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Mathematical Modelling of Human African Trypanosomiasis using Control Measures

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Abstract

Human African Trypanosomiasis (HAT) commonly known as sleeping sickness, is a neglected tropical vector borne disease caused by trypanosome protozoa. It is transmitted by bites of infected tsetse fly. In this paper we first present the vector-host model which describes the general transmission dynamics of HAT. In the tsetse fly population, the HAT is modelled by three compartments while in the human population, the HAT is modelled by four compartments. The next generation matrix approach is used to derive the basic reproduction number, R_0, and also it is proved that if $R_0 \leq 1$ the disease free equilibrium is globally asymptotically stable, which means the disease dies out. The disease persist in the population if the value of $R_0 > 1$. Furthermore, the optimal control model is determined by using the Pontryagin's maximum principle with control measures such as education, treatment and insecticides used to optimize the objective function. The model simulations confirm that the use of the three control measures are very efficient and effective to eliminate HAT in Africa.

Keywords: Human African Trypanosomiasis (HAT), Mathematical modelling, optimal control, Control measures.

1 Introduction

Human African trypanosomiasis (HAT), commonly known as sleeping sickness, is a vector-borne tropical disease which is caused by trypanosoma brucei protozoa species. It is one of the neglected tropical diseases which affects people in sub-Saharan Africa specifically those living in rural areas. HAT is caused by two species of protozoa which are Trypanosoma brucei gambiense (TBG), which causes the chronic form of HAT in central and western Africa and Trypanosoma brucei rhodesiense (TBR), which causes the acute form of the disease in Eastern and southern Africa [1]. The HAT disease has killed millions of people since the beginning of 20^{th} century and it is transmitted from one individual to another by tsetse flies (genus $Glossina$); TBG is transmitted by riverine tsetse species while TBR is transmitted by savanna tsetse species [1]. Rhodesiense HAT is an acute disease that can lead to death if not treated within 6 months while Gambiense HAT is a slow chronic progressive disease which causes death with an average duration of 3 years [2]. The signs and symptoms for both forms of HAT are not specific and their appearances vary from one person to another; at the first stage of HAT, the disease is not severe and the signs and symptoms such as intermittent fever, headache, pruritus, lymphadenopathies, asthenia, anemia, cardiac disorders, endocrin disturbances, musculoskeletal pains and hepatosplenomegaly may be observed while in the second stage of HAT, sleep disorders and neuro-psychiatric disorders are likely to dominate. The HAT disease can be treated by using the drugs such as suramin, eflornithine, melarsoprol and pentamidine.

The disease is reported to affect about 37 sub-Saharan African Countries, it affects much rural areas where there are suitable environments for the tsetse flies to live and reproduce; the peri-urban areas can also be affected. The transmission of HAT can occur during the human activities such as hunting, farming as well as fishing [3]. The transmission of HAT needs the reservoir; *reservoir* is a species that can permanently maintain the pathogen and from which the pathogen can be transmitted to the target population [4]. Rhodesiense HAT is zoonotic which requires a non-human reservoir (animals) for maintaining its population, while in Gambiense HAT, humans act as key reservoir [4].

Mathematical models have been used to study the transmission and effective control of diseases simply and cheaply with no need of expensive and complicated experiments [5]. So far, different models have been developed and formulated by different researchers. One of the important modelling work on HAT, was done by [6]; the model explained the mathematical frame work on transmission of HAT in multiple host populations [6]. Rogers model was generalized by [7] and a new parameter which allows the tsetse flies to feed off multiple hosts was introduced. The model compared the effectiveness of two methods used to control HAT; insecticide treated cattle and the use of trypanocides drugs to treat cattle. They found out that treating cattle with insecticides is more effective and a cheaper approach to control HAT than using trypanocides drugs. [8] developed a model which was based on a constant population with a fixed number of domestic animals, human and tsetse flies in one of the Villages in West Africa. The major findings of their model estimated that the cattle population contribute to about 92% of the total TBR transmission while the rest 8% is the contribution of human population in transmission of the disease. The work in [8] which also formulated a multi-host model was used to study the control of tsetse flies and TBR in Southern Uganda. They found out that the effective application of insecticides brings about a cost-effective method of control and eliminating the disease, they realised that insecticides way for controlling HAT is more effective and efficient in the area where there are few wild hosts.

Due to low mortality rate of the disease and poverty of its sufferers, the efforts toward the control of HAT has reduced. Most attention is given to popular diseases such as HIV/AIDS, Tuberculosis, Malaria and Ebola, although the disease is still a threat to the lives of sub-Saharan African people. Moreover, very few studies have been carried out on applying optimal control theory to HAT transmission models. In this paper, we use optimal control theory to study the transmission dynamics of HAT diseases by using education, treatment and insecticides as the control measures.

The rest of this paper is outlined as follows: Section 2 represents the vector-host model and the underlying assumptions. In section 3 the model equilibria and stabilities are determined whereas in Section 4, the optimal control model is analysed by modifying the previous one to control the HAT by using control measures (education, insecticides and treatment). In addition, the numerical simulations for the optimal control model are done in this section and we use the results obtained to compare the efforts of each control measure to control the HAT in Africa. Finally we provide the conclusion in Section 5.

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2 Model Formulation

In this section, the vector-host model as well as the necessary differential equations to describe the transmission of HAT from tsetse fly to human and vice versa is developed. The transmission of HAT in the human population is modelled using four subclasses; Susceptible S_H, Exposed E_H, Infectious I_H and Recovered R_H. The total human population, N_H, is thus defined by:

$$N_H = S_H + E_H + I_H + R_H.$$

The transmission of HAT in the vector (Tsetse flies) population, is also divided into Susceptible (S_V), Exposed (E_V) and Infectious (I_V). The total population of the tsetse flies, N_V, is also defined by:

$$N_V = S_V + E_V + I_V.$$

We assume a constant population for both host and vector, it is also assumed that the tsetse fly cannot recover from the disease and the infected tsetse fly remains infectious throughout the rest of its life; there is no disease induced death rate for tsetse flies and the recruitment rates are assumed to be constant due to birth and immigration. In

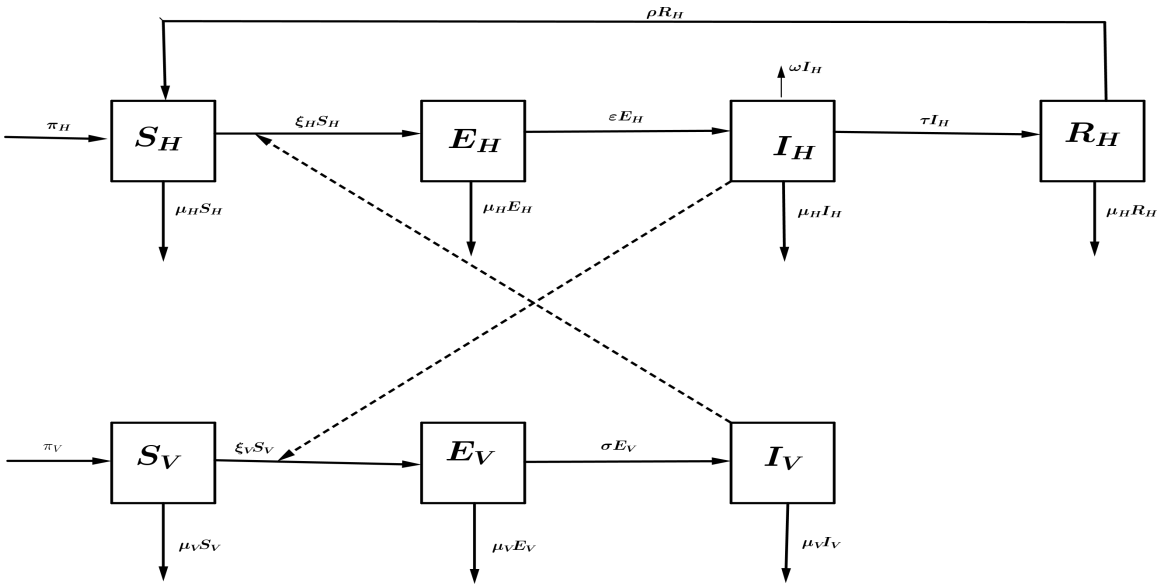

Figure 1: Compartmental model for the transmission of Human African Trypanosomiasis.

our model, the recruitment rate of hosts and vectors are represented by π_H and π_V respectively. The susceptible host gets the disease when bitten by infectious tsetse fly and susceptible tsetse fly gets the disease when it bites an infectious human at the rate a. The natural mortality rate for humans and vectors are represented by μ_H and μ_V respectively. The parameter ω represents the disease induced death rate for humans while ξ_H and ξ_V are the force of infection for humans and vectors respectively. The parameter σ represents per capita rate of a vector becoming infectious, and the rest of the parameters are explained in Table 1. Assuming that the transmission per bite from infectious tsetse-fly to human is a, then the rate of infection per susceptible human is given by

$$\xi_H = \frac{ap_H I_V}{N_V},$$

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and also if we further assume that a is the tsetse-fly biting rate, that is, the average number of bites per tsetse-fly per unit, then the rate of infection per susceptible tsetse-fly can be represented by

$$\xi_V = \frac{ap_V I_H}{N_H}.$$

From the model diagram in Figure (1), the following differential equations are derived:

$$\begin{cases} \frac{dS_H}{dt} &= \pi_H N_H + \rho R_H - \frac{ap_H I_V}{N_V} S_H - \mu_H S_H \\ \frac{dE_H}{dt} &= \frac{ap_H I_V}{N_V} S_H - \varepsilon E_H - \mu_H E_H \\ \frac{dI_H}{dt} &= \varepsilon E_H - \mu_H I_H - \omega I_H - \tau I_H \\ \frac{dR_H}{dt} &= \tau I_H - \rho R_H - \mu_H R_H \\ \frac{dS_V}{dt} &= \pi_V N_V - \mu_V S_V - \frac{ap_V I_H}{N_H} S_V \\ \frac{dE_V}{dt} &= \frac{ap_V I_H}{N_H} S_V - \mu_V E_V - \sigma E_V \\ \frac{dI_V}{dt} &= \sigma E_V - \mu_V I_V. \end{cases} \tag{1}$$

From system (1), the dimensionless technique is used to derive another equivalent differential equations; we denote $s_h = \frac{S_H}{N_H}$, $e_h = \frac{E_H}{N_H}$, $i_h = \frac{I_H}{N_H}$, $r_h = \frac{R_H}{N_H}$, $s_v = \frac{S_V}{N_V}$, $e_v = \frac{E_V}{N_V}$, $i_v = \frac{I_V}{N_V}$ and substitute into system (1), to obtain the following new equivalent equations:

$$\begin{cases} \frac{ds_h}{dt} &= \pi_h + \rho r_h - ap_h i_v s_h - \mu_h s_h \\ \frac{de_h}{dt} &= ap_h i_v s_h - \varepsilon e_h - \mu_h e_h \\ \frac{di_h}{dt} &= \varepsilon e_h - \mu_h i_h - \omega i_h - \tau i_h \\ \frac{dr_h}{dt} &= \tau i_h - \rho r_h - \mu_h r_h \\ \frac{ds_v}{dt} &= \pi_v - \mu_v s_v - ap_v i_h s_v \\ \frac{de_v}{dt} &= ap_v i_h s_v - \mu_v e_v - \sigma e_v \\ \frac{di_v}{dt} &= \sigma e_v - \mu_v i_v. \end{cases} \tag{2}$$

The following table shows the description of the model parameters and variables.

2.1 Positivity and Boundedness of the Solutions

In this subsection we show that system (2) is epidemiologically and mathematically well-defined in the positive invariant region;

$$D = \left\{ (s_h, e_h, i_h, r_h, s_v, e_v, i_v) \in \mathbb{R}^7_+ : n_h \leq \frac{\pi_h}{\mu_h}; n_v \leq \frac{\pi_v}{\mu_v} \right\}. \tag{3}$$

Theorem 1. There exist a domain D in which the solution $(s_h, e_h, i_h, r_h, s_v, e_v, i_v)$ is contained and bounded.

Proof. We provide the proof following the idea by [9]. Given the solution set $(s_h, e_h, i_h, r_h, s_v, e_v, i_v)$ with the positive initial conditions $(s_{h_0}, e_{h_0}, i_{h_0}, r_{h_0}, s_{v_0}, e_{v_0}, i_{v_0})$, we define

$$n_h(s_h, e_h, i_h, r_h) = s_h(t) + e_h(t) + i_h(t) + r_h(t) \text{ and}$$

$$n_v(s_v, e_v, i_v) = s_v(t) + e_v(t) + i_v(t).$$

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Table 1: The description of model variables and parameters

Variable	**Description**
s_h	Susceptible human population
s_v	Susceptible tsetse fly population
e_h,e_v	Exposed human and tsetse fly population respectively
i_h,i_v	Infectious human and tsetse population respectively
r_h	Recovered human population
Parameter	**Description**
π_h	Recruitment rate for human population
π_v	Recruitment rate for tsetse fly population
p_h	Proportion of bites by the infectious vector on susceptible human population
p_v	Proportion of bites by susceptible vector on an Infectious human population
a	The biting rate of the tsetse flies
σ	Per capita rate of a vector becoming infectious
ε	Per capita rate of human becoming infectious
ω	Disease induced death rate
ρ	The rate at which the recovered human can become susceptible again
τ	Recovery rate
μ	Natural death rate
ξ_h	Force of infection for human population
ξ_v	Force of infection for tsetse flies

The derivatives of n_h and n_v with respect to time along the solution of system (2) for human and tsetse flies respectively, are obtained by;

$$\begin{aligned} n_h^{'} &= \frac{ds_h}{dt} + \frac{de_h}{dt} + \frac{di_h}{dt} + \frac{dr_h}{dt}, \\ &= \pi_h - (s_h + e_h + i_h + r_h)\mu_h - \omega i_h, \\ &= \pi_h - n_h\mu_h - \omega i_h. \\ n_v^{'} &= \frac{ds_v}{dt} + \frac{de_v}{dt} + \frac{di_v}{dt}, \\ &= \pi_v - (s_v + e_v + i_v)\mu_v, \\ &= \pi_v - n_v\mu_v. \end{aligned}$$

From these differential equations it follows that $n_h^{'} \leq \pi_h - \mu_h n_h$ and $n_v^{'} \leq \pi_v - \mu_v n_v$. We obtain the solutions as follows;

$$\begin{aligned} n_h &\leq \frac{\pi_h}{\mu_h}\left(1 - \exp(-\mu_h t)\right) + n_h(s_{h_0}, e_{h_0}, i_{h_0}, r_{h_0})\exp(-\mu_h t), \\ n_v &\leq \frac{\pi_v}{\mu_v}\left(1 - \exp(-\mu_v t)\right) + n_v(s_{v_0}, e_{v_0}, i_{v_0})\exp(-\mu_v t). \end{aligned}$$

By taking the limits of both n_h and n_v above as $t \longrightarrow \infty$ we obtain $n_h \leq \frac{\pi_h}{\mu_h}$ and $n_v \leq \frac{\pi_v}{\mu_v}$, hence the solutions are contained in the region D. This implies that all solutions of the human and tsetse fly population are contained in the region D and are non-negative, this guarantee that the positive invariant region for system (2) exists and is

given by;

$$D = \left\{ (s_h, e_h, i_h, r_h, s_v, e_v, i_v) \in \mathbb{R}_+^7 : n_h \leq \frac{\pi_h}{\mu_h}; n_v \leq \frac{\pi_v}{\mu_v} \right\}.$$

□

3 Model Equilibria and Stability Analysis

In this section we give the model equilibria, the basic reproduction number, R_0, and the stabilities at both disease free and endemic equilibrium.

3.1 Disease-free Equilibrium(DFE)

The DFE in system (2) is when there are no HAT infections within the human and tsetse fly population. Thus the existence of the DFE is given by; $E_0 = \left(\frac{\pi_h}{\mu_h}, 0, 0, 0, \frac{\pi_v}{\mu_v}, 0, 0 \right)$.

3.2 Endemic Equilibrium(EE)

The EE is the non-trivial equilibrium point at which the HAT disease persist in both human and tsetse fly population. Thus the EE is obtained as follows; $E_* = (s_h^*, e_h^*, i_h^*, r_h^*, s_v^*, e_v^*, i_v^*)$, where,

$$\begin{cases} s_h^* &= \dfrac{[\pi_h(\rho+\mu_h)+\rho\tau i_h^*]\,[\mu_v(\sigma+\mu_v)(ap_v i_h^*+\mu_v)]}{[a^2\sigma p_h p_v \pi_v i_h^* + \mu_v\mu_h(\sigma+\mu_v)(ap_v i_h^*+\mu_v)]\,(\mu_h+\rho)}, \\ e_h^* &= \dfrac{(\omega+\tau+\mu_h)i_h^*}{\varepsilon}, \\ r_h^* &= \dfrac{\tau i_h^*}{\mu_h+\rho}, \\ s_v^* &= \dfrac{\pi_v}{ap_v i_h^*+\mu_v}, \\ e_v^* &= \dfrac{ap_v\pi_v i_h^*}{(\sigma+\mu_v)(ap_v i_h^*+\mu_v)}, \\ i_v^* &= \dfrac{a\sigma p_v \pi_v i_h^*}{(\sigma+\mu_v)(ap_v i_h^*+\mu_v)\mu_v}, \\ i_h^* &= \dfrac{(\rho+\mu_h)\left[a^2\varepsilon p_h p_v \pi_h \pi_v \sigma - \mu_v^2\mu_h(\varepsilon+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)\right]}{B}, \end{cases} \tag{4}$$

the term

$$B = (ap_v(a\sigma p_h\pi_v(\varepsilon\rho\omega+\mu_h(\rho(\tau+\omega)+\varepsilon(\rho+\tau+\omega)+\mu_h(\varepsilon+\rho+\tau+\omega+\mu_h)))+\mu_h(\varepsilon+\mu_h)(\rho+\mu_h)(\tau+\omega+\mu_h)\mu_v(\sigma+\mu_v))).$$

3.3 Basic Reproduction Number, R_0

The basic reproduction number, R_0, is defined as the number of secondary infections caused by one infected host or vector in a completely susceptible population [10]. The *next generation matrix* approach as done by *Van den Driessche* and *Watmough* in [5, 11] is applied to derive

$$\mathbb{F} = \begin{pmatrix} ap_h i_v s_h \\ 0 \\ ap_v i_h s_v \\ 0 \end{pmatrix} \text{ and } \mathbb{V} = \begin{pmatrix} \mu_h e_h + \varepsilon e_h \\ -\varepsilon e_h + \mu_h i_h + \omega i_h + \tau i_h \\ \mu_v e_v + \delta e_v \\ -\delta e_v + \mu_v i_v \end{pmatrix}.$$

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By denoting matrix $F = \frac{\partial \mathbb{F}}{\partial x_i}$ and $V = \frac{\partial \mathbb{V}}{\partial x_i}$ where $x_i = e_h, i_h, e_v, i_v$, the spectral radius of the next generation matrix FV^{-1} gives the value of R_0.

$$F = \begin{pmatrix} 0 & 0 & 0 & ap_h s_h \\ 0 & 0 & 0 & 0 \\ 0 & ap_v s_v & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \text{ and } V = \begin{pmatrix} \varepsilon + \mu_h & 0 & 0 & 0 \\ -\varepsilon & \mu_h + \omega + \tau & 0 & 0 \\ 0 & 0 & \mu_v + \delta & 0 \\ 0 & 0 & -\delta & \mu_v \end{pmatrix},$$

$$FV^{-1} = \begin{pmatrix} 0 & 0 & \frac{a\delta p_h}{\mu_v(-\delta + \mu_v)} & \frac{-ap_h}{\mu_v} \\ 0 & \frac{ap_v}{\mu_h + \tau + \omega} & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

The spectral radius $\sigma(FV^{-1})$ gives,

$$R_0 = \sigma(FV^{-1}) = \sqrt{\frac{a^2 \varepsilon p_h p_v \pi_h \pi_v \sigma}{\mu_v^2 \mu_h (\varepsilon + \mu_h)(\sigma + \mu_v)(\mu_h + \tau + \omega)}}.$$

One infected human in a population of susceptible vectors will cause R_v infected vectors, like wise, one infected vector in a population will cause R_h infected humans [5]. Therefore the basic reproduction number can be rewritten as $R_0 = \sqrt{R_h R_v}$, where $R_h = \frac{a\varepsilon p_h \pi_h}{\mu_h(\mu_h + \varepsilon)(\mu_h + \tau + \omega)}$ and $R_v = \frac{\sigma a p_v \pi_v}{\mu_v^2(\sigma + \mu_v)}$. Thus, R_0 can also be defined as the square root of the product of the number of infected humans in the susceptible population caused by one infected tsetse fly in its infectious lifetime and the number of infected tsetse flies caused by one infected human during the infectious period [12].

3.4 Local Stability of Disease-Free Equilibrium(DFE)

Theorem 2. If $R_0 \leq 1$ the DFE given by E_0 is locally asymptotically stable in the region defined by Equation (3), it is unstable when $R_0 > 1$.

Proof. The DFE is locally stable if all eigenvalues of Jacobian matrix J_{E_0} are negative. The matrix has all eigenvalues negative only if the trace of $J_{E_0} < 0$ and determinant of $J_{E_0} > 0$. By linearising system (2) around E_0, we obtain the following Jacobian matrix;

$$J_{E_0} = \begin{pmatrix} -\mu_h & 0 & 0 & \rho & 0 & 0 & -ap_h s_h \\ 0 & -(\varepsilon + \mu_h) & 0 & 0 & 0 & 0 & ap_h s_h \\ 0 & \varepsilon & -(\omega + \tau + \mu_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & \tau & -(\rho + \mu_h) & 0 & 0 & 0 \\ 0 & 0 & -ap_v s_v & 0 & -\mu_v & 0 & 0 \\ 0 & 0 & ap_v s_v & 0 & 0 & -(\sigma + \mu_v) & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma & -\mu_v \end{pmatrix}.$$

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The trace of matrix J_{E_0} is such that;

$$\begin{aligned} tr(J_{E_0}) &= -(\mu_h + \varepsilon + \mu_h + \mu_h + \omega + \tau + \rho + \mu_h + \mu_v + \sigma + \mu_v + \mu_v) \\ &= -(4\mu_h + 3\mu_v + \varepsilon + \omega + \tau + \rho + \sigma) < 0. \end{aligned}$$

Using the basic properties of matrix algebra as in [13], it is clear that the eigenvalues $\lambda_1 = -\mu_h$ and $\lambda_2 = -\mu_v$ of the matrix J_{E_0} have negative real parts. The reduced matrix is

$$J_{E_1} = \begin{pmatrix} -(\varepsilon + \mu_h) & 0 & 0 & 0 & ap_h s_h \\ \varepsilon & -(\omega + \tau + \mu_h) & 0 & 0 & 0 \\ 0 & \tau & -(\rho + \mu_h) & 0 & 0 \\ 0 & ap_v s_v & 0 & -(\sigma + \mu_v) & 0 \\ 0 & 0 & 0 & \sigma & -\mu_v \end{pmatrix}.$$

From matrix J_{E_1} the eigenvalue $\lambda_3 = -(\rho + \mu_h)$ has negative real part. The remaining matrix is further reduced by using the reduction techniques, we obtain;

$$J_{E_2} = \begin{pmatrix} -(\varepsilon + \mu_h) & 0 & 0 & ap_h s_h \\ 0 & -(\omega + \tau + \mu_h) & 0 & \frac{ap_h s_h \varepsilon}{\varepsilon + \mu_h} \\ 0 & ap_v s_v & -(\sigma + \mu_v) & 0 \\ 0 & 0 & \sigma & -\mu_v \end{pmatrix}.$$

Using the properties of matrix algebra, the matrix J_{E_2} has eigenvalue $-(\varepsilon + \mu_h)$ which has negative real part. We further reduce to a 2×2 matrix by using the same reduction techniques. The matrix is

$$J_{E_3} = \begin{pmatrix} -(\omega + \tau + \mu_h) & \frac{ap_h s_h \varepsilon}{\varepsilon + \mu_h} \\ \frac{ap_v s_v \sigma}{\sigma + \mu_v} & -\mu_v \end{pmatrix}.$$

From the reduced 2×2 matrix, the trace is negative and the determinant is,

$$\begin{aligned} Det(J_{E_3}) &= (\omega + \tau + \mu_h)\mu_v - \frac{ap_h s_h \varepsilon}{\varepsilon + \mu_h} \times \frac{ap_v s_v \sigma}{\sigma + \mu_v}, \\ &= (\omega + \tau + \mu_h)\mu_v \left[1 - \frac{a^2 \varepsilon p_h p_v \pi_h \pi_v \sigma}{\mu_v^2 \mu_h (\varepsilon + \mu_h)(\sigma + \mu_v)(\mu_h + \tau + \omega)}\right]. \end{aligned}$$

Since

$$R_0 = \sqrt{\frac{a^2 \varepsilon p_h p_v \pi_h \pi_v \sigma}{\mu_v^2 \mu_h (\varepsilon + \mu_h)(\sigma + \mu_v)(\mu_h + \tau + \omega)}},$$

then, by letting $R_T = \dfrac{a^2 \varepsilon p_h p_v \pi_h \pi_v \sigma}{\mu_v^2 \mu_h (\varepsilon + \mu_h)(\sigma + \mu_v)(\mu_h + \tau + \omega)}$, we find our determinant as,

$$Det(J_{E_3}) = (\omega + \tau + \mu_h)\mu_v \left[1 - R_T\right]. \tag{5}$$

The value of R_T can be seen to be positive because all the parameters are positive. As a result, the determinant in (5) is positive if and only if $R_T < 1$. Therefore the DFE is locally stable if $R_T \leq 1$. □

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3.5 Global Stability of Disease-Free Equilibrium(DFE)

To show that the DFE is globally stable, we apply the Lypunov's Theorem in [5].

Theorem 3. The DFE defined by E_0 is globally asymptotically stable in the region defined by Equation (3) if $R_0 \leq 1$. Otherwise unstable if $R_0 > 1$.

Proof. We define the Lypunov's function as

$$V = k_1\left(s_h - s_{h_0} - s_{h_0}\ln\frac{s_h}{s_{h_0}}\right) + k_2 e_h + k_3 i_h + k_4\left(s_v - s_{v_0} - s_{v_0}\ln\frac{s_v}{s_{v_0}}\right) + k_5 e_v + k_6 i_v \tag{6}$$

satisfying system (2), where $k_1, k_2, k_3, k_4, k_5, k_6 > 0$ are to be determined and $s_{h_0} = \dfrac{\pi_h}{\mu_h}$ and $s_{v_0} = \dfrac{\pi_v}{\mu_v}$. We first show that $V > 0$ for all $E \neq \left(\dfrac{\pi_h}{\mu_h}, 0, 0, 0, \dfrac{\pi_v}{\mu_v}, 0, 0\right)$. It is enough to check that,

$$k_1 s_{h_0}\left(\frac{s_h}{s_{h_0}} - 1 - \ln\frac{s_h}{s_{h_0}}\right) > 0,$$
$$k_4 s_{v_0}\left(\frac{s_v}{s_{v_0}} - 1 - \ln\frac{s_v}{s_{v_0}}\right) > 0.$$

The function $g(m) = m - 1 - \ln m$ such that $m = \frac{s_h}{s_{h_0}} = \frac{s_v}{s_{v_0}}$ has minimum value equal to zero when $m = 1$, hence $g(m) > 0$ for all $m > 0$. Thus the Lypunov's function $V > 0$. The function V is radially unbounded because as $|m| \longrightarrow \infty$ the function $g(m) \longrightarrow \infty$. We now take the derivative of V with respect to time and use system (2) to replace the derivatives in the right hand side such that;

$$\begin{aligned}
V' =& k_1\left(1 - \frac{s_{h_0}}{s_h}\right)\frac{ds_h}{dt} + k_2\frac{de_h}{dt} + k_3\frac{di_h}{dt} + k_4\left(1 - \frac{s_{v_0}}{s_v}\right)\frac{ds_v}{dt} + k_5\frac{de_v}{dt} + k_6\frac{di_v}{dt},\\
=& k_1\left(1 - \frac{s_{h_0}}{s_h}\right)\left[\pi_h + \rho r_h - a p_h i_v s_h - \mu_h s_h\right] + k_2\left[a p_h i_v s_h - \varepsilon e_h - \mu_h e_h\right]\\
&+ k_3\left[\varepsilon e_h - \mu_h i_h - \omega i_h - \tau i_h\right] + k_4\left(1 - \frac{s_{v_0}}{s_v}\right)\left[\pi_v - \mu_v s_v - a p_v i_h s_v\right]\\
&+ k_5\left[a p_v i_h s_v - \mu_v e_v - \sigma e_v\right] + k_6\left[\sigma e_v - \mu_v i_v\right],\\
=& 2k_1\pi_h - a p_h s_h k_1 i_v + \rho r_h k_1 - k_1\mu_h s_h - k_1\frac{\pi_h^2}{\mu_h s_h} + \frac{a p_h \pi_h i_v}{\mu_h}k_1 - \frac{\pi_h \rho r_h}{\mu_h s_h}k_1 + k_2 a p_h s_h i_v\\
&- k_2(\varepsilon + \mu_h)e_h + k_3\varepsilon e_h - k_3(\tau + \mu_h + \omega)i_h + 2k_4\pi_v - k_4 a p_v s_v i_h - \mu_v s_v k_4 - \frac{\pi_v^2}{\mu_v s_v}k_4\\
&+ \frac{a p_v i_h \pi_v}{\mu_v}k_4 - k_5(\mu_v + \sigma)e_v + k_5 a p_v s_v i_h + k_6\sigma e_v - k_6\mu_v i_v.
\end{aligned}$$

The terms with r_h are ignored because if s_h, e_h, i_h are globally stable then $r_h \longrightarrow 0$ at any time t and the DFE for system (2) is globally stable. Taking $k_1 = k_2 = \frac{1}{\mu_h + \varepsilon}$, $k_4 = k_5 = \frac{1}{\mu_v + \sigma}$, $k_3 = \frac{1}{\varepsilon}$ and $k_6 = \frac{1}{\sigma}$, the derivative of V with respect to time becomes:

$$V' = -\frac{\pi_h}{\mu_h+\varepsilon}\left(\frac{\pi_h}{\mu_h s_h}+\frac{\mu_h s_h}{\pi_h}-2\right)-\frac{(\tau+\mu_h+\omega)}{\varepsilon}i_h+\frac{ap_h\pi_h}{(\mu_h+\varepsilon)\mu_h}i_v-\frac{\pi_v}{\mu_v+\sigma}\left(\frac{\pi_v}{\mu_v s_v}+\frac{\mu_v s_v}{\pi_v}-2\right)$$

$$-\frac{\mu_v}{\sigma}i_v+\frac{ap_v\pi_v}{\mu_v(\mu_v+\sigma)}i_h,$$

$$=-\left[\frac{\pi_h}{\mu_h+\varepsilon}\left(\frac{\pi_h}{\mu_h s_h}+\frac{\mu_h s_h}{\pi_h}-2\right)+\frac{\pi_v}{\mu_v+\sigma}\left(\frac{\pi_v}{\mu_v s_v}+\frac{\mu_v s_v}{\pi_v}-2\right)\right]$$

$$+\frac{(\tau+\mu_h+\omega)}{\varepsilon}\left(\frac{\varepsilon ap_v\pi_v}{\mu_v(\sigma+\mu_v)(\mu_h+\tau+\omega)}-1\right)i_h+\frac{\mu_v}{\sigma}\left(\frac{a\sigma p_h\pi_h}{\mu_v\mu_h(\mu_h+\varepsilon)}-1\right)i_v,$$

$$=-\left[\frac{\pi_h}{\mu_h+\varepsilon}\left(\frac{\pi_h}{\mu_h s_h}+\frac{\mu_h s_h}{\pi_h}-2\right)+\frac{\pi_v}{\mu_v+\sigma}\left(\frac{\pi_v}{\mu_v s_v}+\frac{\mu_v s_v}{\pi_v}-2\right)\right]$$

$$+\frac{(\tau+\mu_h+\omega)}{\varepsilon}(R_v-1)i_h+\frac{\mu_v}{\sigma}(R_h-1)i_v.$$

The terms $\left(\frac{\pi_h}{\mu_h s_h}+\frac{\mu_h s_h}{\pi_h}-2\right)$ and $\left(\frac{\pi_v}{\mu_v s_v}+\frac{\mu_v s_v}{\pi_v}-2\right)$ are positive because if we suppose $m=\frac{\pi_h}{\mu_h s_h}=\frac{\pi_v}{\mu_v s_v}$, we have $m+\frac{1}{m}-2=\frac{m^2-2m+1}{m}=\frac{(m-1)^2}{m}>0$ for all $m>1$ and since $R_v\leq 1$ and $R_h\leq 1$ then V' is negative. Thus we have $V'<0$ for all $E_0\neq\left(\frac{\pi_h}{\mu_h},0,0,0,\frac{\pi_v}{\mu_v},0,0\right)$. □

Thus, the largest compact invariant set in D is the singleton set E_0. Hence, system (2) is globally asymptotically stable.

3.6 Local Stability of Endemic Equilibrium(EE)

Theorem 4. The unique endemic equilibrium defined by E^* is locally asymptotically stable in the region defined by Equation (3) if $R_0>1$, but is unstable if $R_0\leq 1$.

Proof. We give the proof of this theorem based on the approach used by [9, 14]. From the EE points defined in Equation (4), since all values are positive, we express the value of i_h^* in terms of R_0 to obtain;

$$i_h^*=\frac{\mu_v^2\mu_h(\varepsilon+\mu_h)(\rho+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)}{B}\left[\frac{a^2\varepsilon p_h p_v\pi_h\pi_v\sigma}{\mu_v^2\mu_h(\varepsilon+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)}-1\right],$$

$$=\frac{\mu_v^2\mu_h(\varepsilon+\mu_h)(\rho+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)}{B}\left[R_0^2-1\right],$$

where

$$B=(ap_v(a\sigma p_h\pi_v(\varepsilon\rho\omega+\mu_h(\rho(\tau+\omega)+\varepsilon(\rho+\tau+\omega)+\mu_h(\varepsilon+\rho+\tau+\omega+\mu_h)))+\mu_h(\varepsilon+\mu_h)(\rho+\mu_h)(\tau+\omega+\mu_h)\mu_v(\sigma+\mu_v))).$$

Since the basic reproduction number, $R_0=\sqrt{\frac{a^2\varepsilon p_h p_v\pi_h\pi_v\sigma}{\mu_v^2\mu_h(\varepsilon+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)}}$, if we let

$$R_T=\frac{a^2\varepsilon p_h p_v\pi_h\pi_v\sigma}{\mu_v^2\mu_h(\varepsilon+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)},$$

then we can find i_h^* as,

$$i_h^*=\frac{\mu_v^2\mu_h(\varepsilon+\mu_h)(\rho+\mu_h)(\sigma+\mu_v)(\mu_h+\tau+\omega)}{B}\left[R_T-1\right].$$

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The value of B is clearly positive because all parameters are positive. Hence, $i_h^* > 0$ if and only if $R_T > 1$, implying that the EE is locally asymptotically stable if $R_T > 1$. □

3.7 Global Stability of Endemic Equilibrium(EE)

To show the global stability of the EE we use Lyapunov's Theorem together with the following Lemma.

Lemma 1. Suppose that $y_1, y_2, \cdots, y_n$ are n positive numbers, then their arithmetic mean is greater than or equal to the geometric mean, that's $\dfrac{y_1 + y_2 + \cdots + y_n}{n} \geq (y_1 y_2 \cdots y_n)^{\frac{1}{n}}$.

Theorem 5. The EE defined by E^* is globally asymptotically stable if $R_0 > 1$, otherwise is unstable.

Proof. The proof is based on the idea as explained by [5]. We define the Lyapunov function as

$$V = k_1\left(s_h - s_h^* - s_h^* \ln\frac{s_h}{s_h^*}\right) + k_2\left(e_h - e_h^* - e_h^* \ln\frac{e_h}{e_h^*}\right) + k_3\left(i_h - i_h^* - i_h^* \ln\frac{i_h}{i_h^*}\right)$$

$$+ k_4\left(s_v - s_v^* - s_v^* \ln\frac{s_v}{s_v^*}\right) + k_5\left(e_v - e_v^* - e_v^* \ln\frac{e_v}{e_v^*}\right) + k_6\left(i_v - i_v^* - i_v^* \ln\frac{i_v}{i_v^*}\right)$$

satisfying system (2) with $k_1, k_2, k_3, k_4, k_5, k_6 > 0$ to be determined. The function V is non negative for all $(s_h, e_h, i_h, r_h, s_v, e_v, i_v) \neq (s_h^*, e_h^*, i_h^*, r_h^*, s_v^*, e_v^*, i_v^*)$ and radially unbounded.

We need to prove that $V' < 0$ for all $(s_h, e_h, i_h, r_h, s_v, e_v, i_v) \neq (s_h^*, e_h^*, i_h^*, r_h^*, s_v^*, e_v^*, i_v^*)$. We find the derivative of V with respect to time and replace the derivatives $s_h^{'}, e_h^{'}, i_h^{'}, r_h^{'}, s_v^{'}, e_v^{'}, i_v^{'}$ with system (2). We also ignore the r_h terms because if s_h, e_h, i_h are globally stable then $r_h \longrightarrow 0$ at any time t and EE is globally stable.

$$V^{'} = k_1\left(1 - \frac{s_h^*}{s_h}\right)[\pi_h - ap_h i_v s_h - \mu_h s_h] + k_2\left(1 - \frac{e_h^*}{e_h}\right)[ap_h i_v s_h - (\mu_h + \varepsilon)e_h]$$

$$+ k_3\left(1 - \frac{i_h^*}{i_h}\right)[\varepsilon e_h - (\omega + \tau + u_h)i_h] + k_4\left(1 - \frac{s_v^*}{s_v}\right)[\pi_v - ap_v i_h s_v - \mu_v s_v]$$

$$+ k_5\left(1 - \frac{e_v^*}{e_v}\right)[ap_v i_h s_v - (\mu_v + \sigma)e_v] + k_6\left(1 - \frac{i_v^*}{i_v}\right)[\sigma e_v - u_v i_v].$$

We now substitute $\pi_h = ap_h i_v^* s_h^* + \mu_h s_h^*$ and $\pi_v = ap_v i_h^* s_v^* + \mu_v s_v^*$ at the endemic equilibrium then simplify and put similar terms together to obtain;

$$\begin{aligned}
V' = &- k_1\frac{(s_h - s_h^*)^2 \mu_h}{s_h} + k_1 ap_h i_v^* s_h^* - k_1 ap_h i_v s_h - k_1 ap_h \frac{s_h^{*2} i_v^*}{s_h} + k_1 ap_h i_v s_h^* + k_2 ap_h s_h i_v - k_2(\varepsilon + \mu_h)e_h \\
&- k_2 ap_h s_h i_v \frac{e_h^*}{e_h} + k_2(\varepsilon + \mu_h)e_h^* + k_3\varepsilon e_h - k_3(\omega + \tau + \mu_h)i_h^* - k_3\varepsilon e_h \frac{i_h^*}{i_h} + k_3(\omega + \tau + \mu_h)i_h^* \\
&- k_4\frac{(s_v - s_v^*)^2 \mu_v}{s_v} + k_4 ap_v i_h^* s_v^* - k_4 ap_v i_h s_v - k_4 ap_v \frac{s_v^{*2} i_h^*}{s_v} + k_4 ap_v i_h s_v^* + k_5 ap_v s_v i_h - k_5(\sigma + \mu_v)e_v \\
&- k_5 ap_v s_v i_h \frac{e_v^*}{e_v} + k_5(\sigma + \mu_v)e_v^* + k_6\sigma e_v - k_6\mu_v i_v^* - k_6\sigma e_v \frac{i_v^*}{i_v} + k_6\mu_v i_v^*.
\end{aligned}$$

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We suppose $k_1 = k_2$ and $k_4 = k_5$, and multiply and divide the same equilibrium value to some of the fractions to obtain;

$$\begin{aligned}V' =& -k_1\frac{(s_h - s_h^*)^2\mu_h}{s_h} + k_1 a p_h i_v^* s_h^* - k_1 a p_h \frac{s_h^{*2} i_v^*}{s_h} + k_1 a p_h i_v s_h^* - k_2(\varepsilon+\mu_h)e_h \\ &- k_2 a p_h s_h i_v \frac{e_h^* s_h^* i_v^*}{s_h^* i_v^* e_h} + k_2(\varepsilon+\mu_h)e_h^* + k_3\varepsilon e_h - k_3(\omega+\tau+\mu_h)i_h - k_3\varepsilon e_h\frac{i_h^* e_h^*}{i_h e_h^*} + k_3(\omega+\tau+\mu_h)i_h^* \\ &- k_4\frac{(s_v - s_v^*)^2\mu_v}{s_v} + k_4 a p_v i_h^* s_v^* - k_4 a p_v \frac{s_v^{*2} i_h^*}{s_v} + k_4 a p_v i_h s_v^* - k_5(\sigma+\mu_v)e_v \\ &- k_5 a p_v s_v i_h \frac{e_v^* s_v^* i_h^*}{s_v^* i_h^* e_v} + k_5(\sigma+\mu_v)e_v^* + k_6\sigma e_v - k_6\mu_v i_v^* - k_6\sigma e_v\frac{e_v^* i_v^*}{i_v e_v^*} + k_6\mu_v i_v^*.\end{aligned}$$

We choose $k_3 = k_2\frac{\mu_h+\varepsilon}{\varepsilon}$ such that $k_3(\omega+\tau+\mu_h)i_h^* = k_2(\varepsilon+\mu_h)e_h^*$ and choose $k_6 = k_5\frac{\mu_h+\sigma}{\sigma}$ such that $k_6\mu_v i_v^* = k_5(\sigma+\mu_v)e_v^*$. Now $a p_h s_h^* i_v^* = (\mu_h+\varepsilon)e_h^*$ and $a p_v s_v^* i_v^* = (\mu_v+\sigma)e_v^*$ because $k_1 = k_2$ and $k_4 = k_5$ respectively. We now obtain;

$$\begin{aligned}V' =& -k_1\frac{(s_h - s_h^*)^2\mu_h}{s_h} + k_1 a p_h i_v^* s_h^*\left[3 - \frac{s_h^*}{s_h} - \frac{e_h^* i_v s_h}{s_h^* e_h i_v^*} - \frac{e_h i_h^*}{i_h e_h^*}\right] + k_1 a p_h i_v s_h^* - k_3(\omega+\tau+\mu_h)i_h \\ &+ \left[k_3\varepsilon - k_2(\varepsilon+\mu_h)\right]e_h - k_4\frac{(s_v - s_v^*)^2\mu_v}{s_v} + k_4 a p_v i_h^* s_v^*\left[3 - \frac{s_v^*}{s_v} - \frac{e_v^* i_h s_v}{s_v^* e_v i_h^*} - \frac{e_v i_v^*}{i_v e_v^*}\right] \\ &+ k_4 a p_v i_h s_v^* - k_6\mu_v i_v + \left[k_6\sigma - k_5(\sigma+\mu_v)\right]e_v.\end{aligned}$$

Suppose $k_6 = \frac{k_1 a p_h s_h^*}{\mu_v}$ and $k_3 = \frac{k_4 a p_v s_v^*}{\omega+\tau+\mu_h}$, we then substitute and simplify to get

$$\begin{aligned}V' =& -k_1\frac{(s_h - s_h^*)^2\mu_h}{s_h} + k_1 a p_h i_v^* s_h^*\left[3 - \frac{s_h^*}{s_h} - \frac{e_h^* i_v s_h}{s_h^* e_h i_v^*} - \frac{e_h i_h^*}{i_h e_h^*}\right] - k_4\frac{(s_v - s_v^*)^2\mu_v}{s_v} \\ &+ k_4 a p_v i_h^* s_v^*\left[3 - \frac{s_v^*}{s_v} - \frac{e_v^* i_h s_v}{s_v^* e_v i_h^*} - \frac{e_v i_v^*}{i_v e_v^*}\right].\end{aligned}$$

From Lemma 1 above, the terms

$$k_1 a p_h i_v^* s_h^*\left[3 - \tfrac{s_h^*}{s_h} - \tfrac{e_h^* i_v s_h}{s_h^* e_h i_v^*} - \tfrac{e_h i_h^*}{i_h e_h^*}\right] \text{ and } k_4 a p_v i_h^* s_v^*\left[3 - \tfrac{s_v^*}{s_v} - \tfrac{e_v^* i_h s_v}{s_v^* e_v i_h^*} - \tfrac{e_v i_v^*}{i_v e_v^*}\right] \leq 0.$$

Therefore, $V' < 0$ for all $(s_h, e_h, i_h, r_h, s_v, e_v, i_v) \neq (s_h^*, e_h^*, i_h^*, r_h^*, s_v^*, e_v^*, i_v^*)$ implying that the endemic equilibrium is globally asymptotically stable if $R_0 > 1$. □

4 Analysis of Optimal Control Model

In this section, we formulate the optimal control model by modifying system (2) to an optimal control problem. We thus define some linear functions $c_i(t) = 1$, for $i = 1, 2, 3$. It is important to note that controls are fully effective when $c_i(t) = 1$ and not effective when $c_i(t) = 0$. The forces of infection ξ_h and xi_v which correspond to the human and vector population respectively, are reduced by the factor $(1 - c_1)$; where c_1 measures the level of success obtained due to the effort of educating people on the dangers of exposing their skin, and encouraging them to wear long sleeves and long pants during the day to minimize tsetsefly-human contacts. The factor c_2 represents the effort of treatment to control the disease and the factor c_3 also represent the effort of using insecticides to ensure that the breeding sites of the tsetsefly are minimized. Hence, taking into account the assumptions and extensions

made, we try to find the most effective strategy that reduces the HAT infection in the population at a very minimum cost. With the use of bounded Lebesgue measurable control, we define the objective function to be minimized as

$$J(c_1, c_2, c_3) = \int_0^{t_F} \left(M_1 e_h + M_2 i_h + M_3 e_v + M_4 i_v + \frac{1}{2} k_1 c_1^2 + \frac{1}{2} k_2 c_2^2 + \frac{1}{2} k_3 c_3^2 \right) dt. \tag{7}$$

Thus, the dynamics of the controls that minimizes the objective function is given by

$$\begin{cases} \frac{ds_h}{dt} &= \pi_h + \rho r_h - (1-c_1) a p_h i_v s_h - \mu_h s_h \\ \frac{de_h}{dt} &= (1-c_1) a p_h i_v s_h - \varepsilon e_h - \mu_h e_h \\ \frac{di_h}{dt} &= \varepsilon e_h - \mu_h i_h - \omega i_h - c_2 \tau i_h \\ \frac{dr_h}{dt} &= c_2 \tau i_h - \rho r_h - \mu_h r_h \\ \frac{ds_v}{dt} &= \pi_v - c_3 \mu_v s_v - (1-c_1) a p_v i_h s_v \\ \frac{de_v}{dt} &= (1-c_1) a p_v i_h s_v - c_3 \mu_v e_v - \sigma e_v \\ \frac{di_v}{dt} &= \sigma e_v - c_3 \mu_v i_v, \end{cases} \tag{8}$$

subject to the initial conditions $s_h \geq 0, e_h \geq 0, i_h \geq 0, r_h \geq 0, s_v \geq 0, e_v \geq 0, i_v \geq 0$. The associated effective reproduction number for Equation (8) denoted by R_E is obtained as

$$R_E = \sqrt{\frac{a^2 \varepsilon (1-c_1)^2 p_h \pi_h \pi_v \sigma}{c_3 \mu_h (\varepsilon + \mu_h) \mu_v^2 (\sigma + c_3 \mu_v)(\mu_h + c_2 \tau + \omega)}} = \sqrt{R_c}. \tag{9}$$

The goal is to minimize the exposed and infectious human populations (e_h, i_h), the exposed and infectious vector populations (e_v, i_v) and the cost of implementing the control by the use of possible $c_i, i = 1, 2, 3$. The functional objective includes the social cost which relates to the resources that is needed for educating people on personal protection $\frac{1}{2} k_1 c_1^2$, the application of treatment $\frac{1}{2} k_2 c_2^2$ and spraying of tsetsefly operations $\frac{1}{2} k_3 c_3^2$. The quantities M_1 and M_2 respectively represent the associated cost with minimizing the exposed and infected human population, while M_3 and M_4 also represent the cost associated with minimizing the exposed and infected vector respectively. The quantity t_F is the time period of intervention. As explained in [17], the costs corresponding to $M_1 e_h, M_2 i_h, M_3 e_v$ and $M_4 i_v$ are linear while the cost control functions $\frac{1}{2} k_1 c_1^2$, $\frac{1}{2} k_2 c_2^2$, and $\frac{1}{2} k_3 c_3^2$ should be nonlinear and take a quadratic form. Therefore, we seek to minimize the objective function over the given time interval $[0, t_F]$. Pontryagin's Maximum Principle is used to solve this optimal control problem and the derivation of the necessary conditions. The Lagrangian of the optimal control problem is given by

$$L = \left(M_1 e_h + M_2 i_h + M_3 e_v + M_4 i_v + \frac{1}{2} k_1 c_1^2 + \frac{1}{2} k_2 c_2^2 + \frac{1}{2} k_3 c_3^2 \right). \tag{10}$$

To determine the Lagrangian minimum value, we define the Hamiltonian, H, for the control problem as

$$\begin{aligned} H =& M_1 e_h + M_2 i_h + M_3 e_v + M_4 i_v + \frac{1}{2} k_1 c_1^2 + \frac{1}{2} k_2 c_2^2 + \frac{1}{2} k_3 c_3^2 + \lambda_{s_h} \frac{ds_h}{dt} + \lambda_{e_h} \frac{de_h}{dt} + \lambda_{i_h} \frac{di_h}{dt} \\ &+ \lambda_{r_h} \frac{dr_h}{dt} + \lambda_{s_v} \frac{ds_v}{dt} + \lambda_{e_v} \frac{de_v}{dt} + \lambda_{i_v} \frac{di_v}{dt}, \end{aligned}$$

where $\lambda_{s_h}, \lambda_{e_h}, \lambda_{i_h}, \lambda_{r_h}, \lambda_{s_v}, \lambda_{e_v}, \lambda_{i_v}$ are adjoint variables or co-state variables. The differential equations of adjoint variables are obtained by taking the partial derivatives of the Hamiltonian equation with respect to the state variables which gives:

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$$\begin{cases} \frac{d\lambda_{s_h}}{dt} &= \lambda_{s_h}\mu_h + (\lambda_{s_h} - \lambda_{e_h})(1-c_1)ap_h i_v \\ \frac{d\lambda_{e_h}}{dt} &= -M_1 + (\lambda_{e_h} - \lambda_{i_h})\varepsilon + \lambda_{e_h}\mu_h \\ \frac{d\lambda_{i_h}}{dt} &= -M_2 + (\lambda_{i_h} - \lambda_{r_h})c_2\tau + \lambda_{i_h}(\omega + \mu_h) + (\lambda_{s_v} - \lambda_{e_v})(1-c_1)ap_v s_v \\ \frac{d\lambda_{r_h}}{dt} &= (\lambda_{r_h} - \lambda_{s_h})\rho + \lambda_{r_h}\mu_h \\ \frac{d\lambda_{s_v}}{dt} &= (\lambda_{s_v} - \lambda_{e_v})(1-c_1)ap_v i_h + \lambda_{s_v}\mu_v c_3 \\ \frac{d\lambda_{e_v}}{dt} &= -M_3 + (\lambda_{e_v} - \lambda_{i_v})\sigma + \lambda_{e_v}\mu_v c_3 \\ \frac{d\lambda_{i_v}}{dt} &= -M_4 + (\lambda_{s_h} - \lambda_{e_h})(1-c_1)ap_h s_h + \lambda_{i_v}\mu_v c_3. \end{cases} \tag{11}$$

Theorem 6. Given the optimal controls c_1^*, c_2^*, c_3^* and the solutions $s_h, e_h, i_h, r_h, s_v, e_v, i_v$ of the corresponding state Equations (8) and (7) which minimize $J(c_1, c_2, c_3)$ over the region Ω, then there exist adjoint variables $\lambda_{s_h}, \lambda_{e_h}, \lambda_{i_h}, \lambda_{r_h}, \lambda_{s_v}, \lambda_{e_v}, \lambda_{i_v}$ satisfying

$$-\frac{d\lambda_i}{dt} = \frac{\partial H}{\partial i} \quad i \in \{s_h, e_h, i_h, r_h, s_v, e_v, i_v\},$$

and the optimal solution c_1^*, c_2^*, c_3^* is given by

$$c_1^* = \min\{1, \max(0, \widehat{c_1})\},$$

$$c_2^* = \min\{1, \max(0, \widehat{c_2})\},$$

$$c_3^* = \min\{1, \max(0, \widehat{c_3})\}.$$

Proof. The Pontryagin's Maximum principle described in [15, 16] is applied. The Corollary 4.1 in [16] shows the existence of an optimal control due to the convexity of the integrand J with respect to c_1, c_2, c_3, and Lipschitz property of the state system with respect to the state variables. By using the optimal conditions,

$$\frac{\partial H}{\partial c_1} = 0, \quad \frac{\partial H}{\partial c_2} = 0, \quad \frac{\partial H}{\partial c_3} = 0,$$

we obtain,

$$\begin{cases} \frac{\partial H}{\partial c_1} &= k_1 c_1 + (\lambda_{s_h} - \lambda_{e_h})ap_h i_v s_h + (\lambda_{s_v} - \lambda_{e_v})ap_v i_h s_v = 0, \\ \frac{\partial H}{\partial c_2} &= k_2 c_2 + (\lambda_{r_h} - \lambda_{i_h})\tau i_h = 0, \\ \frac{\partial H}{\partial c_3} &= k_3 c_3 - (\lambda_{s_v}\mu_v s_v + \lambda_{e_v}\mu_v e_v + \lambda_{i_v}\mu_v i_v) = 0. \end{cases} \tag{12}$$

Solving Equation (12) we have,

$$\widehat{c_1} = \frac{(\lambda_{e_h} - \lambda_{s_h})ap_h i_v s_h + (\lambda_{e_v} - \lambda_{s_v})ap_v i_h s_v}{k_1},$$

$$\widehat{c_2} = \frac{(\lambda_{i_h} - \lambda_{r_h})\tau i_h}{k_2},$$

$$\widehat{c_3} = \frac{\lambda_{s_v}\mu_v s_v + \lambda_{e_v}\mu_v e_v + \lambda_{i_v}\mu_v i_v}{k_3}.$$

□

As stated earlier, the lower and upper boundaries for the control parameters are 0 and 1 respectively. If $\widehat{c_1}, \widehat{c_2}, \widehat{c_3} < 1$ then $c_1 = c_2 = c_3 = 0$ and if $\widehat{c_1}, \widehat{c_2}, \widehat{c_3} > 1$ then $c_1 = c_2 = c_3 = 1$ otherwise $c_1 = \widehat{c_1}, c_2 = \widehat{c_2}, c_3 = \widehat{c_3}$. Therefore, for the control parameters c_1^*, c_2^*, c_3^* we obtain the optimum value of the function $J(c_1, c_2, c_3)$.

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4.1 Optimal Control Simulations

The Octave programming language is used to simulate the optimal control model using the set of parameters obtained from previously reported studies and datasets, which have been cited. Some of these parameters are assumed for the sake of illustrations. Table 2 represents the values of the model parameters used for simulations. The following initial conditions were considered,

$$s_h(0) = 30, e_h(0) = 7, i_h(0) = 2, r_h(0) = 0, s_v(0) = 40, e_v(0) = 10, i_v(0) = 3,$$

and the weight constants were assumed to be

$$M_1 = 1, M_2 = 2, M_3 = 2, M_4 = 2, k_1 = 2, k_2 = 10, k_3 = 5.$$

Table 2: Parameters values used for simulations

Parameter	Value	Reference
π_h	0.000215/day	[14]
π_v	0.07/day	[14]
p_h	0.62	[6]
p_v	0.065	[6], [17]
a	varying	Assumed
σ	0.001	Assumed
ε	0.083	[18]
ω	0.004	[3]
ρ	0.02	[6]
τ	0.125	[3]
μ_h	0.00044	Assumed
μ_v	0.034	[17]

The Figures 2 and 3 represent the control profiles at different values of c_1, c_2 and c_3 while the rest of the plots are the graphs of infectious human and vector population plotted against time in days and they represent the effect of optimal controls c_1, c_2 and c_3 in reducing the number of individuals infected. From Figure 4 we observe that, the use of treatment and insecticides only has a significant impact in reducing the number of infectious individuals and they show that this strategy is effective to control tsetse flies and infected human populations. In Figure 5, we observe that the use of education and insecticides reduce the number of infectious individuals but the results depicted in Figure 5(a) shows that this strategy is not effective and efficient to control the infectious human population. From Figure 6, we observe that the use of education and treatment reduce the number of infectious individuals but the results from Figure 6(b) shows that this strategy is not effective and efficient to control the infectious tsetse flies population. Lastly, the results depicted from Figure 7 shows that the strategy of using both education, treatment and insecticides are very efficient and effective to reduce the number of infected individuals. Therefore, the use of both education, treatment and insecticides simultaneously is very efficient and effective to eliminate HAT in Africa.

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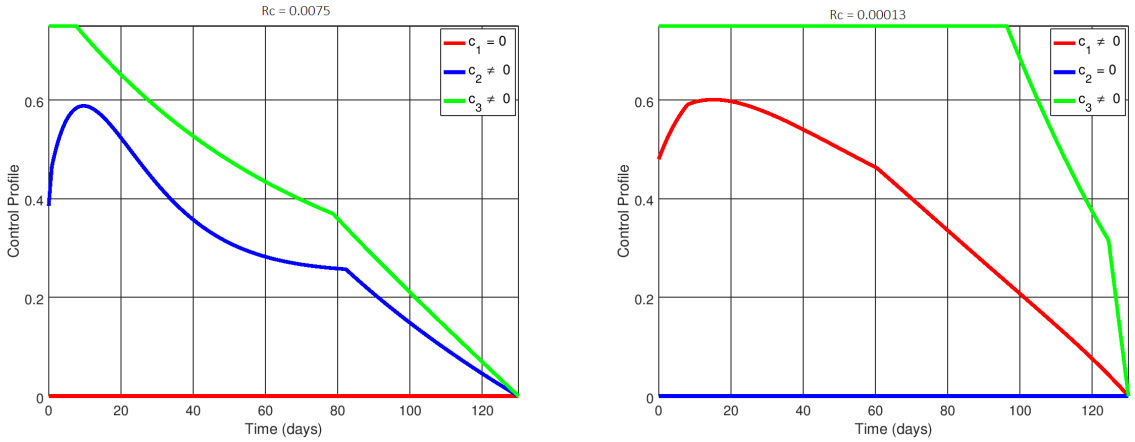
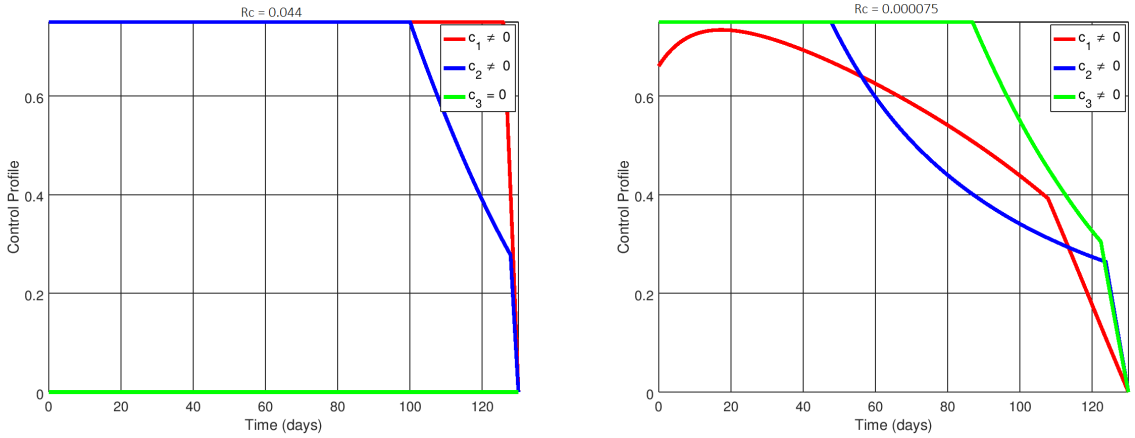


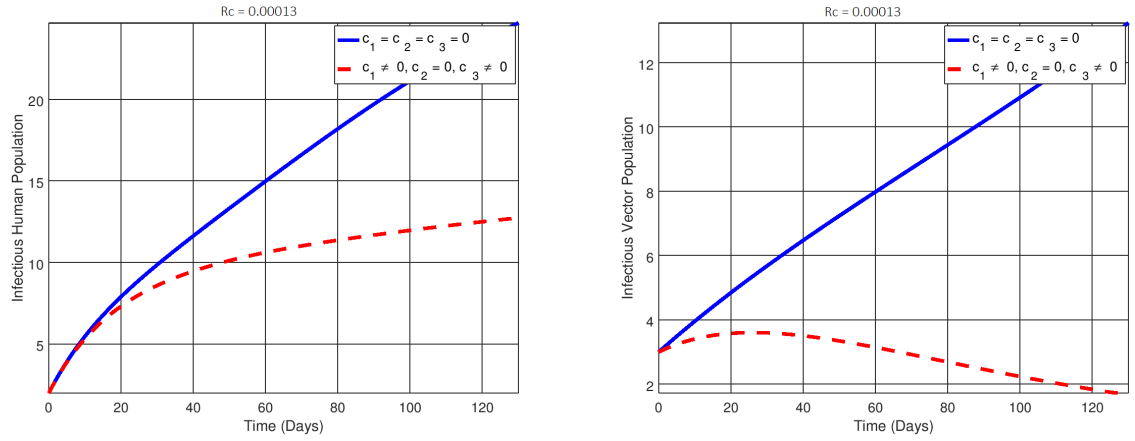
(a) (b)

Figure 2: (a) Control Profile when $c_1 = 0$, $c_2 \neq 0$ and $c_3 \neq 0$. (b) Control profile when $c_1 \neq 0, c_2 = 0$ and $c_3 \neq 0$.



(a) (b)

Figure 3: (a) Control Profiles when $c_1 \neq 0, c_2 \neq 0$ and $c_3 = 0$. (b) Control profile when $c_1 \neq 0, c_2 \neq 0$, and $c_3 \neq 0$.



(a) (b)

Figure 5: Simulations of the model showing the efforts of education and insecticides only on infectious individuals.

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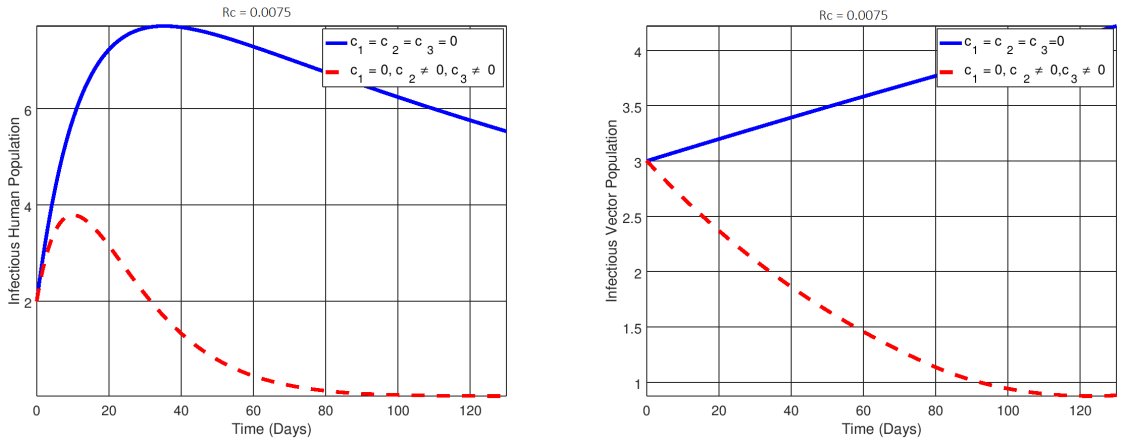
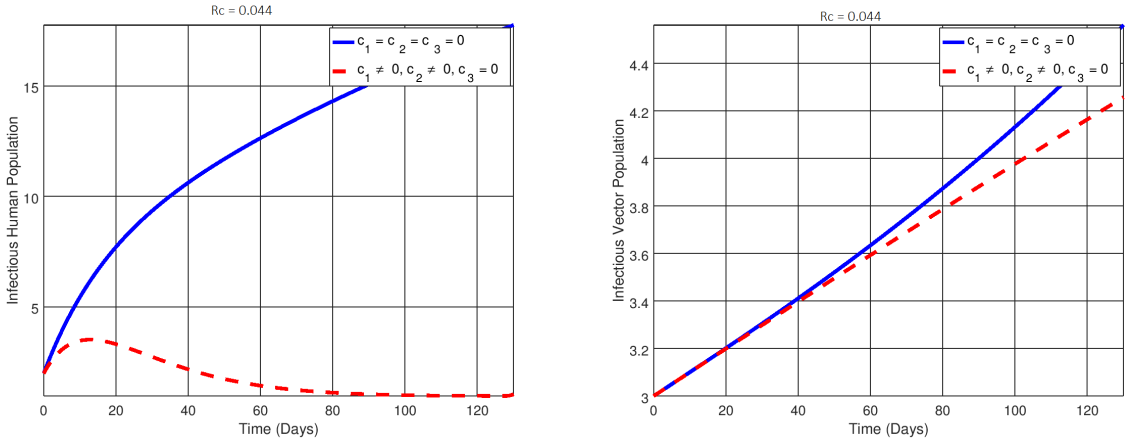


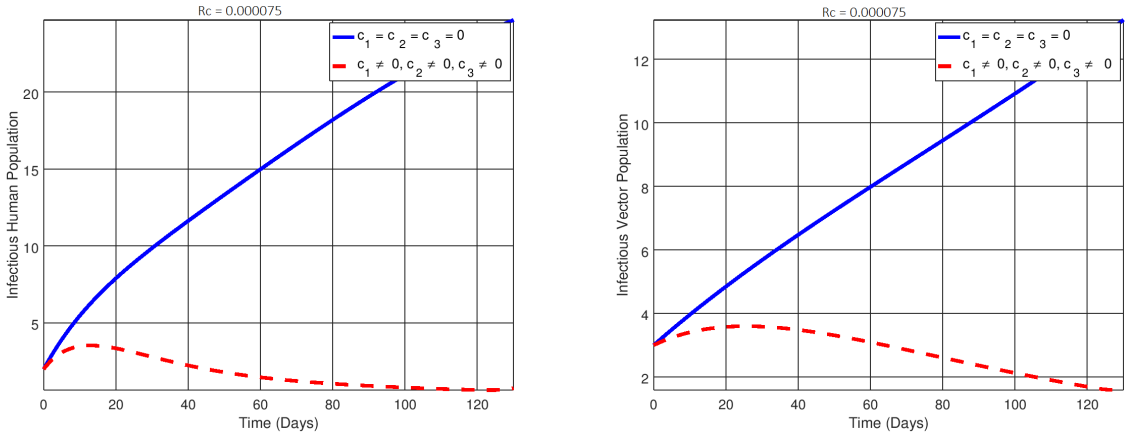
(a) (b)

Figure 4: Simulations of the model showing the efforts of treatment and insecticides only on infectious individuals.



(a) (b)

Figure 6: Simulations of the model showing the efforts of education and treatment only on infectious individuals.



(a) (b)

Figure 7: Simulations of the model showing the efforts of both education, treatment and insecticides on infectious individuals.

In epidemiology, a reproduction number less than unity implies that the disease can be eradicated in the long run. Hence, choosing suitable parameters for the controls c_1, c_2 and c_3, it was observed that the effective reproduction number obtained for Figures $2(a)$, $2(b)$, $3(a)$, $3(b)$, 4, 5, 6, and 7 were 0.0075, 0.00013, 0.044, 0.000075, 0.0075, 0.00013, 0.044 and 0.000075 respectively. This shows that by incorporating all the control measures that is educating individuals, giving treatment and applying insecticides is an effective method to help reduce the number secondary infections in the population which corresponds with eradicating the disease in the long run.

5 Conclusion

In this paper, we studied and analysed the model for transmission of HAT, and determined the basic reproduction number. The local and global stabilities of disease free equilibrium and endemic equilibrium were also proved. For the optimal control model, education, treatment and insecticides as control measures were used to optimize the objective function defined by Equation (7). The numerical simulations of the optimal control model shows that the best strategy to reduce the number of infected individuals is through the use of both education, treatment and insecticides. This is the effective and efficient method to eliminate the disease. Furthermore, the national authorities, Non-Governmental Organizations (NGOs), and stakeholders must not lose their interest in controlling the disease because neglecting this disease may cause the rapid re-occurrence and much effect to the people who are at risk.

6 Conflicts of Interest

The authors declare that they have no conflicts of interest.

7 Acknowledgements

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8 Data Availability Statement

The secondary data supporting this research are from previously reported studies and datasets, which have been cited. The processed data are available in the reference cited at the reference section.

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