ADAMA SCEINCE AND TECHNOLOGY UNIVERSITY
SCHOOL OF APPLIED NATURAL SCIENCES
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A THESIS ON MATHEMATICAL MODELING OF HIV/AIDS TRANSMISSION FROM MOTHER TO CHILDREN WITH TREATMENT

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Contents

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Abbreviation

HIV – Human Immunodeficiency Virus

AIDS – Acquired Immunodeficiency Syndrome

ART-Antiretroviral Therapy

DFE - Disease Free Equilibrium

Abstract

In this research work we developed a mathematical model which describes the dynamic transmission of HIV/AIDS from mother to children with treatment. A nonlinear deterministic mathematical model for the problem is proposed and analyzed qualitatively using the stability theory of differential equations. Local stability of the disease free equilibrium point of the model was established using next generation method. The results show that the disease free equilibrium point is locally asymptotically stable when the threshold parameter is less than unity and unstable at threshold parameter greater than unity. Globally, the disease free equilibrium point is not stable due to existence of forward bifurcation at threshold parameter equal to unity. The endemic equilibrium point is locally asymptotically stable when the threshold parameter is greater than unity, unstable at threshold parameter less than unity and globally asymptotically stable under certain conditions. However, it is shown that using treatment measures (ARVs) and control of the rate of vertical transmission have the effect of reducing the transmission of the disease significantly. Numerical simulation of the model is implemented to investigate the sensitivity of certain key parameters on the spread of the disease.

ARVs, HIV/AIDS, Stability, Bifurication threshold parameter.

Chapter 1

Introduction

1.1 Back ground of the study

Diseases can be transmitted in many ways, some of which can be transmitted by direct physical contact between an infected individual and a susceptible individual. On the other hand, it can also be transmitted from an infected mother to an unborn or newborn offspring, this is called vertical transmission [16]. HIV/AIDS is one of an example that disease can be transmitted vertically. The impact of vertical transmission of HIV/AIDS has been felt mainly in Africa where the level of literacy is low, the poverty level is very high and the quality of health services is generally poor [5].

HIV/AIDS can be transmitted from mother to child during pregnancy, delivery or breastfeeding and is influenced by many factors, including maternal viral load and the type of delivery [17]. According to [2,14] about 20% of the children infected with HIV develop AIDS in the first year of their lives, and most of them die by the age of 4 years; the others, up to 80% of infected children, develop symptoms of HIV/AIDS at school entry age (7-9 years) or even during adolescence. In Africa HIV/AIDS transmission is primarily through heterosexual sex and vertical transmission [8].

In this research work therefore we study and analyze the transmission of HIV/AIDS from mother to children with treatment. Consequently, we formulate anon-linear system of differential equations that models the dynamics of transmission in a population of varying size.

1.2 Statement of the problem

AIDS is an infectious disease in both the developed and developing countries. It is a fatal disease, which destroys the body's immune system, leaving the victim vulnerable to a host of life threatening opportunistic infections, neurological disorders or unusual malignancies. It causes mortality of millions of people and expenditure of enormous amount of money in health care and disease control. The AIDS epidemic has spread rapidly in Africa than any other continent in the world, sub-Saharan countries being the worst hit [6].

The Center of Disease Control (CDC) estimates that from 1981 to 2001, approximately 21 million people died from AIDS worldwide, millions of people all over the world are currently infected with the human immunodeficiency syndrome virus(HIV), about 95% of them are in developing countries[14]. HIV infection spreads rapidly in populations through unsafe sexual interaction with an accompanying risk of vertical transmission. Vertical transmission can occur through transplacental transfer of disease agents [16].

Antiretroviral therapy (ART) provides a maximal and durable suppression of the viral load and helps to slow the disease progression, reduces HIV-related morbidity and mortality and improves the quality of life of the infected person[3]. A lot of mathematicians and scientists have conducted various studies to find a remedy to the HIV/AIDS pandemic. A very important tool that is usually employed in epidemiological studies of this nature is mathematical modeling. It can be used to study the epidemiological patterns for disease control to predict the short and long term transmission dynamics of HIV/AIDS[4].

In this research work we developed a mathematical model using a non linear system of ordinary differential equations to describe the transmission of HIV/AIDS from mother to children in a population with treatment. The analysis of the model will be done using different mathematical tools to get insight of the transmission dynamics. Therefore, being on the existing model and facts of [15] this research work tried to answer the following basic questions.

1. What is the dynamic of HIV/AIDS transmissions from mother to children?
2. How can we develop a mathematical model that describes the dynamics of the transmission of HIV/AIDS with treatment?
3. What are the prevention mechanisms to protect the transmission of HIV/AIDS from mother to children?
4. What are the biological interpretations of the solution of mathematical model problems?

1.3 Objective of the study

1.3.1 General objectives

The general objective of this study is to understand the dynamic transmission of HIV/ AIDS from mother to child with treatment and suggest possible prevention mechanisms.

1.3.2 Specific objectives

The specific objectives of the study are to:

- Develop a mathematical model which describes the dynamics of HIV/AIDS transmission from mother to children with treatment,
- Determine the prevention mechanisms to protect the transmission of HIV/AIDS from mother to children,
- Determine the conditions under which the equilibrium points of the model equations are stable or not, and
- Examine the biological interpretation of the solution of the mathematical problem.

1.4 Significance of the study

This research thesis will help to:

- Give an awareness for the patient mothers to protect their children from the transmission of HIV/AIDS,
- The policy makers to develop prevention mechanisms of HIV/AIDS transmission from mother to children,
- The researcher as the base for the further research on mathematical modeling of HIV/AIDS transmission from mother to children, and
- Give some information about the transmission of HIV/AIDS from mother to children for those who are interested to read this thesis.

Chapter 2

Review literature

The term vertical transmission of a disease is used to mean the transmission of a disease from infected mothers to their unborn or newly born babies[11,15,16]. It is also commonly referred to as mother-to-child transmission. Examples of diseases that can be vertically transmitted include some sexually transmitted diseases such as gonorrhea and syphilis, herpes, tuberculosis and recently, HIV/AIDS. Human immunodeficiency virus (HIV) infection in children is generally more serious than in adults due to faster disease complications and progression[18]. From the start of the HIV epidemic, vertical transmission from mother to child appeared to be a major source of new HIV infections.

Initial studies of HIV-positive pregnant women show that mother to child transmission (MTCT) rates in the absence of any interventions is around 15%–45%, with higher rates seen amongst mothers who become HIV-positive during their pregnancy. Although the exact mechanisms of transmission are unknown, researchers have identified three stages at which transmission from mother to child can occur: during pregnancy (in utero, ante partum), during labour (intra-partum) and during breastfeeding (post-partum). Transmissions in utero are thought to occur via micro transfusion of maternal blood through the placenta, and it is believed that most of these infections take place in the latter stages of pregnancy. Intra-partum transmissions are thought to occur via exposure to maternal cervico-vaginal secretions and blood by the infant through the birth canal during delivery. Finally, most post-partum transmissions take place as a result of breastfeeding, as HIV viraemia can be detected in breast milk [15]. The concentration of infective HIV (high viral

load) in the blood and genital secretions of HIV-infected pregnant women appears to be the best factor associated with the risk of vertical transmission [12].

Vertical transmission of HIV appears to be highest during labour and delivery. Approximately 25 – 38% of vertical transmission occurs in utero and at least 50% of HIV infected children have been infected either per-or post-natally by infected mothers' milk [17]. Clearly, as these three stages have been identified as the likely major stages at which HIV transmission can occur, it is logical that they should be the targets for interventions to prevent transmission from mother to child. Non antiretroviral interventions, such as use of elective caesarean section to prevent intrapartum transmissions, and avoiding breastfeeding to prevent post-partum transmissions, have both been shown to be successful prevention strategies. However, there are limitations to these approaches.

In the developing world, avoiding breastfeeding has proved not to be a viable option in all settings due to increased infant mortality when access to formula milk or clean water is problematic. Although elective caesareans are the preferable mode of delivery for avoiding transmission, emergency caesareans and vaginal deliveries are not always avoidable. Furthermore, neither strategy will impact on ante partum transmissions[17].

Thus, clearly, the need for further intervention is warranted. One obvious intervention is through the use of antiretroviral drugs[17]. Currently available drugs do not completely eradicate HIV infection; therefore, lifelong treatment might be needed. The goal of antiretroviral treatment is to decrease the morbidity and mortality that is generally associated with HIV infection[9]. The current antiretroviral drugs (ARV) are known to be effective in lowering viral loads[10]. Other studies[4,7,8] involving treatment of HIV-infected children have demonstrated further that effective treatment for these children can prolong their survival and significantly improve the quality of their lives. There fore, in this research work we tried to improve the work of [15] depending on the existing model and facts.

Chapter 3

Model Formulation and Analysis

3.1 Model formulation

A non linear mathematical model is proposed and analyzed to study the transmission of HIV/AIDS from mother to children with treatment. In modeling the dynamics, the population at time t is divided into five classes.
These are: Susceptible , infected, pre-AIDS, Treated class and AIDS patients class (SIPTA). Susceptible is free infected HIV-AIDS populations, Infected is HIV-infected population, Pre-AIDS is an HIV-infected population who has symptoms of AIDS before suffer positively AIDS, Treatment population is HIV-AIDS population who are doing the treatment, and AIDS is a population that suffer positively AIDS.

Model Assumptions

The following assumptions were used to simplify the model:

- The susceptible become HIV infected via sexual contacts with infectives which may also lead to the birth of infected new born baby.
- A fraction of new born children are infected during birth and hence are directly recruited into the infective class.
- The susceptible individual under the study is homogeneous, it means that everyone has the same risk to be infected by HIV.
- Individuals in pre-AIDS and AIDS class were isolated, themselves to have not had sexual contact with other and hence they are not capable of producing children.

- In each class the death occurred due to natural mortality and due to AIDS.

- We do not consider direct recruitment of the infected persons but by vertical transmission only.

The variables and parameters which were used in this study are:

The variables:

S(t) : The number of individuals Susceptible.

I(t) : The number of individuals Infected.

P(t) : The number of individuals Pre-AIDS.

T(t) : The number of individual Treatment.

A(t) : The number of AIDS positive individuals.

N(t) : Total population.

The Parameters:

π =Rate of recruitment in to susceptible population.

c = Average number of sexual partner per unit time.

β_i = 1,2,3,4, are sexual contact rate.

δ = Rate of movement from infection class.

ε= Fraction of new borns infected with HIV who dies immediately after birth.

θ=Rate of newborns infected with HIV.

μ=Natural mortality rate.

α=Induced death rate due to AIDS.

σ_1=fraction of δ joining the pre-AIDS class.

γ=Rate of movement of pre-AIDS class individuals in to AIDS class.

σ_2=Fraction of δ joining treated class.

ν=Rate at which AIDS group get treatment.

m = fraction of γ who gets treatment.

κ= Rate at which treated group becomes full blown AIDS.

Based on the above assumptions, we then have the following schematic flow diagram below. From the figure and the assumptions, we can get the following system of

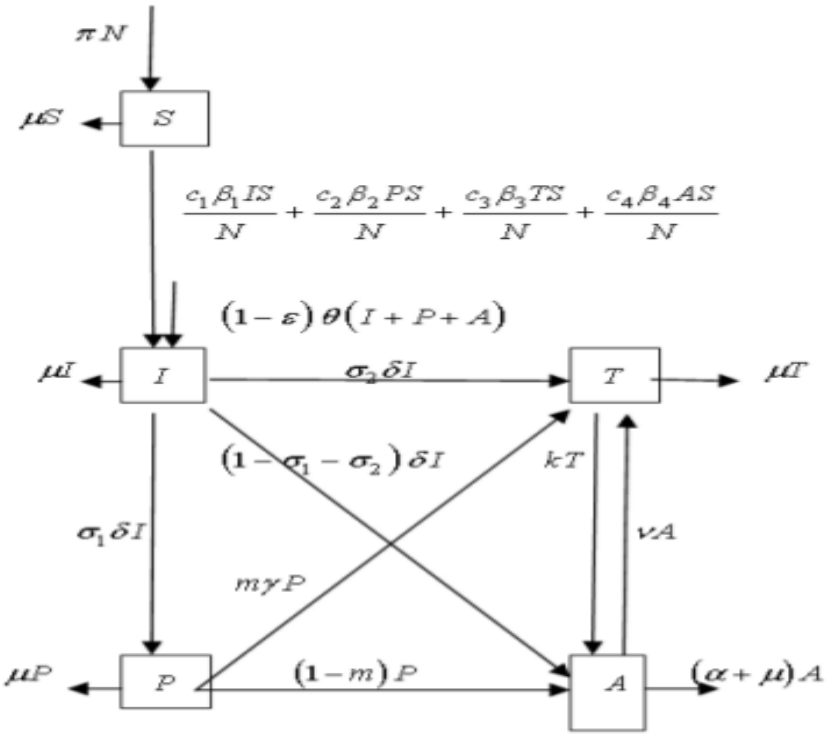

Figure 3.1: Flow diagram of the model[16]

differential equations.

$$\begin{aligned}
\frac{ds}{dt} &= \pi N - \frac{C_1\beta_1 IS}{N} - \frac{C_2\beta_2 PS}{N} - \frac{C_3\beta_3 TS}{N} - \frac{C_4\beta_4 AS}{N} - \mu S \\
\frac{dI}{dt} &= \frac{C_1\beta_1 IS}{N} + \frac{C_2\beta_2 PS}{N} + \frac{C_3\beta_3 TS}{N} + \frac{C_4\beta_4 AS}{N} + (1-\varepsilon)\theta(I+P+A) - (\delta+\mu)I \\
\frac{dP}{dt} &= \sigma_1\delta I - (\gamma+\mu)P \\
\frac{dT}{dt} &= \sigma_2\delta I + m\gamma P + \nu A - (\kappa+\mu)T \\
\frac{dA}{dt} &= (1-\sigma_1-\sigma_2)\delta I + (1-m)\gamma P + \kappa T - (\nu+\alpha+\mu)A
\end{aligned} \tag{3.1}$$

here the initial conditions are taken as: S(0)=S_o, I(o)=I_o, P(o)=P_o, T(0)=T_o and A(0)=A_o. To simplify the model, it is reasonable to assume that the AIDS patients and those in pre-AIDS class are isolated and sexually inactive and hence they are not capable of producing children i.e. $(1-\varepsilon)\theta P = 0 = (1-\varepsilon)\theta A$. And also they do not contribute to viral transmission horizontally i.e, β_2 and β_4 are negligible.

In view of the above assumptions, the system reduces to:

$$\begin{aligned}
\frac{ds}{dt} &= \pi N - \frac{C_1\beta_1 IS}{N} - \frac{C_3\beta_3 TS}{N} - \mu S \\
\frac{dI}{dt} &= \frac{C_1\beta_1 IS}{N} + \frac{C_3\beta_3 TS}{N} + (1-\varepsilon)\theta I - (\delta+\mu)I \\
\frac{dP}{dt} &= \sigma_1\delta I - (\gamma+\mu)P \\
\frac{dT}{dt} &= \sigma_2\delta I + m\gamma P + \nu A - (\kappa+\mu)T \\
\frac{dA}{dt} &= (1-\sigma_1-\sigma_2)\delta I + (1-m)\gamma P + \kappa T - (\nu+\alpha+\mu)A
\end{aligned} \tag{3.2}$$

The total population N at any time t is given by :

N(t) = S(t) + I(t) + P(t) + T(t) + A(t)

This gives :

$\frac{dN}{dt} = (\pi-\mu)N - \alpha A + (1-\varepsilon)\theta$ I

We note that in the absence of the disease and infective, the total population size N is constant for $\pi = \mu$, decline for $\pi < \mu$ and grows exponentially for $\pi > \mu$, so we shall assume that mortality rate μ, will be a function of state variables.

Since the model is homogeneous of degree one, the variable can be normalized by setting:

s = S/N, i = I/N, p = P/N, h = T/N, a = A/N.

This leads to the normalized system, and calculated as follows:

$$\begin{aligned}
\frac{ds}{dt} &= \pi - c_1\beta_1 is - c_3\beta_3 hs - [\pi - \alpha a + (1-\varepsilon)\theta i]s \\
\frac{di}{dt} &= c_1\beta_1 is + c_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i \\
\frac{dp}{dt} &= \sigma_1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p \\
\frac{dh}{dt} &= \sigma_2\delta i + m\gamma p + \nu a - [\pi + \kappa - \alpha a + (1-\varepsilon)\theta i]h \\
\frac{da}{dt} &= (1-\sigma_1-\sigma_2)\delta i + (1-m)\gamma p + \kappa h - [\pi + \nu + \alpha + -\alpha a + (1-\varepsilon)\theta i]a
\end{aligned} \tag{3.3}$$

where s + i + p + h + a = 1

3.2 Model Analysis

The nonlinear system (3.3) will be qualitatively analyzed so as to find the conditions for existence and stability of disease free equilibrium points. Analysis of the model allows us to determine the impact of treatment and vertical transmission of HIV/AIDS infection in a population. Also on finding the reproductive number R_o, one can determine if the disease become endemic in a population or not.

3.2.1 Positivity and boundedness of the solution

The model equations are to be epidemiologically meaningful and well posed; we need to prove that all the state variables are non-negative. It is necessary to prove all solutions of system (3.3) with positive initial data will remain positive for all $t > 0$. This will be established by the following theorem.

Theorem 1

Let $s(0) > 0$, $i(0) \geq 0$, $p(0) \geq 0$, $h(0) \geq 0$, and $a(0) \geq 0$.

Then, the solutions { s, i, p, h, a } of the system(3.3) are positive for all $t \geq 0$.

proof

By using differential equation, from the first equation of the system (3.3), we obtain the inequality expression:

$$\frac{ds}{dt} \leq \pi - \pi S$$
$$\frac{ds}{dt} + \pi s \leq \pi$$

Finding the integrating factor,

$$IF = e^{\int \pi dt} = e^{\pi t}$$
$$\frac{d}{dt} = (\pi s e^{\pi t}) \leq \pi e^{\pi t}$$

integrating both sides,

$$s(t) \leq 1 + ce^{-\pi t}$$

Applying the initial condition,when

$$t = 0,\ s(t)s(0),\ s(0) \leq 1 + c$$
$$s(t) \leq 1 + (s(0) - 1)e^{-\pi t}$$

then,

$$\text{as } t \to \infty,\ s(t) \leq 1$$

therefore,

$$0 \leq s(t) \leq 1$$

Using the second equation of the system 3.3, we get,

$$\frac{di}{dt} \geq -(\delta + \pi)i$$
$$\frac{di}{i} \geq -(\delta + \pi)dt$$

Integrating both sides,

$$i(t) \geq i(0)e^{-(\delta+\pi)t}$$

Applying initial conditions at, t = 0,

$$i(t) \geq i(0)$$
$$\text{as } t \to \infty,\ \text{i(t)} \geq 0$$

Also in the third equation of the system (3.3),

$$\frac{dp}{dt} \geq -(\pi + \gamma)p$$
$$\frac{dp}{p} \geq (\pi + \gamma)dt$$

Integrating both sides we get,

$$\text{p(t)} \geq p(0)e^{-(\pi+\gamma)t}$$

Applying initial conditions,

$$\text{at t= 0,p(t)} \geq p(0)$$
$$\text{when, t} \to \infty\text{,p(t)} \geq 0$$

Similarly using equation four of the system (3.3) we have,

$$\frac{dh}{dt} \geq -(\pi + \kappa)h$$
$$\frac{dh}{h} \geq -(\pi + \kappa)dt$$

Integrating both sides we get,

$$h(t) \geq h(0)e^{-(\pi+\kappa)t}$$

Applying initial conditions at,

$$\text{t= 0, } h(t) \geq h(0)$$

when,

$$t \to \infty, h(t) \geq 0$$

Finally using equation five of the system (3.3) we have,

$$\frac{da}{dt} \geq -(\pi + \nu + \alpha)a$$
$$\frac{da}{a} \geq -(\pi + \nu + \alpha)dt$$

Integrating both sides we get,

$$a(t) \geq a(0)e^{-(\pi+\nu+\alpha)t}$$

Applying initial condition,

$$\text{at t=0, } a(t) \geq a(0)$$

when,

$$t \to \infty, a(t) \geq 0$$

Hence all feasible solution of system (3.3) enters the region:
$\{(s, i, p, h, a) : s(t) > 0, i(t) \geq 0, p(t) \geq 0, h(t) \geq 0, a(t) \geq 0; s + i + p + h + a = 1\}$.

3.2.2 Disease Free Equilibrium (DFE) point

The disease free equilibrium point of the normalized model (3.3) is obtained by setting:

$$\begin{aligned} \frac{ds}{dt} &= 0 \\ \frac{di}{dt} &= 0 \\ \frac{dp}{dt} &= 0 \\ \frac{dh}{dt} &= 0 \\ \frac{da}{dt} &= 0 \end{aligned} \tag{3.4}$$

At disease free equilibrium we have;

s=1, i=0, p=0, h=0, a=0.

Therefore the disease free equilibrium (DFE) point denoted by E_0 of the system (3.3) is given by $E_o = (1, 0, 0, 0, 0)$.

3.2.3 Reproduction Number

The reproduction number R_O is defined as the average number of secondary infections caused by typical infected individual during his or her entire period of infectiousness. This definition is given for the models that represent the spreading of infection in a population.

3.2.4 Local Stability Analysis

In order to assess the local stability of the E_o on the system (3.3), computation of the basic reproduction number is essential. And it is determined using next generation matrix. It is also obtained by taking the largest (dominant) eigenvalue (spectral radius) of the next generation matrix.

Therefore in this model, the infected classes are i, p, h and a classes.

So the differential equations used are:

$$\begin{aligned}
\frac{di}{dt} &= c_1\beta_1 is + c_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i \\
\frac{dp}{dt} &= \sigma_1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p \\
\frac{dh}{dt} &= \sigma_2\delta i + m\gamma p + \nu a - [\pi + \kappa - \alpha a + (1-\varepsilon)\theta i]h \\
\frac{da}{dt} &= (1-\sigma_1-\sigma_2)\delta i + (1-m)\gamma p + \kappa h - [\pi + \nu + \alpha + -\alpha a + (1-\varepsilon)\theta i]a.
\end{aligned} \tag{3.5}$$

Then, from the above differential equations, F and V were obtained by matrix:

$$\left[\frac{\partial F_i(E_o)}{\partial X_j} \right] \left[\frac{\partial V_i(E_o)}{\partial X_j} \right]^{-1} \tag{3.6}$$

where:

F_i is the rate of appearance of new infection in compartment i,

V_i^+ is the transfer of individuals out of the component i by all other means,

E_o is the disease free equilibrium.

The associated matrix at disease free equilibrium is given by:

$$F = \begin{bmatrix} c_1\beta_1 & 0 & c_3\beta_3 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \text{ and}$$

$$V = \begin{bmatrix} \pi + \delta - (1-\varepsilon)\theta & 0 & 0 & 0 \\ -\sigma_1\delta & \pi + \gamma & 0 & 0 \\ -\sigma_2\delta & -m\gamma & \pi + \kappa & -\nu \\ -(1-\sigma_1-\sigma_2)\delta & (1-m)\gamma & -\kappa & \pi + \nu + \alpha \end{bmatrix}$$

After finding V^{-1} and then multiplying matrix FV^{-1}, the basic reproduction number was obtained from the largest eigenvalue of matrix FV^{-1}. Then it can be shown that the eigenvalue of FV^{-1} are (0,0,0,Z), where:

$$Z = \frac{c_1\beta_1}{\pi + \delta - \theta + \theta\varepsilon} + \frac{c_3\beta_3(\sigma_2\pi^2 + \sigma_2\pi\alpha + \sigma_2\gamma\pi + \sigma_2\gamma\alpha + \sigma_1 m\gamma\pi + \sigma_1 m\gamma\alpha + \nu\pi + \nu\gamma + \sigma_1\nu\pi)\delta}{(\pi + \delta - \theta + \theta\varepsilon)(\pi + \gamma)(\alpha\pi + \kappa\pi + \pi^2 + \alpha\kappa + \nu\pi)}.$$

Thus, the basic reproduction number R_0 for the normalized model system (3.3) with treatment and vertical transmission is give by:

$$R_o = \frac{c_1\beta_1}{\pi + \delta - \theta + \theta\varepsilon} + \frac{c_3\beta_3(\sigma_2\pi^2 + \sigma_2\pi\alpha + \sigma_2\gamma\pi + \sigma_2\gamma\alpha + \sigma_1 m\gamma\pi + \sigma_1 m\gamma\alpha + \nu\pi + \nu\gamma + \sigma_1\nu\pi)\delta}{(\pi + \delta - \theta + \theta\varepsilon)(\pi + \gamma)(\alpha\pi + \kappa\pi + \pi^2 + \alpha\kappa + \nu\pi)}.$$

Therefore the disease free equilibrium point of the treatment model system (3.3) is locally asymptotically stable if $R_o < 1$ and unstable if $R_o > 1$.

Remark: It is noted that with high R_o, which is a function of the number of sexual partners c, the number of infective will increase which in turn increase the AIDS patients population.Thus in order to keep the spread of the disease at minimum, the number of sexual partners should be restricted.

3.2.5 The Endemic Equilibrium point

To obtain an endemic equilibrium E^*, we solve the system of equations:

$$\pi - c_1\beta_1 is - c_3\beta_3 hs - [\pi - \alpha a + (1-\varepsilon)\theta i]s = 0$$

$$c_1\beta_1 is + c_3\beta_3 hs + (1-\varepsilon)\theta i - [\pi + \delta - \alpha a + (1-\varepsilon)\theta i]i = 0$$

$$\sigma_1\delta i - [\pi + \gamma - \alpha a + (1-\varepsilon)\theta i]p = 0$$

$$\sigma_2\delta i + m\gamma p + \nu a - [\pi + \kappa - \alpha a + (1-\varepsilon)\theta i]h = 0$$

$$(1-\sigma_1-\sigma_2)\delta i + (1-m)\gamma p + \kappa h - [\pi + \nu + \alpha + -\alpha a + (1-\varepsilon)\theta i]a = 0$$

simultaneously. Solving the system of equation simultaneously, while expressing each equilibrium point in terms of i^* at steady state, we get
$s^*(t)$, $p^*(t)$, $i^*(t)$, $h^*(t)$ and $a^*(t)$ as an endemic equilibrium point.
Thus $E^* = (s^*(t), i^*(t), p^*(t), h^*(t), a^*(t))$ is an endemic equilibrium,
where:
$s^* = \frac{\pi+(1-\varepsilon)\theta i^* - (\pi+\delta-\alpha a^*+(1-\varepsilon)\theta i^*)i^*}{\pi-\alpha a^*+(1-\varepsilon)\theta i^*}$,
$p^* = \frac{\sigma_1\delta i^*}{\pi+\gamma-\alpha a^*+(1-\varepsilon)\theta i^*}$,
$h^* = \frac{\kappa}{\Phi\omega}$,
$a^* = \frac{(1-\sigma_1-\sigma_2)\delta i^*\Phi\omega+(1-m)\sigma_1\gamma\delta i^*\Psi+\kappa(2\delta i^*\Phi+m\gamma\sigma_1\delta i^*}{\Phi(\omega\Psi-\kappa\nu)}$,
with
$\Phi = (\pi + \gamma - \alpha a^* + (1-\varepsilon)\theta i^*)$,
$\Psi = (\pi + \kappa - \alpha a^* + (1-\varepsilon)\theta i^*)$,
$\omega = (\pi + \nu + \alpha - \alpha a^* + (1-\varepsilon)\theta i^*)$, and
$\kappa = \sigma_2\delta i^*\Phi + m\gamma\sigma_1\delta i^* + \frac{\nu(1-\sigma_1-\sigma_2)\delta i^*\Phi\Psi+(1-m)\sigma_1\gamma\delta i^*\Psi+\kappa(\sigma_2\delta i^*\Phi+m\gamma\sigma_1\delta i^*)}{\omega\Psi-\kappa\nu}$.
We note that s^*, p^*, h^* and a^*, are always positive and this will happen if and only if $R_o > 0$.

3.2.6 Global Stability Analysis

Theorem 2

If $R_o > 1$, the endemic equilibrium E^* of the model (3.3) is globally asymptotically stable.

Proof

To establish the global stability of the endemic equilibrium E^*, we construct the following Lyapunov function[16]:

$V(s^*, i^*, p^*, h^*, a^*) = (s - s^* - s^* \ln \frac{s^*}{s}) + (i - i^* - i^* \ln \frac{i^*}{i}) + (p - p^* - p^* \ln \frac{p^*}{p}) + (h - h^* - h^* \ln \frac{h^*}{h} + (a - a^* - a^* \ln \frac{a^*}{a})$

By direct calculation of the derivative of V along the solution of (3.3) we obtain;

$$\frac{dv}{dt} = (\frac{s - s^*}{s})\frac{ds}{dt} + (\frac{i - i^*}{i})\frac{di}{dt} + (\frac{p - p^*}{p})\frac{dp}{dt} + (\frac{h - h^*}{h})\frac{dh}{dt} + (\frac{a - a^*}{a})\frac{da}{dt} \quad (3.7)$$

Which gives; $\frac{d}{dt} = Z - Y$, where:

$Z = [c_1\beta_1 i^* + c_3\beta_3 h^* + \alpha a + \theta i + \varepsilon\theta i]\frac{(\delta - \delta^*)^2}{\delta} + [c_1\beta_1 s + \theta + \alpha a]\frac{(i - i^*)^2}{i} + [\alpha a + \theta i + \varepsilon\theta i]\frac{(p - p^*)^2}{p} + [\alpha a + \theta i + \varepsilon\theta i]\frac{(h - h^*)^2}{h} + [\theta i^* + \varepsilon\theta i]\frac{(a - a^*)^2}{a} + \theta\frac{i^{*3}}{i} + c_3\beta_3 h^*\frac{i^*}{i} + \sigma_1\delta i^*\frac{p^*}{p} + \sigma_2\delta i^*\frac{h^*}{h} + m\gamma p^*\frac{h^*}{h} + \nu a\frac{h^*}{h} + \sigma_1\delta i\frac{a^*}{a} + \sigma_2\delta i\frac{a^*}{a} + \delta i^*\frac{a^*}{a} + \gamma p^*\frac{a^*}{a} + m\gamma p\frac{a^*}{a} + \kappa h^*\frac{a^*}{a} + 3\theta i i^* + \varepsilon\theta i^{*2} + \pi + c_3\beta_3 h + \sigma_1\delta i + \sigma_2\delta i + m\gamma p + \nu a + \alpha a^2 + 3\alpha a^{*2} + \delta i + \sigma_1\delta i^* + \sigma - 2\delta I^* + \gamma p + m\gamma P + \kappa h$

and

$Y = -[c_1\beta_1 i + c_3\beta_3 h + \pi + \alpha a^* + \theta i + \varepsilon\theta i^*]\frac{(s - s^*)^2}{s} - [c_1\beta_1 s^* + \varepsilon\theta + \pi + \alpha a^*]\frac{(i - i^*)^2}{i} - [\pi + \gamma + \alpha a^* + \theta i + \varepsilon\theta i^*]\frac{(p - p^*)^2}{p} - [\pi + \kappa + \alpha a^*\theta i^*]\frac{(a - a^*)^2}{a} - \pi\frac{s^*}{s} - c_3\beta_3 h\frac{i^*}{i} - \sigma_1\delta i\frac{p^*}{p} - \sigma_2\delta i\frac{h^*}{h} - m\gamma p\frac{h^*}{h} - \nu a\frac{h^*}{h} - 3\varepsilon\theta\frac{i^*}{i} - \alpha\frac{a^{*3}}{a} - \delta i\frac{a^*}{a} - \sigma_1\delta i^*\frac{a^*}{a} - \sigma_2\delta i\frac{a^*}{a} - \gamma p\frac{a^*}{a} m\gamma p^*\frac{a^*}{a} - \kappa h\frac{a^*}{a} - 3\varepsilon\theta i i^* - 3\alpha a a^* - \theta i^* - 3\theta i^* - c_3\beta_3 h^* - \sigma_1\delta i^* - \sigma_2\delta i^* - m\gamma p^* - \nu a - \sigma_1\delta i - \sigma_2\delta i - \delta i^* - \gamma p^* - m\gamma p - kh^*.$

Therefore from (3.7), if $Z < Y$ then, $\frac{dv}{dt}$ will be negative definite, implying that $\frac{dv}{dt} < 0$; also $\frac{dv}{dt} = 0$, if and only if $s = s^*, i = i^*, p = p^*, h = h^*, a = a^*$.

Therefore, the largest compact invariant set in $(s^*, i^*, p^*, h^*, a^*) \in \Omega : \frac{dv}{dt} = 0$ is the singleton E^*, where E^* is endemic equilibrium of the normalized model system (3.3). By LaSalle's invariant principle, it then implies that E^* is globally asymptotically stable if $Z<Y$.

3.2.7 Bifurication Analysis

The model has two equilibrium point that is disease free equilibrium point and endemic equilibrium point, so that we have two stability analysis at R_0=1. If $R_0 < 1$, there is a disease free equilibrium point which is asymptotically stable, and the infection dies out, that is the infectives decrease and the susceptible increase to a steady equilibrium state. Conversely if $R_0 > 1$ there is an endemic equilibrium point which is asymptotically stable, and the infection persists, and eventually reaching a steady endemic equilibrium point. Therefore the model exhibits a forward bifurcation for some estimated parameters as shown in figure 3.2 below. As R_0 increase through

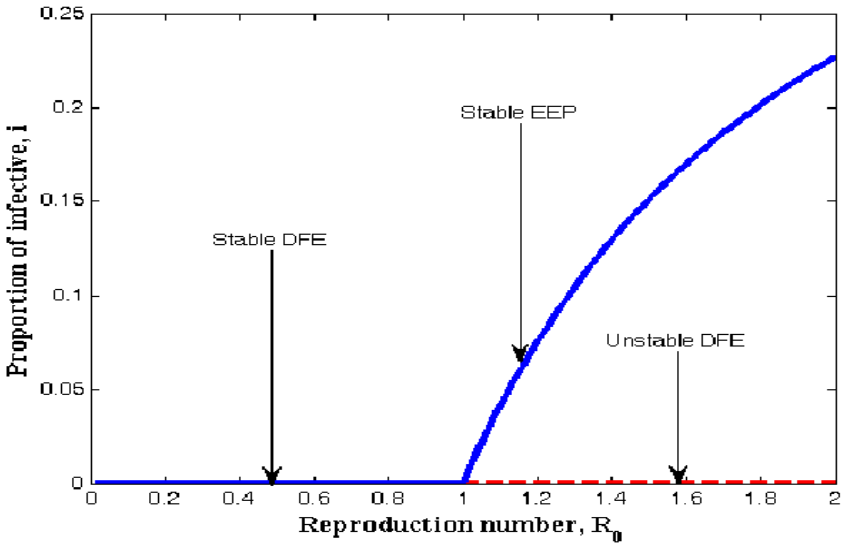

Figure 3.2: Forward bifurication of model(3.3)

1 there is an exchange of stability between the disease-free equilibrium point and endemic equilibrium point. This is referred to as a forward or Transcritical bifurcation, because in the neighborhood of the bifurcation point, the endemic disease prevalence is an increasing function of R_o.

Chapter 4

Numerical simulation of the model

In order to verify the theoretical predictions of the model, the numerical simulations to the model (3.3) are carried out using the following set of estimated parameter values[15]:

$\theta = 0.3, \varepsilon = 0.2, \nu = 0.1, \beta_1 = 0.4, \beta_3 = 0.05, \sigma_1 = 0.2, \sigma_2 = 0.01, \kappa = 0.08, \gamma = 0.9, c_1 = 3, c_3 = 1, m = 0.4, \pi = 0.4, \delta = 0.6, \alpha = 1,$

with the starting values:

S(0)=0.5, i(0)=0.3, p(0)=0.12, h(0)=0.07, a(0)= 0.01. The equilibrium points of the endemic equilibrium E* was obtained as:

S*=0.6028, i*=0.2433, p*=0.2284, h*=0.04236 and a*=0.08929.

Therefore it can be concluded that the system (3.3) is globally stable about this endemic equilibrium point E* for the estimated parameters.

Figure 4.1 below shows that the variation of proportion of population in all classes with both recruitment of susceptible and fraction of new born children which are infected at birth. From the figure it can be seen that susceptible first decrease with time. After undergoing ARV treatment their lives time are prolonged and thus their number increase reaching an equilibrium point.

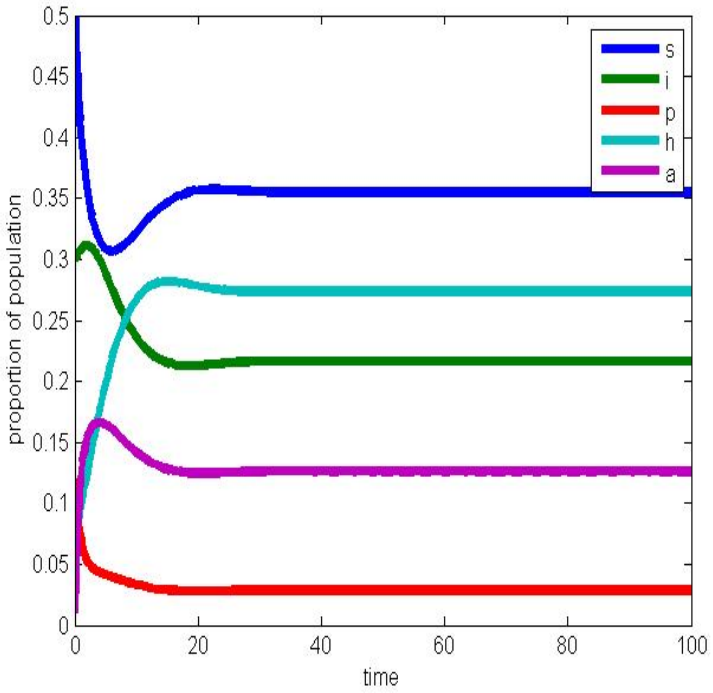

Figure 4.1: Variation of population indifferent class for π=0.1 and θ=0.2

Figures 4.2 – 4.3 below show the variation of susceptible and infective population for different values of number of sexual partners of susceptible with infective C_1, and between susceptible with treated population C_3.

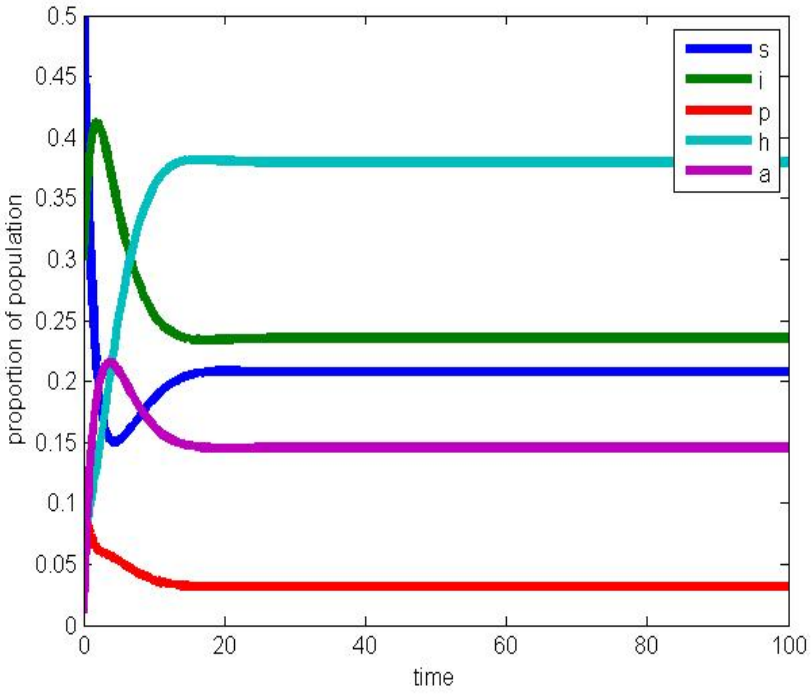

Figure 4.2: Variation of susceptible population for different values of C_1

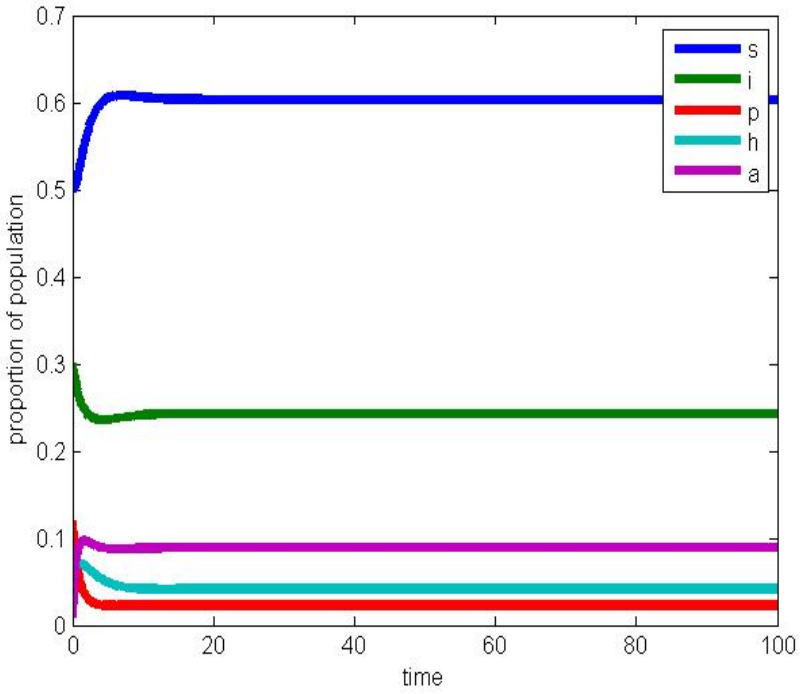

Figure 4.3: Variation of susceptible populationfor different values of C_3

From figure 4.2and 4.3, it is seen that as the number of sexual partners of susceptible with infective C_1 increases with time, susceptible decreases continuously and infective increases continuously. Also it is seen that if the number of sexual partners of susceptible with treated population C_3 increases with time, susceptible first increase and then decrease with time as shown in Fig.4.3 due to the loss of immunity. Thus it can be concluded that, in order to reduce the spread of the disease, the number of sexual partners as well as unsafe sexual interaction with an infective should be restricted.

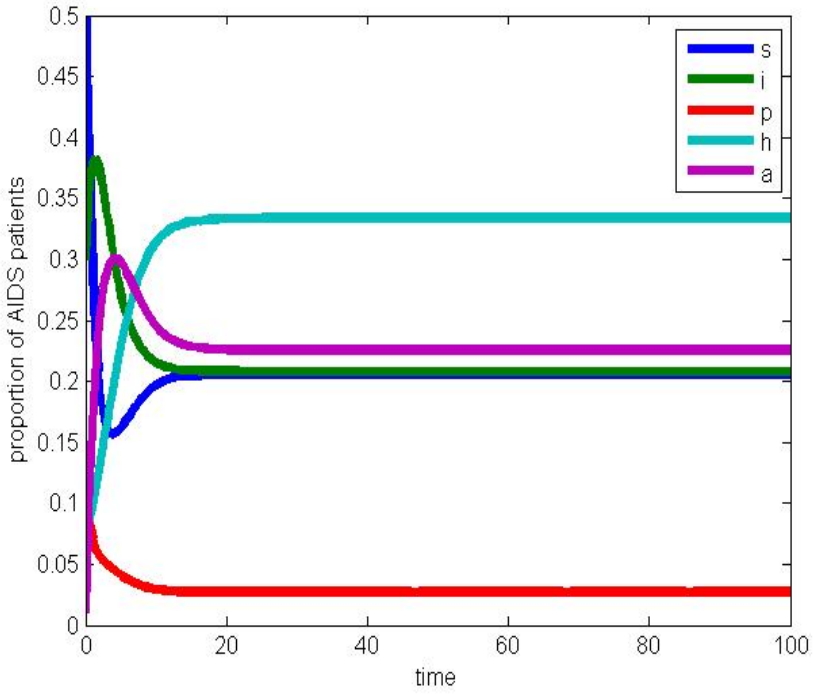

Figure 4.4: Variation of AIDs population for different values of α

From figure 4.4 above It can be seen that as α increases, the population of AIDS patients decrease. It is found that the AIDS induced death rate, can be controlled by ARVs strengthening health education regarding the AIDS disease. It can also be noted that the respective populations tend to the equilibrium level as time progresses. Hence the endemic equilibrium E^* is globally asymptotically stable for the chosen set of parameter value.

Chapter 5

Discussion and conclusion

In this research, a non-linear mathematical model to study the transmission of HIV/AIDS from mother to children with treatments in a population of varying size was proposed. Both qualitative and numerical analysis of the model was done. The model incorporates the assumption that due to sexual interaction of susceptible with infective, the infected babies born increase the growth of infective population directly. It was shown that there exists a feasible region where the model is well posed in which a unique disease free equilibrium point exists. The disease free and endemic equilibrium point was obtained and their stabilities investigated. A numerical study of the model has been conducted to see the effect of certain key parameters on the spread of the diseases. It was established that the disease-free equilibrium is locally asymptotically stable if the basic reproduction number $R_o < 1$ and for $R_o > 1$ it is unstable and the infection is persist in the population.

The endemic equilibrium E^*, which exist only when $R_0 > 1$, is always locally asymptotically stable. The equilibrium endemic is also shown to be globally asymptotically stable under certain conditions. It is found that an increase in the rate of vertical transmission leads to the increase of the population of infective which in turn increases the pre-AIDS and AIDS population. From the numerical simulation, it is shown that by controlling the rate of vertical transmission, the spread of the disease can be reduced significantly.

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