A study of the persistence and extinction of malaria in a family of epidemic models

Divine Wanduku and Broderick Oluyede

Department of Mathematical Sciences, Georgia Southern University, 65 Georgia Ave, Room 3042, Statesboro, Georgia, 30460, U.S.A. E-mail: dwanduku@georgiasouthern.edu; wandukudivine@yahoo.com

Abstract

This paper investigates the deterministic extinction and permanence of a family of SEIRS malaria models with multiple random delays, and with a general nonlinear incidence rate. The conditions for the extinction and permanence of the disease are presented. For the persistence of disease, improved analytical techniques are employed to obtain eventual lower bounds for the states of the system, while extinction results are obtained via analyzing the Lyapunov exponent. The basic reproduction number $R_0^*$ is calculated, and for $R_0^* < 1$, extinction of disease occurs, while for $R_0^* \geq 1$, the disease persists. But if $R_0^* \geq 1$, and the expected survival probability of the plasmodium $E(e^{-(\mu vT_1+\mu T_2)}) < \frac{1}{R_0^*}$, then extinction occurs. Results are interpreted, and numerical simulation examples are presented to (a) compare and evaluate the impacts of the intensity of the incidence rate, and the intensity of response to malaria control, on the persistence of malaria in the human population, and (2) to justify the asymptotic stability of the disease-free equilibrium.

Keywords: Endemic steady state, basic reproduction number, permanence of disease, Lyapunov functional, Incidence function

1. Introduction

Continuing earlier discussions about malaria in Wanduku[17], malaria has exhibited an increasing alarming high mortality rate between 2015 and 2016. In fact, the latest WHO-World Malaria Report 2017[21] estimates a total of 216 million cases of malaria from 91 countries in 2016, which constitutes a 5 million increase in the total malaria cases from the malaria statistics obtained previously in 2015. Moreover, the total death count was 445000, and sub-Saharan Africa accounts for 90% of the total estimated malaria cases. This rising trend in the malaria data, signals a need for more learning about the disease, improvement of
the existing control strategies and equipment, and also a need for more advanced resources etc. to fight and eradicate, or ameliorate the burdens of malaria.

Malaria and other mosquito-borne diseases such as dengue fever, yellow fever, zika fever, lymphatic filariasis, and the different types of encephalitis etc. exhibit some unique biological features. For instance, the incubation of the disease requires two hosts - the mosquito vector and human hosts, which may be either directly involved in a full life cycle of the infectious agent consisting of two separate and independent segments of sub-life cycles, which are completed separately inside the two hosts, or directly involved in two separate and independent half-life cycles of the infectious agent in the hosts. Therefore, there is a total latent time lapse of disease incubation which extends over the two segments of delay incubation times namely:-(1) the incubation period of the infectious agent (or the half-life cycle) inside the vector, and (2) the incubation period of the infectious agent (or the other half-life cycle) inside the human being. See [25, 26]. In fact, the malaria plasmodium undergoes the first developmental half-life cycle called the sporogonic cycle inside the female *Anopheles* mosquito lasting approximately 10 – 18 days, following a successful blood meal obtained from an infectious human being through a mosquito bite. Moreover, the mosquito becomes infectious. The parasite completes the second developmental half-life cycle called the *exo-erythrocytic cycle* lasting about 7-30 days inside the exposed human being[25, 26], whenever the parasite is transferred to human being in the process of the infectious mosquito foraging for another blood meal.

The exposure and successful recovery from a malaria parasite, for example, *falciparum vivae* induces natural immunity against the disease which can protect against subsequent severe outbreaks of the disease. Moreover, the effectiveness and duration of the naturally acquired immunity against malaria is determined by several factors such as the species and the frequency of exposure to the parasites. Furthermore, it has been determined that other biological factors such as the genetics of the human being, for instance, sickle-cell anaemia, duffy negative blood types have bearings on the naturally acquired immunity against different species of malaria[26, 8, 4].

Compartmental mathematical epidemic dynamic models have been used to investigate the dynamics of several different types of infectious diseases including malaria[16, 15, 7]. In general, these models are classified as SIS, SIR, SIRS, SEIRS, and SEIR etc.[10, 6, 19, 18] epidemic dynamic models depending on the compartments of the disease classes directly involved in the general disease dynamics. Some of these studies devote interest to SEIRS and SEIR models[3, 2, 22], which account for the compartment of individuals who are exposed to the disease, *E*, that is, infected but noninfectious individuals. This inclusion of the exposed class of individuals allows for more insights about the disease dynamics during the incubation stage of the disease.

In addition, many of these epidemic dynamic models are improved in reality by including the time delays that occur in the disease dynamics. Generally, two distinct types of delays are studied namely:-disease latency and immunity delay. The disease latency represents
the period of disease incubation, or period of infectiousness which nonetheless is studied as a delay in the disease dynamics. The immunity delay represents the period of effective naturally acquired immunity against the disease after successful recovery from infection. See [18, 20, 11, 1, 2].

Some important investigations in the study of population dynamic models expressed as systems of differential equations are the persistence (or permanence) and extinction of disease in the population, and also disease eradication when the population is in a steady state over sufficiently long time. Several papers in the literature [24, 12, 14, 23, 6, 22] have addressed these topics. The extinction of disease seeks to find conditions that are sufficient for the disease related classes in the population such as, the exposed and infectious classes, to become extinct over sufficiently long time. The persistence or permanence of disease also answers the question about whether a significant number of people in the disease related classes will remain over sufficiently long time. Disease eradication in the steady state population seeks to find conditions sufficient for the disease-free equilibrium population to be stable asymptotically.

The information about these three important properties of systems of differential equations is obtained via analyzing the behavior of the trajectories of the system over time in the neighborhood of the equilibria of the dynamic systems. Indeed, extinction of the disease conditions in the differential equation system can be obtained by conducting a Lyapunov exponential analysis, and to determine convergence to the disease-free equilibrium. Persistence of disease conditions over time in the differential equation system can be obtained by analyzing the behavior of the solution of the system near an endemic steady state. And disease eradication conditions when the differential equation system is in steady state are obtained as sufficient conditions for every trajectory that starts in the neighborhood of the disease-free steady state to remain in the neighborhood of the steady state, and converge asymptotically to the steady state [24, 12, 14, 23, 6, 22].

The primary objectives of this paper include, to investigate (1) the extinction, and (2) the persistence of malaria in a human population in the line of thinking of [24]. In other words, we find conditions that are sufficient for the malaria parasite to become extinct from the population over time, and also conditions that would negatively prevail the disease in the population. Recently, Wanduku [17] presented and studied the following novel family of epidemic dynamic models for malaria with three distributed delays:
\[
\begin{align*}
\frac{dS(t)}{dt} &= B - \beta S(t) \int_{t_0}^{h_1} f_{T_1}(s)e^{-\mu s}G(I(t-s))ds - \mu S(t) + \alpha \int_{t_0}^{\infty} f_{T_3}(r)I(t-r)e^{-\mu r}dr \ dt, \\
\frac{dE(t)}{dt} &= \beta S(t) \int_{t_0}^{h_1} f_{T_1}(s)e^{-\mu s}G(I(t-s))ds - \mu E(t) \\
&\quad - \beta \int_{t_0}^{h_2} f_{T_2}(u)S(t-u) \int_{t_0}^{h_1} f_{T_1}(s)e^{-\mu s}G(I(t-s-u))dsdu \ dt, \\
\frac{dI(t)}{dt} &= \beta \int_{t_0}^{h_2} f_{T_2}(u)S(t-u) \int_{t_0}^{h_1} f_{T_1}(s)e^{-\mu s}G(I(t-s-u))dsdu - (\mu + d + \alpha)I(t) \ dt, \\
\frac{dR(t)}{dt} &= \alpha I(t) - \mu R(t) - \alpha \int_{t_0}^{\infty} f_{T_3}(r)I(t-r)e^{-\mu r}dr \ dt,
\end{align*}
\]

where the initial conditions are given in the following: let \( h = h_1 + h_2 \) and define

\[
(S(t), E(t), I(t), R(t)) = (\varphi_1(t), \varphi_2(t), \varphi_3(t), \varphi_4(t)), \quad t \in (-\infty, t_0],
\]
\[
\varphi_k \in \mathcal{C}((-\infty, t_0], \mathbb{R}_+), \forall k = 1, 2, 3, 4, \quad \varphi_k(t_0) > 0, \forall k = 1, 2, 3, 4,
\]

where \( \mathcal{C}((-\infty, t_0], \mathbb{R}_+) \) is the space of continuous functions with the supremum norm

\[
||\varphi||_\infty = \sup_{t \leq t_0} |\varphi(t)|.
\]

The disease spreads in the human population of total size \( N(t) = S(t) + E(t) + I(t) + R(t) \), where \( S(t), E(t), I(t) \) and \( R(t) \) represent the susceptible, exposed, infectious and naturally acquired immunity classes at time \( t \), respectively. The positive constants \( B \) and \( \mu \) represent the constant birth and natural death rates, respectively. Furthermore, the disease related death rate is denoted \( d \). For simplicity the vector and human natural death rates are the same, and \( \beta \) is the average effective contact rate per infected mosquito per unit time. The recovery rate from malaria with acquired immunity is \( \alpha \). Also, the incubation delays inside the mosquito and human hosts are denoted \( T_1 \) and \( T_2 \), respectively, and the period of effective naturally acquired immunity is denoted \( T_3 \). Moreover, the delays are random variables with arbitrary densities denoted \( f_{T_1}, f_{T_2} \) and \( f_{T_3} \), and their supports given as \( T_1 \in [t_0, h_1], T_2 \in [t_0, h_2] \) and \( T_3 \in [t_0, +\infty) \). The nonlinear incidence function \( G \) which signifies the response to disease transmission by the susceptible class as malaria increases in the population, satisfies the following assumptions

**Assumption 1.1.**  
A1: \( G(0) = 0 \); A2: \( G(I) \) is strictly monotonic on \([0, \infty)\); A3: \( G''(I) < 0 \); A4: \( \lim_{I \to \infty} G(I) = C, 0 \leq C < \infty \); and A5: \( G(I) \leq I, \forall I > 0 \).

More details about the derivation of the model in (1) is given in Wanduku [17]. Whilst permanence of diseases in some delay type systems are known, such as for single finite, or single distributed, and also for some double finite delay systems ( cf. [24, 14, 23, 22],
the permanence of disease in systems with multiple random delays that occur in series is not properly understood in the literature. It appears that only these papers have addressed some properties of differential equation systems with multiple delays in series. Furthermore, as far as we know no other paper has addressed extinction and persistence of malaria in a human population by conducting a Lyapunov exponent analysis, or analyzing the behavior of the trajectories of the differential equation system in the mode of thinking and techniques in [24].

This paper also presents an inherent algorithmic technique to analyze the permanence of diseases in complex multiple distributed delay systems in the line of thinking of [14]. In this regard, the primary goal is to add to the literature an analytic algorithmic method with numerical justification, to investigate deterministic permanence of complex multiple random delay systems.

The rest of this paper is presented as follows:- in Section 2 some preliminary results for (1.1) are presented. In Section 3 the results for the permanence of the disease are presented. Moreover, simulation results for the permanence of the disease in the population are presented in Section 6. In Section 5 the results for the extinction of the disease are presented. Moreover, the numerical simulation results for the extinction of disease are presented in Section 6.

Observe from (1.1) that the equations for $E$ and $R$ decouple from the other two equations in the system. Therefore, the results in this paper will be shown for the decoupled system containing equations for $S$ and $I$. Nevertheless, the following notations are utilized:

$$Y(t) = (S(t), E(t), I(t), R(t))^T, X(t) = (S(t), E(t), I(t))^T, \text{ and } N(t) = S(t) + E(t) + I(t) + R(t).$$

(1.4)

2. Model Validation and Preliminary Results

The results in [Theorem 3.1, Wanduku[17]] show that the system (1.1) has a unique positive solution $Y(t) \in \mathbb{R}_+^4$. Moreover,

$$\limsup_{t \to \infty} N(t) \leq S_0^* = \frac{B}{\mu}. \quad (2.1)$$

Furthermore, there is a positive self invariant space for the system denoted $D(\infty) = \overline{B}_{\mathbb{R}_+^4}(0, \frac{B}{\mu})$, where $D(\infty)$ is the closed ball in $\mathbb{R}_+^4$ centered at the origin with radius $\frac{B}{\mu}$ containing all positive solutions defined over $(-\infty, \infty)$.

In the analysis of the deterministic malaria model (1.1) with initial conditions in (1.2)-(1.3) in Wanduku[17], the threshold values for disease eradication such as the basic repro-
duction number for the disease when the system is in steady state are obtained in both cases where the delays in the system $T_1, T_2$ and $T_3$ are constant, and also arbitrarily distributed.

For $S_0^* = \frac{B}{\mu}$, when the delays in the system are all constant, the basic reproduction number of the disease is given by

$$\hat{R}_0^* = \frac{\beta S_0^*}{(\mu + d + \alpha)}.$$  \hfill (2.2)

Furthermore, the threshold condition $\hat{R}_0^* < 1$ is required for the disease-free equilibrium $E_0 = X_0^* = (S_0^*, 0, 0)$ to be asymptotically stable, and hence, for the disease to be eradicated from the steady state human population.

On the other hand, when the delays in the system $T_i, i = 1, 2, 3$ are random, and arbitrarily distributed, the basic reproduction number is given by

$$R_0 = \frac{\beta S_0^* K_0}{(\mu + d + \alpha)} + \frac{\alpha}{(\mu + d + \alpha)}.$$  \hfill (2.3)

where, $\hat{K}_0 > 0$ is a constant that depends only on $S_0^*$ (in fact, $\hat{K}_0 = 4 + S_0^*$). In addition, malaria is eradicated from the system in the steady state, whenever $R_0 \leq 1$.

The results in [Theorem 5.1, Wanduku[17]] also show that when $R_0 > 1$, and the delays in the system $T_i, i = 1, 2, 3$ are random, and arbitrarily distributed, the deterministic system (1.1) has a unique positive equilibrium state denoted by $E_1 = (S_1^*, E_1^*, I_1^*)$.

3. Permanence of the disease in the deterministic system

The following lemma will be used to establish the results about the permanence of the disease in the population.

Lemma 3.1. Suppose the conditions of [Theorem 5.1, Wanduku[17]] are satisfied, and let the nonlinear incidence function $G$ characterized by the assumptions in Assumption [17] satisfy the additional condition

$$\left(\frac{G(x)}{x} - \frac{G(y)}{y}\right) (G(x) - G(y)) \leq 0, \forall x, y \geq 0.$$  \hfill (3.1)

Then every positive solution $(S(t), I(t))$ of the decoupled deterministic system (1.1) with initial conditions (1.2) and (1.3) satisfies the following conditions:

$$\liminf_{t \to \infty} S(t) \geq v_1 \equiv \frac{B}{\mu + \beta G(S_0)} \quad \text{and} \quad \liminf_{t \to \infty} I(t) \geq v_2 \equiv qI_1^*e^{-(\mu + d + \alpha)(\rho + 1)h},$$  \hfill (3.2)

where $h = h_1 + h_2$, and $\rho > 0$ is a suitable positive constant, $S_1^* < \min\{S_0, S_0^A\}$ and
0 < q < \bar{q} < 1, given that,
\[ q = \frac{B\beta E(e^{-\mu T_1})G(I_1^*) - \mu\alpha E(e^{-\mu T_3})I_1^*}{(B + \alpha E(e^{-\mu T_3})I_1^*) \beta I_1^*}, \quad S^\delta = \frac{B}{k} \left(1 - e^{-k\rho h}\right), \quad k = \mu + \beta G(qI_1^*). \quad (3.3) \]

Proof: Recall, [Theorem 3.1, Wanduku[17]] and (2.1) assert that for \( N(t) = S(t) + E(t) + I(t) + R(t) \), \( \lim_{t \to \infty} N(t) \leq S_0^* = \frac{B}{\mu} \). This implies that \( \lim_{t \to \infty} S(t) \leq S_0^* \). This further implies that for any arbitrarily small \( \epsilon > 0 \), there exists a sufficiently large \( \Lambda > 0 \), such that
\[ I(t) \leq S_0^* + \epsilon, \quad \text{whenever}, \quad t \geq \Lambda. \quad (3.4) \]

Without loss of generality, let \( \Lambda_1 > 0 \) be sufficiently large such that
\[ t \geq \Lambda \geq \max_{(s,r) \in [t_0,h_1] \times [t_0,\infty)} (\Lambda_1 + s, \Lambda_1 + r). \]

It follows from Assumption 1.1 and (1.1) that
\[ \frac{dS(t)}{dt} \geq B - \beta S(t) \int_{t_0}^{h_1} f_{T_1}(s) e^{\mu s} G(S_0^* + \epsilon) ds - \mu S(t), \geq B - [\mu + \beta G(S_0^* + \epsilon)] S(t). \quad (3.5) \]

From (3.5) it follows that
\[ S(t) \geq \frac{B}{k_1} - \frac{B}{k_1} e^{-k_1(t-t_0)} + S(t_0) e^{-k_1(t-t_0)}, \quad (3.6) \]
where \( k_1 = \mu + \beta G(S_0^* + \epsilon) \).

It is easy to see from (3.6)
\[ \liminf_{t \to \infty} S(t) \geq \frac{B}{\mu + \beta G(S_0^* + \epsilon)}. \quad (3.7) \]

Since \( \epsilon > 0 \) is arbitrarily small, then the first part of (3.2) follows immediately.

In the following it is shown that \( \liminf_{t \to \infty} I(t) \geq v_2 \). In order to establish this result, it is first proved that it is impossible that \( I(t) \leq qI_1^* \) for sufficiently large \( t \geq t_0 \), where \( q \in (0, 1) \) is defined in the hypothesis. Suppose on the contrary there exists some sufficiently
large $\Lambda_0 > t_0 > 0$, such that $I(t) \leq qI_1^*, \forall t \geq \Lambda_0$. It follows from (1.1) that

$$S_1^* = \frac{B + \alpha E(e^{-\mu T_3})I_1^*}{\mu + \beta e^{-\mu T_1}G(I_1^*)} = \frac{B}{\mu + \beta e^{-\mu T_1}G(I_1^*)},$$

(3.8)

But, it can be easily seen from (1.1) that

$$B\beta e^{-\mu T_1}G(I_1^*) - \mu \alpha E(e^{-\mu T_3})I_1^* \leq \mu \left(\mu + d + \alpha\right)\left[S_0^* - \frac{\alpha E(e^{-\mu T_3})E(e^{-\mu T_2})S_1^*}{\mu + d + \alpha}\right]I_1^*$$

(3.9)

Therefore, from (3.8), it follows that

$$S_1^* < \frac{B}{\mu + \beta I_1^* q} \leq \frac{B}{\mu + \beta G(qI_1^*)},$$

(3.10)

where $0 < q < \bar{q}$, and $\bar{q}$ is defined in (3.3).

For all vector values $(s, r) \in [t_0, h_1] \times [t_0, \infty)$ define

$$\Lambda_{0,\text{max}} = \max_{(s, r) \in [t_0, h_1] \times [t_0, \infty]} (\Lambda_0 + s, \Lambda_0 + r),$$

(3.11)

It follows from Assumption (1.1) and (1.1) that for all $t \geq \Lambda_{0,\text{max}}$,

$$S(t) \geq \frac{B}{k} - \frac{B}{k} e^{-k(t-\Lambda_{0,\text{max}})} + S(\Lambda_{0,\text{max}})e^{-k(t-\Lambda_{0,\text{max}})},$$

(3.12)

where $k$ is defined in (3.3). For $t \geq \Lambda_{0,\text{max}} + \rho h$, where $h = h_1 + h_2$, and $\rho > 0$ is sufficiently large, it follows from (3.12) that

$$S(t) \geq \frac{B}{k} \left[1 - e^{-k(t-\Lambda_{0,\text{max}})}\right] \geq \frac{B}{k} \left[1 - e^{-k\rho h}\right] = S^\triangle.$$

(3.13)

Hence, from (3.10) and (3.13), it follows that for some suitable choice of $\rho > 0$ sufficiently large, then

$$S^\triangle > S_1^*, \forall t \geq \Lambda_{0,\text{max}} + \rho h.$$
For $t \geq \Lambda_{0,\text{max}} + \rho h$, define

$$V(t) = \int_{t_0}^{t} \int_{t_0}^{h_1} f_{T_2}(u) f_{T_1}(s) e^{-\mu(s+u)} \int_{t-s}^{t} G(I(v-u)) dv ds du$$

$$+ \beta S_{1}^* \int_{t_0}^{h_2} \int_{t_0}^{h_1} f_{T_2}(u) f_{T_1}(s) e^{-\mu(s+u)} \int_{t-u}^{t} G(I(v)) dv ds du. \quad (3.15)$$

It is easy to see from (1.1) and (3.15) that differentiating $V(t)$ with respect to the system (1.1), leads to the following

$$\dot{V}(t) = \beta \int_{t_0}^{h_2} \int_{t_0}^{h_1} f_{T_2}(u) f_{T_1}(s) e^{-\mu(s+u)} G(I(t-s-u))[S(t-u) - S_1^*] ds du$$

$$+ \left[\beta S_{1}^* E(e^{-\mu(T_1+T_2)}) \frac{G(I(t))}{I(t)} - (\mu + d + \alpha)\right] I(t). \quad (3.16)$$

For all $t \geq \Lambda_{0,\text{max}} + \rho h + h > \Lambda_{0,\text{max}} + \rho h + h_2$, it follows from (3.1), (3.14) and (1.1) that

$$\dot{V}(t) \geq \beta \int_{t_0}^{h_2} \int_{t_0}^{h_1} f_{T_2}(u) f_{T_1}(s) e^{-\mu(s+u)} G(I(t-s-u))[S^\Delta - S_1^*] ds du$$

$$+ \left[\beta S_{1}^* E(e^{-\mu(T_1+T_2)}) \frac{G(I^*_1)}{I^*_1} - (\mu + d + \alpha)\right] I(t)$$

$$= \beta \int_{t_0}^{h_2} \int_{t_0}^{h_1} f_{T_2}(u) f_{T_1}(s) e^{-\mu(s+u)} G(I(t-s-u))[S^\Delta - S_1^*] ds du. \quad (3.17)$$

Observe that the union of the subintervals $\bigcup_{(s,u) \in [t_0,h_1]} [t_0 - (s + u), t_0] = [t_0 - h, t_0]$, where $h = h_1 + h_2$. Denote the following

$$i_{\text{min}} = \min_{\theta \in [t_0-h,t_0],(s,u) \in [t_0,h_1]} I(\Lambda_{0,\text{max}} + \rho h + h + s + u + \theta). \quad (3.18)$$

Note that (3.18) is equivalent to

$$i_{\text{min}} = \min_{\theta \in [t_0-h,t_0]} I(\Lambda_{0,\text{max}} + \rho h + h + \theta). \quad (3.19)$$

It is shown in the following that $I(t) \geq i_{\text{min}}, \forall t \geq \Lambda_{0,\text{max}} + \rho h + h \geq \Lambda_{0,\text{max}} + \rho h + u, \forall u \in [t_0, h_2]$.  

Suppose on the contrary there exists $\tau_1 \geq 0$ such that $I(t) \geq i_{\text{min}}$ for all $t \in [\Lambda_{0,\text{max}} + \rho h + h, \Lambda_{0,\text{max}} + \rho h + h + \tau_1] \supset [\Lambda_{0,\text{max}} + \rho h + h, \Lambda_{0,\text{max}} + \rho h + h + u + \tau_1], \forall (s,u) \in [t_0, h_1] \times [t_0, h_2]$

$$I(\Lambda_{0,\text{max}} + \rho h + h + \tau_1) = i_{\text{min}}, \quad \text{and} \quad \dot{I}(\Lambda_{0,\text{max}} + \rho h + h + \tau_1) \leq 0. \quad (3.20)$$
For the value of \( t = \Lambda_{0, \text{max}} + \rho h + h + \tau_1 \), it follows that \( S(t - u) > S^\Delta > S_1^* \), and \( t - s - u \in [\Lambda_{0, \text{max}} + \rho h + h, \Lambda_{0, \text{max}} + \rho h + h + \tau_1] \), \( \forall (s, u) \in [t_0, h_1] \times [t_0, h_2] \), and it can be further seen from (1.1), (3.14) and (3.1) that

\[
\dot{I}(t) \geq \beta E(e^{-\mu(T_1 + T_2)})G(i_{\min})S^\Delta - (\mu + d + \alpha)i_{\min},
\]

\[
= \left[ \beta E(e^{-\mu(T_1 + T_2)}) \frac{G(i_{\min})}{i_{\min}} S^\Delta - (\mu + d + \alpha) \right] i_{\min},
\]

\[
> \left[ \beta E(e^{-\mu(T_1 + T_2)}) \frac{G(I^*_1)}{I^*_1} S_1^* - (\mu + d + \alpha) \right] i_{\min},
\]

\[
= 0. \quad (3.21)
\]

But (3.21) contradicts (3.20). Therefore, \( I(t) \geq i_{\min}, \forall t \geq \Lambda_{0, \text{max}} + \rho h + h \geq \Lambda_{0, \text{max}} + \rho h + u + s, \forall (s, u) \in [t_0, h_1] \times [t_0, h_2] \).

It follows further from (3.10)-(3.18), and the Assumption 1.1 that for \( \forall t \geq \Lambda_{0, \text{max}} + \rho h + h + h \geq \Lambda_{0, \text{max}} + \rho h + h + s + u, \forall (s, u) \in [t_0, h_1] \times [t_0, h_2] \).

\[
\dot{V}(t) \geq \beta \int_{t_0}^{h_1} \int_{t_0}^{h_1} f_{T_2}(u)f_{s}(s)e^{-\mu(s+u)}G(I(t - s - u))[S^\Delta - S_1^*] ds du
\]

\[
> \beta E(e^{-\mu(T_1 + T_2)})G(i_{\min})(S^\Delta - S_1^*) > 0. \quad (3.22)
\]

From (3.22), it implies that \( \limsup_{t \to \infty} V(t) = +\infty \).

On the contrary, it can be seen from [Theorem 3.1, Wanduku(17)], and (2.1) that \( \limsup_{t \to \infty} N(t) \leq S_0^* = \frac{\beta}{\mu} \), which implies that \( \limsup_{t \to \infty} I(t) \leq S_0^* = \frac{\beta}{\mu} \). This further implies that for every \( \epsilon > 0 \) infinitesimally small, there exists \( \tau_2 > 0 \) sufficiently large such that \( I(t) \leq S_0^* + \epsilon, \forall t \geq \tau_2 \). It follows that from Assumption 1.1 that

\[
G(I(t - s - u)) \leq G(I(v - u)) \leq G(I(t - u)) \leq G(I(t)) \leq G(S_0^* + \epsilon), \forall v \in [t - s, t], (s, u) \in [t_0, h_1] \times [t_0, h_2].
\]

From (3.23), it follows that

\[
\limsup_{t \to \infty} G(I(t - s - u)) \leq \limsup_{t \to \infty} G(I(t)) \leq G(S_0^*). \quad (3.24)
\]

It is easy to see from (3.15) and (3.24) that

\[
\limsup_{t \to \infty} V(t) \leq S_0^* + \beta S_1^* G(S_0^*) E \left( (T_1 + T_2)e^{-\mu(T_1 + T_2)} \right) < \infty. \quad (3.25)
\]

Therefore, it is impossible that \( I(t) \leq qI_1^* \) for sufficiently large \( t \geq t_0 \), where \( q \in (0, 1) \).

Hence, the following are possible, (Case(i.)) \( I(t) \geq qI_1^* \) for all \( t \) sufficiently large, and (Case(ii.)) \( I(t) \) oscillates about \( qI_1^* \) for sufficiently large \( t \). Obviously, we need show only
1. It can be seen from Lemma 3.1 (3.2) that when \( \beta \to \infty \), new births over the average lifespan of a human being in the population, which is also the transmission stops, then asymptotically, the smallest total susceptible that remains will be all cases.

Case(ii.). Suppose \( t_1 \) and \( t_2 \) are are sufficiently large values such that

\[
I(t_1) = I(t_2) = qI_1^*, \quad \text{and} \quad I(t) < qI_1^*, \forall (t_1, t_2).
\]

If for all \((s, u) \in [t_0, h_1] \times [t_0, h_2], t_2 - t_1 \leq \rho h + h_2 \), observe that \([t_1, t_1 + \rho h + s + u] \subseteq [t_1, t_1 + \rho h + h_2] \), and it is easy to see from (1.1) by integration that

\[
I(t) \geq I(t_1)e^{-(\mu + \alpha)(t-t_1)} \geq qI_1^*e^{-(\mu + \alpha)(\rho + 1)h} \equiv v_2.
\]

If for all \((s, u) \in [t_0, h_1] \times [t_0, h_2], t_2 - t_1 > \rho h + h_2 \geq \rho h + s + u \), then it can be seen easily that \( I(t) \geq v_2 \), for all \( t \in [t_1, t_1 + \rho h + s + u] \subseteq [t_1, t_1 + \rho h + h] \).

Now, for each \( t \in (\rho h, t_2) \supseteq (\rho h + s + u, t_2), \forall (s, u) \in [t_0, h_1] \times [t_0, h_2], \) one can also claim that \( I(t) \geq v_2 \). Indeed, as similarly shown above, suppose on the contrary for all \((s, u) \in [t_0, h_1] \times [t_0, h_2], \exists T^* > 0 \) such that \( I(t) \geq v_2, \forall t \in [t_1, t_1 + \rho h + h + T^*] \supseteq [t_1, t_1 + \rho h + s + u + T^*] \)

\[
I(t_1 + \rho h + h + T^*) = v_2, \quad \text{but} \quad I(t_1 + \rho h + h + T^*) \leq 0.
\]

It follows from (1.1) and (3.1) that for the value of \( t = t_1 + \rho h + h + T^* \),

\[
I(t) = \beta E(e^{-\mu(T_1+T_2)})G(v_2)S_0 - (\omega + \lambda + \alpha)v_2 \\
> \beta E(e^{-\mu(T_1+T_2)})G(v_2)S_1 - (\omega + \lambda + \alpha)v_2 \\
\geq \beta E(e^{-\mu(T_1+T_2)})G(1)S_1^* - (\omega + \lambda + \alpha)v_2 \\
= 0.
\]

Observe that (3.29) contradicts (3.28). Therefore, \( I(t) \geq v_2 \), for \( t \in [t_1, t_2] \). And since \([t_1, t_2]\) is arbitrary, it implies that \( I(t) \geq v_2 \) for all sufficiently large \( t \). Therefore (3.2) is satisfied.

**Theorem 3.1.** If the conditions of Lemma 3.1 are satisfied, then the system (1.1) is permanent for any total delay time \( h = h_1 + h_2 \) (see [24] for the definition of persistence of a state).

**Remark 3.1.**

1. It can be seen from Lemma 3.1 (3.2) that when \( \beta = 0 \), then \( v_1 = \frac{\beta}{\mu} \). That is, when disease transmission stops, then asymptotically, the smallest total susceptible that remains will be all new births over the average lifespan of a human being in the population, which is also the disease free state \( S_0^* = \frac{\beta}{\mu} \) (see [17]). Also, as the disease transmission rate rises given by \( \beta \to \infty \), then the total susceptible that remains \( v_1 \to 0^+ \). That is, as disease transmission rises, even the new births are either infected, or die from natural or disease related causes
over sufficiently long time leaving only infinitesimally small number of susceptible people. These facts are exhibited in the example presented in the next section.

2. From (3.3), observe that \(e^{-(\mu+d+\alpha)(\rho+1)h}\) is the survival probability from natural death (\(\mu\)), disease mortality (\(d\)), and from infectiousness (\(\alpha\)) over the total duration of the life cycle of the parasite \(h\). Thus, the smallest total infectious class that remains asymptotically \(v_2 \equiv qI_1^*e^{-(\mu+d+\alpha)(\rho+1)h}\) is a fraction \(q \in (0,1)\) of the endemic equilibrium population \(I_1^*\) that survives from all sources of death and disease over the parasite life cycle.

Since \(\frac{1}{(\mu+d+\alpha)}\) is the effective average lifespan of an individual who gets infected by malaria and survives the disease until recovery at rate \(\alpha\) (see [Remark 4.2, [17]]), it follows from (3.2) that as \((\mu+d+\alpha) \to 0^+\) and consequently \(\frac{1}{(\mu+d+\alpha)}\) is sufficiently large, then \(e^{-(\mu+d+\alpha)(\rho+1)h}\) \(\to 1^-\). Moreover, from (3.2), \(v_2 \to qI_1^*\). That is, suppose malaria is still transmitted in the population \(\beta > 0\), so that as described in [1.] above, more susceptible individuals become infected, but the effective average lifespan in the population is high because for example, malaria is effectively treated, and healthier ways to live are encouraged so that less people die from the disease at rate \(0 \leq d << 1\), and also from natural causes at rate \(0 \leq \mu << 1\), then the total infectious class that remains over sufficiently long time \(v_2\) will be a fraction \(q >> qe^{-(\mu+d+\alpha)(\rho+1)h}\) of all those who are infected in the steady state population \(I_1^*\). In other words, a larger number of infectious people remains over time when malaria is treated effectively, and better living standards are encouraged.

3. The question of under what conditions the population ever gets extinct in time can easily be answered from [1.] \& [2.] above. Since as \(\beta \to +\infty\), and \((\mu+d+\alpha) \to \infty\), then \(v_1 \to 0^+\), and \(v_2 \to 0^+\), respectively, from (3.2). Thus, one concludes that extinction is ever possible in time (that is, over sufficiently large time), whenever disease transmission rate is significantly high, and the response to malaria treatment and also the response of the population to improve living standards are very poor. These observations are investigated numerically in the next section.

4. Example for Permanence of malaria

In this study, the examples exhibited in this section are used to facilitate understanding about the influence of malaria transmission rate represented by the rate \(\beta\), and the response to the standards of malaria treatment, and human living conditions which are indicated by the disease related death \((d)\) and natural \((\mu)\) deathrates in the population respectively, on the permanence of the disease in the population. This objective is realized in a simplistic manner by examining the behavior of the trajectories of the different states \((S, E, I, R)\) of the system (1.1) in the neighborhood of the endemic equilibrium \(E_1 = (S_1^*, E_1^*, I_1^*, R_1^*)\) of the system.

Recall [Theorem 5.2, Wanduku[17]] asserts that the endemic equilibrium \(E_1\) exists, whenever the basic reproduction number \(R_0^* > 1\), where \(R_0^*\) is defined in (2.2). It follows that when
the conditions of [Theorem 5.2, Wanduku[17]] are satisfied, then the endemic equilibrium $E_1 = (S^*_1, E^*_1, I^*_1, R^*_1)$ satisfies the following system

$$\begin{align*}
B - \beta S e^{-\mu T_1} G(I) - \mu S + \alpha I e^{-\mu T_3} &= 0 \\
\beta S e^{-\mu T_1} G(I) - \mu E - \beta S e^{-\mu (T_1 + T_2)} G(I) &= 0 \\
\beta S e^{-\mu (T_1 + T_2)} G(I) - (\mu + d + \alpha) I &= 0 \\
\alpha I - \mu R - \alpha I e^{-\mu T_3} &= 0
\end{align*}$$

(4.1)

The following convenient list of parameter values in Table 2 are used to generate and examine the trajectories of the different states of the system (1.1), whenever $R^*_0 > 1$, and the intensities of the malaria incidence rate, and the deathrates of the population in the system continuously change. The following new variables are introduced. (1) The special nonlinear incidence functions $G(I) = a I + I$, $a \geq 0$ in [13] is utilized to generate the numeric results. The variable $a$ is used to scale the malaria transmission rate $\beta$, and it will be called the intensity of the disease transmission rate. The total conversion rate from infectiousness in the population $\theta(\mu + d + \alpha)$, $\theta \geq 0$ is also scaled by the parameter $\theta \geq 0$, and this parameter shall be referred to as the response intensity of malaria regulation.

For the set of parameter values in Table 2, it is easily seen that, $R^*_0 = 80.7854 > 1$. Furthermore, the endemic equilibrium for the system $E_1$ is given as follows: $E_1 = (S^*_1, E^*_1, I^*_1) = (0.2286216, 0.07157075, 0.9929282)$.

Table 1: A list of specific values chosen for the system parameters for the examples in subsection 4.1

| Disease transmission rate | $\beta$ | 0.6277 |
|---------------------------|--------|--------|
| Constant Birth rate      | $B$    | $\frac{22.39}{1000}$ |
| Recovery rate             | $\alpha$ | 0.05067 |
| Disease death rate        | $d$    | 0.01838 |
| Natural death rate        | $\mu$  | 0.002433696 |
| Incubation delay time in vector | $T_1$ | 2 units |
| Incubation delay time in host | $T_2$ | 1 unit |
| Immunity delay time       | $T_3$  | 4 units |

The Euler approximation scheme is used to generate the trajectories for the different states $S(t), E(t), I(t), R(t)$ over the time interval $[0, T]$, where $T = \max(T_1 + T_2, T_3) = 4$. Furthermore, the following initial conditions are used

$$\begin{align*}
S(t) &= 10, \\
E(t) &= 5, \\
I(t) &= 6, \quad \forall t \in [-T, 0], T = \max(T_1 + T_2, T_3) = 4. \\
R(t) &= 2,
\end{align*}$$

(4.2)
4.1. Example 1: Effect of the intensity \( a \geq 0 \) of malaria transmission rate

The effect of continuously changing the intensity \( a \geq 0 \) of the malaria transmission rate and consequently changing the incidence rate of malaria on the permanence of the disease is exhibited in the Figures 1-8.

Figure 1: (a-1), (b-1), (c-1) and (d-1) show the trajectories of the disease states \((S, E, I, R)\), respectively, over sufficiently long time \( t = 1000 \), whenever the intensity of the incidence of malaria \( a = 0.05 \), and the response intensity of malaria regulation is fixed at \( \theta = 1 \). The broken lines represent the endemic equilibrium \( E_1 = (S_1^*, E_1^*, I_1^*) = (5.116312, 0.07157075, 1.229982) \). Furthermore, \( \min(S(t)) = 10, \min(E(t)) = 4.954723, \min(I(t)) = 4.554145 \) and \( \min(R(t)) = 1.839505 \). Moreover, the basic reproduction number in this case is \( R_0^* = 4.03927 > 1 \).
Figure 2: (a-2), (b-2), (c-2) and (d-2) show the trajectories of the disease states $(S, E, I, R)$, respectively, over sufficiently long time $t = 1000$, whenever the intensity of the incidence of malaria $a = 1.5$, and the response intensity of malaria regulation is fixed at $\theta = 1$. The broken lines represent the endemic equilibrium $E_1 = (S_1^*, E_1^*, I_1^*) = (0.1521307, 0.07157075, 0.9892183)$. Furthermore, $\min(S(t)) = 0.3449024$, $\min(E(t)) = -32.03996$, $\min(I(t)) = 6$ and $\min(R(t)) = 1.999992$. Moreover, the basic reproduction number in this case is $R_0^* = 121.1781 > 1$

It is easy to see from Figures 1-8 that for a fixed response intensity of malaria regulation $\theta = 1$, by continuously increasing the intensity of malaria transmission rate from $a = 0.05$ to $a = 1.5$, the smallest value of $S(t)$ denoted $\min S(t)$ decreases over time from $\min S(t) = 10$ to $\min S(t) = 0.3449024$, while the trajectory for $S(t)$ in Figures 1 $(a - 1)$ changes from a monotonic increasing function to a monotonic decreasing function in Figures 8 $(a - 2)$ over long time, respectively. This observation confirms the Remark 3.1 [1.], which asserts that lower transmission rate of malaria allows a larger lower bound for the susceptible state over time and vice versa. That is, the higher malaria transmission rate which results in more susceptible people getting infected, leads to a rise in the infectious population $I(t)$ over time, where $I((t)$ changes from a monotonic decreasing function in Figure 1 $(c - 1)$ to a monotonic increasing in function in Figure 8 $(c - 2)$. Consequently, only a smaller number of susceptibles $S(t)$ remain over time.

4.1.1. Example 2: Effect of the response intensity $\theta \geq 0$ of malaria regulation

The effect of continuously changing the response intensity $\theta \geq 0$ of the malaria regulation, and consequently changing the survival probability rate of malaria patients (see Remark 3.1 [2.]) on the permanence of the disease is exhibited in the Figures 3[8].
Figure 3: (a-3), (b-3), (c-3) and (d-3) show the trajectories of the disease states \((S, E, I, R)\), respectively, over sufficiently long time \(t = 1000\), whenever the intensity of the incidence of malaria is fixed at \(a = 1\), and the response intensity of malaria regulation is \(\theta = 0.05\). The broken lines represent the endemic equilibrium \(E_1 = (S_1^*, E_1^*, I_1^*) = (-0.03663787, 0.003574402, -7.432011)\). Furthermore, \(\min (S(t)) = 10\), \(\min (E(t)) = -7.586546\), \(\min (I(t)) = 6\) and \(\min (R(t)) = 1.999997\). Also, note that all negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in this case is \(R_0 = 32314.16 > 1\).
Figure 4: (a-5), (b-5), (c-5) and (d-5) show the trajectories of the disease states \((S, E, I, R)\), respectively, over sufficiently long time \(t = 1000\), whenever the intensity of the incidence of malaria is fixed at \(a = 1\), and the response intensity of malaria regulation is \(\theta = 20\). The broken lines represent the endemic equilibrium \(E_1 = (S^*_1, E^*_1, I^*_1) = (8.63627, 1.465039, 2.276611)\). Furthermore, \(\min(S(t)) = 9.438989\), \(\min(E(t)) = 4.280227\), \(\min(I(t)) = 3.260888\) and \(\min(R(t)) = -2.913245\). Also, note that all negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in this case is \(R_0^* = 0.2019635 < 1\).
Figure 5: (a-4), (b-4), (c-4) and (d-4) show the trajectories of the disease states \((S, E, I, R)\), respectively, over sufficiently long time \(t = 1000\), whenever the intensity of the incidence of malaria is fixed at \(a = 1\), and the response intensity of malaria regulation is \(\theta = 100\). The broken lines represent the endemic equilibrium \(E_1 = (S_1^*, E_1^*, I_1^*) = (-67.80324, 8.093293, -3.868886)\). Furthermore, \(\min(S(t)) = 10, \min(E(t)) = 4.93237, \min(I(t)) = 0.3626737\) and \(\min(R(t)) = -22.35532\). Also, note that all negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in this case is \(R_0^* = 0.00807854 < 1\).

It is easy to see from Figures 3-4 that for a fixed intensity of malaria transmission rate \(a = 1\), by continuously increasing the response intensity of malaria regulation from \(\theta = 0.05\) to \(\theta = 100\), the smallest value of \(I(t)\) denoted \(\min I(t)\) continuously decreases over time from \(\min I(t) = 6\) to \(\min I(t) = 0.3626737\), while the trajectory for \(I(t)\) in Figures 3 (c-3) changes from a monotonic increasing function to a monotonic decreasing function in Figure 4 (c-4) and Figure 5 (c-4) over long time, respectively. This observation confirms the Remark 3.1 [2], which asserts that smaller values of \(\theta(\mu + d + \alpha) \rightarrow 0^+\), and consequently larger values for the effective average lifespan of an individual who gets infected and recovers from disease \(\frac{1}{(\mu + d + \alpha)}\), allow for an eventual lower bound for the infectious state over time and vice versa.

Also observe that the basic reproduction number \(R_0^*\) decreases across from \(R_0^* = 32314.16 > 1\) to \(R_0^* = 0.2019635 < 1\) and \(R_0^* = 0.00807854 < 1\), as \(\theta\) increases from \(\theta = 0.05\) to \(\theta = 100\), which signifies that the increase in the response to treatment or malaria control is effectively leading to eradication of the malaria parasite, which results in an increase in the number of susceptible people in the population as depicted in Figure 5 (a-4), where the susceptible state \(S(t)\) becomes a monotonic increasing function, changing from a monotonic decreasing function in Figure 3 (a-3) and Figure 4 (a-5), as \(\theta\) increases in value.
4.2. Example 3: Joint effects the intensities of malaria transmission and response to malaria regulation

The joint effects of continuously changing the response intensity $\theta \geq 0$ of the malaria regulation, and consequently changing the survival probability rate of malaria patients, as well as continuously changing the intensity $a \geq 0$ of malaria transmission rate, on the permanence of the disease is exhibited in the Figures 6-7.

Figure 6: (a-6), (b-6), (c-6) and (d-6) show the trajectories of the disease states $(S,E,I,R)$, respectively, over sufficiently long time $t = 1000$, whenever the intensity of the incidence of malaria is $a = 1.5$, and the response intensity of malaria regulation is $\theta = 1.5$. The broken lines represent the endemic equilibrium $E_1 = (S^*_1, E^*_1, I^*_1) = (0.247531, 0.1074215, 1.149901)$. Furthermore, $\min(S(t)) = 0.467897$, $\min(E(t)) = -31.35931$, $\min(I(t)) = 6$ and $\min(R(t)) = 1.999997$. Also, note that all negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in this case is $R^*_0 = 53.85694 > 1$. 
Figure 7: (a-7), (b-7), (c-7) and (d-7) show the trajectories of the disease states \((S, E, I, R)\), respectively, over sufficiently long time \(t = 1000\), whenever the intensity of the incidence of malaria is \(a = 20\), and the response intensity of malaria regulation is \(\theta = 100\). The broken lines represent the endemic equilibrium \(E_1 = (S_1^*, E_1^*, I_1^*) = (7.998663, 8.093293, 5.768778)\). Furthermore, \(\min(S(t)) = 0.08683528\), \(\min(E(t)) = -2617.125\), \(\min(I(t)) = 6\) and \(\min(R(t)) = 2\). Also, note that all negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in this case is \(R_0^* = 0.1615708 < 1\).

Observe from Figures 6-7 that as the values of \(\theta \geq 0\) and \(a \geq 0\) continuously increase from \((\theta, a) = (1.5, 1.5)\) to \((\theta, a) = (100, 20)\), the trajectory for \(S(t)\), continuously decreases monotonically over time with a continuously decreasing minimum value from \(\min(S(t)) = 0.467897\) to \(\min(S(t)) = 0.08683528\), while the trajectory for \(I(t)\) continuously increases monotonically over time and saturates at a maximum value \(\max(I(t)) = 145.0695\) exhibited in Figure 7 (c – 7). In addition, the trajectory for the removed class \(R(t)\), monotonically increases over time with minimum and maximum values rising in the ranges \((\min(R(t)), \max(R(t))) = (2, 7.964306)\) and \((\min(R(t)), \max(R(t))) = (2, 1812.767)\) in Figures 6-7 respectively. Furthermore, the basic reproduction number also decreases from \(R_0^* = 53.85694 > 1\) to \(R_0^* = 0.1615708 < 1\), respectively.

These observations suggests that increasing the intensity of the malaria transmission rate, and also increasing the response intensity to malaria regulation results in more people removed from the disease with natural immunity than they are infected, if the intensity of the response to malaria control \(\theta\) is higher than the intensity of malaria transmission \(a\). Indeed, this is evident from Figure 6 (d – 6) and Figure 7 (d – 7), where \(R(t)\) continuously increases as \((\theta, a)\) continuously increases from \((\theta, a) = (1.5, 1.5)\) to \((\theta, a) = (100, 20)\). The rise in the infectious population \(I(t)\) in Figure 6 (c – 6) and Figure 7 (c – 7), which saturates in Figure 7 (c – 7), is attributed to the increase in disease transmission rate as \(a \geq 0\) increases from \(a = 1.5\) to \(a = 20\). However, since \(\theta = 100 >> 20 = a\), signifying that the response to malaria regulation is significantly larger than the disease transmission rate, it implies that
recovery from disease with natural immunity $R(t)$ over time dominates the transmission of malaria to susceptible people $S(t)$ over time. Finally, despite the rise in malaria transmission as $a \geq 0$ increases from $a = 1.5$ to $a = 20$, the decline in the basic reproduction number $R_0^*$ from $R_0^* = 53.85694 > 1$ to $R_0^* = 0.1615708 < 1$, signifies that the malaria parasite is getting eradicated as more people respond positively to malaria treatment, and are removed with natural immunity.

5. Extinction of disease

In this section, the extinction of malaria from the system (1.1) is investigated. It will be shown that the extinction of the disease from the population depends only on the basic reproduction number $R_0^*$ in (2.2) and (2.3), or on the expected survival probability rate $E(e^{-\mu v T_1 + \mu T_2})$ of the malaria parasites, where $\mu_v$ is the natural death rate of the mosquitoes, over the complete life cycle of the parasites of length $T_1 + T_2$. The following lemmas will be used to establish the extinction results, whenever the conditions of [Theorem 3.1, Wanduku[17]] hold.

**Lemma 5.1.** Suppose the conditions of [Theorem 3.1, Wanduku[17]] hold, then the unique solution $Y(t) \in D(\infty), t \geq t_0$ of the system (1.1) also lies in the space

$$D_{\text{expl}}(\infty) = \left\{ Y(t) \in \mathbb{R}^4 : \frac{B}{\mu + d} \leq N(t) = S(t) + E(t) + I(t) + R(t) \leq \frac{B}{\mu}, \forall t \in (-\infty, \infty) \right\},$$

(5.1)

where $D_{\text{expl}}(\infty) \subset D(\infty)$. Moreover, the space $D_{\text{expl}}(\infty)$ is also self-invariant with respect to the system (1.1).

Proof: Suppose [Theorem 3.1, Wanduku[17]] holds, then it follows from (1.1) and (1.4) that the total population $N(t) = S(t) + E(t) + I(t) + R(t)$ satisfies the following inequality

$$[B - (\mu + d)N(t)]dt \leq dN(t) \leq [B - (\mu)N(t)]dt. \quad (5.2)$$

It is easy to see from (5.2) that

$$\frac{B}{\mu + d} \leq \liminf_{t \to \infty} N(t) \leq \limsup_{t \to \infty} N(t) \leq \frac{B}{\mu}, \quad (5.3)$$

and (5.1) follows immediately.
Lemma 5.2. Let [Theorem 3.1, Wanduku17] hold, and define the following Lyapunov functional in $D^{\text{expl}}(\infty)$,

$$
\dot{V}(t) = V(t) + \beta \left[ \int_{t_0}^{t} f(t_2(u)) f(t_1(s)) e^{-(\mu_0 s + \mu u)} \int_{t-u}^{t} S(\theta) G(I(\theta - s)) \frac{G(I(\theta))}{I(t)} d\theta dsdu \right. \\
+ \left. \int_{t_0}^{t} \int_{t_0}^{t} f(t_2(u)) f(t_1(s)) e^{-(\mu_0 s + \mu u)} \int_{t-s}^{t} S(t) G(I(\theta)) \frac{G(I(\theta))}{I(t)} d\theta \right],
$$

where $V(t) = \log I(t)$. It follows that

$$
\limsup_{t \to \infty} \frac{1}{t} \log I(t) \leq \frac{\beta}{\mu} \frac{B}{E} \left( e^{-(\mu_0 T_1 + \mu T_2)} - (\mu + d + \alpha) \right).
$$

Proof:
The differential operator $\dot{V}$ applied to the Lyapunov functional $\dot{V}(t)$ with respect to the system (1.1) leads to the following

$$
\dot{V}(t) = \beta \left[ \int_{t_0}^{t} f(t_2(u)) f(t_1(s)) e^{-(\mu_0 s + \mu u)} \int_{t-u}^{t} S(\theta) G(I(\theta - s)) \frac{G(I(\theta))}{I(t)} d\theta dsdu \right. \\
+ \left. \int_{t_0}^{t} \int_{t_0}^{t} f(t_2(u)) f(t_1(s)) e^{-(\mu_0 s + \mu u)} \int_{t-s}^{t} S(t) G(I(\theta)) \frac{G(I(\theta))}{I(t)} d\theta \right].
$$

Since $S(t), I(t) \in D^{\text{expl}}(\infty)$, and $G$ satisfies the conditions of Assumption 1.1 it follows easily from (1.6) that

$$
\dot{V}(t) \leq \beta \frac{B}{\mu} \frac{E}{e^{-(\mu_0 T_1 + \mu T_2)}} - (\mu + d + \alpha).
$$

Now, integrating both sides of (5.7) over the interval $[t_0, t]$, it follows from (5.7) and (5.4) that

$$
\log I(t) \leq \dot{V}(t) \\
\leq \dot{V}(t_0) + \left[ \beta \frac{B}{\mu} \frac{E}{e^{-(\mu_0 T_1 + \mu T_2)}} - (\mu + d + \alpha) \right] (t-t_0).
$$

Dividing both sides of (5.8) by $t$, and taking the limit supremum as $t \to \infty$, it is easy to see that (5.8) reduces to

$$
\limsup_{t \to \infty} \frac{1}{t} \log I(t) \leq \left[ \beta \frac{B}{\mu} \frac{E}{e^{-(\mu_0 T_1 + \mu T_2)}} - (\mu + d + \alpha) \right].
$$

And the result (5.9) follows immediately from (5.9).

The conditions for extinction of the infectious population over time can be expressed in terms of two important parameters for the disease dynamics namely - (1) the basic repro-
duction number $R^*_0$ in (2.2), and (2) the expected survival probability rate of the parasites $E(e^{-(\mu_1 T_1 + \mu T_2)})$, defined in [Theorem 5.1, Wanduku[17]].

**Theorem 5.1.** Suppose the conditions for Lemma 5.2 are satisfied, and let the basic reproduction number $R^*_0$ be defined as in (2.2). In addition, let one of the following conditions hold

1. $R^*_0 \geq 1$ and $E(e^{-(\mu_1 T_1 + \mu T_2)}) < \frac{1}{R^*_0}$, or
2. $R^*_0 < 1$.

Then

$$\limsup_{t \to \infty} \frac{1}{t} \log (I(t)) < -\lambda. \quad (5.10)$$

where $\lambda > 0$ is some positive constant. In other words, $I(t)$ converges to zero exponentially.

Proof:
Suppose Theorem 5.1 [1.] holds, then from (5.5),

$$\limsup_{t \to \infty} \frac{1}{t} \log (I(t)) < \beta B \mu \left( E(e^{-(\mu_1 T_1 + \mu T_2)}) - \frac{1}{R^*_0} \right) \equiv -\lambda, \quad (5.11)$$

where the positive constant $\lambda > 0$ is taken to be as follows

$$\lambda \equiv (\mu + d + \alpha) - \beta \frac{B}{\mu} E(e^{-(\mu_1 T_1 + \mu T_2)}) = \beta \frac{B}{\mu} \left( \frac{1}{R^*_0} - E(e^{-(\mu_1 T_1 + \mu T_2)}) \right) > 0. \quad (5.12)$$

Also, suppose Theorem 5.1 [2.] holds, then from (5.5),

$$\limsup_{t \to \infty} \frac{1}{t} \log (I(t)) \leq \beta \frac{B}{\mu} e^{-(\mu_1 T_1 + \mu T_2)} - (\mu + d + \alpha)$$

$$< \beta \frac{B}{\mu} - (\mu + d + \alpha) = -(1 - R^*_0)(\mu + d + \alpha) \equiv -\lambda, \quad (5.13)$$

where the positive constant $\lambda > 0$ is taken to be as follows

$$\lambda \equiv (1 - R^*_0)(\mu + d + \alpha) > 0. \quad (5.14)$$

**Remark 5.1.** Theorem 5.1 [Theorem 3.1, Wanduku[17]] and Lemma 5.1 signify that all trajectories of the solution $(S(t), I(t))$ of the decoupled system containing equations for $S$ and $I$ in the system (1.1) that start in $D^{expl}(\infty) \subset D(\infty)$ remain bounded in $D^{expl}(\infty)$. Moreover, on the phase plane of the solution $(S(t), I(t))$, the trajectory of the infectious state $I(t)$, $t \geq t_0$ ultimately turn to zero exponentially, whenever either the expected survival probability rate
of the malaria parasites satisfy $E(e^{-\mu T_1 + \mu T_2}) < \frac{1}{R}^*$, for $R > 1$, or whenever the basic production number of the disease satisfy $R < 1$. Furthermore, the Lyapunov exponent from (5.10) is estimated by the term $\lambda$, defined in (5.12) and (5.14).

It follows from (5.10) that when either of the conditions in Theorem 5.1[1.-2.] hold, then the infectious population $I(t)$ dies out exponentially, whenever $\lambda$ in (5.12) and (5.14) is positive, that is, $\lambda > 0$. In addition, the rate of the exponential decay of each trajectories of the infectious population $I(t)$ in each scenario of Theorem 5.1[1.-2.] is given by the estimate $\lambda > 0$ of the Lyapunov exponent in (5.12) and (5.14).

The conditions in Theorem 5.1[1.-2.] can also be interpreted as follows. Recall [17, Remark 4.2], the basic reproduction number $R^*$ in (2.2) (similarly in (2.3)) represents the expected number of secondary malaria cases that result from one infective placed in the steady state disease free population $S_0^* = \frac{B}{\mu}$. Thus, $\frac{1}{R^*} = \frac{(\mu + d + \alpha)}{\beta S_0^*}$, for $R^* \geq 1$, represents the probability rate of infectious persons in the secondary infectious population $\beta S_0^*$ leaving the infectious state either through natural death $\mu$, diseases related death $d$, or recovery and acquiring natural immunity at the rate $\alpha$. Thus, $\frac{1}{R^*}$ is the effective probability rate of surviving infectiousness until recovery with acquisition of natural immunity. Moreover, $\frac{1}{R^*}$ is a probability measure provided $R^* \geq 1$.

In addition, recall [17, Theorem 5.1&5.2] asserts that when $R^* \geq 1$, and the expected survival probability $E(e^{-\mu T_1 + \mu T_2})$ is significantly large, then the outbreak of malaria establishes a malaria endemic steady state population $E_1$. The conditions for extinction of disease in Theorem 5.1[1.], that is $R^* \geq 1$ and $E(e^{-\mu T_1 + \mu T_2}) < \frac{1}{R^*}$ suggest that in the event where $R^* \geq 1$, and the disease is aggressive, and likely to establish an endemic steady state population, if the expected survival probability rate $E(e^{-\mu T_1 + \mu T_2})$ of the malaria parasites over their complete life cycle of length $T_1 + T_2$, is less than $\frac{1}{R^*}$- the effective probability rate of surviving infectiousness until recovery with natural immunity, then the malaria epidemic fails to establish an endemic steady state, and as a result, the disease ultimately dies out at an exponential rate $\lambda$ in (5.12). This result suggests that, malaria control policies should focus on vector control strategies such as genetic modification techniques in order to reduce the chances of survival of the malaria parasites inside the mosquitoes, and in the human beings.

In the event where $R^* < 1$ in Theorem 5.1[2.], extinction of disease occurs exponentially over sufficiently long time, regardless of the survival of the parasites. Moreover, the rate of extinction is $\lambda$ in (5.14).

Theorem 5.1 characterizes the behavior of the trajectories of the $I(t)$ coordinate of the solution $(S(t), I(t))$ of the decoupled system containing equations for $S$ and $I$ in the system (1.1) in the phase plane. The question remains about how the trajectories for the $S(t)$ behave asymptotically in the phase plane.

The following result describes the average behavior of the trajectories of the susceptible population $S(t)$ over sufficiently long time, and also states conditions for the asymptotic stability in the mean, in the event where the conditions of Theorem 5.1 are satisfied.
Theorem 5.2. Suppose any of the conditions in the hypothesis of Theorem 5.1 are satisfied. It follows that in $D^{\exp}(\infty)$, the trajectories of the susceptible state $S(t)$ of the solution $(S(t), I(t))$ of the decoupled system containing equations for $S$ and $I$ in the system (1.1) satisfy

$$
\lim_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi) d\xi = \frac{B}{\mu}.
$$

That is, the susceptible population is persistent over long-time in the mean (see definition of persistence in the mean in [24]), and hence, asymptotically stable. Moreover, the average value of the susceptible population over sufficiently long time is the disease-free equilibrium $S^*_0 = \frac{B}{\mu}$.

Proof:
Suppose either of the conditions in Theorem 5.1 hold, then it follows clearly from Theorem 5.1 that for every $\epsilon > 0$, there is a positive constant $K_1(\epsilon) \equiv K_1 > 0$, such that $I(t) < \epsilon$, whenever $t > K_1$.

It follows from (5.16) that

$$I(t - s) < \epsilon, \quad \text{whenever } t > K_1 + h_1, \forall s \in [t_0, h_1].$$

In $D^{\exp}(\infty)$, define

$$V_1(t) = S(t) + \alpha \int_{t_0}^{\infty} f_{T_3}(r)e^{\mu r} \int_{t-r}^{t} I(\theta) d\theta dr.$$  

The differential operator $\dot{V}_1$ applied to the Lyapunov functional $V_1(t)$ in (5.18) leads to the following

$$\dot{V}_1(t) = g(S, I) - \mu S(t),$$

where

$$g(S, I) = B - \beta S(t) \int_{t_0}^{h_1} f_{T_3}(s)e^{-\mu s}G(I(t - s)) ds + \alpha E(e^{-\mu T_3})I(t).$$

Estimating the right-hand-side of (5.19) in $D^{\exp}(\infty)$, and integrating over $[t_0, t]$, it follows from (5.16)-(5.17) that

$$V_1(t) \leq V_1(t_0) + B(t - t_0) + \int_{t_0}^{K_1} \alpha I(\xi) d\xi + \int_{K_1}^{t} \alpha I(\xi) d\xi - \mu \int_{t_0}^{t} S(\xi) d\xi,$$

$$\leq V_1(t_0) + B(t - t_0) + \frac{B}{\mu}(K_1 - t_0) + \alpha(t - K_1)\epsilon - \mu \int_{t_0}^{t} S(\xi) d\xi.$$
Thus, dividing both sides of (5.21) by \( t \) and taking the limit supremum as \( t \to \infty \), it follows that

\[
\limsup_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi) d\xi \leq \frac{B}{\mu} + \frac{\alpha}{\mu} \epsilon. \tag{5.22}
\]

On the other hand, estimating \( g(S, I) \) in (5.20) from below and using the conditions of Assumption 1.1 and (5.17), it is easy to see that in \( D^{\text{expl}}(\infty) \),

\[
g(S, I) \geq B - \beta S(t) \int_{t_0}^{h_1} f_{T_1}(s)e^{-\mu v_s}(I(t-s))ds \geq B - \beta \frac{B}{\mu} E(e^{-\mu v_{T_1}})\epsilon, \forall t > K_1 + h_1,
\]

Moreover, for \( t \in [t_0, K_1 + h_1] \), then

\[
g(S, I) \geq B - \beta \left( \frac{B}{\mu} \right)^2. \tag{5.23}
\]

Therefore, applying (5.23)-(5.24) into (5.19), then integrating both sides of (5.19) over \([t_0, t]\), and diving the result by \( t \), it is easy to see from (5.19) that

\[
\frac{1}{t} S(t) \leq \frac{1}{t} S(t_0) + B(1 - t_0/t) - \frac{1}{t} \beta \left( \frac{B}{\mu} \right)^2 (K_1 + h_1 - t_0) - \frac{1}{t} \beta \frac{B}{\mu} \epsilon[1 - \frac{K_1 + h_1}{t}] - \frac{1}{t} \mu \int_{t_0}^{t} S(\xi) d\xi. \tag{5.25}
\]

Observe that in \( D^{\text{expl}}(\infty) \), \( \lim_{t \to \infty} \frac{1}{t} V_1(t) = 0 \), and \( \lim_{t \to \infty} \frac{1}{t} V_1(t_0) = 0 \). Therefore, rearranging (5.25), and taking the limit infimum of both sides as \( t \to \infty \), it is easy to see that

\[
\liminf_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi) d\xi \geq \frac{B}{\mu} - \frac{1}{\mu} \beta \frac{B}{\mu} \epsilon. \tag{5.26}
\]

It follows from (5.22) and (5.26) that

\[
\frac{B}{\mu} - \frac{1}{\mu} \beta \frac{B}{\mu} \epsilon \leq \liminf_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi) d\xi \leq \limsup_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi) d\xi \leq \frac{B}{\mu} + \frac{\alpha}{\mu} \epsilon. \tag{5.27}
\]

Hence, for \( \epsilon \) arbitrarily small, the result in (5.15) follows immediately from (5.27). Note, the asymptotic stability of the disease-free equilibrium state for \( S(t) = S_0^* \) is explained further in the Theorem 5.3.

**Theorem 5.3.** Suppose any of the conditions in the hypothesis of Theorem 5.1-2 are satisfied. Also, suppose the conditions of Theorem 5.2 hold. It follows that in \( D^{\text{expl}}(\infty) \), the
disease-free equilibrium for the susceptible state \( S(t) \), denoted \( S^*_0 = \frac{B}{\mu} \), and the infectious state \( I(t) \), denoted as \( I^*_0 = 0 \), of the solution \( (S(t), I(t)) \) of the decoupled system containing equations for \( S \) and \( I \) in the system \((1.1)\) is asymptotically stable. That is, \( E_0 = (S^*_0, I^*_0) = (\frac{B}{\mu}, 0) \) is asymptotically stable.

Proof:
From [Theorem 4.1, [17]], \( E_0 = (S^*_0, I^*_0) = (\frac{B}{\mu}, 0) \) is clearly a disease-free equilibrium. It is left to show that every trajectory that starts near \( E_0 \) remains near \( E_0 \), and converges asymptotically at \( E_0 \). Indeed, clearly if the hypothesis of Theorem 5.1[1.-2.] hold, then all trajectories in the phase-plane for the infectious state \( I(t) \) converge asymptotically and exponentially to \( I^*_0 = 0 \). It is left to show that if the trajectories of the susceptible state \( S(t) \) from Theorem 5.2 [5.15], converge asymptotically in the mean to \( S^*_0 = \frac{B}{\mu} \), then they converge asymptotically to \( S^*_0 = \frac{B}{\mu} \).

Indeed, if on the contrary, there exist a trajectory for \( S(t) \) starting near \( S^*_0 = \frac{B}{\mu} \) that does not stay near \( S^*_0 = \frac{B}{\mu} \) asymptotically, that is, suppose there exists some \( \epsilon_0 > 0 \) and \( \delta(t_0, \epsilon_0) > 0 \), such that \( ||S(t_0) - S^*_0|| < \delta \), but \( ||S(t) - S^*_0|| \geq \epsilon_0, \forall t \geq t_0 \), then clearly from (5.15), either

\[
S^*_0 = \lim_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi)d\xi \geq S^*_0 + \epsilon_0 \quad \text{or} \quad S^*_0 = \lim_{t \to \infty} \frac{1}{t} \int_{t_0}^{t} S(\xi)d\xi \leq S^*_0 - \epsilon_0.
\]  

(5.28)

Thus, \( \epsilon_0 \) must be zero, otherwise (5.28) is a contradiction. Hence, \( E_0 = (S^*_0, 0) \) is asymptotically stable.

**Remark 5.2.** Theorem 5.2, Theorem 5.1, [Theorem 3.1, Wanduku [14]] and Lemma 5.1 signify that all trajectories of the solution \((S(t), I(t)), t \geq t_0 \) of the decoupled system containing equations for \( S \) and \( I \) in the system \((1.1)\) that start in \( D^{ex}(\infty) \subset D(\infty) \) remain bounded in \( D^{ex}(\infty) \). Moreover, the trajectories of the infectious state \( I(t), t \geq t_0 \) of the solution \((S(t), I(t)), t \geq t_0 \) in phase plane, ultimately turn to zero exponentially, whenever either the expected survival probability rate the malaria parasite satisfy \( E(e^{-(\mu T_1 + \mu T_2)}) < \frac{1}{R_0^*} \), for \( R_0^* \geq 1 \), or whenever the basic production number satisfy \( R_0^* < 1 \). Furthermore, the rate of the exponential decrease of the infectious population from (5.10) is estimated by the term \( \lambda \), defined in (5.12) and (5.14).

In addition, Theorem 5.2 asserts that when either the expected survival probability rate the malaria parasites satisfy \( E(e^{-(\mu T_1 + \mu T_2)}) < \frac{1}{R_0^*} \), for \( R_0^* \geq 1 \), or whenever the basic production number satisfy \( R_0^* < 1 \), the susceptible population remains strongly persistent in the mean over sufficiently large time, moreover, every trajectory of the susceptible state \( S(t) \) that starts in \( D^{ex}(\infty) \) remain bounded in \( D^{ex}(\infty) \), and on average the trajectories converge to the disease free steady state population \( S^*_0 = \frac{B}{\mu} \).

From Theorem 5.3 since \((S(t), I(t)) = E_0 = (S^*_0, 0) = (\frac{B}{\mu}, 0) \) is the disease-free equilibrium of the decoupled system containing equations for \( S \) and \( I \) in the system \((1.1)\), and from
(5.15), every trajectory for the susceptible state $S(t)$ converges asymptotically to $S_0^* = \frac{B}{\mu}$ on average, the disease-free steady state $(S(t), I(t)) \equiv E_0 = (S_0^*, 0) = (\frac{B}{\mu}, 0)$ must be asymptotically stable.

In other words, over sufficiently long time, the population that remains will be all susceptible malaria-free people, and the population size will be equal to the disease free steady state population $S_0^* = \frac{B}{\mu}$ of the system (1.1).

6. Example for extinction of disease

The examples exhibited in this section are used to facilitate understanding about the conditions for extinction of the disease in the population over time in Theorem 5.2. This objective is achieved in a simplistic manner by examining the behavior of the trajectories of the different states $(S, E, I, R)$ of the system (1.1) over sufficiently long time.

The following convenient list of parameter values in Table 2 are used to generate and examine the trajectories of the different states of the system (1.1), whenever the conditions of Theorem 5.2 are satisfied. The Euler approximation scheme is used to generate trajectories

| Parameter Value                        | Value  |
|----------------------------------------|--------|
| Disease transmission rate $\beta$      | 0.0006277 |
| Constant Birth rate $B$                | 22.39/1000 |
| Recovery rate $\alpha$                 | 0.55067 |
| Disease death rate $d$                 | 0.011838 |
| Natural death rate $\mu$               | 0.6 |
| Incubation delay time in vector $T_1$  | 2 units |
| Incubation delay time in host $T_2$    | 1 unit |
| Immunity delay time $T_3$              | 4 units |

for the different states $S(t), E(t), I(t), R(t)$ over the time interval $[0, T]$, where $T = \max(T_1 + T_2, T_3) = 4$. The special nonlinear incidence functions $G(I) = \frac{\beta I}{1 + I}$, $a = 0.05$ in [13] is utilized to generate the numeric results. Furthermore, the following initial conditions are used

$$
\begin{align*}
S(t) &= 10, \\
E(t) &= 5, \\
I(t) &= 6, \quad \forall t \in [-T, 0], T = \max(T_1 + T_2, T_3) = 4. \\
R(t) &= 2,
\end{align*}
$$

(6.1)
Figure 8: (a-1), and (b-1), show the trajectories of the states \((S, I)\), respectively, over sufficiently long time \(t = 1000\), whenever the intensity of the incidence of malaria is \(a = 0.05\). Also, note that any negative values have no meaningful interpretation, except a significance of extinction of the population if the negative values occur over sufficiently long time. Moreover, the basic reproduction number in (2.2) in this case is \(R_0^* = 2.014926e - 05 < 1\), the estimate of the Lyapunov exponent or rate of extinction of the disease in (5.14) is \(\lambda = 1.162485 > 0\). The broken line in (b-1) signify the origin, while the broken line in (a-1) signify the disease-free-equilibrium \(S_0^* = \frac{B}{\mu} = 0.03731667\). The minimum value for \(S(t)\) over time is \(\min(S(t)) = 1.392842\), which is closer to \(S_0^* = \frac{B}{\mu} = 0.03731667\). The minimum value of \(I(t)\) over time is \(\min(I(t)) = 0.05678687\), near zero.

Figure 8 is used to verify the results about the extinction of the infectious population over time in Theorem 5.1 and the long-term behavior of the susceptible population \(S(t)\) in Theorem 5.2. Indeed, it can be observed that for the given parameter values in Table 2 and the initial conditions for the system (1.1) in (6.1), it follows that the basic reproduction number in (2.2) in this scenario is \(R_0^* = 2.014926e - 05 < 1\). Therefore, the condition of Theorem 5.1(a.) is satisfied, and from (5.14), the estimate of the Lyapunov exponent or the rate of extinction of the malaria population \(I(t)\) is \(\lambda = 1.162485 > 0\). That is,

\[
\limsup_{t \to \infty} \frac{1}{t} \log (I(t)) \leq -\lambda = -1.162485.
\]  

(6.2)

The Figure 8(b-1) confirms that over sufficiently large time, when \(\lambda > 0\), then the infectious population becomes extinct. Furthermore, note that the basic reproduction number in (2.2) in this scenario is \(R_0^* = 2.014926e - 05 < 1\), which signifies that the disease is getting eradicated from the population over time, and the susceptible population seen in Figure 8(a-1) over sufficiently long time, approaches the disease-free equilibrium state \(S_0^* = \frac{B}{\mu} = 0.03731667\).

Indeed, note that the minimum value for the trajectory of \(S(t)\) in Figure 8(a-1) over long time is \(\min(S(t)) = 1.392842\) near \(S_0^* = \frac{B}{\mu} = 0.03731667\). This suggests that the
susceptible population is asymptotically stable on average over sufficiently long time near \( S_0^* = \frac{B}{\mu} = 0.03731667 \) as shown in Theorem 5.2. Also, note that the general decrease in the susceptible population \( S(t) \) in Figure 8(a-2) over time is accounted for by the intensity of the incidence rate of malaria \( a = 0.05 \).

7. conclusion

The extinction and persistence of malaria in a family of SEIRS models is studied. Lyapunov functional, Lyapunov exponential analysis, and other analytic techniques are used to examine the trajectories of the system near the endemic and disease-free steady states of the system. The analytic results for extinction dependent on the basic reproduction, and the expected probability of the survival of the malaria parasites. Moreover, numerical simulation results are presented to show the extinction of disease, and the asymptotic stability of the disease-free steady state population.

Also, from the above analysis, for the permanence of disease in the population, an extensive inherent algorithmic technique to analyze the permanence of disease in a complex multiple distributed delay system is presented in the proof of Lemma 3.1. The sufficient conditions for the permanence of disease are exhibited, and interpreted. Numerical simulation results are presented to investigate the impacts of malaria transmission rate and response to malaria regulation such as malaria treatment and improved living standards, on the permanence of the disease in the population.

8. References

References

[1] K. L. Cooke Stability analysis for a vector disease model. Rocky Mountain Journal of Mathematics 9 (1979), no. 1, 31-42

[2] KL Cooke , P. van den Driessche, Analysis of an SEIRS epidemic model with two delays, J Math Biol. 1996 Dec; 35(2):240-60.

[3] M. De la Sen, S. Alonso-Quesada, , A. Ibeas, On the stability of an SEIR epidemic model with distributed time-delay and a general class of feedback vaccination rules, Applied Mathematics and Computation Volume 270, 1 November 2015, Pages 953976

[4] D. L. Doolan, C. Dobano, J. K. Baird, Acquired Immunity to Malaria, clinical microbiology reviews, Vol. 22, No. 1, Jan. 2009, p. 1336

[5] S. Gao, Z. Teng, D. Xie, The effects of pulse vaccination on SEIR model with two time delays, Applied Mathematics and Computation Volume 201, Issues 12, 15 (2008), Pages 282292
[6] A. Gray, D. Greenhalgh, L. Hu, X. Mao, and J. Pan, A Stochastic Differential Equation SIS Epidemic Model, SIAM J. Appl. Math., 71(3), (2011) 876902

[7] M.Y. Hyun, Malaria transmission model for different levels of acquired immunity and temperature dependent parameters (vector). Rev. Saude Publica 2000, 34 (3), 223231

[8] L. Hviid, Naturally acquired immunity to Plasmodium falciparum malaria, Acta Tropica 95(3):270-5, October 2005

[9] Y. Kuang, delay Differential Equations with Applications in population Dynamics, Academic Press, boston. 1993

[10] A. Korobeinikov, P.K. Maini, A Lyapunov function and global properties for SIR and SEIR epidemiological models with nonlinear incidence, Math. Biosci. Eng. 1 (1) (2004) 5760.

[11] Y. N. Kyrychko, K. B. Blyussb, Global properties of a delayed SIR model with temporary immunity and nonlinear incidence rate, Nonlinear Analysis: Real World Applications Volume 6, Issue 3, July 2005, Pages 495-507

[12] A. Lahrouz, L. Omari, extinction and stationary distribution of a stochastic SIRS epidemic model with non-linear incidence, Statistics & Probability Letters 83(4):(2013)960968

[13] S.M. Moghadas, A.B. Gumel, Global Statbility of a two-stage epidemic model with generalized nonlinear incidence, Mathematics and computers in simulation 60 (2002), 107-118

[14] W. ma, M. Song, Y. Takeuchi, Global stability of ab SIR epidemic model with time delay, applied mathematics letters, 17 (2004)1141-1145

[15] CN Ngonghala, GA Ngwa, MI Teboh-Ewungkem, Periodic oscillations and backward bifurcation in a model for the dynamics of malaria transmission. Math Biosci (2012), 240(1):4562

[16] L. Pang, S. Ruan, S. Liu, Z. Zhao, X. Zhang, Transmission dynamics and optimal control of measles epidemics, Applied Mathematics and Computation 256 (2015) 131147

[17] D. Wanduku, Threshold conditions for a family of epidemic dynamic models for malaria with distributed delays in a non-random environment, International Journal of Biomathematics Vol. 11, No. 6 (2018) 1850085 (46 pages), DOI: 10.1142/S1793524518500857
[18] D. Wanduku, Complete Global Analysis of a Two-Scale Network SIRS Epidemic Dynamic Model with Distributed Delay and Random Perturbation, Applied Mathematics and Computation Vol. 294 (2017) p. 49 - 76

[19] D. Wanduku, G.S. Ladde, Fundamental Properties of a Two-scale Network stochastic human epidemic Dynamic model, Neural, Parallel, and Scientific Computations 19(2011) 229-270

[20] D. Wanduku, G.S. Ladde, Global properties of a two-scale network stochastic delayed human epidemic dynamic model, nonlinear Analysis: Real World Applications 13(2012)794-816

[21] World malaria report 2017. Geneva: World Health Organization; 2017. Licence: CC BY-NC-SA 3.0 IGO.

[22] Zhichao Jianga, b, Wanbiao Mab, Junjie Wei, Global Hopf bifurcation and permanence of a delayed SEIRS epidemic model, Mathematics and Computers in Simulation Volume 122, April 2016, Pages 3554

[23] T. Zhang, Z. teng, Global behavior and permanence of SIRS epidemic model with time delay, nonlinear analysis: RWA 9(2008)1409-1424

[24] M. Zhien, C. Guirong, Pesistence and extinction of a population in a pollulted environment, Mathematical Biosciences, 101:75-97(1990)

[25] http://www.who.int/denguecontrol/human/en/

[26] https://www.cdc.gov/malaria/about/disease.html
Extinction function ($Q$)

Intensity ($\sigma^2_1 = \sigma^2_2 = \sigma$)
(a–1) Sample path for $S(t)$

(b–1) Sample path for $I(t)$
(a−2) Sample path for $S(t)$

(b−2) Sample path for $I(t)$
(a–3) Sample path for $S(t)$

(b–3) Sample path for $I(t)$