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In honour of Prof. Ekhaguere at 70

The asymptotic behaviour of malaria dynamics equilibrium solution with non-drug compliant human compartment

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Abstract. In this paper, we develop a mathematical model to study and analyze malaria dynamics involving ordinary differential equations for the human and mosquito populations. The model incorporates a class of non-drug compliant humans in the infective class. An equivalent system is obtained, which has two equilibria: a disease free-equilibrium and an endemic equilibrium. The existence and stability analyses of the disease-free and endemic equilibria are obtained. We establish local stability of disease-free equilibrium points by solving the linearized system and calculating a classical epidemiology threshold, R_m, called the basic reproduction number, which is obtained from next generation matrix. Local stability of endemic equilibrium points is also determined.

Keywords: malaria, non-drug compliant human, equilibrium, basic reproduction number, additive compound matrix, stability.

1. Introduction

Malaria is one of the most important public health problems. It has been rated as one of the top three killers among communicable diseases (Sachs and Malaney, 2002). The estimated annual mortality rate attributed to malaria ranges from 700,000-2.7 million worldwide and more than 75 percent of them are African children and expectant mothers who have less immunity (Kumar et al.,2007). Sub-Sahara Africa (SSA) and Southeast Asia are the most malaria-affected regions.

Protozoan parasite of genus plasmodium is the main cause for malaria disease which is transmitted between humans through the bite of female anopheles mosquitoes(Mandal et al.,2011). There are five species of the plasmodium parasite which can infect humans; they are plasmodium falciparum, plasmodium vivax, plasmodium ovale, plasmodium malariae and plasmodium knowlesi and the most serious form of the disease is caused by plasmodium falciparum(Wei,2008). Malaria caused by plasmodium vivax, plasmodium ovale and plasmodium malariae causes milder diseases in humans that is not generally fatal(Pongsumpon et al.,2009). A fifth specie, plasmodium knowlesi causes malaria in macaques but can also infect humans(Malaria,2010). Malaria symptoms include temperature with headache, shivering, muscle pains, diarrhoea and vomiting with attacks appearing in two to three days depending on the plasmodium species.

Mathematical modelling of spread of malaria has attracted constant interest of researchers. A great deal of papers published during the last three decades are concerned with local and global stability of equilibria of malaria dynamics. Among numerous results concerned with the existence and stability of equilibria of malaria dynamics, we would like to mention especially Sir Ronald Ross who introduced the first deterministic differential equation malaria model in which the human population was structured as susceptible-Infected-Susceptible (SIS) compartment model and the mosquito. He showed that bringing a mosquito population to certain threshold was sufficient to eliminate malaria. Dietz et al. (1974) proposed a model that accounts for acquired immunity in a mass action model. Macdonald (1957) used a model in which he assumed the amount of infective material to which a population is exposed remains unchanged and also showed that reducing the number of mosquitoes is an inefficient control strategy that would have little effect on the epidemiology of malaria in areas of intense transmission. Bailey (1982) and Aron (1988) models take into account that acquired immunity to malaria depends on the exposure.

During the last decades, various mathematical models have been used for infectious diseases es-

pecially for malaria (Ngwa et al.,2000; Olumese, 2005; Sachs, 2002; Tumwiine et al., 2005). Gosh et al.(1996), studied the environmental effect on a susceptible/infected/susceptible(SIS) model for bacteria and the spread of carrier-dependent infectious diseases, like cholera, diarrhoea. Castilho (2006) specifically applied optimal control methods in a simplified susceptible-infective-removed (SIR) model, to study the best strategy for educational campaigns during the outbreak of an epidemic. Xiefel et al.(2007) applied optimal control methods to study the outbreak of severe respiratory syndrome(SARS) using Pontryagin's Maximum Principle and genetic algorithm. Jia(2008) formulated and examined a compartmental mathematical model for malaria transmission that includes incubation periods for both infected human host and mosquitoes. Elsady(2008) studied the mathematical effect of improving the function of the thymus on the viral growth and T cell population of an HIV-immune dynamic system. Rafikov et al.(2009) formulated a continuous model for malaria vector with the aim of studying how genetically modified mosquitoes should be introduced in the environment using optimal control problem strategies. Makinde and Okosun(2011) presented impact of optimal control strategies on malaria spread with infective immigrants. With a view to preventing the human-mosquito contacts, it is inevitable to incorporate a class of vigilant humans who adhere to the malaria vector control measures of the World Health Organization(Obabiyi, Olaniyi, 2016). All these work did not consider the non-drug compliance problem.

The model we consider in this paper differs from that of previous work because it incorporates a new class of non-drug compliant human(who are given medication by their doctors and nearly half do not take the drug or do not take it as prescribed, and most will stop the treatment as soon as they are feeling better) into the population in order to investigate the role and effect of non-drug compliant humans in malaria spread so as to make decisions in controlling the disease. Thus our model is based on the susceptible-exposed-infectious-non-drug compliant-recovered($S_H E_H I_H I_{NH} R_H$) in human population and susceptible-infective($S_V I_V$) for the mosquito vector population. The paper is organized as follows: In section 2, model formulation is obtained. Section 3 deals with the stability analyses of the equilibrium solution. Section 4 deals with discussion of results and concludes the modelling work.

1.1 *Compartmental Model Formulation for the Transmission Dynamics of Malaria*

The model sub-divides the total human population denoted by N_H, into sub-populations of susceptible human hosts (S_H), exposed human hosts, i.e.,those exposed to malaria parasites(E_H), infectious human hosts (I_H), non-drug compliant human hosts (I_{NH}) and recovered human hosts (R_H) so that $N_H = S_H + E_H + I_H + I_{NH} + R_H$.

The total mosquito vector population, denoted by N_v, is sub-divided into susceptible mosquito vectors (S_v), infected mosquito vectors (I_V) so that $N_v = S_v + I_v$.

Susceptible humans are recruited at a rate Λ_H; susceptible humans (S_H) acquire malaria through contact with infectious mosquitoes (I_V), with which infectious mosquitoes injects sporozoites along with saliva into small blood vessels(Nakul et al., 2006) and susceptible humans move to the exposed human compartment (E_H) at a rate $\frac{abS_H I_V}{N_H}$. Exposed humans are those who have parasites in them and the parasites are in asexual stages. They do not have gametocytes and they cannot transmit malaria to the susceptible mosquitoes.

The parasites in the exposed human move down to the liver where they undergo nuclear division and thousands of them are released into the blood stream as merozoites which develop to form gametocytes(Nakul et al., 2006). At this stage, the exposed humans move to infectious human compartment(I_H) at a rate $\alpha_v E_H$. A proportion of infectious humans(I_H), who do not comply to drug move to non-drug compliant human compartment(I_{NH}) at a rate $(1-\theta)\tau I_H$, where $(1-\theta)$, is the proportion of infectious humans who do not comply to drug and τ is the drug efficacy and the proportion of infectious humans who comply to drug move to the recovered human compartment(R_H) at a rate $\theta\tau I_H$, where θ is the proportion of infectious humans who comply to drug. Recovered humans(R_H), after some period of time, lose their immunity at a rate γR_H and return to the susceptible class(Nakul et al., 2006) μ_N is non-drug compliance induced death and μ_H is the natural death rate.

Susceptible mosquitoes(S_V) are recruited at a rate Λ_V and acquire malaria through contacts with

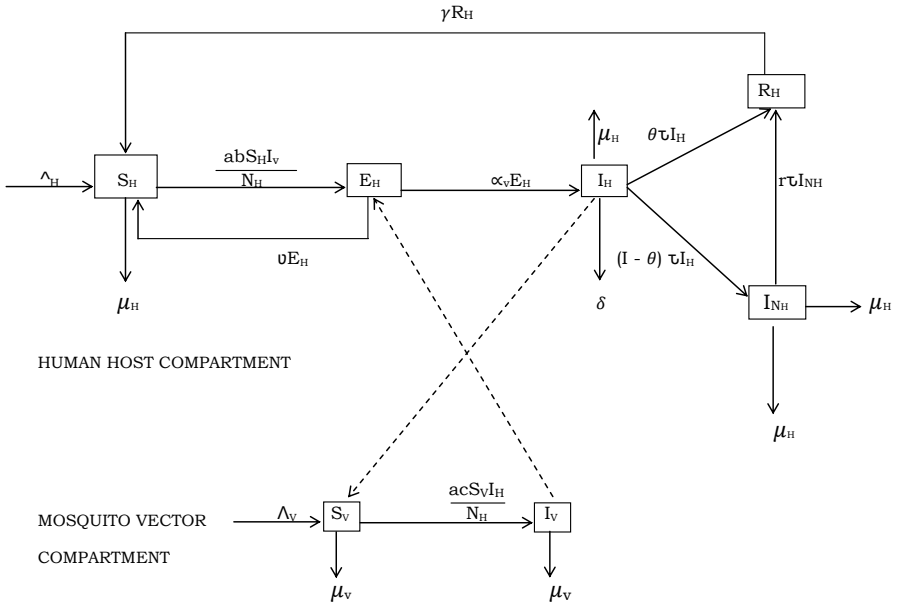

Figure 1. Compartmental diagram for malaria model incorporating non-drug compliant human compartment

infected humans(I_H) and non-drug compliant humans at a rate $\frac{acS_V(I_H+I_{NH})}{N_H}$. Mosquitoes never recover from infection and suffer death due to natural causes and various control measures.

The model has the following variables and parameters and the unit of time is days:

Let $\theta\tau$ be the portion of infected humans with drug compliance and $(1-\theta)\tau$ be the portion of the infected humans with non-drug compliance.

$S_H(t)$ = the number of susceptible human hosts at time t
$E_H(t)$ = the number of exposed human hosts at time t
$I_H(t)$ = the number of infectious human hosts at time t
$I_{NH}(t)$ = the number of non-drug compliant human hosts at time t
$R_H(t)$ = the number of recovered human hosts at time t
$S_V(t)$ = the number of susceptible mosquito vectors at time t
$I_V(t)$ = the number of infected mosquito vectors at time t
$N_H(t)$ = total human population 5668123 [Central Intelligence Agency(CIA)] $m = \frac{N_V}{N_H}$ = the number of female mosquitoes per human host
a = the average daily biting rate on man by a single mosquito(infection rate) 0.29/day [Ishikawa et al.,(2003), Laxminarayan, R.(2004)]
b = the proportion of bites on man that produce an infection 0.75 [Laxminarayan, R.(2004)]
c = the probability that a mosquito becomes infectious 0.09 [Kbenesh et al. (2009)]
γ = the per capita loss of immunity in human hosts $0.000017/day$ [Ishikawa et al.,(2003)]
r = the rate at which non-drug compliant human hosts are educated $0.00019/day$ [Coutinho et al.,(2005)]
δ = the per capita death rate of infected human hosts due to the disease $0.05day^{-}1$ [Okosun et al.,(2011)]
τ = drug efficacy $0.01 - 0.07$ [Okosun et al., 2011]
ν = the rate of recovery of human hosts from the disease $0.038day^{-}1$ [Aguas et al.(2008), Akbari et al.(2012)]
Λ_H = recruitment rate of humans $100/day$ [Okosun et al.(2011)]
Λ_V = recruitment rate of mosquitoes $1000/day$ [Okosun et al.(2011)]
μ_H = natural death rate in humans $0.00004/day$ [Nakul et al., 2006]
μ_V = natural death rate in mosquitoes $0.1429/day$ Nakul et al.,(1996)]
μ_N = non-drug compliance induced death rate 0.05 [Okosun et al., 2011]
α_V = probability of human getting infected $0.8333/day$ [Okosun et al., 2011]

1.2 *Assumptions of the model (malaria model)*

The following assumptions were made in order to formulate the equations of the model:
(a). Exposed humans progress to either become susceptible or infectious.
(b). All mosquitoes are born susceptible.
(c). All humans are born susceptible and there is no vertical transmission.
(d). Mosquitoes never recover from infection, that is, there is no recovered compartment for mosquito population.
(e). Some infectious humans who take their drugs as prescribed by their doctors(i.e., they complete treatment) get treated fully and move to the recovered compartment.
(f). Some infectious humans who take their drugs but stop the treatment as soon as they are feeling better(i.e., they do not complete treatment) get treated partially and move to the non-drug compliant human compartment and when a susceptible mosquito bites them, it becomes infectious.
(g). Some infectious humans who do not take their drugs move to the non-drug compliant human compartment.
(h). Proportion of active parasites are still in the blood of partially treated humans, (i.e., those who stop the treatment as soon as they are feeling better). They do not complete treatment.
(i). Infectious humans progress to either become recovered or non-drug compliant.
(j). Infectious humans who do not comply to drug may either die or survive.
(k). A proportion of susceptible humans is infected by infectious mosquitoes and susceptible mosquitoes become infected when in contact with a proportion of infectious humans
(l). Recovered humans have some immunity that can be lost and are again susceptible to reinfection.
(m). Infected susceptible mosquitoes are the exposed mosquitoes who are not yet infectious.
Note: Recovery rate corresponds to how quickly parasites are cleared from the human host due to treatment.

Applying the assumptions, definitions of variables, parameters and descriptions of terms above, the malaria model is formulated:

$$\frac{dS_H}{dt} = \Lambda_H - \frac{abS_H I_V}{N_H} + \nu E_H + \gamma R_H - \mu_H S_H \tag{1.1}$$

$$\frac{dE_H}{dt} = \frac{abS_H I_V}{N_H} - \nu E_H - \alpha_v E_H - \mu_H E_H \tag{1.2}$$

$$\frac{dI_H}{dt} = \alpha_v E_H - \tau I_H - \delta I_H - \mu_H I_H \tag{1.3}$$

$$\frac{dI_{NH}}{dt} = (1-\theta)\tau I_H - \mu_N I_{NH} - r\tau I_{NH} - \mu_H I_{NH} \tag{1.4}$$

$$\frac{dR_H}{dt} = \theta\tau I_H - \gamma R_H + r\tau I_{NH} - \mu_H R_H \tag{1.5}$$

$$\frac{dS_V}{dt} = \Lambda_V - \frac{acS_V(I_H + I_{NH})}{N_H} - \mu_V S_V \tag{1.6}$$

$$\frac{dI_V}{dt} = \frac{acS_V(I_H + I_{NH})}{N_H} - \mu_V I_V \tag{1.7}$$

2. Stability analysis

2.1 *Local stability of disease-free equilibrium*

In this section, we state and prove conditions that guarantee local stability of the disease-free equilibrium E_0

Lemma 1: If the unique solution of the linearized system decays exponentially and approaches the equilibrium point E_0 and if $R_m < 1$, then the disease-free equilibrium point E_0 is locally

asymptotically stable.

Proof: The local stability of equilibrium solution of model (1.1)-(1.7) in the absence of infection, called the disease-free equilibrium is analyzed. In the absence of infection, the model reduces to:

$$\frac{dS_H}{dt} = \Lambda_H + \gamma R_H - \mu_H S_H \tag{2.1}$$

$$\frac{dR_H}{dt} = -(\gamma + \mu_H) R_H \tag{2.2}$$

$$\frac{dS_V}{dt} = \Lambda_V - \mu_V S_V \tag{2.3}$$

We first solve for the disease-free equilibrium solution by setting the right-hand sides of (2.1)-(2.3) to zero and the system takes the form

$$\Lambda_H + \gamma R_H - \mu_H S_H = 0 \tag{2.4}$$

$$-(\gamma + \mu_H) R_H = 0 \tag{2.5}$$

$$\Lambda_V - \mu_V S_V = 0 \tag{2.6}$$

Solving for the equilibrium points yields

$$E_o = (\frac{\Lambda_H}{\mu_H}, 0, \frac{\Lambda_V}{\mu_V}) \tag{2.7}$$

We next solve the system to know if the unique solution of the system (2.1)-(2.3) is approaching the equilibrium solution in the future(i.e. as t grows large).

From (2.2),

$$\frac{dR_H}{dt} = -(\gamma + \mu_H) R_H$$

Solving this, we have

$$R_H = R_H^o e^{-(\gamma + \mu_H)t} \tag{2.8}$$

where $R_H(0) = R_H^o$.

This shows that the recovered human is approaching the equilibrium solution as t approaches infinity. From (2.1) and (2.8), we have

$$\frac{dS_H}{dt} = \Lambda_H + \gamma R_H^o e^{-(\gamma + \mu_H)t} - \mu_H S_H$$

which implies

$$S_H = \frac{\Lambda_H}{\mu_H} - R_H^o e^{-(\gamma + \mu_H)t} + (S_H^o - \frac{\Lambda_H}{\mu_H} + R_H^o) e^{-\mu_H t} \tag{2.9}$$

where $S_H(0) = S_H^o$. This shows that the susceptible human decays exponentially. Now, for mosquito population, we have from (2.3)

$$S_V = \frac{\Lambda_v}{\mu_v} + (S_v^o - \frac{\Lambda_v}{\mu_v}) e^{-\mu_v t} \tag{2.10}$$

We have established that the disease-free equilibrium point E_0 is locally asymptotically stable. Next we find R_m. But before then, it is easier to analyze our model in terms of proportions of quantities instead of actual population. This can be done by scaling the population of each class by the total species populations. To do this, we first determine the total population sizes by $N_H = S_H + E_H + I_H + I_{NH} + R_H$ and $N_V = S_V + I_V$ or from the differential equations

$$\frac{dN_H}{dt} = \Lambda_H - \mu_H N_H - \delta I_H - \mu_N I_{NH} \tag{2.11}$$

$$\frac{dN_V}{dt} = \Lambda_V - N_V \mu_V \tag{2.12}$$

which are derived by adding Eqs. (1.1)-(1.5) for the human population and (1.6) and (1.7) for mosquito vector population. Now we do the scaling by making the transformation

$$s_h = \frac{S_H}{N_H};\ e_h = \frac{E_H}{N_H};\ i_h = \frac{I_H}{N_H};\ i_{nh} = \frac{I_{NH}}{N_H};\ r_h = \frac{R_H}{N_H};\ s_v = \frac{S_V}{N_V};\ i_v = \frac{I_V}{N_V};\ m = \frac{N_V}{N_H}$$

in the classes $S_H, E_H, I_H, I_{NH}, R_H, S_V$ and I_V in the population respectively. This is done by differentiating the fractions with respect to time t and simplifying as follows:

$$\begin{aligned}
\frac{ds_h}{dt} &= \frac{1}{N_H}\left[\frac{dS_H}{dt} - s_h\frac{dN_H}{dt}\right] \\
&= \lambda_h - abms_h i_v + \nu e_h + \gamma r_h - \mu_H s_h - \lambda_h s_h + \mu_H s_h + \delta s_h i_h + \mu_N s_h i_{nh} \\
&= \lambda_h(1 - s_h) - abms_h i_v + \nu e_h + \gamma r_h + \delta s_h i_h + \mu_N s_h i_{nh} \\
\frac{de_h}{dt} &= \frac{1}{N_H}\left[\frac{dE_H}{dt} - e_h\frac{N_H}{dt}\right] \\
&= abms_h i_v - (\nu + \alpha_v + \lambda_h - \delta i_h - \mu_N i_{nh})e_h \\
\frac{di_h}{dt} &= \frac{1}{N_H}\left[\frac{dI_H}{dt} - i_h\frac{dN_H}{dt}\right] \\
&= \alpha_v e_h - (\tau + \delta + \lambda_h + \mu_N i_{nh})i_h + \delta i_h^2 \\
\frac{di_{nh}}{dt} &= \frac{1}{N_H}\left[\frac{dI_{NH}}{dt} - i_{nh}\frac{dN_H}{dt}\right] \\
&= (\tau - \theta\tau)i_h - (r\tau + \lambda_h)i_{nh} + \delta i_h i_{nh} \\
\frac{dr_h}{dt} &= \frac{1}{N_H}\left[\frac{dR_H}{dt} - r_h\frac{dN_H}{dt}\right] \\
&= \theta\tau i_h - (\gamma + \lambda_h)r_h + r\tau i_{nh} + \delta r_h i_h + \mu_N r_h i_{nh} \\
\frac{ds_v}{dt} &= \frac{1}{N_V}\left[\frac{dS_V}{dt} - s_v\frac{dN_V}{dt}\right] \\
&= \lambda_v(1 - s_v) - acsv(i_h + i_{nh}) \\
\frac{di_v}{dt} &= \frac{1}{N_V}\left[\frac{dI_V}{dt} - i_v\frac{dN_V}{dt}\right] \\
&= acs_v(i_h + i_{nh}) - \lambda_v i_v
\end{aligned}$$

subject to the restrictions $s_h + e_h + i_h + i_{nh} + r_h = 1$ and $s_v + i_v = 1$. Using the relations $r_h =$

$1 - s_h - e_h - i_h - i_{nh}$ and $s_v = 1 - i_v$ lead to system

$$\frac{ds_h}{dt} = \lambda_h(1 - s_h) - abms_h i_v + \nu e_h + \gamma r_h + \delta s_h i_h + \mu_N s_h i_{nh} \tag{2.13}$$

$$\frac{de_h}{dt} = abms_h i_v - (\nu + \alpha_v + \lambda_h - \delta i_h - \mu_N i_{nh})e_h \tag{2.14}$$

$$\frac{di_h}{dt} = \alpha_v e_h - (\tau + \delta + \lambda_h + \mu_N i_{nh})i_h + \delta i_h^2 \tag{2.15}$$

$$\frac{di_{nh}}{dt} = (\tau - \theta\tau)i_h - (r\tau + \lambda_h)i_{nh} + \delta i_h i_{nh} \tag{2.16}$$

$$\frac{di_v}{dt} = aci_h(1 - i_v) + aci_{nh}(1 - i_v) - \lambda_v i_v \tag{2.17}$$

in the feasible region (i.e. where the model makes biological sense) $T = \{(s_h, e_h, i_h, i_{nh}, i_v) \in R_+^5 : 0 \le s_h, 0 \le s_h, 0 \le e_h, 0 \le i_h, 0 \le i_{nh} \le 1, s_h + e_h + i_h + i_{nh} \le 1, 0 \le i_v \le 1\}$ that can be shown to be positively invariant with respect to the system(2.13)-(2.17) where R_+^5 denotes the nonnegative cone of R^5 including its lower dimensional faces. We denote the boundary and the interior of T by ∂T and T respectively. Equilibrium points are obtained by setting the right hand-sides of (2.13)-(2.17) to zero and the system takes the form

$$\lambda_h(1 - s_h) - abms_h i_v + \nu e_h + \gamma r_h + \delta s_h i_h + \mu_N s_h i_{nh} = 0 \tag{2.18}$$

$$abms_h i_v - (\nu + \alpha_v + \lambda_h - \delta i_h - \mu_N i_{nh})e_h = 0 \tag{2.19}$$

$$\alpha_v e_h - (\tau + \delta + \lambda_h + \mu_N i_{nh})i_h + \delta i_h^2 = 0 \tag{2.20}$$

$$(\tau - \theta\tau)i_h - (r\tau + \lambda_h)i_{nh} + \delta i_h i_{nh} = 0 \tag{2.21}$$

$$aci_h(1 - i_v) + aci_{nh}(1 - i_v) - \lambda_v i_v = 0 \tag{2.22}$$

The model has a steady state, E_0, called the disease-free equilibrium where $E_0 = (1, 0, 0, 0, 0)$. We obtain the reproductive number R_m by expressing (2.13)-(2.17) as the difference between the rate of new infection in each infected compartment F and the rate of transfer between each infected compartment G.

Note: R_m is defined as the number of secondary infectious cases produced by one primary case introduced into an entirely susceptible population at the disease-free equilibrium.

$$\begin{bmatrix} \frac{de_h}{dt} \\ \frac{di_h}{dt} \\ \frac{di_{nh}}{dt} \\ \frac{i_v}{dt} \end{bmatrix} = F - G = \begin{bmatrix} abms_h i_v \\ 0 \\ 0 \\ acs_v(i_h + i_{nh}) \end{bmatrix} - \begin{bmatrix} (\nu + \alpha_v + \lambda_h - \delta i_h - \mu_N i_{nh})e_h \\ -\alpha_v e_h + (\tau + \delta + \lambda_h + \mu_N i_{nh})i_h + \delta i_h^2 \\ -\tau i_h + \theta\tau i_h + (tau + \lambda_h)i_{nh} + \delta i_h i_{nh} \\ \lambda_v i_v \end{bmatrix}$$

The Jacobian matrices J_F and J_G of F and G are found about E_0.

$$S = J_F J_G^{-1} = \begin{bmatrix} 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \frac{ac}{\lambda_v} \\ 0 & 0 & 0 & \frac{ac}{\lambda_v} \\ \frac{abm}{\nu + \alpha_v + \lambda_h} & \frac{abm\alpha_v}{H_T(\nu + \alpha_v + \lambda_h)} & -\frac{abm\alpha_v\tau(\theta - 1)}{(r\tau + \lambda_h)H_T(\nu + \alpha_v + \lambda_h)} & 0 \end{bmatrix}$$

R_m is the maximum eigenvalue of S given as

$$R_m = \frac{Ka^2bmc}{H_T\lambda_v}, \text{ where } H_T = \tau + \delta + \lambda_h \text{ and } K = \frac{\alpha_v(r\tau - \theta\tau + \tau + \lambda_h)}{(\nu r\tau + r\tau\alpha_v + r\tau\lambda_h + \nu\lambda_h + \alpha_v\lambda_h + \lambda_h^2)}.$$

Since the unique solution of system (3.1)-(3.3) decays exponentially and $R_m < 1$, the disease-free equilibrium is locally asymptotically stable.

2.2 *Local Stability of Endemic Equilibrium* E_1

For the existence and uniqueness of endemic equilibrium $E_1 = (s_h^*, e_h^*, i_h^*, i_{nh}^*, i_v^*)$, its coordinates should satisfy the conditions $s_h^* > 0, e_h^* > 0, i_h^* > 0, i_{nh}^* > 0, i_v^* > 0$. Adding Eqs. (2.18)-(2.22), we have

$\lambda_h(1 - s_h^* - e_h^* - i_h^* - i_{nh}^*) + \gamma(1 - s_h^* - e_h^* - i_h^* - i_{nh}^*) - \delta i_h^*(1 - s_h^* - e_h^* - i_h^* - i_{nh}^*) + \mu_N i_{nh}^*(s_h^* - e_h^* - i_h^* - i_{nh}^*) + aci_h^*(1 - i_v^*) + aci_{nh}^*(1 - i_v^*) - \theta\tau i_h^* - r\tau i_{nh}^* - \lambda_v i_v^* = 0$

From Eq.(2.22), $aci_h^*(1 - i_v^*) + aci_{nh}^*(1 - i_v^*) - \lambda_v i_v^* = 0$ and $\mu_N i^* nh(s_h^* - e_h^* - i_h^*) = 0$. This gives

$(1 - s_h^* - e_h^* - i_h^* - i_{nh}^*)(\lambda_h + \gamma - \delta i_h^*) - \theta\tau i_h^* - r\tau i_{nh}^* = 0$
$(1 - s_h^* - e_h^* - i_h^* - i_{nh}^*)(\lambda_h + \gamma - \delta i_h^*) = \theta\tau i_h^* - r\tau i_{nh}^*$

since $s_h^* > 0, e_h^* > 0, i_h^* > 0, r_h^* > 0$ and $r_h^* = 1 - e_h^* - i_h^* - i_{nh}^* > 0$. Also since $\theta > 0, \tau > 0$ and $i_{nh}^* > 0$, then $\lambda_h + \gamma - \delta i_{nh}^* > 0$, $-\delta i_h^* > -(\lambda_h + \gamma)$, $\delta i_h^* < (\lambda_h + \gamma)$.

Dividing through by δ gives $i_h^* < \frac{\lambda_h + \gamma}{\delta}$. Thus, an endemic equilibrium point exists, where i_h^* lies in the interval $\left(0, \min\left\{1, \frac{\lambda_h+\gamma}{\delta}\right\}\right)$. $\delta < \lambda_h + \gamma$ is of significant importance and plays a great role when malaria persists. It shows that mortality rate due to malaria should be less than that at which the susceptible human population is refilled due to birth and loss of immunity to malaria.

In order to analyze the stability of the endemic equilibrium, the additive compound matrices approach as in [Mouldowney,(1990); Li et. al.,(1995)] is used. We first compute the Jacobian matrix J_E of (2.18)-(2.22). At the steady state, the Jacobian matrix is given by

$$J_E = \begin{bmatrix} \Psi_1 & \nu - \gamma & -\gamma + \delta s_h & -\gamma + \mu_N s_h & -abms_h \\ abmi_v & \Psi_2 & \delta e_h & \mu_N e_h & abms_h \\ 0 & \alpha_v & \Psi_3 & -\mu_N i_h & 0 \\ 0 & 0 & \tau - \theta\tau + \delta i_{nh} & -(\lambda_h + r\tau - \delta i_h) & 0 \\ 0 & 0 & ac(1 - i_v) & ac(1 - i_v) & \Psi_4 \end{bmatrix} \tag{2.23}$$

where

$$\Psi_1 = -(\lambda_h + \gamma + abmi_v - \delta i_h - \mu_N i_{nh})$$
$$\Psi_2 = -(\nu + \lambda_h + \alpha_v - \mu_N i_{nh} - \delta i_h)$$
$$\Psi_3 = -H_T + 2\delta i_h - \mu_N i_{nh}$$
$$\Psi_4 = -\lambda_v - aci_h - aci_{nh}$$

From the Jacobian matrix, the first additive compound matrix is given by

$$J_E^{[1]} = \begin{bmatrix} -(K-\delta i_h^*) & 0 & 0 & 0 & 0 \\ 0 & -(M-\delta i_h^*) & 0 & 0 & 0 \\ 0 & 0 & -(N+2\delta i_h^*) & 0 & 0 \\ 0 & 0 & 0 & -(F-\delta i_h^*) & 0 \\ 0 & 0 & 0 & 0 & -E \end{bmatrix} \tag{2.24}$$

where $K = \lambda_h + \gamma + abmi_v + \mu_N i_{nh}^*$, $M = \lambda_h + \nu + \alpha_v + \mu_N i_{nh}^*$, $N = H_T + \mu_N i_{nh}^*$, $F = \lambda_h - r\tau$, $E = aci_h^* + aci_{nh}^* - \lambda_v$.

The following lemma stated and proved in McCluskey and Van den Driessche [McCluskey et. al.(2004)] is used to demonstrate the local stability of endemic equilibrium point E_1.

Lemma 2: Let M be a 5×5 matrix. If $tr(M)$, $det(M)$, and $det(M^{[1]})$ are all negative, then all eigenvalues of M have negative have negative real part.

Proof. From the Jacobian matrix J_E in Eq.(4.0.19), we have

$$\begin{aligned} tr(J_{E_1}) &= -\lambda_h - \gamma - abmi_v^* + \delta i_h^* + \mu_N i_{nh}^* - \nu - \lambda_h - \alpha_v + \mu_N i_{nh}^* + \delta i_h^* - H_T + 2\delta i_h^* \\ &\quad -\mu_N i_{nh}^* - \lambda_h - r\tau + \delta i_h^* - aci_h^* - aci_{nh}^* - \lambda_v \\ &= 4\delta i_h^* - 3\lambda_h - \gamma - abmi_v^* - H_T - \lambda_v - \nu - \alpha_v + \mu_N i^* nh \\ &\quad -r\tau - aci_h^* - aci_{nh}^* \ < \ 0 \end{aligned} \tag{2.25}$$

In order to determine $det(J_{E_1})$, the following simplified form of equations of system (2.18)-(2.22) is used:

$$\begin{aligned} -\frac{\lambda_h + \nu e_h^* + \gamma(1 - e_h^* - i_h^* - i_{nh}^*)}{s_h^*} &= -(\lambda_h + \gamma + abmi_v^* - \delta i_h^* - \mu_N i_{nh}^*) \\ -\frac{abms *_h i_v^*}{e_h^*} &= -(\nu + \alpha_v + \lambda_h - \delta i_h^* - \mu_N i_{nh}^*) \end{aligned} \tag{2.26}$$

$$-H_T + 2\delta i_h^* - \mu_N i_{nh}^* = -\frac{K*}{i_h^*} + \delta i_h^* - \mu_N i_{nh}^* \tag{2.27}$$

$$-(\lambda_h + r\tau - \delta i_h^*) = -\frac{U^* \tau i_h^*}{i_{nh}^*} \tag{2.28}$$

$$-\lambda_h - aci_h^* - aci_{nh}^* = -\frac{S^*}{i_v^*} \tag{2.29}$$

$$ac(1 - i_v^*) = \frac{N^*}{i_h^*} \tag{2.30}$$

$$\tau - \theta\tau + \delta i_{nh}^* = \frac{Z^*}{i_h^*} \tag{2.31}$$

where $K^* = \alpha_v e_h^* - \mu_N i_{nh}^*$, $U^* = 1 - \theta$, $S^* = aci_h^* + aci_{nh}^*$, $N^* = \lambda_v i_v^* + aci_{nh}^* i_v^* - aci_{nh}^*$, $Z^* = (r\tau + \lambda_h) i_{nh}^*$ ■

Note: $\lambda_v = \dfrac{aci_h^*(1 - i_v^*) + aci_{nh}^*(1 - i_v^*)}{i_v^*}$ is used to get (2.30)

So from the Jacobian matrix J_{E_1} and the simplified expressions (2.26)-(2.32), we have

$$det(J_{E_1}) = \begin{bmatrix} \Psi_1^* & \nu-\gamma & -\gamma+\delta s_h^* & -\gamma+\mu_N s_h^* & -abms_h^* \\ abmi_v^* & \Psi_2^* & \delta e_h^* & \mu_N e_h^* & abms_h^* \\ 0 & \alpha_v & \Psi_3^* & -\mu_N i_h^* & 0 \\ 0 & 0 & \tau-\theta\tau+\delta i_{nh}^* & \Psi_4^* & 0 \\ 0 & 0 & ac(1-i_v^*) & ac(1-i_v^*) & \Psi_5^* \end{bmatrix} \tag{2.32}$$

where

$$\begin{aligned} \Psi_1^* &= -(\lambda_h+\gamma+abmi_v^*-\delta i_h^*-\mu_N i_{nh}^*) \\ \Psi_2^* &= -(\nu+\lambda_h+\alpha_v-\mu_N i_{nh}^*-\delta i_h^*) \\ \Psi_3^* &= -H_T+2\delta i_h^*-\mu_N i_{nh}^* \\ \Psi_4^* &= -(\lambda_h+r\tau-\delta i_h^*) \\ \Psi_5^* &= -\lambda_v-aci_h^*-aci_{nh}^* \end{aligned}$$

$$= \begin{bmatrix} \Psi_1^* & \nu-\gamma & -\gamma+\delta s_h^* & -\gamma+\mu_N s_h^* & -abms_h^* \\ abmi_v^* & -\dfrac{abms_h^* i_v^*}{e_h^*} & \delta e_h^* & \mu_N e_h^* & abms_h^* \\ 0 & \alpha_v & \Psi_2^* & -\mu_N i_h^* & 0 \\ 0 & 0 & \dfrac{Z^*}{i_h^*} & -\dfrac{U^*\tau i_h^*}{i_{nh}^*} & 0 \\ 0 & 0 & \dfrac{N^*}{i_h^*} & \dfrac{N^*}{i_h^*} & -\dfrac{S^*}{i_v^*} \end{bmatrix} \tag{2.33}$$

where

$$\begin{aligned} \Psi_1^* &= -\frac{\lambda_h+\nu e_h^*+\gamma(1-e_h^*-i_h^*-i_{nh}^*)}{s_h^*} \\ \Psi_2^* &= -\frac{K^*}{i_h^*}+\delta i_h^*-\mu_N i_{nh}^* \end{aligned}$$

$$\det(J_{E_1}) = -\left[\frac{1}{G}(\lambda_h+\gamma-\delta i_h^*)\right](A\phi abms_h^* i_v^* + Babms_h^* e_h^* + C\phi\alpha_v e_h^{*2} + Da^2b^2m^2 s_h^{*2} e_h^{*2} i_v^{*2}\alpha_v) \tag{2.34}$$

where

$$\begin{aligned} A &= si_h^{*3}d\tau u + si_h^{*2}z\mu_N i_{nh}^* + si_h^{*2}k\tau u - \alpha_v e_h^* z i_{nh}^* n i_v^* - \alpha_v e_h^* z i_{nh}^* n - \alpha_v e_h^* nu\tau i_h^{*2} \\ B &= i_v^* si_h^{*3}dv\tau u - i_v^* si_h^{*2} i_{nh}^* vz\mu_N - i_v^* si_v^{*2}kv\tau u - i_v^* si_h^{*3}\gamma d\tau u + i_v^* si_h^{*2}\gamma i_{nh}^* z\mu_N + i_v^* si_h^{*2}\gamma k\tau u \\ &\quad -s_h^* i_v^* \alpha_v i_h^{*3} s\tau u\delta + i_v^*\alpha_v\gamma i_h^{*3} s\tau u - s_h^* i_v^*\alpha_v z i_{nh}^* i_h^* s\mu_N + i_h^*\alpha_v z i_{nh}^*\gamma i_h^* s \\ C &= -\delta u\tau i_h^{*3} s - z i_{nh}^*\mu_N s i_h^* \\ D &= z i_{nh}^* n + nu\tau i_h^{*2} \\ G &= s_h^* e_h^* i_h^{*2} i_{nh}^* i_v^* \\ \phi &= \frac{\lambda_h+\nu e_h^*+\gamma(1-e_h^*-i_h^*-i_{nh}^*)}{s_h^*} \end{aligned}$$

Since $\delta < \lambda_h + \gamma$, the $det(J_{E_1})$ is negative. From the first additive compound matrix $J^{[1]}_{E_1}$, $det(J^{[1]}_{E_1}) < 0$ is demonstrated as follows:

For the endemic equilibrium point $E_1 = (s^*_h, e^*_h i^*_h, i^*_{nh}, i^*_v)$, let $P = diag(s^*_h, e^*_h, i^*_h, i^*_{nh}, i^*_v)$ be the diagonal matrix. Then the matrix $J^{[1]}_{E_1}$ is similar to the matrix given by

$$PJ^{[1]}_{E_1}P^{-}1 = \begin{bmatrix} -(K-\delta i^*_h) & 0 & 0 & 0 & 0 \\ 0 & -(M-\delta i^*_h) & 0 & 0 & 0 \\ 0 & 0 & -(N+2\delta i^*_h) & 0 & 0 \\ 0 & 0 & 0 & -(F-\delta i^*_h) & 0 \\ 0 & 0 & 0 & 0 & -E \end{bmatrix}.$$

Since similarity preserves the eigenvalues, then matrix $J^{[1]}_{E_1}$ is stable if the matrix $PJ^{[1]}_{E_1}p^{-}1$ is stable. This can be done by examining if the matrix $PJ^{[1]}_{E1}P^{-}1$ is diagonally dominant in rows, since its diagonal elements are negative

$$h_1 = -(\lambda_h + \gamma - 3\delta i^*_h + abmi^*_v + \mu_N i^*_{nh}) \tag{2.35}$$

$$h_2 = -(\lambda_h + \nu - \alpha_v + \mu_N i^*_{nh} - \delta i^*_h) \tag{2.36}$$

$$h_3 = -(H_T + \mu_N i^*_{nh} - 2\delta i^*_h) \tag{2.37}$$

$$h_4 = -(\lambda_h - r\tau - \delta i^*_h) \tag{2.38}$$

$$h_5 = -(aci^*_h + aci^*_{nh} - \lambda_v) \tag{2.39}$$

Clearly, all values $h_1, h_2, h_3, h_4, h_5 < 0$ and so all the diagonals are negative. Thus from Lemma 2, the system has a local stability at the endemic equilibrium point.

3. Discussion

We propose a model with incidence of dynamics of malaria within human hosts and mosquito vectors in which the class of the non-drug compliant human hosts is incorporated into the system, which is the portion of the infective who do not take their drug or stop taking it as soon as they are feeling better. The class of the recovered human is refilled by the individuals who are educated to take their drug with proper follow-up and the infected individuals who comply to drug. The model was then reformulated in terms of the proportions of the classes of the respective populations. Model analyses were carried out. Disease-free and endemic equilibrium solution were obtained and their stability was analysed respectively.

It was established that for the unique solution of the system to approach the disease-free equilibrium solution exponentially and basic reproduction number, $R_0 < 1$, the disease-free equilibrium is locally asymptotically stable so that the disease always dies out, and if $R_0 > 1$, the disease-free equilibrium is unstable. We observe that in order to reduce the basic reproduction number below 1, intervention strategies need to be focused on treatment and reduction on the contact between mosquito vector and human host.

Since non-drug compliant human compartment increases the rate of spread of malaria in the society, there is need to increase the parameter r which reduces the number of non-drug compliant human compartment. There is also need for treated bed nets and insecticides that would reduce the mosquito population.

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