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BIFURCATION ANALYSIS OFA MATHEMATICAL MODEL FOR MALARIA TRANSMISSION UNDER TREATMENT AND CONTROL

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Abstract

The bifurcation analysis of a mathematical model for malaria transmission under treatment and control were studied. The equations were modeled compartmentally. The basic reproduction number was calculated using the spectral radius of the new generation matrix. The disease free equilibrium is stable for $R_0 < 1$ and unstable otherwise. Also $R_0 = 1$ is the perfect bifurcation of the model, since it is found that at $R_0 = 1$ the endemic and disease free equilibrium coincides. It was observed that the interaction between mosquitoes and recovered humans was negligible that is $R_0 << 1$ and the average number of infection by an infectious human reduces and this implies that adequate treatment and control reduces malaria transmission.

Keywords: Bifurcation, basic reproductive number, stability, new generation matrix, MATLAB.

1.0 INTRODUCTION.

A bifurcation occurs when a small change in the parameter values of a system causes a sudden qualitative or topological change in the system.[1]

Several researchers have studied the bifurcation analysis of a mathematical model for Malaria transmission under oscillations, backward bifurcation and other aspects of bifurcations with resounding results see for instance[2,3,4,5,6,7]

Nakul et al [3] considered the bifurcation of a mathematical model for malaria transmission using compartments and analyzed their model for transmission of malaria with four compartments for the human population and three compartments for the mosquitoes. They proved the existence of an equilibrium point with no disease. For instance Imo and Ateatima [8] worked on a mathematical model for the dynamics of malaria transmission, oscillations and backward bifurcations using a deterministic model that explicitly integrates the demography and life style of malaria vector and its interaction with the human population, culminating in the existence of non-trivial disease free and endemic steady states, which can be to instability via a Hopf bifurcation as a parameter is varied in the parameter space. Similar results have shown stability and backward bifurcation in a malaria transmission model with applications to the control of malaria see for instance [7,9,10]

Malaria is caused when an infected female anopheles mosquito bites a human being, the plasmodium parasite in form of sporozite is injected into the human system via saliva. The developmental process of the sporozite through schizont, to merozoite is what causes malaria in humans. [6]

Initially the treatment of malaria was not known owing to the fact that the actual cause of it was unknown. Historically, malaria was thought of as being the result of inhaling bad air. Malaria has its origin from Italy "Malaria or bad air" but scientists discovered that the real cause of malaria is the single-celled plasmodium parasite, see [6,8,13].

The first treatment of malaria commenced with quinine treatment from Spain followed by the Chloroquine. This was short lived as malaria started developing resistance towards these treatments which led to aggressive research into drugs for the treatment [6]. It should be observed that just as there are many drugs for the treatment of malaria, it has also developed resistance to many and this led to stronger quest and desire to eliminate malaria.

Since the vector carrying plasmodium, anopheles mosquito are known, the only way of fighting malaria is through the control of mosquitoes. World Health Organization(WHO) recommends mosquito treated nets, neat environments, clearing of stagnant water and bushes. These help in reducing the mosquito population since they are deprived of their breeding places. [6].

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Motivated by the above literature and ongoing research in this direction, the aim of this paper the 'bifurcation analysis of a mathematical model for malaria transmission under treatment and control' is to construct a mathematical model and a bifurcation analysis for malaria transmission under treatment and control and to proffer control measures for the eradication of malaria in the society. The basic reproduction number will be calculated using the spectral radius of the new generation matrix. The model consists of the following equations:

Model parameters

S_h -Susceptible humans, E_h -Exposed humans,I_h-Infectious humans, R_h-Recovered humans

S_m -Susceptible mosquitoes, E_m-Exposed mosquitoes, I_m-Infectious mosquitoes

π - Immigration rate for humans. Humans x Time^{-1}

ζ_h - Per capita birth rate of humans. Time $^{-1}$

ζ_m - Per capita birth rate of mosquitoes. Time $^{-1}$

ρ_v - Number of times one mosquito would want to bite or per capita biting rate of mosquito. This depends on the mosquitoes gonotrophic cycle ie interval between laying of eggs and preference for human blood meal (anthropophilic rate) and availability of humans.

λ_{hm} - Probability of transmission of infection from an infectious human to a susceptible mosquito when it bites the human.

$\widehat{\lambda_{hm}}$ - Probability of transmission of infection from a recovered human ie asymptomatic carrier to a susceptible mosquito when it bites the human.

τ_h - Per capita rate of progression of humans from exposed class to infectious class. $\frac{1}{\tau_h}$ is the average of such progression.

λ_{mh} - Probability of transmission from the infectious mosquito to a susceptible human given that the mosquito bites the human.

τ_m - Per capita rate of progression of mosquitoes from exposed class to infectious class. $\frac{1}{\tau_m}$ is the average of such movement.

γ_h - Per capita recovery rate for humans under treatment. $\frac{1}{\gamma_h}$ is the average rate of recovery.

δ - Disease induced death rate for humans. Time $^{-1}$

ε_h - Rate of loss of immunity for humans. $\frac{1}{\varepsilon_h}$ is the average loss of immunity.

μ - Natural death rate of humans. Humans x Time $^{-1}$

μ_1 - Natural death rate of mosquitoes. Time $^{-1}$

μ_2 - Death rate of mosquitoes as a result of human control.

μ_3 - Death rate of mosquitoes as a result of quest for blood meal.

S_h -Susceptible humans, E_h -Exposed humans,I_h-Infectious humans, R_h-Recovered humans

S_m -Susceptible mosquitoes, E_m-Exposed mosquitoes, I_m-Infectious mosquitoes

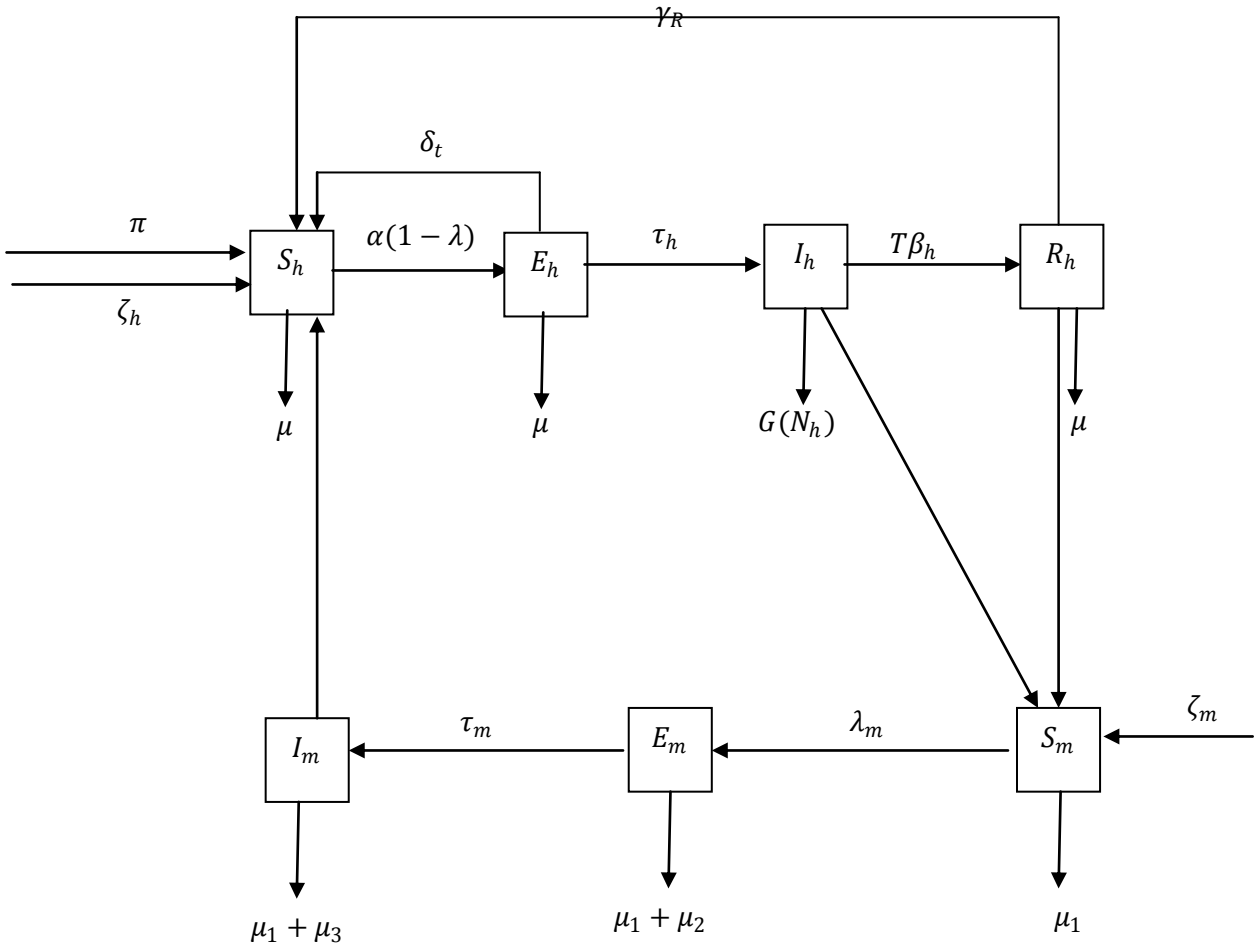


Fig 1. **Flow Diagram showing the Transmission Dynamics of Malaria**

2. GOVERNING EQUATIONS

$$\left.\begin{aligned}
&\frac{dS_h}{dt} = \Psi + \gamma_R + \delta_t E_h - \mu S_h - \alpha(1-\lambda)S_h \\
&\frac{dE_h}{dt} = \alpha(1-\lambda)S_h - \mu E_h - \delta_t E_h - \tau_h E_h \\
&\frac{dI_h}{dt} = \tau_h E_h - (\mu+\delta)I_h - T\beta_h I_h \\
&\frac{dR_h}{dt} = T\beta_h I_h - \mu R - \gamma R \\
&\frac{dS_m}{dt} = \zeta_m - \mu_1 S_m - \lambda_m S_m \\
&\frac{dE_m}{dt} = \lambda_m S_m - (\mu_1+\mu_2)E_m - \tau_m E_m \\
&\frac{dI_m}{dt} = \tau_m E_m - (\mu_1+\mu_3)I_m
\end{aligned}\right\} \quad (1.0)$$

The total number of humans is given by

$N_h = S_h + E_h + I_h + R_h$

And the total number of mosquitoes is given by

$N_m = S_m + E_m + I_m$

Also

$G(N_h) = \mu + \delta$

$$\alpha = \frac{(\lambda_{mh}\rho_v I_m)}{(N_h)} \qquad and \quad \lambda_m = \frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}$$

At any time t_1 the population of humans is given by

$$\frac{dN_h}{dt} = \Psi - \mu N_h - \delta I_h \quad - \quad - \quad - \quad - \quad - \quad (1.1)$$

And the mosquito population is

$$\frac{dN_m}{dt} = \zeta_m - \mu_1 N_m - \mu_2 E_m - \mu_3 I_m$$
$$= \zeta_m - (\mu_1 N_m + \mu_2 E_m + \mu_3 I_m) \quad - \quad - \quad - \quad - \quad - \quad (1.2)$$

2.0 Analysis of the Model

We analyze the model to see if the model is biologically meaningful and mathematically well posed.

2.1 INVARIANT REGION AND POSITIVITY OF THE MODEL SOLUTIONS

The invariant region can be obtained by this theorem.

Theorem

The solution set $(S_h,\ E_h,\ I_h,\ R_h,\ S_m,\ E_m,\ I_m) \in R_+^7$ of the system (1.1) are contained in the feasible solution Ω.

Proof: Let $(S_h,\ E_h,\ I_h,\ R_h,\ S_m,\ E_m,\ I_m) \in R_+^7$ for all t > 0

We show that the region Ω is positively invariant so that it is sufficient to consider the dynamics of the model system.

But $\frac{dN_h}{dt} \leq \Psi - \mu N_h - \delta I_h$

$$\frac{dN_h}{dt} \leq \Psi - \mu N_h$$

In the absence of disease, ie $I_h = 0$.

$$\frac{dN_h}{dt} + \mu N_h \leq \Psi \quad - \quad - \quad - \quad - \quad - \quad - \quad (1.3)$$

The integrating factor for (1.3) is (IF) = $e^{\int \mu dt} = e^{\mu t}$

Multiplying both sides of (1.3) by $e^{\mu t}$

$$e^{\mu t}\frac{dN_h}{dt} + \mu N_h e^{\mu t} \leq \Psi e^{\mu t}$$

$$\frac{d}{dt}(N_h e^{\mu t}) \leq \Psi e^{\mu t}$$

Integrating both sides

$$N_h e^{\mu t} \leq \frac{\Psi}{\mu} e^{\mu t} + c$$

Where c is the constant of integration

Dividing through by $e^{\mu t}$

$$N_h \leq \frac{\Psi}{\mu} + ce^{-\mu t}$$

$$for\ t = 0, \qquad N_h = N_h(0) = N_{h0}$$

$$N_{h0} \leq \frac{\Psi}{\mu} + c$$

$$N_{h0} - \frac{\Psi}{\mu} \leq c$$

$$N_h \leq \frac{\Psi}{\mu} + (N_{h0} - \frac{\Psi}{\mu})e^{-\mu t}$$

$$N_h \leq \frac{\Psi}{\mu}(1 - e^{-\mu t}) + N_{h0}e^{-\mu t} \quad - \quad - \quad - \quad - \quad - \quad (1.4)$$

Using a standard comparison theorem [3]

$$at\ t = 0, \qquad N_h \leq N_{h0}$$

$$t = \infty, \qquad N_h \leq \frac{\Psi}{\mu}$$

Hence the total population size,

$N_h(t) \to \frac{\Psi}{\mu}\ as\ t \to \infty,\ similarly\ for\ the\ vector\ (mosquito), the\ total\ population\ size\ N_m(t) \to \frac{\zeta_m}{\mu_1}\ as\ t \to \infty.$

TInfected variables of the two populations tend to zero as time goes to infinity, in this manner the region Ω is attracting the solutions in R_+^7.

Also assume that $S_h \geq 0, E_h \geq 0, I_h \geq 0, R_h \geq 0, S_m \geq 0, E_m \geq 0, I_m \geq 0$

$$\frac{dS_h}{dt} = \Psi + \gamma_R + \delta_t E_h - \mu S_h - \alpha(1 - \lambda)S_h$$

$\frac{dS_h}{dt} = \Psi + \gamma_R + \delta_t E_h - \mu S_h - \alpha(1-\lambda)S_h > -(\mu + \alpha(1-\lambda))S_h$

$\frac{dS_h}{dt} \geq -\big(\mu + \alpha(1-\lambda)\big)S_h$

$\int \frac{1}{S_h} dS_h \geq -\int \big(\mu + \alpha(1-\lambda)\big)dt$

$\ln S_h \geq -(\mu t + \alpha t(1-\lambda) + c)$

$\ln S_h \geq -\big(\mu + \alpha(1-\lambda)\big)t + c$

$S_h \geq e^{-(\mu+\alpha(1-\lambda))t}.e^c$

$S_h \geq Ae^{-(\mu+\alpha(1-\lambda))t}$

For t=0

$S_h \geq A$

$S_h(t) \geq S_h(0)e^{-(\mu+\alpha(1-\lambda))t}$

$S_h(t) \geq 0$

From the second equation

$\frac{dE_h}{dt} = \alpha(1-\lambda)S_h - \mu E_h - \delta_t E_h - \tau_h E_h$

$\frac{dE_h}{dt} = \alpha(1-\lambda)S_h \geq -(\mu + \delta_t + \tau_h)E_h$

$\int \frac{1}{E_h} dE_h \geq \int -(\mu + \delta_t + \tau_h)dt$

Therefore

$E_h(t) \geq E_h(0)e^{-(\mu+\delta_t+\tau_h)t} \geq 0$

Thus, the feasible set for the model system (4.1) is given by

$$\left\{ \begin{pmatrix} S_h \\ E_h \\ I_h \\ R_h \\ S_m \\ E_m \\ I_m \end{pmatrix} \in R_+^7 \;\middle|\; \begin{matrix} S_h \geq 0 \\ E_h \geq 0 \\ I_h \geq 0 \\ R_h \geq 0 \\ S_m \geq 0 \\ E_m \geq 0 \\ I_m \geq 0 \\ N_h \leq 0 \\ N_m \leq 0 \end{matrix} \right\}$$

It implies that the model equations are positively invariant. Hence the model is mathematically well posed and biologically meaningful (Gumel and Niger 2008).

Equilibrium States

2.2 Disease free equilibrium

Under disease free- state. It is assumed that there is no disease ie the population of both humans and mosquitoes are free of malaria infection which implies that

$E_h = I_h = R_h = 0 \quad and \quad E_m = I_m = 0$

Thus

$\frac{dS_h}{dt} = 0$

But $N_h = S_h + E_h + I_h + R_h$

$\Rightarrow \quad \frac{dN_h}{dt} = \Psi - \mu N_h - \delta I_h$

$But \quad I_h = 0$

$\frac{dN_h}{dt} = \Psi - \mu N_h$

$\Psi - \mu N_h = 0$

$N_h = \frac{\Psi}{\mu}$

Now let the disease Free State be
$(S_h^e, \quad E_h^e, \quad I_h^e, \quad R_h^e)\ for\ humans\ and\ \ (S_m^e, \quad E_m^e, \quad I_h^e)\ for\ mosquitoes.$
From equation 1.0, we have

$$\frac{dS_h}{dt} = \Psi + \gamma_R + \delta_t E_h - \mu S_h - \alpha(1-\lambda)S_h$$

$$E_h = I_h = R_h = 0$$

$$\Psi - \mu S_h^e = 0$$

$$S_h^e = \frac{\Psi}{\mu}$$

For the mosquitoes, we have

$$\frac{dN_m}{dt} = \zeta_m - \mu_1 N_m - \mu_2 E_m - \mu_3 I_m$$

But at disease free -state, $E_m = I_m = 0$

$$\frac{dN_m}{dt} = \boldsymbol{\zeta_m - \mu_1 N_m}$$

$$\zeta_m - \mu_1 N_m = 0$$

$\Rightarrow N_m = S_m$ at disease free state.
The disease free equilibrium is given as

$$\zeta_m - \mu_1 S_m = 0$$

$$\zeta_m - \mu_1 S_m^e = 0$$

$$S_m^e = \frac{\zeta_m}{\mu_1}$$

Disease free equilibrium = $(\frac{\Psi}{\mu}, 0, 0, 0, \ \frac{\boldsymbol{\zeta_m}}{\boldsymbol{\mu_1}}, 0, 0)$
Now considering the force of infection and the interacting dynamics of the mosquito – human population, we have

$$\frac{dS_h}{dt} = \Psi + \gamma_R + \delta_t E_h - \mu S_h - \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h \quad - - - - \quad (1.5)$$

$$\frac{dE_h}{dt} = \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h - \mu E_h - \delta_t E_h - \tau_h E_h \quad - - - - \quad (1.6)$$

$$\frac{dI_h}{dt} = \tau_h E_h - (\mu+\delta)I_h - T\beta_h I_h \quad - - - - \quad (1.7)$$

$$\frac{dR_h}{dt} = T\beta_h I_h - \mu R - \gamma R \quad - - - - \quad (1.8)$$

$$\frac{dS_m}{dt} = \zeta_m - \mu_1 S_m - \left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m \quad - - - - \quad (1.9)$$

$$\frac{dE_m}{dt} = \left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m - (\mu_1+\mu_2)E_m - \tau_m E_m \quad - - - \quad (1.10)$$

$$\frac{dI_m}{dt} = \tau_m E_m - (\mu_1+\mu_3)I_m \quad - - - -$$

2.3 Local Stability of disease free equilibrium

The disease free equilibrium for system (1.1) is locally asymptotically stable if $R_0 < 1$ and unstable if $R_0 > 1$.
From (1.1) and the Jacobian matrix (J) of the malaria model (1.1) with
$S_h = N_h - (E_h + I_h + R_h)\ and\ \ S_m = N_m - (E_m + I_m)$

$$J0 = \begin{pmatrix} -(\mu+\delta_t+\tau_h) & 0 & 0 & 0 & 0 \\ \tau_h & -(\mu+\delta+T\beta_h) & 0 & 0 & 0 \\ & T\beta_h & -(\mu+\gamma) & 0 & 0 \\ 0 & 0 & 0 & -(\mu_1+\mu_2+\tau_m) & 0 \\ 0 & 0 & 0 & \tau_m - (\mu_1+\mu_3)/J - \lambda I/ = 0 & \end{pmatrix}$$

$$\begin{vmatrix} -(\mu+\delta_t+\tau_h+\lambda) & 0 & 0 & 0 & 0 \\ \tau_h & -(\mu+\delta+T\beta_h+\lambda) & 0 & 0 & 0 \\ 0 & T\beta_h & -(\mu+\gamma+\lambda) & 0 & 0 \\ 0 & 0 & 0 & -(\mu_1+\mu_2+\tau_m+\lambda) & 0 \\ 0 & 0 & 0 & \tau_m & -(\mu_1+\mu_3+\lambda) \end{vmatrix} = 0$$

The Eigen-values are

$\lambda_1 = -(\mu + \delta_t + \tau_h)$

$\lambda_2 = -(\mu + \delta + T\beta_h)$

$\lambda_3 = -(\mu + \gamma)$

$\lambda_4 = -(\mu_1 + \mu_2 + \tau_m)$

$\lambda_5 = -(\mu_1 + \mu_3)$

Since all the Eigen-values of the Jacobian matrix are negative, it implies that the Disease free equilibrium is stable if $R_0 < 1$ and unstable at $R_0 > 1$.

2.4 Endemic equilibrium

In the presence of the malaria disease, that is $E_h \neq 0, I_h \neq 0, E_m \neq 0, I_m \neq 0$, the model has an equilibrium point called the endemic equilibrium denoted by E^* and is given by

$E^* = (S_h^*, \quad E_h^*, \quad I_h^*, \quad R_h^*, \quad S_m^*, \quad E_m^*, \quad I_m^*) \neq 0$

That is E^* is the steady state endemic equilibrium point whereby the disease persists in the population. Its co-ordinates should satisfy the following conditions for its existence and uniqueness of particular point.

$0 < S_h^*, 0 < E_h^*, 0 < I_h^*, 0 < R_h^*, 0 < S_m^*, 0 < E_m^*, 0 < I_m^*$

So from the model equation, we have the first order system of differential equation expressed as

$S_h^{'} = E_h^{'} = I_h^{'} = R_h^{'} = S_m^{'} = E_m^{'} = I_m^{'}$

We compute endemic equilibrium as

$\Psi + \gamma_R + \delta_t E_h - \mu S_h - \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h = 0$ - - - - (1.11)

$\frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h - (\mu + \delta_t + \tau_h)E_h = 0$ - - - - (1.12)

$\tau_h E_h - \big((\mu + \delta) + T\beta_h\big)I_h = 0$ - - - - (1.13)

$T\beta_h I_h - (\mu + \gamma)R = 0$ - - - - (1.14)

$\zeta_m - \mu_1 S_m - \left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m = 0$ - - - - (1.15)

$\left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m - (\mu_1 + \mu_2)E_m - \tau_m E_m = 0$- - - - - (1.16)

$\tau_m E_m - (\mu_1 + \mu_3)I_m = 0$ - - - - (1.17)

$I_m^* = \frac{\tau_m E_m^*}{\mu_1 + \mu_3}$ - - - - - - - (1.18)

$E_m^* = \frac{\left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m^*}{\mu_1 + \mu_2 + \tau_m}$

$\boldsymbol{E_m^*} = \frac{(\lambda_{hm}\rho_v I_h + \widehat{\lambda_{hm}}\rho_v R_h)}{N_h(\mu_1 + \mu_2 + \tau_m)}S_m^*$ - - - - - - - (1.19)

$S_m^* = \dfrac{\zeta_m}{\mu_1 + \left(\frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)}$

$S_m^* = \frac{N_h\zeta_m}{N_h\mu_1 + \lambda_{hm}\rho_v I_h^* + \widehat{\lambda_{hm}}\rho_v R_h^*}$ - - - - - - (1.20)

$R_h^* = \frac{T\beta_h I_h}{\mu + \gamma}$ - - - - - - (1.21)

$I_h^* = \frac{\tau_h E_h^*}{\mu + \delta + T\beta_h}$ - - - - - - (1.22)

$E_h^* = \dfrac{\frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)}{\mu + \delta_t + \tau_h}$

$E_h^* = \frac{\lambda_{mh}\rho_v(1-\lambda)}{N_h(\mu + \delta_t + \tau_h)}I_m^*$ - - - - - - (1.23)

$S_h^* = \dfrac{\Psi + \gamma_R + \delta_t E_h}{\mu + \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)}$

$S_h^* = \frac{N_h(\Psi + \gamma_R + \delta_t E_h^*)}{\mu N_h + \lambda_{mh}\rho_v I_m(1-\lambda)}$ - - - - - - (1.24)

2.5 Local stability of the endemic equilibrium

The long term dynamics of a disease is characterized by the stability at the endemic equilibrium. In order to determine the long-term dynamics of malaria, we investigate the stability of equation (4.1) at the endemic equilibrium (EE). The endemic equilibrium of the model is given by

$$S_h^*,\quad E_h^*,\quad I_h^*,\quad R_h^*,\quad S_m^*,\quad E_m^*,$$

$$I_m^* = \frac{N_h(\Psi+\gamma_R+\delta_t E_h^*)}{\mu N_h+\lambda_{mh}\rho_v I_m(1-\lambda)}, \frac{\lambda_{mh}\rho_v(1-\lambda)}{N_h(\mu+\delta_t+\tau_h)}I_m^*, \frac{\tau_h E_h^*}{\mu+\delta+T\beta_h}, \frac{T\beta_h I_h}{\mu+\gamma}, \frac{N_h\zeta_m}{N_h\mu_1+\lambda_{hm}\rho_v I_h^*+\widehat{\lambda_{hm}}\rho_v R_h^*},$$

$$\frac{(\lambda_{hm}\rho_v I_h+\widehat{\lambda_{hm}}\rho_v R_h)}{N_h(\mu_1+\mu_2+\tau_m)}S_m^*, \frac{\tau_m E_m^*}{\mu_1+\mu_3}.$$

Theorem 1.2.

A unique positive endemic equilibrium EE exists for the model (1.1) if and only if $R_0 > 1$.

Proof. If $R_0 = 1$, we observe that the following: $(S_h^*,\ E_h^*,\ I_h^*,\ R_h^*,\ S_m^*,\ E_m^*,\ I_m^*) = (S_h^e, 0, 0, 0, S_m^e, 0, 0)$. Thus, the EE coincide with the DFE when $R_0 = 1$. On the other hand, if $R_0 < 1$, we saw that $E_h^* < 0,\ I_h^* < 0,\ R_h^* < 0,\ E_m^* < 0,\ I_m^* < 0$ which does not make sense epidemiologically since population is always non negative. Thus, we say that EE do not exist when $R_0 < 1$. However, when $R_0 > 1$, we discover that $S_h^* > 0, E_h^* > 0,\ I_h^* > 0,\ R_h^* > 0, S_m^* > 0,\ E_m^* > 0,\ I_m^* > 0$. Therefore, we say that EE exists for the model (1.1)

if and only if $R_0 > 1$.

Theorem 1.2: When $R_0 > 1$, the endemic equilibrium EE is locally asymptotically stable.

Proof. The Jacobian J^* of the model (4.1) evaluated at the EE is given by

$$J^* = \begin{pmatrix} -\mu & \delta_t & 0 & 0 & 0 & 0 & -\lambda_{mh}\rho_v(1-\lambda) \\ 0 & -(\mu+\delta_t+\tau_h) & 0 & 0 & 0 & 0 & \lambda_{mh}\rho_v(1-\lambda) \\ 0 & \tau_h & -(\mu+\delta+T\beta_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & T\beta_h & -(\mu+\gamma) & 0 & 0 & 0 \\ 0 & 0 & -\frac{\lambda_{hm}\rho_v\tau_m\mu}{\mu_1\varphi} & -\frac{\hat{\lambda}_{hm}\rho_v\tau_m\mu}{\mu_1\varphi} & -\mu_1 & 0 & 0 \\ 0 & 0 & \frac{\lambda_{hm}\rho_v\tau_m\mu}{\mu_1\varphi} & \frac{\hat{\lambda}_{hm}\rho_v\tau_m\mu}{\mu_1\varphi} & 0 & -(\mu_1+\mu_2+\tau_m) & 0 \\ 0 & 0 & 0 & 0 & 0 & \tau_m & -(\mu_1+\mu_3) \end{pmatrix}$$

Clearly, det. $(J^*) > 0$ if $R_0 > 1$. Thus, by Ruth-Hurwitz criterion for local stability, the EE is locally asymptotically stable if $R_0 > 1$.

Epidemiologically, this implies that there will be malaria outbreak whenever $R_0 > 1$, based on our model formulation.

3.0 Results

3.1 Basic reproduction number

The new generation matrix is the product of $F\,V^{-1}$, where F is the matrix of new infection terms and V is the matrix of all the worsening terms.

Hence

$$\frac{dE_h}{dt} = \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h - (\mu+\delta_t+\tau_h)E_h$$

$$\frac{dI_h}{dt} = \tau_h E_h - \big((\mu+\delta)+T\beta_h\big)I_h$$

$$\frac{dE_m}{dt} = \left(\frac{\lambda_{hm}\rho_v I_h}{N_h}+\frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m - (\mu_1+\mu_2)E_m - \tau_m E_m$$

$$\frac{dI_m}{dt} = \tau_m E_m - (\mu_1+\mu_3)I_m$$

$$\frac{dR_h}{dt} = T\beta_h I_h - (\mu+\gamma)R$$

$$\frac{dS_h}{dt} = \Psi+\gamma_R+\delta_t E_h - \mu S_h - \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h$$

$$\frac{dS_m}{dt} = \zeta_m - \mu_1 S_m - \left(\frac{\lambda_{hm}\rho_v I_h}{N_h}+\frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h}\right)S_m$$

$R_0 = \gamma(FV^{-1}),$ $\quad where\ R_0\ is\ the\ Reproductive\ number.$
$where\ \gamma(A)\ is\ the\ spectral\ radius\ of\ the\ matrix\ A\ and\ the\ spectral\ radius\ \gamma(FV^{-1}).$

$$F_i = \begin{pmatrix} \frac{\lambda_{mh}\rho_v I_m}{N_h}(1-\lambda)S_h \\ 0 \\ 0 \\ \frac{\lambda_{hm}\rho_v I_h}{N_h} + \frac{\widehat{\lambda_{hm}}\rho_v R_h}{N_h} S_m \\ 0 \end{pmatrix} \qquad V_i = \begin{pmatrix} (\mu + \delta_t + \tau_h)E_h \\ \big((\mu+\delta) + T\beta_h\big)I_h - \tau_h E_h \\ (\mu+\gamma)R - T\beta_h I_h \\ (\mu_1+\mu_2+\tau_m)E_m \\ (\mu_1+\mu_3)I_m - \tau_m E_m \end{pmatrix}$$

The Jacobian of $F_i\ and\ V_i\ with\ respect\ to\ E_h, I_h, R_h, E_m\ and\ I_m$ are

$$F = \begin{pmatrix} 0 & 0 & 0 & 0 & \lambda_{mh}\rho_v(1-\lambda) \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & \frac{\lambda_{hm}\rho_v\tau_m\mu}{\mu_1\Psi} & \frac{\widehat{\lambda_{hm}}\rho_v\tau_m\mu}{\mu_1\Psi} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ (\mu+\delta_t+\tau_h) & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$V = \begin{pmatrix} -\tau_h & \big((\mu+\delta)+T\beta_h\big) & 0 & 0 & 0 \\ 0 & -T\beta_h & (\mu+\gamma) & 0 & 0 \\ 0 & 0 & 0 & (\mu_1+\mu_2+\tau_m) & 0 \\ 0 & 0 & 0 & -\tau_m & (\mu_1+\mu_3) \end{pmatrix}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{(\mu+\delta_t+\tau_h)} & 0 & 0 & 0 & 0 \\ \frac{\tau_h}{(\mu+\delta_t+\tau_h)((\mu+\delta)+T\beta_h)} & \frac{1}{((\mu+\delta)+T\beta_h)} & 0 & 0 & 0 \\ \frac{\tau_h T\beta_h}{(\mu+\delta_t+\tau_h)((\mu+\delta)+T\beta_h)(\mu+\gamma)} & \frac{T\beta_h}{((\mu+\delta)+T\beta_h)(\mu+\gamma)} & \frac{1}{(\mu+\gamma)} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ \frac{1}{(\mu_1+\mu_2+\tau_m)} & 0 & 0 & 0 & 0 \\ 0 & \frac{\tau_m}{(\mu_1+\mu_2+\tau_m)(\mu_1+\mu_3)} & \frac{1}{(\mu_1+\mu_3)} & & \end{pmatrix}$$

$$FV^{-1} = \begin{pmatrix} 0 & 0 & 0 & k & l \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ m & n & p & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

$$k = \lambda_{mh}\rho_v(1-\lambda)\left(\frac{\tau_h}{(\mu_1+\mu_2+\tau_m)(\mu_1+\mu_3)}\right) \qquad l = \frac{\hat{\lambda}_{hm}\rho_v}{\Psi\mu_1(\mu_1+\mu_3)}$$

$$m = \left(\left(\left(\frac{\lambda_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)}\right)\right)+\left(\frac{\hat{\lambda}_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h T\beta_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)(\mu+\gamma)}\right)\right)$$

$$n = \frac{\lambda_{hm}\rho_v\mu}{\Psi\mu_1(\mu+\delta+T\beta_h)}+\left(\frac{\hat{\lambda}_{hm}\rho_v\mu}{\Psi\mu_1(\mu+\delta+T\beta_h)(\mu+\gamma)}\right) \qquad p = \frac{\hat{\lambda}_{hm}\rho_v\mu}{\Psi\mu_1(\mu+\gamma)}$$

The eigenvalues of the above matrix is computed as

$$/A-\lambda I/=0$$

$$\begin{vmatrix} -\lambda & 0 & 0 & k & l \\ 0 & -\lambda & 0 & 0 & 0 \\ 0 & 0 & -\lambda & 0 & 0 \\ m & n & p & -\lambda & 0 \\ 0 & 0 & 0 & 0 & -\lambda \end{vmatrix} = 0$$

From the five eigen-values, the dominant eigen-value of the matrix FV^{-1} is $\lambda = km$
Therefore the basic reproduction number $R_0 = km, hence$

$$R_0 = \left(\left(\lambda_{mh}\rho_v(1-\lambda)\right)\left(\frac{\tau_h}{(\mu_1+\mu_2+\tau_m)(\mu_1+\mu_3)}\right)\right)\left(\left(\left(\frac{\lambda_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)}\right)\right)+\left(\frac{\hat{\lambda}_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h T\beta_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)(\mu+\gamma)}\right)\right) \quad 1.2.1$$

The basic reproduction number can be used to determine the local stability of the disease free equilibrium point.

3.2 Estimation of Parameters

Table 1.2: The Values of Parameters curled from Nakul et al determining the important parameters in malaria transmission

Baseline values and ranges for parameters for the malaria model (1.1). descriptions of the parameters are as given below table 1.0 explanation for the values are given in Appendix A.				
Parameters	**Dimension**	**Baseline high**	**Baseline low**	**Range**
π	Humans x Days^{-1}	0.033	0.041	0.002-0.27
ζ_h	Days^{-1}	1.1 x 10^{-4}	5.5 x 10^{-5}	2.7 x 10^{-5} – 1.4 10^{-4}
Ψ	Days^{-1}	0.03311		
ζ_m	Days^{-1}	0.13	0.13	0.02 – 0.27
ρ_v	Days^{-1}	0.50	0.33	0.10 – 1.0
δ_t	Days^{-1}	19	4.3	0.10 – 50
λ_{hm}	1	0.48	0.24	0.072 – 0.64
$\hat{\lambda}_{hm}$	1	0.048	0.024	0.0072 – 0.64
γ	Days^{-1}	0.0035	0.0035	0.0014 – 0.017
τ_h	Days^{-1}	0.10	0.10	0.067 – 0.20
τ_m	Days^{-1}	0.91	0.83	0.029 – 0.33
δ	Days^{-1}	9.0 x 10^{-5}	1.8 x 10^{-5}	
β_h	Days^{-1}	5.5 x 10^{-4}	2.7 x 10^{-3}	1.1 x 10^{-2} – 5.5 x 10^{-5}
μ_1	Days^{-1}	1.6 x 10^{-3}	8.8 x 10^{-6}	1.0 x 10^{-6} x 100 x 10^{-3}
μ_2	Days^{-1}	0.033	0.033	0.0010 – 0.10
μ_3	Mosquitoes^{-1} x Days^{-1}	2.0 x 10^{-2}	4.0 x 10^{-5}	1.0 x 10^{-6} x 1.0 x 10^{-3}

Calculating Basic Reproduction Number

$$R_0 = \left((\lambda_{mh}\rho_v(1-\lambda))\left(\frac{\tau_h}{(\mu_1+\mu_2+\tau_m)(\mu_1+\mu_3)}\right)\right)\left(\left(\left(\frac{\lambda_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)}\right)\right)\right.$$
$$\left.+\left(\frac{\hat{\lambda}_{hm}\rho_v\mu}{\Psi\mu_1}\right)\left(\frac{\tau_h T\beta_h}{(\mu+\delta_t+\tau_h)(\mu+\delta+T\beta_h)(\mu+\gamma)}\right)\right)$$

$$R_0 = \left((0.28x0.50(1-0.45))\right)$$

$$\left(\left(\frac{0.10}{(0.0016+0.033+0.91)(0.0016+0.02)}\right)\left(\left(\left(\frac{0.48x0.50x0.0004}{0.3311+0.0016}\right)\left(\frac{0.10}{(0.0004+19+0.10)(0.00009+0.75+0.00055)}\right)\right)\right.\right.$$
$$\left.\left.+\left(\frac{0.048x0.50x0.0004}{0.3311+0.0016}\right)\left(\frac{0.10}{((0.0004+19+0.10)(0.00009+0.75+0.00055)(0.0004+0.0035)}\right)\right)\right)$$

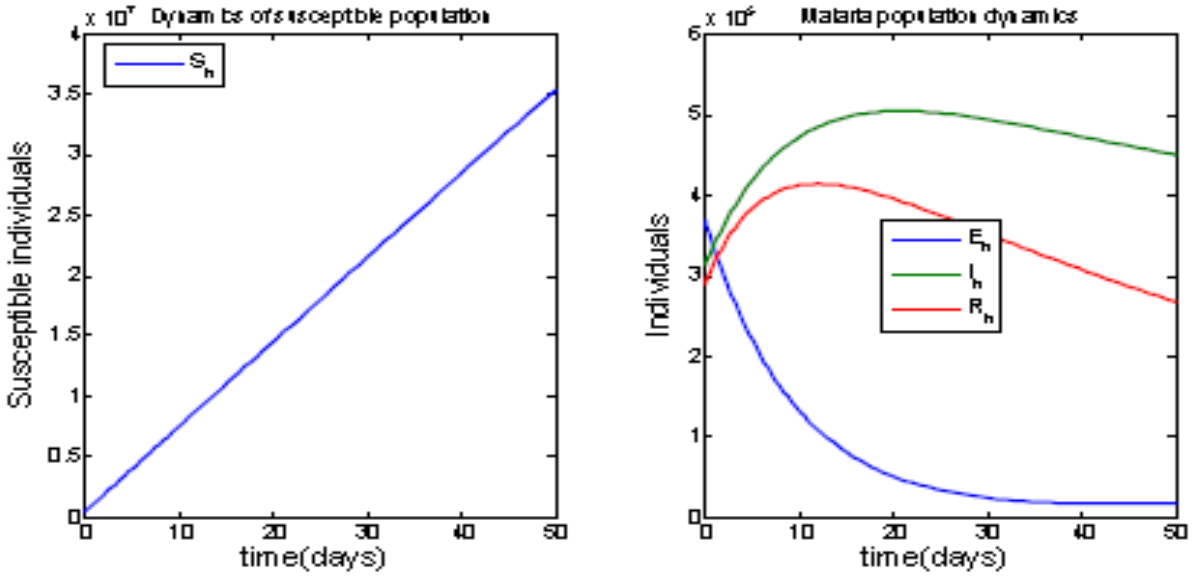
$R_0 = 0.3967$

Therefore, since $R_0 = 0.3967 < 1$, it means that malaria can be eradicated from the population with time.

4.0 Numerical Simulations

In this section, we present the numerical analysis of the model. A numerical simulation of the model (1.1) is conducted to find out the dynamics of the disease in the human population. The simulations were conducted using MATLAB. The initial conditions were $S_h = 326250$, $E_h = 125000$, $I_h = 65200$ $R_h = 57250$, $S_m = 30500$, $E_m = 25350$, $I_m = 19200$. The simulation was run in years.

Figure 1.2: This portrait shows dynamics of the first compartment of the model, which is human population. It is divided into two i.e. susceptible and exposed, infected and recovered. This is at a normal condition without control or treatment



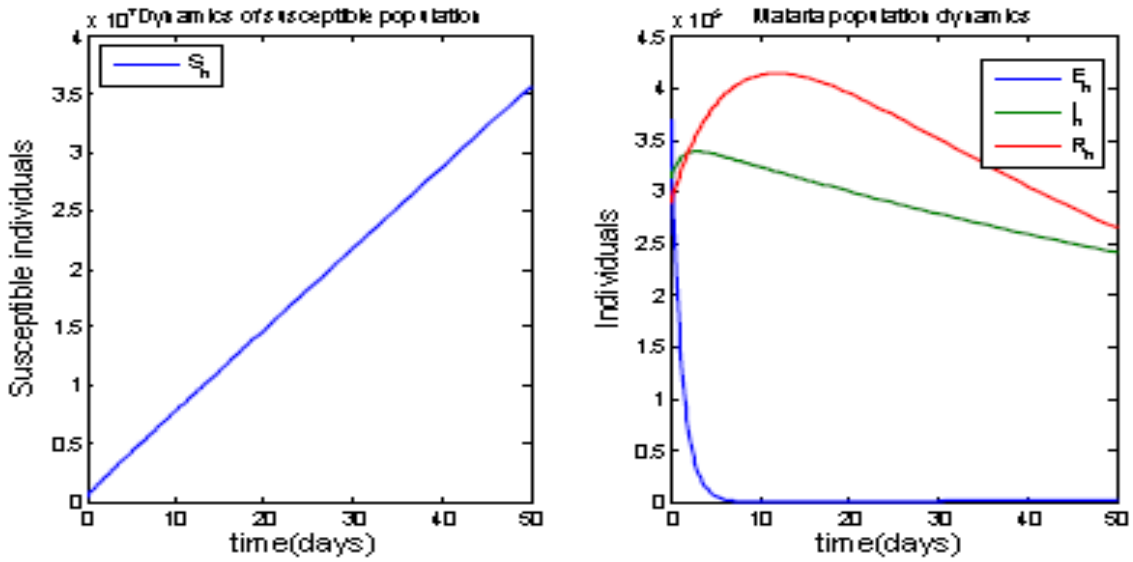
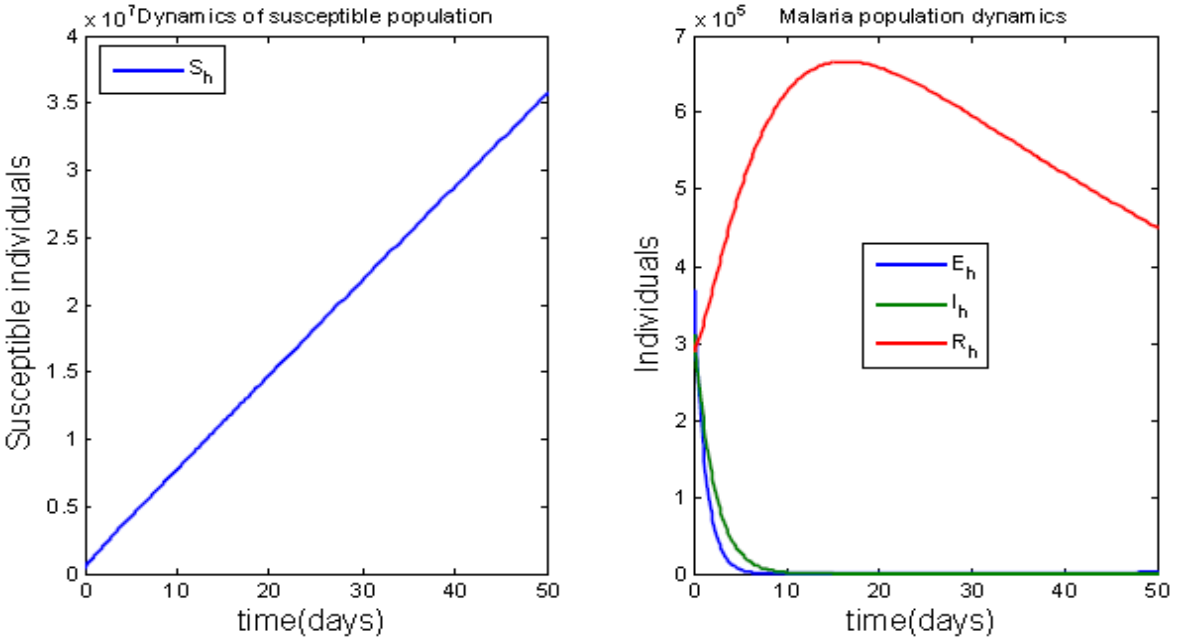


Figure 1.3: This is also the dynamics of the human population, but at this point there is increase in which the exposed class is been treated and controlled.



5. DISCUSSION AND CONCLUSIONS

From the work it is seen that the population was divided into two the human population and the mosquito population. The disease free equilibrium was derived and it was observed that the disease free equilibrium is stable if $R_0 < 1$ and unstable if $R_0 > 1$.

From the interaction of the vector and human, it was stated that the mosquitoes interact with both the infectious humans and recovered humans, but if adequate control is carried out the interaction between the mosquitoes and recovered humans will be negligible, and so the reproduction number decreases. That is to say with adequate control and treatment malaria transmission will be minimal. The average number a human can infect in his life time will be far less than one and so the disease is shown to die off the population with time.

From the numerical simulations carried out from figures 1.2 to figure 1.4

Figure 1.2:- It is seen from the graph that the transmission model as stated in our earlier flow diagram with all the parameters inclusive, it can be seen that the infectious and exposed class are on the increase.

Figure 1.3:- Here there is an introduction of control and treatment on the exposed and infectious classes and this led to a decrease in the population of the infectious class. This tells us that if adequate control measures are applied in the exposed class and the infectious adequately treated, then malaria will reduce in the population.

Figure 1.4:- The graph shows that an increase in the rate at which the infectious class is been treated causes increase in recovered humans and consequently decrease in the number of infectious humans.

So from these we can conclude that adequate control measures and treatment of early signs of malaria are the best measures to control malaria transmission in a particular population. Also avoidance of interaction between mosquitoes and infectious or recovered persons reduces the risk of malaria incidence.

Also at $R_0 = 1$, the disease free coincides with the endemic state, this implies that

$R_0 = 1$is a perfect bifurcation of the model.

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REFERENCES

[1]. Perko L- Differential equations and Dynamical Systems. Text in Applied Mathematics. Spinger-Verlag.:291

[2]. Buonomo B De-Leon C.V – Stability and bifurcation analysis of a vector – bias model of malaria transmission. Mathematical Biosciences, Elsevier 242(1) (2012):59-57

[3]. Chitnis, N, Cushing, J.M and Hyman, J.M – Bifurcation analysis of a mathematical model of malaria transmission. SIAM journal of Applied Mathematics 67(1) (2006) :24 – 45.

[4]. Ngonghala, C.N, Miranda I.T, Gideon, A.N – Persistent oscillations and backward bifurcation in a malaria model with varying human and mosquito population implications of control. Journal of Mathematical Biology. Springer Berling Heidelberg. 70(7)(2015): 1581 – 1622.

[5]. Pariyaporn, R.P, Chinviriyasit, W. Chinviriyasit S - The effect of incidence function in backward bifurcation for malaria model with temporary immunity (Elsevier Mathematical Biosciences vol. 265(2015): 47 – 64.

[6]. Understanding malaria - U.S Department of Health and Human Services. National Institute of Allergy and Infectious Diseases NIH publication N0 07 – 7139, Feb. 2007.

[7]. Xiaomei Feng, Shigui, R, Zhidong, T, Wang K – Stability and backward bifurcation in a malaria transmission model with applications to the control of malaria in China. Elsevier Inc.266(2015):52-64

[8]. Udo, I.E and Udofa,A.I. – Mathematical model for the dynamics of malaria transmission oscillations and backward bifurcation. International lever of Natural Sciences 2 (2013):31 – 42.

[9]. Chitinis N –Using mathematical models in controlling the spread of malaria:- A PhD dissertation submitted to the faculty of the graduate school interdisciplinary program in Applied Mathematics University of Arizona (2005)

[10]. Abdullahi M. B, Yahaya A.H, Farah A.A – A mathematical model of malaria and effectiveness of drugs. Applied mathematical Sciences 7(2013): 3079 – 3095.

[11]. Mutua,J.M, Feng-Bin W, Naveen, K.V – Modeling malaria and typhoid co – injection dynamics (Mathematical Biosciences. 264(20115): 128 – 144.

[12]. Mwanga, G.G – Mathematical modeling and optimal control of malaria. PhD thesis presented to Lappeenranta University of Technology, Lappeenranta, Finland, Dec. 2014.

[13]. Niger A.M and Gumel A.B - Mathematical Analysis of the Role of Repeated Exposure on Malarial Transmission Dynamics, Differential Equation and Dynamical Systems. 3(2008): 251-287.

[14]. MATLAB (7.5.0.324, R2007b).