# MODELING HIV/AIDS CO INFECTION WITH MALARIA AND TUBERCULOSIS: THE ROLE OF TREATMENT AND COUNSELING

***Okongo, M.K.[1*], George, L.[2], Musundi, S.W.[1] and Magana, A.M.[1]***
*[1]Chuka University, P. O. Box 109-60400, Kenya*
*[2]Masinde Muliro University of Science and Technology, Kenya*
*Email addresses: markokongo@yahoo.com; glawi@mmust.ac.ke; swmusundi@chuka.ac.ke; adielmagana@yahoo.com*

**Citation:** Okongo, M.K., George, L., Musundi, S.W. and Magana, A.M. (2017). Modeling Hiv/Aids Co Infection with Malaria and Tuberculosis: The Role of Treatment and Counseling. In: Isutsa, D.K. and Githae, E.W. *Proceedings of the Third Chuka University International Research Conference held in Chuka University, Chuka, Kenya from 26th to 28th October, 2016. 142 to 156 pp***.**

## ABSTRACT
HIV/AIDS remains one of the leading causes of death worldwide with its effects most devastating in Sub-Saharan Africa due to its dual infection with malaria and tuberculosis. This study presents a co-infection deterministic model defined by a system of ordinary differential equations for HIV/AIDS, malaria and tuberculosis. The HIV/AIDS model is analysed to determine the conditions for the stability of the equilibria points and assess the role of treatment and counseling in controlling the spread of co-infections. This study shows that effective counseling reduces the value of the reproduction number for HIV/AIDS ( $R_H$ ) to less than unity eliminating the problem. Numerical simulations show that applying anti-retroviral (ARV) treatment without effective counseling increases the value of $R_H$, worsening the HIV/AIDS problem. However, ARV treatment coupled with effective counseling reduces the value of $R_H$ to a level below one eliminating the disease. Also when the proportion of those receiving ARV treatment without effective counseling increases, the value of $R_H$ also increases to a level above one. Therefore, strategies for control of HIV/AIDS should emphasize counseling and not only treatment.

**Keywords**: *HIV/AIDS, Tuberculosis, Malaria, Stability, Counseling, Treatment*

## BACKGROUND INFORMATION
Research at the interface of mathematics and biology is increasing, and virtually any advance in disease dynamics to day requires a sophisticated mathematical approach in order to map out the parameters necessary for control and containment of epidemic outbreaks. Infectious diseases, alongside cardiovascular diseases and cancer, have been the main threat to human health. Acute and chronic respiratory diseases, especially pulmonary tuberculosis, malaria and HIV/AIDS are responsible for a large portion of mortality especially in developing countries (Kramer et al., 2010).

Globally HIV/AIDS has killed more than 35 million people since it was first discovered in 1981 and almost 70 million people have been infected with the HIV/AIDS virus making it one of the most destructive epidemics in recorded history (World Health Organization (WHO), 2013). It remains one of the leading causes of death in the world with its effects most devastating in Sub-Saharan Africa. One of the key factors that fuels the high incidence of HIV/AIDS in Sub-Saharan Africa is its dual infection with malaria and tuberculosis (Martin et al., 1995). World Health Organization statistics show that tuberculosis (TB) is the most common illness and the leading cause of death among people living with HIV/AIDS, accounting for one in four HIV/AIDS related deaths and at least one-third of the 34 million people living with HIV/AIDS worldwide are infected with latent TB. Persons co infected with TB and HIV/AIDS are 21-34 times more likely to develop active TB disease than persons without HIV/AIDS. In 2011, there were an estimated 1.1 million HIV/AIDS positive new TB cases globally and about 79% of these people live in Sub-Saharan Africa (WHO, 2013).

According to the World Health Organization report of April 2008, malaria increases the viral load in HIV/AIDS patients. Conversely HIV/AIDS increases the risk of malaria infection and accelerate development of clinical symptoms of malaria with the greatest impact on the immune suppressed persons (WHO, 2008). Since the co-infections were recorded, malaria has seen a 28% increase in its prevalence and malaria related death rates have also nearly doubled for those with co infections (Centre for Desease Control (CDC), 2007). The co infection between malaria and HIV-1 is the commonest in Sub-Saharan Africa and, to a lesser extent, in other developing countries. It is estimated that 22 million Africans are infected with HIV-1, and around 500 million are suffering from malaria annually (WHO, 2013).

Hohman and Kami (2009), discovered that HIV/AIDS and malaria have similar global distributions. The discovery motivated a study on the impact of HIV/AIDS and malaria co infection and established that globally, 500 million people are infected with malaria annually resulting in one million deaths yearly. Thirty three million people get infected with HIV/AIDS and 2 million die from it every year. The study further showed that those with HIV/AIDS have more frequent episodes of symptomatic malaria and that malaria increases HIV/AIDS plasma viral load and decrease $CD4+$ cells. During episodes of parasitemia, HIV/AIDS infected people have an increase in viremia leading to potential increase in risk of HIV/AIDS transmission. A comparison of the geographical distributions of HIV/AIDS, TB and malaria especially in Africa, reveal that these three diseases have similar geographical distributions suggesting a possible existence of HIV/AIDS, TB and malaria co infection. This may be due to shared risk factors and/or the presence of opportunistic infections.

Audu et al. (2005) investigated the possible impact of co infections of tuberculosis and malaria on the $CD4+$ cell counts of HIV/AIDS patients and established the following: The healthy control group recorded a median $CD4+$ cell counts of 789 cells/ul (789 cells per $mm^3$ of blood); subjects infected with HIV/AIDS only recorded a median $CD4+$ cell counts of 386 cell/μl; subjects co infected with HIV/AIDS and TB recorded a median $CD4+$ cell counts of 268 cell/μl; subjects co infected with HIV/AIDS and malaria recorded a median $CD4+$ cell counts of 211 cell/μl and those co infected with HIV/AIDS, malaria and TB recorded the lowest median $CD4+$ cell counts of 182 cell/μl. Motivated by these findings, this study aims at developing a deterministic model exploring the joint dynamics of the simultaneous co infections of HIV/AIDS, TB and malaria incorporating treatment and counselling for the HIV/AIDS infected population. It represents the first deterministic mathematical model incorporating HIV/AIDS, TB and Malaria co infections within a single model to gain insights into their combined transmission dynamics and determine effective control strategies.

**Model Formulation and Description**

To study the dynamics of HIV/AIDS, malaria and TB co infection, a deterministic model is formulated described by a system of ordinary differential equations. The model sub-divide the human population into the following epidemiological classes:

$S_H(t)$ - Susceptible population at time t, $I_M(t)$ - Malaria infected population at time t,
$I_H(t)$ - HIV cases at time t, $I_A(t)$ - AIDS cases at time t, $I_T(t)$ - TB cases at time t.
$I_{HM}(t)$ - Those co infected with malaria and HIV at time t, $I_{AM}(t)$ - Those co infected with malaria and AIDS at time t, $I_{MT}(t)$ - Those co infected with malaria and TB at time t,
$I_{HT}(t)$ - Those co infected with HIV and TB at time t, $I_{AT}(t)$ - Those co infected with AIDS and TB at time t, $I_{HMT}(t)$ - Those co infected with HIV, Malaria and TB at time t,

$I_{AMT}(t)$ - Those co infected with AIDS, Malaria and TB at time t. The total human population ($N_H(t)$) is therefore denoted by: $N_H(t) = S_H(t) + I_M(t) + I_H(t) + I_A(t) + I_T(t) + I_{HM}(t) + I_{AM}(t) + I_{MT}(t) + I_{HT}(t) + I_{AT}(t) + I_{HMT}(t) + I_{AMT}(t)$. The vector (mosquito) population at time t denoted by $N_V(t)$ is sub-divided into the following classes: $S_V(t)$ - Vector susceptibles at time t, $I_V(t)$ - Vector infected population at time t. The total vector population $N_V(t)$ is given by $N_V(t) = S_V(t) + I_V(t)$.

**Definition of Parameters**

It is assumed that susceptible humans are recruited into the population at a constant rate either by birth or recovery from malaria and TB. They acquire infection with either HIV/AIDS, malaria or TB and move to the infectious classes. Susceptible mosquitoes are recruited into the mosquito population at a constant rate. They acquire malaria infection following a blood meal feeding on infected malaria humans, becomes infectious and move to the infectious class. The recruitment rate of humans into the susceptible population is denoted by $\Lambda_H$ while that of vectors (mosquitoes) is denoted by $\Lambda_V$ and are both assumed to be constant. The natural death rate of humans is given by $d_n$ while that of vectors is given by $d_v$. The death rates due to AIDS, malaria and TB in humans are $d_a$, $d_m$ and $d_t$ respectively. The parameters $d_{am}$, $d_{mt}$, $d_{at}$ and $d_{amt}$ account for the combined death rates in the $I_{AM}$, $I_{MT}$, $I_{AT}$ and $I_{AMT}$ classes respectively. The parameters $r_m$ and $r_t$ are the recovery rates from malaria and TB respectively due to effective treatment. It is assumed that the recovered individuals do not acquire temporary immunity to either or both diseases thus become susceptible again. The model assumes that susceptible humans cannot simultaneously get infected with malaria, HIV/AIDS and TB since the transmission mechanics are completely different for the three diseases. The model further assumes that humans acquire HIV/AIDS through sexual contacts between an infective and a susceptible. The average force of infection for HIV/AIDS denoted $\lambda_{ah}$ is given by

$$\lambda_{ah} = \frac{\beta_a(1-\delta)c_1(I_H + I_{HM} + I_{HT})}{N_H} \qquad (2.1.1)$$

where $\beta_a$ is the average transmission probability of HIV/AIDS between an infective and a susceptible per sexual contact and $c_1$ is the per capita number of sexual contacts of susceptible humans with HIV/AIDS infected individuals per unit time. The parameter $\delta$ measures the effectiveness of counselling through condom use and a reduction in the number of sexual partners, where $0 \le \delta \le 1$. Effective counselling reduces the value of the parameter $c_1$. The model assumes that the classes $I_{HMT}$, $I_A$, $I_{AM}$, $I_{AT}$ and $I_{AMT}$ do not transmit the virus due to acute ill health and noticeable AIDS symptoms. Define $\alpha_1$ as the number of bites per human per mosquito (biting rate of mosquitoes), $\beta_m$ as the transmission probability of malaria in humans per bite thus the force of infection with malaria for humans, denoted $\lambda_{mh}$ is given by

$$\lambda_{mh} = \frac{\alpha_1 \beta_m I_V}{N_H} \qquad (2.1.2)$$

Whereas the average force of infection with malaria for vectors, denoted $\lambda_{mv}$ is given by

$$\lambda_{mv} = \frac{\alpha_1 \beta_v(I_M + I_{HM} + I_{MT} + I_{AM} + I_{HMT} + I_{AMT})}{N_H} \qquad (2.1.3)$$

where $\beta_v$ is the transmission probability of malaria in vectors from any infected human.

Finally the average force of infection for TB denoted $\lambda_{th}$ is given by:

$$\lambda_{th} = \frac{\beta_t c_2(I_T + I_{HT} + I_{MT} + I_{HMT} + I_{AMT} + I_{AT})}{N_H} \qquad (2.1.4)$$

where $\beta_t$ is the transmission probability of TB in humans and $c_2$ is the average per capita contact rate of susceptible humans with TB infected individuals. The rate of progression from HIV to AIDS for the untreated HIV cases is $p$. The parameters $\theta_1 p$, $\theta_2 p$ and $\theta_3 p$ account for increased rates of progression to AIDS for individuals co infected with HIV - TB, HIV - malaria and HIV - malaria - TB respectively where $\theta_1 < \theta_2 < \theta_3$. Define $\alpha$ as the proportion of the HIV/AIDS infected population receiving effective treatment. This involves the administration of ARV'S that keeps the HIV patients from progressing to

AIDS while transferring the AIDS patients back to the HIV classes. The modification parameters $e^h{}_m$, $e^h{}_t$ and $e^h{}_{mt}$ account for the reduced susceptibility to infection with HIV for individuals in the $I_M$, $I_T$ and the $I_{MT}$ classes respectively due to reduced sexual activity as a result of ill health where $e^h{}_m < 1$, $e^h{}_t < 1$, $e^h{}_{mt} \ll 1$. The parameters $e^m{}_a$ , $e^m{}_h$ , $e^m{}_{ht}$, $e^m{}_{at}$, account for the increased susceptibility to infection with malaria for individuals already infected with AIDS, HIV, HIV - TB and AIDS - TB respectively due to suppressed immune system where $e^m{}_a > 1$, $e^m{}_h > 1$, $e^m{}_{ht} > 1$, $e^m{}_{at} > 1$. It is also clear that $e^m{}_a < e^m{}_{at}$ and $e^m{}_h < e^m{}_{ht}$. The parameters $e^t{}_h$, $e^t{}_a$, $e^t{}_{mh}$, and $e^t{}_{am}$ account for the increased susceptibility to infection with TB for individuals already infected with HIV, AIDS, HIV malaria and AIDS - malaria respectively due to suppressed immune system where $e^t{}_h > 1$, $e^t{}_a > 1$, $e^t{}_{hm} > 1$, $e^t{}_{am} > 1$. Again $e^t{}_h < e^t{}_{hm}$ and $e^t{}_a < e^t{}_{am}$. Malaria and TB does not lead to the depletion of the $CD4^+$ cell counts, however their association with HIV/AIDS leads to a significant reduction in the $CD4+$ cell counts within an individual leading to faster progression to AIDS.

**The Model Equations**

Combining all the aforementioned assumptions and definitions, the model for the transmission dynamics of HIV/AIDS, TB and malaria is given by the following system of differential equations:

$$
\begin{aligned}
\frac{dS_H(t)}{dt} &= \Lambda_H + r_m I_M(t) + r_t I_T(t) - \lambda_{ah} S_H(t) \\
&\quad -\lambda_{mh} S_H(t) - \lambda_{th} S_H(t) - d_n S_H(t) \qquad (2.2.1)\\
\frac{dI_M(t)}{dt} &= \lambda_{mh} S_H(t) + r_t I_{MT}(t) - r_m I_M(t) - e^h_m \lambda_{ah} I_M(t) \\
&\quad -\lambda_{th} I_M(t) - d_n I_M(t) - d_m I_M(t). \\
\frac{dI_H(t)}{dt} &= \lambda_{ah} S_H(t) + r_m I_{HM}(t) + r_t I_{HT}(t) - (1-\alpha) p I_H(t) \\
&\quad -e^m_h \lambda_{mh} I_H(t) - e^t_h \lambda_{th} I_H(t) - d_n I_H(t) + \alpha I_A(t). \\
\frac{dI_A(t)}{dt} &= (1-\alpha) p I_H(t) + r_m I_{AM}(t) + r_t I_{AT}(t) - e^m_a \lambda_{mh} I_A(t) \\
&\quad -e^t_a \lambda_{th} I_A(t) - d_a I_A(t) - d_n I_A(t) - \alpha I_A(t) \\
\frac{dI_T(t)}{dt} &= \lambda_{th} S_H(t) + r_m I_{MT}(t) - e^h_t \lambda_{ah} I_T(t) - \lambda_{mh} I_T(t) \\
&\quad -d_n I_T(t) - d_t I_T(t) - r_t I_T(t) \\
\frac{dI_{HM}(t)}{dt} &= e^m_h \lambda_{mh} I_H(t) + e^h_m \lambda_{ah} I_M(t) + r_t I_{HMT}(t) - r_m I_{HM}(t) - e^t_{hm} \lambda_{th} I_{HM}(t) + \\
&\quad \alpha I_{AM}(t) - d_m I_{HM}(t) - (1-\alpha)\theta_2 p I_{HM}(t) - d_n I_{HM}(t) \\
\frac{dI_{AM}(t)}{dt} &= (1-\alpha)\theta_2 p I_{HM}(t) + e^m_a \lambda_{mh} I_A(t) - r_m I_{AM}(t) - d_m I_{AM}(t) - \alpha I_{AM}(t) \\
&\quad + r_t I_{AMT}(t) - e^t_{am} \lambda_{th} I_{AM}(t) - d_n I_{AM}(t) - d_a I_{AM}(t) - d_{am} I_{AM}(t). \\
\frac{dI_{MT}(t)}{dt} &= \lambda_{th} I_M(t) + \lambda_{mh} I_T(t) - r_m I_{MT}(t) - e^h_{mt} \lambda_{ah} I_{MT}(t) - r_t I_{MT}(t) \\
&\quad -d_m I_{MT}(t) - d_n I_{MT}(t) - d_t I_{MT}(t) - d_{mt} I_{MT}. \\
\frac{dI_{HT}(t)}{dt} &= e^h_t \lambda_{ah} I_T(t) + r_m I_{HMT}(t) + e^t_h \lambda_{th} I_H(t) - e^m_{ht} \lambda_{mh} I_{HT}(t) - (1-\alpha)\theta_1 p I_{HT}(t) \\
&\quad -d_n I_{HT}(t) - d_t I_{HT}(t) - r_t I_{HT}(t) + \alpha I_{AT}(t) \\
\frac{dI_{AT}(t)}{dt} &= e^t_a \lambda_t I_A(t) + r_m I_{AMT}(t) + (1-\alpha)\theta_1 p I_{HT}(t) - \alpha I_{AT}(t) \\
&\quad -e^m_{at} \lambda_{mh} I_{AT}(t) - d_n I_A(t) - d_a I_{AT}(t) - d_t I_{AT}(t) - r_t I_{AT}(t) - d_{at} I_{AT}.
\end{aligned}
$$

$$
\begin{aligned}
\frac{dI_{HMT}(t)}{dt} &= e_{ht}^{m}\lambda_m I_{HT}(t) + e_{hm}^{t}\lambda_{th} I_{HM}(t) + e_{mt}^{h}\lambda_{ah} I_{MT}(t) + \alpha I_{AMT}(t) \\
&\quad -r_m I_{HMT}(t) - d_m I_{HMT}(t) - d_n I_{HMT}(t) \\
&\quad -(1-\alpha)\theta_3 p I_{HMT}(t) - d_t I_{HMT}(t) - r_t I_{HMT}(t) - d_{mt} I_{HMT} \\
\frac{dI_{AMT}(t)}{dt} &= e_{at}^{m}\lambda_{mh} I_{AT}(t) + e_{am}^{t}\lambda_{th} I_{AM}(t) + (1-\alpha)\theta_3 p I_{HMT}(t) \\
&\quad -r_m I_{AMT}(t) - d_m I_{AMT}(t) - d_a I_{AMT}(t) - \alpha I_{AMT}(t) \\
&\quad -d_n I_{AMT}(t) - d_t I_{AMT}(t) - r_t I_{AMT}(t) - d_{amt} I_{AMT} \\
\frac{dS_V(t)}{dt} &= \Lambda_V - \lambda_{mv} S_V(t) - d_v S_V(t) \\
\frac{dI_V(t)}{dt} &= \lambda_{mv} S_V(t) - d_v I_V(t).
\end{aligned}
$$

**Positivity and Boundedness of Solutions**

The model system 2.2.1 describes living populations therefore the associated state variables are non-negative for all time $t \geq 0$. The solutions of this model with positive initial data therefore remain positive for all time $t \geq 0$.

**Lemma 3.1.** *Let the initial data set be* $\{(S_H(0), S_V(0) > 0), (I_M(0), I_H(0), I_A(0), I_T(0), I_{HM}(0), I_{AM}(0), I_{MT}(0), I_{HT}(0), I_{AT}(0), I_{HMT}(0), I_{AMT}(0), I_V(0))\} \in \Psi$. *Then the solution set* $\{(S_H, S_V, I_M, I_H, I_A, I_T\ I_{HM}, I_{AM}, I_{MT}, I_{HT}, I_{AT}, I_{HMT}, I_{AMT}, I_V\}(t)$ *is positive for all time* $t > 0$.

Proof. Consider the first equation of 2.2.1 at time t

$$
\frac{dS_H}{dt} = \Lambda_H + r_m I_M + r_t I_T - \lambda_{ah} S_H - \lambda_{mh} S_H - \lambda_{th} S_H - d_n S_H
$$

then

$$
\frac{dS_H}{dt} \geq -(\lambda_{ah} + \lambda_{mh} + \lambda_{th} + d_n) S_H
$$

$$
\int \frac{dS_H}{S_H} \geq -\int (\lambda_{ah} + \lambda_{mh} + \lambda_{th} + d_n) d(t)
$$

$$
S_H(t) \geq S_H(0) e^{-\int (\lambda_{ah} + \lambda_{mh} + \lambda_{th} + d_n) d(t)} \geq 0
$$

From the second equation of 2.2.1 at time t

$$
\frac{dI_M}{dt} = \lambda_{mh} S_H + r_t I_{TM} - r_m I_M - e_m^a \lambda_{ah} I_M - \lambda_{th} I_M - d_n I_M - d_m I_M.
$$

then

$$
\frac{dI_M}{dt} \geq -(r_m + e_m^a \lambda_{ah} + \lambda_{th} + d_n + d_m) I_M.
$$

$$
\frac{dI_M}{I_M} \geq -\int (r_m + e_m^a \lambda_{ah} + \lambda_{th} + d_n + d_m) dt.
$$

$$
I_M(t) \geq I_M(0) e^{-\int (r_m + e_m^a \lambda_{ah} + \lambda_{th} + d_n + d_m) dt} \geq 0.
$$

We can proceed in a similar manner and show that all the state variables are positive for all time t.

**Lemma 3.2.** *The solutions of the model 2.2.1 are uniformly bounded in a proper subset*

$\Psi = \Psi_H \times \Psi_V$

Proof. Let $\{(S_H, I_M, I_H, I_A, I_T\ I_{HM}, I_{AM}, I_{MT}, I_{HT}, I_{AT}, I_{HMT}, I_{AMT}\}(t) \in \mathbb{R}^{12}_+$, be any solution with non-negative initial conditions. The rate of change of the total human population with time is given by:

$$\frac{dN_H}{dt} = \Lambda_H - d_n N_H - (I_M + I_{HM}(t) + I_{AM} + I_{MT} + I_{HMT} + I_{AMT})d_m -$$

$$(I_T + I_{MT} + I_{HT} + I_{AT} + I_{HMT} + I_{AMT})d_t - (I_A + I_{AM} + I_{AT} + I_{AMT})d_a$$

$$-d_{am} I_{AM} - d_{mt}(I_{MT} + I_{HMT}) - d_{at} I_{AT} - d_{amt} I_{AMT}$$

The model system 2.2.1 has a varying human population size $\frac{dN_H}{dt} \neq 0$ and therefore a trivial equilibrium is not feasible. Whenever $N_H > \frac{\Lambda_H}{d_n}$, then $\frac{dN_H}{dt} < 0$. Since $\frac{dN_H}{dt}$ is bounded by $\Lambda_H - d_n N_H$, a standard comparison theorem by (Birkoff and Rota, 1989) shows that $0 \leq N_H(t) \leq N_H(0)e^{-d_n} + \frac{\Lambda_H}{d_n}(1 - e^{-d_n})$, where $N_H(0)$ represents the value of $N_H(t)$ evaluated at the initial values of the respective variables. Thus as $t \to \infty$, we have, $0 \leq N_H(t) \leq \frac{\Lambda_H}{d_n}$. In particular, $N_V(t) \leq \frac{\Lambda_H}{d_n}$, if $N_0 \leq \frac{\Lambda_H}{d_n}$. This shows that $N_H$ is bounded and all the feasible solutions of the human only component of model 2.2.1 starting in the region $\Psi_H$ approach, enter or stay in the region, where:

$$\Psi_H = \{(S_H, I_M, I_H, I_A, I_T, I_{MH}, I_{MA}, I_{MT}, I_{HT}, I_{TA}, I_{MHT}, I_{MAT}) : N(t) \leq \frac{\Lambda_H}{d_n}\}.$$

Similarly let $\{(S_V, I_V\}(t) \in \mathbb{R}^2_+$, be any solution with non-negative initial conditions. The rate of change of the total vector population with time is given by:
$\frac{dN_V}{dt} = \Lambda_V - (S_V(t) - I_V(t))d_v$. $\frac{dN_V}{dt} \neq 0$ and therefore a trivial equilibrium is not feasible. Whenever $N_V > \frac{\Lambda_V}{d_v}$, then $\frac{dN_V}{dt} < 0$. Since $\frac{dN_V}{dt}$ is bounded by $\Lambda_V - d_v N_V$, a standard comparison theorem by Birkoff and Rota (1989), shows that $0 \leq N_V(t) \leq N_V(0)e^{-d_v} + \frac{\Lambda_V}{d_v}(1 - e^{-d_v})$, where $N_V(0)$ represents the value of $N_V(t)$ evaluated at the initial values of the respective variables. Thus as $t \to \infty$, $0 \leq N_V(t) \leq \frac{\Lambda_V}{d_v}$. In particular, $N(t) \leq \frac{\Lambda_V}{d_v}$, if $N_0 \leq \frac{\Lambda_V}{d_v}$. This shows that $N_V$ is bounded and all the feasible solutions of the vector only component of model 2.2.1 starting in the region $\Psi_V$ approach, enter or stay in the region, where: $\Psi_V = \{(S_V, I_V) : N_V \leq \frac{\Lambda_V}{d_v}\}$. □.

**HIV/AIDS Model**

Before analyzing the full model (HIV/AIDS, Malaria and TB), it is instructive to gain insights into the dynamics of the HIV/AIDS only model, HIV/AIDS-malaria co infection model and the HIV/AIDS-TB co infection model.

$$\begin{aligned}
\frac{dS_H(t)}{dt} &= \Lambda_H - \lambda_{ah} S_H(t) - d_n S_H(t) \\
\frac{dI_H(t)}{dt} &= \lambda_{ah} S_H(t) - (1-\alpha)pI_H(t) - d_n I_H(t) + \alpha I_A(t). \qquad (4.0.2) \\
\frac{dI_A(t)}{dt} &= (1-\alpha)pI_H(t) - d_a I_A(t) - d_n I_A(t) - \alpha I_A(t)
\end{aligned}$$

where, $N_H = S_H + I_H + I_A$, and $\lambda_{ah} = \frac{\beta_a(1-\delta)c_1 I_H}{N_H}$. For this model, it can be shown that the region, $\Omega_H = \{(S_H, I_H, I_A) \in \mathbb{R}^3_+ : N_H \leq \frac{\Lambda_H}{d_n}\}$, is positively-invariant and attracting. Thus, 4.0.2 is mathematically well posed and its dynamics can be considered in $\Omega_H$.

**The Basic Reproduction Number $R_0$**

The basic reproduction number $R_0$ is defined as the average number of secondary infections an infectious individual would cause over his infectious period in an entirely susceptible population. The basic reproduction number *RH* for the HIV/AIDS only model is defined as the number of secondary HIV/AIDS infections due to a single HIV/AIDS infective individual. When $R_H < 1$, then an infectious individual is causing, on average, less than one new infection and thus the disease does not invade the population. On the other hand, when $R_H > 1$ then an infectious individual is causing, on average, more than one new infection and thus the disease invades and persist in the population.

**Local Stability of Disease-Free Equilibrium (DFE)**

The model 4.0.2 has a DFE, obtained by setting the right-hand sides of the equations in the model to zero given by

$$\mathcal{E}_0^h = (S_H^* + I_H^* + I_A^*) = (\frac{\Lambda_H}{d_n}, 0, 0)$$

Define $Fi$ as the rate of appearance of new infections in the class or compartment i and $V_i = V_i^- - V_i^+$, where $V_i^-$ is the rate of transfer of individuals out of compartment i, and $V_i^+$ is the rate of transfer of individuals into compartment i by all other means. Therefore:

$$\mathcal{F}_i = \begin{pmatrix} \frac{\beta_a(1-\delta)c_1 I_H}{N_H} S_H \\ 0 \end{pmatrix}$$

and

$$\mathcal{V}_i = \begin{pmatrix} (1-\alpha)pI_H + d_n I_H - \alpha I_A \\ d_a I_A + d_n I_A + \alpha I_A - (1-\alpha)pI_H \end{pmatrix}$$

The Jacobian of $\mathcal{F}_i$ and $\mathcal{V}_i$ at the DFE denoted by $F$ and $V$ respectively are given by:

$$F = \begin{pmatrix} \beta_a(1-\delta)c_1 & 0 \\ 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (1-\alpha)p + d_n & -\alpha \\ -(1-\alpha)p & d_a + d_n + \alpha \end{pmatrix}$$

The basic reproduction number $R_H$ is by definition the spectral radius of the matrix $FV^{-1}$ and is given by:

$$R_H = \frac{c_1(1-\delta)(\alpha + d_a + d_n)\beta_a}{(\alpha d_n + d_a d_n + d_n^2 + d_a p - \alpha d_a p + d_n p - \alpha d_n p)} \quad (4.1.1)$$

It measures the average number of new HIV infections generated by a single HIV/AIDS infected individual in a population where a certain fraction of infected individuals are treated and counselled.

**Lemma 4.1.1:** *The DFE of the HIV Model is locally asymptotically stable (LAS) if $R_H < 1$, and unstable otherwise.*

Parameter values for the HIV/AIDS model

| Symbol | Parameter | Value ($yr^{-1}$) | Source |
|---|---|---|---|
| $\Lambda_H$ | Recruitment rate of humans | $0.4 \times 40 \times 10^6$ | Kenya demographics profile (2014) |
| $d_n$ | Natural death rate of humans | 0.016667 | Kenya demographics profile (2014) |
| $d_a$ | HIV/AIDS-induced death rate | 0.4 | WHO report (2014a) |
| $p$ | Progression rate from HIV to AIDS (untreated) | 0.1 | Baryama and Mugisha (2007) |
| $\alpha$ | Proportion of the HIV/AIDS victims treated | 0.6 | Kenya NACC report (2014) |
| $\beta_a$ | Transmission probability of HIV/AIDS | 0.019 | Baryama and Mugisha (2007) |
| $c_1$ | Per capita number of sexual contacts | 9 | Kenya NACC report (2014) |
| $\delta$ | Effectiveness of counseling | Variable | |

Lemma 4.1.1 follows from Theorem two by Van, P. and Watmough, J. (2002). This lemma is illustrated graphically in figure 1 showing total infected population $(I_H + I_A)$ against time in years, with $R_H$ = 0.517234.

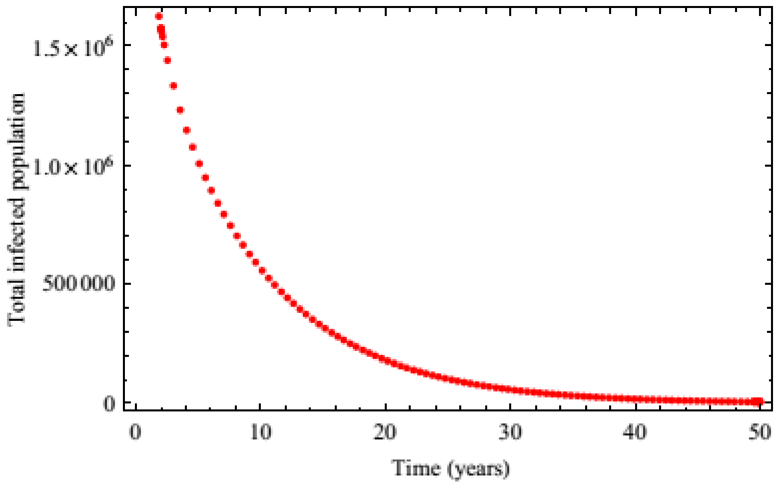


**Figure 1: HIV/AIDS local disease free equilibrium**

**Simulating the Role of Counseling and Treatment**

From equation 4.1.1, it is evident that strategies for the reduction of HIV/AIDS infections in humans should target the reduction of the parameter $c_1$ (per capita number of sexual contacts) through counseling. Effective counseling where $\delta = 1$, reduces the value of $c_1$ and $R_H$ to zero eliminating the HIV/AIDS problem. The graph of $R_H$ against $c_1$ is shown in fig 2.

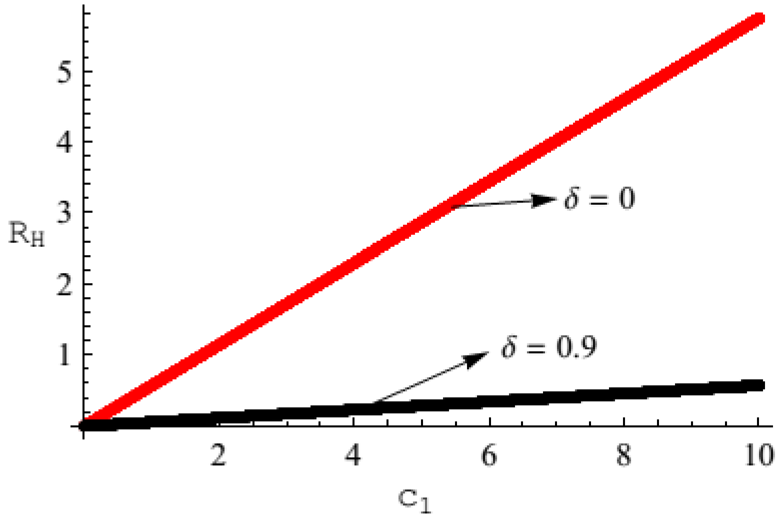


**Figure 2: The role of treatment and counseling ($\alpha = 0.6$)**

Figure 2 shows that effective counseling ($\delta = 0.9$) reduces the value of $R_H$ to less than unity and therefore very effective in controlling the HIV/AIDS problem.

Figure 3 combines the parameters for ARV treatment ($\alpha$) and counseling ($\delta$) within the same graph. The graph shows that ARV treatment without effective counseling ($\alpha = 0.6$ and $\delta = 0$), increases the value of $R_H$, worsening the HIV/AIDS problem. However ARV treatment coupled with effective counseling ($\alpha = 0.6$ and $\delta = 0.9$) reduces the value of $R_H$ to a level below one eliminating the disease. This figure suggests that there is a threshold level of counseling below which ARV treatment is disastrous. Above the threshold level, ARV treatment and counseling would be very effective.

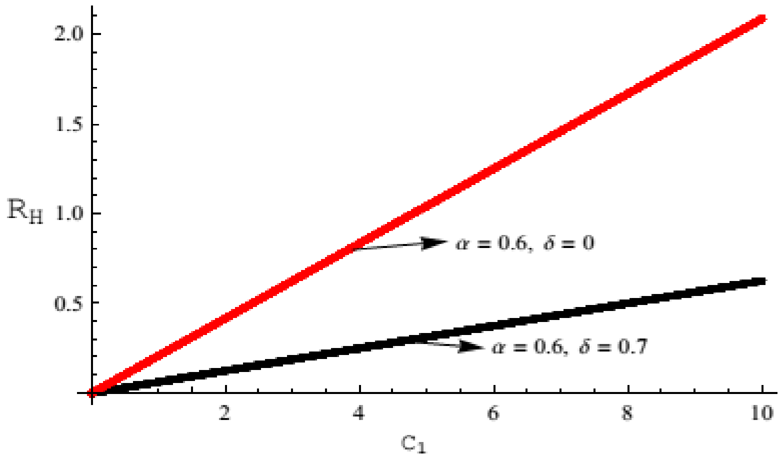


**Figure 3: Simulation result of $R_H$ against per capita number of sexual contacts ( $c_1$)**

When the proportion of those receiving ARV treatment without effective counseling increases, the value of $R_H$ also increases to a level above one, however effective counselling maintains the value of $R_H$ below unity as shown in figure 4. Therefore strategies for the control of HIV/AIDS should emphasize counseling and not only treatment.

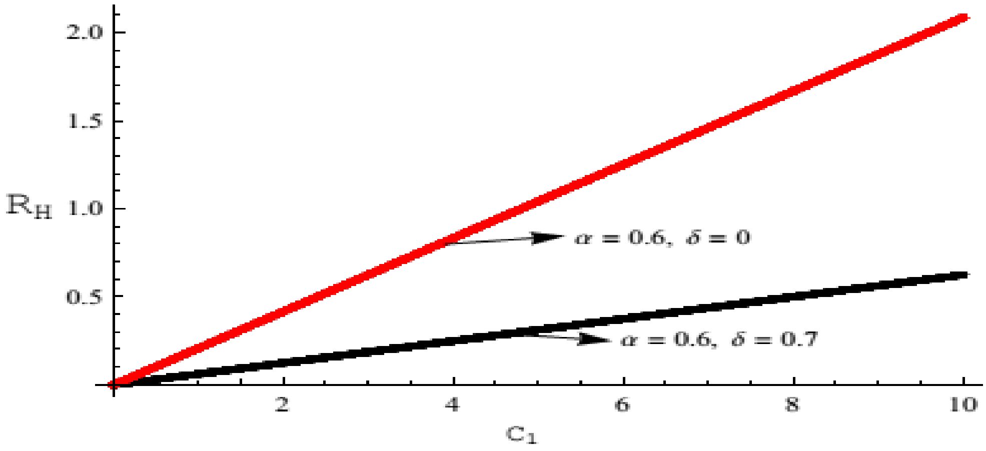


**Figure 4: Simulation result of $R_H$ against per capita number of sexual contacts ($c_1$)**

To further investigate the potential impact of counseling and treatment on disease progression, we carry out sensitivity analysis of the reproduction number with respect to counselling and treatment. The sensitivity index of $R_H$ with respect to $\delta$ is given by:

$$R_H^{\delta} = -\frac{\delta}{1-\delta} \quad (5.0.2)$$

The negative sign in equation 5.0.2 indicates that there is an expected decline in the rate of new HIV/AIDS infections when counseling is scaled up. Similarly, The sensitivity index of $R_H$ with respect to $\alpha$ is given by:

$$R_H^{\alpha} = \frac{\alpha A_1\{-\frac{\beta_a c_1 A_2 A_3(1-\delta)}{A_1^2} + \frac{\beta_a c_1(1-\delta)}{A_1}\}}{\beta_a c_1 A_2(1-\delta)} \quad (5.0.3)$$

$$A_1 = \alpha d_n + d_a d_n + d_n^2 + d_a p - \alpha d_a p + d_n p - \alpha d_n p$$
$$A_2 = \alpha + d_a + d_n$$
$$A_3 = d_n - d_a p - d_n p$$

Numerical simulations shows that the sensitivity index of $R_H$ with respect to treatment is positive indicating that an increase in the proportions of those treated leads to an increase in new HIV cases as shown in figure 5.

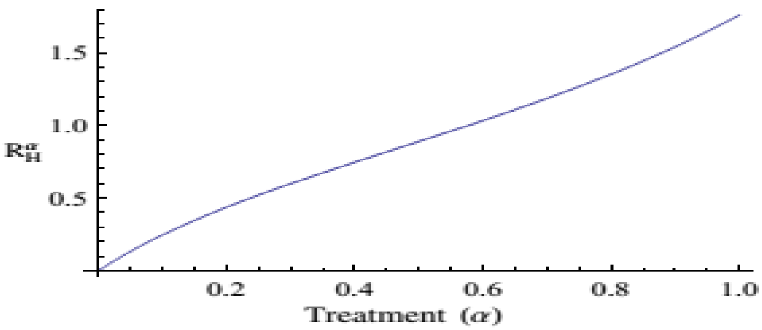


**Figure 5: Simulation result of the sensitivity index of $R_H$ with respect to treatment**

Biologically, lemma 4.1.1 implies that HIV/AIDS can be eliminated from the community when $R_H <$ 1. This is only true if the initial sizes of the sub-populations of the model are in the basin of attraction of:

$$\mathcal{E}_0^h = (S_H^* + I_H^* + I_A^*) = (\frac{\Lambda_H}{d_n}, 0, 0)$$

To ensure that elimination of the virus is independent of the initial sizes of the sub-populations, it is necessary to show that the DFE is globally asymptotically stable.

**Global Stability of Disease-Free Equilibrium (DFE)**
The global asymptotic stability (GAS) of the disease-free state of the model is investigated using the theorem by Castillo-Chavez et al. (2002). The model is rewritten as follows:

$$\frac{dX}{dt} = H(X, Z) \qquad (5.0.4)$$

$$\frac{dZ}{dt} = G(X, Z), \quad G(X, 0) = 0 \qquad (5.0.5)$$

where the components of the column-vector $X \in R^m$ denote the uninfected population and the components of $Z \in R^n$ denote the infected population. $E^0 = (X^*, 0)$ denotes the disease free equilibrium of this system. The fixed point $E^0 = (X^*, 0)$ is globally asymptotically stable (GAS) equilibrium for this system provided that $R_0 < 1$ and the following two conditions satisfied:

**(H1)** For $\frac{dX}{dt} = H(X, 0)$, $X^*$ is globally asymptotically stable
**(H2)** $G(X, Z) = PZ - \widehat{G}(X, Z)$, $\widehat{G}(X, Z) \geq 0$ for $(X, Z) \in \Omega_H$,

where $P = D_Z G(X^*, 0)$ is an M-matrix (the off diagonal elements of P are non negative) and $\Omega_H$ is the region where the model makes biological sense. The disease-free equilibrium is now denoted as $E^0 = (X^*, 0)$, $X^* = \frac{\Lambda_H}{d_n}$

**Theorem 5.1.** *The fixed point* $E^0 = (X^*, 0)$ *is a globally asymptotically stable equilibrium of system 4.0.2 provided that* $R_H < 1$ *and the assumptions* ***H1*** *and* ***H2*** *are satisfied.*

*Proof.* From the system 4.0.2

$$H(X, 0) = (\ \Lambda_H - d_n\ )$$
$$G(X, Z) = PZ - \widehat{G}(X, Z)$$

Where

$$P = \begin{pmatrix} \beta_a(1-\delta)c_1 - (1-\alpha)p - d_n & \alpha \\ (1-\alpha)p & -(d_a + d_n + \alpha) \end{pmatrix}$$

and

$$\widehat{G} = \begin{pmatrix} \beta_a(1-\delta)c_1 I_H(1 - \frac{S_H}{N_H} \\ 0 \end{pmatrix}$$

□

Notice that $G = (X, Z) \geq 0$ in $\Omega_H$. Therefore the DFE of model 4.0.2 is globally asymptotically stable if $R_H < 1$. This shows that HIV/AIDS will be completely eliminated from the community if the epidemiological threshold, $R_H$ can be brought to a value less than unity independent of the initial sizes of the sub-populations as shown numerically in figure 6.

**Figure 6: Numerical simulation of the global stability of the disease free equilibrium**

**Existence and Stability of the Endemic Equilibrium**
To find conditions for the existence of an equilibrium for which HIV/AIDS is endemic in the population, the steady states of the system 4.0.2 are determined by solving

$$E_1^* = f(S_H^*, I_H^*, I_A^*) = 0.$$

The equations for the population proportions are considered by first scaling the sub-populations for $S_H$, $I_H$ and $I_A$ using the following set of new variables: $S_H = \frac{SH}{NH}$

$i_H = \frac{I_H}{N_H}$, $i_A = \frac{I_A}{N_H}$. The system 4.2.1, is therefore given by:

$$\begin{aligned} \frac{ds_H}{dt} &= \frac{\Lambda_H}{N_H} - \lambda_{ah}s - s(\frac{\Lambda_H}{N_H} - d_a i_A) \\ \frac{di_H}{dt} &= \lambda_{ah}s - (1-\alpha)pi_H + \alpha i_A - i_H(\frac{\Lambda_H}{N_H} - d_a i_A) \\ \frac{di_A}{dt} &= (1-\alpha)pi_H - d_a i_A - \alpha i_A - i_A(\frac{\Lambda_H}{N_H} - d_a i_A) \end{aligned} \qquad (4.2.7)$$

At the steady states, $\frac{dN_H}{dt} = 0$ and $\frac{\Lambda_H}{N_H} - d_a i_A = d_n$. By setting $s_H = (1 - i_H - i_A)$, the coordinates of the endemic equilibrium of the system 4.2.7 satisfy:

$$i_A^* = \frac{(1-\alpha)pi_H}{d_a + d_n + \alpha} \qquad (4.2.8)$$

$$i_H^* = \frac{\{\beta_1(1-\delta)c_1\pi_1 + \alpha(1-\alpha)p\} - \{d_n\pi_1 + p\pi_1(1-\alpha)\}}{\beta_1(1-\delta)c_1\{\pi_1 + p(1-\alpha)\}} \qquad (4.2.9)$$

where $\pi_1 = \alpha + d_a + d_n$. Since $i_H^*$ is positive, then $\{\beta_1(1-\delta)c_1\pi_1 + \alpha(1-\alpha)p\} > \{d_n\pi_1 + p\pi_1(1-\alpha)\}$ which indicates the existence of only one unique endemic equilibrium point suggesting that there is no bifurcation. When $\{\beta_1(1-\delta)c_1\pi_1 + \alpha(1-\alpha)p\} < \{d_n\pi_1 + p\pi_1(1-\alpha)\}$, then the model has no positive equilibrium. It can also be verified by the theorem by Castillo-Chavez and Song (2002), that the model 4.2.7 has a unique endemic equilibrium which is LAS whenever $R_H > 1$ as follows: The equations in 4.2.7 are solved in terms of the force of infection at steady-state of $\lambda_{ah}$, given by

$$\lambda_{ah}^* = \frac{\beta_a c_1(1-\delta)I_H^*}{S_H^* + I_H^* + I_A^*} \qquad (4.2.10)$$

Setting the right hand sides of the mo del 4.0.2 to zero and noting that

$$S_H^* = \frac{\Lambda_H}{\lambda_{ah} + d_n} \quad (4.2.11)$$

$$I_H^* = \frac{\lambda_{ah} S_H^* + \alpha I_A^*}{d_n + (1-\alpha)p}$$

$$I_A^* = \frac{(1-\alpha)pI_H^*}{d_a + d_n + \alpha}$$

using 4.2.11 in the expression for $\lambda_{ah}^*$ in 4.2.10 shows that the nonzero endemic equilibria of the model satisfy

$$a_{11}\lambda_{ah}^* - a_{12} = 0 \quad (4.2.12)$$

where $a_{12} = R_H - 1$ and $a_{11} = \frac{a_{12}}{\lambda_{ah}^*}$. It is clear that $a_{11} > 0$, and $a_{12} > 0$ for $R_H > 1$. Thus, the non linear system 4.2.1 has only one unique positive solution,
This endemic equilibrium is illustrated in figure 7 showing the total infected population against time in years.

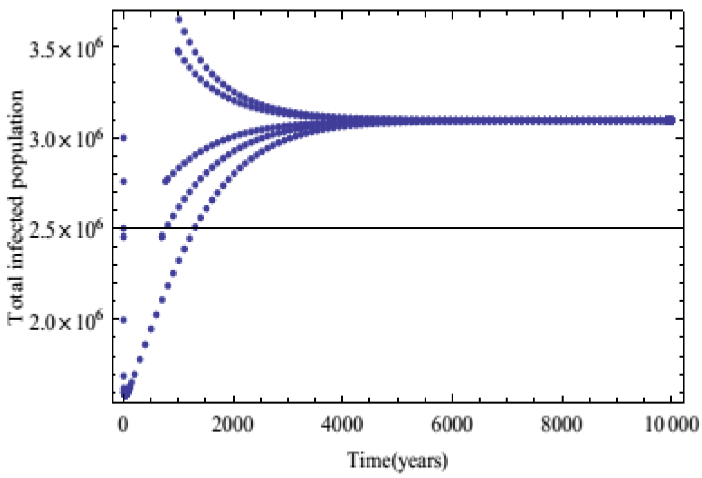


**Figure 7: The global stability of the endemic equilibrium, $R_H$ = 1 .03447.**

**Lemma 6.1.** *The HIV model 4.0.2 has a unique endemic equilibrium whenever $R_H$ >1, and no endemic equilibrium otherwise.*

When an endemic equilibrium point of a disease is unique and stable, then we would expect easier management of the disease because there is no bifurcation and therefore reducing the value of $R_H$ to less than one eliminates the disease. In summary, the HIV Model 4.0.2 has a globally-asymptotically stable DFE whenever $R_H > 1$, and a unique endemic equilibrium point whenever $R_H > 1$. This study shows that effective counseling reduces the value of the reproduction number for HIV/AIDS ($R_H$) to less than unity eliminating the HIV/AIDS problem. When the proportion of those receiving ARV treatment without effective counseling increases, the value of $R_H$ also increases to a level above one, however effective counseling maintains the value of $R_H$ below unity therefore strategies for the control of HIV/AIDS should emphasize counseling and not only treatment.

**ACKNOWLEDGEMENTS**
The authors are very grateful to Dr. Ochieng Ombaka (Chuka University, Department of Physical sciences) for many excellent comments that have enhanced the model as well as the clarity of the paper.

**REFERENCES**

Abu-Raddad, L.J., Patnaik, P. and Kublin, J.G. (2006). Dual infection with HIV/AIDS and malaria fuels the spread of both diseases in Sub-Saharan Africa, Science 314(5805): 1603-1606.

Allman, E.S. and Rhodes, J.A. (2004). An introduction to mathematical models in biology, New York: Cambridge University Press, 365-382.

Anderson, R.M and May, R.M. (1993). Infectious diseases of humans: Dynamics and control, Oxford University Press: United Kingdom, 114 - 513.

Audu, R.A., Onwujekwe, D.I, Onubogu, C.C., Adedoyin, J.A., Onyejepu, N., Mafe, A.G., Onyewuche, J., Oparaugo, C., Enwuru, C., Aniedobe, M., Musa, A.Z. and Idigbe, E.O. (2005). Impact of co infections of tuberculosis and malaria on the $CD4^+$ cell counts of HIV/AIDS patients in Nigeria, Annals of African Medicine, 4(1): 10-13.

Bernoulli, D. (1766), Essai d`une. nouvelle analyse de la mortalite causee par la petite verole et des avantages de l`inoculation pour la prevenir, in memoires de mathematiques et de physique, Academie Royale des Sciences, Paris, 11-235.

Bhunu, C., Garira, W. and Mukandavire, Z. (2009). Modeling HIV/AIDS and tuberculosis co infection, Bulletin of Mathematical Biology, 71: 1745–1780.

Centre for Disease Control and Prevention (CDC), (2007). Incorporating HIV prevention into the medical care of persons living with malaria: MMWR 2006; 55 (No. RR-14):1-17. http:www.cdc.gov/malaria/facts.htm, Accessed on August, 22nd, 2013.

Diekmann, O. and Heesterbeek, J. (2000). Mathematical epidemiology of infectious diseases. Chichester: Wiley, 28(4): 365-382.

Chuncky, C.K. (2012). Modeling the transmission dynamics of HIV/AIDS-malaria co infection with treatment: Published Msc. Dissertation, University of Dar es Salaam. Tanzania, 35-88.

French, N., Nakiyingi, J., Lugada, E., Watera, C., Whitworth, J. and Gilks, C. (2001). Increasing rates of malarial fever with deteriorating immune status in HIV-1 infected Ugandan adults. AIDS Bulletin, 15: 899-906.

Granich, R.M., Gilks, C.F., Dye, C., Decock, K.M. and William, B.G. (2008), Universal voluntary HIV testing with immediate antiretroviral therapy as a strategy for elimination of HIV transmission, Journal of Mathematical Biology, 28(1): 365–382.

Hamer, W. H. (1906). Epidemic disease in England, Lancet 1, England, 234-423.

Hohman, S. and Kim, K. (2009). The impact of HIV and malaria co infection: What is known and suggested avenues for further study, Interdisciplinary perspectives on infectious diseases, 201(8):617-654.

Kamal, B., David, M., Svetlana, R., Ana, M., Tameru. F. and Sharquetta, T. (2007). Mathematical model of HIV and malaria co infection in Sub-Saharan Africa, Alabama State University: USA, AL(5): 361-371.

Kermack, W. O. and Mckendric, A.G. (1927). Contributions to the mathematical theory of epidemics, part 1, Proc. R. Sec., London, A115: 700-721.

Kirschner, D. (1999). Dynamics of co infection with Mycobacterium tuberculosis and HIV-1. Theory of Population Biology, 55: 94-109.

Kivihya, L., Ochola, J., Otieno, G. and Muthami L. (1994). Clinical and immunological markers in Kenyan pulmonary tuberculosis patients with and without HIV-1, East African Medical Journal, 71(24): 373-375.

Kramer, A., Mirjam, K. and Klaus, K. (2010). Modern infectious disease epidemiology. In: Springer (Ed.). Statistics for biology and health, Science and Business Media, Germany LLC. 210-219.

Lih-Ing, W. R., Zhilan, F. and Carlos, C. (2009). Modeling TB and HIV co infections, Mathematical Biosciences and Engineering, 6(4): 815–837.

Lima, V.D, Johnston, K., Hogg, S.R., Harrigan, P.R., Anema, A. and Montaner, J.S. (2008). Expanded access to highly active anti-retroviral therapy - A potentially powerful strategy to curb down the growth of HIV epidemic, American Journal of Infectious Diseases, 198:59-67.

Martin, D., Sim, J. and Sole, G. (1995). $CD4^+$ lymphocyte count in African patients co infected with HIV and tuberculosis, Journal of Acquired Immune Deficiency Syndrome, 8, 386 - 391.
Mckendric, A.G. (1926). Applications of mathematics to medical problems, Proceedings of Edinburgh mathematical society, 44: 324 – 356.
Mukandavire, Z., Gumel, A., Garira, W. and Tchuenche, J.M. (2009). Mathematical analysis of a model for HIV malaria co infection, Mathematical Biosciences and Engineering, 6(2):333-362.
Oluwaseun, S., Chandra, N. and Abba, B. 2008. Mathematical analysis of the transmission dynamics of HIV/TB co infection in the presence of treatment. Mathematical Biosciences and Engineering, 1: 145–174.
Ronald, R. (1902). The Prevention of malaria, John Murray, London. 127 – 386.
S-F. Shu Schmitz (2000a). A mathematical model of HIV transimission in homosexuals with genetic heterogenity, Journal of Theoretical Medicine,bf 2:285–296.
[70] S-F. Shu Schmitz (2000b). Treatment and vaccination against HIV/AIDS in homosexuals with genetic heterogenity, Math. Biosci.,167:1–18.
Van, P. and Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. Mathematical Biosciences. 180: 29-48.
World Health Organization (WHO), (2008), Malaria and HIV interactions and their implications for Public Health Policy, WHO Press, Geneva, Switzerland, 453 - 463.
World Health Organization (WHO), (2013), HIV - Associated TB facts: Challenges and key issues, http://www.who.int/tb/challenges/hiv/, Accessed on 13th, August, 2013.
World Health Organization (WHO), (2014), The World Health Report; HIV/AIDS global maps, Global prevalence of HIV/AIDS, malaria and tuberculosis, http://www.google.com/imgres?, Accessed on 5th, February, 2014.
Xiao, D. and Bossert, W.H. (2010). An intra-host mathematical model on interaction between HIV and malaria, Bulletin of Mathematical Biology, 72(7): 1892-1911.

******