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AN SIA MODEL OF HIV TRANSMISSION IN GHANA

BY

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DECLARATION

I hereby declare that this submission is my own work towards the MPhil and that, to the best of my knowledge; it contains no material previously published by another person nor material which has been accepted for the award of any other degree of the university, except where due acknowledge has been made in the text.

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May God richly bless you.

DEDICATION

I dedicate this work to my entire household, especially my mum, dad and brothers.

I also dedicate this work to all my friends who stood by me in times of difficulty. I appreciate all their love and effort.

Thank you all for your prayers and encouragement especially when things seemed impossible.

ABSTRACT

In this thesis an SIA compartment model of the transmission dynamics of HIV/AIDS is developed using Ghana Data.

The resulting system of three non-linear differential equations was analyzed in respect of stability of the three equilibrium points namely the disease free which was found to be unstable and two endemic equilibrium points which were found to be stable. Further analysis to determine the conditions for the breakout of epidemic were done using the basic reproductive number of the infection.

Simulations of solutions of the model in various scenarios were also performed. It was found that the rate of transition from HIV infected to AIDS relative to the rate of transition from susceptible to HIV infected state would need to be increased in order to effectively control the spread of the disease.

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CHAPTER ONE

INTRODUCTION

1.0 Overview

The origin of HIV and AIDS has puzzled scientists ever since the illness first came to light in the early 1980s. For over twenty years it has been the subject of fierce debate and the cause of countless arguments, with everything from a promiscuous flight attendant to a suspect vaccine programme being blamed.

The first recognized cases of AIDS occurred in the USA in the 1980s. A number of gay men in New York and California suddenly began to develop rare opportunistic infections and cancers that seemed stubbornly resistant to any treatment. At this time, AIDS did not yet have a name, but it quickly became obvious that all the men were suffering from a common syndrome.

The discovery of HIV, the Human Immunodeficiency Virus, was made soon after. While some were initially resistant to acknowledge the connection (and indeed some remain so today), there is now clear evidence to prove that HIV causes AIDS.

The significance of this risk factor was particularly profound in the African region, accounting for 19.4% of the total burden of disease in Africa. Most of this burden is directly attributable to HIV/AIDS, though other sexually transmitted infections (STIs) also comprise an important element. Interventions to limit the spread of HIV are therefore urgently needed in Africa especially.

1.1 Background

Human immunodeficiency virus (HIV) is a lentivirus (a member of the retrovirus family), and like all viruses of this type, it attacks the immune system. Lentiviruses are in turn part of a larger group of viruses known as retroviruses that causes acquired immunodeficiency syndrome (AIDS), a condition in humans in which the immune system begins to fail, leading to life-threatening opportunistic infection. The name 'lentivirus' literally means 'slow virus' because they take such a long time to produce any adverse effects in the body. They have been found in a number of different animals, including cats, sheep, horses and cattle.

However, the most interesting lentivirus in terms of the investigation into the origins of HIV is the Simian Immunodeficiency Virus (SIV) that affects monkeys, which is believed to be at least 32,000 years old. In fact, it is generally accepted that HIV is a descendant of a Simian Immunodeficiency Virus because certain strains of SIV bear a very close resemblance to HIV-1 and HIV-2.

There are only two species of HIV known to exist: HIV-1 and HIV-2. HIV-1 is the virus that was initially discovered and termed both LAV and HTLV-III.

It is more virulent, more infective, and is the cause of the majority of HIV infections globally. The lower infectivity of HIV-2 compared to HIV-1 implies that fewer of those exposed to HIV-2 will be infected per exposure. Because of its relatively poor capacity for transmission, HIV-2 is largely confined to West Africa.

HIV-2 for example corresponds to SIVsm, a strain of the Simian Immunodeficiency Virus found in the sooty mangabey (also known as the White-collared monkey), which is indigenous to western Africa.

The most virulent, pandemic strain of HIV, namely HIV-1, was until recently more difficult to place. Until 1999, the closest counterpart that had been identified was SIVcpz, the SIV found in chimpanzees. However, this virus had certain significant differences from HIV.

1.1.1 *How HIV-1 Originated*

In February 1999 a group of researchers from the University of Alabama announced that they had found a type of SIVcpz that was almost identical to HIV-1. This particular strain was identified in a frozen sample taken from a captive member of the sub-group of chimpanzees known as Pan Troglodytes (P.t. troglodytes), which were once common in west-central Africa.

The researchers (led by Paul Sharp of Nottingham University and Beatrice Hahn of the University of Alabama) made the discovery during the course of a 10-year long study into the origins of the virus. They claimed that this sample proved that chimpanzees were the source of HIV-1, and that the virus had at some point crossed species from chimps to humans.

Their final findings were published two years later in Nature magazine. In this article, they concluded that wild chimps had been infected simultaneously with two different simian immunodeficiency viruses which had "viralse" to form a third virus that could be passed on to other chimps and, more significantly, was capable of infecting humans and causing AIDS.

These two different viruses were traced back to a SIV that infected red-capped mangabeys and one found in greater spot-nosed monkeys. They believe that the hybridization took place inside chimps that had become infected with both strains of SIV after they hunted and killed the smaller species of monkey.

They also concluded that three 'groups' of HIV-1 namely Group M, N and O came from the SIV found in P.t troglodytes, and that each group represented a separate crossover 'event from chimps to humans.

1.1.2 *How HIV-2 Originated*

Until recently, the origins of the HIV-2 virus had remained relatively unexplored. HIV-2 is thought to come from the SIV in Sooty Mangabeys rather than chimpanzees, but the crossover to humans is believed to have happened in a similar way (i.e. through the butchering and consumption of monkey meat).It is far rarer, significantly less infectious and progresses more slowly to AIDS than HIV-1. As a result, it infects far fewer people, and is mainly confined to a few countries in West Africa.

By analyzing samples of the two different subtypes of HIV-2 (A and B) taken from infected individuals and SIV samples taken from sooty mangabeys, Dr. Vandamme concluded that subtype A had passed into humans around 1940 and subtype B in 1945 (plus or minus 16 years or so). Her team of researchers also discovered that the virus had originated in Guinea-Bissau and that its spread was most likely precipitated by the independence war that took place in the country between 1963 and 1974. Her theory was backed up by the fact that the first European cases of HIV-2 were discovered among Portuguese veterans of the war, many of whom had received blood transfusions or unsterile infections following injury, or had possibly had relationships with local women.

HIV is a retrovirus and like most of the viruses in this family of viruses the Retroviridae, only replicates in dividing cells.

HIV has some unfortunate unique properties even within this retrovirus family such as using the mRNA processing of the cell it invades to synthesis its own viral RNA. Although studies (Ho et al. 1995) have shown the dynamics of viral replication is very high in vivo the immune system can counteract this replication from 5 to 10years or more depending on the initial infection. Cases of haemophiliacs who have been given contaminated blood have succumbed in a matter of months.

Infections by the virus HIV-1, the most common variety, has many highly complex characteristics, most of which are still not understood. The fact that the disease progression can last more than 10years from the first day of infection is just one of them. Another is that while most viral infections can be eliminated by an immune response, HIV is only briefly controlled by it. HIV primarily infects a class of white blood cells or lymphocytes, called CD4 T-cells, but also infect other cells such as dendritic cells. The virus has a high affinity for a receptor present on the cell surface of each of these cells which guides the virus to their location in vivo.

When the CD4 T-cell count, normally around 1000/μL, decreases to 200/μL or below, a patient is characterized as having AIDS. There are very specific clearly (Morb Mort Week Report 42(No. RR-17), Table 308-1 and Table 308-2, December 18, 1992) which are used to diagnose the AIDS; the CD4 T-cell count is not the only factor. The categories are regularly updated. These are used by the Centers for Disease Control for surveillance purposes. For example, if a patient with the virus has a CD4T-cell count greater than 500/μL but has, or has had one of a variety of diseases then a formal diagnosis is made and registered. The reason for the fall in the T-cell count is unknown. T-cells are normally replenished very quickly in the body, so the infection may affect the source of new T-cells or the life span of preexisting ones. Although HIV can kill cells that it infects, only a small fraction of CD4 T-cells are infected at any given time.

Because of the central role of CD4 T-cells in immune regulation, their depletion has widespread deleterious effects on the functioning of the immune system as a whole and this is what leads to AIDS.

HIV infection has four basic stages: incubation period, acute infection, latency stage and AIDS. The initial incubation period upon infection is asymptomatic and usually lasts between two and four weeks. The second stage, acute infection, lasts an average of 28 days and can include symptoms such as fever, lymphadenopathy (swollen lymph nodes), pharyngitis(sore throat), and rash, myalgia(muscle pain), malaise, and mouth and esophageal sores.

The latency stage, which occurs third, shows few or no symptoms and last anywhere from two weeks to twenty years and beyond. AIDS, the fourth and final stage of HIV infection shows as symptoms of various opportunistic infections.

Infections with HIV occur by the transfer of bodily fluids such as blood, semen, vaginal fluid, breast milk. Within these bodily fluids, HIV is present as both free virus particles and virus within infected immune cells. The four major routes of transmission are unsafe sex, contaminated needles, breast milk, and transmission from an infected mother to her baby at birth (perinatal transmission). Screening of blood products for HIV has largely eliminated transmission through blood transfusion or infected blood products in the developed world.

HIV infection in humans is considered pandemic by the World Health Organization (WHO). Nevertheless, complacency about HIV may play a key role in HIV risk. From its discovery in 1981 to 2006, AIDS killed more than 25 million people.

HIV infects about 0.6% of the world's population. In 2005 alone, AIDS claimed an estimated 2.4-3.3 million lives, of which more than 570,000 were children. A third of these deaths are occurring in Sub-Saharan Africa, retarding economic growth and increasing poverty.

According to current estimates, HIV is set to infect 90 million people in Africa, resulting in a minimum estimate of 18 million orphans.

HIV infects primarily vital cells in the human immune system such as helper T cells (to be specific, $CD4^+$ T cells), macrophages, and dendritic cells. HIV infection leads to low levels of $CD4^+$ T cells through three main mechanisms: First, direct viral killing of infected cell; second, increased rates of apoptosis in infected cells; and third, killing of infected $CD4^+$ by CD8 cytotoxic lymphocytes that recognize infected cells. When $CD4^+$ T cell numbers decline below a critical level, cell-mediated immunity is lost, and the body becomes progressively more susceptible to opportunistic infections.

Most untreated people infected with HIV-1 eventually develop AIDS. These individuals mostly die from opportunistic infections or malignancies associated with the progressive failure of the immune system. HIV progresses to AIDS at a variable rate affected by viral, host, and environmental factors; most will progress to AIDS within 10years of HIV infection: some will have progressed much sooner and some will take much longer. Treatment with anti-retrovirals increases the life expectancy of people infected with HIV has progressed to diagnosable AIDS, the average survival time with antiretroviral therapy was estimated to be more than 5years as of 2005. Without antiretroviral therapy, someone who has AIDS typically dies within a year.

The history of HIV is a complex one.

Twenty years ago, little was known about the mysterious illness that was killing thousands of people. The history of HIV tells us that scientists struggled for a cause and even more important a solution. Then an American scientist named Robert Gallo co-discovered a virus later known as HIV that seemed to be the culprit.

His research and findings opened the door to a new field of medicine and science dedicated to finding answers to the epidemic of the 20th century HIV and AIDS.

In the mids 80's Gallo and his team co-discovered the virus they believed to be responsible for the killer disease known as AIDS. In addition, Gallo and his team developed a test that identified the virus in humans-the HIV antibody blood test. This test makes possible the early identification of infected people, allowing for early and better treatment resulting in long life expectancies for those living with HIV.

Since the mid-1980's, numerous models have been developed to describe the immune system and its interaction with HIV. These models are deterministic and stochastic models. Stochastic models aim to account for the early events in the disease when there are few infected cells and a small number of viruses.

Most models have been deterministic. Deterministic models, which attempt to reflect the dynamic changes in mean cell numbers, are more applicable to later stages of the process when the population is large. These models typically consider the dynamics of the CD4 cells, latently infected cells and virus populations as well as the effects of drug therapy.

Because of the ethics, among other things, of doing experiments on humans, fundamental information has been lacking about the dynamics of HIV infection.

For example, since the disease takes an average of 10years to develop it was widely thought that the components of the disease process would also be slow.

A combination of mathematical modeling and experiments has shown this is not the case, by showing that there are a number of different timescales in HIV infection. The current understanding of the rapidity of HIV infection has totally changed the manner in which HIV is treated in patients and has had a major impact in extending patients lives;

1.2 Statement of the Problem

Since the first cases of AIDS were identified in the United States nearly two decades ago, HIV/AIDS has emerged as one of the leading challenges for global public health. Particularly in sub-Saharan Africa, where the overwhelming majority of HIV and AIDS cases appear, the epidemic continues to take a massive human toll.

This pandemic has not only taken a massive toll on human lives but also affected developmental agenda of most developing countries including Ghana. It has also denied majority of our effective labor force the strength to function properly thereby reducing our total output as a nation.

Scientist/researchers have over the years since the emergence of this life threatening diseases have worked tirelessly to bring this pandemic under control, adapting different mathematical techniques and almost always end up with some quantitative and qualitative questions to answer: how many people are infected with the HIV each day?, where are these people resident?, how many new cases will be administered in the future?, and how to control the disease?

An understanding of the magnitude and trajectory of the HIV/AIDS epidemic, as well as the uncertainty around these parameters, is critically important both for planning and developmental purposes.

1.3 Objectives of the Research

As a motivation for this research, it is important not to let our arms down in our effort to prevent and control the HIV/AIDS epidemic in our country, Ghana. Countries including Ghana are dealing with the growing impact of the epidemics on the youngest and most productive population groups; increasing numbers in children and adolescents; worsening situation among the poor and marginalized population; a continuous aggravation of the existent health problems; and above all, the diversion of resources from other health, welfare and educational priorities.

If mathematical models based on the underlying transmission mechanism of HIV/AIDS might help the medical and scientific communities understand better how the disease spreads in the community then we have to support it as mathematicians.

The specific objectives of the study are to;

1. To construct an SIA compartmental model of HIV/AIDS, i.e. comprising the Susceptible, Infected (without AIDS) and Infected with AIDS compartments.
2. Investigate solutions and the stability of the equilibria of the model analytically and using Ghana data.
3. Also investigate the role of the basic reproductive number.
4. Based on the above findings, determine implications for intervention.

1.4 Methodology

Many mathematical models have been developed and applied to the HIV/AIDS epidemic since its initial occurrence (Knox, 1986; Anderson, et al., 1986; Anderson, 1988; Dietz et al., 1983; Dietz, 1988; Brauer, 1993; Brauer and Castillo, 2001; Castillo et al., 1994; Chowell et al., 2004).

These mathematical models are proposed based on the nature and the type of disease one is looking at.

Considering the process of a disease that fits the SIR framework we have a flow of individuals from the susceptible group to the infected group and then to the removed group (identified here with AIDS group).

Susceptible →Infected →Removed (AIDS)

We therefore seek to apply the following mathematical methods to model the HIV/AIDS dynamics:

We construct a compartmental model, in which the total population is divided into three groups (variables), a susceptible population, the population with the HIV infection and the population which are infected and show symptoms of AIDS.

We then develop systems of non-linear differential equations based on the compartmental model, after which we find the steady state equilibria and hence establish the points at which the system will attain stability by first linearizing the systems of nonlinear differential equations. This linearization is done by finding the jacobian matrix and solving to get the eigenvalues.

We will go ahead and find the basic reproductive ratio.

The data for the thesis is specifically from Ghana data which was collected from WHO website and the evaluations are carried out using numerical simulations with MatLab.

1.5 Structure of the Thesis

The thesis is organized in five chapters, each chapter containing an introductory note of what should be expected in the respective chapters.

In chapter one, we looked at the historical background, statement of the problem, objective of the thesis, methodology, justification and the structure of the thesis. Chapter two deals with a review of related research, chapter three also deals with the methodology which involves the mathematical methods for modeling, chapter four involves the stability analysis of the model and we gave a concluding note and some recommendations in the chapter five of this thesis.

CHAPTER TWO

REVIEW OF RELATED LITERATURE

2.0 Introduction

Mathematical models provide a unified and flexible approach to the study of the spread of AIDS and other infectious diseases. This chapter presents briefly, a review of some of the papers that use mathematical models to study the epidemiology of AIDS.

In general, modeling the transmission of AIDS in a population is carried out by way of compartmental models. The population is divided into the susceptible, infective and removed individuals. Each infective is infectious during a random period of time. While infected, it behaves independently of the others and is able to contact susceptible, which will then become infective. After that period, the individual is removed, by death for example, and plays no further role in the propagation of the disease.

2.1 Mathematical Models for HIV Dynamics

Mathematical models play an important role in the understanding of the dynamics of the transmission of HIV.

We present a few of such models that are related to this thesis.

One of such known models was presented by (Ho et al. 1995). Their work examines the pathogenesis of the dynamical process of HIV using a model based on a simple equation expressing the rate of change of the viral concentration depending on time. This work was

extended by (Perelson et al., 1996) including the dynamics of infected T-cells and the non-infectious viral loads.

As a consequence of the above mentioned articles, several models began to include biological processes into the mathematical models. Some of these are compartmental models (Murray et al., 1998; Callaway and Perelson, 2002) and some more recent works using delay differential models as in (Nelson et al., 2000; Nelson and Perelson, 2002).

We begin with a simple Susceptible-Infected-Recovered (SIR) model. We consider a variation of this model proposed by (Tassier, 2005). As a variant on this thesis, SIR can also stand for Susceptible-Infected-Removed if people are allowed to die from their infection and thus leave the population under consideration.

Thus we have three groups or states in which we can place individuals and the number of people in each group was treated as a time series data where we have a number of infected individuals as well as susceptible and recovered individuals at each point in time.

From his model of the disease he noted that each individual in the population is in one of the three groups.

From his work he mentioned that an individual potentially moves from the susceptible to the infected group when he comes in contact with an infected person.

He then supposed that each infected person contacts γ individuals in each period of time on average. Now each contact may not result in transmission of the disease. Perhaps only α percent of the contacts result in transmission.

Thus the potential number of transmissions may be at most $\gamma * \alpha$.

He then defined $\beta = \gamma * \alpha.\beta$ is the average of transmissions possible from a given infected person in each period.

Now, we must remember that there are three groups in the population. If we assume that individuals are mixed randomly then each potential transmission may be from an infected person to a susceptible person which results in a new infected person. Or a transmission may occur from an infected person to another infected person which results in nothing happening since the person is already infected or the potential transmission may occur from an infected person to a recovered or immune person. In this case again nothing changes. Since only s_t percent of the population is susceptible each infected person generates only βs_t new infections each period.

Each infected person recovers (or is removed or dies) at some rate. Let the fraction of the infected group that recovers be κ.

Tassier (2005) then described the SIR process given the current state of the population in period t described by S_t, I_t and R_t. With this he wrote a series of differential equations that describe the motion of the system. He actually carried out this by first describing the susceptible population by beginning period t with S_t individuals in the susceptible population. We then lose on average $\beta s_t I_t$ from the population.

From all the analysis Troy Tassier made from his model, he concluded on the fact that if a disease removes its carriers quickly the disease is not likely to have a long life itself.

Greenhalgh (1997) also wrote a paper on Mathematical modeling of the spread of HIV/AIDS amongst injecting drug users and in his paper he developed and analyzed a model for the spread of HIV/AIDS amongst a population of injecting drug users. His model was based on what is originally due to Kaplan (1989).

Greenhalgh (1997) then ended up with deriving the differential equations which describe the progress of the disease amongst the addicted population and the proportion of needles which are infected.

Another paper written by Altman (1994) on the topic Susceptible-Infected-Removed epidemic models with dynamic partnerships also looks into how well an extension of the classical, stochastic, Susceptible-Infected-Removed (SIR) epidemic model could be used to allow for disease transmission through a dynamic network of partnerships.

M. Altman actually came up with some deductions of which the Markov model with partnerships was considered. In his model he made a couple of assumptions which are:

1. Removal from the infectious state occurs at a constant rate.

2. Unpaired individuals begin a partnership at a constant rate, partnerships dissolve at a constant rate, and partnerships behave independently. Therefore the interval during which two individuals are unpaired and paired are independent, exponentially distributed random variables.

3. Partnerships always begin with a contact, which may or may not be effective, and thereafter effective contacts occur at a constant rate. Therefore, the contacts other than the initiating contact may be modeled as Poisson processes.

4. An effective contact between an infectious individual and susceptible individual results in transmission.

In his paper, he wrote that to understand the initial dynamics of the model, we look at what happens when a few cases are introduced into a large population of susceptible individuals. So long as these initial cases are distributed randomly in the population, it suffices to consider what happens when a single initial case is introduced.

The independence of the partnership processes implies that the secondary cases arising from a particular infectious individual are unlikely to be partners of each other, and thus the number of infected individuals will initially grow like a branching process, just as for the classical model. The threshold for a major epidemic is when the average number of secondary cases produced by an isolated initial case, R_0, is greater than 1.

He denoted the initial case by individual i. The number of secondary case is the sum over the N other individuals of the probability that i transmits to the other individual. The individuals are identical, so it suffices to compute the probability that i transmits to some individual j. The key to computing this probability, and more generally to understanding the dynamics of the epidemic, is to consider the configuration of the dyad (i, j). since each individual can be in one of three possible disease states and the individuals may or may not be partners at a given time, there are 18 possible configurations for the dyad. These configurations will be denoted by two letters, indicating the disease status of the two individuals in the dyad. A centered dot was used to indicate that i and j are unpaired, a dash to indicate that they are paired. For example, let $S-S$ denote the configuration where both are susceptible and they are partners, $I \cdot S$ denote the

configuration where i is infected and j is susceptible and they are not partners, etc. Each dyad will move among the possible configurations according to a Markov process.

After his consideration of the so many possibilities in the transmission dynamic, M. Altman came up with a diagrammatic representation of the transmission rates among the states for a dyad of individuals, from first infection to transmission or removal.

In his diagram, external sources of infection are ignored. $I \cdot S$ refers to the state where the first individual is infectious, the second is susceptible and they are not currently partners, $R-S$ refers to the state where the first individual is removed, the second is susceptible and they are currently partners, etc. The dyad begins with one infected and one susceptible individual, either in state $I \cdot S$ or state $I-S$.

In this model external infection is assumed to be negligible for large populations with independent partnership processes, which is why the branching process approximation is valid. This reduced diagram has three absorbing states: I– I, R · S, and R– S.

This paper has been concerned with the initial dynamics and the final size of the epidemic.

López-Cruz (2006) wrote a paper on SI epidemic titled structured SI epidemic models with applications to HIV epidemic. In her paper she actually divided the work into three main parts. The first parts dealt with effect of age structure on $S-I$ epidemic models in the form of Ordinary Differential Equations and Delay Differential Equations, respectively. López-Cruz finally came up with an $S-I$ epidemic model which represents contagious disease dynamics in single patch (Brauer and Castillo, 2001; Brauer, 2002; Edelstein, 2005).

The birth rate is dependent on the total population N but it is more realistic to depend on the sexually active population in the case of one sex models and depend on the sexually active female population in the case of two sex models. In the second $S-I$ model, the infection term is modified for non constant total populations$\frac{C_N SI}{S+I}$ and C_N is the maximum number of infections an infected individual can cause in a unit of time. It assumed a constant recruitment which is not realistic. Taking into consideration the modeling issues above described, these models are improved by the following research: An $S-I$ model is developed in Hwang and Kuang (2005) to study the host extinction dynamics in a simple parasite-host interaction model. Those can be applied to the study of epidemiological trends of diseases and conditions that permit global stability. For example, consider that the disease divides the population into susceptible and infected subpopulations.

Assume that the newborn of infected individuals could be a susceptible individual, the main difference with the above mentioned models.

By standard results (Thieme, 2003), the solutions of the system exist, are unique, positive, uniformly eventually bounded and defined on $[0, \infty)$. For the stability results of the general $S-I$ model, it could be reviewed in (Hwang and Kuang, 2005) as a particular case.

A paper written by Abdulkarim (2007) on SIR Epidemic Model with Application to Transmission Dynamics of HIV/AIDS also considered how the SIR epidemic model could be used to analyze how the transmission of the epidemic from one state or population group to the other. In his paper, he examined the Susceptibles-Infectives-Removed/Recovered, (SIR)

epidemic model and applied it to horizontal transmission of HIV/AIDS in a homogeneous mixing population with the additional assumption that the AIDS virus does not kill. Instead; AIDS infectives are removed from circulation until death by non disease induced factors.

Also the stability of the equilibrium point are examined through the basic reproductive number of the infection and trace-determinant condition of the Jacobian matrix at the equilibrium point, for a system of non-linear differential equation.

Then also in his paper, Abdulkarim (2007) considered a series of models with some parameter definition which actually defined the various aspects of the disease modeling process.

In his model, he assumed that the death rate is the same as the birth rate and that the deaths in the class of infectives, denoted by A in the SIR epidemic model, reduces it to a simple SIA model, where the removed/recovered class forms the class of AIDS infectives, without disease induced death. Since they are assumed, non-sexually active and are quarantined. They do not contribute to transmission dynamics of the infection.

To have an AIDS free stable population, the product of the net transmission of HIV-infection and the average length of infection for AIDS should be less than unity.

After his model to study the transmission of the disease and the equilibrium state, Abdulkarim (2007) then went on to model for the possibility of existence of an endemic equilibrium point.

The identified endemic equilibrium point E_l is not stable. However, Mugisha et al. (2005) and Heffeman et al. (2005) gave insights into the use of the basic reproductive number R_0 in analyzing the stability of the endemic equilibrium point.

They observed that if $R_1 > 1$, then the system has an asymptotically stable endemic equilibrium and the disease-free equilibrium is unstable. However, if $R_1 < 1$, then the disease-free equilibrium is locally asymptotically stable while the endemic equilibrium is unstable.

Abdulkarim (2007) then adapted the above stated approach and, using the next generation operator by Diekmann (Herfferman et al., 2005), he categorized the population into two classes.

This requirement is also obtained using the determinant or trace method of investigating stability of equilibrium points for systems of two non-linear differential equations.

After a series of analyses made with respect to the various models, Abdulkarim concluded that increasing the birth rate, decreasing AIDS progression rate and minimizing net transmission for both cases may eradicate HIV/AIDS, but would give a long incubation period for AIDS.

CHAPTER THREE

MATHEMATICAL MODEL

3.0 Introduction to Disease Modeling

Mathematical models have been used in epidemiology for at least 250 years, taking as a somewhat arbitrary starting point Daniel Bernoulli's study, published in 1760, on the advantages of smallpox vaccination. Mathematical models are commonly understood to have two distinct roles: to predict and to facilitate understanding.

By far the largest, best-understood group of models is deterministic and expressed in terms of differential equations. These can be simple models such as the SI, SIR or SEIR models, which consist of one, two and three equations, respectively or more complicated aggregations of states. These deterministic models model the behavior of epidemiologically relevant classes. These classes are sometimes referred to as compartments and this type of model are compartmental models. The SI epidemic model, for example, models two states, a susceptible state (S) and an infectious state (I). The $SEIR$ model adds an exposed state (E) for those who are exposed but not yet infectious and a recovered state. The SIR model only adds a recovered or removed state (R).

Usually the choice between such models is dictated by the natural history of the disease: for example, is there a recovered state that is immune? Is there an exposed state that is not infectious? Generally, the simpler the model is, the more transparent its behavior and the more understandable its results. At the same time, too much simplicity can obviously be a barrier to the accuracy of prediction.

Some of these models are SIS model, SIR model, SIRS and SI model respectively.

3.0.1 *The SIS Model*

Some infections do not confer any long lasting immunity. Such infections do not have a recovered state and individuals become susceptible again after infection.

This type of disease can be modeled by SIStype. The total population N is divided into two compartments with $N = S + I$, where S is the number of individuals in the susceptible class, I is the number of individuals who are infectious. The SIS model since one typical pathway is through S, then I, and then back to S, as shown below.

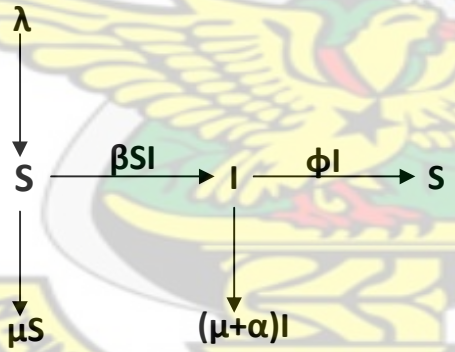

Fig.3.1: The transfer diagram for the SIS model.

The transfer diagram leads to the following systems of differential equations for this SIS model are:

$$\frac{dS}{dt} = \lambda - \beta SI - \mu S + \Phi I$$

$$\frac{dI}{dt} = \beta SI - (\Phi + \mu + \alpha)I \quad (1)$$

The parameters are positive constants. The constant λ is the recruitment rate of susceptible corresponding to births and immigration, μ is the per capital natural mortality rate.

We assume that a disease may be fatal to some infectious death rate from infectious class, α. And Φ the rate at which individuals infectious and return to susceptible class and they don't acquire immunity.

Which, together with $N = S + I$, implies:

$$\frac{dN}{dt} = \lambda - \mu N - \alpha I \quad (2)$$

Thus the total population size N may vary in time. In the absence of disease, the population size N converges to the equilibrium λ/μ .It follows from (2) that $\lim_{supt\to\infty} N \leq \lambda/\mu$.

3.0.2 *The SIR and SIRS Models*

Some infectious disease confers permanent immunity and other disease confers temporal acquired immunity. These types of disease can be modeled by SIR and SIRS models, respectively.

The total population N is divided into three compartments with $N = S + I + R$, where S is the number of individuals in the susceptible class, I is the number of individuals who are infectious and R is the number of individuals recovered.

The SIRS model since one typical pathway is through S, then I, then R, and then back to S, as shown below:

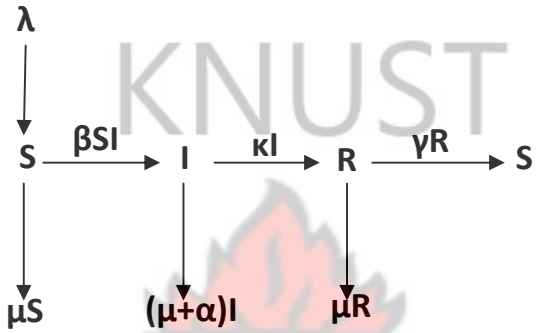

Fig.3.2: The transfer diagram for the SIRS model.

The transfer diagram leading to the following systems of differential equations for this SIRS model are:

$$\frac{dS}{dt} = \lambda - \beta SI - \mu S + \gamma R,$$

$$\frac{dI}{dt} = \beta SI - (\kappa + \mu + \alpha)I, \qquad (3)$$

$$\frac{dR}{dt} = \kappa I - (\mu + \gamma)R.$$

Where parameters $\lambda, \mu, \beta, \kappa$ and α are positive constants and γ is a non-negative constant. Here we assume that κ is the rate at which infectives recover, if the recovered individuals acquired permanent immunity.

This, together with $N = S + I + R$ implies,

$$\frac{dN}{dt} = \lambda - \mu N - \alpha I. \quad (4)$$

Thus the total population size N may vary in time. In the absence of disease, the population size N converges to the equilibrium λ/μ .

3.0.3 *The SI Epidemic Model*

The SI epidemic model is a prelude to the SIA model. In this model we consider, we consider only two population groups in which we have the class of the susceptibles and the class of the infectives which is a combination of the infected and those infectives with full-blown AIDS.

This type of disease can be modeled bySItype. The total population N is divided into two compartments with$N = S + I$, where S is the number of individuals in the susceptible class, I is the number of individuals who are infectious. The SI model has one typical pathway and that is through S, then I, as shown below.

Based on the flow diagram below, we generate our systems of nonlinear differential equation.

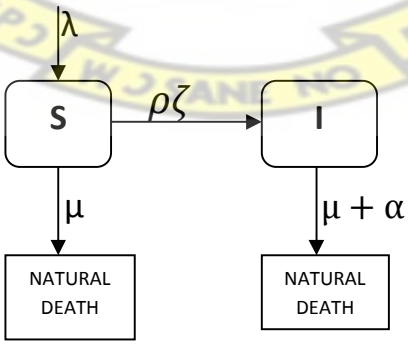

Fig.3.3: A flow diagram of the SI model.

The transfer diagram leads to the following systems of differential equations for the SI model.

$$\frac{dS}{dt} = \lambda - \rho\zeta S - \mu S$$

$$\frac{dI}{dt} = \rho\zeta S - (\mu + \alpha)I \qquad (5)$$

The parameters are positive constants. The constant λ is the recruitment rate of susceptible corresponding to births and immigration, μ is the per capita natural mortality rate.

Which, together with $N = S + I$, implies:

$$\frac{dN}{dt} = \lambda - \mu N - \alpha I \qquad (6)$$

Thus the total population size N may vary in time. In the absence of disease, the population size N converges to the equilibrium λ/μ.It follows from (6) that $\lim_{supt\to\infty} N \leq \lambda/\mu$.

From the system of nonlinear differential equations, we first consider the existence of equilibria.

For any value of parameters, the model always has a disease-free equilibrium $E_0 = (N, 0)$.

To find the positive equilibrium set:

That is

$$\frac{dS}{dt} = \frac{dI}{dt} = 0$$

In equation(5), if at $t = 0$, an infected individual is introduced into an otherwise infection-free population of susceptibles, we have initially $S = N$ and $I = 0$, and the disease-free equilibrium point is determined as

$$(S, I) \longrightarrow (N, 0).$$

When the epidemic starts, the system (5) evolves to a steady state when

$$\frac{dS}{dt} = \frac{dI}{dt} = 0$$

From (6), Since

$$\frac{dN}{dt} = \lambda - \mu N - \alpha I$$

It implies that

$$\lambda - \rho\zeta S - \mu S = 0$$

$$\rho\zeta S - (\mu + \alpha)I = 0$$

Solving for the various population groups, S and I we get

$$S^* = \frac{(\alpha + \mu)N^*}{\eta\zeta}$$

$$I^* = \frac{(\lambda - \mu N^*)}{\alpha}$$

We then investigate the behavior of the flow near equilibrium solutions using the linearization technique

The Jacobian matrix for the SI model is therefore given by:

$$J = \begin{pmatrix} -\frac{\eta\zeta I}{N} - \mu & -\frac{\eta\zeta S}{N} \\ \frac{\eta\zeta I}{N} & \frac{\eta\zeta S}{N} - (\mu + \alpha) \end{pmatrix}$$

Where $\rho = \eta I/N$

Considering the zero endemic equilibrium point, we will first shift the variables so that the origin is at the equilibrium $(S^*, I^*) = (N, 0) \rightarrow (0, 0)$ and the Jacobian matrix at the disease-free equilibrium point is obtained as,

$$J = \begin{pmatrix} -\mu & -\eta\zeta \\ 0 & \eta\zeta - (\mu + \alpha) \end{pmatrix}$$

That means that any term with higher powers of S^* and I^* are very small, so we neglect them.

Solving for the eigenvalues of the Jacobian matrix at the equilibrium points.

$$det\begin{pmatrix} -\mu - T & -\frac{\eta\zeta S}{N} \\ 0 & \eta\zeta - (\mu + \alpha) - T \end{pmatrix} = 0$$

$therefore$:

$$T = -\mu \; and \; \eta\zeta - (\alpha + \mu)$$

Where T is our eigenvalue.

Considering the non-zero endemic equilibrium point (S^*, I^*), we establish the stability of the equilibrium point (S^*, I^*) by finding the Jacobian matrix at the endemic equilibrium point and hence the eigenvalues of such Jacobian matrix:

Therefore for:

$$(S^*, I^*) = \left(\frac{(\alpha+\mu)N^*}{\eta\zeta}, \frac{(\lambda-\mu N^*)}{\alpha}\right)$$

$$J = \begin{pmatrix} -\frac{\eta\zeta I}{N} - \mu & -\frac{\eta\zeta S}{N} \\ \frac{\eta\zeta I}{N} & \frac{\eta\zeta S}{N} - (\mu+\alpha) \end{pmatrix}$$

$$J(S^*, I^*) = \begin{pmatrix} \frac{-\eta\zeta(\lambda-\mu N^*) - \alpha\mu N^*}{\alpha N^*} & -(\alpha+\mu) \\ \frac{\eta\zeta(\lambda-\mu N^*)}{\alpha N^*} & 0 \end{pmatrix} \tag{3.7}$$

(S^*, I^*) Is the non-zero endemic equilibrium point, thus the population of each type, provided (S^*, I^*) are all positive quantities.

Solving for the eigenvalues of the Jacobian matrix (3.7) above, we get

$$det\begin{pmatrix} \frac{-\eta\zeta(\lambda-\mu N^*) - \alpha\mu N^*}{\alpha N^*} - T & -(\alpha+\mu) \\ \frac{\eta\zeta(\lambda-\mu N^*)}{\alpha N^*} & -T \end{pmatrix} = 0$$

⇒

$$\left(\left(\frac{-\alpha\mu N^* - \eta\zeta(\lambda - \mu N^*)}{\alpha N^*} - T\right)T - \frac{\eta\zeta(\alpha+\mu)(\lambda - \mu N^*)}{\alpha N^*}\right) = 0$$

Hence

$$T_1, T_2 = \frac{-(\alpha\mu N^* + \eta\zeta(\lambda - \mu N^*))}{2\alpha N^*} \pm \sqrt{\left(\frac{(\alpha\mu N^* + \eta\zeta(\lambda - \mu N^*))}{2\alpha N^*}\right)^2 - \frac{\eta\zeta(\alpha+\mu)(\lambda - \mu N^*)}{\alpha N^*}}$$

Where T is the eigenvalue of the Jacobian Matrix (3.7).

Now, I would want to find the reproductive number for this model first with a simple method. In this method for finding R_0, we survey to have increase and decrease of infectives, therefore we have,

If

$$\frac{dI}{dt} > 0$$

then

$$\rho\zeta S - (\alpha+\mu)I > 0$$

$$\rho\zeta S > (\alpha+\mu)I$$

⇒

$$\frac{\rho\zeta S}{(\alpha+\mu)I} > 1$$

Where

$$\rho = \frac{\eta I}{N}$$

It implies that

$$\frac{\eta\zeta S}{N(\mu+\upsilon)} > 1 \quad \text{but at t} = 0, \text{S} \approx \text{N}$$

⇒

$$\frac{\eta\zeta}{(\mu+\upsilon)} > 1$$

If we take

$$R_0 = \frac{\eta\zeta}{(\mu+\upsilon)}$$

Therefore: $\frac{dI}{dt} > 0$, we have $R_0 > 1$.

Also if $\frac{dI}{dt} < 0$ we will get $R_0 < 1$ by similar computation as we did in the above calculation.

From the response we got from the SI epidemic model, we would want to consider a more complicated but precise model and this model is the SIA epidemic model where the infectives are compartmented into the infective class and those infectives showing symptoms of AIDS.

An SIA epidemic model of HIV/AIDS is as modeled below:

3.1 Model Parameters and Assumptions

We formulate an HIV/AIDS model by considering the population of individuals in the different groups or stages. At time t, there are $S(t)$ human susceptibles, $I(t)$ infectives who are the infected and infectious individuals that have not yet developed AIDS symptoms, $A(t)$ AIDS patients who are infected and with AIDS symptoms and $R(t)$ are individuals who dieof the AIDS. Susceptibles have sexual contacts at a rate ζ with a probability of transmission at one sexual encounter denoted by ρ. A proportion of these sexual contacts are with infectives. Let us assume there is a constant immigration rate λ of susceptible into a population of size N. We assume that susceptibles die naturally at a rate μ. We also assume AIDS patients also die a natural death at a rate μ. In addition we assume uniform mixing with the different population groups and also sexual contacts within susceptibles do not result in any transmission and thus do not feature in the model. Also, sexual contacts within infectives which give rise to issues about the role of re-infections are ignored.

Table 3.1: Presented below is a table of parameters, their descriptions and their values

Parameters	Descriptions	Values/1000
λ	Recruitment rate	28.74 births
μ	Natural death rate	9.10 deaths
ρ	Transmission probability	Not known
ζ	Number of sexual contacts	Not known
υ	Rate of progression to AIDS	10.91
σ	HIV/AIDS induced death rate	0.76 deaths

Source: WHO (2009 Ghana data)

3.2 Derivation of Equations for the SIA Model

The equations derived are for the *SIA* model for the transmission process as shown in the description of each epidemiological class below, together with a pictorial representation of the flow diagram of the disease on which I base my model.

3.2.1 *Susceptibles,* $S(t)$

Consider a constant recruitment rate λ to the susceptible population per unit time. Recruited individuals consist of maturing young persons joining the sexually active age group at a predetermined age. The recruitment term can be rewritten in terms of birth rate, maturation rates and rates of mother-to-child transmission with time lags.

Susceptibles are removed through infection or by natural death. We let μ be the natural death rate for the sexually active adults. The removal rate of susceptible through infection is the number of new HIV infections per unit time. This rate is important in calculating HIV incidence which by definition is the number of new infected persons in a specified time period divided by the number of uninfected persons that were exposed for this same time period.

3.2.2 *Number of New HIV Infections*

Let each susceptible have ζ sexual contacts per unit time. Assume that a proportion I/N of these contacts are with infectives and at each of these contacts with infectives, a susceptible has a probability ρ of getting infected.

Let $\rho\zeta$ be a function of the number of AIDS cases given by $\eta(A)$, then the total probability of one susceptible getting HIV infected from any of their sex contacts per unit time is $(\eta(A(t)))\ /\ N$. This is the expression for the force of infection. The force of infection is the probability that a susceptible will get HIV infections per unit time is given by $\eta(A(t))IS/N$.

3.2.3 *Infectives,* $I(t)$

Infectives are recruited through new HIV infections described above and removed through progression to AIDS at rate υ and through natural death at rate μ. $1/\upsilon$ is the duration spent in the infective stage and $1/\mu$ is the life expectancy of the adult population. Both of these rates assumed constant in the model.

3.2.4 *AIDS Cases, $A(t)$*

AIDS cases are recruited through progression from the infective stage to the AIDS stage and removed through AIDS accelerated deaths at rate $\sigma + \mu$ where $1/\sigma$ is the average duration spent in the AIDS stage if natural deaths are assumed constant in the model. However, allowing for variability in σ could be necessary given the advances in medical interventions and in charges in medical seeking behaviors for persons living with HIV/AIDS.

3.2.5 *A flow diagram of the disease as modeled by the system below:*

Presented below is a flow diagram that represents the SIA epidemic model for HIV/AIDS based on which we generate our systems of nonlinear differential equation.

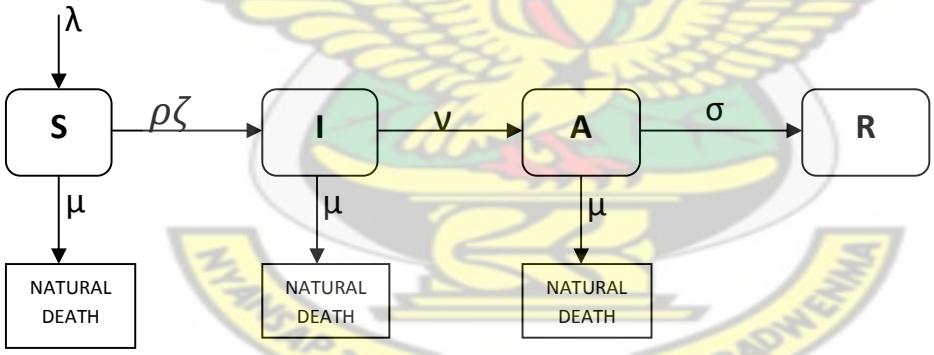

Fig.3.4: A flow diagram of the disease as modeled by the system of equations.

3.2.6 *Model Equations*

As the first step in the modeling process, we identify the independent and dependent variables. The independent variable is time t, measured in days. We consider two related sets of dependent variables.

The first set of dependent variable counts people in the groups, each as a function of time:

$S = S(t)$,is the number of susceptible individuals,

$I = I(t)$,is the number of infected individuals, and

$A = A(t)$,is the number of AIDS patients.

The second set of dependent variables represents the fraction of the total population in each of the categories.

So, if N is the total population, we have

$s(t) = S(t)/N$, the susceptible fraction of the population,

$i(t) = I(t)/N$, the infected fraction of the population, and

$a(t) = A(t)/N$, the proportion of AIDS patients in the entire population.

Looking at the two sets of dependent variables, though it seems more natural to work with population counts, working with the fraction will be my option since calculation with the fractions will make my work simpler.

It is also noted that the two set of dependent variables are proportional to each other, so either set will give us the same information about the progress of the epidemic.

From the descriptions and assumptions on the dynamics of the epidemic made above, the following are the model equations.

$$\frac{dS}{dt} = \lambda - \mu S - \rho\zeta S \tag{3.0}$$

$$\frac{dI}{dt} = \rho\zeta S - \mu I - \upsilon I \tag{3.1}$$

$$\frac{dA}{dt} = \upsilon I - \mu A - \sigma A \tag{3.2}$$

Then for the scaled variables, we have the non-linear differential equation presented below:

$$\frac{ds}{dt} = \lambda - \mu s(t) - \rho\zeta s(t) \tag{3.4}$$

$$\frac{di}{dt} = \rho\zeta s(t) - \mu i(t) - \upsilon i(t) \tag{3.5}$$

$$\frac{da}{dt} = \upsilon i(t) - \mu a(t) - \sigma a(t) \tag{3.6}$$

$$s(t) + i(t) + a(t) = 1 \tag{3.4}$$

Where N is the total size of the population and $\rho = \eta I/N$. Thus, S, I, A are all bounded above by N.

The mathematical formulation of the epidemic problem is completed given initial conditions such as

$$S(0) = S_0 > 0, I(0) = I_0 > 0, A(0) = A_0 > 0$$

3.3 Stability of Fixed Point of the Nonlinear SIA Epidemic Equations

3.3.1 *Determination of Stability by Linearization*

Let $f:\mathbb{R}^n \to \mathbb{R}^n$ be a C^1 map and suppose that p is a point such that $f(p) = 0$, that is, p is a fixed point for the differential equation below:

$$x'(t) = f(x(t)).$$

The linear part of f at p, denoted $Df(p)$, is the matrix of partial derivatives at p; For $x \in \mathbb{R}^n$, $f(x) \in \mathbb{R}^n$, so we can write:

$$f(x) = \begin{pmatrix} f_1(x) \\ f_2(x) \\ . \\ . \\ . \\ f_n(x) \end{pmatrix}$$

The function f_i are called the component functions of f.

We define

$$Df(p) = \begin{pmatrix} \frac{\partial f_1}{\partial x_1}(p) & \frac{\partial f_1}{\partial x_2}(p) & \dots & \frac{\partial f_1}{\partial x_n}(p) \\ \frac{\partial f_2}{\partial x_1}(p) & \frac{\partial f_2}{\partial x_2}(p) & \dots & \frac{\partial f_2}{\partial x_n}(p) \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\partial f_n}{\partial x_1}(p) & \frac{\partial f_n}{\partial x_2}(p) & \dots & \frac{\partial f_n}{\partial x_n}(p) \end{pmatrix}$$

Since f is C^1, Taylor's theorem for functions of several variables says that

$$f(x) = Df(p)(x-p) + g(x),$$

Where $f(p) = 0$ and g is a function that is small near p in the sense that

$$\lim_{x \to p} \frac{|g(x)|}{|x-p|} = 0$$

3.3.2 *Proof of Linearization of the SIA Epidemic Model:*

Consider the system of *SIA* epidemic model

$$\dot{S} = f(S, I, A)$$

$$\dot{I} = g(S, I, A)$$

$$\dot{A} = h(S, I, A)$$

and suppose that (S^*, I^*, A^*) is a fixed point.

That is

$$f(S^*, I^*, A^*) = 0$$

$$g(S^*, I^*, A^*) = 0$$

$$h(S^*, I^*, A^*) = 0.$$

Let

$$U = S - S^*$$

$$V = I - I^*$$

$$W = A - A^*$$

denote the components of a small disturbance from the fixed point. To see whether the disturbance grows or decays, we need to derive differential equations for U, V and W.

Let's do the U-equation first:

$\dot{U} = \dot{S}$(Since S^* is a constant)

$= f(S^* + U, I^* + V, A^* + W)$ (by substitution)

$= f(S^*, I^*, A^*) + U\frac{\partial f}{\partial s} + V\frac{\partial f}{\partial I} + W\frac{\partial f}{\partial A} + O(U^3, V^3, W^3, UVW)$

(Taylor's series expansion)

$= U\frac{\partial f}{\partial s} + V\frac{\partial f}{\partial I} + W\frac{\partial f}{\partial A} + \mathrm{O}(U^3, V^3, w^3, UVW)$ $since\ f(U^*, V^*, W^*) = 0$

It should be noted that these partial derivatives will be evaluated at the fixed point (S^*, I^*, A^*); that is they are numbers and not functions. Also, the notation $\mathrm{O}(S^*, I^*, A^*)$ denote quadratic terms in U, V and W. since U, V and W are small, these quadratic terms are extremely small.

Similarly, we find $V$and W. That is:

$$\dot{V} = U\frac{\partial g}{\partial S} + V\frac{\partial g}{\partial I} + W\frac{\partial g}{\partial A} + \mathrm{O}(S^*, I^*, A^*)$$

.

$$\dot{W} = U\frac{\partial h}{\partial S} + V\frac{\partial h}{\partial I} + W\frac{\partial h}{\partial A} + \mathrm{O}(S^*, I^*, A^*).$$

Hence the disturbance (U, V, W) evolves according to

$$\begin{pmatrix} \dot{U} \\ \dot{V} \\ \dot{W} \end{pmatrix} = \begin{pmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} & \frac{\partial f}{\partial A} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} & \frac{\partial g}{\partial A} \\ \frac{\partial h}{\partial S} & \frac{\partial h}{\partial I} & \frac{\partial h}{\partial A} \end{pmatrix} \begin{pmatrix} U \\ V \\ W \end{pmatrix} + quadratic\ terms. \qquad (3.5)$$

The matrix

$$J = \begin{pmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} & \frac{\partial f}{\partial A} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} & \frac{\partial g}{\partial A} \\ \frac{\partial h}{\partial S} & \frac{\partial h}{\partial I} & \frac{\partial h}{\partial A} \end{pmatrix}_{(S^*, I^*, A^*)}$$

is called the Jacobian matrix at the fixed point(S^*, I^*, A^*).

Now since the quadratic terms in (1) are tiny, it's tempting to neglect them altogether. If we do that, we obtain the linearized system

$$\begin{pmatrix} \dot{U} \\ \dot{V} \\ \dot{W} \end{pmatrix} = \begin{pmatrix} \frac{\partial f}{\partial S} & \frac{\partial f}{\partial I} & \frac{\partial f}{\partial A} \\ \frac{\partial g}{\partial S} & \frac{\partial g}{\partial I} & \frac{\partial g}{\partial A} \\ \frac{\partial h}{\partial S} & \frac{\partial h}{\partial I} & \frac{\partial h}{\partial A} \end{pmatrix} \begin{pmatrix} U \\ V \\ W \end{pmatrix}$$

3.3.3 *Calculations*

Theorem 1.0:

Let $S(t), I(t)$ and $A(t)$ be solution to model $(3.0) - (3.2)$

1. If $R_0 \leq 1$, then $\lim_{t\to\infty} I(t) = 0$ and we have a disease free equilibrium.
2. If $R_0 > 1$, then $\lim_{t\to\infty}(S(t), I(t), A(t)) = (\frac{\upsilon+\mu}{\rho\zeta}, \frac{(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon}, \frac{\lambda-\mu N^*}{\sigma})$

3.3.3.1 *Steady State Equilibrium*

Because of the biological meaning of the components $\big(S(t), I(t), A(t)\big)$, we focus on the model in the first octant of $\mathbb{R}^3$.we first consider the existence of equilibria of system $(3.0) - (3.3)$. For any value of parameters, model $(3.0) - (3.3)$ always has a disease-free equilibrium $E_0 = (N, 0,0)$.

To find the positive equilibrium set:

That is

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = 0$$

In equation $(3.0) - (3.3)$, if att $= 0$, an infected individual is introduced into an otherwise infection-free population of susceptible, we have initially $S = N, I = 0, \text{and } A = 0$ and the disease-free equilibrium point is determined as

$$(S, I, A) \longrightarrow (N, 0, 0).$$

When the epidemic starts, the system $(3.0) - (3.3)$ evolves to a steady state when

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dA}{dt} = 0$$

Since

$$N = S(t) + I(t) + A(t)$$

$$\frac{dN}{dt} = \lambda - \mu S - \mu I - \mu A - \sigma A$$

$$= \lambda - \mu N - \sigma A$$

It implies that

$$\lambda - \rho\zeta S - \mu S = 0$$

$$\rho\zeta S - \upsilon I - \mu I = 0$$

$$\upsilon I - \sigma A - \mu A = 0$$

Solving for the various population groups, S, I, A we get

$$S^* = \frac{(\upsilon + \mu)N^*}{\eta\zeta}$$

$$I^* = \frac{(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon}$$

$$A^* = \frac{(\lambda - \mu N^*)}{\sigma}$$

$$(S^*, I^*, A^*) = \left(\frac{(\upsilon + \mu)N^*}{\eta\zeta}, \frac{(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon}, \frac{(\lambda - \mu N^*)}{\sigma}\right)$$

3.3.3.2 *Linearization of Equation*

In this section we investigate the behavior of the flow near equilibrium solutions using the linearization technique and connect it to the Hartman-Grobman theorem, which relates a nonlinear system to the corresponding linear one near the equilibrium.

The Jacobian matrix for the SIA model is therefore given by:

$$J = \begin{pmatrix} -\frac{\eta\zeta I}{N} - \mu & -\frac{\eta\zeta S}{N} & 0 \\ \frac{\eta\zeta I}{N} & \frac{\eta\zeta S}{N} - (\upsilon + \mu) & 0 \\ 0 & \upsilon & -(\sigma + \mu) \end{pmatrix}$$

Where $\rho = \eta I/N$

Considering the zero endemic equilibrium point, we will first shift the variables so that the origin is at the equilibrium $(S^*, I^*, A^*) = (N, 0, 0) \rightarrow (0, 0, 0)$and the Jacobian matrix at the disease-free equilibrium point is obtained as,

$$J(N,0,0) = \begin{pmatrix} -\mu & -\eta\zeta & 0 \\ 0 & \eta\zeta - (\upsilon + \mu) & 0 \\ 0 & \upsilon & -(\sigma + \mu) \end{pmatrix} \tag{3.6}$$

we are only considering small derivatives from the equilibrium, so that S^*, I^*, A^* are small.

That means that any term with higher powers of S^*, I^* and $A^*$are very small, so we neglect them.

Solving for the eigenvalues of the Jacobian matrix (3.6),we get

$$\det\begin{pmatrix} -\mu - T & -\eta\zeta & 0 \\ 0 & \eta\zeta - (\upsilon + \mu) - T & 0 \\ 0 & \upsilon & -(\sigma + \mu) - T \end{pmatrix} = 0$$

$$\Rightarrow \quad (\mu + T)((\sigma + \mu) + T)(\eta\zeta - (\upsilon + \mu) - T) = 0$$

$therefore$: $(\mu + T) = 0,$

$$(\sigma + \mu) + T = 0 \quad \text{or}$$

$$\left(\eta\zeta - \left((\upsilon + \mu)\right) - T\right) = 0$$

Hence

$$T = -\mu, -(\sigma + \mu) \; and \; \eta\zeta - (\upsilon + \mu)$$

Where T is our eigenvalue.

Considering the non-zero endemic equilibrium point (S^*, I^*, A^*), we find the Jacobian matrix at the endemic equilibrium point:

$$(S^*, I^*, A^*) = (\frac{(\upsilon + \mu)N^*}{\eta\zeta}, \frac{(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon}, \frac{(\lambda - \lambda N^*)}{\sigma})$$

.

$$J(S^*, I^*, A^*) = \begin{pmatrix} \frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & -(\mu + \upsilon) & 0 \\ \frac{\eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & 0 & 0 \\ 0 & \upsilon & -(\sigma + \mu) \end{pmatrix} \quad (3.7)$$

(S^*, I^*, A^*) is non-zero endemic equilibrium point, thus the population of each type, provided (S^*, I^*, A^*) are all positive quantities.

Solving for the eigenvalues of the Jacobian matrix (3.5) above, we get

$$det \begin{pmatrix} \frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} - T & -(\mu + \upsilon) & 0 \\ \frac{\eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & -T & 0 \\ 0 & \upsilon & -(\sigma + \mu) - T \end{pmatrix} = 0$$

⇒

$$\left(\left(\frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} - T\right)T - (\mu+\upsilon)\frac{\eta\zeta(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*}\right)\big((\sigma+\mu)+T\big)$$

$$= 0$$

Therefore

$$\big((\sigma+\mu)+T\big) = 0$$

or

$$\left(\left(\frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} - T\right)T - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*}\right) = 0$$

Hence

$$T = -(\sigma+\mu),$$

and

$$\frac{-(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}$$

$$\pm\sqrt{\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*}}$$

Where T is the eigenvalue of the JacobianMatrix (3.7).

Further analysis of these results will be carried out in the chapter IV of this thesis.

3.4 Reproductive Number

One of the fundamental questions of mathematical epidemiology is to find threshold conditions that determine whether an infectious disease will spread in a susceptible population when the disease is introduced into the population.

The threshold conditions are characterized by the so-called reproductive number, the reproduction number, the reproductive ratio, basic reproductive value, basic reproductive rate, or contact number, commonly denoted by R_0 in mathematical epidemiology.

In epidemiology, the basic reproduction number of an infection is the mean number of secondary cases a typical single infected case will cause in a population with no immunity to the disease in the absence of interventions to control the infection or it is the average number of susceptible who can be infected by a typical infective in a population in which everybody is considered as susceptible.

The reproductive number defines the direction of the disease. This can be written mathematically as:

$$R_0 = T^* * (infectious\ period) + 1$$

$$infectious\ period = \frac{1}{Rate\ of\ change}$$

and T^* $is\ the\ dominant\ eigenvalue$.

The basic reproductive rate is affected by several factors including the duration of infectivity of affected patients, the infectiousness of the organism, and the number of susceptible people in the population that the affected patients are in contact with.

3.4.1 *Calculations*

Now, I would want to find the reproductive number for this model first with a simple method. In this method for finding R_0, we survey to have increase and decrease of infectives, therefore we have:

If

$$\frac{dI}{dt} > 0$$

then

$$\rho\zeta S - (\mu + \upsilon)I > 0$$

$$\rho\zeta S > (\mu + \upsilon)I$$

$$\Rightarrow$$

$$\frac{\rho\zeta S}{(\mu + \upsilon)I} > 1$$

Where

$$\rho = \frac{\eta I}{N}$$

It implies that

$$\frac{\eta\zeta S}{N(\mu + \upsilon)} > 1 \qquad \text{but at t} = 0, \text{S} \approx \text{N}$$

$$\Rightarrow$$

$$\frac{\eta\zeta}{(\mu + \upsilon)} > 1$$

If we take

$$R_0 = \frac{\eta\zeta}{(\mu + \upsilon)}$$

Therefore: $\frac{dI}{dt} > 0$, we have$R_0 > 1$.

Also if $\frac{dI}{dt} < 0$ we will get $R_0 < 1$ by similar computation as we did in the above calculation.

It should be noted that the basic reproductive number 3.6.1 can be used to determine the dynamics of the model (3.0) − (3.2), hence further analysis of these result will be made in the chapter IV of this thesis.

CHAPTER FOUR

ANALYSIS AND NUMERICAL SIMULATIONS OF THE MODEL

4.0 Introduction:

In this section, we will be looking at the implications of the results we got in the chapter three of my thesis. This will involve a study of the significance of the various eigenvalues and the reproductive number as well as the MatLab simulation result to the stability of the system of differential equations.

4.1 Analytic Study of Results:

In this section, we are going to present a detailed study into the results we obtained in the chapter III of this thesis. Although numerical solutions are very important besides analytic result, it is very necessary to use both tools to establish explicit conclusions to our study.

From chapter III, we considered the zero endemic equilibrium point and the Jacobian matrix at the disease-free equilibrium point were obtained as:

$$J(N,0,0) = \begin{pmatrix} -\mu & -\eta\zeta & 0 \\ 0 & \eta\zeta - (\upsilon + \mu) & 0 \\ 0 & \upsilon & -(\sigma + \mu) \end{pmatrix} \tag{4.3}$$

We only considered small derivatives from the equilibrium, so that S^*, I^*, A^* are small.

That means that any term with higher powers of S^*, I^* and A^* are very small, so we neglected them.

Solving for the eigenvalues of the Jacobian matrix (4.3) we got

$$\det\begin{pmatrix} -\mu - T & -\eta\zeta & 0 \\ 0 & \eta\zeta - (\upsilon + \mu) - T & 0 \\ 0 & \upsilon & -(\sigma + \mu) - T \end{pmatrix} = 0$$

Hence

$$T_1, T_2 \; and \; T_3 = -\mu, -(\sigma + \mu) \; and \; \eta\zeta - (\upsilon + \mu)$$

Where the $T's$ are our eigenvalues.

From the above jacobian matrix, we are getting negative values of the eigenvalue given that $\mu \; and \; (\sigma + \mu)$ are all positive for any positive values of $\mu, \sigma \; and \; \upsilon$. From the first two results of our eigenvalues, it is so obvious that we obtain negative values.

This goes to explain the fact that at the non-endemic equilibrium point, the state of the system can be estimated in either of two ways, that is the system experiences a nodal sink provided $\eta\zeta < (\upsilon + \mu)$ and hence the system will be in a state of total stability and this explains that either there is no body in the population infected with the HIV/AIDS disease or there are some infectives in the population but the disease spread are completely under control.

Now if $\eta\zeta > (\upsilon + \mu)$, then the system will now have a saddle point.

Considering the non-zero endemic equilibrium point (S^*, I^*, A^*), we found the Jacobian matrix at the endemic equilibrium point:

$$(S^*, I^*, A^*) = (\frac{(\upsilon + \mu)N^*}{\eta\zeta}, \frac{(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon}, \frac{(\lambda - \lambda N^*)}{\sigma})$$

.

$$J(S^*, I^*, A^*) = \begin{pmatrix} \frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & -(\mu + \upsilon) & 0 \\ \frac{\eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & 0 & 0 \\ 0 & \upsilon & -(\sigma + \mu) \end{pmatrix} \quad (4.4)$$

(S^*, I^*, A^*) is the non-zero endemic equilibrium point. Thus the population of each type, provided (S^*, I^*, A^*) are all positive quantities.

Solving for the eigenvalues of the Jacobian matrix (3.5) above, we got

$$det\begin{pmatrix} \frac{-\mu\sigma\upsilon N^* - \eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} - T & -(\mu + \upsilon) & 0 \\ \frac{\eta\zeta(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*} & -T & 0 \\ 0 & \upsilon & -(\sigma + \mu) - T \end{pmatrix} = 0$$

Therefore:

$$T_1 = -(\sigma + \mu),$$

Or

$$T_2, T_3 = \frac{-(\mu\sigma\upsilon N^* + \eta\zeta(\sigma + \mu)(\lambda - \mu N^*))}{2\sigma\upsilon N^*} \pm \sqrt{\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma + \mu)(\lambda - \mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu + \upsilon)(\sigma + \mu)(\lambda - \mu N^*)}{\sigma\upsilon N^*}}$$

Where T_1, T_2, T_3 are the eigenvalue of the Jacobian Matrix (4.4).

From the above results of the eigenvalues, we can study the entire system by considering the nature of the eigenvalues. From the result of the eigenvalues above we realize that, its first value T_1 is negative for positive values of the respective rates, μ *and* σ.

Also considering the second set of values for the eigenvalues, we will use the discriminate analysis to establish the behavior of the system with such an eigenvalue. We can now conclude on the behavior of the system based on the analysis on the operations below.

Considering the case where $\lambda > \mu N^*$ for all the cases below, Then if:

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} < 0$$

Then the eigenvalues T_2 *and* T_3, are complex conjugate, this goes to explain the fact that in this case the system will have a spiral sink at $\lambda > \mu N^*$ since T_1, T_2 *and* T_3 have a negative real part.

Since we realize that the eigenvalues of the Jacobian matrix have a negative real value and two complex conjugate with negative real part at $\lambda > \mu N^*$, if the discriminant is less than zero, then the system experiences a spiral sink at the equilibrium. That means the system have a certain form of oscillatory behavior at equilibrium while its solution still moves to stable direction.

In other words, the system behaves in a damped oscillatory manner with a certain period determined by the parameters.

Also if

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} > 0$$

Then we will get two real eigenvalues ,T_2 *and* T_3. This goes to explain the fact that the system will be a nodal sink at $T_2 < 0$ *and* $T_3 < 0$ but the system will experience a saddle point at either$T_2 > 0$ *or* $T_3 > 0$ *or both* for $\lambda > \mu N^*$seeing $T_1 < 0$.

Since we have a negative real value and two distinct real values if the discriminant is greater than zero, it implies that the system experiences a nodal sink at the equilibrium if and only if the two distinct real values are both negative else the system experiences a saddle point . This means the system moves to stable direction if and only if the two distinct real values are both negative else the system experiences a state of instability.

If:

$$\left(\frac{(\mu\sigma\upsilon N^{*}+\eta\zeta(\sigma+\mu)(\lambda-\mu N^{*}))}{2\sigma\upsilon N^{*}}\right)^{2}-\frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^{*})}{\sigma\upsilon N^{*}}=0,$$

Then

$$T=\frac{-(\mu\sigma\upsilon N^{*}+\eta\zeta(\sigma+\mu)(\lambda-\mu N^{*}))}{2\sigma\upsilon N^{*}}$$

This implies that at the case where $\lambda > \mu N^{*}$,we will get one repeated eigenvalues, T which is negative hence a nodal sink is established.

Considering the case where the discriminant is equal to zero. This measures a stable system since the eigenvalues of the Jacobian matrix have a negative real value and one repeated value hence a nodal sink is established.

Also:

Considering the case where $\lambda < \mu N^*$ for all the cases below, Then if:

$$\left(\frac{(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*))}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} < 0$$

Then the eigenvalues T_2 *and* T_3, are complex conjugate, this goes to explain the fact that in this case the system will have a saddle point at $\lambda < \mu N^*$ since $T_1 < 0$ *while* T_2 *and* T_3 both have a positive real part.

Also if:

$$\left(\frac{\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} > 0$$

Then we will get two real eigenvalues,T_2 *and* T_3. This goes to explain the fact that the system will be a saddle point at either $T_2 > 0$ *or* $T_3 > 0$ *or both* for $\lambda < \mu N^*$ seeing that $T_1 < 0$.

If:

$$\left(\frac{\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}\right)^2 - \frac{\eta\zeta(\mu+\upsilon)(\sigma+\mu)(\lambda-\mu N^*)}{\sigma\upsilon N^*} = 0,$$

Then

$$T_2, T_3 = \frac{-\left(\mu\sigma\upsilon N^* + \eta\zeta(\sigma+\mu)(\lambda-\mu N^*)\right)}{2\sigma\upsilon N^*}$$

This implies that at the case where $\lambda < \mu N^*$, we will get one repeated eigenvalue, T which are positive hence a saddle point is established.

From the above analysis, we realize that at $\lambda < \mu N^*$, the eigenvalues of the Jacobian matrix will have a negative real value and two complex conjugate with positive real part if the discriminant is less than zero, a negative real value and two distinct real values or a negative real value and one repeated real value which are positive, hence the system experiences a saddle point at the equilibrium with all the cases considered at $\lambda < \mu N^*$. That means the system experience a state of instability at all the cases where $\lambda < \mu N^*$. In other words, the system will experience an outbreak of the disease.

In all the analysis made in our analytic study, when given the model parameter values, the period of the oscillation plays a role in predicting further, the behavior of the infections.

We also considered what the reproductive number is and the relationship it has with rate of change of infectives in the population and hence, can be used to determine the dynamics of the model $(3.0) - (3.2)$.

The reproductive number defines the direction of the disease. This can be written mathematically as:

$$R_0 = T^* * (infectious\ period) + 1$$

$$infectious\ period = \frac{1}{Rate\ of\ change}$$

and T^* *is the dominant eigenvalue*.

Now, calculating for the reproductive number of model $(3.0) - (3.2)$, using the simple method. In this method for finding R_0, we survey to have increase and decrease of infectives, therefore we have,

If

$$\frac{dI}{dt} > 0$$

then

$$\rho\zeta S - (\mu + \upsilon)I > 0$$

$$\rho\zeta S > (\mu + \upsilon)I$$

$$\Rightarrow \quad \frac{\rho\zeta S}{(\mu + \upsilon)I} > 1$$

Where

$$\rho = \frac{\eta I}{N}$$

It implies that

$$\frac{\eta\zeta S}{N(\mu + \upsilon)} > 1 \quad \text{but at t} = 0, \text{S} \approx \text{N}$$

⇒

$$\frac{\eta\zeta}{(\mu+\upsilon)} > 1$$

If we take

Then for $\frac{dI}{dt} > 0$, we have $R_0 > 1$.

Now, $if\ the\ system\ enters\ a\ stage\ where\ R_0 > 1$, then it is said to be asymptotically unstable and this implies that there will be a serious outbreak of the HIV/AIDS epidemic in the country provided the rate of change of infectives is positive.

Also:

$$if\ \frac{dI}{dt} < 0, we\ will\ get\ R_0 < 1$$

$by\ similar\ computation\ as\ in\ the\ above\ calculation,$ this will imply that the system will be in a state of total stability and hence the entire population will be free from the opportunistic infection(HIV-epidemic).

We also looked at when the system will develop an epidemic using the basic reproductive rate. In doing this we consider the case where the infection rate is greater than zero, which means that we have increasing number of infectives in the system and this will give us a reproductive rate which is greater than 1, hence the system experiences an outbreak of HIV/AIDS epidemic since the system is asymptotically unstable in this case.

We also consider the case where the infection rate is negative, which means that we have decreasing number of infectives in the system and this will result in a case where the reproductive rate is less than 1, hence the system experiences stability which implies that the entire population will be free from the opportunistic infection.

Infact, the results of our numerical simulations is a confirmation of the results we had in the analytic study as well as the graphical results.

4.2 Numerical Simulation:

This section will be established based on the idea of mathematical simulations using MatLab. In this respect we present computer simulations of the system $(3.0) - (3.2)$.

We take the parameters of the system as presented in the tables below taken our total population as $\mathrm{N} = 24791073$.

We finally complete the model by given each differential equation an initial condition. Since none of the population is immune at the beginning of the epidemic, we assume that almost everyone in the population is susceptible. We also assume a trace level of infection in the population, that is:

$$\mathrm{S}(0) = 24791073, \quad \mathrm{I}(0) = 15, \quad \mathrm{A}(0) = 0$$

In terms of the scaled variables, the initial conditions are:

$$s(0) = 1,$$

$$i(0) = 6.051 \times 10^{-7},$$

$$a(0) = 0$$

This will be the variables with which the graphing will be appropriately presented.

For each table of parameter values, we have graphical results to our differential model as well as the phase portrait.

Table 4.1: Parameter values in respect of low rate of infection with a high rate of conversion from infectives to AIDS and low AIDS accelerated death rates

Parameters of the system	λ	μ	ρ	ζ	υ	σ
Values of the (Parameters)/year	13249.5	0.00025	0.06	2	0.825	0.524

We also assume values for the different population groups such that if $(S(0), I(0), A(0)) = (24791073,15,0)$ then $E_0 = (24791073,0,0)$ and $R_0 = 0.1455 < 1$.

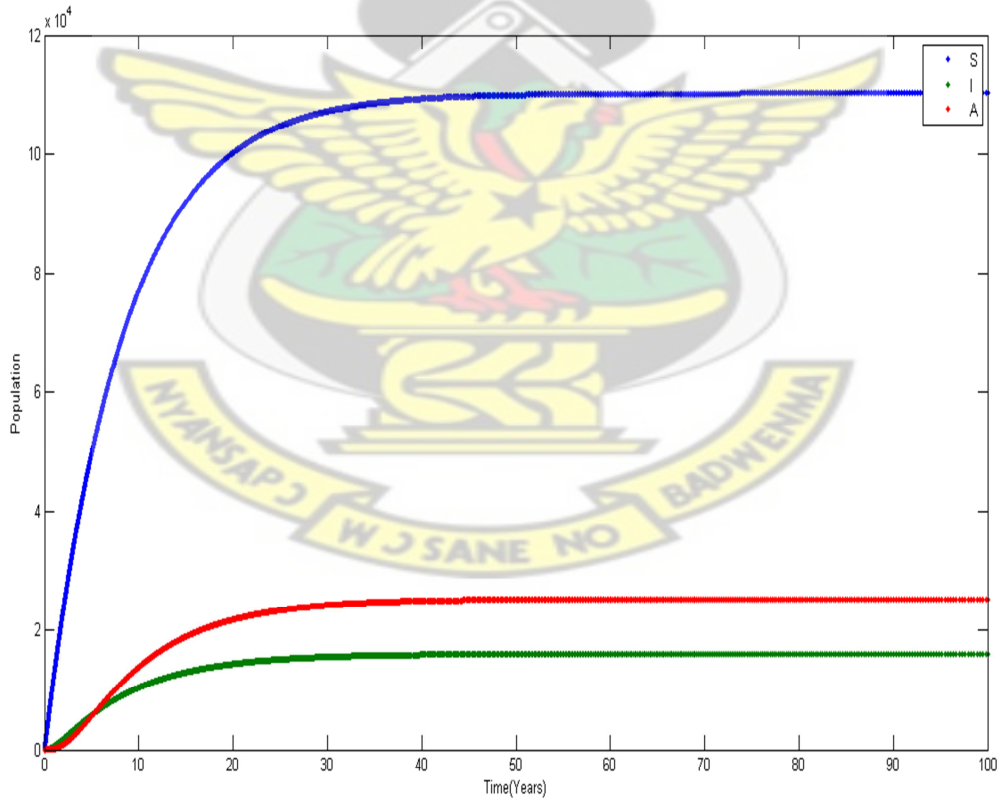

Fig. 4.1a: Numerical solution of the model with parameters from Table 4.1.

The above graph (Fig. 4.1a), gives the proportion of susceptible, infective and AIDS patients with time, showing that the system is stable as the proportion of susceptible in the population takes a sharp increase until its size attains equilibrium after 40year of growth as compared to the other class of population.

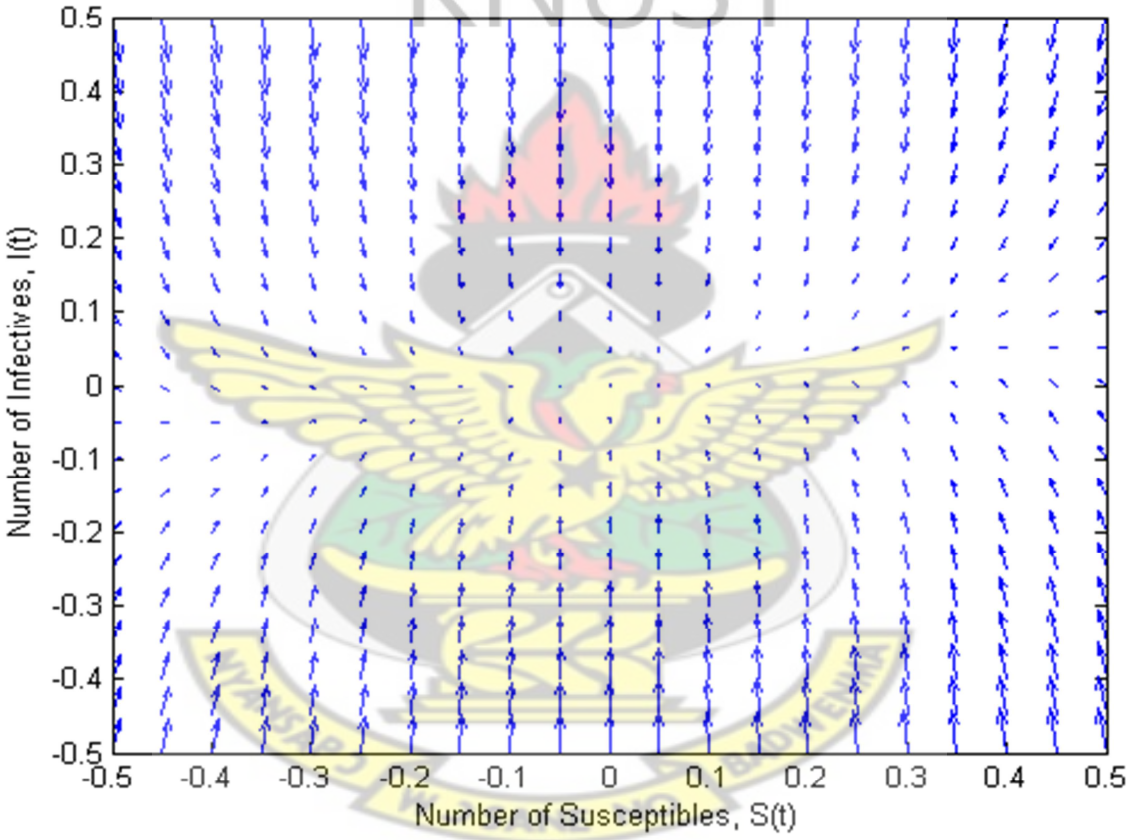

Fig. 4.1b: A phase portrait showing the stability situation of the differential model.

The above phase portrait (Fig. 4.1b) is a representation of a stable system with all the field lines converging at a point. This figure demonstrates a stability situation called a nodal sink.

Table 4.2: Parameter values in respect of high rate of infection with a high rate of conversion from infectives to AIDS and high AIDS accelerated death rates

Parameters of the system	λ	μ	ρ	ζ	υ	σ
Values of the (Parameters)/year	13249.5	0.00025	0.06	12	0.825	2.334

We also assume values for the different population groups such that if $(S(0), I(0), A(0)) = (24791073,15,0)$ then $E_0 = (24791073,0,0)$ and $R_0 = 0.87273 < 1$.

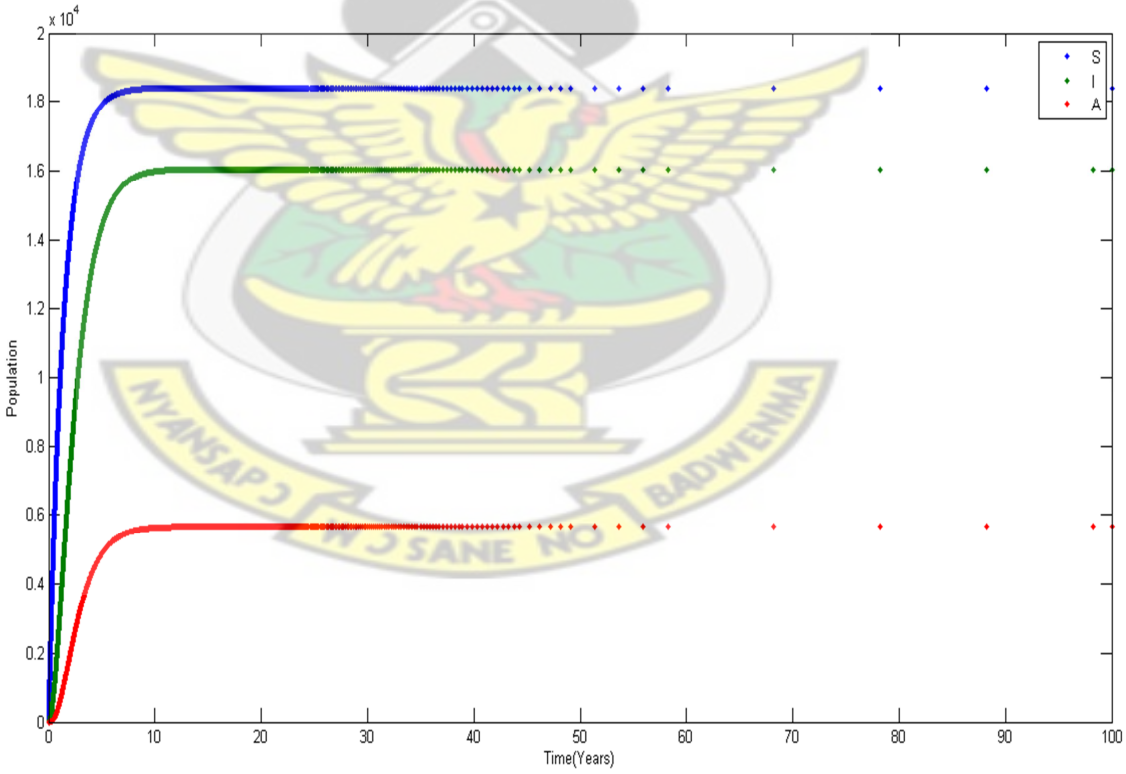

Fig. 4.2a: Numerical solution of the model with parameters from Table 4.2.

The above graph (Fig. 4.2a) gives the proportion of susceptible, infective and AIDS patients with time, Showing that the system is stable as the proportion of susceptible in the population takes a sharp increase until its size attains equilibrium before 10year of growth with those infected also increasing at a relatively low rate as compared to the susceptible growth with less AIDS patients.

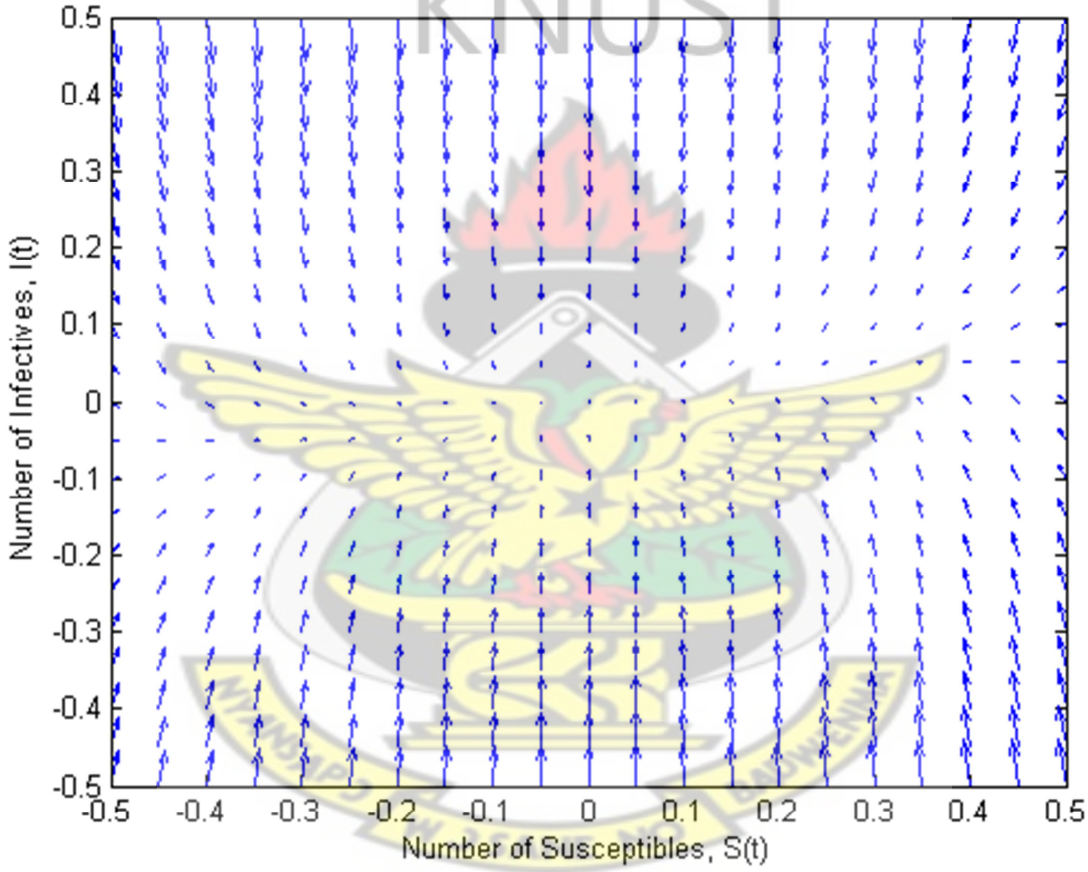

Fig. 4.2b: A phase portrait showing the stability situation of the differential model.

The above phase portrait (Fig. 4.2b) is a representation of a stable system with all the field lines converging at a point. This figure demonstrates a stability situation called a nodal sink.

Table 4.3: Parameter values in respect of low rate of infection with a low rate of conversion from infectives to AIDS and high AIDS accelerated death rates

Parameters of the system	λ	μ	ρ	ζ	υ	σ
Values of the (Parameters)/year	13249.5	0.00025	0.06	4	0.225	2.524

We also assume values for the different population groups such that $(S(0), I(0), A(0)) = (24791073,15,0)$. Then $E^*(S^*, I^*, A^*) = (14.078,31344.134,2793.872)$ and $R_0 = 1.0667 > 1$

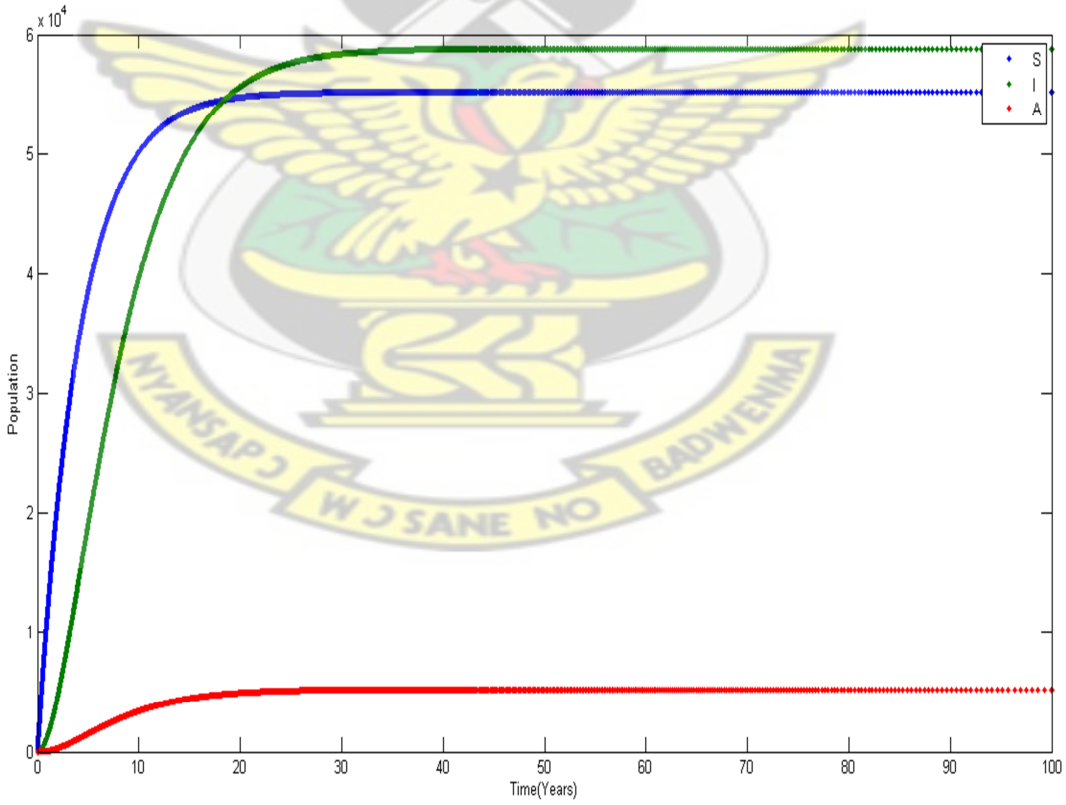

Fig. 4.3a: Numerical solution of the model with parameters from Table 4.3.

The above graph (Fig. 4.3a) gives the proportion of susceptible, infective and AIDS patients with time, showing that the system is unstable as the proportion of susceptible and infectives in the population takes a sharp increase until they both attain convergence at time greater than 15years but less than 20years whilst the AIDS cases registers a very low proportion of people. We also noticed that the size of the susceptible population takes a short time to stabilize unlike those belonging to the infected class who take averagely longer time to attain a constant value. In fact this is enough prove of the fact that the system will be unstable.

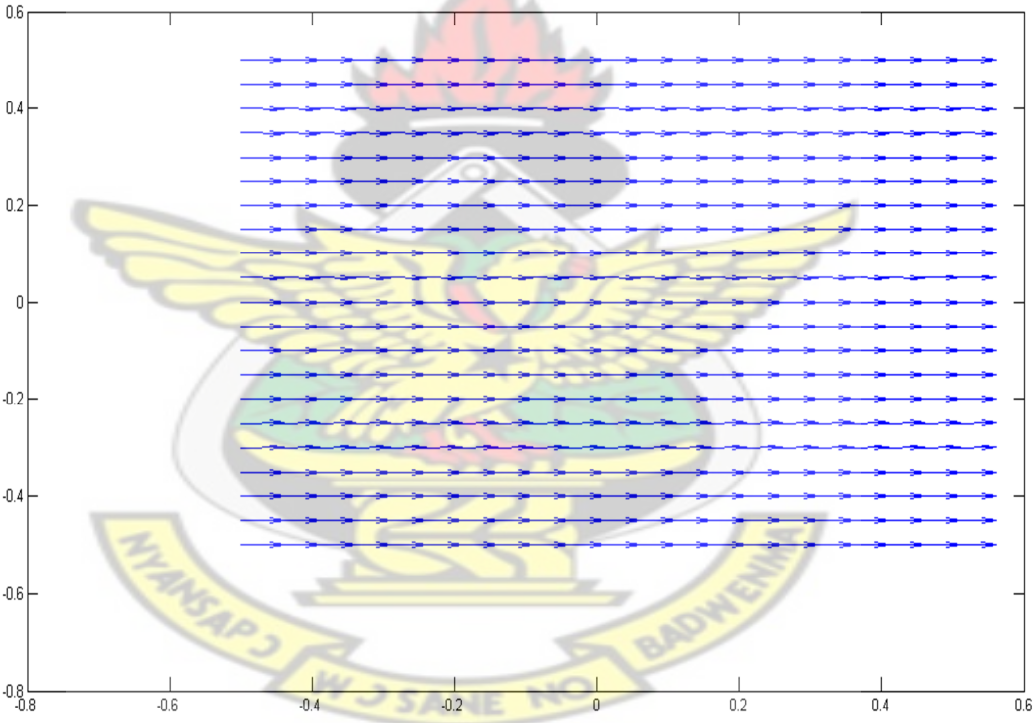

Fig. 4.3b: A phase portrait showing the stability situation of the differential model.

The above phase portrait (Fig. 4.3b) is a representation of an unstable system with some of the field lines moving away from the origin. This figure demonstrates a situation of instability called a saddle.

Table 4.4: Parameter values in respect of high rate of infection with a high rate of conversion from infectives to AIDS and low AIDS accelerated death rates

Parameters of the system	λ	μ	ρ	ζ	υ	σ
Values of the (Parameters)/year	13249.5	0.00025	0.06	14	0.825	0.524

We also assume values for the different population groups such that $(S(0), I(0), A(0)) = (24791073,15,0)$. Then $E^*(S^*, I^*, A^*) = (14.733,8551.632,13457.503)$ and $R_0 = 1.0182 > 1$

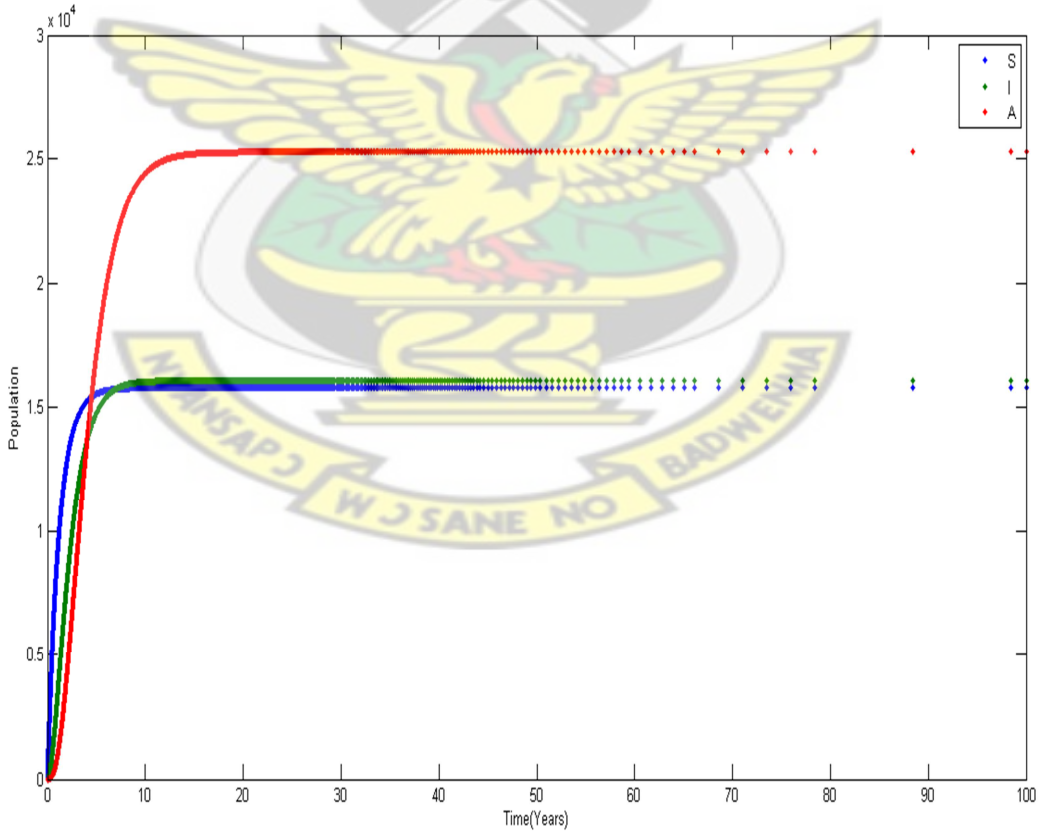

Fig. 4.4a: Numerical solution of the model with parameters from Table 4.3.

The above graph (Fig. 4.4a) gives the proportion of susceptible, infective and AIDS patients with time. We realize a system with an epidemic as it's clearly demonstrated by the graph. This has a high progression of the infectives into the AIDS zone and fairly high proportion of people leaving the susceptible group into the infective class, hence an unstable system.

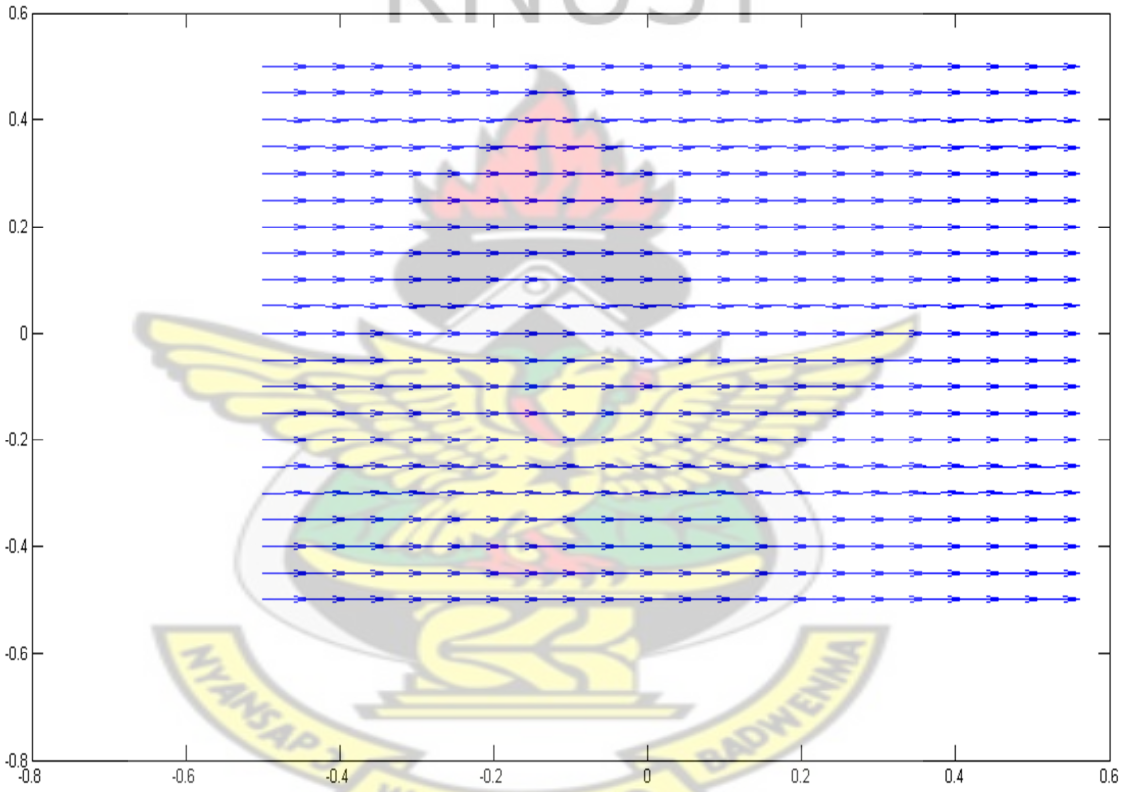

Fig. 4.4b: A phase portrait showing the stability situation of the differential model.

The above phase portrait (Fig. 4.4b) is a representation of an unstable system with some of the field lines moving away from the origin. This figure demonstrates a situation of instability called a saddle.

CHAPTER FIVE

CONCLUSION AND RECOMMENDATIONS

5.0 Introduction

At present, however, almost all the developing countries have increasingly realized the necessity of social consciousness in preventing the HIV/AIDS epidemic. Also different protective measures against diseases are found to be effective.

One main goal of mathematical epidemiology is to understand how to control or eradicate diseases. We therefore seek to explain the dynamical behavior of the nonlinear differential equation and how different types of models are used to capture the essential behavioral of a population and the biological features (Natural history) of the infection.

In this section of the thesis, we seek to give a description and analysis of the various mathematical techniques used to mimic the operations of the real-life process described in the SIA epidemic model as presented in the *CHAPTER IV* of this thesis.

These mathematical techniques used in the analysis of the model are analytic study and numerical simulations using MatLab.

5.1 Conclusion

We have investigated the transmission dynamics of an SIA epidemic model with positive immigration. We have also characterized the equilibrium and thresholds and shown how they are affected by the immigration profile.

Much of the theory at the basis of the modern control of infectious diseases (Anderson and May, 1991) has been developed around the equilibrium analysis of the basic SIR age-structured model in a closed stationary population in which the recruitment of susceptible occurs at birth only.

After a series of analysis made with respect to the various models, we realize in conclusion that in almost all the cases where $\lambda > \mu N^*$, the system realized a total stability but in all the cases where $\lambda < \mu N^*$ the system is always unstable.

We are also able to establish that in situations where net transmission rates is very small as compared to the rate of progression to AIDS, the system experience stability. Hence increasing the birth rate (immigration rate), increasing AIDS progression rate relative to the net transmission rate and Minimizing net Transmission for almost all cases may eradicate HIV/AIDS, but would give long incubation period for AIDS since from our assumption $\upsilon \gg \mu$.

5.2 Recommendations

The findings of this thesis provide useful inputs to policy formulation and execution in the fight against the spread of HIV/AIDS.

In order to control the epidemic, the transition of persons from the susceptible to the infective populations should be reduced to the barest minimum.

This can be achieved by conscientising the entire populace on the risks and prevention methods. Civil society and other identifiable groups should be involved in engaging society on the epidemic with particular emphasis on abstinence as the safest option. For instance, religious bodies should be encouraged to make HIV testing mandatory prior to wedlock. Medical studies suggest that transmission rate depends mainly on the males given their socio-economic status in society; hence educational campaigns should be targeted mainly on them.

Also the issue of the accessibility and affordability of the antiretroviral drugs should be reduced and provision of appropriate medical care to the infected will reduce the rate of progression to full – blown AIDS relative to the transmission of susceptible to infective.

However, decreasing the transmission rate is a necessary condition but that alone is not a sufficient mechanism to control the spread of the epidemic. Other essential parameters such as an increased immigration rate (albeit considered unacceptable), and reduced progression rate affects the spread of the disease.

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