{(\pi_{v1} + \pi_{v2})}{\mu_m} + K5e^{-\mu_m(t)}$$

$$\lim_{t\to\infty} N_v(t) = \frac{(\pi_{v1} + \pi_{v2})}{\mu_m}$$

3.4 Model Analysis

Since the right hand side of the system (3.3.1) is a vector (multi-variables polynomial) function of class C^∞, by the Cauchy-Piccard theorem [Wouk, 1963] the exists a unique (local) solution of the system (3.3.1). For the rest of the analysis, we assume that the solution of (3.3.1) is nonnegative (to ensure a nonnegative population at all time).

3.4.1 Boundedness of Solution

Proposition 3.4.1. *The functions $S_{h_1}, I_{h_1}, R_{h_1}, S_{v_1}, I_{v_1}, S_{h_2}, I_{h_2}, R_{h_2}, S_{v_2}, I_{v_2}$ solutions of the system (3.3.1) are bounded.*

Proof. Consider total human population for both patches

$$N_h = N_{h1} + N_{h2}, \tag{3.4.1}$$

where

$$N_{h1} = S_{h1} + I_{h1} + R_{h1}, \quad N_{h2} = S_{h2} + I_{h2} + R_{h2}. \tag{3.4.2}$$

Differentiating (3.4.1)) with respect to t and taking into account for (3.3.1), we get

$$\begin{aligned}
N_h^{'} &= N_{h1}^{'} + N_{h2}^{'} \\
&= S_{h1}^{'} + I_{h1}^{'} + R_{h1}^{'} + S_{h2}^{'} + I_{h2}^{'} + R_{h2} \\
&= \pi_{h1} + \pi_{h2} - \mu_{h1}(S_{h1} + I_{h1} + R_{h1}) - \mu_{h2}(S_{h2} + I_{h2} + R_{h2}) - d_1 I_{h1} - d_2 I_{h2} \\
&= \pi_{h1} + \pi_{h2} - \mu_{h1} N_{h1} - \mu_{h2} N_{h2} - d_1 I_{h1} - d_2 I_{h2} \\
&\leq \pi_{h1} + \pi_{h2} - \mu_h (N_{h1} + N_{h2}) - d_1 I_{h1} - d_2 I_{h2} \\
&\leq \pi_{h1} + \pi_{h2} - \mu_h N_h - d_1 I_{h1} - d_2 I_{h2} \\
&\leq \pi_{h1} + \pi_{h2} - \mu_h N_h \quad (\text{since } I_{h1}, I_{h2} \geq 0),
\end{aligned} \tag{3.4.3}$$

where $\mu_h \leq min\{\mu_{h1}, \mu_{h2}\}$. Solve the differential inequality (3.4.3), we get

$$N_h(t) \leq \frac{\pi_{h1} + \pi_{h2}}{\mu_h} + \left(N_h(0) - \frac{\pi_{h1} + \pi_{h2}}{\mu_h} \right) e^{-\mu_h t} = N_h(0) e^{-\mu_h t} + (1 - e^{-\mu_h t}) \frac{\pi_{h1} + \pi_{h2}}{\mu_h}.$$

If $N_h(0) \leq \frac{\pi_{h1}+\pi_{h2}}{\mu_h}$, then $N_h(t) \leq \frac{\pi_{h1}+\pi_{h2}}{\mu_h}$ for all $t > 0$. However, if $\frac{\pi_{h1}+\pi_{h2}}{\mu_h} < N_h(0)$, then $N_h(t) \leq N_h(0)$ for all $t > 0$. In either cases we always have $N_h(t) \leq \max\left(N_h(0), \frac{\pi_{h1}+\pi_{h2}}{\mu_h}\right)$ for all $t \geq 0$. This shows that the total human population N_h is bounded.

In the same manner, we consider the total mosquito population for both patches

$$N_v = N_{v1} + N_{v2}, \tag{3.4.4}$$

where

$$N_{v1} = S_{v1} + I_{v1}, \quad N_{v2} = S_{v2} + I_{v2}. \tag{3.4.5}$$

Differentiating (3.4.4) with respect to t and accounting for (3.3.1), we get

$$\begin{aligned}
N_v^{'} &= S_{v1}^{'} + I_{v1}^{'} + S_{v2}^{'} + I_{v2}^{'} \\
&= \pi_{v1} + \pi_{v2} - \mu_{v1}(S_{v1} + I_{v1}) - \mu_{v2}(S_{v2} + I_{v2}) \\
&= \pi_{v1} + \pi_{v2} - \mu_{v1} N_{v1} - \mu_{v2} N_{v2} \\
&\leq \pi_{v1} + \pi_{v2} - \mu_m (N_{v1} + N_{v2}) \\
&\leq \pi_{v1} + \pi_{v2} - \mu_m N_v,
\end{aligned} \tag{3.4.6}$$

where $\mu_m \leq min\{\mu_{v1}, \mu_{v2}\}$. Therefore,

$$N_v(t) \leq \frac{\pi_{v1} + \pi_{v2}}{\mu_m} + \left(N_v(0) - \frac{\pi_{v1} + \pi_{v2}}{\mu_m}\right) e^{-\mu_m t}, \tag{3.4.7}$$

which is bounded above by $\max\left(N_v(0), \frac{\pi_{v1}+\pi_{v2}}{\mu_m}\right)$.
Since the sub-populations are nonnegative et the total population is bounded, then they are bounded as well. □

3.4.2 Equilibrium Point

There are four equilibrium points for the system (3.3.1):

(i) The Zika free Equilibrium (ZFE) Z_0 which occurs when both communities (connected via immigration) do no longer have a single case of Zika Virus infection. It is given by $Z_0 = \left(S^o_{h1}, 0, 0, S^0_{v1}, 0, S_{h2^o}, 0, 0, S^o_{v2}, 0\right)$, where

$$S^o_{v1} = \frac{\pi_{v1}}{\mu_{v1}}, \quad S^o_{v2} = \frac{\pi_{v2}}{\mu_{v2}}, \quad S^o_{h1} = \frac{\pi_{h1}\lambda_2 + \pi_{h1}\mu_{h2} + \pi_{h2}\lambda_2}{\lambda_1\mu_{h2} + \lambda_2\mu_{h1} + \mu_{h1}\mu_{h2}}, \quad S^o_{h2} = \frac{\lambda_1\pi_{h1} + \lambda_1\pi_{h2} + \mu_{h1}\pi_{h2}}{\lambda_1\mu_{h2} + \lambda_2\mu_{h1} + \mu_{h1}\mu_{h2}}.$$

(ii) The Zika free endemic equilibrium Z_1 which occurs when Zika is prevalent in the first patch but not present in the second patch. Assuming no immigration (i.e., $\lambda_1 = \lambda_2 = 0$), it is given by

$$Z_1 = (S^*_{h1}, I^*_{h1}, R^*_{h1}, S^*_{v1} I^*_{v1}, S^*_{h2}, 0, 0, S^*_{v2}, 0)$$

, where

$$\begin{aligned}
S^*_{v2} &= \frac{\pi_{v2}}{\mu_{v2}}, \\
S^*_{h2} &= \frac{\pi_{h2}}{\mu_{h2}}, \\
I^*_{h1} &= \frac{c_2c_3\mu_{h1}\mu^1_{v1} - \beta_{v1h1}\beta_{h1v1}\pi_{v1}\pi_{h1}c_3}{(\alpha_1\sigma_1 - c_2c_3)\beta_{v1h1}\beta_{h1v1}\pi_{v1} - c_2c_3\mu_{h1}\beta_{h1v1}} \\
S^*_{h1} &= \frac{c_3\pi_{h1} + (\sigma_1\alpha_1 - c_2c_3)}{c_3\mu_{h1}} I^*_{h1}, \\
R^*_{h1} &= \frac{\alpha_1}{c_3} I^*_{h1}, \\
I^*_{v1} &= \frac{\beta_{h1v1}\pi_{v1} I^*_{h1}}{\beta_{h1v1} I^*_{h1} + \mu^2_{v1}}, \\
S^*_{v1} &= \frac{\pi_{v1} - \mu_{v1} I^*_{h1}}{\mu_{v1}}.
\end{aligned}$$

(iii) The Zika free endemic equilibrium Z_2 which occurs when Zika is prevalent in the second patch but not present in the first patch. Assuming no immigration, it is given by $Z_2 = (S^*_{h1}, 0, 0, S^*_{v1}, 0, S^*_{h2}, I^*_{h2}, R^*_{h2}, S^*_{v2}, I^*_{v1})$, where

$$
\begin{aligned}
S^*_{v1} &= \frac{\pi_{v1}}{\mu_{v1}}, \\
S^*_{h1} &= \frac{\pi_{h1}}{\mu_{h1}}, \\
I^*_{h2} &= \frac{c_0 c_1 \mu_{h2} \mu^2_{v2} - \beta_{v2h2}\beta_{h2v2}\pi_{v2}\pi_{h2}c_1}{(\alpha_2\sigma_2 - c_0c_1)\beta_{v2h2}\beta_{h2v2}\pi_{v2} - c_0c_1\mu_{h2}\beta_{h2v2}} \\
S^*_{h2} &= \frac{c_1\pi_{h2} + (\sigma_2\alpha_2 - c_0c_1)}{c_1\mu_{h2}} I^*_{h2}, \\
R^*_{h2} &= \frac{\alpha_2}{c_1} I^*_{h2}, \\
I^*_{v2} &= \frac{\beta_{h2v2}\pi_{v2} I^*_{h2}}{\beta_{h2v2} I^*_{h2} + \mu^2_{v2}}, \\
S^*_{v2} &= \frac{\pi_{v2} - \mu_{v2} I^*_{h2}}{\mu_{v2}}.
\end{aligned}
$$

(iv) The Zika Endemic Equilibrium (ZEE) Z_3 which occurs when Zika is prevalent in both patches. It is given by $Z_3 = (S^{**}_{h1}, I^{**}_{h1}, R^{**}_{h1}, S^{**}_{v1}, I^{**}_{v1}, S^{**}_{h2}, I^{**}_{h2}, R^{**}_{h2}, S^{**}_{v2}, I^{**}_{v2})$, where

$$
\begin{aligned}
R^{**}_{h1} &= \frac{\alpha_1}{c_3} I^{**}_{h1}, R^{**}_{h2} = \frac{\alpha_2}{c_1} I^{**}_{h2}, \\
S^{**}_{v1} &= \frac{\pi_{v1}}{\beta_{h1v1} I^{**}_{h1} + \mu_{v1}}, \\
S^{**}_{v2} &= \frac{\pi_{v2}}{\beta_{h2v2} I^{**}_{h2} + \mu_{v2}} \\
I^{**}_{v1} &= \frac{\pi_{v1}\beta_{h1v1} I^{**}_{h1}}{\mu_{v1}(\beta_{h1v1} I^{**}_{h1} + \mu_{v1})}, \\
I^{**}_{v2} &= \frac{\pi_{v1}\beta_{h2v2} I^{**}_{h2}}{\mu_{v2}(\beta_{h2v2} I^{**}_{h2} + \mu_{v2})} \\
S^{**}_{h2} &= \frac{\pi_{h2}}{(\mu_{h2} + \lambda_2 + \beta_{v2h2} I^{**}_{v2})} + \frac{\lambda_1 S^{**}_{h1}}{(\mu_{h2} + \lambda_2 + \beta_{v2h2} I^{**}_{v2})} + \frac{\sigma_2\alpha_2 I^{**}_{h2}}{c_1(\mu_{h2} + \lambda_2 + \beta_{v2h2} I^{**}_{v2})}, \\
I^{**}_{h1} &= \frac{\beta_{v1h1} I^{**}_{v1} S^{**}_{h1}}{c_2}, I^{**}_{h2} = \frac{\beta_{v2h2} I^{**}_{v2} S^{**}_{h2}}{c_4}
\end{aligned}
$$

$$
\begin{aligned}
S_{h1}^{**} =& \frac{(\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v1}^{**})(\mu_{h1}+\lambda_2+\beta_{v2h2}I_{v2}^{**})}{(\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v1}^{**})(\mu_{h2}+\lambda_2+\beta_{v2h2}I_{v2}^{**})-\lambda_1\lambda_2}\Bigg(\frac{\pi_{h1}}{\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v1}^{**}} \\
&+\frac{\lambda_2\pi_{h2}}{(\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v2}^{**})(\mu_{h2}+\lambda_2+\beta_{v2h2}I_{v2}^{**})}+\frac{\sigma_1\alpha_1 I_{h1}^{**}}{c_3(\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v1}^{**})} \\
&+\frac{\lambda_2\sigma_2\alpha_2 I_{h2}^{**}}{c_1(\mu_{h1}+\lambda_1+\beta_{v1h1}I_{v1}^{**})(\mu_{h2}+\lambda_2+\beta_{v2h2}I_{v2}^{**})}\Bigg).
\end{aligned}
$$

3.4.3 Basic Reproduction Number

We use the next generation matrix [Diekmann et al., 2010, van den Driessche, 2017] approach to find the basic reproduction number of (3.3.1). The matrices for the newly infected and for transfer and death into the disease compartments are respectively

$$
\mathbb{F} = \begin{bmatrix}
0 & \frac{\beta_{v1h1}g_1}{g_2} & 0 & 0 \\
\frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & 0 & 0 \\
0 & 0 & 0 & \frac{\beta_{v2h2}g_3}{g_4} \\
0 & 0 & \frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0
\end{bmatrix}
$$

and

$$
\mathbb{V} = \begin{bmatrix}
\mu_{h1}+d_1+\alpha_1 & 0 & 0 & 0 \\
0 & \mu_{v1} & 0 & 0 \\
0 & 0 & \mu_{h2}+d_2+\alpha_2 & 0 \\
0 & 0 & 0 & \mu_{v2}
\end{bmatrix},
$$

where

$$
\begin{aligned}
&g_1 = \pi_{h1}\lambda_2+\pi_{h1}\mu_{h2}+\pi_{h2}\lambda_2, g_2 = \lambda_1\mu_{h2}+\lambda_2\mu_{h1}+\mu_{h1}\mu_{h2}, \\
&g_3 = \lambda_1\pi_{h1}\mu_{h2}+\lambda_1\lambda_2\pi_{h1}+\lambda_1\lambda_2\pi_{h2}+\pi_{h2}\mu_{h2}\mu_{h1}+\pi_{h1}\lambda_1\mu_{h2}+\pi_{h2}\lambda_1\mu_{h1}, \\
&g_4 = {\mu_{h2}}^2\mu_{h1}+\lambda_1{\mu_{h2}}^2+2\lambda_2\mu_{h2}\mu_{h1}+\lambda_1\lambda_2\mu_{h2}+{\lambda_2}^2\mu_{h1}.
\end{aligned}
$$

The next generation matrix $\mathbb{FV}^{-1}$ is

$$\mathbb{FV}^{-1} = \begin{bmatrix} 0 & \frac{\beta_{v1h1}g_1}{g_2\mu_{v1}} & 0 & 0 \\ \frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}(\mu_{h1}+d_1+\alpha_1)} & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta_{v2h2}g_3}{g_4\mu_{v2}} \\ 0 & 0 & \frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}(\mu_{h2}+d_2+\alpha_2)} & 0 \end{bmatrix}$$

and has four eigenvalues

$$\lambda^{(1)} = \frac{\sqrt{g_4\left(\mu_{h2}+d_2+\alpha_2\right)\beta_{v2h2}g_3\beta_{h2v2}\pi_{v2}}}{g_4\left(\mu_{h2}+d_2+\alpha_2\right)\mu_{v2}}, \quad \lambda^{(2)} = -\frac{\sqrt{g_4\left(\mu_{h2}+d_2+\alpha_2\right)\beta_{v2h2}g_3\beta_{h2v2}\pi_{v2}}}{g_4\left(\mu_{h2}+d_2+\alpha_2\right)\mu_{v2}}$$

$$\lambda^{(3)} = \frac{\sqrt{g_2\left(\mu_{h1}+d_1+\alpha_1\right)\beta_{h1v1}\pi_{v1}\beta_{v1h1}g_1}}{g_2\left(\mu_{h1}+d_1+\alpha_1\right)\mu_{v1}}, \quad \lambda^{(4)} = -\frac{\sqrt{g_2\left(\mu_{h1}+d_1+\alpha_1\right)\beta_{h1v1}\pi_{v1}\beta_{v1h1}g_1}}{g_2\left(\mu_{h1}+d_1+\alpha_1\right)\mu_{v1}}.$$

Thus the basic reproduction number R_0 which is the spectral radius $\rho(\mathbb{FV}^{-1})$ (dominant maximum eigenvalue) of the next generation operator $\mathbb{FV}^{-1}$ is given by

$$R_0 = \max(R_1, R_2),$$

where

$$R_1 = \frac{\beta_{h1v1}\sqrt{\pi_{v1}g_1}}{\mu_{v1}\sqrt{g_2\left(\mu_{h1}+d_1+\alpha_1\right)}}, \quad R_2 = \frac{\beta_{h2v2}\sqrt{g_3\pi_{v2}}}{\mu_{v2}\sqrt{g_4\left(\mu_{h2}+d_2+\alpha_2\right)}}.$$

We note that R_1 and R_2 are the basic reproduction number of Zika in patches 1 and 2 respectively. By definition, the basic reproduction number is the average number of secondary infections caused by a single infected individual during his entire period of infectiousness.

3.4.4 Stability Analysis

Theorem 3.4.2. *The Zika free equilibrium Z_0 is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$.*

Proof. The Jacobian matrix evaluate at Z_0 is given by

$$J(Z_0) = \begin{bmatrix} -\lambda_1 - \mu_{h1} & 0 & \sigma_1 & 0 & -\frac{\beta_{v1h1} g_1}{g_2} & \lambda_2 & 0 & 0 & 0 & 0 \\ 0 & -c_2 & 0 & 0 & \frac{\beta_{v1h1} g_1}{g_2} & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_1 & -c_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & -\mu_{v1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & 0 & -\mu_{v1} & 0 & 0 & 0 & 0 & 0 \\ \lambda_1 & 0 & 0 & 0 & 0 & -\lambda_2 - \mu_{h2} & 0 & \sigma_2 & 0 & -\frac{\beta_{v2h2} g_3}{g_4} \\ 0 & 0 & 0 & 0 & 0 & 0 & -c_0 & 0 & 0 & \frac{\beta_{v2h2} g_3}{g_4} \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -c_4 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & -\frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & -\mu_{v2} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & 0 & -\mu_{v2} \end{bmatrix}$$

where $c_0 = (\mu_{h2} + d_2 + \alpha_2)$, $c_2 = (\mu_{h1} + d_1 + \alpha_1)$, $c_3 = (\mu_{h1} + \sigma_1)$ and $c_4 = (\mu_{h2} + \sigma_2)$. It eigenvalues are

$$\lambda^{(1)} = -c_3, \quad \lambda^{(2)} = -\mu_{v1}, \quad \lambda^{(3)} = -c_4, \quad \lambda^{(4)} = -\mu_{v2}$$

$$\lambda^{(5)} = -\frac{1}{2}\left[\lambda_1 + \mu_{h1} + \lambda_2 + \mu_{h2} + \sqrt{(\lambda_1 + \mu_{h1} - \lambda_2 - \mu_{h2})^2 + 4\lambda_1\lambda_2}\right]$$

$$\lambda^{(6)} = -\frac{1}{2}\left[\lambda_1 + \mu_{h1} + \lambda_2 + \mu_{h2} - \sqrt{(\lambda_1 + \mu_{h1} - \lambda_2 - \mu_{h2})^2 + 4\lambda_1\lambda_2}\right]$$

$$\lambda^{(7)} = -\frac{1}{2}\left[c_2 + \mu_{v1} + \sqrt{(c_2 - \mu_{v1})^2 + \frac{4\beta_{h1v1}^2 g_1 \pi_{v1}}{\mu_{v1} g_2}}\right]$$

$$\lambda^{(8)} = -\frac{1}{2}\left[c_2 + \mu_{v1} - \sqrt{(c_2 - \mu_{v1})^2 + \frac{4\beta_{h1v1}^2 g_1 \pi_{v1}}{\mu_{v1} g_2}}\right]$$

$$\lambda^{(9)} = -\frac{1}{2}\left[c_0 + \mu_{v2} + \sqrt{(c_0 - \mu_{v2})^2 + \frac{4\beta_{h2v2}^2 g_3 \pi_{v2}}{\mu_{v2} g_4}}\right]$$

$$\lambda^{(10)} = -\frac{1}{2}\left[c_0 + \mu_{v2} - \sqrt{(c_0 - \mu_{v2})^2 + \frac{4\beta_{h2v2}^2 g_3 \pi_{v2}}{\mu_{v2} g_4}}\right]$$

We note that if $\lambda^{(i)} + \lambda^{(j)} < 0$ and $\lambda^{(i)}\lambda^{(j)} > 0$, then $\lambda^{(i)}$ and $\lambda^{(j)}$ are both negative. We have:

$$\lambda^{(5)} + \lambda^{(6)} = -(\lambda_1 + \mu_{h1} + \lambda_2 + \mu_{h2}) < 0$$

$$\lambda^{(5)}\lambda^{(6)} = (\lambda_1 + \mu_{h1})(\lambda_2 + \mu_{h2}) - \lambda_1\lambda_2 = \lambda_1\mu_{h2} + \lambda_2\mu_{h1} + \mu_{h1}\mu_{h2} > 0.$$

Likewise we have

$$\lambda^{(7)} + \lambda^{(8)} = -(c_2 + \mu_{v1}) < 0 \lambda^{(7)}\lambda^{(8)} = c_2\mu_{v1} - \frac{\beta_{h1v1}^2 g_1 \pi_{v1}}{\mu_{v1} g_2} = c_2\mu_{v1}(1 - R_1^2) = c_2\mu_{v1}(1 + R_1)(1 - R_1),$$

and

$$\lambda^{(9)} + \lambda^{(10)} = -(c_0 + \mu_{v2}) < 0 \lambda^{(9)}\lambda^{(10)} = c0\mu_{v2} - \frac{\beta_{h2v2}^2 g_3 \pi_{v2}}{\mu_{v2} g_4} = c_0\mu_{v2}(1 - R_2^2) = c_0\mu_{v2}(1 + R_2)(1 - R_2).$$

If $R_1 > 1$ or $R_2 > 1$, then $\lambda^{(7)}\lambda^{(8)} < 0$ or $\lambda^{(9)}\lambda^{(10)} < 0$. As a result, at least two eigenvalues will have opposite signs and the equilibrium point Z_0 will be unstable. However, if both $R_1 < 1$ (i.e., $\lambda^{(7)}\lambda^{(8)} > 0$) and $R_2 < 0$ (i.e., $\lambda^{(9)}\lambda^{(10)} > 0$), then Z_0 is stable. □

Theorem 3.4.3. *Zika free equilibrium Z_0 is globally asymptotically stable when $R_0 < 1$.*

Proof. Define a Lyapunov function as follows:

$$L(I_{h1}, I_{h2}, I_{v1}, I_{v2}) = \frac{\pi_{v1}\beta_{h1v1} I_{h1}}{\mu_{v1}} + c_2 I_{v1} + \frac{\pi_{v2}\beta_{h2v2} I_{h2}}{\mu_{v2}} + c_0 I_{v2}$$

Differentiating with respect to t,

$$\begin{aligned} L' &= \frac{\pi_{v1}\beta_{h1v1} I'_{h1}}{\mu_{v1}} + c_2 I'_{v1} + \frac{\pi_{v2}\beta_{h2v2} I'_{h2}}{\mu_{v2}} + c_0 I'_{v2} \\ &= \frac{\pi_{v1}\beta_{h1v1}}{\mu_{v1}}\left[\beta_{v1h1} I_{v1} S_{h1} - c_2 I_{h1}\right] + c_2\left[\beta_{h1v1} I_{h1} S_{v1} - \mu_{v1} I_{v1}\right] \\ &+ \frac{\pi_{v2}\beta_{h2v2}}{\mu_{v2}}\left[\beta_{v2h2} I_{v2} S_{h2} - c_0 I_{h2}\right] + c_0\left[\beta_{h2v2} I_{h2} S_{v2} - \mu_{v2} I_{v2}\right] \end{aligned}$$

By expansion and collection of terms, we have

$$\begin{aligned} L' &= \left[\frac{\pi_{v1}\beta_{v1h1}\beta_{h1v1} S_{h1}}{\mu_{v1}} - c_2\mu_{v1}\right] I_{v1} + \left[\frac{\pi_{v2}\beta_{v2h2}\beta_{h2v2} S_{h2}}{\mu_{v1}} - c_0\mu_{v2}\right] I_{v2} \\ &+ \left[c_2\beta_{h1v1} S_{v1} - \frac{c_2\pi_{v1}\beta_{h1v1}}{\mu_{v1}}\right] I_{h1} + \left[c_0\beta_{h2v2} S_{v2} - \frac{c_0\pi_{v2}\beta_{h2v2}}{\mu_{v2}}\right] I_{h2} \end{aligned}$$

At Zika free equilibrium, $S_{h1} = \frac{g_1}{g_2}, S_{h2} = \frac{g_3}{g_4}$ such that,

$$L^{'} = \left[\frac{\pi_{v1}\beta_{v1h1}\beta_{h1v1}}{\mu_{v1}}\frac{g_1}{g_2} - c_2\mu_{v1}\right]I_{v1} + \left[\frac{\pi_{v2}\beta_{v2h2}\beta_{h2v2}}{\mu_{v1}}\frac{g_3}{g_4} - c_0\mu_{v2}\right]I_{v2}$$
$$+ \left[c_2\beta_{h1v1}S_{v1} - \frac{c_2\pi_{v1}\beta_{h1v1}}{\mu_{v1}}\right]I_{h1} + \left[C_0\beta_{h2v2}S_{v2} - \frac{c_0\pi_{v2}\beta_{h2v2}}{\mu_{v2}}\right]I_{h2}$$

$S_{v1} = S_{v2} = 0$ Then

$$L' = c_2\mu_{v1}\left[\frac{\pi_{v1}\beta_{v1h1}\beta_{h1v1}g_1}{c_2\mu_{v1}^2 g_2} - 1\right]I_{v1} + c_0\mu_{v2}\left[\frac{\pi_{v2}\beta_{v2h2}\beta_{h2v2}g_3}{c_0\mu_{v2}^2 g_4} - 1\right]I_{v2} = c_2\mu_{v1}(R_1^2 - 1)I_{v1} + c_0\mu_{v2}(R_2^2 - 1)I_{v2}$$

Thus $L^{'} < 0$ if $R_1 < 1$ and $R_2 < 1$. Hence, Zika free equilibrium is globally asymptotically stable if $R_1 \leqslant 1$ and $R_2 \leqslant 1$ □

From the above theorem, the stability Z_0 indicates that the populations of both patches could be disease free over time provided that each infected individual infects at most one susceptible (i.e., $R_1 < 1$ and $R_2 < 1$) during his entire period of infectiousness.

Theorem 3.4.4. *Zika free endemic equilibrium Z_1 is locally asymptotically stable if $R_1 > 1$ and $R_2 < 1$, and unstable if $R_1 < 1$ or $R_2 > 1$.*

Proof. The Jacobian matrix evaluated at $Z_1 = (S_{h1}^*, I_{h1}^*, R_{h1}^*, S_{v1}^* I_{v1}^*, S_{h2}^*, 0, 0, S_{v2}^*, 0)$ is given by

$$J(Z_1) = \left(\begin{array}{ccccc|ccccc}
-\beta_{v1h1}I_{v1}^* - \mu_{h1} & 0 & 0 & 0 & -\beta_{v1h1}S_{h1}^* & 0 & 0 & 0 & 0 & 0 \\
\beta_{v1h1}I_{v1}^* & -c_2 & 0 & 0 & \beta_{v1h1}S_{h1}^* & 0 & 0 & 0 & 0 & 0 \\
0 & \alpha_1 & -c_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & -\beta_{v1h1}S_{v1}^* & 0 & \beta_{v1h1}I_{h1}^* - \mu_{v1} & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & \beta_{v1h1}S_{v1}^* & 0 & \beta_{v1h1}I_{h1}^* & -\mu_{v1} & 0 & 0 & 0 & 0 & 0 \\
\hline
0 & 0 & 0 & 0 & 0 & -\mu_{h2} & 0 & \sigma_2 & 0 & -\frac{\beta_{v2h2}\pi_{h2}}{\mu_{h2}} \\
0 & 0 & 0 & 0 & 0 & 0 & -c_0 & 0 & 0 & \frac{\beta_{v2h2}\pi_{h2}}{\mu_{h2}} \\
0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -c_4 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & -\frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & -\mu_{v2} & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & \frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & 0 & -\mu_{v2}
\end{array}\right).$$

The matrix $J(Z_1)$ is diagonal bloc matrix. Its eigenvalues are also eigenvalues of the bloc diagonal matrices. The eigenvalue of the second bloc matrix

$$A_2 = \begin{pmatrix} -\mu_{h2} & 0 & \sigma_2 & 0 & -\frac{\beta_{v2h2}\pi_{h2}}{\mu_{h2}} \\ 0 & -c_0 & 0 & 0 & \frac{\beta_{v2h2}\pi_{h2}}{\mu_{h2}} \\ 0 & \alpha_2 & -c_4 & 0 & 0 \\ 0 & -\frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & -\mu_{v2} & 0 \\ 0 & \frac{\beta_{h2v2}\pi_{v2}}{\mu_{v2}} & 0 & 0 & -\mu_{v2} \end{pmatrix}$$

are

$$\lambda^{(1)} = -\mu_{h2} < 0, \quad \lambda^{(2)} = -c_4 < 0, \quad \lambda^{(3)} = -\frac{1}{2}\left[c_0 + \mu_{v2} + \sqrt{(c_0 - \mu_{v2})^2 + \frac{4\beta_{h2v2}^2\pi_{v2}^2}{\mu_{v2}^2}}\right]$$

$$\lambda^{(4)} = -\frac{1}{2}\left[c_0 + \mu_{v2} - \sqrt{(c_0 - \mu_{v2})^2 + \frac{4\beta_{h2v2}^2\pi_{v2}^2}{\mu_{v2}^2}}\right], \quad \lambda^{(5)} = -\mu_{v2} < 0.$$

with

$$\begin{aligned} \lambda^{(3)} + \lambda^{(4)} &= -(c_0 + \mu_{v2}) < 0, \\ \lambda^{(3)}\lambda^{(4)} &= c_0\mu_{v2} - \frac{\beta_{h2v2}^2\pi_{v2}\pi_{h2}}{\mu_{v2}\mu_{h2}} \\ &= c_0\mu_{v2}(1 - R_2^2) \quad (\text{since } \lambda_1 = \lambda_2 = 0 \text{ and } R_2 = \frac{\beta_{h2v2}\pi_{v2}\pi_{h2}}{\mu_{v2}^2\mu_{h2}}) \\ &= c_0\mu_{v2}(1 + R_2)(1 - R_2). \end{aligned}$$

If $R_2 > 1$, then $\lambda^{(3)}$ and $\lambda^{(4)}$ have opposite signs and the equilibrium point Z_1 is unstable. We assume now that $R_2 < 1$. Then $\lambda^{(3)} < 0$ and $\lambda^{(4)} < 0$. The eigenvalue of the first bloc matrix

$$A_1 = \begin{pmatrix} -\beta_{v1h1}I_{v1}^* - \mu_{h1} & 0 & 0 & 0 & -\beta_{v1h1}S_{h1}^* \\ \beta_{v1h1}I_{v1}^* & -c_2 & 0 & 0 & \beta_{v1h1}S_{h1}^* \\ 0 & \alpha_1 & -c_3 & & \\ 0 & -\beta_{v1h1}S_{v1}^* & 0 & \beta_{v1h1}I_{h1}^* - \mu_{v1} & \\ 0 & \beta_{v1h1}S_{v1}^* & 0 & \beta_{v1h1}I_{h1}^* & -\mu_{v1} \end{pmatrix}$$

cannot be obtained explicitly. The Routh Hurwitz criteria for stability shall be used to investigated the sign of the eigenvalues of the matrix A_1. The characteristic polynomial associated to A_1 is given by

$$p(x) = -(x + c_3)(a_4x^4 + a_3x^3 + a_2x^2 + a_1x + a_0),$$

where

$$a_4 = 1, a_3 = \mu_{v1} + d_1 + c_2 + \beta_{h1v1} I^*_{v1} + \mu_{h1},$$

$$a_1 = \left(\beta_{h1v1} I^*_{h1} - \mu_{v1}\right)\left(c_2\mu_{v1} + \beta_{h1v1} I^*_{v1}(c_2 + \mu_{v1})\right) + \beta_{h1v1} I^*_{v1} c_2 \mu_{v1} - \beta^2_{h1v1} S^*_{h1} S^*_{v1}(\mu_{v1} + \mu_{h1})$$

$$\begin{aligned} a_2 = \mu_{v1}\left(\beta_{h1v1} I^*_{h1} + \beta_{h1v1} I^*_{v1} + \mu_{v1} + \mu_{h1} + c_2\right) + \left(\beta_{h1v1} I^*_{h1}\right. \\ \left. + \mu_{v1}\left(c_2 + \beta_{h1v1} I^*_{v1} + \mu_{h1}\right) + \beta_{h1v1} I^*_{v1} c_2 + \mu_{h1} - \beta^2_{h1v1} S^*_{h1} S^*_{v1}, \end{aligned}$$

$$a_0 = c_2\mu_{v1}\left(\beta_{h1v1} I^*_{v1} + \mu_{h1}\right)\left(\beta_{h1v1} I^*_{h1} + \mu_{v1}\right) - \beta^2_{h1v1} S^*_{h1} S^*_{v1} \mu_{h1}\mu_{v1}.$$

It can be verified that $a_1 > 0$, $a_2 > 0$, $a_0 > 0$, $a_1 a_2 > a_0 a_3$ and $(a_1 a_2 - a_0 a_3)_3 > a_1^2 a_4$ provided $R_1 > 1$. Moreover, if $R_1 < 1$, then $a_0 < 0$. By the Routh Hurwitz criteria for stability, the endemic equilibrium $Z_1$is asymptotically stable if $R_1 > 1$ and $R_2 < 1$, and unstable if $R_1 < 1$ or $R_2 > 1$. □

The above theorem indicates the possibility of the disease to persist within the first community provided that each single infected infects more than one susceptible (i.e., $R_1 > 1$) of the community during his infectiousness period, and to be overcome over time in the second community provided that each single infected infects less than one (in average) susceptible (i.e., $R_2 < 1$) of the community during his infectiousness period and there is no migration (i.e., $\lambda_1 = \lambda_2 = 0$).

Theorem 3.4.5. *Zika free endemic equilibrium Z_2 is locally asymptotically stable if $R_1 < 1$ and $R_2 > 1$, and unstable if $R_1 > 1$ or $R_2 < 1$.*

Proof. The Jacobian matrix evaluated at Z_2 is given by

$$J(Z_2) = \left(\begin{array}{ccccc|ccccc} -\mu_{h1} & 0 & \sigma_1 & 0 & -\frac{\beta_{v1h1}\pi_{h1}}{\mu_{h1}} & 0 & 0 & 0 & 0 & 0 \\ 0 & -c_2 & 0 & 0 & \frac{\beta_{v1h1}\pi_{h1}}{\mu_{h1}} & 0 & 0 & 0 & 0 & 0 \\ 0 & \alpha_1 & -c_3 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & -\frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & -\mu_{v1} & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & 0 & -\mu_{v1} & 0 & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 0 & -\beta_{v2h2}I_{v2} - \mu_{h2} & 0 & 0 & 0 & -\beta_{v2h2}S_{h2} \\ 0 & 0 & 0 & 0 & 0 & \beta_{v2h2}I_{v2} & -c_0 & 0 & 0 & \beta_{v2h2}S_{h2} \\ 0 & 0 & 0 & 0 & 0 & 0 & \alpha_2 & -c_4 & 0 & 0 \\ \hline 0 & 0 & 0 & 0 & 0 & 0 & -\beta_{h2v2}S_{v2} & 0 & -\beta_{h2v2}I_{h2} - \mu_{v2} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \beta_{h2v2}S_{v2} & 0 & \beta_{h2v2}I_{h2} & -\mu_{v2} \end{array}\right). \quad (3.4.8)$$

The matrix $J(Z_2)$ is a diagonal bloc. Its eigenvalues are eigenvalues of the bloc diagonal matrices. The eigenvalue of the first bloc matrix

$$B_1 = \begin{pmatrix} -\mu_{h1} & 0 & \sigma_1 & 0 & -\frac{\beta_{v1h1}\pi_{h1}}{\mu_{h1}} \\ 0 & -c_2 & 0 & 0 & \frac{\beta_{v1h1}\pi_{h1}}{\mu_{h1}} \\ 0 & \alpha_1 & -c_3 & 0 & 0 \\ 0 & -\frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & -\mu_{v1} & 0 \\ 0 & \frac{\beta_{h1v1}\pi_{v1}}{\mu_{v1}} & 0 & 0 & -\mu_{v1} \end{pmatrix}$$

are

$$\lambda^{(1)} = -\mu_{h1} < 0, \quad \lambda^{(2)} = -c_3 < 0, \quad \lambda^{(3)} = -\frac{1}{2}\left[c_2 + \mu_{v1} + \sqrt{(c_2 - \mu_{v1})^2 + \frac{4\beta_{h1v1}^2\pi_{v1}\pi_{h1}}{\mu_{v1}\mu_{h1}}}\right],$$

$$\lambda^{(4)} = -\frac{1}{2}\left[c_2 + \mu_{v1} - \sqrt{(c_2 - \mu_{v1})^2 + \frac{4\beta_{h1v1}^2\pi_{v1}\pi_{h1}}{\mu_{v1}\mu_{h1}}}\right], \lambda^{(5)} = -\mu_{v1} < 0.$$

with

$$\begin{aligned} \lambda^{(3)} + \lambda^{(4)} &= -(c_2 + \mu_{v1}) < 0, \lambda^{(3)}\lambda^{(4)} = c_1\mu_{v1} - \frac{\beta_{h1v1}^2\pi_{v1}\pi_{h1}}{\mu_{v1}\mu_{h1}} \\ &= c_1\mu_{v1}(1 - R_1^2) \quad (\text{since } \lambda_1 = \lambda_2 = 0 \text{ and } R_1 = \frac{\beta_{h1v1}\pi_{v1}\pi_{h1}}{\mu_{v1}^2\mu_{h1}}) \\ &= c_2\mu_{v1}(1 + R_1)(1 - R_1). \end{aligned}$$

If $R_1 > 1$, then $\lambda^{(3)}$ and $\lambda^{(4)}$ have opposite signs and the equilibrium point Z_2 is unstable. We assume now that $R_1 < 1$. Then $\lambda^{(3)} < 0$ and $\lambda^{(4)} < 0$. In the same manner (as in Theorem 3.4.4), it can be shown using the Routh Hurwitz criteria that all the eigenvalues of the first bloc matrix $J(Z_2)$ have negative real parts if $R_2 > 1$, and there is at least one positive real part eigenvalue of $J(Z_2)$ if $R_2 < 1$. □

Likewise banning migration (i.e., $\lambda_1 = \lambda_2 = 0$) between the two communities, the above theorem indicates the possibility of the disease to persist within the second community provided that each single infected infects more than one susceptible (i.e., $R_2 > 1$) of the community during his infectiousness period, and to be overcome over time in the first community provided that each single infected infects less than one (in average) susceptible (i.e., $R_1 < 1$) of the community during his infectiousness period.

3.5 Sensitivity Analysis

For the purpose of knowing the parametric data with higher influence on the metapopulation mathematical models, we conducted sensitivity analysis to determine the parameter values and model robustness. In a bid to help us determine the parameters that have a high impact on Ebola transmission dynamics in the EVD model and the Zika transmission dynamics in the ZVD model and their respective reproduction number (R_i). In carrying out the sensitivity analysis of the Ebola and Zika Metapopulation model, we employ normalised forward sensitivity index of a variable to a parameter as described in Chitins et al [Chitnis et al., 2006]. Defined as the ratio of some relative change in the variable to the relative change in the parametric values of the system. While the sensitivity index is defined using partial derivatives when the variable is a differentiable function of the parameter.

Definition 3.5.1. *The normalized forward-sensitivity index, of a variable R, to a parameter M, denoted by* $\Psi_M^{R_0}$ *,which is defined as a ratio of the relative change in the variable to the relative change in the parameter*

3.5.1 Sensitivity Analysis of Ebola

In order to determine the parameters or factors most essential in the transmission dynamics and spread of the disease, we perform a sensitivity analysis of the formulated model (3.2.1) in the sense of Chitnis et al [Chitnis et al., 2006] (2008). The sensitivity indices of the basic reproduction numberR_0,for first and second patch to the parameters of the Ebola model analysis (3.2.1) are computed as follows:

$$
\begin{cases}
\Psi_{\alpha_1}^{R_0} = \frac{\alpha_1}{R_0} \times \frac{\partial R_0}{\partial \alpha_1} = -0.00069 \\
\Psi_{\alpha_2}^{R_0} = \frac{\alpha_2}{R_0} \times \frac{\partial R_0}{\partial \alpha_2} = -0.00098 \\
\Psi_{\omega_1}^{R_0} = \frac{\omega_1}{R_0} \times \frac{\partial R}{\partial \omega_1} = -0.499 \\
\Psi_{\omega_2}^{R_0} = \frac{\omega_2}{R_0} \times \frac{\partial R_0}{\partial \omega_2} = -0.794 \\
\Psi_{\mu_1}^{R_0} = \frac{\mu_1}{R_0} \times \frac{\partial R_0}{\partial \mu_1} = -0.50 \\
\Psi_{\mu_2}^{R_0} = \frac{\mu_2}{R_0} \times \frac{\partial R_0}{\partial \mu_2} = -0.50 \\
\Psi_{\kappa_1}^{R_0} = \frac{\kappa_1}{R_0} \times \frac{\partial R_0}{\partial \kappa_1} = 0.371e-5 \\
\Psi_{\kappa_2}^{R_0} = \frac{\kappa_2}{R_0} \times \frac{\partial R_0}{\partial \kappa_2} = 0.371e-5 \\
\Psi_{\tau_1}^{R_0} = \frac{\tau_1}{R_0} \times \frac{\partial R_0}{\partial \tau_1} = -0.00998 \\
\Psi_{\tau_2}^{R_0} \frac{\tau_2}{R_0} \times \frac{\partial R_0}{\partial \tau_2} = -0.00967 \\
\Psi_{\beta_1}^{R_0} = \frac{\beta_1}{R_0} \times \frac{\partial R_0}{\partial \beta_1} = \left(\frac{(\omega_2 A_2 + A_1(\mu_2\omega_2))(\kappa_2+\mu_2)(\tau_2+\alpha_2+\mu_2)\kappa_1}{\mu_1\mu_2+\mu_1\omega_2+\mu_2\omega_1} \right) \\
\Psi_{\beta_2}^{R_0} = \frac{\beta_2}{R_0} \times \frac{\partial R_0}{\partial \beta_2} = 1.56 \\
\Psi_{a}^{R_0} = \frac{a}{R_0} \times \frac{\partial R_0}{\partial a} = 0.435 \\
\Psi_{A_1}^{R_0} = \frac{A_1}{R_0} \times \frac{\partial R_0}{\partial A_1} = 0.0001276 \\
\Psi_{A_2}^{R_0} = \frac{A_2}{R_0} \times \frac{\partial R_0}{\partial A_2} = 0.000122
\end{cases}
\tag{3.5.1}
$$

In a similar manner, we can obtain the sensitivity indices of the basic reproduction number, R_0, to parameters of the Zika model.

3.5.2 Sensitivity Analysis of Zika

In order to determine the parameters or factors most essential in the transmission dynamics and spread of the disease, we perform a sensitivity analysis of the formulated model (3.5.1) in the sense of Chitnis et al [Chitnis et al., 2006] Consequently, the sensitivity indices of the basic reproduction number R_0, to the parameters of the Zika model analysis (3.5.1) are computed as follows:

$$
\begin{cases}
\Psi_{\alpha_1}^{R_0} = \frac{\alpha_1}{R_0} \times \frac{\partial R_0}{\partial \alpha_1} = -\frac{R_0}{2(\mu_{h1}+d_1+\alpha_1)} = -0.24 \\
\Psi_{\alpha_2}^{R_0} = \frac{\alpha_2}{R_0} \times \frac{\partial R}{\partial \alpha_2} = -\frac{R_1}{2(\mu_{h1}+d_2+\alpha_2)} = -0.2477 \\
\Psi_{\pi_{h1}}^{R_0} = \frac{\pi_{h1}}{R_0} \times \frac{\partial R_0}{\partial \pi_{h1}} = 0.27 \\
\Psi_{\pi_{h2}}^{R_0} = \frac{\pi_{h2}}{R_0} \times \frac{\partial R_0}{\partial \pi_{h2}} = 0.25 \\
\Psi_{\mu_{h1}}^{R_0} = \frac{\mu_{h1}}{R_0} \times \frac{\partial R_0}{\partial \mu_{h1}} = -\frac{1}{2} \\
\Psi_{\mu_{h2}}^{R_0} = \frac{\mu_{h2}}{R_0} \times \frac{\partial R_0}{\partial \mu_{h2}} = -\frac{1}{2} \\
\Psi_{\lambda_1}^{R_0} = \frac{\lambda_1}{R_0} \times \frac{\partial R_0}{\partial \lambda_1} = 0.004 \\
\Psi_{\lambda_2}^{R_0} = \frac{\lambda_2}{R} \times \frac{\partial R}{\partial \lambda_2} = 0.0047 \\
\Psi_{\sigma_1}^{R_0} = \frac{\sigma_1}{R_0} \times \frac{\partial R_0}{\partial \sigma_1} = 0 \\
\Psi_{\sigma_2}^{R_0} = \frac{\sigma_2}{R_0} \times \frac{\partial R_0}{\partial \sigma_2} = 0 \\
\Psi_{\mu_{v1}}^{R_0} = \frac{\mu_{v1}}{R_0} \times \frac{\partial R_0}{\partial \mu_{v1}} = -0.25 \\
\Psi_{\mu_{v2}}^{R_0} = \frac{\mu_{v2}}{R_0} \times \frac{\partial R_0}{\partial \mu_{v2}} = -0.35 \\
\Psi_{\beta_{v_1h_1}}^{R_0} = \frac{\beta_{v_1h_1}}{R_0} \times \frac{\partial R_0}{\partial \beta_{v_1h_1}} = 0.27 \\
\Psi_{\beta_{v_2h_2}}^{R_0} = \frac{\beta_{v_2h_2}}{R_0} \times \frac{\partial R_0}{\partial \beta_{v_2h_2}} = 0.27 \\
\Psi_{\beta_{h_1v_1}}^{R_0} = \frac{\beta_{h_1v_1}}{R_0} \times \frac{\partial R_0}{\partial \beta_{h_1v_1}} = 0.25 \\
\Psi_{\beta_{h_2v_2}}^{R_0} = \frac{\beta_{h_2v_2}}{R_0} \times \frac{\partial R_0}{\partial \beta_{h_2v_2}} = 0.25 \\
\Psi_{\pi_{v1}}^{R_0} = \frac{\pi_{v1}}{R_0} \times \frac{\partial R_0}{\partial \pi_{v1}} = 0.27 \\
\Psi_{\pi_{v2}}^{R_0} = \frac{\pi_{v2}}{R_0} \times \frac{\partial R_0}{\partial \pi_{v2}} = 0.25
\end{cases}
\tag{3.5.2}
$$

It is established (from the above theorems) that the basis reproduction number plays an important role to understand the asymptotic disease dynamics within the population. The progression of the disease reduces as the basic reproduction number decreases. Since $\frac{\partial R_1}{\partial \beta_{h1v1}} = \frac{R_1}{\beta_{h1v1}} > 0$ and $\frac{\partial R_2}{\partial \beta_{h2v2}} = \frac{R_2}{\beta_{h2v2}} > 0$, R_1 (resp. R_2) decreases as β_{h1v1} (resp. β_{h2v2}) decreases. Likewise,since $\frac{\partial R_1}{\partial \alpha_1} = -\frac{R_1}{2(\mu_{h1}+d_1+\alpha_1)} < 0$ and $\frac{\partial R_2}{\partial \alpha_1} = -\frac{R_2}{2(\mu_{h2}+d_2+\alpha_2)} < 0$, to reduce R_1 (resp. R_2) one can increase the recovery rate α_1 (resp. α_2). To apply these strategies, We consider their implementation cost. We will investigate the optimal value of parameters which ensures low infection and low

cost.

Chapter 4

Optimal Control Analysis and Its Application

4.1 Introduction

Optimal control theory is a mathematical strategic tool used in decision making which includes an appropriate use of several strategies while trying to reduce the occurrence of diseases in cost-effective ways. Optimal control theory have previously being applied to diverse epidemiological problems [Wang and Zhao, 2004,Oke et al., 2018,Lenhart and Workman, 2007]. [Lenhart and Workman, 2007] explored techniques for improving multi-dose drug schedules, treatment times and drug toxicities in cancer chemotherapy. Also, [Bonyah et al., 2016] used the optimal control theory strategy to investigate several optimal control strategies of of the spread of Ebola. With options of controlling infection by vaccination of susceptible, education of individuals on healthy living and minimizing exposed and infected. [Momoh and Fügenschuh, 2018] examined the possibility of implementing a combined control strategies in order to determine the most cost-effective one. We however employ quadratic objective function in measuring the control cost for Ebola Virus Disease treatment and Zika Virus Disease treatment. As much as the possibility of individuals staying in their respective communities as a control strategy in reducing the transmission of any of both disease in both patches. With great adherence to healthy Education and Governmental

health policies.

4.2 Formulation of optimal control model for Ebola and Zika Virus Model

In the previous section, control options have been considered as constants. without much consideration on cost associated with the implementation of the control Strategy. Hence, we formulate a corresponding optimal control problem for the model in system (3.2.1) and (3.5.1) using strict adherence to no movement with both patch, education, wearing long covering as protective gear for the Zika model and a healthy living and abstinence from infected individual for the Ebola model to reduce prevalence and economic burdens. Similar technique have been used successfully to determine the relevant control strategies with optimal cost in communities not linked together as the case of a metapopulation [Kassa and Hove-Musekwa, 2014,Kumar and Srivastava, 2017]. We use a quadratic term for the rate of application of a our control with the goal of minimizing the number of movement in and out of both patches for both Ebola and Zika model.

4.2.1 Optimal Control for Ebola Disease Model

The introducing of control strategies on the rate of isolating the infected humans, maintenance of proper hygiene, with effect of safety precaution and adherence to adequate campaigns from World Health Organization (WHO), African Centre for Disease Control (ACDC) as well as other health organizations in Africa and across the globe regarding Ebola virus infection. The control functions being employed, monitoring the effect of immigration reduction or movement from one patch to another as an effect of educational campaigns and adherence to such campaign. Because in case of Ebola and its spread, It is of great importance has to emphasize on educational campaign because it is a fact that Ebola virus spreads through human-to-human transmission, which is not by close and direct contact of which ever kind of an infected bodily fluids also via exposure to objects and contaminated environment. Which makes controlled treatment, proper isolation and safe burial of infected individual of great importance. Vaccination and Monitoring most infectious fluids are blood,

$$
\begin{cases}
\frac{dS_1}{dt} = A_1 - (1-u_1)\beta_1 S_1 I_1 - (\mu_1+\omega_1)S_1 + \omega_2 S_2 + aR_1 \\
\frac{dE_1}{dt} = (1-u_1)\beta_1 S_1 I_1 - (\delta u_3 + \kappa_1 + \mu_1)E_1 \\
\frac{dI_1}{dt} = (\delta u_3 + \kappa_1)E_1 - (1-u_4)(\alpha_1 + \mu_1 + \tau_1)I_1 \\
\frac{dR_1}{dt} = (1-u_4)(\alpha_1)I_1 - \mu_1 R_1 - aR_1 \\
\frac{dS_2}{dt} = A_2 - (1-u_2)\beta_2 S_2 I_2 - (\mu_2+\omega_2)S_2 + \omega_1 S_1 + aR_2 \\
\frac{dE_2}{dt} = (1-u_2)\beta_2 S_2 I_2 - (\delta u_3 + \kappa_2 + \mu_2)E_2 \\
\frac{dI_2}{dt} = (\delta u_3 + \kappa_2)E_2 - (1-u_4)(\alpha_2 + \mu_2 + \tau_2)I_2 \\
\frac{dR_2}{dt} = (1-u_4)(\alpha_2)I_2 - \mu_2 R_2 - aR_2
\end{cases}
\tag{4.2.1}
$$

where u_1 is the fraction of susceptible human who do not travel from one patch to patch two adhering to educational campaign at time t,u_2 is the fraction of susceptible human who do not travel from two patch to patch one adhering to educational campaign at time t, u_3 is the controlled treatment, isolation and safe burial of infected individuals as a means of controlling and preventing the spread at time t and u_4 is the effectiveness of vaccine as well as other treatment at time t. Hence, our goal is to minimize the number of infected individuals with Ebola virus while at the same time keeping the cost of treatment very low.

To determine optimal control for the system (4.2.1) investigating the optimal efforts by defining the objective functional

$$
J(u_1, u_2, u_3, u_4) = \int_0^T [B_1 E_1 + B_2 E_2 + B_3 I_1 + B_4 I_2
$$

$$+\frac{1}{2}\left(c_1u_1^2+c_2u_2^2+c_3u_3^2+c_4u_4^2\right)dt$$

with $S_1(0)\geqslant 0, E_1(0)\geqslant 0, I_1(0)\geqslant 0, R_1(0)\geqslant 0, S_2(0)\geqslant 0, E_2(0)\geqslant 0, I_2(0)\geqslant 0, R_2(0)\geqslant 0$. We assume cost of treatments is nonlinear and objective functional takes a quadratic nature. The coefficients B_1 and B_2 are balancing cost factors due to the size and importance of objective functional. Hence, we seek to find an optimal control, u_1^*, u_2^*, u_3^* and u_4^* such that

$$\mathrm{J}(\mathrm{u}_1^*,u_2^*,u_3^*,\mathrm{u}_4^*)=\min J(u_1,u_2,u_3),(u_1,u_2,u_3,\mathrm{u}_4)\in\Omega \quad (4.2.2)$$

subject to system (2.1), where Ω is a Lebesgue measurable function defined from $[0,T]$ to $[0,1]$. Applying Pontryagin's Maximum Principle[ref]to solve optimal control problem satisfying necessary conditions corresponding to the given state variables.

The Hamiltonian H from the objective functional (3.18) which is subject to system (2.1) is

$$\begin{aligned}H=B_1E_1+B_2E_2+B_3I_1+B_4I_2+\frac{1}{2}\left(c_1u_1^2+c_2u_2^2+c_3u_3^2+c_4u_4^2\right)\\+\lambda_{S_1}\frac{dS_1}{dt}+\lambda_{E_1}\frac{dE_1}{dt}+\lambda_{I_1}\frac{dI_1}{dt}+\lambda_{R_1}\frac{dR_1}{dt}+\lambda_{S_2}\frac{dS_2}{dt}+\lambda_{E_2}\frac{dS_2}{dt}+\lambda_{I_2}\frac{dI_2}{dt}+\lambda_{R_2}\frac{dR_2}{dt}\end{aligned} \quad (4.2.3)$$

where $\lambda_{S_1},\lambda_{E_1},\lambda_{I_1},\lambda_{R_1},\lambda_{S_2},\lambda_{E_2},\lambda_{I_2},\lambda_{R_2}$ are adjoint variables which satisfy the adjoint system

$$\begin{aligned}H=B_1E_1+B_2E_2+B_3I_1+B_4I_2+\frac{1}{2}\left(c_1u_1^2+c_2u_2^2+c_3u_3^2+c_4u_4^2\right)\\+\lambda_{S_1}\left[A_1-(1-u_1)\beta_1S_1I_1-(\mu_1+\omega_1)S_1+\omega_2S_2+aR_1\right]\\+\lambda_{E_1}[(1-u_1)\beta_1S_1I_1-(\delta u_3+\kappa_1+\mu_1)E_1]\\+\lambda_{I_1}[(\delta u_3+\kappa_1)E_1-(1-u_4)(\alpha_1+\mu_1+\tau_1)I_1]\\+\lambda_{R_1}[(1-u_4)(\alpha_1)I_1-\mu_1R_1-aR_1]\\+\lambda_{S_2}[A_2-(1-u_2)\beta_2S_2I_2-(\mu_2+\omega_2)S_2+\omega_1S_1+aR_2]\\+\lambda_{E_2}[(1-u_2)\beta_2S_2I_2-(\delta u_3+\kappa_2+\mu_2)E_2]\\+\lambda_{I_2}[(\delta u_3+\kappa_2)E_2-(1-u_4)(\alpha_2+\mu_2+\tau_2)I_2]\\+\lambda_{R_2}[(1-u_4)(\alpha_2)I_2-\mu_2R_2-aR_2]\end{aligned} \quad (4.2.4)$$

We then have to determine the Adjoint Variables by partially differentiating the Hamiltonian with respect to each of the state variables as given above

Theorem 14. *To establish an optimal control set u_1, u_2, u_3 and u_4 that minimizes J over U , there are adjoint variables, $\lambda_{S_1}, \lambda_{E_1}, \lambda_{I_1}, \lambda_{R_1}, \lambda_{S_2}, \lambda_{E_2}, \lambda_{I_2}, \lambda_{R_2}$ satisfying*

$$\frac{d\lambda_i}{dt} = -\frac{\partial H}{\partial i}$$

and with transversality conditions $\lambda_i(t_f) = 0$, where,

$$i = S_1, E_1, I_1, R_1, S_2, E_2, I_2, R_2 \tag{4.2.5}$$

Furthermore,

$$u_1^* = max\left\{0, min\left(1, \frac{-(\lambda_{S1} + \lambda_{E1})\beta_1 S_1 I_1}{2c_1}\right)\right\} \tag{4.2.6}$$

$$u_2^* = max\left\{0, min\left(1, \frac{\beta_2 S_2 I_2(-\lambda_{S2} - \lambda_{E2})}{2c_2}\right)\right\} \tag{4.2.7}$$

$$u_3^* = max\left\{0, min\left(1, \frac{\delta E_1(\lambda_{E1} - \lambda_{I1}) + \delta E_2(\lambda_{E2} - \lambda_{I2})}{2c_3}\right)\right\} \tag{4.2.8}$$

$$u_4^* = max\left\{0, min\left(1, \frac{\lambda_{R1}\alpha_1 I_1 - \lambda_{I1}(\alpha_1 + \mu_1 + \tau_1)I_1 - \lambda_{I2}(\alpha_2 + \mu_2 + \tau_2)I_2 + \lambda_{R2}\alpha_2 I_2}{2c_4}\right)\right\} \tag{4.2.9}$$

Proof. Suppose $U^* = (u_1^*, u_2^*, u_3^*, u_4^*)$ is an optimal control and $S_1, E_1, I_1, R_1, S_2, E_2, I_2, R_2$ are the corresponding state solutions.Applying the Pontryagin's Maximum Principle [Pontryagin, 1987] there exist adjoint variables satisfying:

$$\frac{d\lambda_{S1}}{dt} = -\frac{\partial H}{\partial S_1}; \frac{d\lambda_{E1}}{dt} = -\frac{\partial H}{\partial E_1}; \frac{d\lambda_{I1}}{dt} = -\frac{\partial H}{\partial I_1}; \frac{d\lambda_{R1}}{dt} = -\frac{\partial H}{\partial R_1};$$
$$\frac{d\lambda_{S2}}{dt} = -\frac{\partial H}{\partial S_2}; \frac{d\lambda_{E2}}{dt} = -\frac{\partial H}{\partial E_2}; \frac{d\lambda_{I2}}{dt} = -\frac{\partial H}{\partial I_2}; \frac{d\lambda_{R2}}{dt} = -\frac{\partial H}{\partial R_2};$$

$$\frac{d\lambda_{S1}}{dt} = -\frac{\partial H}{\partial S_1} = -[\lambda_{S1}(-(1-u_1)\beta_1 I_1 - (\mu_1 + \omega_1))] \tag{4.2.10}$$
$$-\lambda_{S1}[-(1-u_1)\beta_1 I_1 - (\mu_1 + \omega_1)]$$

$$\frac{d\lambda_{E1}}{dt} = -\frac{\partial H}{\partial E_1} = -[B_1 - \lambda_{E1}(\delta u_3 + \kappa_1 + \mu_1)] \tag{4.2.11}$$
$$-B_1 + \lambda_{E1}(\delta u_3 + \kappa_1 + \mu_1)$$

$$\frac{d\lambda_{I1}}{dt} = -\frac{\partial H}{\partial I_1} = -[B_3 - \lambda_{I1}(1-u_4)(\alpha_1+\mu_1+\tau_1)] \tag{4.2.12}$$

$$-B_3 + \lambda_{I1}(1-u_4)(\alpha_1+\mu_1+\tau_1)$$

$$\frac{d\lambda_{R1}}{dt} = -\frac{\partial H}{\partial R_1} = -\lambda_{R1}(-\mu_1 - a) \tag{4.2.13}$$

$$\lambda_{R1}(\mu_1 + a)$$

$$\frac{d\lambda_{S2}}{dt} = -\frac{\partial H}{\partial S_2} = -[\lambda_{S2}(-(1-u_2)\beta_1 I_2 - (\mu_2+\omega_2))] \tag{4.2.14}$$

$$-\lambda_{S2}[-(1-u_2)\beta_2 I_2 - (\mu_2+\omega_2)]$$

$$\frac{d\lambda_{E2}}{dt} = -\frac{\partial H}{\partial E_2} = -[B_2 - \lambda_{E2}(\delta u_3 + \kappa_2 + \mu_2)] \tag{4.2.15}$$

$$-B_2 + \lambda_{E2}(\delta u_3 + \kappa_2 + \mu_2)$$

$$\frac{d\lambda_{I2}}{dt} = -\frac{\partial H}{\partial I_2} = -[B_4 - \lambda_{I2}(1-u_4)(\alpha_2+\mu_2+\tau_2)] \tag{4.2.16}$$

$$-B_4 + \lambda_{I2}(1-u_4)(\alpha_2+\mu_2+\tau_2)$$

$$\frac{d\lambda_{R2}}{dt} = -\frac{\partial H}{\partial R_2} = -\lambda_{R2}(-\mu_2 - a) \tag{4.2.17}$$

$$\lambda_{R2}(\mu_2 + a)$$

4.2.2 Characterization

$$\frac{\partial H}{\partial u_1} = 2u_1c_1 + \lambda_{S1}\beta_1 S_1 I_1$$

$$\frac{\partial H}{\partial u_1} = 0$$

$$2u_1c_1 = -\lambda_{S1}\beta_1 S_1 I_1 - \lambda_{E1}\beta_1 S_1 I_1$$

$$u_1^* = \frac{-(\lambda_{S1}+\lambda_{E1})\beta_1 S_1 I_1}{2c_1}$$

$$\frac{\partial H}{\partial u_2} = 2u_2c_2 + \lambda_{S2}\beta_2 S_2 I_2 + \lambda_{E2}\beta_2 S_2 I_2$$

$$\frac{\partial H}{\partial u_2} = 0$$

$$2u_2c_2 = -\lambda_{S2}\beta_2 S_2 I_2 - \lambda_{E2}\beta_2 S_2 I_2$$

$$u_2^* = \frac{\beta_2 S_2 I_2(-\lambda_{S2} - \lambda_{E2})}{2c_2}$$

$$\frac{\partial H}{\partial u_3} = 2u_3c_3 + \lambda_{E1}\delta E_1 + \lambda_{I1}\delta E_1 - \lambda_{E2}\delta E_2 + \lambda_{I2}\delta E_2$$

$$\frac{\partial H}{\partial u_3} = 0$$

$$2u_3c_3 = \lambda_{E1}\delta E_1 - \lambda_{I1}\delta E_1 + \lambda_{E2}\delta E_2 - \lambda_{I2}\delta E_2$$

$$u_3^* = \frac{\delta E_1(\lambda_{E1} - \lambda_{I1}) + \delta E_2(\lambda_{E2} - \lambda_{I2})}{2c_3}$$

$$\frac{\partial H}{\partial u_4} = 2u_4c_4 + \lambda_{I1}(\alpha_1 + \mu_1 + \tau_1)I_1 - \lambda_{R1}\alpha_1 I_1 + \lambda_{I2}(\alpha_2 + \mu_2 + \tau_2)I_2 - \lambda_{R2}\alpha_2 I_2$$

$$\frac{\partial H}{\partial u_1} = 0$$

$$2u_4c_4 = \lambda_{R1}\alpha_1 I_1 - \lambda_{I1}(\alpha_1 + \mu_1 + \tau_1)I_1 - \lambda_{I2}(\alpha_2 + \mu_2 + \tau_2)I_2 + \lambda_{R2}\alpha_2 I_2$$

$$u_4^* = \frac{\lambda_{R1}\alpha_1 I_1 - \lambda_{I1}(\alpha_1 + \mu_1 + \tau_1)I_1 - \lambda_{I2}(\alpha_2 + \mu_2 + \tau_2)I_2 + \lambda_{R2}\alpha_2 I_2}{2c_4}$$

$$U_i^* = \begin{cases} 0 & u_1 \leq 0 \\ 1 & u_1 \geq 1 \end{cases}$$

where i=1,2,3,4

$$\mathrm{U}_1^* = max\left\{1, \frac{\lambda_{R1}\alpha_1 I_1 - \lambda_{I1}(\alpha_1+\mu_1+\tau_1)I_1 - \lambda_{R2}\alpha_2 I_2}{2c_4}\right\} \quad \square$$

4.2.3 Ebola Control Strategy

The strategy employed for the effective control of EVD is to combine the effects of adherence to no movement restriction in both patches as well as the control treatment, which indeed aided the effect of the Virus in both patches considered. From Figure 4, which shows the reduction in the Susceptible human in both patches as a result of effective control to the movement within patches. The Strategy involving the use of no movement order within $u_1(t)$ which is the fraction of susceptible human who do not travel from one patch to patch two adhering

to educational campaign and $u_2(t)$ which is the fraction of susceptible human who do not travel from two patch to patch one. Where , $u_1(t) = 0$ while considering the second patch and $u_2(t) = 0$ while considering the control strategy for the fist patch which is seen in Figure(4.1-4.3) , we observe that the optimal strategy adopted resulted in a drastic reduction in the susceptible individuals. Similarly, Figure 4.3 shows that the infected population dropped with the control strategy from 100 to 70 in less than 10 days of the adherence of the strategy and further reduction in the first 100 days.

4.3 Optimal Control Zika

With constant and adequate campaigns from WHO and health organizations in South America, Europe and across the globe regarding Zika virus infection. We propose some control strategy considering the vector transmission which seems prevalent than sexual transmission protection and abstinence possibly which seems to have reduced due to adherence to the health advice of sexual. Five control parameters are introduced for constructing the control model. The control variable $u_1(t)$ is the personal preventive strategy and measures adopted to protect oneself from contracting ZVD such as insect repellent or mosquito net to reduce the contacts between human and wearing of long sleeve clothing which covers the body properly. While $u_2(t)$ is the use of insecticide spraying to kill mosquitoes. $u_3(t)$ is the rate of treatment of those infected with ZVD. $u_4(t)$ is the efforts deployed to reduce the movement of infected people from patch one to patch two. Through screening and testing. While $u_5(t)$ is the efforts deployed to reduce the movement of infected people from patch two to patch one. Through screening and testing. Five control parameters are introduced to construct the control model:

- $u_1(t)$ for the personal preventive strategy from contracting ZVD (such as insect repellent, or mosquito net and wearing of long sleeve clothing which covers the body properly)
- $u_2(t)$ to increase the death rate of mosquito (via insecticide spraying for instance), hence reduce contact between susceptible host and mosquito
- $u_3(t)$ for recovered/treated infected host
- $u_4(t)$ for the efforts deployed to reduce the movement of infected people from patch one to patch two (through

screening and testing)

- $u_5(t)$ for the efforts deployed to reduce the movement of infected people from patch two to patch one.

The model with control variables is given by

$$\begin{cases} \frac{dS_{h1}}{dt} = \pi_{h1} - \mu_{h1}S_{h1} - (1-u_1)\beta_{v1h1}S_{h1}I_{v1} - (1-u_4)\lambda_1 S_{h_1} + (1-u_5)\lambda_2 S_{h_2} + \sigma_1 R_{h1} \\ \frac{dI_{h1}}{dt} = (1-u_1)\beta_{v1h1}S_{h1}I_{v1} - (\mu_{h1} + d_1 + u_3)I_{h1} \\ \frac{dR_{h1}}{dt} = u_3 I_{h1} - (\mu_{h1} + \sigma_1)R_{h1} \\ \frac{dS_{v_1}}{dt} = \pi_{v_1} - (1-u_2)\beta_{h1v1}S_{v1}I_{h1} - (\mu_{v_1} + (u_1+u_2)\mu_{max1})S_{v1} \\ \frac{dI_{v_1}}{dt} = (1-u_2)\beta_{h1v1}S_{v1}I_{h1} - (\mu_{v_1} + (u_1+u_2)\mu_{max1})I_{v1} \\ \frac{dS_{h_2}}{dt} = \pi_{h2} - \mu_{h2}S_{h2} - (1-u_1)\beta_{v2h2}S_{h2}I_{v2} + (1-u_4)\lambda_1 S_{h_1} - (1-u_5)\lambda_2 S_{h_2} + \sigma_2 R_{h2} \\ \frac{dI_{h_2}}{dt} = (1-u_1)\beta_{v2h2}S_{h2}I_{v2} - (\mu_{h2} + d_2 + u_3)I_{h2} \\ \frac{dR_{h_2}}{dt} = u_3 I_{h2} - (\mu_{h2} + \sigma_2)R_{h2} \\ \frac{dS_{v_2}}{dt} = \pi_{v_2} - (1-u_2)\beta_{h2v2}S_{v2}I_{h2} - (\mu_{v_2} + (u_1+u_2)\mu_{max2})S_{v2} \\ \frac{dI_{v_2}}{dt} = (1-u_2)\beta_{h2v2}S_{v2}I_{h2} - (\mu_{v_2} + (u_1+u_2)\mu_{max2})I_{v2}, \end{cases} \tag{4.3.1}$$

with nonnegative initials conditions. Our aim is to investigate the optimal efforts needed to control the disease dynamics and minimize the cost of implementing the controls u_1, u_2, u_3, u_4 and u_5 over a finite time T. We choose controls with quadratic cost and consider the objective functional (similarly with some authors in the literature [Adams et al., 2004, De Souza et al., 2000, Lenhart and Yong, 1992, Kirschner et al., 1997])

$$J(u_1,u_2,u_3,u_4,u_5) = \int_0^T \left[A_1 I_{h1} + A_2 I_{h2} + A_3 I_{v1} + A_4 I_{v2} + \frac{1}{2}\left(w_1 u_1^2 + w_2 u_2^2 + w_3 u_3^2 + w_4 u_4^2 + w_5 u_5^2\right) \right] dt, \tag{4.3.2}$$

where the coefficients A_1, A_2, A_3 and A_4 are balancing cost factors due to the size and w_1, w_2, w_3, w_4 and w_5 are positive weights. We seek to find an optimal control $(u_1^*, u_2^*, u_3^*, u_4^*, u_5^*)$ such that

$$J(u_1^*, u_2^*, u_3^*, u_4^*, u_5^*) = \min_{\Omega} J(u_1,u_2,u_3,u_4,u_5) \tag{4.3.3}$$

subject to system (4.3.1)), where $\Omega = \{(u_1,u_2,u_3,u_4,u_5) | u_i : [0,T] \to [0,1] measurable, i = 1,\ldots,5\}$. To solve the

optimal control problem we apply the Pontryagin's Maximum Principle [Pontryagin et al., 1962] which reduces to minimizing the Hamiltonian pointwise with respect to the control variables. The Hamiltonian is given by

$$\begin{aligned} H &= A_1 I_{h1} + A_2 I_{h2} + A_3 I_{v1} + A_4 I_{v2} + \frac{1}{2}\left(w_1 u_1^2 + w_2 u_2^2 + w_3 u_3^2 + w_4 u_4^2 + w_5 u_5^2\right) \\ &+ \theta_1 \frac{dS_{h1}}{dt} + \theta_2 \frac{dI_{h1}}{dt} + \theta_3 \frac{dR_{h1}}{dt} + \theta_4 \frac{dS_{v1}}{dt} + \theta_5 \frac{dI_{v1}}{dt} \\ &+ \theta_6 \frac{dS_{h2}}{dt} + \theta_7 \frac{dI_{h2}}{dt} + \theta_8 \frac{dR_{h2}}{dt} + \theta_9 \frac{dS_{v2}}{dt} + \theta_{10} \frac{dI_{v2}}{dt}. \end{aligned} \tag{4.3.4}$$

that is,

$$\begin{aligned} H &= A_1 I_{h1} + A_2 I_{h2} + A_3 I_{v1} + A_4 I_{v2} + \frac{1}{2}\left(w_1 u_1^2 + w_2 u_2^2 + w_3 u_3^2 + w_4 u_4^2 + w_5 u_5^2\right) \\ &+ \theta_1 \left[\pi_{h1} - \mu_{h1} S_{h1} - (1-u_1)\beta_{v1h1} S_{h1} I_{v1}\right] + \theta_2[(1-u_1)\beta_{v1h1} S_{h1} I_{v1} - (\mu_{h1} + d_1 + u_3) I_{h1}] \\ &+ \theta_3[u_3 I_{h1} - (\mu_{h1} + \sigma_1) R_{h1}] + \theta_4[\pi_{v_1} - (1-u_2)\beta_{h1v1} S_{v1} I_{h1} - (\mu_{v_1} + (u_1+u_2)\mu_{max1}) S_1] \\ &+ \theta_5[(1-u_2)\beta_{h1v1} S_{v1} I_{h1} - (\mu_{v_1} + (u_1+u_2)\mu_{max1}) I_{v1}] \\ &+ \theta_6[\pi_{h2} - \mu_{h2} S_{h2} - (1-u_1)\beta_{v2h2} S_{h2} I_{v2} + (1-u_4)\lambda_1 S_{h_1} - (1-u_5)\lambda_2 S_{h_2} + \sigma_2 R_{h2}] \\ &+ \theta_7[(1-u_1)\beta_{v2h2} S_{h2} I_{v2} - (\mu_{h2} + d_2 + u_3) I_{h2}] + \theta_8[u_3 I_{h2} - (\mu_{h2} + \sigma_2) R_{h2}] \\ &+ \theta_9[\pi_{v_2} - (1-u_2)\beta_{h2v2} S_{v2} I_{h2} - (\mu_{v_2} + (u_1+u_2)\mu_{max2}) S_{v2}] \\ &+ \theta_{10}[(1-u_2)\beta_{h2v2} S_{v2} I_{h2} - (\mu_{v_2} + (u_1+u_2)\mu_{max2}) I_{v2}] \end{aligned} \tag{4.3.5}$$

where $\theta_1, \theta_2, \theta_3, \theta_4, \theta_5, \theta_6, \theta_7, \theta_8, \theta_9, \theta_{10}$ are adjoint variables which satisfy the adjoint system

Hence, we determine the adjoint variables by partially differentiating the Hamiltonian with respect to each of the state variables

Theorem 4.3.1. *For an optimal control set u_1, u_2, u_3, u_4 and u_5 that minimizes J over U , there are adjoint variables, $\theta_1, \theta_2, \theta_3, \theta_4, \theta_5, \theta_6, \theta_7, \theta_8, \theta_9, \theta_{10}$ satisfying*

$$\frac{d\theta_i}{dt} = -\frac{\partial H}{\partial i}$$

and with transversality conditions $\theta_i(t_f) = 0$, where,

$$i = S_{h1}, I_{h1}, R_{h1}, S_{v1}, I_{h1}, S_{h2}, I_{h2}, R_{h2}, S_{v2}, I_{v2} \tag{4.3.6}$$

Furthermore,

$$u_1^* = max\left\{0, min\left(1, \frac{\begin{array}{r}\theta_2\beta_{v1h1}S_{h1}I_{v1} + \theta_4\left(\mu_{max1}S_{v1} + \beta_{h1v1}S_{v1}I_{h1}\right) + \theta_5\left(\beta_{h1v1}S_{v1}I_{h1} + \mu_{max1}I_{v1}\right.\\ \left. - \theta_1\beta_{v1h1}S_{h1}I_{v1} - \theta_6\beta_{v2h2}S_{h2}I_{v2}\right.\\ \left. + \theta_7\beta_{v2h2}S_{h2}I_{v2} + \theta_9\mu_{max2}S_{v2} + \theta_{10}\mu_{max2}I_{v2}\right.\end{array}}{2w_1}\right)\right\} \tag{4.3.7}$$

$$u_2^* = max\left\{0, min\left(1, \frac{\begin{array}{r}\theta_4\mu_{max1}S_{v1} + \theta_5\mu_{max1}I_{v1}\\ + \theta_9(\mu_{max2}S_{v2} - \beta_{h2v2}S_{v2}I_{h2}) - \theta_{10}\mu_{max2}I_{v2}\end{array}}{2w_2}\right)\right\} \tag{4.3.8}$$

$$u_3^* = max\left\{0, min\left(1, \frac{\theta_2 I_{h1} - \theta_3 I_{h1} + \theta_7 I_{h2} - \theta_8 I_{h2}}{2w_3}\right)\right\} \tag{4.3.9}$$

$$u_4^* = max\left\{0, min\left(1, \frac{\theta_6\lambda_1 S_{h1} - \theta_1 S_{h2}}{2w_4}\right)\right\} \tag{4.3.10}$$

$$u_5^* = max\left\{0, min\left(1, \frac{\lambda_2 S_{h2}(\theta_1 - \theta_6)}{2w_5}\right)\right\} \tag{4.3.11}$$

Proof. Suppose $U^* = (u_1^*, u_2^*, u_3^*, u_4^*, u_5^*)$ is an optimal control and $S_{h1}, I_{h1}, R_{h1}, S_{v1}, I_{h1}, S_{h2}, I_{h2}, R_{h2}, S_{v2}, I_{v2}$ are the corresponding state solutions. Applying the Pontryagin's Maximum Principle [Pontryagin, 1987] there exist adjoint variables satisfying:

$$\begin{array}{r}\frac{d\theta_1}{dt} = -\frac{\partial H}{\partial S_{h1}}, \theta_{S_{h1}}(t_f) = 0, \frac{d\theta_2}{dt} = -\frac{\partial H}{\partial I_{h1}}, \theta_{I_{h1}}(t_f) = 0,\\ \frac{d\theta_3}{dt} = -\frac{\partial H}{\partial R_{h1}}, \theta_{R_{h1}}(t_f) = 0, \frac{d\theta_4}{dt} = -\frac{\partial H}{\partial S_{v1}}, \theta_{S_{v1}}(t_f) = 0,\\ \frac{d\theta_5}{dt} = -\frac{\partial H}{\partial I_{v1}}, \theta_{I_{v1}}(t_f) = 0, \frac{d\theta_6}{dt} = -\frac{\partial H}{\partial S_{h2}}, \theta_{S_{h2}}(t_f) = 0, \frac{d\theta_7}{dt} = -\frac{\partial H}{\partial I_{h2}}, \theta_{I_{h2}}(t_f) = 0,\\ \frac{d\theta_8}{dt} = -\frac{\partial H}{\partial R_{h2}}, \theta_{R_{h2}}(t_f) = 0, \frac{d\theta_9}{dt} = -\frac{\partial H}{\partial S_{v2}}, \theta_{S_{v2}}(t_f) = 0, \frac{d\theta_{10}}{dt} = -\frac{\partial H}{\partial I_{v2}}, \theta_{I_{v2}}(t_f) = 0,\end{array} \tag{4.3.12}$$

with transversality conditions given as;

$$S_{h1} = I_{h1} = R_{h1} = S_{v1} = I_{h1} = S_{h2} = I_{h2} = R_{h2} = S_{v2} = I_{v2} = 0$$

We can determine the behaviour of the control by differentiating the Hamiltonian, $\mathcal{H}$ with respect to the controls $(u_1, u_2, u_3, u_4, u_5)$ at a time t.On the interior of the control set, such that $0 < uj < 1$ for all $(j = 1, 2, 3, 4, 5)$, we obtain

$$\begin{aligned}
0 = \frac{\partial H}{\partial u_1} &= 2u_1 w_1 + \theta_1 \beta_{v1h1} S_{h1} I_{v1} - \theta_2 \beta_{v1h1} S_{h1} I_{v1} \\
&\quad - \theta_4 \mu_{max1} I_{v1} + \theta_6 \beta_{v2h2} S_{h2} I_{v2} - \theta_7 \beta_{v2h2} S_{h2} I_{v2} \\
&\quad - \theta_9 \mu_{max2} S_{v2} - \theta_{10} \mu_{max2} I_{v2}, \\
0 = \frac{\partial H}{\partial u_2} &= 2w_2 u_2 - \theta_4 \mu_{max1} S_{v1} \\
&\quad - \theta_5 \mu_{max1} I_{v1} + \theta_9 \mu_{max2} S_{v2} + \theta_9 \beta_{h2v2} S_{v2} I_{h2} - \theta_{10} \mu_{max2} I_{v2}, \\
0 = \frac{\partial H}{\partial u_3} &= 2w_3 u_3 - \theta_2 I_{h1} + \theta_3 I_{h1} - \theta_7 I_{h2} + \theta_8 I_{h2} \\
0 = \frac{\partial H}{\partial u_4} &= 2w_4 u_4 + \theta_1 \lambda_1 S_{h1} - \theta_6 \lambda_1 S_{h1} \\
0 = \frac{\partial H}{\partial u_5} &= 2w_5 u_5 - \theta_1 \lambda_2 S_{h2} + \theta_6 \lambda_2 S_{h2}
\end{aligned} \tag{4.3.13}$$

Therefore, we have that

$$\frac{d\theta_1}{dt} = -\frac{\partial H}{\partial S_{h1}}; \frac{d\theta_2}{dt} = -\frac{\partial H}{\partial I_{h1}}; \frac{d\theta_3}{dt} = -\frac{\partial H}{\partial R_{h1}}; \frac{d\theta_4}{dt} = -\frac{\partial H}{\partial S_{v1}}; \frac{d\theta_5}{dt} = -\frac{\partial H}{\partial I_{v1}};$$
$$\frac{d\theta_6}{dt} = -\frac{\partial H}{\partial S_{h2}}; \frac{d\theta_7}{dt} = -\frac{\partial H}{\partial I_{h2}}; \frac{d\theta_8}{dt} = -\frac{\partial H}{\partial R_{h2}}; \frac{d\theta_9}{dt} = -\frac{\partial H}{\partial S_{v2}}; \frac{d\theta_{10}}{dt} = -\frac{\partial H}{\partial I_{v2}}$$

$$\frac{d\theta_1}{dt} = -\frac{\partial H}{\partial S_{h1}} = -[\theta_1(-\mu_{h1} - (1-u_1)\beta_{v1h1} I_{v1} - (1-u_4)\lambda_1) + \theta_2((1-u_1)\beta_{v1h1} I_{v1}) + \theta_6((1-u_4)\lambda_1)] \tag{4.3.14}$$

$$-[(-\theta_1 \mu_{h1} - \theta_1(1-u_1)\beta_{v1h1} I_{v1} - \theta_1(1-u_4)\lambda_1) + \theta_2(1-u_1)\beta_{v1h1} I_{v1} + \theta_6(1-u_4)\lambda_1]$$

$$\theta_1' = -\frac{\partial H}{\partial S_{h1}} = -\theta_1(-\mu_{h1} - (1-u_1)\beta_{v1h1} I_{v1} - (1-u_4)\lambda_1) - \theta_2(1-u_1)\beta_{v1h1} I_{v1} - \theta_6(1-u_4)\lambda_1$$

$$\frac{d\theta_2}{dt} = -\frac{\partial H}{\partial I_{h1}} = -[A_1 - \theta_2(\mu_{h1} + d_1 + u_3) + \theta_3 u_3 - \theta_4(1-u_1)\beta_{h1v1} S_{v1} + \theta_5(1-u_1)\beta_{h1v1} S_{v1}] \tag{4.3.15}$$

$$\theta_2' = -\frac{\partial H}{\partial I_{h1}} = -A_1 + \theta_2(\mu_{h1} + d_1 + u_3) - \theta_3 u_3 + \theta_4(1-u_1)\beta_{h1v1} S_{v1} - \theta_5(1-u_1)\beta_{h1v1} S_{v1}$$

$$\frac{d\theta_3}{dt} = -\frac{\partial H}{\partial R_{h1}} = -[\theta_1\sigma_1 - \theta_3 c_3] \tag{4.3.16}$$

$$\theta_3^{'} = -\frac{\partial H}{\partial R_{h1}} = \theta_3 c_3 - \theta_1\sigma_1$$

$$\frac{d\theta_4}{dt} = -\frac{\partial H}{\partial S_{v1}} = -[-\theta_4(\mu_{v1} + (u_1+u_2)\mu_{max1}) - (1-u_1)\beta_{h1v1}I_{h1} + \theta_5(1-u_1)\beta_{h1v1}I_{h1}] \tag{4.3.17}$$

$$\theta_4^{'} = -\frac{\partial H}{\partial S_{v1}} = \theta_4(\mu_{v1} + (u_1+u_2)\mu_{max1}) + \theta_4(1-u_1)\beta_{h1v1}I_{h1} - \theta_5(1-u_1)\beta_{h1v1}I_{h1}$$

$$\frac{d\theta_5}{dt} = -\frac{\partial H}{\partial I_{v1}} = -[A_3 - \theta_1(1-u_1)\beta_{v1h1}S_{h1} + \theta_2(1-u_1)\beta_{v1h1}S_{h1} - \theta_5(\mu_{v1} + (u_1+u_2)\mu_{max1})] \tag{4.3.18}$$

$$\theta_5^{'} = -\frac{\partial H}{\partial I_{v1}} = -A_3 + \theta_1(1-u_1)\beta_{v1h1}S_{h1} - \theta_2(1-u_1)\beta_{v1h1}S_{h1} + \theta_5(\mu_{v1} + (u_1+u_2)\mu_{max1})$$

$$\frac{d\theta_6}{dt} = -\frac{\partial H}{\partial S_{h2}} = -[\theta_6(-\mu_{h2} - (1-u_1)\beta_{v2h2}I_{v2} - (1-u_5)\lambda_2) + \theta_7((1-u_1)\beta_{v2h2}I_{v2}) + \theta_1((1-u_5)\lambda_2)] \tag{4.3.19}$$

$$\theta_1^{'} = -\frac{\partial H}{\partial S_{h1}} = -\theta_1(1-u_5)\lambda_2 + \theta_6(\mu_{h2} + (1-u_1)\beta_{v2h2}I_{v2} + (1-u_5)\lambda_2) - \theta_7(1-u_1)\beta_{v2h2}I_{v2}$$

$$\frac{d\theta_7}{dt} = -\frac{\partial H}{\partial I_{h2}} = -[A_2 - \theta_7(\mu_{h2} + d_2 + u_3) + \theta_8 u_3 - \theta_9(1-u_2)\beta_{h2v2}S_{v2} + \theta_{10}(1-u_2)\beta_{h2v2}S_{v2}] \tag{4.3.20}$$

$$\theta_7^{'} = -\frac{\partial H}{\partial I_{h2}} = -A_2 + \theta_7(\mu_{h2} + d_2 + u_3) - \theta_8 u_3 + \theta_9(1-u_2)\beta_{h2v2}S_{v2} - \theta_{10}(1-u_2)\beta_{h2v2}S_{v2}$$

$$\frac{d\theta_8}{dt} = -\frac{\partial H}{\partial R_{h2}} = -[\theta_6\sigma_2 - \theta_8 c_4] \tag{4.3.21}$$

$$\theta_8^{'} = -\frac{\partial H}{\partial R_{h2}} = \theta_8 c_4 - \theta_6\sigma_2$$

$$\frac{d\theta_9}{dt} = -\frac{\partial H}{\partial S_{v2}} = -[-\theta_9(\mu_{v2} + (u_1+u_2)\mu_{max2}) - (1-u_2)\beta_{h2v2}I_{h2} + \theta_{10}(1-u_2)\beta_{h2v2}I_{h2}] \tag{4.3.22}$$

$$\theta_9^{'} = -\frac{\partial H}{\partial S_{v2}} = \theta_9(\mu_{v2} + (u_1+u_2)\mu_{max2}) + \theta_9(1-u_2)\beta_{h2v2}I_{h2} - \theta_{10}(1-u_2)\beta_{h2v2}I_{h2}$$

$$\frac{d\theta_{10}}{dt} = -\frac{\partial H}{\partial I_{v2}} = -[A_4 - \theta_1(1-u_1)\beta_{v2h2}S_{h2} + \theta_7(1-u_1)\beta_{v2h2}S_{h2} - \theta_{10}(\mu_{v2} + (u_1+u_2)\mu_{max2})] \tag{4.3.23}$$

$$\theta_{10}^{'} = -\frac{\partial H}{\partial I_{v2}} = -A_4 + \theta_6(1-u_1)\beta_{v2h2}S_{h2} - \theta_7(1-u_1)\beta_{v2h2}S_{h2} + \theta_{10}(\mu_{v2} + (u_1+u_2)\mu_{max2})$$

$$u_1^* = \frac{\begin{array}{r}\theta_2\beta_{v1h1}S_{h1}I_{v1} + \theta_4\left(\mu_{max1}S_{v1} + \beta_{h1v1}S_{v1}I_{h1}\right) + \theta_5\left(\beta_{h1v1}S_{v1}I_{h1} + \mu_{max1}I_{v1}\right.\\ \left. - \theta_1\beta_{v1h1}S_{h1}I_{v1} - \theta_6\beta_{v2h2}S_{h2}I_{v2}\right.\\ \left. + \theta_7\beta_{v2h2}S_{h2}I_{v2} + \theta_9\mu_{max2}S_{v2} + \theta_{10}\mu_{max2}I_{v2}\right.\end{array}}{2w_1}$$

$$u_2^* = \frac{\begin{array}{r}\theta_4\mu_{max1}S_{v1} + \theta_5\mu_{max1}I_{v1}\\ + \theta_9(\mu_{max2}S_{v2} - \beta_{h2v2}S_{v2}I_{h2}) - \theta_{10}\mu_{max2}I_{v2}\end{array}}{2w_2}$$

$$u_3^* = \frac{\theta_2 I_{h1} - \theta_3 I_{h1} + \theta_7 I_{h2} - \theta_8 I_{h2}}{2w_3} u_4^* = \frac{\theta_6\lambda_1 S_{h1} - \theta_1 S_{h2}}{2w_4}$$

$$u_5^* = \frac{\lambda_2 S_{h2}(\theta_1 - \theta_6)}{2w_5}$$

$$u_1^* = max\left\{0, min\left(1, \frac{\begin{array}{r}\theta_2\beta_{v1h1}S_{h1}I_{v1} + \theta_4\left(\mu_{max1}S_{v1} + \beta_{h1v1}S_{v1}I_{h1}\right) + \theta_5\left(\beta_{h1v1}S_{v1}I_{h1} + \mu_{max1}I_{v1}\right.\\ \left. - \theta_1\beta_{v1h1}S_{h1}I_{v1} - \theta_6\beta_{v2h2}S_{h2}I_{v2}\right.\\ \left. + \theta_7\beta_{v2h2}S_{h2}I_{v2} + \theta_9\mu_{max2}S_{v2} + \theta_{10}\mu_{max2}I_{v2}\right.\end{array}}{2w_1}\right)\right\} \tag{4.3.24}$$

$$u_2^* = max\left\{0, min\left(1, \frac{\begin{array}{r}\theta_4\mu_{max1}S_{v1} + \theta_5\mu_{max1}I_{v1}\\ + \theta_9(\mu_{max2}S_{v2} - \beta_{h2v2}S_{v2}I_{h2}) - \theta_{10}\mu_{max2}I_{v2}\end{array}}{2w_2}\right)\right\} \tag{4.3.25}$$

$$u_3^* = max\left\{0, min\left(1, \frac{\theta_2 I_{h1} - \theta_3 I_{h1} + \theta_7 I_{h2} - \theta_8 I_{h2}}{2w_3}\right)\right\} \tag{4.3.26}$$

$$u_4^* = max\left\{0, min\left(1, \frac{\theta_6\lambda_1 S_{h1} - \theta_1 S_{h2}}{2w_4}\right)\right\} \tag{4.3.27}$$

$$u_5^* = max\left\{0, min\left(1, \frac{\lambda_2 S_{h2}(\theta_1 - \theta_6)}{2w_5}\right)\right\} \tag{4.3.28}$$

$$U_i^* = \begin{cases} 0 & u_1 \leq 0 \\ u_i & 0 < u_1 < 1 \\ 1 & u_1 \geq 1 \end{cases}$$

where i=1,2,3,4,5

$\mathrm{U}_1^* = max\left\{1, \frac{\lambda_2 S_{h2}(\theta_1 - \theta_6)}{2w_5}\right\}$ □

4.3.1 Zika Control Strategy

$u_1(t)$ for the personal preventive strategy from contracting ZVD (such as insect repellent, or mosquito net and wearing of long sleeve clothing which covers the body properly)

$u_2(t)$ to increase the death rate of mosquito (via insecticide spraying for instance), hence reduce contact between susceptible host and mosquito

$u_3(t)$ for recovered/treated infected host

$u_4(t)$ for the efforts deployed to reduce the movement of infected people from patch one to patch two (through screening and testing)

$u_5(t)$ for the efforts deployed to reduce the movement of infected people from patch two to patch one. For our Zika Virus model, We employed effective control strategy for the ZVD with combined effects of adherence to the personal preventive strategy from contracting ZVD, to increase the death rate of mosquito and treatment of infected host. While restriction of movement to and fro each patch is another control strategy, which indeed aided the effect of the Virus in both patches considered. Figure (4.5 - 4.6), which shows the reduction in the Susceptible human population in both patches as a result of effective control to the movement within patches. while considering the control strategy for the first patch which is seen in Figure(4.5 - 4.6), we observe that the

optimal strategy adopted resulted in a drastic reduction in the susceptible individuals. Similarly, Figure 4.6(a) shows that the infected population dropped with the control strategy from 100 to 70 in less than 10 days of the adherence of the strategy and further reduction in the first 100 days as well as the very drastic reduction in the susceptible individuals in both patches as seen in Figure 4.5(a&b).

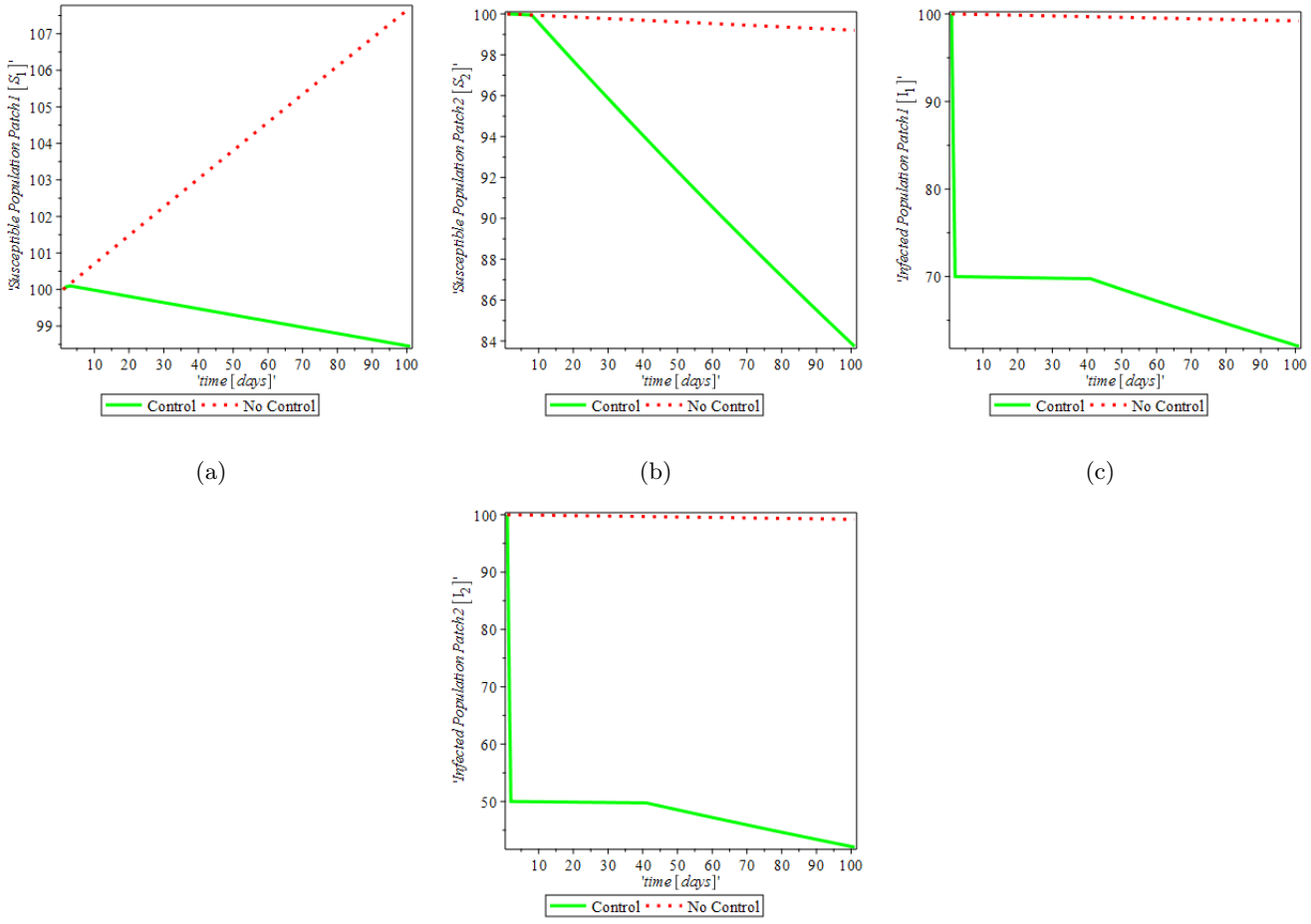
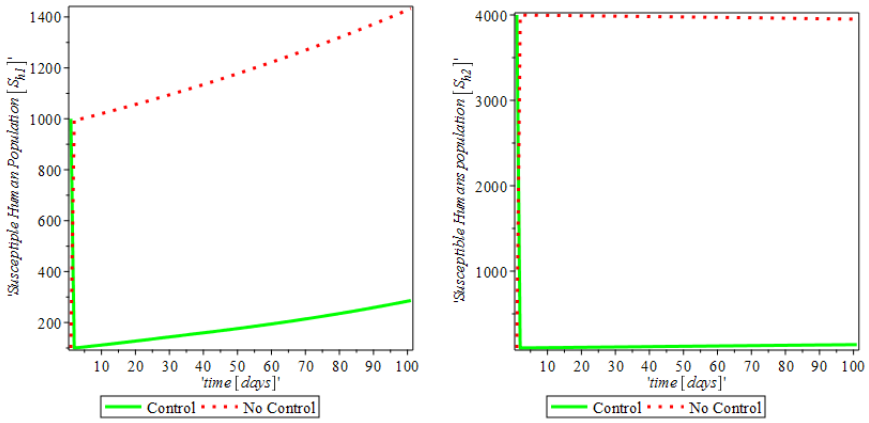


Figure 4.1: Diagram depicting the Control Strategy Case of the persistence of Ebola virus disease in the infected and recovered human population.



(a) Susceptible population S_{h1} (b) Susceptible population S_{h2}

Figure 4.2: Diagram depicting the Control Strategy Case of a Zika disease in Susceptible Class.

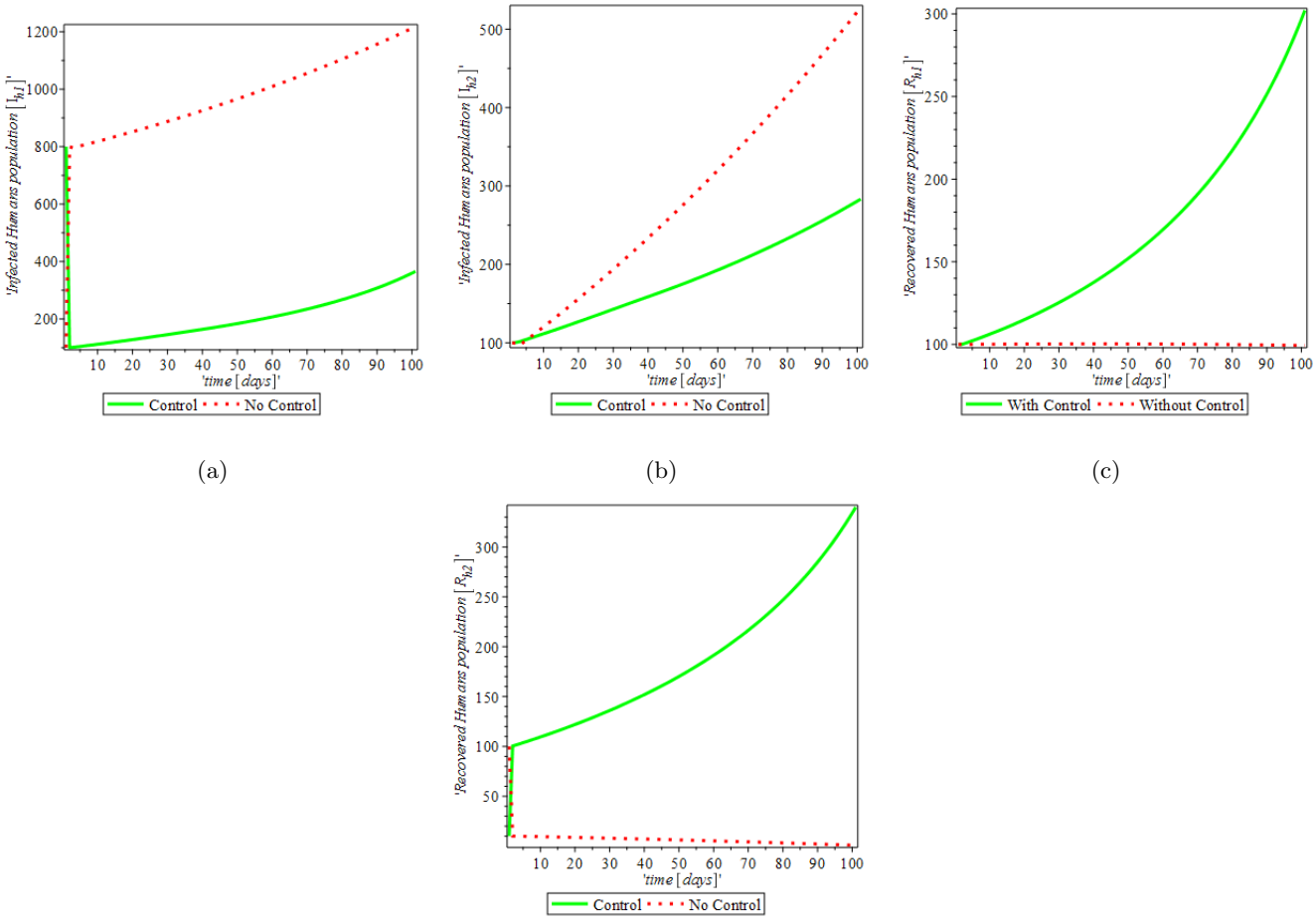


Figure 4.3: Diagram depicting the Control Strategy Case of the persistence of Zika virus disease in the infected and recovered human population .

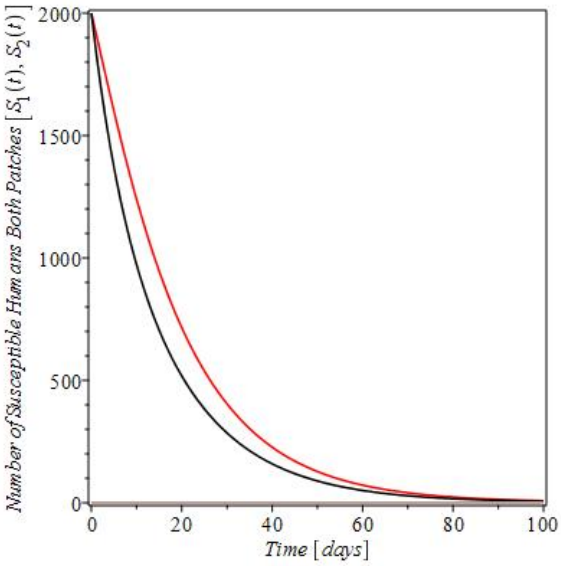
Chapter 5

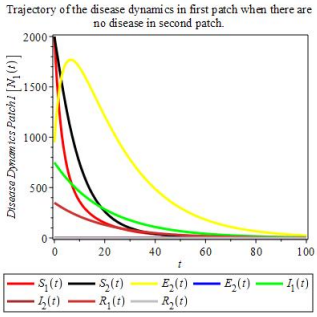
Simulations and Discussion of Results

In order to understand the overall picture of the EVD and ZVD behaviours respectively, this chapter provides numerical simulations of each of the formulated models using a Matlab software package and Maple software package. The results of the simulations are discussed with the aid of figures as well as the implications of the theoretical results obtained in Chapter 4.

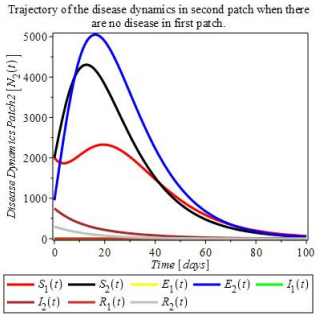
5.0.1 EVD Numerical Simulation and Discussions

The Numerical model parameters of the Ebola virus disease (EVD) which have been well and widely used in different existing literature's where used peculiar to each metapopulation,



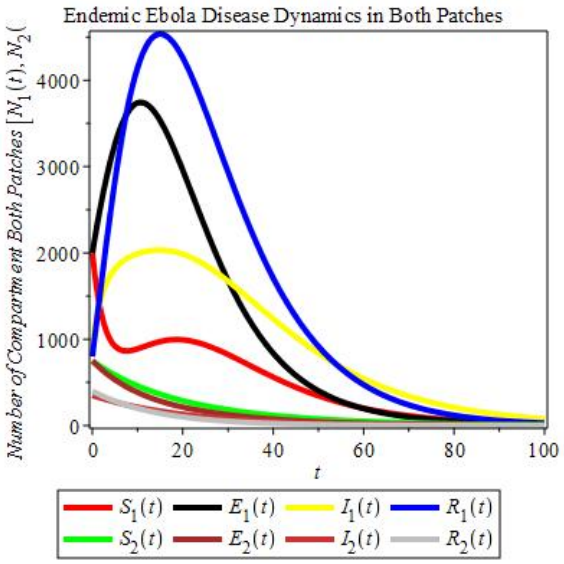


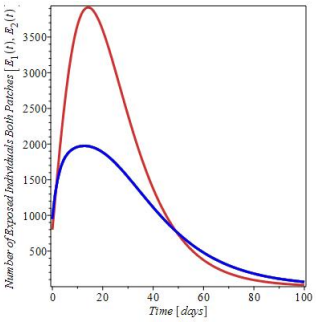
(a) Endemic Free population in patch1



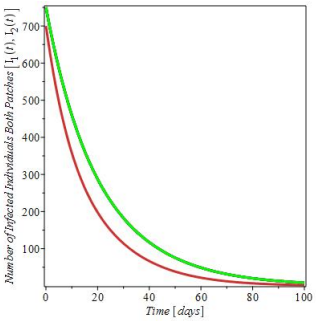
[Endemic Free population in Patch2]

while others (EVD) model parameters were logically estimated for the purpose of illustrations of the model analyses. Pictures of the dynamical behavior of EVD in the presence of movement of susceptible human from one patch to another is given by the numerical simulations of the model (2.1).All the numerical simulations were





(c) Exposed population



(d) Infected population

executed in MAPLE 18

Table 5.1: Parameters value used in the EVD simulations

Parameters	Value	Reference
α_1	0.176/yr	[6]
α_2	0.146/yr	[6]
β_1	1.7/yr	Assumed
β_2	1.8/yr	Assumed
τ_1	0.10/yr	[24]
τ_2	0.20/yr	[24]
μ_1	0.039/yr	[24]
μ_2	0.046/yr	[24]
ω_1	0.95/yr	[50]
ω_2	0.88/yr	[50]
κ_1	0.20	[57]
κ_2	0.17	[57]
π_1	0.013/yr	Assumed
π_2	0.023/yr	Assumed
a	0.06/yr	[54]

it is obvious that the the simulation gives approximation for solutions $S_1(t), E_1(t), I_1(t), R_1(t), S_2(t), E_2(t), I_2(t), R_2(t)$, are presented in graphs respectively. In each case two different movement of susceptible individuals in both patches are considered. It appears that numerical results show that the Ebola model (2.1)exhibits the traditional threshold behaviour which get to reduce with time. We also considered for the non-incidence and transmission of the virus in sub-population, showing the effect of the trajectory of EVD as it converges to the disease free equilibrium. We also took note that the behaviour of the system remains similar for close values of the derivative parameter in both patches.

5.1 ZVD Simulations

In this section, we perform numerical simulations to illustrate the theoretical results in our Zika Metapopulation Mathematical model analysis. We used the parameters values: [Srivastav et al., 2018] $d_1 = d_2 = 0.05/day$, $\mu_{h1} = 0.019896/yr$, $\mu_{v1} = 0.025312/yr$, $\mu_{h2} = 0.019897/yr$, $\mu_{v2} = 0.025312/yr$.

We also assumed $\pi_{h1} = 50/yr$, $\pi_{v1} = 70/yr$, $\pi_{h2} = 110/yr$, $\pi_{v2} = 75/yr$, $\alpha_1 = 0.013/yr$, $\alpha_2 = 0.023/yr$,and considered the initial conditions $S_{h1}(0) = 1000$, $I_{h1}(0) = 50$, $R_{h1}(0) = 0$, $S_{v1}(0) = 4000$, $I_{v1}(0) = 80$, $S_{h2}(0) = 800$, $I_{h2}(0) = 5$, $R_{h2}(0) = 2$, $S_{v2}(0) = 2500$ and $I_{v2}(0) = 50$.

In Figure fig1, we assume a very low disease rate transmission. Even though movement is allowed between patches (since $\lambda_1 \neq 0$ and $\lambda_2 \neq 0$), it is observed that the two patches will be disease free in less than a year. In Figure fig2, we consider the case of high disease transmission rate in the first patch and low rate in the second patch. It is observed when movement between patches is banned that the disease will become endemic in the first patch (with an average of 575 secondary new infections per single infected) and will be overcome in the second patch. Moreover, the infected population will be prevalent in the first patch. A similar (reverse) observation can be seen in Figure fig3. We observe in Figure fig4 that the disease will become endemic in both patches when the disease transmission rates are high (resulting to a minimum of 9879 secondary new infections per single infected).

5.2 Discussion of Results

The Zika model considered a two patch model for the transmission dynamics of Zika Virus with transmission coefficient of susceptible mosquito with infected human and transmission coefficient of susceptible human with infected mosquito with movement within the two patches were analyzed. For the model, It was found that the basic reproduction ratio $R_1 \leq 1$ and $R_2 \leq 1$ for both patches gives a solution limits to the disease-free equilibrium. We also presented scenarios of Zika-free endemic equilibrium where $R_1 \leq 1$ and $R_2 \geq 1$ or $R_1 \geq 1$ and $R_2 \leq 1$ depending on the patch that Zika is prevalent and the patch that movement is restricted. Meaning that the disease persist within any of the community provided that each single infected infects more than one susceptible and the scenario presented is subdued with time in any of the community provided that each single infected infects less

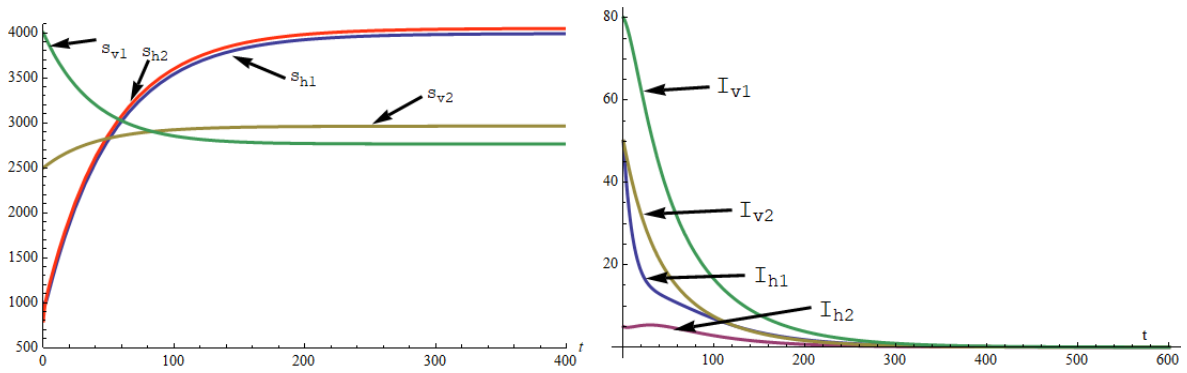
than one susceptible on the average assuming there is no migration. The basic reproduction ratio in both patch plays an important role in the determination to understand the disease dynamics with the population because they are sensitive to the changes of mosquito related parameters, such as the coefficient of transmission between human and mosquitoes. We formulated an optimal control problem of Zika virus infection in both patches.Figure (2a) shows the combined variations in the susceptible human and vector in both patches with movement to and from each patch. Figure (2b) shows the combined variational effect of Zika dynamics when the transmission coefficient for susceptible vector and human as well as infected vector and human is so small, the infection reduces and goes to 0 with time t.

Figure (3a & b) Shows the variation in the transmission dynamics showing the rate of coefficient of susceptible mosquito with infected human as well as transmission coefficient of susceptible human with infected vector in both patches. While Figure (3c&d)shows the variational increase in the transmission coefficient of infective human and vector ($I_{h1} and I_{v1}$) in patch 1 and the decrease in the transmission coefficient of infective human and vector ($I_{h2} and I_{v2}$) in patch 2.

Figure(4a) shows the variation in the Zika virus transmission coefficient of susceptible mosquito with infected human and susceptible human with infected mosquito in both patches with significant decrease in the susceptible human (S_{h2}) with time t due to the reduced rate of infected vector and no movement within both patches. Figure(4b) shows the effect of the increased rate of transmission coefficient of susceptible human with infected mosquito (β_{v2h2}) and Figure (4c) the decrease in the transmission coefficient of susceptible mosquito with infected human as well as transmission coefficient of susceptible human with infected vector going to 0 with time t. Figure (5) Shows the variation in the infective human in both patches ($I_{h1} and I_{h2}$) and Infective vector ($I_{v1} and I_{v2}$) in both patches, while there exist movement within both patches. with the increase in the rate of recovery in patches 1 compared to patch 2.

Table 5.2: Parameters value used in the simulations

Parameters	Value	Reference
π_{h1}	50/yr	Assumed
π_{v1}	70/yr	Assumed
π_{h2}	110/yr	Assumed
π_{v2}	75/yr	Assumed
d_1	0.05/day	[9]
d_2	0.05/day	[9]
μ_{h1}	0.019896/yr	[24]
μ_{v1}	0.025312/yr	[24]
μ_{h2}	0.019897/yr	[24]
μ_{v2}	0.025312/yr	[24]
σ_1	0.0005	[5]
σ_1	0.017456	[5]
α_1	0.013/yr	Assumed
α_2	0.023/yr	Assumed



(e) Susceptible population

(f) Infected population

Figure 5.1: Case of a Zika disease free population ($\beta_{v1h1} = \beta_{h1v1} = \beta_{v2h2} = \beta_{h2v2} = 0.1/12000$, $\lambda_1 = 0.5$, $\lambda_2 = 0.5001$, $R_1 = 0.60447$, $R_2 = 0.591132$).

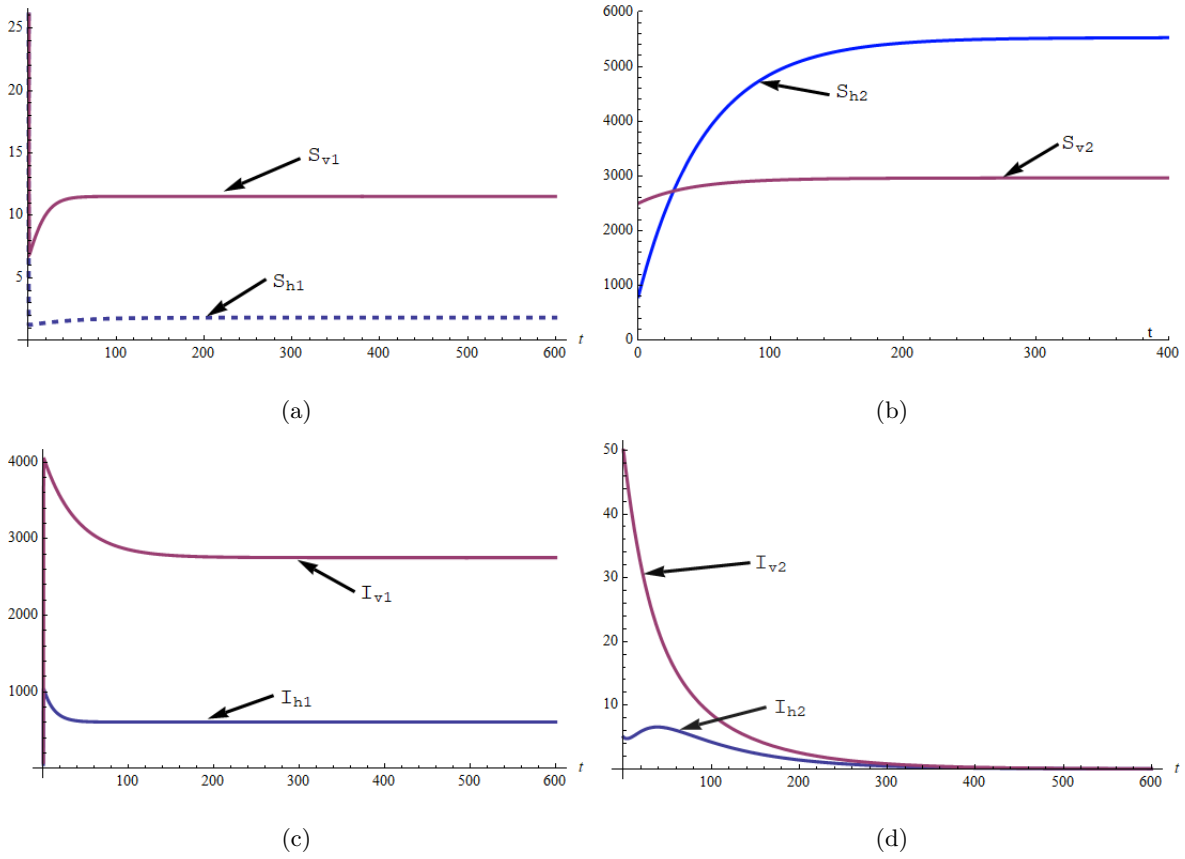


Figure 5.2: Case of the persistence of Zika virus disease in the first population only ($\beta_{v1h1} = \beta_{h1v1} = 0.1/10$, $\beta_{v2h2} = \beta_{h2v2} = 0.1/12000$, $\lambda_1 = \lambda_2 = 0$, $R_1 = 575.517$, $R_2 = 0.695544$).

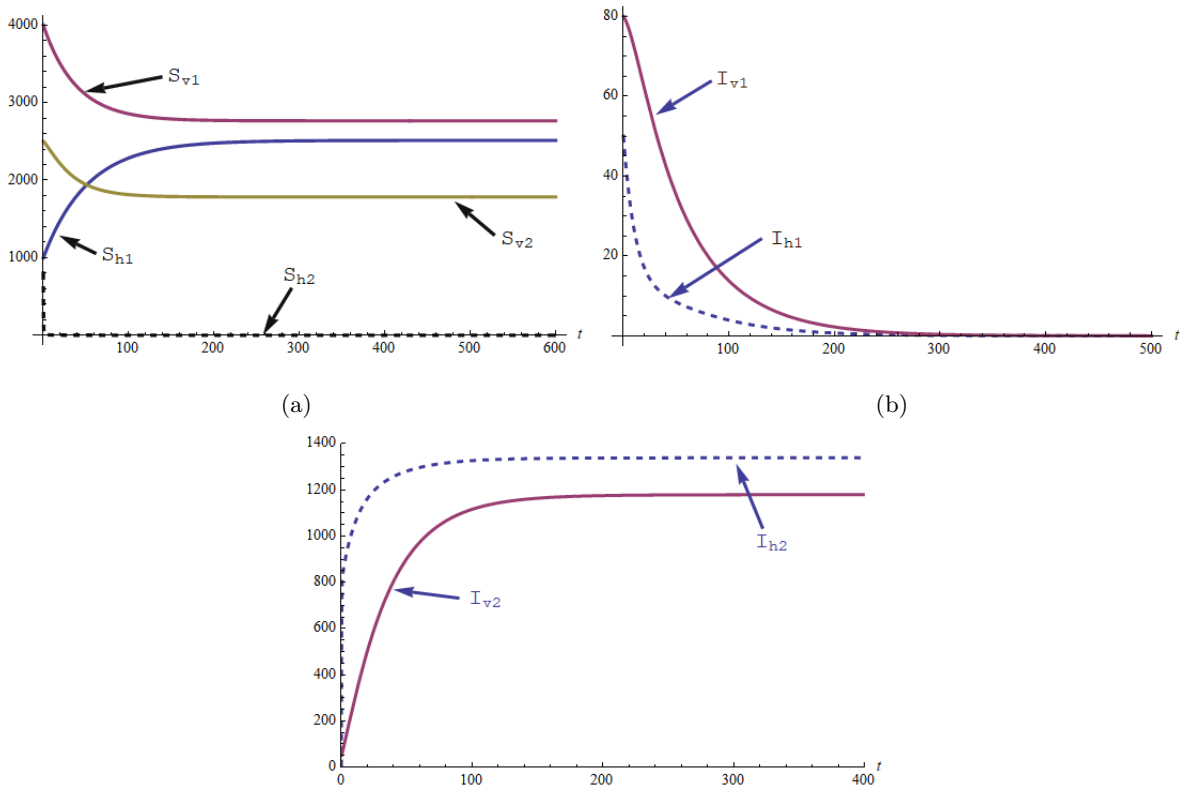


Figure 5.3: Case of the persistence of Zika virus disease in the second population only ($\beta_{v1h1} = \beta_{h1v1} = 0.1/12000$, $\beta_{v2h2} = 0.1$, $\beta_{h2v2} = 0.1/8000$, $\lambda_1 = \lambda_2 = 0$, $R_1 = 0.479597$, $R_2 = 1.04332$).

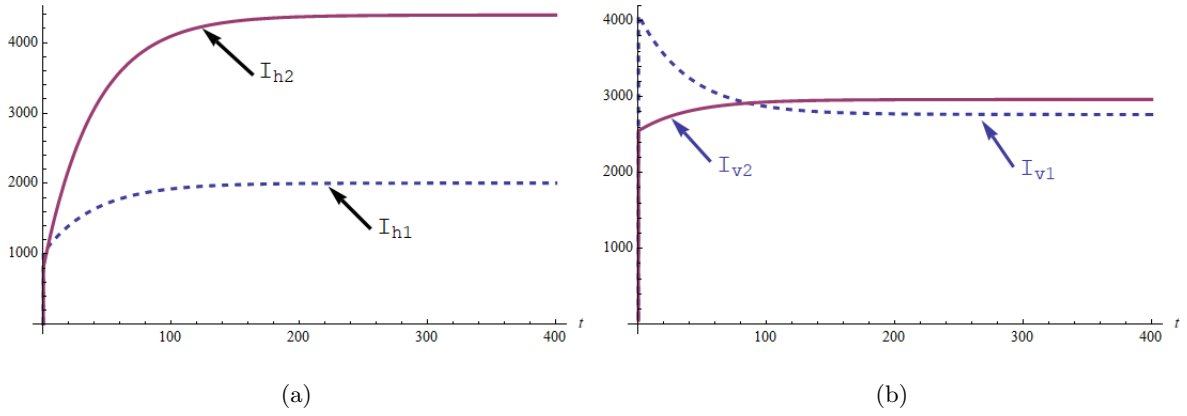


Figure 5.4: Case of the persistence of Zika virus disease in both populations ($\beta_{v1h1} = \beta_{h1v1} = \beta_{v2h2} = \beta_{h2v2} = 0.1$, $\lambda_1 = 0.5$, $\lambda_2 = 0.5001$, $R_1 = 10727.8$, $R_2 = 9878.99$).

Chapter 6

Conclusion

In this study, we investigated the impact of metapopulation on disease transmission dynamics. We took critical look at the effect of metapopulation on Ebola virus disease transmission dynamics in West Africa and the effect of metapopulation on Zika virus disease transmission dynamics in South America. We determined an appropriate optimal control strategy for disease transmission elimination or control. Also, we derived and analysed a etapopulation deterministic model for both EVD and ZVD where we performed an optimal control analysis of the metapopulation model. We began with historical background on both Ebola and Zika virus disease respectively in Chapter 1 as well as explanation of basic mathematical tools used in mathematical modeling techniques. While in Chapter 2, we discussed and reviewed literature on both Ebola disease model and Zika disease model, with special interest on transmission of disease in linked communities. The formulation of both Ebola disease model and Zika disease model was presented in Chapter 3, with qualitative analysis of the four compartment model for each of the two patch considered for the EVD model and five compartment model for each of the two patch considered for the ZVD model which are feasible epidemiologically and mathematically well-posed. We investigated the existence and stability of both EVD and ZVD models with their peculiarities: like Ebola-free endemic equilibrium (EFEE) and Zika-free endemic equilibrium (ZFEE) for each patch of both model, we also applied the next generation matrix technique in deriving the invasion reproduction number R_i where $i = 1, 2$ for EVD and ZVD model. The respective basic reproduction number was used to show that Ebola-free equilibrium (EFEE) and Zika-free equilibrium (ZFEE) are locally asymptotically stable whenever $R_i < 1$ and unstable otherwise. However, the stability

analysis of the model beyond small region near the equilibria was checked. We explored the global dynamical behavior of the model around the equilibria. Also, a suitable Lyapunov function was constructed at both the Ebola free equilibrium (EFE) and the Zika free equilibrium (ZFE) respectively to prove that the model is globally asymptotically stable. A sensitivity analysis checking the effectiveness of parametric values was carried out with a view to examining the factors most responsible for diseases transmission with both patch. In Chapter 4, Optimal control strategy was carried out, where we seek strategy to reduced the effect of disease transmission within linked communities for both metapopulation model respectively. For the Ebola Control we have namely,anti movement within patches campaign for patch 1 $u_1(t)$ and $u_2(t)$ for patch 2. While $u_3(t)$ is the controlled treatment and $u_4(t)$ is the adequate inoculation of vaccine. We established existence of an optimal control by applying the Pontryagin's Maximum Principle [Pontryagin, 1987]. Which we used to explain the essence of the control strategy [Wang et al., 2019]. Furthermore, we saw the effectiveness of proper control strategy in the reduction of both disease as the rate of transmission of disease reduced as shown in the Numerical simulations carried out with relevant data relied upon from World health Ogranisation (WHO) and Centre for Disease Control (CDC). Thus we conclude that with the increase fraction of vaccaination of the EVD as seen as a control strategy and proper adherence to education and restriction of movement in and out of disease prevalent communities. Also it is easy to observe the reproduction numbers R_i where $i = 1, 2$ for both patches and both disease dynamics can be reduced below one by increasing the awareness in movement within patches for both disease dynamics. So also the numerical simulation suggest that the rate of transmission of both EVD and ZVD be deceased as increases in this affects the equilibrium level of both Model.

Future works

Further extensions to this work could be:

- To develop a fractional differential metapopulation model in disease transmission dynamics for linked communities.
- To investigate the delay differential equation metapopulation model in disease transmission dynamics in linked communities.

- To develop and analyse sex-structured, age-structured and mother to child transmission dynamics of Zika virus disease.
- To develop and analyse effect of metapopulation on transmission of disease in not linked, while considering air travels and migration. Example is the recent COVID-19 pandemic.

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