

GLOBAL STABILITY OF $SEIR - SEI$ MODEL OF MALARIA TRANSMISSION

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ABSTRACT. In this paper, we have developed a deterministic dynamic model of malaria transmission governed by a non-linear system of differential equations. We consider global dynamic of the model by finding the basic reproduction number (\mathcal{R}_0) using Next Generation Matrix. Direct method of Lyapunov function is employed to show the global stability analysis of disease-free equilibrium (E_0) and endemic equilibrium (E_1). The results illustrate that malaria would become extinct in the neighbourhood whenever $\mathcal{R}_0 \leq 1$. Also, malaria would persist in the neighbourhood whenever $\mathcal{R}_0 > 1$ regardless of the number of infectious humans at initial stage of the population as endemic equilibrium is globally stable.

1. INTRODUCTION

Malaria is a life-threatening disease caused by parasites that are transmitted to people through the bites of infected female *Anopheles* mosquitoes. It is preventable and curable. Malaria still remains one of the most leading mortality rate after HIV/ AIDS in Africa [1]. In fact, an estimated 405, 000 mortality of humans in which 272,000 of under aged 5 years children were recorded worldwide in 2018 according to WHO [2]. Roll-Back Malaria (RBM) programme

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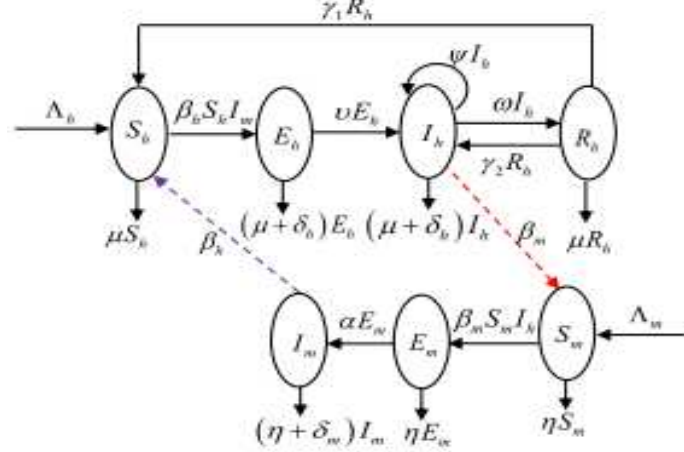
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was instigated to focus on two important areas namely, prevention and treatment of malaria. Because of this, Roll-Back Malaria Partnership makes public new strategies to curb malaria globally by 2030 [3]. Ghana and Nigeria are listed to be among the top 10 countries in Africa that had risen cases in mortality rates in 2018. Many researchers have developed mathematical models on malaria such as [4–9]. Currently, no study has considered exposed-class, disease-induced death rates, nonlinear force of infection, and newborn birth rates with the global stability at the same time. Many researchers developed epidemiological mathematical models on global stability and considered various approaches [10]–[15]. This work focuses on the analysis of the Globally Asymptotically Stability (GAS) for both disease-free and endemic equilibrium to the proposed malaria model.

2. MATERIALS AND METHODS

This developed model is an extension of Budhwar and Daniel [15] integrated with the rate of newborn birth with human infection, the exposed mosquito population compartment, the disease-induced death rate and the rate of relapse in the human population which comprises the exposed and infected compartments. The total population of humans $N_h(t)$ can be defined as $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ where $S_h(t)$, $E_h(t)$, $I_h(t)$ and $R_h(t)$ represent susceptible humans, exposed humans, infectious o humans and recovered humans respectively. Similarly, the total population of mosquitoes $N_m(t)$ can be defined as $N_m(t) = S_m(t) + E_m(t) + I_m(t)$ where $S_m(t)$, $E_m(t)$ and $I_m(t)$ represent susceptible mosquitoes, exposed mosquitoes and infectious mosquitoes respectively. Λ_h is the recruitment rate of the humans, v is the rate of exposed in humans, ω is the recovery rate of humans, γ_2 is the relapse rate of humans (the rate at which humans with low immunity return from recovered class back to infectious class), ψ is the rate of newborn's birth with infection of humans, μ is the natural death rate of humans, δ_h is the disease-induced death rate of humans, γ_1 is the loss of immunity rate of humans, Λ_m is the recruitment rate of mosquitoes, δ_m is the disease-induced death rate of mosquitoes, β_m is the rate of interaction between human and mosquito and β_h is the rate of interaction between human and mosquito. The flow chart of host-vector (human-mosquito) populations is shown in figure 1.

FIGURE 1. Flow chart of the model



2.1. Assumptions of the Model. Some of the assumptions used in the model are listed below

- (i) Mosquitoes are assumed not to recover from the parasites.
- (ii) The human population has a low or incomplete immunity to malaria.
- (iii) The exposed class can also transmit the disease.
- (iv) There is relapse of the infection after treatment.
- (v) Malaria is contracted only from infected mosquitoes.
- (vi) Newborn births can be affected by malaria.

The differential equations of the flow chart in figure 1 are

$$\begin{aligned}
 (2.1) \quad & \frac{dS_h(t)}{dt} = \Lambda_h - \beta_h S_h(t) I_m(t) - \mu S_h(t) + \gamma_1 R_h(t) \\
 & \frac{dE_h(t)}{dt} = \beta_h S_h(t) I_m(t) - (v + \mu + \delta_h) E_h(t) \\
 & \frac{dI_h(t)}{dt} = v E_h(t) - (\omega + \mu + \delta_h - \psi) I_h(t) + \gamma_2 R_h(t) \\
 & \frac{dR_h(t)}{dt} = \omega I_h(t) - (\gamma_1 + \gamma_2 + \mu) R_h(t) \\
 & \frac{dS_m(t)}{dt} = \Lambda_m - \beta_m S_m(t) I_h(t) - \eta S_m(t) \\
 & \frac{dE_m(t)}{dt} = \beta_m S_m(t) I_h(t) - (\alpha + \eta) E_m(t) \\
 & \frac{dI_m(t)}{dt} = \alpha E_m(t) - (\eta + \delta_m) I_m(t).
 \end{aligned}$$

2.2. Basic Properties of the Model.

2.2.1. Positivity of the Solution. Consider the positivity solution of the state variables of model (2.1) with non-negative initial conditions.

Theorem 2.1. *Let $S_h(0), E_h(0), I_h(0), R_h(0), S_m(0), E_m(0), I_m(0)$ be non-negative, then the solutions $(S_h(t), E_h(t), I_h(t), R_h(t), S_m(t), E_m(t), I_m(t))$ of the model (2.1) are non-negative for all $t > 0$.*

Proof. Let $t^* = \sup\{t > 0 : S_h(t) > 0, E_h(t) > 0, I_h(t) > 0, R_h(t) > 0, S_m(t) > 0, E_m(t) > 0, I_m(t) > 0\}$ then $t^* > 0$. From the first equation in the model (2.1), we say that

$$\frac{dS_h(t)}{dt} = \Lambda_h + \gamma_1 R_h(t) - \beta_h S_h(t) I_m(t) - \mu S_h(t) \geq \Lambda_h - [\beta_h I_m(t) - \mu] S_h(t).$$

This can be written as

$$\frac{d}{dt} \left[S_h(t) \exp^{\int_0^t \beta_h I_m(s) ds + \mu t} \right] \geq \Lambda_h \exp^{\int_0^t \beta_h I_m(s) ds + \mu t}.$$

Integrating both sides from $t = 0$ to $t = t^*$ and to make $S_h(t^*)$ subject of the formula, we obtain

$$\begin{aligned} S_h(t^*) \geq S_h(0) \left[\exp^{-\int_0^{t^*} \beta_h I_m(s) ds + \mu t^*} \right] &+ \left[\exp^{-\int_0^{t^*} \beta_h I_m(s) ds + \mu t^*} \right] \\ &\times \left[\int_0^{t^*} \Lambda_h \exp^{-\int_0^{t^*} \beta_h I_m(y) dy + \mu x} dx \right] > 0. \end{aligned}$$

As a result, $S_h(t^*)$ being > 0 the sum of positive terms is positive [19]. By same argument, it can also be proved that $E_h(t) > 0, I_h(t) > 0, R_h(t) > 0, S_m(t) > 0, E_m(t) > 0, I_m(t) > 0$ for all $t > 0$. \square

2.2.2. Boundedness of the Solution. It is very important to show the boundedness solution of the model (2.1).

Theorem 2.2. *All solutions $(S_h(0), E_h(0), I_h(0), R_h(0), S_m(0), E_m(0), I_m(0))$ of the malaria model (2.1) are bounded. Therefore, from (2.1), if*

$$\begin{aligned} \limsup_{t \rightarrow \infty} N_h(t) &\leq \frac{\Lambda_h}{\mu} \\ \limsup_{t \rightarrow \infty} N_m(t) &\leq \frac{\Lambda_m}{\eta} \end{aligned}$$

then $N_h(t) = S_h(t) + E_h(t) + I_h(t) + R_h(t)$ and $N_m(t) = S_m(t) + E_m(t) + I_m(t)$.

Proof. With the proof of boundedness, $0 < E_h(t) \leq N_h(t)$, $0 < I_h(t) \leq N_h(t)$, $0 < E_m(t) \leq N_m(t)$ and $0 < I_m(t) \leq N_m(t)$. Adding the human population and the mosquito population from (2.1), we obtain respectively

$$(2.2) \quad \begin{aligned} \frac{dN_h(t)}{dt} &= \Lambda_h - \mu N_h(t) - \delta_h E_h(t) - \delta_h I_h(t) + \psi I_h(t) \\ \frac{dN_m(t)}{dt} &= \Lambda_m - \eta N_m(t) - \delta_m I_m(t). \end{aligned}$$

All solutions of model (2.1) are bounded. Hence, equation (2.2) is given by

$$\begin{aligned} \Lambda_h - (\mu + 2\delta_h - \psi) N_h(t) &\leq \frac{dN_h(t)}{dt} \leq \Lambda_h - \mu N_h(t) \\ \Lambda_m - (\eta + \delta_m) N_m(t) &\leq \frac{dN_m(t)}{dt} \leq \Lambda_m - \eta N_m(t). \end{aligned}$$

Therefore, this can now be written as

$$\begin{aligned} \frac{\Lambda_h}{(\mu + 2\delta_h - \psi)} &\leq \liminf_{t \rightarrow \infty} N_h(t) \leq \limsup_{t \rightarrow \infty} N_h(t) \leq \frac{\Lambda_h}{\mu} \\ \frac{\Lambda_m}{(\eta + \delta_m)} &\leq \liminf_{t \rightarrow \infty} N_m(t) \leq \limsup_{t \rightarrow \infty} N_m(t) \leq \frac{\Lambda_m}{\eta}. \end{aligned}$$

□

2.2.3. Invariant Region. Consider the model (2.1) with non-negative initial conditions, all the state variables must be meaningful mathematically, biologically, epidemiological and positively invariant in the region Ω , see Olaniyi et al. [4].

Theorem 2.3. *The region $\Omega = \Omega_h \cup \Omega_m \subset \mathbb{R}_+^4 \times \mathbb{R}_+^3$ is positively invariant for the model (2.1) with non-negative initial conditions \mathbb{R}_+^7 .*

Proof. Let Ω_h represent feasible region of human population and Ω_m represent feasible region of mosquito population of the model (2.1). Therefore, the feasible region of the model (2.1) can be written as

$$\Omega = \Omega_h \cup \Omega_m \subset \mathbb{R}_+^4 \times \mathbb{R}_+^3$$

with

$$\begin{aligned} \Omega_h &= \left\{ (S_h, E_h, I_h, R_h) \in \mathbb{R}_+^4 : S_h + E_h + I_h + R_h \leq \frac{\Lambda_h}{\mu} \right\} \\ \Omega_m &= \left\{ (S_m, E_m, I_m) \in \mathbb{R}_+^3 : S_m + E_m + I_m \leq \frac{\Lambda_m}{\eta} \right\}. \end{aligned}$$

To reaffirm the positive invariance of Ω , the following steps are considered for the solution in $\Omega \forall t > 0$. Model (2.1) is the rate of change of human and mosquito populations and this follows that

$$\begin{aligned}\frac{dN_h(t)}{dt} &\leq \Lambda_h - \mu N_h(t) \\ \frac{dN_m(t)}{dt} &\leq \Lambda_m - \eta N_m(t).\end{aligned}$$

Therefore, by the standard comparison theorem by Lakshmikantham et al. [16], we obtain

$$\begin{aligned}N_h(t) &\leq N_h(0)e^{-\mu t} + \frac{\Lambda_h}{\mu}(1 - e^{-\mu t}) \\ N_m(t) &\leq N_m(0)e^{-\eta t} + \frac{\Lambda_m}{\eta}(1 - e^{-\eta t}).\end{aligned}$$

In particular, $N_h(t) \leq \frac{\Lambda_h}{\mu}$ if $N_h(0) \leq \frac{\Lambda_h}{\mu}$ and $N_m(t) \leq \frac{\Lambda_m}{\eta}$ if $N_m(0) \leq \frac{\Lambda_m}{\eta}$. Hence the region Ω is positive invariant. It sufficient to consider the dynamics of the flow formulated by model (2.1) in Ω . \square

2.2.4. Existence of Equilibrium Point of the Model. It is very important to examine the model (2.1) quantitatively to study the condition of existence of equilibrium points as well as to know what will finally occur to the disease as time goes on. These questions may arise thus:

- (i) will the disease (malaria) become extinct? Or
- (ii) will this disease be found in the population and turn out to be endemic?

To answer the above questions, it is necessary to consider the long-term behaviour of the solutions. This behaviour could be determined mainly on the equilibrium points. For equilibrium point, setting the derivatives on the right hand side of model (2.1) to be zero, then to show that disease free equilibrium exists, let $E_h = I_h = E_m = I_m = 0$ to obtain

$$(2.3) \quad E_0 = \left(\frac{\Lambda_h}{\mu}, 0, 0, 0, \frac{\Lambda_m}{\mu}, 0, 0\right)$$

Therefore, equation (2.3) shows that disease free equilibrium exists.

2.2.5. *Basic Reproduction Number* (\mathcal{R}_0). We derive \mathcal{R}_0 of the disease free equilibrium (DFE) by using next generation matrix method. Therefore, if matrix \mathbf{F} stands for new infection terms and \mathbf{V} stands for the remaining transfer terms of the DFE, then \mathbf{FV}^{-1} is called "Next Generation" Matrix.

$$\mathbf{F} = \begin{pmatrix} 0 & 0 & 0 & \frac{\beta_h \Lambda_h}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_m \Lambda_m}{\eta} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}$$

and

$$\mathbf{V} = \begin{pmatrix} v + \mu + \delta_h & 0 & 0 & 0 \\ -v & \omega + \mu + \delta_h - \psi & 0 & 0 \\ 0 & 0 & \alpha + \eta & 0 \\ 0 & 0 & -\alpha & \eta + \delta_m \end{pmatrix}.$$

Multiplying \mathbf{F} with the inverse matrix of \mathbf{V} and since, the basic reproduction number (\mathcal{R}_0) is the dominant or largest eigenvalue corresponding to the Spectral radius of matrix (\mathbf{FV}^{-1}) . According to Anderson and May [17], the basic reproduction number can be expressed as $\mathcal{R}_0 = \rho(\mathbf{FV}^{-1})$ where ρ is the Spectral radius. Therefore, the basic reproduction number is given by

$$\mathcal{R}_0 = \sqrt{\frac{v\beta_h\Lambda_h}{\mu(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)} \frac{\alpha\beta_m\Lambda_m}{\eta(\alpha + \eta)(\eta + \delta_m)}}.$$

3. GLOBAL STABILITY ANALYSIS

3.1. Global Stability of the Disease-Free Equilibrium (DFE).

Theorem 3.1. *If $\mathcal{R}_0 \leq 1$ then the disease free equilibrium E_0 given by equation (2.3) is globally asymptotically stable. Otherwise, it is unstable.*

Proof. Olaniyi et al. [18], consider the formed Lyapunov function of the type

$$\mathfrak{F} = a_1 E_h + a_2 I_h + a_3 E_m + a_4 I_m$$

where $a_1 = \frac{v}{\mu(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)}$, $a_2 = \frac{1}{(\omega + \mu + \delta_h - \psi)}$, $a_3 = \frac{\eta\mathcal{R}_0}{\beta_m\Lambda_m}$ and $a_4 = \frac{\eta(\alpha + \eta)\mathcal{R}_0}{\beta_m\alpha\Lambda_m}$. It is clearly shown that a_1, a_2, a_3 and a_4 are all positive.

Therefore, the derivative of \mathfrak{F} can be written as

$$\begin{aligned}
 \dot{\mathfrak{F}} &= a_1 \dot{E}_h + a_2 \dot{I}_h + a_3 \dot{E}_m + a_4 \dot{I}_m \\
 \dot{\mathfrak{F}} &= \frac{v}{\mu(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)} (\beta_h S_h I_m - (v + \mu + \delta_h) E_h) \\
 &\quad + \frac{1}{(\omega + \mu + \delta_h - \psi)} (v E_h - (\omega + \mu + \delta_h - \psi) I_h + \gamma_2 R_h) \\
 (3.1) \quad &\quad + \frac{\eta \mathcal{R}_0}{\beta_m \Lambda_m} (\beta_m I_h S_m - (\alpha + \eta) E_m) \\
 &\quad + \frac{\eta(\alpha + \eta) \mathcal{R}_0}{\beta_m \alpha \Lambda_m} (\alpha E_m - (\eta + \delta_m) I_m) .
 \end{aligned}$$

From the equations (3.1), we obtain

$$\begin{aligned}
 \dot{\mathfrak{F}} &= \left(\frac{v \beta_h S_h}{(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)} - \frac{\eta(\alpha + \eta)(\eta + \delta_m) \mathcal{R}_0}{\beta_m \Lambda_m \alpha} \right) I_m \\
 &\quad + \left(\frac{\eta \mathcal{R}_0 S_m}{\Lambda_m} - 1 \right) I_h + \left(\frac{\gamma_2}{(\omega + \mu + \delta_h - \psi)} \right) R_h \\
 &\leq \left[\frac{v \beta_h \Lambda_h}{\mu(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)} - \frac{\eta(\alpha + \eta)(\eta + \delta_m) \mathcal{R}_0}{\beta_m \Lambda_m \alpha} \right] I_m \\
 &\quad + (\mathcal{R}_0 - 1) I_h \\
 &= \left[\left(\sqrt{\frac{v \beta_h \Lambda_h \eta(\alpha + \eta)(\eta + \delta_m)}{\alpha \beta_m \Lambda_m \mu(v + \mu + \delta_h)(\omega + \mu + \delta_h - \psi)}} \right) I_m + I_h \right] (\mathcal{R}_0 - 1) .
 \end{aligned}$$

The above result, $\dot{\mathfrak{F}} \leq 0$ provided $\mathcal{R}_0 \leq 1$ as well as $\dot{\mathfrak{F}} = 0$ provided that $\mathcal{R}_0 = 1$ or $I_h = 0$ and $I_m = 0$. This means that the highest invariance set in $\{(S_h, E_h, I_h, R_h, S_m, E_m, I_m) \in \mathbb{R}_+^7 : \dot{\mathfrak{F}} = 0\}$ is the singleton DFE (E_0) and by LaSalle's Invariance Principle according to LaSalle [19], DFE (E_0) is globally asymptotically stable in \mathbb{R}_+^7 . Epidemiologically, the prove of theorem 3.1 shows that malaria would become extinct in the neighbourhood whenever $\mathcal{R}_0 \leq 1$ regardless of the number of humans in model (2.1) at initial stage of the population. \square

3.2. Global stability analysis of endemic equilibrium.

Theorem 3.2. *If $\mathcal{R}_0 > 1$ then model (2.1) has a unique endemic equilibrium (E_1) whenever $\mathcal{R}_0 > 1$ and no endemic equilibrium otherwise.*

Proof. For equilibrium point, setting the derivatives on the right hand side of model (2.1) to be zero and let $S_h = S_h^*, E_h = E_h^*, I_h = I_h^*, R_h = R_h^*, S_m = S_m^*, E_m = E_m^*$ and $I_m = I_m^*$ to establish the existence of endemic equilibrium points as $E_1 = (S_h^*, E_h^*, I_h^*, R_h^*, S_m^*, E_m^*, I_m^*)$. Therefore, the model (2.1) becomes

$$(3.2) \quad \begin{aligned} S_h^* &= \frac{\Lambda_h + \gamma_1 R_h^*}{\mu + \beta_h I_m^*}; & E_h^* &= \frac{\beta_h I_m^* S_h^*}{(v + \mu + \delta_h)}; & I_h^* &= \frac{v E_h^* + \gamma_2 R_h^*}{\omega + \mu + \delta_h - \psi} \\ R_h^* &= \frac{\omega I_h^*}{\gamma_1 + \mu + \gamma_2}; & S_m^* &= \frac{\Lambda_m}{\eta + \beta_m I_h^*}; & E_m^* &= \frac{\beta_m I_h^* S_m^*}{(\alpha + \eta)} \\ I_m^* &= \frac{\alpha E_m^*}{\eta + \delta_m}. \end{aligned}$$

For convenience, let $x_1 = (v + \mu + \delta_h)$, $x_2 = (\omega + \mu + \delta_h - \psi)$ and $x_3 = (\gamma_1 + \gamma_2 + \mu)$. By substitution method and making I_h subject of formula, equation (3.2) becomes

$$(3.3) \quad \mathcal{A} I_h^* + \mathcal{B} = 0$$

where $\mathcal{A} = (x_2 \eta (v \gamma_1 \omega + x_1 \gamma_2 \omega - x_1 x_2 x_3) \mathcal{R}_0^2 + v \Lambda_h \beta_m (\omega \gamma_2 - x_2 x_3))$ and $\mathcal{B} = v \Lambda_h \eta (x_2 x_3 (\mathcal{R}_0^2 - 1) + \omega \gamma_2)$. Hence, equation (3.3) can be defined as $I_h^* = \frac{-\mathcal{B}}{\mathcal{A}} \leq 0$ if $\mathcal{B} \geq 0$ at $\mathcal{R}_0 \leq 1$, and endemic equilibrium does not exist.

Moreover, $I_h^* = \frac{\mathcal{B}}{\mathcal{A}} > 0$ if $\mathcal{B} < 0$ at $\mathcal{R}_0 > 1$. Therefore, there exists the endemic equilibrium only at $\mathcal{R}_0 > 1$. This shows that model (2.1) has a unique endemic that is positive equilibrium whenever $\mathcal{R}_0 > 1$. \square

Theorem 3.3. *If $\mathcal{R}_0 > 1$ then the endemic equilibrium of model (2.1) given by $E_1 = (S_h^*, E_h^*, I_h^*, R_h^*, S_m^*, E_m^*, I_m^*)$ is globally asymptotically stable in the interior of the region \mathbb{R}_+^7 .*

Proof. Following Olaniyi *et al.* [18], and Shuai and Van Den Driessche [20], the equation below is made of the following Goh-Volterra type Lyapunov function:

$$(3.4) \quad \begin{aligned} \mathcal{T} &= S_h - S_h^* - S_h^* \ln \frac{S_h}{S_h^*} + E_h - E_h^* - E_h^* \ln \frac{E_h}{E_h^*} \\ &+ k_1 (I_h - I_h^* - I_h^* \ln \frac{I_h}{I_h^*}) + k_2 (S_m - S_m^* - S_m^* \ln \frac{S_m}{S_m^*}) \\ &+ k_3 (E_m - E_m^* - E_m^* \ln \frac{E_m}{E_m^*}) + k_4 (I_m - I_m^* - I_m^* \ln \frac{I_m}{I_m^*}) \end{aligned}$$

where $k_1 = \frac{\beta_h S_h^* I_m^*}{v E_h^*}$, $k_2 = k_3 = \frac{\beta_h S_h^* I_m^*}{\beta_m S_m^* I_h^*}$ and $k_4 = \frac{\beta_h S_h^* I_m^*}{\alpha E_m^*}$. Differentiating equation (3.4) with respect to time and If $R_h \rightarrow R_h^*$ as time, $t \rightarrow \infty$ in equation (3.2) and model (2.1) then using substitution method as well as simplifying to obtain

$$\begin{aligned} \dot{\mathcal{T}} = & \mu S_h^* \left(2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*} \right) + \frac{\beta_h S_h^* I_m^*}{\beta_m I_h^*} \left(2 - \frac{S_m^*}{S_m} - \frac{S_m}{S_m^*} \right) + \beta_h S_h^* I_m^* \\ & \left(6 - \frac{S_h^*}{S_h} - \frac{I_h^* E_h}{I_h E_h^*} - \frac{S_h I_m E_h^*}{S_h^* I_m^* E_h} - \frac{S_m^*}{S_m} - \frac{I_m^* E_m}{I_m E_m^*} - \frac{S_m I_h E_m^*}{S_m^* I_h^* E_m} \right) \leq 0. \end{aligned}$$

Therefore, since arithmetic mean is greater than the geometric mean, then the following inequalities hold:

$$\begin{aligned} 2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*} \leq 0, \quad 2 - \frac{S_m^*}{S_m} - \frac{S_m}{S_m^*} \leq 0 \quad \text{and} \\ \left(6 - \frac{S_h^*}{S_h} - \frac{I_h^* E_h}{I_h E_h^*} - \frac{S_h I_m E_h^*}{S_h^* I_m^* E_h} - \frac{S_m^*}{S_m} - \frac{I_m^* E_m}{I_m E_m^*} - \frac{S_m I_h E_m^*}{S_m^* I_h^* E_m} \right) \leq 0. \end{aligned}$$

□

For that reason, $\dot{\mathcal{T}} \leq 0$ for $\mathcal{R}_0 > 1$. Since all the parameters are non-negative with $\dot{\mathcal{T}} = 0$ provided that, $S_h = S_h^*$, $E_h = E_h^*$, $I_h = I_h^*$, $S_m = S_m^*$, $E_m = E_m^*$ and $I_m = I_m^*$. Meanwhile $R_h \rightarrow R_h^*$ as time, $t \rightarrow \infty$ and so by LaSalle's invariance principle (LaSalle [19]) the endemic equilibrium E_1 is globally asymptotically stable whenever $\mathcal{R}_0 > 1$. Epidemiologically, Theorem 3.3 means that malaria will persist in the neighbourhood whenever $\mathcal{R}_0 > 1$ regardless of the number of infectious humans at initial stage of the population.

4. CONCLUSION AND FUTURE WORK

A deterministic mathematical model was developed for the transmission dynamics of malaria. Basic properties of the model were analyzed. The basic reproduction number (\mathcal{R}_0) of the model showed that the disease free equilibrium is stable whenever $\mathcal{R}_0 < 1$ or globally asymptotically stable. Otherwise unstable. Therefore, the outcomes revealed that eradication in the neighbourhood was contingent largely on the basic reproduction number (\mathcal{R}_0) of the autonomous model. Meanwhile, the numerical simulation aspect was not considered in this work, this gives space for further research. Lastly, the study of

global stability for both disease-free and infectious equilibriums reveals that the epidemic will become extinct and will turn out to be present respectively.

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