SCITECH
RESEARCH ORGANISATION

Volume 15, Issue 1
Published online: April 11, 2019|

Journal of Progressive Research in Mathematics
www.scitecresearch.com/journals

Analysis of Treatment and Counseling in an HIV/AIDS Malaria Co infection Model using the Reproduction Number.

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Abstract
This study proposes a model that describes the dynamics of HIV/AIDS Co infection with Malaria using systems of nonlinear ordinary differential equations. The basic reproduction number (R_0) is the average number of secondary infections an infectious individual would cause during the infectious period in an entirely susceptible population. This study has shown that treatment (ARV) and counseling for HIV/AIDS infected individuals have insignificant effect on the spread of malaria, however HIV/AIDS counseling strategy is very effective in controlling the spread of malaria, HIV/AIDS and HIV/AIDS - Malaria co infections. The study further showed that the co infections of HIV/AIDS and malaria reduces the number of HIV/AIDS cases in the population but increases the malaria cases which could be due to the fact that malaria increases the rate of progression from HIV to AIDS leading to more HIV/AIDS deaths reducing the number of the HIV/AIDS cases while HIV/AIDS compromises the immune system thus the HIV/AIDS individuals become easily susceptible to malaria infection increasing the prevalence of malaria in the community.

Keywords: Equilibria; Co-infection; Reproduction Number.

1.0 Introduction
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 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 (Kramer *et al*., 2010).

HIV/AIDS increases the risk of malaria infection and accelerate the development of clinical symptoms of malaria with the greatest impact on the immune suppressed persons while Malaria infection increases the progression rate from HIV to AIDS (WHO, 2008). From the time the co infection of HIV/AIDS and malaria was recorded, malaria has seen a 28 percent increase in its prevalence and malaria related death rates have also nearly doubled for those with the co infection (Centre for Disease Control (CDC), 2007).

The normal CD^+ cell counts in a healthy HIV negative adult vary from 500 cells/μl (500 cells per mm3 of blood) to 1500 cells/μl (Kramer *et al*., 2010). Audu *et al*. (2005) investigated the possible impact of co infections of tuberculosis and malaria on the CD^+ cell counts of HIV/AIDS patients and established the following: The healthy control group recorded a median CD^+ cell counts of 789 cells/μl; subjects infected with HIV/AIDS only recorded a median CD^+ cell counts of 386 cells/μl; subjects co infected with HIV/AIDS and TB recorded a median CD^+ cell counts of 268 cells/μl; subjects co infected with HIV/AIDS and malaria recorded a median CD^+ cell counts of 211 cells/μl and those co infected with HIV/AIDS, malaria and TB recorded the lowest median CD^+ cell counts of 182 cells/μl.

The basic reproduction number (R_0) is defined as the average number of secondary infections an infectious individual would cause during the infectious period in an entirely susceptible population. The basic reproduction number (R_H) for the HIV/AIDS model is defied 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. The basic reproduction number R_H is obtained using the next generation operator approach (Diekmann *et al*, 1990).

2.0 The Model Equations

In this study, a deterministic model exploring the joint dynamics of HIV/AIDS and TB co infections at the population level within a single model is developed. The model is described by a system of ordinary differential equations. The total human population $N_H(t)$ is the sum of the following epidemiological classes: $S_H(t)$ - Susceptible population at time t, $I_M(t)$ - Malaria infected individuals at time t, $I_H(t)$ - HIV infected individuals at time t, $I_A(t)$ - AIDS individuals at time t, $I_{HM}(t)$ - Individuals co infected with malaria and HIV at time t, $I_{AM}(t)$ - Individuals co infected with malaria and HIV and have progressed to AIDS at a given time t. $N_H(t)$ is therefore given by $N_H(t) = SH(t)+I_M(t)+I_H(t)+I_A(t)+I_{HM}(t)+I_{AM}(t)$ and the total vector population $N_V(t)$ is given by $N_V(t) = S_V(t) + I_V(t)$.

The model equations are given by the system of equations below.

$$
\begin{aligned}
\frac{dS_H(t)}{dt} &= \Lambda_H + r_m I_M(t) - \lambda_{ah} S_H(t) - \lambda_{mh} S_H(t) - d_n S_H(t) \\
\frac{dI_M(t)}{dt} &= \lambda_{mh} S_H(t) - r_m I_M(t) - e_m^h \lambda_{ah} I_M(t) - d_n I_M(t) - d_m I_M(t). \\
\frac{dI_H(t)}{dt} &= \lambda_{ah} S_H(t) + r_m I_{HM}(t) - (1-\alpha) p I_H(t) - e_h^m \lambda_{mh} I_H(t) - \\
&\quad d_n I_H(t) + \alpha I_A(t) \\
\frac{dI_A(t)}{dt} &= (1-\alpha) p I_H(t) + r_m I_{AM}(t) - e_a^m \lambda_{mh} I_A(t) - d_a I_A(t) - \\
&\quad d_n I_A(t) - \alpha I_A(t) \\
\frac{dI_{HM}(t)}{dt} &= e_h^m \lambda_{mh} I_H(t) + e_m^h \lambda_{ah} I_M(t) - r_m I_{HM}(t) + \alpha I_{AM}(t) \\
&\quad -d_m I_{HM}(t) - (1-\alpha)\theta_2 p I_{HM}(t) - d_n I_{HM}(t)
\end{aligned}
$$

$$\begin{aligned}
\frac{dI_{AM}(t)}{dt} &= (1-\alpha)\theta_2 p I_{HM}(t) + e_a^m \lambda_{mh} I_A(t) - r_m I_{AM}(t) - d_m I_{AM}(t) - \\
&\quad \alpha I_{AM}(t) - d_n I_{AM}(t) - d_a I_{AM}(t) - d_{ma} I_{AM}(t). \\
\frac{dS_V(t)}{dt} &= \Lambda_V - \lambda_{mv} S_V(t) - d_v S_V(t) \\
\frac{dI_V(t)}{dt} &= \lambda_{mv} S_V(t) - d_v I_V(t)
\end{aligned}$$

$$\frac{dN_H}{dt} = \Lambda_H - d_n N_H - d_m(A_{AM} + d_a B_{AM}) - d_{am} I_{AM}$$

$$A_{AM} = (I_{HM} + I_M + I_{AM}), \text{ and } B_{AM} = (I_A + I_{AM}), \quad \frac{dN_V}{dt} = \Lambda_V - d_v N_V.$$

The forces of infection are given by: $\lambda_{ah} = \frac{\beta_a(1-\delta)c_1(I_H+I_{MH})}{N_H}$, $\lambda_{mh} = \frac{\alpha_1\beta_m I_V}{N_H}$ and

$\lambda_{mv} = \frac{\alpha_1\beta_v(I_M+I_{MH}+I_{MA})}{N_H}$.

Let $\Psi_{H2} = \{(S_H, I_M, I_H, I_A, I_{MH}, I_{MA}) : N(t) \leq \frac{\Lambda_H}{d_n}\}$ and $\Psi_{V2} = \{(S_V, I_V) : N_V \leq \frac{\Lambda_V}{d_v}\}$

For this model it can be shown that the solutions are uniformly bounded in a proper subset $\Psi_{H1} = \Psi_{H2} \times \Psi_{V2}$, which is positively-invariant and attracting thus, the model is mathematically well posed and its dynamics can be considered in Ψ_H. Scaling the sub-populations using the following set of new variables, $s_H = \frac{S_H}{N_H}$, $i_H = \frac{I_H}{N_H}$, $i_A = \frac{I_A}{N_H}$, $i_M = \frac{I_M}{N_H}$, $i_{HM} = \frac{I_{HM}}{N_H}$, $i_{AM} = \frac{I_{AM}}{N_H}$, yield the system of equations given as

$$
\begin{aligned}
\frac{ds_H(t)}{dt} &= \frac{\Lambda_H}{N_H} + r_m i_M(t) - \lambda_{ah} s_H(t) - \lambda_{mh} s_H(t) \\
&\quad -s_H[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{ma} i_{AM}(t)] \\
\frac{di_M(t)}{dt} &= \lambda_{mh} s_H(t) - r_m i_M(t) - e_m^h \lambda_{ah} i_M(t) \\
&\quad -i_M[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{am} i_{AM}(t)] \\
\frac{di_H(t)}{dt} &= \lambda_{ah} s_H(t) + r_m i_{HM}(t) - (1-\alpha) p i_H(t) - e_h^m \lambda_{mh} i_H(t) + \alpha i_A(t) \\
&\quad -i_H[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{am} i_{AM}(t)] \\
\frac{di_A(t)}{dt} &= (1-\alpha) p i_H(t) + r_m i_{AM}(t) - e_a^m \lambda_{mh} i_A(t) - \alpha i_A(t) \\
&\quad -i_A[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{am} i_{AM}(t)] \\
\frac{di_{HM}(t)}{dt} &= e_h^m \lambda_{mh} i_H(t) + e_m^h \lambda_{ah} i_M(t) - r_m i_{HM}(t) + \alpha i_{AM}(t) - (1-\alpha)\theta_2 p i_{HM}(t) \\
&\quad -i_{HM}[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{am} i_{AM}(t)] \\
\frac{di_{AM}(t)}{dt} &= (1-\alpha)\theta_2 p i_{HM}(t) + e_a^m \lambda_m i_A(t) - r_m i_{AM}(t) - d_m i_{AM}(t) - \alpha i_{AM}(t) \\
&\quad -i_{MA}[\frac{\Lambda_H}{N_H} - d_n - (d_m A_{AM}(t) + d_a B_{AM}(t) + d_{am} i_{AM}(t)] \\
\frac{ds_V(t)}{dt} &= \frac{\Lambda_V}{N_V}(t) - \lambda_{mv} s_V(t) - s_V \frac{\Lambda_V}{N_V}(t) \\
\frac{di_V(t)}{dt} &= \lambda_{mv} s_V(t) - i_V \frac{\Lambda_V}{N_V}(t).
\end{aligned}
$$

The feasible region Ψ_{H1} (where the model makes biological sense) is given by

$\Psi_{H1} = \{ s_H, i_M, i_H, i_A, i_{HM}, i_{AM}, s_V, i_V \in R_+^8 : 0 \leq s_H + i_M + i_H + i_A + i_{MH} + i_{AM} \leq 1 ; 0 \leq 0 \leq s_V + i_V \leq 1 \}$. It can be shown that the above region is positively invariant with respect to the system, where R_+^8, denotes the non-negative cone of R^8 including its lower dimensional faces. The boundary and the interior of Ψ_{H1} is denoted by $\partial\Psi_{H1}$ and $\widehat{\Psi}_{H1}$ respectively.

3.0 Disease-Free Equilibrium Point of the Model

In the absence of infection by either or both diseases, the model , has a steady state solution called the DFE given by $\varepsilon_{hm}^{0} = s_H, i_M, i_H, i_A, i_{HM}, i_{AM}, s_V, i_V = (1,0,0,0,0,0,1,0)$. To study the stability of the DFE, the basic reproduction number (R_{HT}) which governs the qualitative dynamics of the model is first obtained. Define $\mathbb{F}_i$ 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 the Jacobian of $\mathbb{F}_i$ and v_i at the DFE denoted by F and V respectively is given by:

$$F = \begin{pmatrix} 0 & 0 & 0 & 0 & 0 & \alpha_1\beta_m \\ 0 & \beta_a(1-\delta)c_1 & 0 & \beta_a(1-\delta)c_1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ \alpha_1\beta_v & 0 & 0 & \alpha_1\beta_v & \alpha_1\beta_v & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} h_1 & 0 & 0 & 0 & 0 & 0 \\ 0 & h_2 & -\alpha & -r_m & 0 & 0 \\ 0 & -(1-\alpha)p & h_3 & 0 & -r_m & 0 \\ 0 & 0 & 0 & h_4 & -\alpha & 0 \\ 0 & 0 & 0 & -(1-\alpha)\theta_2 p & h_5 & 0 \\ 0 & 0 & 0 & 0 & 0 & d_v \end{pmatrix}$$

Where $h_1 = (r_m + d_m + d_n), h_2 = (1-\alpha)p + d_n, h_3 = d_a + \alpha + d_n, h_4 = r_m + d_m + (1-\alpha)\theta_2 p + d_n, h_5 = r_m + d_m + \alpha + d_a + d_n.$

The basic reproduction number $R_0 = R_{HM}$ is by definition is the spectral radius of the matrix FV^{-1} and is given by: $R_{HM} = \max\{R_M, R_H\}$, where

$$R_M = \frac{\alpha_1\sqrt{\beta_m\beta_v}}{\sqrt{d_m d_v + d_n d_v + d_v r_m}}$$

$$R_H = \frac{\beta_a(1-\delta)c_1 h_3\{(\alpha-1)\alpha p\theta_2 + h_5 h_4\}}{(1-\alpha)p\theta_2 D + E(h_5-\alpha)h_4}$$

$$D = -(\alpha^2 d_n + \alpha d_a d_n + \alpha d_n + \alpha d_a p + \alpha d_n p) + \alpha^2 d_a p + \alpha^2 d_n p.$$

$$E = \alpha d_n + d_a d_n + d_n^2 + d_a p - \alpha d_a p + d_n p - \alpha d_n p.$$

Lemma 1. *The DFE of the HIV/AIDS-Malaria model is locally asymptotically stable (LAS) if* $R_{HM} < 1$, *and unstable otherwise*

Proof. Lemma 1 follows from Theorem 2 by Van and Watmough (2002).

Table 1.
Parameter Values for the HIV/AIDS - Malaria Co Infection Model

Symbol	Parameter	Value (day^{-1})	Source
Λ_H	Recruitment rate of humans	4.38356×10^4	Kenya demographics profile (2014)
d_n	Natural death rate of humans	4.56630×10^{-5}	Kenya demographics profile (2014)
d_a	HIV/AIDS-induced death rate	1.09589×10^{-3}	WHO report (2014a)
p	Progression rate from HIV to AIDS (untreated)	2.73972×10^{-3}	Baryama and Mugisha(2007)
α	Proportion of the HIV/AIDS victims treated	1.64384	Kenya NACC report (2014)
β_a	Transmission probability of HIV/AIDS	0.019	Baryama and Mugisha (2007)
α_1	Mosquito biting rate	0.7	Lawi *et al.* (2011)
β_m	Transmission probability of malaria in humans	0.8333	Lawi *et al.* (2011)
c_1	Per capita number of sexual contacts	2.46575×10^{-2}	Kenya NACC report (2014)
δ	Effectiveness of counseling	Variable	
r_m	Proportion of malaria victims treated	1.86301×10^{-3}	WHO report (2013)
d_m	Death rate due to malaria	0.00714	WHO report (2014b)
β_v	Transmission probability of malaria in vectors	$(0-1)$	Chiyaka *et al.*(2007)
θ_2	Increased Progresion rate from HIV to AIDS due to malaria	1.5	Estimated
Λ_V	Recruitment rate of vectors	6	Chiyaka *et al.* (2007)
d_v	Death rate of mosquitoes	0.1429	Lawi *et al* (2011)

4.0 The Role of Treatment and Counseling

The reproduction number (R_M) represents the total number of secondary malaria infections in humans caused by one infected mosquito. Numerical simulation of the reproduction number (R_M) against malaria treatment (r_m) is depicted in figure 1 using the set of parameters in table 1. Figure 1 shows that malaria treatment a lone, without strategies to reduce the mosquito biting rate (α_1) may not eliminate malaria from the community therefore strategies for the reduction of malaria infections in humans should not only target malaria treatment but also the reduction of mosquito biting rate α_1 by encouraging the use of insecticide treated nets, vector elimination or reduction (spraying) and draining stagnant water (breeding grounds)

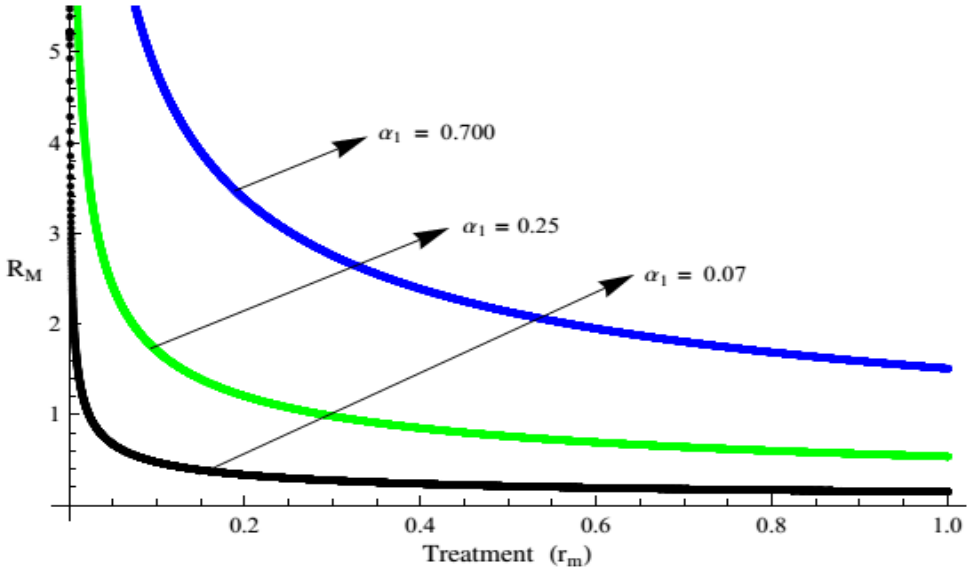

Figure 1: Malaria Reproduction Number (R_H) against Treatment.
Assuming that $R_H > R_M$, implying that $R_H = R_{HM}$, then the graph of R_H against ARV treatment with and without counseling is shown in figure 2

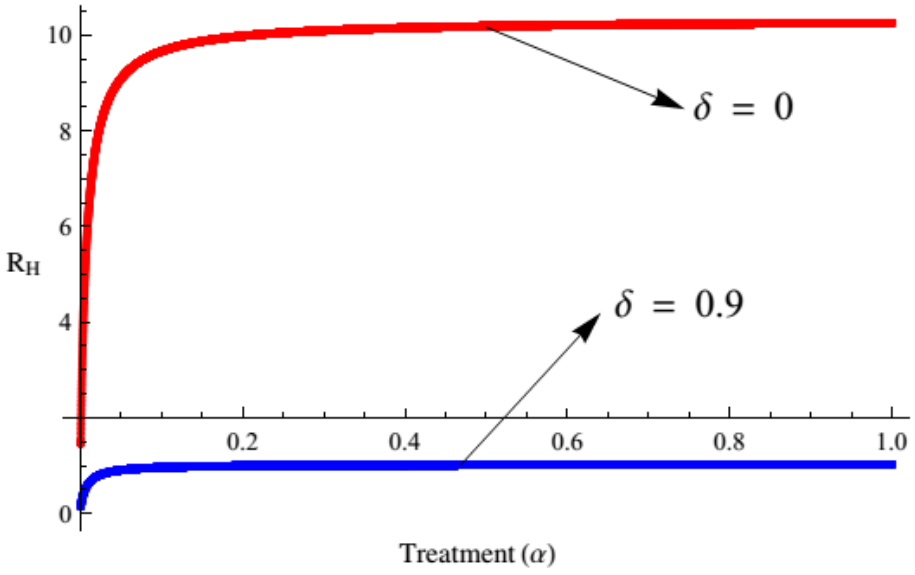

Figure 2: Simulation of R_H against HIV/AIDS Treatment with δ = 0 and 0.9.

Figure 2 shows that an effective HIV/AIDS counseling strategy where δ = 0.9 reduces the value of the reproduction number ($R_{HM} = R_H$) to a level below unity indicating that counseling is very effective in controlling the spread of the HIV/AIDS - malaria co infection.

Figure 3 shows that the effects of scaling up malaria treatment is not significant in reducing the value of R_{HM}.

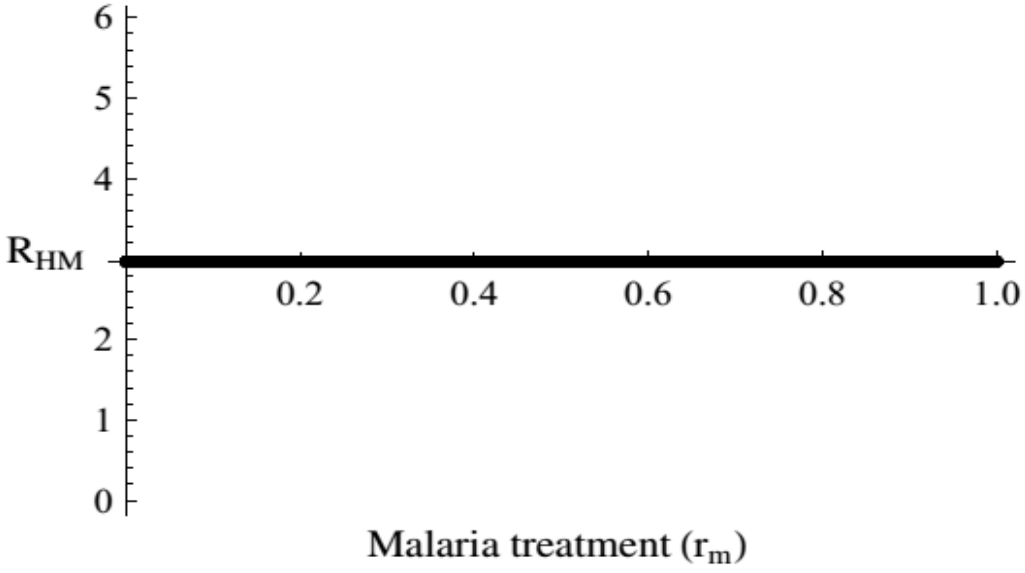

Figure 3: Simulation of R_{HM} against Malaria Treatment

HIV/AIDS incidence in the absence and presence of malaria is analysed in figure 4. The figure depicts the graph of HIV/AIDS infected individuals ($I_H + I_A$) against time in days. The graph shows that co infections of HIV/AIDS and malaria reduces the number of HIV/AIDS cases in the population. This could be due to the fact that malaria increases the rate of progression from HIV to AIDS leading to more HIV/AIDS deaths reducing the number of the HIV/AIDS cases.

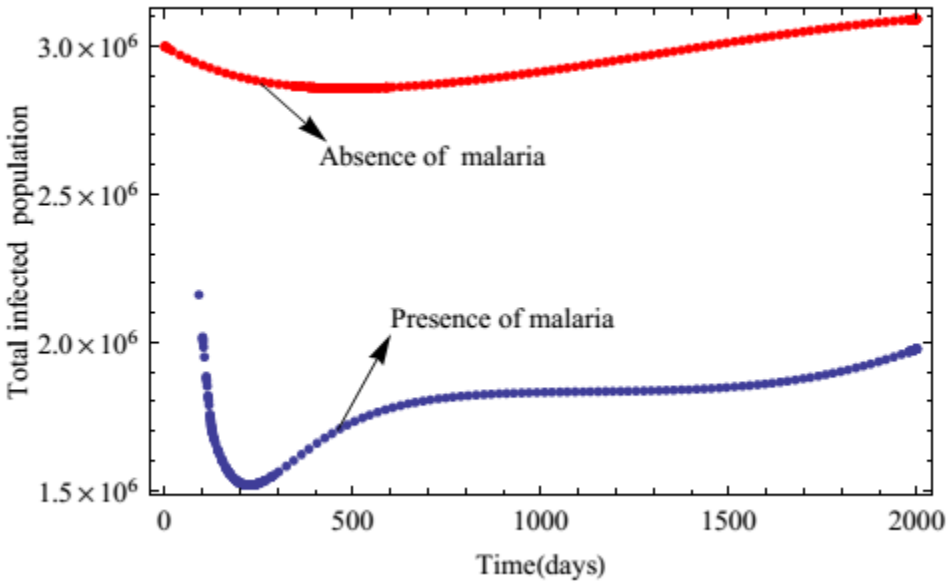

Figure 4: Simulation of HIV/AIDS - Malaria Co Infection against Time in Days.

Figure 5 shows the graph of the malaria infected individuals (I_M) against time in days in the presence and absence of HIV/AIDS. The simulation indicates that co infections of malaria and HIV/AIDS increases the malaria cases in the population. The increase in the malaria cases in the population could be due to the compromised immune system of HIV/AIDS victims as a result of the co infection.

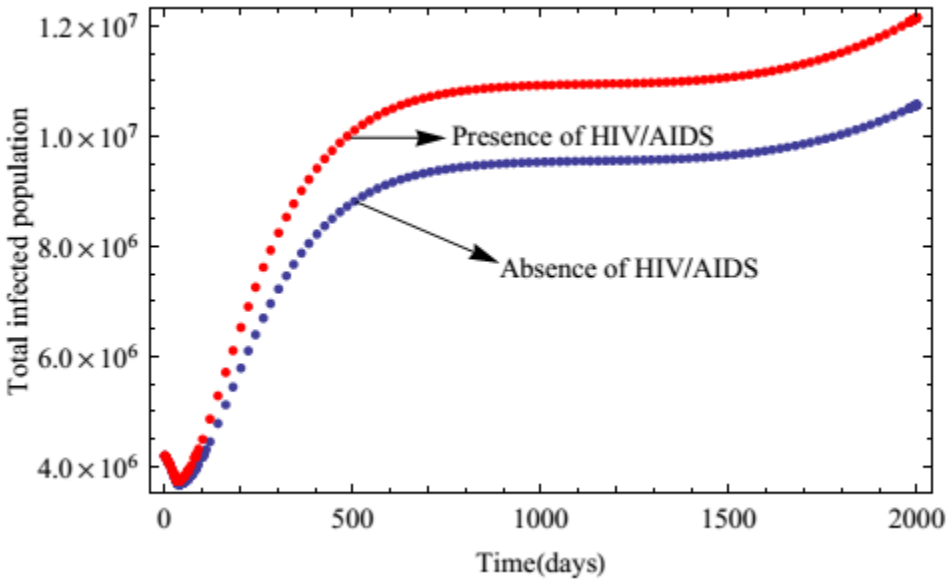

Figure 5: Simulation of Malaria with and without HIV/AIDS.

5. Conclusion

This study has shown that treatment (ARV) and counseling for HIV/AIDS infected individuals have insignificant effect on the spread of malaria, however HIV/AIDS counseling strategy is very effective in controlling the spread of malaria, HIV/AIDS and HIV/AIDS - Malaria co infections. The study further showed that the co infections of HIV/AIDS and malaria reduces the number of HIV/AIDS cases in the population but increases the malaria cases which could be due to the fact that malaria increases the rate of progression from HIV to AIDS leading to more HIV/AIDS deaths reducing the number of the HIV/AIDS cases while HIV/AIDS compromises the immune system thus the HIV/AIDS individuals become easily susceptible to malaria infection increasing the prevalence of malaria in the community.

6. Recommendations

Biologically, lemma 1 implies that HIV/AIDS can be eliminated from the community (when $R_{HM} < 1$) if the initial sizes of the sub-populations of the model are in the basin of attraction of ε_{hm}^{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.

7. Conflicts of interest

There are no conflicts to declare

8. Acknowledgements

Thanks to Prof. Adiel Magana of the department of biological sciences of Chuka university for his insightful contribution to this work.

REFERENCES

[1] 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 $C\ D\ 4^{+}$ cell counts of HIV/AIDS patients in Nigeria. *Annals of African Medicine*, 4(1): 10-13.

[2] Baryama, F. and Mugisha, T. (2007). Comparison of single - stage and staged progression models for HIV/AIDS models. *International Journal of Mathematics and Mathematical Sciences*, 12(4): 399 - 417.

[3] Chiyaka, C., Garira W. and Dube, S. (2007). Transmission model of endemic human malaria in a partially immune population. *Mathematical and Computer Modeling* 46: 806-822.

[4] Centre for Disease Control and Prevention (CDC). (2007). Incorporating HIV prevention into the medical care of persons living with malaria: MMWR 2006: 55 (No. RR14):1-17. http:www.cdc.gov/malaria/facts.htm, Accessed on August, 22nd, 2013.

[5] Diekmann, O., Heesterbeek, J. and Metz, J. (1990). On the definition and computation of the basic reproductive ratio, R_0 in models of infectious diseases in heterogeneous populations. *Journal of Mathematical Biology*, 28(1): 365-382.

[6] Juan, P. and Castillo, C. (2009). Mathematical modeling of tuberculosis epidemics. *Mathematical Biosciences and Engineering*, (6) 2: 209 - 237.

[7] Kenya demographics profile. (2014). Accessed on 3rd August 2015 at www.indexmundi.com/kenya/demographicsprofle 2014.

[8] Kenya National AIDS Control Council (NACC) Report.(2014). Accessed on 03/08/ 2015 at http://www.kaisernetwork.org.

[9] Kramer, A., Mirjam, K. and Klaus, K. (2010). Modern infectious disease epidemiology. In: Springer (Ed.), *Statistics for Biology, Health, Science and Business Media*, Germany LLC. 210 - 219.

[10] Lawi, G. O., Mugisha, J. Y. and Omolo - Ongati, N. (2011), Mathematical model for malaria and meningitis co-infection among children. *Applied Mathematical Sciences*, Vol. 5: 47, 2337 – 2359 .

[11] 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.

[12] World Health Organization (WHO). (2014a). The World Health Report; HIV/AIDS global maps, Global prevalence of HIV/AIDS, malaria and tuberculosis. ttp://www.google.com/imgres?, Accessed on 5th, February, 2014.

[13] World Health Organization (WHO). (2014b). World Malaria Report 2013; Country profiles. http://www.google.com/imgres?, Accessed on 5th, February, 2014.

[14] World Health Organization (WHO). (2008). Malaria and HIV interactions and their implications for public health policy. WHO Press, Geneva, Switzerland, 453 – 463.

[15] Van, P. and Watmough, J. (2002). Reproduction numbers and the sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical Biosciences*, 180(200): 29-48.