MODELING THE EFFECTIVENESS OF CONTROL MEASURES TOWARDS HIV/AIDS AND PNEUMONIA CO-INFECTION

BY

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DECLARATION

DECLARATION BY THE STUDENT

I, the undersigned declare that this thesis is my original work and has not been presented for academic purposes in this University or any other University whatsoever. No part of this thesis may be reproduced without prior written permission of the author and/or University of Eldoret.

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DEDICATION

I dedicate this thesis to my parents who pointed the way, my family who helped me all through until the success of this journey, and my friends and relatives for encouragement.

I hope this work will inspire my children in their studies and lives.

ABSTRACT

The lungs are a principal target of HIV-associated complications and persons with HIV-infection are at an increased risk for a wide spectrum of opportunistic Pneumonias. In this research an HIV/AIDS and Pneumonia co-infection model is presented and analyzed. The Pneumonia and HIV/AIDS sub-models are also presented and analyzed separately without any intervention strategy. Pneumonia is presented as a S.I.R. (Susceptible Infectious Recovered) simple epidemic model. On the other hand the HIV/AIDS is presented as an S.E.I.A. (Susceptible Exposed Infectious AIDS) model. The HIV/AIDS-only model has a globally asymptotically stable disease-free equilibrium when its corresponding reproduction number is less than unity. We proceed to analyze the full HIV/AIDS-Pneumonia co-infection model. The thresholds and equilibria quantities for the models are determined and stabilities analyzed. Secondly, parameters are used for the numerical simulations of the model system from data for both Pneumonia and HIV/AIDS cases sampled from Kapsabet District Hospital in Nandi County, Kenya for the period 2002 – 2011. Thirdly, the effectiveness of control of Pneumonia through treatment and management of HIV/AIDS epidemic through Education Awareness are studied. The minimum threshold for treatment is 97% and 72% for education computed both analytically and also by numerical simulation of the model system through Runge-Kutta method encoded in MATLAB.

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF SYMBOLS AND NOTATIONS

HIV	Human Immuno-deficiency Virus.
AIDS	Acquired Immune Deficiency
ARV's	Anti-Retrovirals
TB	Tuberculosis
PCP	Pneumocystis Carinii Pneumonia
CMV	Cytomegalovirus
W.H.O	World Health Organization
UNAIDS	Joint United Nations Programme on HIV/AIDS.
LMIC	Low and Middle Income Countries
PMNs	Polymorph Nuclear Leukocytes
CDC	Center for Disease Control
CE	Co-infection equilibrium
DFE	Disease Free Equilibrium
H1N1	Influenza A
SIR	Susceptible Infectious and Recovered/Removed/Immune
SI	Susceptible Infectious
SIA	Susceptible, Infective and the AIDS cases
WAIFW	Who Acquires Infection From Whom
RK-4	4^{TH} Order Runge-Kutta Numerical Scheme
SARS	Severely Acute Respiratory Syndrome

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I thank the Almighty God for His protection, guidance and providing me with energy, wisdom and knowledge.

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May God bless you all.

CHAPTER ONE

INTRODUCTION

Among the HIV-associated pulmonary complications, opportunistic pneumonias are major causes of morbidity and mortality. Pneumonia refers to any inflammation of the lungs. According to Huang **et al.,** (2010), the lungs are a principal target of HIV-associated complications and persons with HIV-infection are at an increased risk for a wide spectrum of opportunistic Pneumonias, neoplasms and Pulmonary conditions. It can involve both lungs, one lung or one part of a lung.

According to Huang **et al.,** (2010), Bacterial Pneumonia is the most frequent opportunistic infection in the United States of America and Europe. The incidence of bacterial pneumonia among persons with HIV infection is greater than that among persons without HIV. In those with HIV, bacterial pneumonia is frequently recurrent, and recurrent pneumonia is an AIDS-defining condition. It further says that bacterial pneumonia may be the first manifestation of underlying HIV infection and thus the presence of HIV infection should be considered in any person presenting with bacterial pneumonia, especially if the individual has no other risk factors for pneumonia or if the pneumonia is recurrent.

According to Guide 4 Living (2011) - (an independent information journal online) Pneumonia requires hospitalization and can even lead to death .The spectrum of HIV-associated opportunistic pneumonias is broad and includes bacterial, mycobacterial, fungal, viral, and parasitic pneumonias. It further says that *Pneumocystis Carinii Pneumonia* (known as **PCP**) is one of the most common AIDS-related illnesses which can develop in up to 85% of people with HIV if they don't receive preventative

treatment. In the early days of AIDS, it used to be one of the biggest killers but now thanks to improved medicines the death rate from the illness has dropped from around 30% down to 14%. PCP is an incredibly serious infection which mainly affects the lungs causing a severe form of pneumonia. It's rarely seen in people who are not infected with HIV. It has been known to develop in the liver, spleen, lymph nodes and eyes but these cases are extremely unusual. Caused by a very common fungal organism, *Pneumocystis Carinii Pneumonia* only attacks people with a very weak immune system. The same journal states that it generally appears in people when their CD4+ count goes below 200. This is the point at which a person is defined as having full blown AIDS, hence PCP's reputation as a defining AIDS related illness. Like everyone who gets pneumonia, whether HIV positive or not, sufferers are likely to experience weight loss, fatigue and general weakness due to the illness. The initial signs are difficulty in breathing, rasping breath sounds and a very dry irritating cough. Some people may cough up large amounts of phlegm or have pain or tightness in their chest. The same journal staes that it is an illness that can kill someone with a very weak immune system so it's important that patients with these symptoms see their doctor immediately.Unfortunately for someone with an immune system that is shot to pieces, the likelihood of getting PCP more than once is very high. And after each bout the likelihood of surviving it gets lower - up to 78% of people with HIV survive the first bout of PCP but the figure drops dramatically to 40% if the pneumonia strikes a second time. And if an HIV positive person smokes, studies have found that they can develop *Pneumocystis Carinii Pneumonia* three times faster than someone with HIV who doesn't smoke – basically because not only is the immune system weak but the lungs are being damaged by the effects of smoke as well. For some people the

diagnosis of PCP is also the first time they hear they are HIV positive or, even worse, that they have full blown AIDS.

According to Huang **et al .,** (2010), PCP has been increasingly reported especially in Sub-Saharan Afica with Kenya being part of it.

According to Abdu-Raddad **et al .,** (2006), HIV/AIDS has killed an estimate of 25 million

people. The World Health Organization (WHO) report of 2004 states that AIDS was discovered in 1981 and has become one of the leading causes of death, globally, affecting mostly impoverished people already suffering from poor nutrition and health. While HIV does not kill, it causes the immune system to become defenseless against other opportunistic diseases it could normally fight off. Corbett (2002) states that opportunistic infections are fungal, bacterial or viral infections or a combination of these. Common HIV opportunistic infections are malaria, tuberculosis (TB) and pneumonia. Mathematical models of co-infection have been formulated by Kamal **et al .,** (2007),Wai-ki **et al .,**(2008) and Bhunu **et al .,** (2009).

The HIV/AIDS epidemic has had a major impact throughout the world. In December 2007, the World Health Organization (WHO)/Joint United Nations Programme on HIV/AIDS (UNAIDS) estimated that there are 33 million people living with HIV. Most of these people are unaware of their HIV infection and, as a result, unknowingly contribute to the spread of the infection.

The epidemic has disproportionately affected people residing in areas of the world that have fewer resources to combat the disease. The WHO/UNAIDS(2008) estimated that there were 2.7 million people who were newly infected with HIV in 2007 and

greater than 95% of these new infections occurred among persons residing in Low and Middle Income Countries (LMIC). Sub-Saharan Africa accounts for an estimated 22 million cases of HIV/AIDS and has an estimated prevalence of 5% in adults ages 15-49. In these LMIC, WHO/UNAIDS, (2008) says that the HIV/AIDS epidemic has often over-burdened the under-resourced health care infrastructure. It states that in addition to providing antiretroviral therapy to those with HIV infection, accurate diagnosis and appropriate treatment and prevention of HIV-associated opportunistic pneumonias are both important strategies for reducing the morbidity and mortality from HIV/AIDS.

This thesis Mathematically Models HIV/AIDS and Pneumonia co-infection and formulates a model to test the effectiveness of control measures in controlling Pneumonia and managing HIV/AIDS.

1.1. BACKGROUND OF THE STUDY

A mathematical model is a description of a system using mathematical concepts and language. The process of developing a mathematical model is termed mathematical modeling. According to Matt **et al .,** (2008) mathematical models are used not only in the natural sciences (such as physics, biology, medicine, earth science, meteorology) and engineering disciplines (e.g. Computer science, artificial intelligence), but also in the social sciences (such as economics, psychology, sociology and political science); engineers, statisticians, operation research, analysts and economists use mathematical models most extensively. Simple models have additional value as they are the building blocks of models that include more detailed structure. Detailed models are difficult to solve analytically and hence their usefulness for theoretical purposes is limited, although their strategic value may be high.

One of the early triumphs of mathematical epidemiology was the formulation of a simple model by Kermack W.O. and McKendrick that predicted behavior very similar to the behavior observed in countless epidemics. According to Matt **et al .,** (2008), The Kermack-McKendrick model is a compartmental model based on relatively simple assumptions on the rates of flow between different classes of members of the population. The basic compartmental models to describe the transmission of communicable diseases are contained in a sequence of 3 papers in Kermack W.O. and McKendrick in 1927, 1932 and 1933. The Kermack-McKendrick epidemic model is a special model. The general model included dependence on age of infection, that is, the time since becoming infected.

According to Daley **et al .,** (1999) many of the early developments in the mathematical modeling of communicable diseases date back to the late 18^{th} century. The first known result in mathematical epidemiology is a defence of the practice of inoculation against smallpox in 1760 by Daniel Bernoulli, a member of a famous family of mathematicians (8 spread over 3 generations) who had trained as a physician. The first contributions to modern mathematical epidemiology are due to P.D En'ko between 1873 and 1894. According to Daley **et al .,** (1999), the foundations of the entire approach to epidemiology based on compartmental models was laid by Sir Ross R.A., W.H. Hamer, A.G. McKendrick , W.O Kermack and J. Brownlee (statistician). Dr Ross was awarded the second Nobel Prize in Medicine for his demonstration of the dynamics of the transmission of malaria between mosquitoes and humans. Daley **et al .,** (1999) state that after Ross formulated a mathematical model that predicted that malaria outbreaks could be avoided if the mosquito population could be reduced below a critical threshold level, field trials supported his conclusions and led to brilliant successes in malaria control.

According to Matt **et al .,**(2008) mathematical modeling now plays a key role in policy making, including health-economic aspects; emergency planning and risk assessment; control-programme evaluation; and monitoring of surveillance data. In research, it is essential in study design, analysis (including parameter estimation) and interpretation.

With infectious diseases frequently dominating news headlines, public health and pharmaceutical industry professionals, policy makers, and infectious disease researchers, increasingly need to understand the transmission patterns of infectious diseases, to be able to interpret and critically-evaluate both epidemiological data, and the findings of mathematical modeling studies. Recently there has been rapid progress in developing models and new techniques for measurement and analysis, which have been applied to outbreaks and emerging epidemics, such as Influenza A (H1N1) and SARS. According to Matt **et al .,** (2008) a simple but powerful new technique for assessing the potential of different methods to control an infectious-disease outbreak was recently developed.

1.2. STATEMENT OF THE PROBLEM

The HIV epidemic has been a major cause of morbidity and mortality worldwide. Among the HIV-associated pulmonary complications, opportunistic pneumonias are major causes of morbidity and mortality. The lungs are a principal target of human immunodeficiency virus (HIV)-associated complications and persons with HIV infection are at an increased risk for a wide spectrum of opportunistic pneumonias, neoplasms, and pulmonary conditions. The magnitude of the HIV/AIDS epidemic has led to an unprecedented worldwide effort to provide life-saving antiretroviral therapy and in addition to providing antiretroviral therapy to those with HIV infection,

accurate diagnosis and appropriate treatment and prevention of HIV-associated opportunistic pneumonias are both important strategies for reducing the morbidity and mortality from HIV/AIDS. The challenge of HIV infection is that the clinical and radiographic presentations of HIV-associated opportunistic pneumonias overlap and also that persons with HIV infection may present with more than one concurrent pneumonia.

Mathematical modeling in co-infection of HIV/AIDS and opportunistic infection is an area where most researchers are currently concerned. This is because mathematical models provide rigorous simulations to determine important parameters and effectiveness of various control strategies without necessarily carrying out clinical trials hence reducing time and costs. It is for this reason that in this thesis, we are concerned with Mathematical Modeling of HIV/AIDS and Pneumonia co-infection and formulating a model to test the effectiveness of Treatment in controlling Pneumonia and checking the effectiveness of Education in controlling the spread of HIV/AIDS.

1.3. OBJECTIVES OF THE STUDY

- To determine equilibria quantities for the model and analyze stabilities of the full Pneumonia and HIV/AIDS co-infection model.
- Modeling the effectiveness of Treatment of Pneumonia and the effectiveness of Education in controlling the spread of HIV/AIDS.

1.4. SIGNIFICANCE OF THE STUDY

The result of this study will be beneficial to the following parties:

1.4.1. THE GOVERNMENT

HIV/AIDS is a major concern to all governments. In Kenya, huge sums of money are used to find a lasting solution to HIV/AIDS pandemic and also loss of reproductive workforce and innocent children and mothers. Opportunistic infections including pneumonia are major killers. Effective management and treatment of pneumonia and government intensifying education on condom use and use of ARV's can prevent the spread of HIV and prolong the lives of those infected by HIV/AIDS.

Increase access of information to the public through education on control and management of Pneumonia and HIV/AIDS co-infection.

1.4.2. OTHER RESEARCHERS

Mathematically model HIV/AIDS and other opportunistic infections with a view to notifying health authorities of effectively treating opportunistic infections and providing ARV's.

Research on the effectiveness of these and other control measures in Kenya.

CHAPTER TWO

LITERATURE REVIEW

2.1 INTRODUCTION TO SIMPLE EPIDEMIC MODELS

This chapter starts with the simplest theoretical epidemiological models relating to both Pneumonia and HIV/AIDS. This chapter presents the mathematical equations describing these models, together with the kinds of model analyses that have proved useful to epidemiologists. These approaches encompass both deterministic and probabilistic frameworks. According to Matt **et al.,** (2008), the preliminary models will ignore a number of well-known and important heterogeneities such as differential susceptibility to infection, contact networks, variation immunological responses and transmissibility.

According to Earn **et al .,** (1998), the process of modeling in epidemiology has the ultimate aim of attempting to understand the prevalence and distribution of a species, together with the factors that determine incidence, spread and persistence. Diets (1967) state that in epidemiological models, each individual host is considered as a patch of resource for the pathogen, with transmission and recovery analogous to dispersal and extinction.

In this chapter Pneumonia is presented as a S.I.R (Susceptible-S, Infectious-I and Recovered-R) model while HIV/AIDS is presented as both a S.I. fatal infection model and a S.I.R. (Susceptible-S, Infectious-I and Removed-R) model.

2.2 THE PNEUMONIA S.I.R MODEL

Pneumonia is an example of an infectious disease categorized as acute. The term acute refers to “fast” infections, where relatively rapid immune responses remove pathogens after a short period of time (days or weeks). The development of models focusses on acute infections, assuming the pathogen causes illness for a period of time followed by lifelong immunity. According to Diets (1967), this is mathematically best described by the S-I-R models. This formalism, which was initially studied in depth by Kermack **et al .,**(1927), categorizes hosts within the population as Susceptible (S), Infected (I) and Recovered (R).

This epidemic model divides the host population (humans) into a small number of compartments, each containing individuals that are identical with respect to the disease in question. According to Brauer **et al .,** (2008), the SIR model contains 3 compartments:

1. Susceptible (S): Individuals, who have no immunity to the infectious agent, so might become infected if exposed.
2. Infectious (I): individuals who are currently infected.
3. Recovered (R): individuals who have successfully cleared the infection.

The progression from S to I involves disease transmission which is determined by 3 distinct factors: the prevalence of infected, the underlying population contact structure and the probability of transmission given contact.

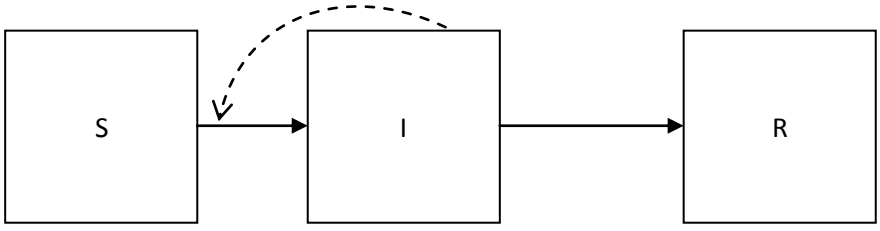

Figure 2.1. Flow diagram illustrating the essential epidemiological characteristics (Source: Brauer et al., 2008)

The force of infection λ is defined as the per capita rate at which individuals contract the infection. The transmission term is described by βSI .

2.2.1 THE PNEUMONIA SIR MODEL WITHOUT DEMOGRAPHY

To introduce the model equations, we consider a "closed population" without demographics (no births, deaths or immigration). We also assume homogeneous mixing, where intricacies affecting the pattern of contacts are discarded, yielding βSI as the transmission term. According to Matt **et al**., (2008) since underlying epidemiological probabilities are constant, we get the following SIR equations:

$$\frac{dS}{dt} = -\beta SI \qquad (2.1)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \qquad (2.2)$$

$$\frac{dR}{dt} = \gamma I \qquad (2.3)$$

The parameter γ is called the removal or recovery rate. Its reciprocal, $\frac{1}{\gamma}$ determines the average infectious period.

Using S, I and R to represent proportions, S+I+R =1, hence knowing S and I will allow us to calculate R. These equations have the initial conditions $S(0)>0, I(0)>0$ and $R(0)=0.$

Despite its extreme simplicity, the model equations (2.1) to (2.3) cannot be solved explicitly. An exact analytical expression for the dynamics of S and I cannot be obtained through time. The model is solved numerically.

2.2.2 THE THRESHOLD PHENOMENON

According to Matt **et al.**, (2008) ,"Threshold phenomenon" by Kermack and McKendrick (1927) of equations (2.1) to (2.3) states that if the initial fraction of susceptibles $S(0)$ is less than $\frac{\gamma}{\beta}$, then $\frac{dI}{dt}<0$ and the infection "dies out".

We can re-write equation (2.2) in the form $\frac{dI}{dt}=I(\beta S-\gamma)$

(2.4)

Hamer, W.H., (1897) states that initially the proportion of susceptibles in the population must exceed this critical threshold for an infection to invade. Alternatively, we can interpret this results as requiring $\frac{\gamma}{\beta}$, the relative removal rate, to be small enough to permit the disease to spread.

2.2.3 THE BASIC REPRODUCTION RATIO, R_0

The basic reproductive ratio R_0 is the inverse of the relative removal rate and is one of the most important quantities in epidemiology. Diekman **et al.,** (2000) defines the basic reproduction number as the average number of secondary cases arising from an average primary case in an entirely susceptible population. The basic reproductive

ratio R_0 measures the maximum reproductive potential for an infectious disease. Lloyd-Smith **et al .,** (2005) states that assuming everyone in the population is initially susceptible, $S(0)=1$. A pathogen can invade if only $R_0>1$. Any infection, on average, which cannot successfully transmit to more than one new host is not going to spread.

Anderson **et al .,**(1982) state that due to difference in demographic rates, rural-urban gradients and contact structure, different human populations may be associated with different values for the same disease. The value of R_0 depends on both the disease and the host population. According to Anderson et al., (1982), R_0 is the rate at which new cases are produced by an infectious individual (when the entire population is susceptible) multiplied by the average infectious period:

i) For an infectious disease with an average infectious period given by $\frac{1}{\gamma}$ and a transmission rate β, its basic reproductive ratio R_0 is determined by $\frac{\beta}{\gamma}$.

ii) In a closed population, an infectious disease with a specified R_0 value can invade only if there is a threshold fraction of susceptible cases greater than $\frac{1}{R_0}$.

iii) Vaccination can be used to reduce the proportion of susceptible cases below $\frac{1}{R_0}$ and hence eradicate the disease.

2.2.4 EPIDEMIC BURNOUT

The above observations are informative about the initial stages, after an infectious agent has been introduced. We can also learn about the long-term (or asymptotic state). Dividing equation (2.1) by (2.3):

$$\frac{dS}{dR} = -\frac{\beta S}{\gamma} = -R_0 S \qquad (2.5)$$

Upon integrating with respect to R, we obtain

$$S(t) = S(0)e^{-R(t)R_0} \qquad (2.6)$$

assuming $R(0) = 0$.

As the epidemic develops, the number of susceptibles declines and with a delay to take the infectious period into account, the number of recovered increases. S always remains above zero because e^{-RR_0} is always positive. There will always be some susceptibles in the population who escape infection. From this simple model, the chain of transmission breaks due to the decline in infectives, not due to a complete lack of susceptible.

According to Waltman., (1974), this approach to model analysis can shed light on the fraction of the population who eventually contract an infection. The author says that it is possible to remove the variable I from the system by dividing equation (2.1) by (2.3). By definition, S+I+R =1 and the epidemic ends when I =0. Equation (2.6) can be rewritten as:

$$S(\infty) = 1 - R(\infty) = S(0)e^{-R(\infty)R_0} \Rightarrow 1 - R(\infty) - S(0)e^{-R(\infty)R_0} = 0$$

(2.7)

Where $R(\infty)$ is the final proportion of recovered individuals, which is equal to the total proportion of the population that get infected.

2.2.5 THE PNEUMONIA S.I.R. MODEL WITH DEMOGRAPHY

The aim is to explore the longer-term persistence and endemic dynamics of an infectious disease, then demographic processes will be important. The most important ingredient necessary for endemicity in a population is the influx of new susceptibles through births.

Brauer (2002), introduces demography into the SIR model by assuming that there is a natural host "life-span", $\frac{1}{\mu}$ years and the rate at which individuals (in any epidemiological class) suffer natural mortality is given by μ (This factor is independent of the disease). It is assumed that mortality acts only on the recovered class.

Putting all these assumptions together, we get the generalized SIR model:

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

(2.8) $$\frac{dI}{dt} = \beta SI - \gamma I - \mu I$$

(2.9)

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

(2.10)

Hethcote (2000) says that maternally derived immunity needs to be explicitly incorporated into models.

If we assume that the entire population is susceptible (S =1), then the average number of new infections per infectious individual is the transmission rate multiplied by the infectious period:

$$R_0 = \frac{\beta}{\gamma + \mu} \qquad (2.11)$$

This model has proved very useful for:

1. Establishing disease prevalence at equilibrium.
2. Determining the conditions necessary for endemic equilibrium stability.
3. Identifying the underlying oscillatory dynamics and predicting the threshold level necessary for eradication.

2.2.6 EQUILIBRIUM ANALYSIS

The dynamics of the system is governed by n coupled Ordinary Differential Equations (ODEs in the SIR equations are 3):

$$\frac{dN_i}{dt} = f_i\left(N_1, N_2, ..., N_n\right), i = 1, 2, ..., n \qquad (2.12)$$

Mathematical results have established that for a series of equations (2.12), the stability of an equilibrium point is determined by the sign of the eigenvalues of the Jacobian matrix. For a system of n ODEs, there will be n eigenvalues and stability is ensured if the real part of all eigenvalues are less than zero.

A Jacobian matrix, J is given by:

$$J = \begin{pmatrix} \frac{\partial f_1^*}{\partial N_1} & \frac{\partial f_1^*}{\partial N_2} & \cdots & \frac{\partial f_1^*}{\partial N_n} \\ \frac{\partial f_2^*}{\partial N_1} & \frac{\partial f_2^*}{\partial N_2} & \cdots & \frac{\partial f_2^*}{\partial N_n} \\ . & . & . & . \\ . & . & . & . \\ . & . & . & . \\ \frac{\partial f_n^*}{\partial N_1} & \frac{\partial f_n^*}{\partial N_2} & \cdots & \frac{\partial f_n^*}{\partial N_n} \end{pmatrix}$$

f_i^* refer to the functions $f_i\left(N_1, N_2, ..., N_n\right)$ evaluated at equilibrium. The eigenvalues λ_i are the solutions of $\det\left(J - \lambda_i I\right) = 0$ where I is the identity matrix of the same order as J.

Applying these ideas to the SIR system of equations, Jacobian is worked out:

$$J = \begin{pmatrix} -\beta I^* - \mu & -\beta S^* & 0 \\ \beta I^* & \beta S^* - (\mu + \gamma) & 0 \\ 0 & \gamma & -\mu \end{pmatrix}$$

To obtain the characteristic polynomial, we subtract λ_i from the diagonal elements and calculate the determinant. This gives:

$$\left(\beta I^* - \mu - \lambda\right)\left(\beta S^* - (\mu + \gamma) - \lambda\right)(-\mu - \lambda) + \left(\beta I^*\right)\left(\beta S^*\right)(-\mu - \lambda) = 0$$

(2.13)

Solving equation (2.13) at DFE, gives the solutions as:

$$\lambda_1 = \lambda_2 = -\mu \text{ and } \lambda_3 = \beta - (\mu + \gamma)$$

(2.14)

For this equilibrium to be stable, we need to ensure all eigenvalues are negative. For a system of n ODEs, there will be n eigenvalues less than zero – these eigenvalues are usually complex numbers. This is to ensure that a small perturbation from the

equilibrium eventually does not grow. Hence the stability criterion becomes $\beta < \mu + \gamma,$ which translates into ensuring $R_0 < 1.$

The endemic equilibrium is feasible only when $R_0 > 1$ but it is always stable.

Endemic equilibrium is obtained by setting (2.9) to 0 i.e.

$$I\left(\beta S - \left(\gamma + \mu\right)\right) = 0$$

(2.15)

One universal condition on population variables is that they cannot be negative. Endemic equilibrium is biologically feasible if $R_0 > 1$. Utilizing $S^* + I^* + R^* = 1$, the endemic equilibrium condition is given by:

$$\left(S^*, I^*, R^*\right) = \left(\frac{1}{R_0}, \frac{\mu}{\beta}\left(R_0 - 1\right), 1 - \frac{1}{R_0} - \frac{\mu}{\beta}\left(R_0 - 1\right)\right)$$

(2.16)

The equilibrium is approached via oscillatory dynamics. The period of these damped oscillations, T, is:

$$T \approx 2\pi\sqrt{AG}$$

(2.17) where A is the Transmission rate and G is the infectious period where $A = \frac{1}{\mu\left(R_0 - 1\right)}$ denotes the mean age at infection and G determines the typical period of a host's infectivity and is given by $G = \frac{1}{\mu + \gamma}.$

2.2.7 OSCILLATORY DYNAMICS

According to Matt **et al .,**., (2008), an important issue for any dynamical system concerns the manner in which a stable equilibrium is eventually approached. The SIR system is an excellent example of a "damped oscillator", which means the inherent dynamics contain a strong oscillatory component, but the amplitude of these

fluctuations declines over time as the system equilibrates. From (2.17), the period of oscillations changes with the transmission rate and the infectious period. The period of oscillations becomes longer as the reproductive ratio approaches one; this is also associated with a slower convergence towards the equilibrium.

2.2.8 MEAN AGE AT INFECTION

According to Anderson **et al .,** (1991), the mean age at infection is the mean time from birth to infection. The average period spent in the susceptible class (is the inverse of the force of infection) is $\frac{1}{\beta I^*}$.

We calculate the average age at which susceptibles are infected by taking (2.8) and calculating the mean time an individual remains susceptible (the mean time from birth to infection). Upon substituting for I^* from (2.17), the mean age at infection (A_1) is obtained as $A_1 \approx \frac{1}{\mu(R_0 - 1)}$

(2.18)

This equation can be rephrased as $R_0 - 1 \approx \frac{L}{A_1}$ where L is the host's life expectancy.

2.2.9 INFECTION-INDUCED MORTALITY

According to Matt (2008), numerous infectious diseases including Pneumonia are associated with mortality risk. We incorporate a mortality probability into the SIR model. This is the probability, ρ , of an individual in the I class dying from the infection before either recovering or dying from natural cases. This quantity is estimated from clinical studies or case observations. Mathematically, this translates to the following equation:

$$\frac{dI}{dt} = \beta SI - (\gamma + \mu) I - \frac{\rho}{1-\rho}(\gamma + \mu) I$$

(2.19)

In order to convert this to a mortality rate, set $m = \frac{\rho}{1-\rho}(\gamma + \mu)$.

The equation for the infection dynamics give

$$\frac{dI}{dt} = \beta SI - (\gamma + \mu) I - mI$$

(2.20)

Note that as ρ approaches unity, new infectives die almost instantaneously and R_0 drops to zero.

2.3 AIDS: FATAL INFECTIONS

Here infecteds are assumed to remain infectious for an average period of time $\left(\frac{1}{\gamma}\right)$, after which they succumb to an infection.

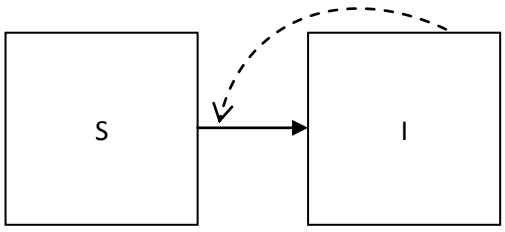

Figure 2.2.0: The SI model: (Source: Brauer et al., 2008)

Assuming frequency-dependent transmission, the equations describing the SI model are:

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

(2.21)

$$\frac{dI}{dt} = \frac{\beta SI}{N} - (\gamma + \mu) I$$

(2.22)

The endemic equilibrium $S^* = \frac{v}{\beta - \gamma}, I^* = \frac{v(\beta - \gamma - \mu)}{(\beta - \gamma)(\gamma + \mu)}$ is feasible as long as $R_0 = \frac{\beta}{(\mu + \gamma)} > 1$ and is always locally stable.

Assuming pseudo mass-action transmission, such that the contact rate scales with density, we obtain:

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

(2.23)

$$\frac{dI}{dt} = \beta SI - (\mu + \gamma) I$$

(2.24)

For this system, the endemic equilibrium $S^* = \frac{\gamma + \mu}{\beta}$ and $I^* = \frac{v}{\gamma + \mu} - \frac{\mu}{\beta}$ is feasible as long as $R_0 = \frac{\beta v}{(\mu + \gamma)\mu} > 1$ and is always locally stable.

2.3.1 HIV/AIDS WITHOUT IMMUNITY: THE S.I.S. MODEL

Numerous infectious diseases including HIV/AIDS confer no long-lasting immunity. Individuals get infected multiple times throughout their lives with no apparent immunity.

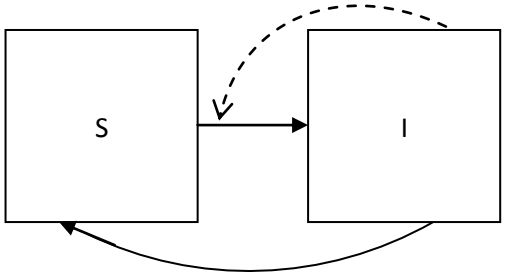

Figure 2.2.1: The S.I.S. model:

These SIS models shown in Figure 2.2.1. are described by a pair of coupled ordinary differential equations:

$$\frac{dS}{dt} = \gamma I - \beta IS \qquad (2.25)$$

$$\frac{dI}{dt} = \beta SI - \gamma I \qquad (2.26)$$

2.3.2 RISK-STRUCTURE: SEXUALLY TRANSMITTED INFECTIONS

The concepts of modeling population heterogeneity with the particular examples of sexually transmitted infections and 2 groups (high risk and low risk) are introduced. In Garnett **et al .,** (2000), The two-class model demonstrates the necessary tools and techniques. Garnett **et al .,**(2000), states that HIV/AIDS is an epidemic since 1983 and this has prompted research activity focussed on modelling these STIs and asserting effective means of control.

2.3.2.1 MODELING RISK STRUCTURE

The sets of equations are derived for the various risk groups within the population and from these equations develop a robust generic framework to explain the interaction between risk and epidemiological dynamics as shown in Figure 2.2.2.1.

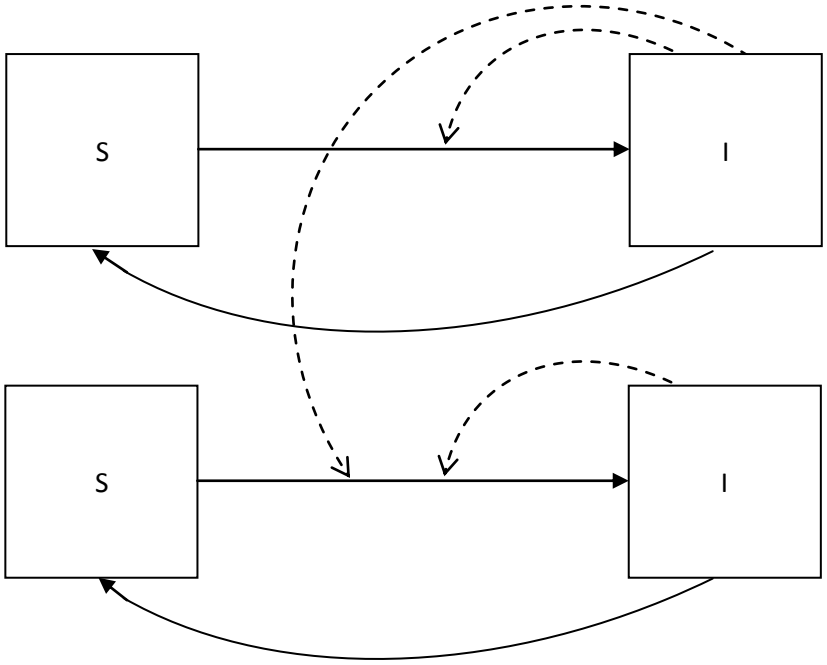

Figure 2.2.2.1: High-Risk and Low-Risk groups (Source: Matt et al., 2008).

The number of susceptible and infectious group within the group are denoted by S_H and I_H respectively and the total number in the high-risk group by $N_H = S_H + I_H$. Using a frequency approach, S_H and I_H refer to the proportion of the entire population that are susceptible or infectious respectively. A disease free population has $S_H = n_H < 1$. The dynamics of either group is derived from two basic events, infection and recovery. (We do not allow the movement of individuals between risk groups). We let β_{HH} denote transmission to high risk from high risk, β_{HL} denote transmission to low risk from high risk and β_{LL} denote transmission to low risk from

low risk. Putting these elements together, we arrive at the following differential equation:

$$\frac{dI_H}{dt} = \beta_{HH} S_H I_H + \beta_{HL} S_H I_L$$

(2.28)

$$\frac{dI_L}{dt} = \beta_{LH} S_L I_H + \beta_{LL} S_L I_L$$

(2.29)

There are 4 transmission parameters represented by a matrix β called the WAIFW(Who Acquires Infection From Whom) matrix:

$$\beta = \begin{pmatrix} \beta_{HH} & \beta_{HL} \\ \beta_{LH} & \beta_{LL} \end{pmatrix}$$

This matrix is a convenient way of capturing the mixing between different social groups.

2.3.2.2 INITIAL DYNAMICS

For unstructured models, the simple parameter β was vital in determining the basic reproductive ratio, R_0 and hence the rate of increase in infection following invasion. Heesterbeck (2002), says that to calculate the actual value of R_0, an eigenvalue approach is required to deal with the recursive nature of transmission. The initial behaviour of a structure model depends on the initial conditions, not just R_0.

2.3.2.3 EQUILIBRIUM PREVALENCE

This is the calculation of the prevalence of infection at equilibrium. Mathematically, this is where the rates of change are zero.

Remembering that $S_H = n_H - I_H$, we need to solve:

$$0 = \beta_{HH}\left(n_H - I_H\right)I_H + \beta_{HL}\left(n_H - I_H\right)I_L - \gamma I_H,$$
$$0 = \beta_{LH}\left(n_L - I_L\right)I_H + \beta_{LL}\left(n_L - I_L\right)I_L - \gamma I_L.$$

These equations contain quadratic terms and hence analytic solution is impossible. We solve the above equilibrium equations numerically or by iterating the model forward to find the equilibrium levels.

2.3.2.4 GENERALIZING THE MODEL

The matrix formulation of β can be adapted to model the interaction of multiple groups (eg high-, medium- and low-risk groups). Infected individuals in group i obey the following differential equation: $\frac{dI_i}{dt} = \sum_j \beta_{ij} S_i I_j - \gamma_i I_i$

(2.30)

where the matrix form of β is used to parameterise transmission between the groups. The contact rates are specified as a matrix of values. We specify the number of infected (or susceptible) individuals in each class as a vector. The full set of equations becomes:

$\frac{d\underline{I}}{dt} = \underline{S} \otimes \left(\beta \underline{I}\right) - \underline{\gamma} \otimes \underline{I}$,where $\otimes$ is the Kronecker product which refers to the piecewise multiplication of 2 vectors. If R_0 >1, the infection can successfully invade. If R_0 <1, the infection will always die out.

2.3.2.5 AGE-STRUCTURED EPIDEMIC MODELS

In the S.I.R. model, there are 3 compartments:

1. Susceptible (S):individuals who become infected if exposed.
2. Infectious (I): individuals who are currently infected and can transmit the infection to susceptible individuals whom they get in contact with.
3. Removed (R): individuals who are immune to the infection.

Ianneli., (1995) supposes an age-structured population in which there is an infectious disease of S.I.R. type. We introduce functions $S(t,a), I(t,a), R(t,a)$ *and* $\rho(t,a)$ representing the age distribution (a) at time t of susceptible, infective, removed members and disease prevalence respectively so that

$$S(t,a)+I(t,a)+R(t,a)=\rho(t,a)$$

The rate of change in time of a function $S(t,a)$ of time and age is $S_t(t,a)+S_a(t,a)$

The following system of equations describes the transmission dynamics of the disease in the age-structured population:

$$\begin{aligned}
&S_t(t,a)+S_a(t,a)=-\left[\mu(a)+\lambda(t,a)\right]S(t,a),\\
&I_t(t,a)+I_a(t,a)=\lambda(t,a)S(t,a)-\left[\mu(a)+\gamma(a)+\delta(a)\right]I(t,a),\\
&R_t(t,a)+R_a(t,a)=-\mu(a)R(t,a)+\gamma(a)I(t,a).
\end{aligned}$$

Here $\mu(a)$ is the natural death rate in each class, $\gamma(a)$ is the recovery rate which in the HIV/AIDS case is 0, $\delta(a)$ is the disease death rate and $\lambda(t,a)$ is the infection rate.

To this system of p.d.e's we must add the initial conditions:

$$S(0,a)=\phi(a), I(0,a)=\varphi(a), R(0,a)=0$$

(2.31)

where ϕ and φ are the initial conditions of susceptibles and infectives respectively.

In addition, the birth or renewal condition is given by:

$$S(t,0)=\int_0^\infty \beta(a)\rho(t,a)da$$

(2.32)

Further analysis requires some assumption on the nature of the infection term $\lambda(t,a)$. One possibility is intracohort mixing given as, $\lambda(t,a)=f(a)I(t,a)$ corresponding to the assumption that infection can be transmitted only between individuals of the same age.

Another possibility is intercohort mixing, $\lambda(t,a)=\int_0^\infty b(a,\alpha)I(t,\alpha)d\alpha$, with $b(a,\alpha)$ giving the rate of infection from contacts between an infective of age α with a susceptible of age a .

2.3.4 A SIMPLE AGE-STRUCTURED S.I.A. AIDS MODEL:

The population is divided into the groups of susceptibe individuals, infective individuals and the AIDS cases, denoted by S, I and A respectively. A simple age-structured epidemic model is considered in which HIV/AIDS is spread in a population of ages $[a_0,\infty]$, where a_0 is the minimal sexually active age. Assume that there is an input flow, $\Lambda(a)$ for all ages a , entering only the susceptible group. We

further assume that the number of susceptible of age a_0 is a constant B and that no individuals with age a_0 are infected yet.

Let $\mu(a)$ be the natural death rate of all individuals in the population, $\gamma(a)$ be the HIV developing rate for infective individuals and $\delta(a)$ is the AIDS induced death rate of AIDS cases.

According to Hyman **et al.,**(1994), the transmission dynamics are governed by the following system of equations:

$$
\begin{aligned}
&(i).S_t(t,a)+S_a(t,a)=\Lambda(a)-\big(\mu(a)+\lambda(t,a)\big)S(t,a)\\
&(ii).S(t,a_0)=B,\\
&(iii).S(0,a)=\phi(a),\\
&(iv).I_t(t,a)+I_a(t,a)=-\big(\mu(a)+\gamma(a)\big)I(t,a)+\lambda(t,a)S(t,a)\\
&(v).I(t,a_0)=0,\\
&(vi).I(0,a)=\phi(a),\\
&(vii).A_t(t,a)+A_a(t,a)=-\delta(a)A(t,a)+\gamma(a)I(t,a),\\
&(viii).A(t,a_0)=0,\\
&(ix).A(0,a)=0,
\end{aligned}
\qquad (2.33)
$$

where ϕ and φ are the initial distributions and infectives respectively.

The infection rate is determined by:

$$\lambda(t,a)=r(a)\int_{a_0}^{\infty}\beta(a,a')\rho(t,a,a')\frac{I(t,a')}{T(t,a')}da' \qquad (2.34)$$

where $T(t,a)=S(t,a)+I(t,a)$ is the total number of sexually active individuals, $r(a)$ is the number of partners that an individual of age a has per unit of time,

$\beta(a,a')$ is the transmission probability of a susceptible individual of age a infected by an infected partner of age a' and $\rho(a,a',t)$ is the rate of pair formation between individuals of ages a and a'.

The transmission probability is described by $\beta(a,a') = f(a)g(a')$, where $f(a)$ is the susceptibility of individuals of age a and $g(a')$ is the infectiousness of individuals of age a'. Then:

$$\lambda(t,a) = r(a)\, f(a) \int_{a_0}^{\infty} g(a')\rho(t,a,a') \frac{I(t,a')}{T(t,a')} da' \qquad (2.35)$$

The Reproduction number in mathematical epidemiology determines whether an infectious disease spreads in a susceptible population when the disease is introduced into the population.

According to Jacques **et al .,**(1991), Reproduction number is derived by determining the condition for local stability of the infection-free equilibrium. Model (2.33) has an infection-free equilibrium,

$$(S,I,A) = (S^0(a),0,0)$$

(2.36)

where $S^0(a) = Be^{(} - M(a)) + e^{-M(a)} \int_{a_0}^{a} e^{M(x)\Lambda(x)} dx$ with $M(a) = \int_{a_0}^{a} \mu(S) dS.$

2.4 THE CONTROL OF EPIDEMICS

According to Daley **et al .,**(1999), one of the purposes of modeling epidemics is to provide a rational basis for policies designed to control the spread of a disease. We consider two models for epidemics to illustrate possible prevention policies of:

a) Control of Pneumonia by Treatment.

b) Control of spread of HIV/AIDS epidemic by Education Awareness Campaign.

Modelling is of vital importance in evaluating the likely effects of spreading a disease deliberately as a means of biological control. Often the data available to decision makers are inadequate, as for example in the case of HIV/AIDS in Africa or South East Asia. Yet policies need to be formulated, if only on the basis of rough qualitative measures. One may, for example, need to know the likely effects of spending funds on two alternative policies, or the optimal method of immunizing a population. Here, exact models may not be easy to formulate, though one tries to make all modeling as realistic as possible. Accurate data may be impossible to obtain, but one should always be in a position to minimize the cost of a policy or to compare the effects of policy A against those of policy B. Examination of the control methods discussed in this chapter shows that they use and extend the simple methods discusssed previously.

When a policy depends on a single variable, it is relatively easy to minimize the cost. If two policies are to be compared, one can examine their respective costs and choose the cheaper policy. Alternatively, if the criterion is not cost, one can rank the policies with respect to the criterion selected. The control methods we describe are in terms of the general model with pairwise transmission rate β and removal rate γ.

According to Fenner et al**.,** (1988), strategies are aimed at one or more of the following results:

- Depressing the number of susceptibles in the population and where possible, to below the threshold level $\rho_1 \equiv \frac{\gamma}{\beta}$ described in the Kermack-McKendrick criticality theorem.
- Accelerating the rate of removal of infectives to reduce their mixing with the population of susceptibles i.e. decreasing β thereby increasing ρ_1 .
- Lowering the pairwise rate of infectious contact between infectives and susceptibles (i.e. decreasing β thereby increasing ρ_1).

For example, Treating some or all of the population reduces the initial number S_0

of susceptibles; operating a screening program or raising public awareness of higher disease prevalence may raise γ or lower β (or both); discouraging the assembly of large crowds reduces β.

According to Fenner **et al .,** (1988), immunization has long been used as a method for controlling the spread of an epidemic. The fact that parents are sometimes lax in ensuring that their children are immunized against preventable diseases like pneumonia (especially bacterial pneumonia) has resulted in their random recurrence. In considering immunization as a technique for controlling the spread of a disease, at least two policy questions arise, both subsumed in the pursuit of maximum effect with minimum effort:

a) How widespread can (or, should) the immunization be, and

b) Which susceptibles should be immunized for this effort to produce the best effect (e.g. should individuals be immunized at random, or should groups such as schools or families be targetted)?

These questions involve detailed modelling of the population where the immunization takes place, and in estimating its effect given some description of how the disease spreads. If infection spreads homogeneously through the population, then question (b) is void. Any quasi-realistic description of the spread of contagious infection usually requires recognition that the population in which the process occurs is inhomogeneous. Yet even when the population is subdivided into groups of individuals belonging to different strata, those in a given strata are assumed to mix homogeneously amongst themselves and to behave similarly towards individuals of other srata. The neutral term 'stratum' describe such sub-populations within which individuals are regarded as identical apart from their disease status, noting that it may cover spatial variability or distinct social behaviour. Anderson **et al .,** (1991), describe an optimal immunization strategy within a spatially heterogeneous population.

Becker and Dietz (1995,1996) have considered a population of a number of smaller units (households, clubs or schools) and computed the effects of different strategies determined by the characteristics of these units. The four particular strategies they discussed were:

(i) Random immunization of individuals;

(ii) Households chosen at random and all their members immunized;

(iii)Preferential selection of large households for immunization;

(iv)Immunization of a fixed fraction of members in every household.

The AIDS epidemic has spread rapidly throughout the world. But its effect has been more limited in countries where a campaign for information and education has been sponsored by the state or by a foundation eg in Switzerland.

According to Daley **et al.,**(1999), a 'STOP-AIDS' advertising campaign launched in February 1987 by the Swiss AIDS Foundation to provide the population with detailed knowledge of the AIDS infection and its spread, and to discourage risk-prone behaviour by recommending the use of condoms in sexual contacts with multiple or casual patners, mutual faithfulness between sexual partners, and the use of clean needles in drug usage(i.e. no exchanges between users).

O'Neill (1995), has also studied epidemic models in which behavioural change plays a role.

CHAPTER THREE

METHODOLOGY

3.1. MODEL DESCRIPTION OF PNEUMONIA AND HIV/AIDS INFECTIONS

This section discusses the Pneumonia and HIV/AIDS model. It is assumed that the Pneumonia and HIV/AIDS model is similar to the HIV/AIDS and Tuberculosis co-infection model as discussed by Bhunu **et al .,** (2009) and the HIV/AIDS and Malaria co-infection model in Sub-Saharan Africa by Kamal **et al .,** (2007).

3.2. PNEUMONIA AND HIV/AIDS CO-INFECTION MODEL DESCRIPTION

The model subdivides the human population into the following sub-population of susceptible individuals *(S)*, those individuals infected with Pneumonia *(* I_p *)*, those who have recovered from Pneumonia *(*R_p*)*, those infected with HIV-only but showing no clinical symptoms of AIDS *(* I_H*)*, HIV-infected displaying AIDS symptoms *(* A_H *)*, HIV-infected individuals (pre-AIDS) class displaying Pneumonia symptoms *(* I_{pH} *)*, and AIDS individuals dually infected with Pneumonia *(*A_{pH} *)*. It is assumed that susceptible humans are recruited into the population at per capita rate Λ. Susceptible individuals acquire HIV infection following contact with HIV-infected individuals at a rate λ_H and acquire Pneumonia infection at a rate λ_p .

The total population size at time t is $N(t)$ and is given by

$$N(t) = S(t) + I_p(t) + R_p(t) + I_H(t) + A_H(t) + I_{pH}(t) + A_{AP}(t)$$

3.2.1. PARAMETERS OF THE MODEL

This section gives the parameters used in developing the model.

σ: Recovery rate from Pneumonia

μ: Natural death rate of persons in all classes.

η_P: Relative infectiousness of individuals infected with Pneumonia

η_{PH}: Relative infectiousness of dually infected victims.

η_H: Relative infectiousness of all HIV cases

η_A: Relative infectiousness of all AIDS classes

θ: Increased susceptibility to Pneumonia due to HIV infection

α: Increased susceptibility to HIV after recovery from Pneumonia Infection

β_H: Effective contact rate of HIV infection

β_P: Effective contact rate of Pneumonia infection

ψ: Force of Pneumonia re-infection

δ: Increased HIV infection rate of Pneumonia infectives

d_P: Accelerated Pneumonia death rate

ρ: Rate of HIV progression to AIDS

$\gamma\rho$: Progression rate to AIDS for HIV victims exposed to Pneumonia

d_A: AIDS accelerated death rate

e: Education parameter in managing the spread of HIV/AIDS infection.

tr: Treatment parameter in controlling the spread and healing Pneumonia infection.

HIV force of infection $\lambda_H = \frac{\beta_H}{N}[(I_H + I_{PH}) + \eta_A(A_H + \eta_{PH}A_{PH})]$

Pneumonia force of infection $\lambda_P = \frac{\beta_P}{N}[I_P + A_{AP} + I_{PH}]$

The above-mentioned 2 forces of infection are derived.

3.2.2. ASSUMPTIONS

The following assumptions are used in the analysis of the model:

Pneumonia undergoes SIR

HIV undergoes Susceptible Exposed Infected AIDS (SEIA) stages.

AIDS cases are seriously sick and cannot contribute to new HIV infectives

The model assumes a closed population with no migration.

The model is not an age-structured model.

3.2.3. MODEL EQUATIONS

The model equations are derived from the flow chart in Figure 3.1. below.

$$S' = \Lambda - (\lambda_p + \lambda_H)S - \mu S$$

$$I_p' = \lambda_p(S + \psi R_p) - \delta\lambda_H I_p - (\mu + \sigma + d_p)I_p$$

$$R_p' = \sigma I_p - (\alpha\lambda_H + \mu + \psi\lambda_p)R_p$$

$$I_H' = \lambda_H S + \alpha\lambda_H R_p - \theta\lambda_p I_H - (\rho + \mu)I_H$$

(3.1)

$$I_{pH}' = \theta\lambda_p I_H + \delta\lambda_H I_p - \gamma\rho I_{pH} - (\mu + d_p)I_{pH}$$

$$A_H' = \rho I_H - \theta\eta_p\lambda_p A_H - (\mu + d_A)A_H$$

$$A_{AP}' = \gamma\rho I_{pH} + \theta\eta_p\lambda_p A_H - (\mu + d_A + d_p)A_{AP}$$

Where ($'$) denote differentiation with respect to time.

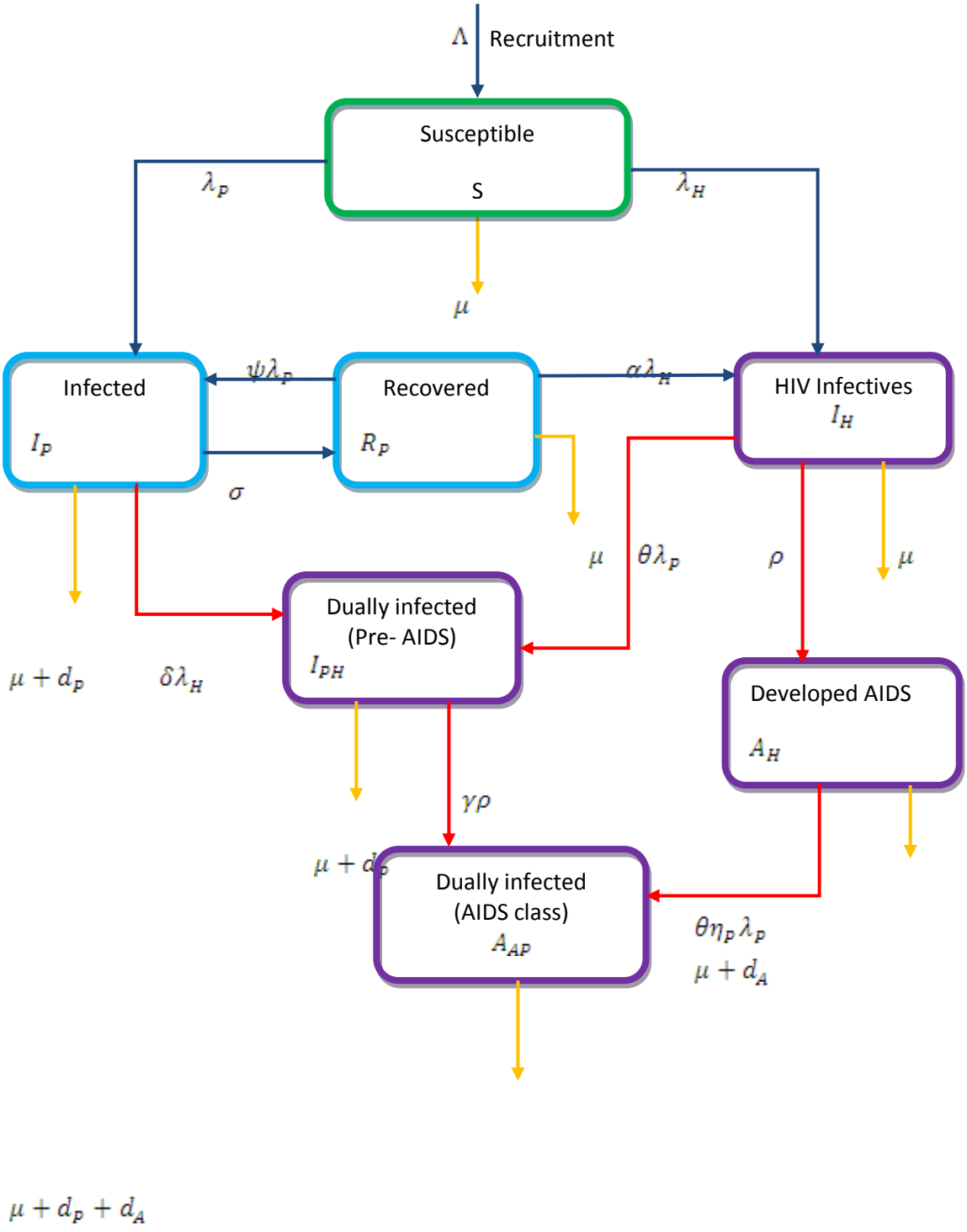
Λ Recruitment
Susceptible
S
λ_P
λ_H
μ
Infected
I_P
$\psi\lambda_P$
Recovered
R_P
$\alpha\lambda_H$
HIV Infectives
I_H
σ
μ
$\theta\lambda_P$
ρ
μ
Dually infected
(Pre- AIDS)
I_{PH}
$\mu + d_P$
$\delta\lambda_H$
Developed AIDS
A_H
$\gamma\rho$
$\mu + d_P$
Dually infected
(AIDS class)
A_{AP}
$\theta\eta_P\lambda_P$
$\mu + d_A$
$\mu + d_P + d_A$

Figure 3.1: HIV-Pneumonia Co-infection Flow chart (Source: Author, 2012)

3.2.4. INITIAL CONDITIONS

All the 7 variables are positive.

$$S(0) = S_0 \geq 0,\ I_p(0) = I_{p_0} \geq 0,\ R_p(0) = R_{p_0} \geq 0,\ I_H(0) = I_{H_0} \geq 0,$$

(3.2)

$$I_{PH}(0) = I_{PH_0} \geq 0,\ A_H(0) = A_{H_0} \geq 0,\ A_{AP}(0) = A_{AP_0} \geq 0$$

3.2.5. REGION OF STUDY

This model studies Heptagonal (seven) positive region given as

$$\xi := \{S(t),\ I_p(t),\ R_p(t),\ I_H(t),\ A_H(t),\ I_{PH}(t),\ A_{AP}(t)\} \in R_+^7;\ N(t) \leq \frac{\Lambda}{\mu}$$

(3.3)

Which is positively invariant with respect to the model system (3.1).

3.2.6. POSITIVITY AND BOUNDEDNESS OF SOLUTIONS

The model system (3.1) describes human population. It is necessary to prove that all the variables $\{S(t),\ I_p(t),\ R_p(t),\ I_H(t),\ A_H(t),\ I_{PH}(t),\ A_{AP}(t)\}$ are non-negative for all time. Solutions of the model system (3.1) with positive initial data remain positive for all time $t \geq 0$ and are bounded in ξ.

Theorem 1. *Let* $S(t) \geq 0, I_p(t) \geq 0, R_P(t) \geq 0, I_H(t) \geq 0, A_H(t) \geq 0, I_{PH}(t) \geq 0, A_{AP}(t) \geq 0$. *The solutions* $\{S(t),\ I_p(t),\ R_p(t),\ I_H(t),\ A_H(t),\ I_{PH}(t),\ A_{AP}(t)\}$ *of the model system (3.1) are positive for* $t \geq 0$. *For the model system (3.1), the region* ξ *is positively invariant and all the solutions starting in* ξ *either approach, enter or stay in* ξ .

Proof:

Under the given initial conditions, it is easy to prove that the components of solutions of the model system (3.1) are positive; if not, we assume a contradiction: that there exists a first time

t_1 :

$S(t_1)=0, S'(t_1)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_1$ or there exists a t_2 :

$I_P(t_2)=0, I_P'(t_2)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_2$

Or there exists a t_3 :

$R_P(t_3)=0, R_P'(t_3)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_3$

Or there exists a t_4 :

$I_H(t_4)=0, I_H'(t_4)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_4$

Or there exists a t_5 :

$A_H(t_5)=0, A_H'(t_5)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_5$

Or there exists a t_6 :

$I_{PH}(t_6)=0, I_{PH}'(t_6)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$
for $0<t<t_6$

Or there exists a

t_7 :

$A_{AP}(t_7)=0, A_{AP}{}'(t_7)<0, S(t)>0, I_p(t)>0, R_P(t)>0, I_H(t)>0, A_H(t)>0, I_{PH}(t)>0, A_{AP}(t)>0$ for $0<t<t_7$.

Evaluating the first equation of system (3.1) at t_1, we obtain;

$S'(t_1)=\Lambda$ ($\Lambda > 0$ is positive and thus a contradiction. We therefore state that there exist no such first time and thus $S(t) \geq 0$ for all $t \geq 0$.

In the second case, we have $I_P{}'(t_2)=\lambda_P\left(S(t_2)+\psi R_P(t_2)\right)>0$ which is a contradiction meaning that $I_P(t)\geq 0$ for all $t\geq 0$.

In the third case, $R_P{}'(t_3)=\delta I_P(t_3)>0$ which is a contradiction meaning that $R_P(t)\geq 0$ for all $t\geq 0$.

In the fourth case, $I_H{}'(t_4)=\lambda_H S(t_4)+\alpha\lambda_H R_P(t_4)>0$ which is a contradiction meaning that $I_H(t)\geq 0$ for all $t\geq 0$.

In the fifth case, $I_{PH}{}'(t_5)=\theta\lambda_P I_H(t_5)+\delta\lambda_H I_P(t_5)>0$ which is a contradiction meaning that $I_{PH}(t)\geq 0$ for all $t\geq 0$.

In the sixth case, $A_H{}'(t_6)=\rho I_H(t_6)>0$ which is a contradiction meaning that $A_H(t)\geq 0$ for all $t\geq 0$.

In the seventh case, $A_{AP}{}'(t_7)=\gamma\rho I_{PH}(t_7)+\theta\eta\rho\lambda_P A_H(t_7)>0$ which is a contradiction meaning that $A_{AP}(t)\geq 0$ for all $t\geq 0$.

3.2.7. BOUNDEDNESS

Note that equation (1) of system (3.1) can be expressed in form of an inequality as shown below;

$$S' \geq -(\lambda_p + \lambda_H)S - \mu S$$

(3.4)

By separation of variables, the solution of (3.4) is given by,

$$S(t) \geq S_0 e^{-(\lambda_P + \lambda_H + \mu)t}$$

(3.5)

For $0 \leq \lambda_p + \lambda_H + \mu \leq 1$ the solution of equation (3.5) is always positive and bounded above by S_0 for all positive time, $t \geq 0$.

Equation (2) of system (3.1) can be expressed in the form of an inequality as:

$$I_P{}' \geq -\delta\lambda_H I_P - \left(\mu + \delta + d_p\right) I_P$$

(3.6)

By separation of variables, the solution of (3.6) is given by

$$I_P(t) \geq I_{P_0} e^{-(\delta\lambda_H + \mu + \delta + d_P)t}$$

(3.7)

for $0 \leq \delta\lambda_H + \mu + \delta + d_P \leq 1$. The solution of (3.7) is always positive and bounded above I_{P_0} for all positive time, $t \geq 0$.

Equation (3) of system (3.1) can be expressed in the form of an inequality as:

$$R_P{}' \geq -\left(\alpha\lambda_H + \mu + \psi\lambda_P\right) R_P$$

(3.8)

By separation of variables, the solution of (3.8) is given by

$$R_P(t) \geq R_{P_0} e^{-(\alpha\lambda_H + \mu + \psi\lambda_P)t}$$

(3.9)

For $0 \leq \alpha\lambda_H + \mu + \psi\lambda_P \leq 1$. The solution of (3.9) is always positive and bounded above R_{P_0} for all positive time, $t \geq 0$.

Equation (4) of system (3.1) can be expressed in the form of an inequality as:

$$I_H{}' \geq -\theta\lambda_P I_H - (\rho + \mu) I_H$$

(3.10)

By separation of variables, the solution of (3.10) is given by

$$I_H(t) \geq I_{H_0} e^{-(\theta\lambda_P + \rho + \mu)t}$$

(3.11)

for $0 \leq \theta\lambda_P + \rho + \mu \leq 1$. The solution of (3.11) is always positive and bounded above I_{H_0} for all positive time, $t \geq 0$.

Equation (5) of system (3.1) can be expressed in the form of an inequality as:

$$I_{PH}{}' \geq -(\gamma\rho + \mu + d_P) I_{PH}$$

(3.12)

By separation of variables, the solution of (3.12) is given by

$$I_{PH}(t) \geq I_{PH_0} e^{-(\gamma\rho + \mu + d_P)t}$$

(3.13)

for $0 \le \gamma\rho + \mu + d_P \le 1$. The solution of (3.13) is always positive and bounded above I_{PH_0} for all positive time, $t \ge 0$.

Equation (6) of system (3.1) can be expressed in the form of an inequality as:

$$A_H{}' \ge -\left(\theta\eta\rho\lambda_P + \mu + d_A\right)A_H \tag{3.14}$$

By separation of variables, the solution of (3.14) is given by

$$A_H(t) \ge A_{H_0} e^{-(\theta\eta\rho\lambda_P + \mu + d_A)t} \tag{3.15}$$

for $0 \le \theta\eta\rho\lambda_P + \mu + d_A \le 1$. The solution of (3.15) is always positive and bounded above A_{H_0} for all positive time, $t \ge 0$.

Equation (7) of system (3.1) can be expressed in the form of an inequality as:

$$A_{AP}{}' \ge -(\mu + d_A + d_P)A_{AP} \tag{3.16}$$

By separation of variables, the solution of (3.16) is given by

$$A_{AP}(t) \ge A_{AP_0} e^{-(\mu + d_A + d_P)t} \tag{3.17}$$

for $0 \le \mu + d_A + d_P \le 1$. The solution of (3.17) is always positive and bounded above A_{AP_0} for all positive time, $t \ge 0$.

3.3. EQUILIBRIUM POINTS

Let $\bar{X}' = f(\bar{X})$ represent the system (3.1) expressed in vector notation, where

$\bar{X} = \{S(t), I_P(t), R_P(t), I_H(t), A_H(t), I_{PH}(t), A_{AP}(t)\}^T$ and $(.)^T$ denotes transpose.

Then equilibrium points are obtained by solving $f(\bar{X}) = \bar{0}$.

3.3.1. Disease Free Equilibrium (DFE)

In the absence of either disease, the DFE is obtained as,

$$(S^0, I_P^0, R_P^0, I_H^0, A_H^0, I_{PH}^0, A_{AP}^0) = (\tfrac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0)$$

(3.18)

3.3.2. Stability of the system at DFE

Matrix of linearization about a fixed point is used to determine stability of the system at that fixed point by examining the sign of the eigenvalues. The system is stable if all the eigenvalues are bounded to the left of the imaginary axis.

3.3.3. Linearization matrix M

This is obtained using equation (2.12) as;

$$M = \begin{pmatrix} a & -\frac{\beta}{N}S^* & 0 & -\frac{\beta}{N}S^* & -\frac{\beta\eta_A}{N}S^* & -\frac{\beta\eta_A}{N}S^* & b \\ \lambda_P^* & c & \lambda_P^*\psi & 0 & -\frac{\delta\beta\eta_A}{N}I_P^* & \frac{\beta}{N}(S^* + \psi R_P^*) & -\delta\frac{\beta}{N}\eta_A I_P^* \\ 0 & \sigma - \frac{\psi\beta}{N}R_P^* & d & -\frac{\alpha\beta}{N}R_P^* & -\frac{\beta}{N}(\alpha+\psi)R_P^* & -\frac{\alpha\eta_A\beta}{N}R_P^* & e \\ \lambda_H^* & -\frac{\theta\beta}{N}I_H^* & \alpha\lambda_H^* & f & k & \frac{\eta_A\beta}{N}(\alpha R_P^* + S^*) & g \\ 0 & h & 0 & n & j & \frac{\beta}{N}\eta_A\delta I_P^* & \delta\frac{\beta}{N}\eta_A\eta_{PH}I_P^* \\ 0 & -\frac{\beta}{N}\theta\eta_P A_H^* & 0 & \rho & \frac{\theta\eta_P\beta}{N}A_H^* & l & -\frac{\beta}{N}\theta\eta_P A_H^* \\ 0 & \frac{\beta}{N}\theta\eta_P A_H^* & 0 & 0 & \gamma\rho + \frac{\theta\eta_P\beta}{N}A_H^* & \theta\eta_P\lambda_P^* & m \end{pmatrix}$$

(3.19)

where $-\lambda_H^* = \frac{\beta}{N}[(I_H^* + I_{PH}^*) + \eta_A(A_H^* + \eta_{PH}A_{AP}^*)]$, and $-\lambda_P^* = \frac{\beta}{N}[I_P^* + A_{AP}^* + I_{PH}^*]$

with

$a = -\lambda_H^* - \lambda_P^* - \mu,$,

$b = -\frac{\beta(\eta_A\eta_{PH}+1)S^*}{N}$

$c = \frac{\beta}{N}S^* - \delta\lambda_H - (\mu + \sigma + d_P),$

$d = -(\alpha\lambda_H^* + \mu + \psi\lambda_P^*)$

$e = -\frac{\beta}{N}(\alpha\eta_A\eta_{PH} + \psi)R_P^*$

$f = \frac{\beta}{N}(S^* + \alpha R_P^*) - (\theta\lambda_P^* + \rho + \mu)$

$g = \frac{\beta}{N}[\eta_A\eta_{PH}(S^* + \alpha R_P^*) - \theta I_P^*]$

$h = \frac{\beta}{N}(\theta I_H^* + \delta\lambda_H^*)$

$j = \frac{\beta}{N}(\theta I_H^* + \delta I_P^*) - (\gamma\rho + \mu + d_P)$

$k = \frac{\beta}{N}(S^* + \alpha R_P^* - \theta I_H^*)$

$l = -(\theta\eta_P\lambda_P^* + \mu + d_A)$

$m = \frac{\theta\eta_P\beta}{N}A_H^* - (\mu + d_A + d_P)$

$n = \theta\lambda_P^* + \frac{\beta}{N}\delta I_P^*$

Note that this is a 7X7 matrix since we are dealing with 7 equations.

3.3.4. Pneumonia only Model Equations

Pneumonia force of infection can be expressed as $\lambda_p = \frac{\beta}{N}[I_p + A_{AP} + I_{pH}]$ and the expressions for S$^{/}$, $I_p^{/}$ and $R_p^{/}$ are;

$$S' = \Lambda - \lambda_p S - \mu S$$

$$I_p' = \lambda_p(S + \psi R_p) - (\mu + \sigma + d_p)I_p$$

(3.20)

$$R_p' = \sigma I_p - (\mu + \psi\lambda_p)R_p$$

3.3.4.1. Population

The population N(t) can be expressed at any time t as

$N(t) = S(t) + I_p(t) + R_p(t)$, and the Force of infection of Pneumonia infection as

$\lambda_p = \beta \frac{I_p}{N}$

3.3.4.2. Equilibrium points

3.3.4.2.1. Disease Free Equilibrium (DFE)

The DFE of Pneumonia infection is written as

$$(S^0,\ I_p^0,\ R_p^0) = (\tfrac{\Lambda}{\mu},\ 0,\ 0)$$

(3.21)

Stability of DFE

This is obtained by evaluating linearization matrix about the fixed point (DFE)

$$M_p = \begin{pmatrix} -(\lambda_p^* + \mu) & -\frac{\beta}{N}S^* & 0 \\ \lambda_p^* & \frac{\beta}{N}(S^* + \psi R_p^*) - (\mu + \sigma + d_p) & \lambda_p^* \psi \\ 0 & \sigma - \frac{\psi\beta}{N}R_p^* & -(\mu + \psi\lambda_p^*) \end{pmatrix}$$

(3.22)

where $\lambda_p^* = \beta\frac{I_p}{N}$.

The equilibrium point of system (3.20) is stable if all the eigenvalues of M_p evaluated at DFE are negative. Stability matrix (3.22) evaluated at DFE yields

$$M_p|_{DFE} = \begin{pmatrix} -\mu & -\frac{\beta v}{\mu} & 0 \\ 0 & \frac{\beta v}{\mu} - (\mu + \sigma + d_p) & 0 \\ 0 & \sigma & -\mu \end{pmatrix}$$

(3.23)

The eigenvalues of $M_p|_{DFE}$ are;

$$\lambda_1 = -\mu, \qquad \lambda_2 = \frac{\beta v}{\mu} - (\mu + \sigma + d_p), \qquad \lambda_3 = -\mu$$

Clearly, the first and the third eigenvalues are negative. The system is stable if the second eigenvalue is negative.

That is, $\frac{\beta v}{\mu} - (\mu + \sigma + d_p) < 0$ or

$$\frac{\beta v}{\mu(\mu+\sigma+d_p)} < 1 := R_1$$

(3.24)

This condition implies that the eigenvalues of the linearization matrix $M_p|_{DFE}$ are all negative and the system (3.20) is locally asymptotically stable at DFE.

3.3.4.2.2. Endemic Equilibrium Point (EEP)

With the assumption that the Pneumonia recovered class have equal likely hood as those who have not contracted Pneumonia before, to be re-infected with Pneumonia, that is, $\psi = 1$, we have the endemic equilibrium point (EEP) defined as;

$$(S^e,\ I_P^e,\ R_P^e) = \left(\frac{vN^2}{\beta I_P^e + \mu N}\ ,\ I_P^e\ ,\ \frac{\sigma N I_P^e}{\beta I_P^e + \mu N}\right) \tag{3.25}$$

where $I_P^e = \frac{\mu v N(R_1 - 1)}{\beta v - \mu\sigma R_1}$.

Stability of EEP

The EEP is stable if the eigenvalues of the Jacobian matrix linearized about EEP has all eigenvalues with the real part less than zero.

Using matrix (3.22), the stability matrix is written as;

$$M_p|_{EEP} = \begin{pmatrix} -(\lambda_p^* + \mu) & -\frac{\beta}{N}S^e & 0 \\ \lambda_p^* & \frac{\beta}{N}(S^e + R_p^e) - (\mu + \sigma + d_p) & \lambda_p^* \\ 0 & \sigma - \frac{\beta}{N}R_p^e & -\left(\beta\frac{I_p}{N} + \mu\right) \end{pmatrix}$$

$$M_p|_{EEP} = \begin{pmatrix} -(\beta\frac{I_p^e}{N} + \mu) & -\frac{v\beta N}{\beta I_p^e + \mu N} & 0 \\ \beta\frac{I_p^e}{N} & \frac{v\beta N + \sigma\beta I_p^e}{\beta I_p^e + \mu N} - (\mu + \sigma + d_p) & \beta\frac{I_p^e}{N} \\ 0 & \sigma - \frac{\sigma\beta I_p^e}{\beta I_p^e + \mu N} & -\left(\beta\frac{I_p^e}{N} + \mu\right) \end{pmatrix}$$

$$M_p|_{EEP} = \begin{pmatrix} -\mu R_1 \frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1} & -\frac{\beta v}{\mu R_1}\frac{(\beta v-\mu\sigma R_1)}{(\beta v-\mu\sigma)} & 0 \\ \frac{\beta\mu v(R_1-1)}{\beta v-\mu\sigma R_1} & \frac{\beta v}{\mu R_1}-(\mu+\sigma+d_p) & \frac{\beta\mu v(R_1-1)}{\beta v-\mu\sigma R_1} \\ 0 & \frac{\sigma}{R_1}\frac{(\beta v-\mu\sigma R_1)}{(\beta v-\mu\sigma)} & -\mu R_1\frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1} \end{pmatrix}$$

(3.26)

The first eigenvalue of the stability matrix $M_p|_{EEP}$ in (3.26) is given by the characteristic roots of the equation

$$\left|M_p|_{EEP} - \lambda I\right| = 0$$

The characteristic roots are all negative if $Det(A) > 0$ and $Tra(A) < 0$.

This result can be summarized in the following lemma.

Lemma 1.

The Pneumonia only model system (3.20) has a stable endemic equilibrium if $R_1 > 1$.

Proof.

The characteristic roots of the Jacobian matrix (3.26) linearized about the equilibrium point (3.25) are obtained from the characteristic equation;

$$\left(-\lambda-\mu R_1\frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1}\right)\left[\lambda^2+\mu R_1\frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1}\lambda+\frac{\beta v(R_1-1)}{R_1}\right]=0$$

Clearly,

$$\lambda_1 = -\mu R_1\frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1}$$

(3.27)

The other two λ_2 and λ_3 are obtained from the characteristic equation;

$$\lambda^2+\mu R_1\frac{(\beta v-\mu\sigma)}{\beta v-\mu\sigma R_1}\lambda+\frac{\beta v(R_1-1)}{R_1}=0$$

(3.28)

This second order characteristic equation is equivalent to;

$$\lambda^2 - Tra(A)\lambda + Det(A) = 0$$

which can equally be obtained from a $A_{2\times 2}$ matrix.

The trace and determinant are given by,

$$Tra(A) = -\mu R_1 \frac{(\beta v - \mu\sigma)}{\beta v - \mu\sigma R_1}$$

$$Det(A) = \frac{\beta v(R_1 - 1)}{R_1}$$

The eigenvalues are both negative if $Det(A) > 0$ and $Tra(A) < 0$ where $A = M_{P/EEP} - \lambda I$.

Given that $R_1 > 1$ corresponding to endemic equilibrium point, the sign of the first eigenvalue (3.27) is negative if

$$\frac{(\beta v - \mu\sigma)}{\beta v - \mu\sigma R_1} > 0$$

This implies that

$$\beta v - \mu\sigma > \beta v - \mu\sigma R_1$$

or $-1 > -R_1$ or $R_1 > 1$.

Similarly, the other two eigenvalues λ_2 and λ_3 are negative if

$$Det(A) = \frac{\beta v(R_1 - 1)}{R_1} > 0$$

This clearly holds if $R_1 > 1$. Lastly we should have

$$Tra(A) = -\mu R_1 \frac{(\beta v - \mu\sigma)}{\beta v - \mu\sigma R_1} < 0$$

This is true if $\frac{(\beta v - \mu\sigma)}{\beta v - \mu\sigma R_1} > 0$ or $R_1 > 1$ as described for the first eigenvalue.

3.3.5. HIV only model

3.3.5.1. Model Equations

The model equations for the HIV only case are given as,

$$S' = \Lambda - \lambda_H S - \mu S$$

$$I_H' = \lambda_H S - (\rho + \mu) I_H$$

(3.29)

$$A_H' = \rho I_H - (\mu + d_A) A_H,$$

And the corresponding Population N(t) is

$$N(t) = S(t) + I_H(t) + A_H(t)$$

The HIV force of infection is $\lambda_H = \frac{\beta}{N}[I_H + \eta_A A_H]$

3.3.5.2. Equilibrium points

3.3.5.2.1. Disease Free Equilibrium for HIV/AIDS-only case

$$E^0 := (S^0 \;\; I_H^0 \;\; A_H^0) = \left(\frac{\Lambda}{\mu}, 0, 0\right)$$

(3.30)

Stability of HIV/AIDS only case

Linearization matrix for the DFE for HIV/AIDS infection is

$$M_H = \begin{pmatrix} -\frac{\beta}{N}(I_H^0 + \eta_A A_H^0) - \mu & -\frac{\beta}{N} S^0 & -\frac{\beta}{N}\eta_A S^0 \\ \frac{\beta}{N}(I_H^0 + \eta_A A_H^0) & \frac{\beta}{N} S^0 - (\rho + \mu) & \frac{\beta}{N}\eta_A S^0 \\ 0 & \rho & -(\mu + d_A) \end{pmatrix}$$

(3.31)

The equilibrium is stable if the eigenvalues of M_H evaluated at DFE has negative real parts with $S^0 = \frac{\Lambda}{\mu}$ i.e:

$$M_H|_{DFE} = \begin{pmatrix} -\mu & -\frac{\beta}{N}\frac{\Lambda}{\mu} & 0 \\ 0 & \frac{\beta}{N}\frac{\Lambda}{\mu} - (\rho+\mu) & 0 \\ 0 & \rho & -(\mu+d_A) \end{pmatrix}$$

(3.32)

The eigenvalues of (3.32) are all negative if $\frac{\beta}{N}\frac{\Lambda}{\mu} - (\rho+\mu) < 0$

The stability criterion is then defined as,

$$R_2 := \frac{\beta\Lambda}{\mu N(\rho+\mu)} < 1$$

With $\Lambda = vN$, the basic reproductive number for HIV only model system (3.29) R_2 is given by

$$R_2 = \frac{\beta v}{\mu(\rho+\mu)}$$

(3.33)

The system (3.29) is Locallly Asymptotically Stable (LAS) if $R_2 < 1$.

3.3.5.2.2. Endemic Equilibrium Point (EEP)

With the existence of HIV, the symptomatic equilibrium with chronic infection is defined by

$$E^e := (S^E, I_H^E, A_H^E) = (S^E, I^E, A^E)$$

(3.34)

where

$$S^E = \frac{vN}{\mu R_1}\frac{\rho\eta+\mu+d_A}{\rho\eta}, \quad I^E = \frac{(\mu+d_A)N[vN-\mu S^E]}{\beta S^E[\rho\eta+\mu+d_A]} \quad \text{and} \quad A^E = \frac{\rho N[vN-\mu S^E]}{\beta S^E[\rho\eta+\mu+d_A]}.$$

Stability of EEP

Using the analogy of the linearization matrix (3.31), the corresponding matrix for EEP evaluated at E^s is given by;

$$M_H|_{E^s} = \begin{pmatrix} -\frac{\beta}{N}(I_H^E + \eta_A A_H^E) - \mu & -\frac{\beta}{N}S^E & -\frac{\beta}{N}\eta_A S^E \\ \frac{\beta}{N}(I_H^E + \eta_A A_H^E) & \frac{\beta}{N}S^E - (\rho + \mu) & \frac{\beta}{N}\eta_A S^E \\ 0 & \rho & -(\mu + d_A) \end{pmatrix}$$

(3.35)

The equilibrium point E^s is stable if the eigenvalues of linearization matrix (3.35) have negative real parts. Thus,

$$M_H|_{E^s} = \begin{pmatrix} -\mu N[R_2 - k] - \mu & -\frac{\beta v}{\mu R_2}k & -\eta_A\frac{\beta v}{\mu R_2}k \\ \mu N[R_2 - k] & \frac{\beta v}{\mu R_2}k - (\rho + \mu) & \eta_A\frac{\beta v}{\mu R_2}k \\ 0 & \rho & -(\mu + d_A) \end{pmatrix}$$

where $k = \frac{\mu + d_A + \eta\rho}{\eta\rho}$

$Trace[M_H|_{E^s}] = -\mu N[R_2 - k] - \mu + \frac{\beta v}{\mu R_2}k - (\rho + \mu) - (\mu + d_A) < 0$ if $R_2 - k > 0$ and $\frac{\beta v}{\mu R_2}k - (\rho + \mu) < 0$.

These two conditions when simplified results into the condition that,

$$Trace[M_H|_{E^s}] < 0 \;\; if \; R_2 \geq 1$$

Also,

$$Det[M_H|_{E^s}] = \frac{\beta v}{R_2}(\mu + d_A + \eta_A\rho) - \mu N[R_2 - k](\rho + \mu)(\mu + d_A) + \mu(\mu + \rho)\left[\frac{\beta v}{\mu R_2}k - (\rho + \mu)\right] > 0$$

when $\frac{\beta v}{R_2}(\mu + d_A + \eta_A\rho) - \mu N[R_2 - k](\rho + \mu)(\mu + d_A) > 0$. This condition simplify to the condition that;

$$1 \leq R_2 < \frac{\eta_A \rho k^2}{N(\mu + d_A)}$$

(3.36)

We thus conclude that all the eigenvalues of $M_H|_{E^s}$ have negative real part if the inequality above is satisfied.

The inequality (3.36) suggests that the Endemic Equilibrium point (EEP) is locally asymptomatically stable if the reproductive ration R_2 is less than the bifurcation parameter $R_c := \frac{\eta_A \rho k^2}{N(\mu + d_A)}$ after which the system becomes unstable.

3.3.6. Analysis of the full model

In this section the full model is analyzed in system (3.1) without any intervention.

Disease Free Equilibrium

In the absence of any disease, DFE defined in (3.18) is given as,

$$(S^0, I_P^0, R_P^0, I_H^0, A_H^0, I_{PH}^0, A_{AP}^0) = (\frac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0)$$

(3.37)

Stability of the system at DFE

Matrix of linearization about a fixed point is used to determine stability of the system at that fixed point by examining the sign of the eigenvalues. The system is stable if all the eigenvalues are bounded to the left of the imaginary axis.

Linearization matrix M defined in (3.19) is evaluated at DFE to obtain,

$$M|_{DFE} = \begin{pmatrix} -\mu & -\frac{\beta v}{\mu} & 0 & -\frac{\beta v}{\mu} & -\eta_A \frac{\beta v}{\mu} & -\eta_A \frac{\beta v}{\mu} & 0 \\ 0 & a_{22} & 0 & 0 & 0 & \frac{\beta v}{\mu} & 0 \\ 0 & \sigma & -\mu & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{\beta v}{\mu} - (\rho + \mu) & \frac{\beta v}{\mu} & \eta_A \frac{\beta v}{\mu} & \frac{\beta v}{\mu} \eta_A \eta_{PH} \\ 0 & 0 & 0 & 0 & -(\gamma\rho + \mu + d_p) & 0 & 0 \\ 0 & 0 & 0 & \rho & 0 & -(\mu + d_A) & 0 \\ 0 & 0 & 0 & 0 & \gamma\rho & 0 & -(\mu + d_A + d_p) \end{pmatrix}$$

(3.38)

where $a_{22} = \frac{\beta v}{\mu} - (\mu + \sigma + d_p)$. The eigenvalues of linearization matrix of the full model $M|_{DFE}$ are;

$\lambda_1 = -\mu,\ \lambda_2 = -\mu,\ \lambda_3 = -(\gamma\rho + \mu + d_p),\ \lambda_4 = -(\mu + d_A),\ \lambda_5 = -(\mu + d_A + d_p), \lambda_6 = \frac{\beta v}{\mu} - (\mu + \sigma + d_p),\ \lambda_7 = \frac{\beta v}{\mu} - (\rho + \mu)$

All the eigenvalues except the sixth and the seventh are clearly less than zero i.e. negative. The sixth and the seventh are negative if $R_1 < 1$ and $R_2 < 1$ respectively.

The dominant eigenvalues of the linearization matrix of the full model at disease free equilibrium is R_1 and R_2 and these correspond to the reproduction numbers for the Pneumonia transmission model and the HIV/AIDS transmission model, respectively. Thus, the basic reproduction number, R_0, for the full model is given by

$$R_0 = \max\{R_1, R_2\}$$

(3.39)

The following Theorem follows from Driesche (2002), (Theorem 2).

Theorem 2. *The disease-free equilibrium point, E^0, is locally asymptotically stable for*

$R_0 < 1$ and unstable for $R_0 > 1$.

Proof.

The Jacobian matrix of the system (3.1) linearized about the equilibrium point E^0 is given in (3.38). The trace and determinant of this matrix is,

$$Trace[M|_{E^0}] = -7\mu - \gamma\rho - 2d_p - 2d_A - d_p + 2\frac{\beta v}{\mu} - \sigma - \rho < 0$$

for $R_0 < 1$.

$$Det[M|_{E^0}] = -\mu^2(\gamma\rho + \mu + d_p)(\mu + d_A)(\mu + d_A + d_p)\left[\frac{\beta v}{\mu} - (\mu + \sigma + d_p)\right]\left[\frac{\beta v}{\mu} - (\rho + \mu)\right] > 0$$

when the following conditions are satisfied.

Case I: $R_1 < 1$ and $R_2 > 1$.

Case II: $R_1 > 1$ and $R_2 > 1 - \frac{\rho\eta\beta v}{\mu(\mu+d_A)}$

Case I corresponds to management of pneumonia not to spread and persistence of HIV in the population.

Case II corresponds to persistence of Pneumonia in the population and presence of HIV if $\frac{\rho\eta\beta v}{\mu(\mu+d_A)} < 0$ and management of HIV if $0 < \frac{\rho\eta\beta v}{\mu(\mu+d_A)} < 1$.

3.4. MODELING THE CONTROL OF PNEUMONIA INFECTION BY TREATMENT AND MANAGING HIV/AIDS INFECTION BY EDUCATION

Assumptions are the same as in equation (3.2.2), the initial conditions are same as in (3.2.4), the region of study is as in (3.2.5) and all the solutions are positive and bounded as in (3.2.6).

The new HIV force of infection after education is

$$\lambda_{He} = (1-e)\frac{\beta_H}{N}\left[(I_H + I_{PH}) + \eta_A(A_H + \eta_{PH}A_{PH})\right] \tag{3.40}$$

Where e is the education awareness campaign parameter on HIV/AIDS.

The new Pneumonia Force of infection after treatment is

$$\lambda_{Pt} = (1-tr)\frac{\beta_P}{N}\left[I_P + A_{AP} + I_{PH}\right] \tag{3.41}$$

Where tr is the treatment parameter on Pneumonia infection.

The model equations in (3.1) become:

$$\begin{aligned}
S' &= \Lambda - (\lambda_{Ptr} + \lambda_{He})S - \mu S \\
I_p' &= \lambda_{Ptr}(S + \psi R_p) - \delta\lambda_{He}I_p - (\mu + \sigma + d_p)I_p \\
R_p' &= \sigma I_p - (\alpha\lambda_{He} + \mu + \psi\lambda_{Ptr})R_p \\
I_H' &= \lambda_{He}S + \alpha\lambda_{He}R_p - \theta\lambda_{Ptr}I_H - (\rho + \mu)I_H \\
A_H' &= \rho I_H - \theta\eta_p\lambda_{Ptr}A_H - (\mu + d_A)A_H
\end{aligned} \tag{3.42}$$

$$I'_{PH} = \theta\lambda_{Ptr}I_H + \delta\lambda_{He}I_P - \gamma\rho I_{PH} - (\mu + d_p)I_{PH}$$

$$A'_{AP} = \gamma\rho I_{PH} + \theta\eta_P\lambda_{Ptr}A_H - (\mu + d_A + d_P)A_{AP}$$

The Disease Free Equilibrium after education awareness campaign and treatment of Pneumonia is obtained as in equation (3.18).

3.4.1. LINEARIZATION MATRIX M_1

Linearization of a matrix about a fixed point is used to determine the stability of the system at that fixed point by examining the sign of the eigenvalues. This is a 7×7 matrix obtained by derivation using equation (2.12) as:

$$M_1 = \begin{pmatrix} -\lambda_{Ptr} - \lambda_{He} - \mu & a_1 & 0 & a_2 & a_3 & a_4 & a_5 \\ b_1 & b_2 & \lambda_{Ptr}\psi & b_3 & b_4 & b_5 & b_6 \\ 0 & c_1 & c_2 & c_3 & c_4 & c_5 & c_6 \\ \lambda_{He} & d_1 & \alpha\lambda_{He} & d_2 & d_3 & d_4 & d_5 \\ 0 & e_1 & 0 & \rho & e_2 & e_3 & e_4 \\ 0 & f_1 & 0 & f_2 & f_3 & f_4 & f_5 \\ 0 & g_1 & 0 & 0 & \theta\eta_P\lambda_{Ptr} & g_2 & g_3 \end{pmatrix}$$

(3.43)

where:

$$a_1 = -\frac{\beta_P}{N}S(1-tr)$$

$$a_2 = -(1-e)\frac{\beta_H}{N}\eta_A S$$

$$a_3 = -(1-e)\frac{\beta_H}{N}S$$

$$a_4 = -\left\{(1-e)\frac{\beta_H}{N} + (1-tr)\frac{\beta_P}{N}\right\}S$$

$$a_5 = -(1-tr)\frac{\beta_P}{N}S$$

$$b_1 = (1-tr)\frac{\beta_P}{N}\left[I_P + A_{AP} + I_{PH}\right]$$
$$b_2 = -\delta\lambda_{He} - \mu - \delta - d_P$$
$$b_3 = -(1-e)\delta I_P \frac{\beta_H}{N}$$
$$b_4 = -(1-e)\delta I_P \eta_A \frac{\beta_H}{N}$$
$$b_5 = (1-tr)\frac{\beta_P}{N}(s + \psi R_P) - \delta I_P (1-e)\frac{\beta_H}{N}$$
$$b_6 = -(1-tr)\delta I_P \frac{\beta_P}{N}$$

$$c_1 = \delta - R_P(\lambda_{He} + \psi\lambda_{Ptr})$$
$$c_2 = -(\alpha\lambda_{He} + \mu + \psi\lambda_{Ptr})$$
$$c_3 = -\alpha R_P (1-e)\frac{\beta_H}{N}$$
$$c_4 = -R_P \frac{\beta_H}{N}$$
$$c_5 = -\alpha(1-e)R_P \frac{\beta_H}{N} - \psi(1-tr)R_P \frac{\beta_P}{N}$$
$$c_6 = -\psi(1-tr)\frac{\beta_P}{N}$$

$$d_1 = -\theta I_H (1-tr)\frac{\beta_P}{N}$$
$$d_2 = \alpha R_P (1-e)\frac{\beta_H}{N} - \theta\lambda_{Pt} - (\rho + \mu) + s(1-e)\frac{\beta_H}{N}$$
$$d_3 = s(1-e)\eta_A \frac{\beta_H}{N} + \alpha R_P (1-e)\eta_A$$
$$d_4 = (s + \alpha R_P)(1-e)\frac{\beta_H}{N} - \theta I_H (1-tr)\frac{\beta_P}{N}$$
$$d_5 = -\theta I_H (1-tr)\frac{\beta_P}{N}$$

$$e_1 = -\theta\eta_P A_H (1-tr)\frac{\beta_P}{N}$$
$$e_2 = -\theta\eta_P\lambda_{Pt} - (\mu + d_A)$$
$$e_3 = -\theta\eta_P A_H (1-tr)\frac{\beta_P}{N}$$
$$e_4 = -\theta\eta_P A_H (1-tr)\frac{\beta_P}{N}$$

$$f_1 = \theta I_H (1-tr)\frac{\beta_P}{N} + \delta\lambda_{He}(\mu + d_A)$$

$$f_2 = \theta\lambda_{Pt} + \delta I_P (1-e)\frac{\beta_H}{N}$$

$$f_3 = \delta I_P (1-e)\eta_A \frac{\beta_H}{N}$$

$$f_4 = \theta I_H (1-tr)\frac{\beta_P}{N} + \delta I_P (1-e)\frac{\beta_H}{N} - \gamma\rho - \mu - d_P$$

$$f_5 = \theta I_H (1-tr)\frac{\beta_P}{N}$$

$$g_1 = \theta\eta_P A_H (1-tr)\frac{\beta_P}{N}$$

$$g_2 = \gamma\rho + \theta\eta_P A_H (1-tr)\frac{\beta_P}{N}$$

$$g_3 = \theta\eta_P A_H (1-tr)\frac{\beta_P}{N} - (\mu + d_A + d_P)$$

3.4.2. Analysis of the full model

This section analyzed the full model in system (3.42) under the same assumptioons in (3.2.2.).

Disease Free Equilibrium

In the absence of any disease, the DFE is defined as,

$$(S^0, I_P^0, R_P^0, I_H^0, A_H^0, I_{PH}^0, A_{AP}^0) = (\tfrac{\Lambda}{\mu}, 0, 0, 0, 0, 0, 0)$$

(3.44)

Stability of the system at DFE

As mentioned earlier, the Matrix of linearization about a fixed point is used to determine stability of the system at that fixed point by examining the sign of the

eigenvalues. The system is stable if all the eigenvalues are bounded to the left of the imaginary axis.

Linearization matrix M defined in (3.43) is evaluated at DFE to obtain,

$$M_1/_{DFE} = \begin{pmatrix} a_{11} & a_{12} & 0 & a_{13} & a_{14} & a_{15} & a_{16} \\ 0 & a_{21} & 0 & 0 & 0 & a_{22} & 0 \\ 0 & \delta & a_{31} & 0 & 0 & a_{32} & 0 \\ \lambda_{He} & 0 & \alpha\lambda_{He} & a_{41} & a_{42} & a_{43} & 0 \\ 0 & \delta\lambda_{He} & 0 & \rho & a_{51} & 0 & 0 \\ 0 & \delta\lambda_{He} & 0 & 0 & 0 & a_{61} & 0 \\ 0 & 0 & 0 & 0 & 0 & \gamma\rho & a_{77} \end{pmatrix} \tag{3.45}$$

where

$$a_{11} = -(1-e)\frac{\beta_H}{N}\left[\eta_A(\eta_{PH}A_{PH})\right] - \mu, a_{12} = -\frac{\nu\beta_P}{\mu}(1-tr), a_{13} = -(1-e)\frac{\nu\beta_H}{\mu},$$

$$a_{14} = -(1-e)\frac{\nu\beta_H\eta_A}{\mu}, a_{15} = -\left\{(1-e)\frac{\nu\beta_H}{\mu} + (1-tr)\frac{\nu\beta_P}{\mu}\right\}, a_{16} = -(1-tr)\frac{\nu\beta_P}{\mu},$$

$$a_{21} = -\delta\lambda_{He} - \mu - \delta - d_P, a_{22} = (1-tr)\frac{\nu\beta_P}{\mu}, a_{31} = -(\alpha\lambda_{He} + \mu),$$

$$a_{32} = (1-tr)\frac{\nu\beta_P}{\mu}, a_{41} = -(\rho+\mu) + (1-e)\frac{\nu\beta_H}{\mu}, a_{42} = (1-e)\eta_A\frac{\nu\beta_H}{\mu},$$

$$a_{43} = (1-e)\frac{\nu\beta_H}{\mu}, a_{51} = -(\mu + d_A), a_{61} = -(\gamma\rho + \mu + d_P),$$

$$a_{71} = -(\mu + d_A + d_P).$$

All the eigenvalues are clearly less than zero, if and only if $a_{41} < 0$ and $a_{21} < 0$. That is,

$$\frac{(1-e)\nu\beta_H}{\mu(\rho+\mu)} < 1 := (1-e)R_2 \tag{3.46}$$

and

$$\frac{(1-tr)\beta v}{\mu(\mu+\sigma+d_P)} < 1 := (1-tr)R_1$$

(3.47)

The dominant eigenvalues of the linearization matrix of the full model at disease free equilibrium is $(1-tr)R_1$ and $(1-e)R_2$ and these correspond to the reproduction numbers for the Pneumonia transmission model (equation 3.47) and the HIV/AIDS transmission models with intervention (equation 3.46), respectively.

3.4.3. THRESHOLD VALUES FOR INTERVENTION STRATEGIES

For stability matrix M_1 the system is stable if equation (3.46) and (3.47) are satisfied. In terms of e and tr, these equations gives the minimum threshold values as:

$$e > 1 - \frac{\mu(\rho+\mu)}{v_H \beta_H}$$

(3.48)

$$tr > 1 - \frac{\mu(\mu+\delta+d_p)}{v_P \beta_P}$$

(3.49)

Solving equations (3.48) and (3.49) analytically using the data in Table (4.1), these values are:

tr>0.97 and e>0.72

(3.50)

CHAPTER FOUR

RESULTS

4.1. NUMERICAL RESULTS AND ANALYSIS OF PNEUMONIA AND HIV/AIDS

To bring out the analytical solutions in the previous section clearly, we illustrate the analytic results with specific numerical examples. We use the model discussed in section 3.2. A complete list of parameters and their estimated values that we use for the numerical simulations of the model system are given in Table 4.1. The majority of the values have been approximated from data taken from Kapsabet District Hospital (a public hospital in Nandi county in Kenya).

The following data is available at the hospital for inpatient incidences of both pneumonia and HIV/AIDS infections and deaths as from 2002 to 2011.

Table 4.1.1. Pneumonia and HIV/AIDS Incidences and deaths at Kapsabet District Hospital from 2002 to 2011

YEAR	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011
PNEUMONIA INCIDENCES	502	123	415	357	285	421	170	340	267	356
HIV/AIDS INCIDENCES	470	502	568	454	508	481	357	499	478	578
PNEUMONIA & HIV/AIDS INCIDENCES	972	625	983	811	793	902	527	839	745	934
PNEUMONIA &HIV/AIDS DEATHS	151	87	320	470	510	496	324	290	281	294
RECOVERED PNEUMONIA	490	105	400	345	275	407	163	329	262	334
PNEUMONIA DEATHS	12	18	15	12	10	14	7	11	5	22
HIV/AIDS DEATHS	139	69	305	368	500	482	317	279	276	272

Table 4.1.2: Parameter Definitions

Parameter	Definition of the Parameter	Value	Source
σ	Recovery rate from pneumonia	0.0005180	Calculated
μ	Natural death rate of persons in all classes	0.0000756	Caculated
η_p	Relative infetiousness of individuals infected with pneumonia	0.0059910	Calculated
η_{pH}	Relative infetiousness of dually infected victims	0.0036600	Calculated
η_H	Relative infetiousness of all AIDS cases.	0.0045780	Caculated
θ	Increased susceptibility to pneumonia due to HIV infection.	0.0160000	Calculated
α	Increased susceptibility to HIV after recovery from pneumonia infection	0.0056200	Calculated
β_{H}	Effective contact rate of HIV infection	0.0052372	Caculated
β_{P}	Effective contact rate of Pneumonia infection	0.0077480	Calculated
ψ	Force of pneumonia re-infection.	1.6000000	Calculated
δ	Increased HIV infection rate of pneumonia infectives	0.0011400	Caculated
d_P	Accelerated pneumonia death rate	0.0000370	Calculated
ρ	Rate of HIV progression to AIDS	0.0051500	Calculated
γ_p	Progression rate to AIDS for HIV victims exposed to pneumonia.	0.0079000	Caculated
d_A	AIDS accelerated death rate.	0.0022890	Calculated
Λ	Human recruitment rate.	0.1320000	Calculated
e	Education parameter in managing HIV/AIDS.	0.1 - 0.9	Caculated
tr	Treatment parameter in controlling pneumonia	0.1 - 0.99	Calculated

4.2. GRAPHICAL SIMULATION OF RESULTS

Using the data provided in Table 4.1.1 and Table 4.1.2, the numerical results are generated for the dynamics of model (3.1) using MATLAB numerical solver which generate results for Runge-Kutta 4 (RK-4) of order 4. The 4th order Runge Kutta is chosen because of its computational speed and increased level of accuracy for solving non stiff ordinary differential equations. The results are illustrated for the following situation:

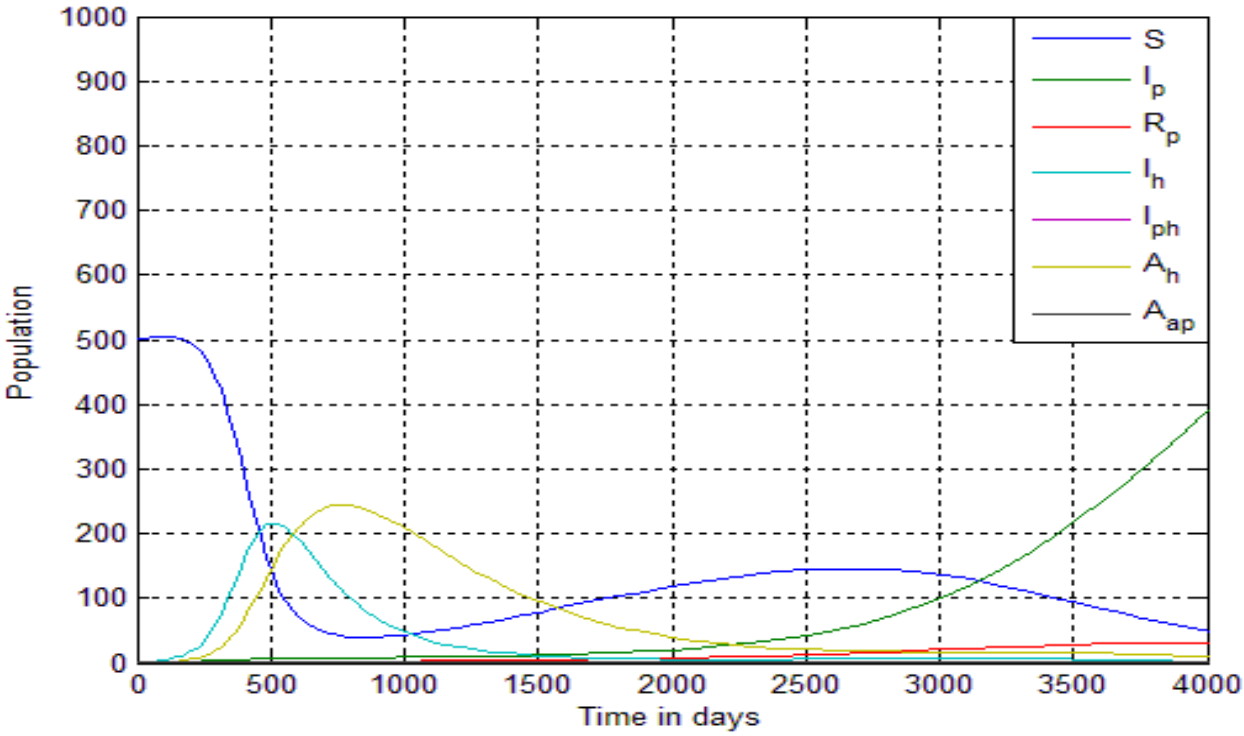

Figure 4.1.1 Population dynamics of various class populations in absence of any Intervention

When no intervention at all is used, that is where there is no treatment of Pneumonia cases and no education awarenes campaign about HIV/AIDS is conducted, the total susceptible population from time zero will be infected so that by the end of around 700 days, (two years), there will be less than 50 uninfected people, over 200 HIV infected people and over 200 AIDS cases, and by then Pneumonia will start to

develop. By the end of 10 years, Pneumonia cases will have risen to almost 400 cases and a few recovered, while all the HIV/AIDS cases will be less than 50, because most of them will have died.

If treatment of Pneumonia only is addressed, while HIV not intervened, the population dynamics will change slightly, with the susceptibles increasing. The required minimum threshold percentage of treatment required to cause an effect is calculated from Equation (3.49), and found to be 0.97. This is also confirmed form the plot of treatment against the reproductive ratio. The reduction of reproductive ratio to less than one is achieved at a minimum treatment of 97%. This means a total of 360 cases must be treated for the threshold to be achieved. This is shown in Figure 4.1.2 bvelow.

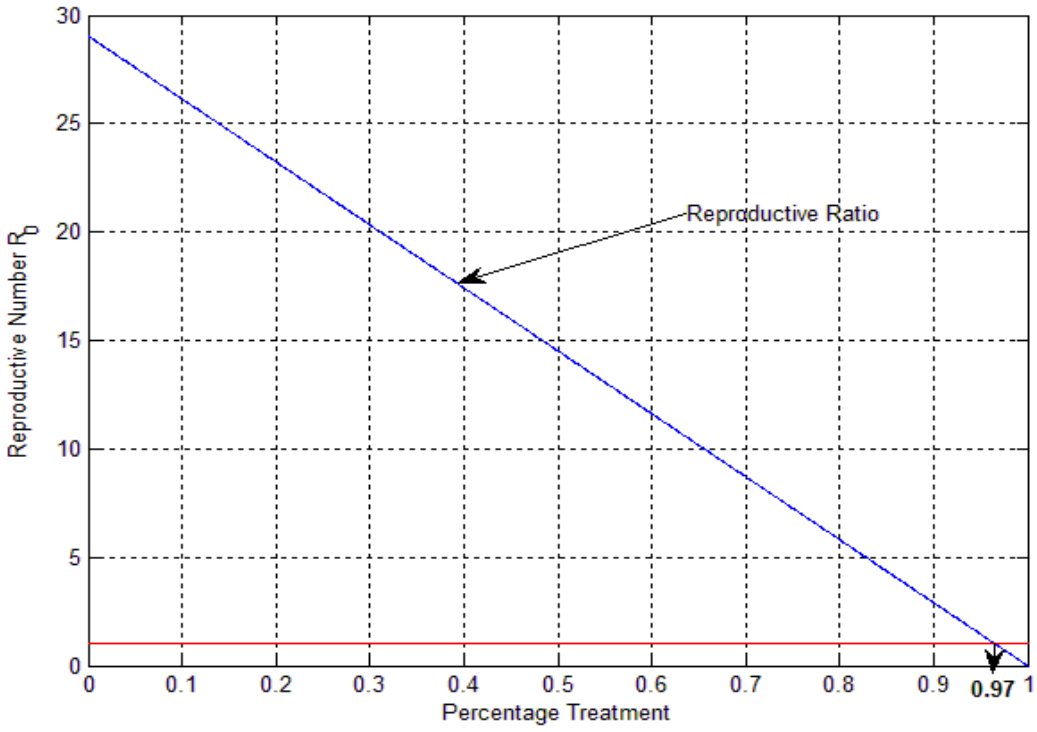

Figure 4.2.2. Minimum treatment threshold of Pneumonia cases to achieve less than one reproductive ratio.

Similarly, the minimum level of education, (awareness campaign) that must be achieved, to cause an effect in HIV cases, and thus reduce the number of infected people is expressed in equation (3.50) and evaluated to be 72%. This is also simulated in the figure below, using the available data. It requires that at least 72% of the masses are aware of the preventive and control measures of HIV/AIDS. The graph below, Figure 4.2.3 illustrates the education threshold required. Reproductive number is plot against percentage level of education.

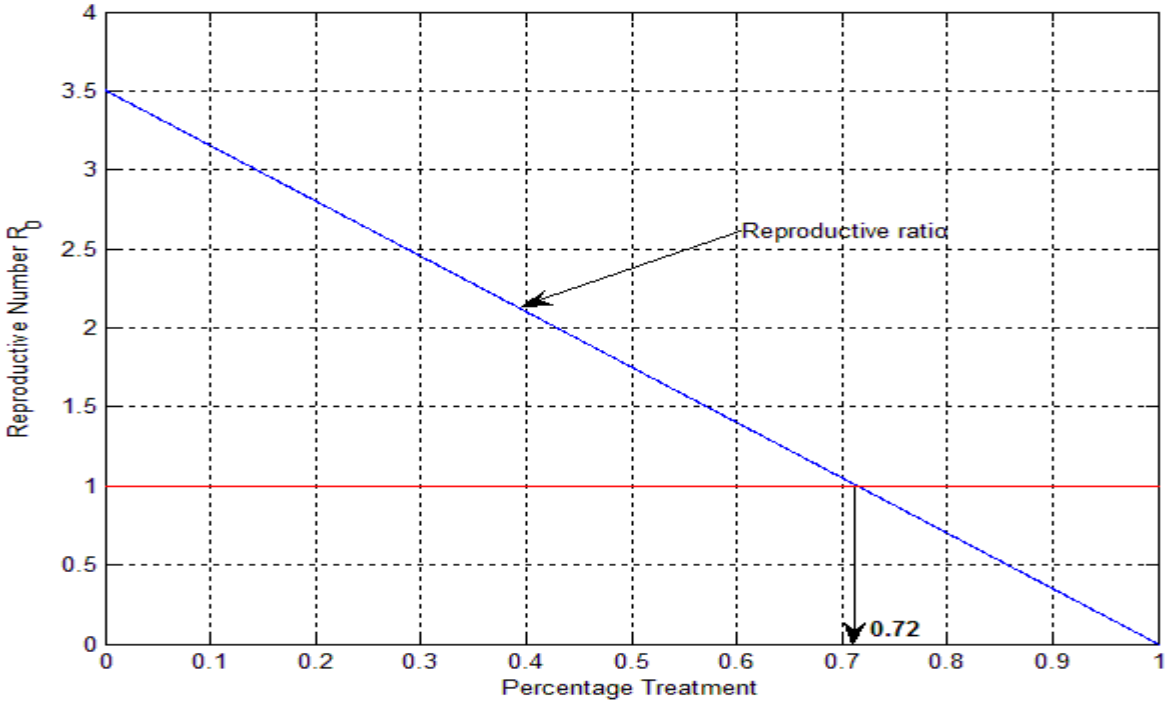

Figure 4.2.3. Minimum Education necessary to bring Reproductive ratio of HIV/AIDS infection to below one

The intervention of both HIV/AIDS and Pneumonia by the said methods, at a level below threshold levels, say 50% for each, shows significant improvement of the susceptible cases and reduced number of infectives. Figure 4.2.4 below shows the simulated results for a 50-50 intervention strategy. It is evident that the susceptibles will remain as high as over 200 even after 10 years of endemic situation and the HIV/AIDS cases is slightly above 100. Meanwhile, the maximum Pneumonia cases is

below 200, unlike in the first case which was over 400 cases. This clearly shows an improvement of the situation. Figure 4.2.5 shows a 75%-75% strategy. The results simulated shows great improvement, with over 400 susceptibles, around 70 pneumonia recovered cases and only 300 pneumonia cases. We also note that HIV/AIDS cases will not be severe, and the graph shows less than 50 cases even after 11 years. This is illustrated in Figure 4.2.5 below.

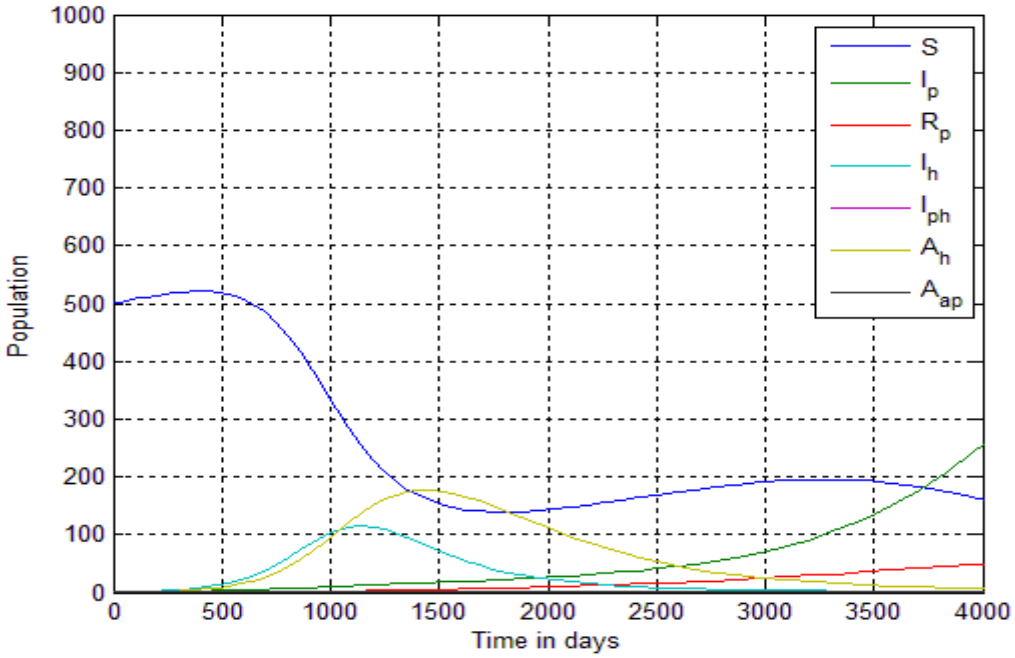

Figure 4.2.4. Population dynamics at 50% treatment of Pneumonia and 50% awareness education campaign against HIV/AIDS

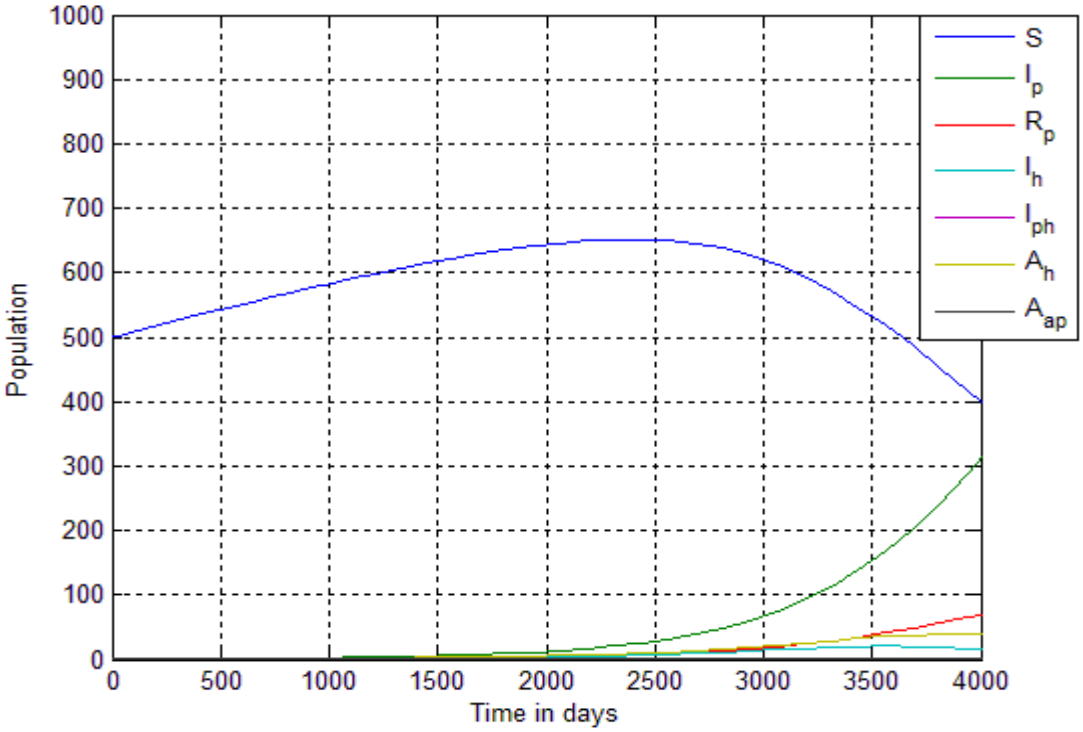

Figure 4.2.5. Treatment and Awareness Education campaign both at 75% each.

In this 75% - 75% strategy, the infected cases of Pneumonia is still as high as 300 cases while the AIDS cases decreased to approximately 70 and the HIV cases the lowest (approximately 20) in a total population of 650 people after 11years.

HIV is the primary disease and Pneumonia is a secondary disease whose dynamics are driven by the HIV/AIDS cases. There is need therefor for control HIV even more than Pneumonia, because, the later is an opportunistic disease and in absence of HIV/AIDS, its incidence is very low. The treatment of pneumonia only do not change the dynamics of the co-infection so much, and it is evident in Figure 4.2.6 below, illustrating 95% treatment of Pneumonia alone, with no intervention to HIV/AIDS. This graph at the same time demonstrates the significance of awareness education campaign as an HIV/AIDS control strategy. Althogh Pneumonia is significantly reduced, the masses are still affected by HIV/AIDS

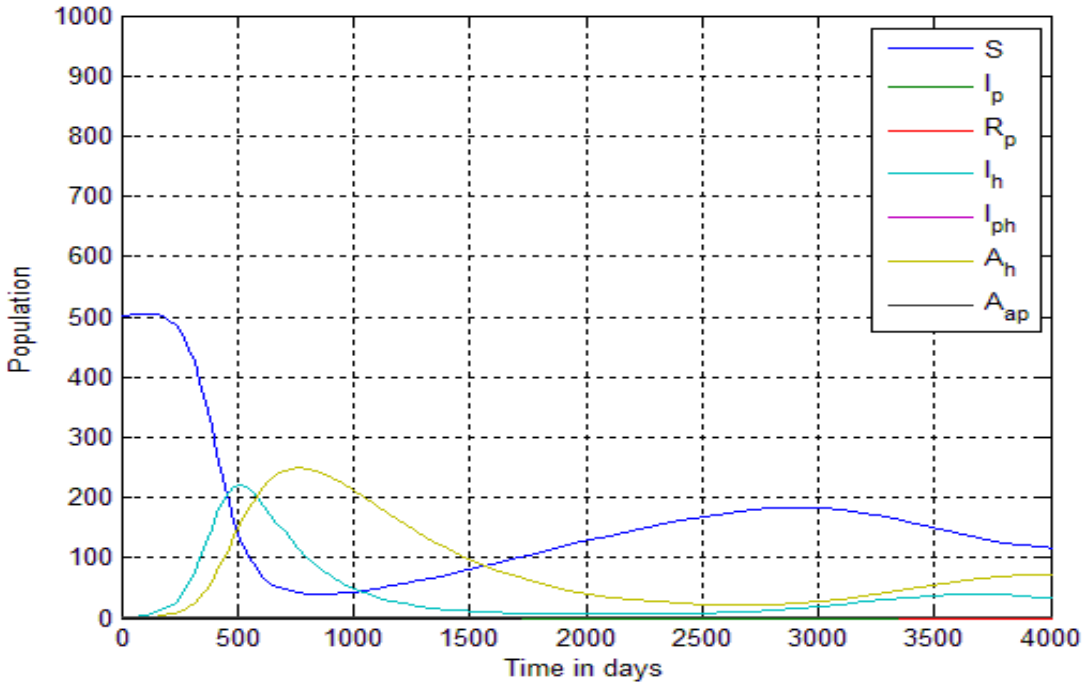

Figure 4.2.6. Single strategy of 95% treatment of Pneumonia with no intervention of HIV/AIDS

If the threshold values are observed, that is 97% treatment and 72% education, a cumulative value of less than 100 people will contract HIV and out of these, over 50 will live with AIDS while around 50 will die of AIDS related cases after 11 years. The total Pneumonia cases will be less than 50 and the susceptibles will remain as high as 370. This is the way forward in reserving rh masses from contracting the deadly HIV disease. The graph in Figure 4.2.7 illustrates the result if intervention is at least greater than the minimum threshold values.

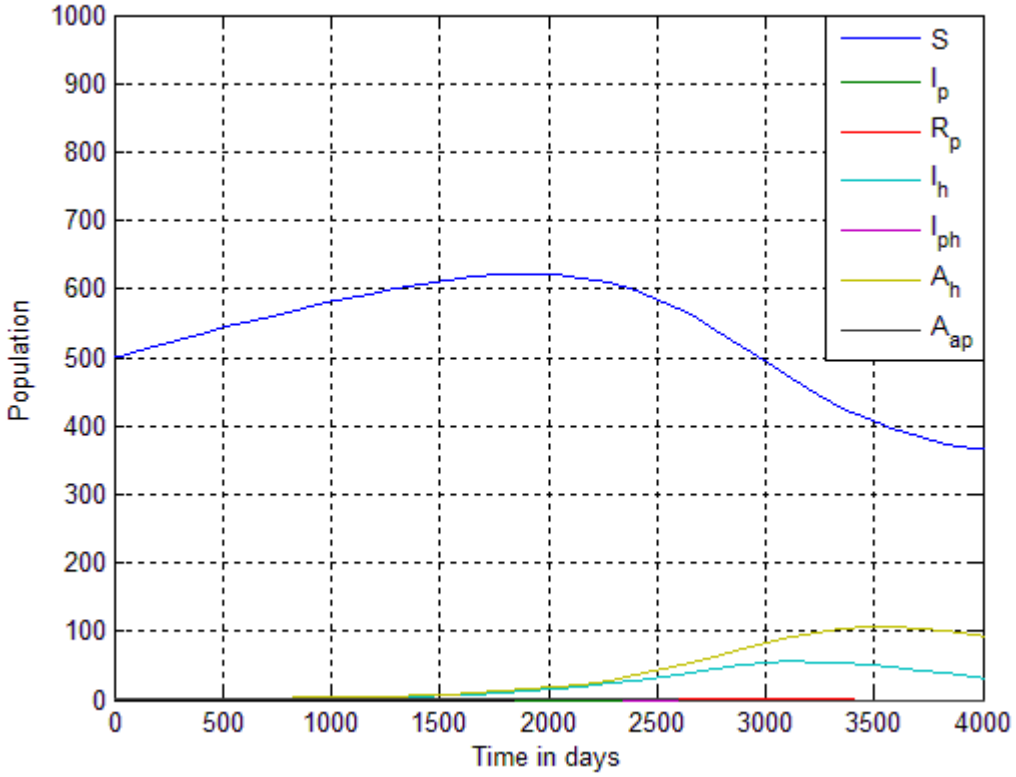

Figure 4.2.7. Effects of a minimum threshold of 97% treatment of Pneumonia and 72% Education on HIV/AIDS Co-infection

Simulation for a period of over 30 years shows that the susceptible population will oscillate then stabilize at a value greater than 470, while HIV only cases will remain at values less than 20 and people living with HIV/AIDS will remain at values less than 50. This represents a situation wher people dying of HIV is minimized and those already infected are able to live with the disease by controlling opportunistic diseases by use of Anti-retrovirals. The people living with HIV/AIDS and Pneumonia co-infection will be eradicated completely. Figure 4.2.8 illustretes the long term dynamics at minimum threshold values of intervention strategies.

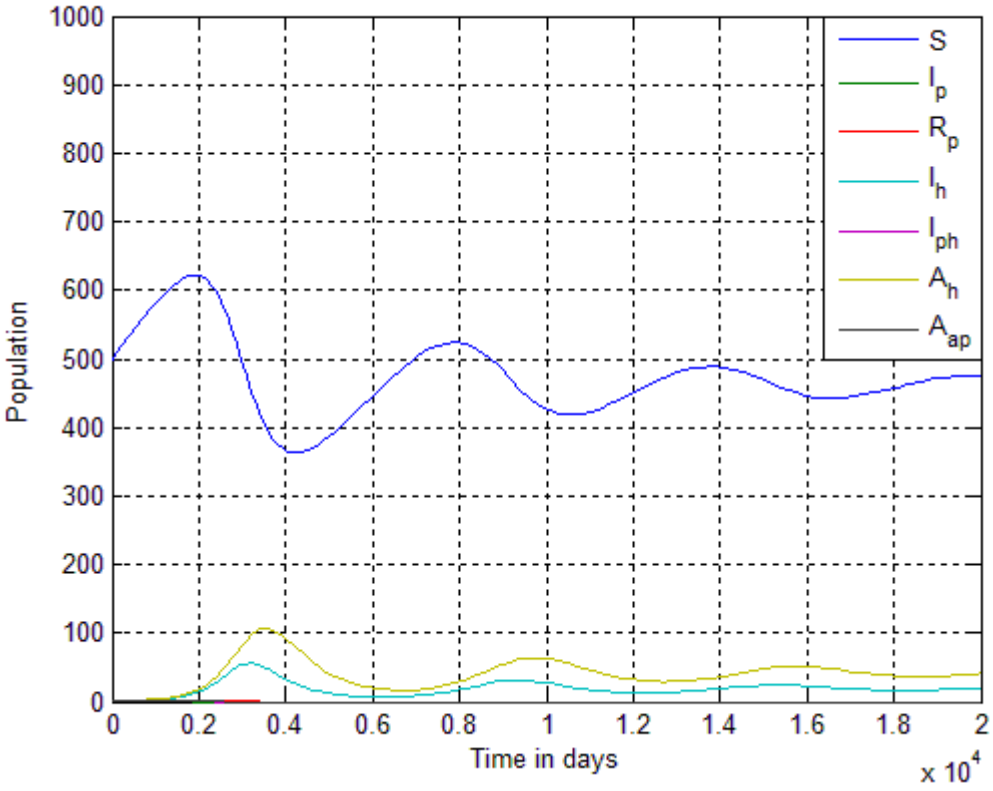

Figure 4.2.8. Long term dynamics of HIV/AIDS Co-infection dynamics for a period of over 50 years

CHAPTER FIVE

CONCLUSION AND RECOMMENDATION

5.1 CONCLUSION

In this particular thesis we have Mathematically modelled the Pneumonia and HIV/AIDS co-infection. We have provided rigorous simulations to determine important parameters and effectiveness of various control strategies without necessarily carrying out clinical trials hence reducing time and costs. In this thesis, a Mathematical Model of HIV/AIDS and Pneumonia co-infection is formulated and analyzed to test the effectiveness of Treatment in controlling Pneumonia and checking the effectiveness of Education in controlling the spread of HIV/AIDS. This objective has thus been achieved with a minimum threshold of 97% treatment of Pneumonia cases (485 people in 500 cases) and a minimum threshold of 72% in HIV/AIDS cases (educating a minimum of 360 people in 500 cases). This gives the required epidemic burn-out of the 2 infections. The minimum threshold and the required graphs were achieved by numerically simulating the data using MATLAB which generate results using 4^{th} – order Runge-Kutta scheme. At the minimum threshold, the reproduction numbers of both Pneumonia (97%) and HIV/AIDS (72%) are less than 1 as generated using MATLAB simulation code. This agrees with the analytic results computed in chapter 3 which calculation gives the minimum threshold for education at $e > 0.72\ (72\%)$ and minimum threshold for treating Pneumonia at $tr > 0.97\ (97\%)$.

5.2 RECOMMENDATIONS

From the results obtained analytically and justified using the data obtained from Kapsabet District Hospital, it is recommended that the proposed intervention strategy is implemented and strictly adhered to in order to achieve the desired results. In a period of over 11 years, the there will be less than 20 cases of new incidences of HIV and less than 50 people living with HIV/AIDS. There will be no pneumonia related deaths and no HIV-Pneumonia co-infection. The cost factors need to be asssessed on how the strategy will be implemented but the most effective way is incorporating HIV/AIDS awareness education materials in School Syllabus, so that the students are taught by their teachers. Also a small group of peer counsellors can be trained to reach the masses in the village.

In this study, the results presented depicts a situation created using assumptions which does not necessarily hold in every day life. Our model assumes that the masses under study is a closed population and there is zero emigration and transfer of individuals from one point to the other. We have also assumed that apart from Pneumonia, there is no other opportunistic disease and the only cause of death is either AIDS or Pneumonia. This is not always true and it is recommended that a detailed study of a model including a parameter to account for the effect of other opportunistic diseases is conducted.

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APPENDICES

Appendix I: MATLAB Simulation Code for Effects of Education on HIV

```
function Effects of Education on HIV/AIDS Pneumonia Treatment
Simulation Code %Includes the effect of CD8 on the viral population
tspan = [0, 5000];
global N;
N = 500;% Total Population
Iv = [N; 1; 0; 1; 0; 0; 0];
[t,dy] = ode45(@red4lag,tspan,Iv);
%.........................................
figure;
plot(t,dy)
axis([0 4000 0 1000]);
%title('HIV/Pneumonia dynamics');
xlabel('Time in days')
ylabel('Population')
legend('S','I_p','R_p','I_h', 'I_{ph}','A_h','A_{ap}');
grid,hold on;
%-----------------------------------------------------------------
-----
function dy = red4lag(t,v)
dy = zeros(7, 1);% dimension of solution vector
global N;
%N = 600;% Total Population
g = 0.000518;% Recovery rate from Pneumonia (sigma)
a = 0.132;% Constant recruitment rate (Delta)
u = 0.0000756;% Natural death rate (mu)
c = 1.6;% Force of Pneumonia re-infection (phi)
d = 0.00299;%0.05114;% Increased HIV infection rate of Pneumonia
infectives (delta)
np = 0.005991;% Relative infectiousness of individuals infected with
Pneumonia (eta_p)
nph = 0.00366;% Relative infectiousness of dually infected victims.
eta_ph)
nh = 0.004578;% Relative infectiousness of all HIV cases (eta_h)
o = 0.016;% Increased susceptibility to Pneumonia due to HIV
infection (theta)
al = 0.00562;% Increased susceptibility to HIV after recovery from
Pneumonia Infection (alpha)
beh = 0.02034;%0.075 Effective contact rate of HIV infection (beta-h)
bep = 0.005244;%0.075 Effective contact rate of Pneumonia
infection(beta-p)
dp = 0.0000370;%0.03041;% Accelerated Pneumonia death rate (d_p)
p = 0.00515;% Rate of HIV progression to AIDS (rho)
y = 0.0079;% Progression rate to AIDS for HIV victims exposed to
Pneumonia (gamma)
da = 0.002289;% AIDS accelerated death rate (d_a)
e = 0.72;% Education (e)
tr = 0.97;% Treatment (tr)
%.........................................................
dy = [a - (1-tr)*(bep/N)*(v(2)+v(5)+v(7))*v(1)-(1-
e)*(beh/N)*(v(4)+v(5))*v(1) - u*v(1)
    (1-tr)*(bep/N)*(v(2)+v(5)+v(7))*(v(1) + c*v(3))- d*v(2)*(1-
e)*(beh/N)*(v(4)+v(5))-(u+g+dp)
```

```
    g*v(2)- (al*(1-e)*(beh/N)*(v(4)+v(5)) + u + c*(1-
tr)*(bep/N)*(v(2)+v(5)+v(7)))*v(3)
    v(1)*(1-e)*(beh/N)*(v(4)+v(5)) + al*(1-
e)*(beh/N)*(v(4)+v(5))*v(3) - o*(1-tr)*(bep/N)*(v(2)+v(5)+v(7))*v(4)-
(p+u)*v(4)
    o*(1-tr)*(bep/N)*(v(2)+v(5)+v(7))*v(4)+d*(1-
e)*(beh/N)*(v(4)+v(5))*v(2)-y*p*v(5)-(u+dp)*v(5)
    p*v(4)-o*np*(1-tr)*(bep/N)*(v(2)+v(5)+v(7))*v(6)-(u+da)*v(6)
    y*p*v(5)+o*np*(1-tr)*(bep/N)*(v(2)+v(5)+v(7))*v(6)-
(u+da+dp)*v(7)];
```

Appendix II: MATLAB Simulation Code for minimum percentage of Education for effective control of HIV/AIDS infection

```
function Minimum Education Simulation Code
%Parameters
N = 500;% Total Population
g = 0.000518;% Recovery rate from Pneumonia (sigma)
a = 0.132;% Constant recruitment rate (Delta)
u = 0.0000756;% Natural death rate (mu)
c = 1.6;% Force of Pneumonia re-infection (phi)
d = 0.00299;%0.05114;% Increased HIV infection rate of Pneumonia
infectives (delta)
np = 0.005991;% Relative infectiousness of individuals infected with
Pneumonia (eta_p)
nph = 0.00366;% Relative infectiousness of dually infected victims.
(eta_ph)
nh = 0.004578;% Relative infectiousness of all HIV cases (eta_h)
o = 0.016;% Increased susceptibility to Pneumonia due to HIV
infection (theta)
al = 0.00562;% Increased susceptibility to HIV after recovery from
Pneumonia Infection (alpha)
beh = 0.02034;%0.075 Effective contact rate of HIV infection (beta-h)
bep = 0.005244;%0.075 Effective contact rate of Pneumonia infection
(beta-p)
dp = 0.0000370;%0.03041;% Accelerated Pneumonia death rate (d_p)
p = 0.00515;% Rate of HIV progression to AIDS (rho)
y = 0.0079;% Progression rate to AIDS for HIV victims exposed to
Pneumonia (gamma)
da = 0.002289;% AIDS accelerated death rate (d_a)
%e = 0.5;% Education (e)
%tr = 0.966;% Treatment (tr)
%.....................................................................
tr=[0:0.001:1];
R0 = 1;
%R1 = ((1-tr)*(bep*a)/(u*N*(u+g+dp)))
for tr = 0:0.001:1;
    R1 = ((1-tr)*(bep*a)/(u*N*(u+g+dp)));
    plot(tr,R1,'-'), hold on, gr
    plot(tr,R0,'r'),grid on
end
grid
xlabel('Percentage Treatment')
ylabel('Reproductive Number R_0')
tr = 1- ((u*N*(p+u))/(bep*a))
```

Appendix III: MATLAB Simulation Code for minimum Treatment Simulaton Code

```
function Minimum Treatment Simulation Code
%Parameters
N = 500;% Total Population
g = 0.000518;% Recovery rate from Pneumonia (sigma)
a = 0.132;% Constant recruitment rate (Delta)
u = 0.0000756;% Natural death rate (mu)
c = 1.6;% Force of Pneumonia re-infection (phi)
d = 0.00299;%0.05114;% Increased HIV infection rate of Pneumonia
infectives (delta)
np = 0.005991;% Relative infectiousness of individuals infected with
Pneumonia (eta_p)
nph = 0.00366;% Relative infectiousness of dually infected victims.
(eta_ph)
nh = 0.004578;% Relative infectiousness of all HIV cases (eta_h)
o = 0.016;% Increased susceptibility to Pneumonia due to HIV
infection (theta)
al = 0.00562;% Increased susceptibility to HIV after recovery from
Pneumonia Infection (alpha)
beh = 0.02034;%0.075 Effective contact rate of HIV infection (beta-h)
bep = 0.005244;%0.075 Effective contact rate of Pneumonia infection
(beta-p)
dp = 0.0000370;%0.03041;% Accelerated Pneumonia death rate (d_p)
p = 0.00515;% Rate of HIV progression to AIDS (rho)
y = 0.0079;% Progression rate to AIDS for HIV victims exposed to
Pneumonia (gamma)
da = 0.002289;% AIDS accelerated death rate (d_a)
%e = 0.5;% Education (e)
%tr = 0.966;% Treatment (tr)
%.....................................................................
tr=[0:0.001:1];
R0 = 1;
%R1 = ((1-tr)*(bep*a)/(u*N*(u+g+dp)))
for tr = 0:0.001:1;
    R1 = ((1-tr)*(bep*a)/(u*N*(u+g+dp)));
    plot(tr,R1,'-'), hold on, gr
    plot(tr,R0,'r'),grid on
end
grid
xlabel('Percentage Treatment')
ylabel('Reproductive Number R_0')
tr = 1- ((u*N*(p+u))/(bep*a))
```