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Local Stability Analysis of Host-Vector Malaria Disease Model

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ABSTRACT

Many infectious diseases including malaria are preventable, yet it still poses a threat and thus remains endemic in many communities due to lack of appropriate, sufficient and timely control policies. Strategies for controlling the spread of infectious disease include a reduction in both infected populations via treatment and a possible reduction in the susceptible population through vaccination or sensitization. In this paper, we gleaned on some existing model and thus carry out a modification by incorporating a vector reduction parameter as a new control strategy. We determine the basic reproduction number of the modified model and also investigated the existence and stability of the disease-free equilibrium (DFE) points. We showed that the disease free equilibrium state is locally asymptotically stable if $R_o < 1$ and unstable if otherwise. This shows that if $R_o < 1$, malaria can be controlled in the population. Finally, numerical simulations of the model carried out using the fourth-order Runge-Kutta numerical scheme in Matlab shows that malaria can be eliminated in the shortest possible time

1. Introduction

Malaria is an infectious disease caused by protozoan of genius Plasmodium parasite and transmitted between humans through bites of female Anopheles mosquitoes. It remains one of the most prevalent and lethal human infections throughout the world. An estimated 40% of the world's population lives in malaria endemic areas with most recorded cases and deaths occurring in sub-Saharan Africa [1]. Children under the age of five and pregnant women are the most vulnerable to the severe forms of malaria. Each year 2-3 million children die from *Plasmodium falciparum* malaria and up to 500 million people throughout the world suffer from malaria clinical disease [2]. Four species of the parasite, namely: P. falciparum, P. vivax, P. ovale, and P. malariae infects human. The parasite requires two hosts to complete its life cycle - the vector female *Anopheles* mosquito and human. The bites/bloodmeals of infected mosquitoes are the mode of transmission of the parasite between the human hosts. The symptoms in an infected human include bouts of fever, headache, vomiting flu-like, anemia (destroying red blood cell) and malaria can kill by clogging the capillaries that carry blood to the brain (cerebral malaria) or other vital organs [3]. On the average the incubation period of Plasmodium falciparum is about 12 days in humans. Infection can be expressed in three ways. Prevalence of infection, or parasite rate, describes the proportion of the population harboring malaria parasites. Parasitaemia describes the density of parasites within a host, and is thought to be an important factor determining the severity of disease in humans [4]. Intensity of infection describes the number of separate infections received by a host as

different strains of parasites differ in their antigenic properties [5]. Thus, intensity is certainly important in determining the level of acquired immunity. It might also contribute to severity of disease [6], possibly by determining the probability of a human becoming infected with a virulent parasite strain.

In the recent years, global eradication and control efforts have led to a surge of activities leading to many studies and publications [7]. Control strategies and intervention program have been adopted worldwide. Some of which include the use of anti-malaria vaccines, insecticides-treated bed nets (ITNs), control of breeding environment, and biological control among others. These are largely used in malaria endemic countries especially those in Sub-Saharan Africa and have somewhat led to the reduction in the spread of the disease. The proportion of the population sleeping under an ITN increased from less than 2% in 2000 to an estimated 55% in 2015 (range: 50–58%). Ensuring access to ITNs has been critical to increasing the proportion of the population sleeping under an ITN. Nearly 500 million ITNs were delivered to countries in sub-Saharan Africa between 2013 and 2015, and the proportion of the population with access to an ITN increased to an estimated 67% in 2015 (range: 61–71%) [3].

1.1. Role of Mathematical Model

Mathematical models play a key role in the control of malaria. It is of great importance and tasking to review all types of models in one article. In this article a historical path has been considered, and an attempt is made to take into account some of those mathematical models, which are primarily focused on the transmission dynamics of the infection in the host and vector populations, using the epidemiological compartment modeling approach [8, 9]. [10] derived a model where humans move through multiple Susceptible Exposed-Infectious-Recovered (SEIR) stages, where a history is kept of previous infections. They include a sub model for the mosquito population with subdivisions for juveniles and adults. They used the steady state value for the adult mosquito population, from this sub model, as the input into their model for malaria transmission. In this paper, we modified the existing model of [11] by including a vector reduction parameter in order to determine its impact as a control measure for the spread of malaria.

1.2. Definition of Terms

Susceptible: The number of individuals who can be infected but have not yet contracted the malaria but may contract it when exposed to its mode of transmission

Infected: The number of individuals from susceptible compartment who have been infected of malaria.

Recovered: The number of individuals from infected and treated compartment who have recovered naturally or clinically and back to normal status of health.

Vaccination: The introduction of a vaccine or serum into a living organism to confer immunity

WHO: World Health Organization

R_o: The expected number of secondary cases produced by a single (typical) infection in a completely susceptible population

2. The Model Equation

We present here the model equations in [11] in term of actual population and their parameters

2.1. Model Equations in Proportion

$$\frac{dS_H}{dt} = \lambda_h N_H - \frac{abS_H I_V}{N_H} + \gamma R_H - \mu_h S_H - \alpha S_H \quad (1)$$

$$\frac{dI_H}{dt} = \frac{abS_H I_V}{N_H} - rI_H - \delta I_H - \mu_h I_H \quad (2)$$

$$\frac{dR_H}{dt} = rI_H - \gamma R_H - \mu_h R_H + \alpha S_H \quad (3)$$

$$\frac{dS_V}{dt} = \lambda_v N_V - \frac{acS_V I_H}{N_H} - \mu_v S_V \quad (4)$$

$$\frac{dI_V}{dt} = \frac{acS_V I_H}{N_H} - \mu_v I_V \quad (5)$$

2.2. Assumptions

The following assumptions are made in order to formulate the equations of the model:

a. The infected human host who recovered naturally having acquired some level of immunity are moved to the recovered class.
b. Mosquito never recovers from infection, as it is regulated by mortality of its individual.
c. Mosquitoes bite human host randomly (independent of their infective status).

We incorporated a vector reduction parameter *k* in the vector population. Thus, our emerging model equation is illustrated as follows:

$$\frac{dS_H}{dt} = \lambda_h N_H - \frac{abS_H I_V}{N_H} + \gamma R_H - \mu_h S_H - \alpha S_H \quad (6)$$

$$\frac{dI_H}{dt} = \frac{abS_H I_V}{N_H} - rI_H - \delta I_H - \mu_h I_H \quad (7)$$

$$\frac{dR_H}{dt} = rI_H - \gamma R_H - \mu_h R_H + \alpha S_H \quad (8)$$

$$\frac{dS_V}{dt} = \lambda_v N_V - \frac{acS_V I_H}{N_H} - \mu_v S_V - k_1 S_V \quad (9)$$

$$\frac{dI_V}{dt} = \frac{acS_V I_H}{N_H} - \mu_v I_V - k_2 I_V \quad (10)$$

The total population sizes N_H and N_V can be determined by $S_H + I_H + R_H = N_H$ and $S_V + I_V = N_V$ from the differential equations

$$\frac{dN_H}{dt} = (\lambda_h - \mu_h)N_H - \delta I_H \quad (11)$$

and

$$\frac{dN_V}{dt} = \lambda_v N_v - S_v(\mu_v + k_1) - I_v(\mu_v + k_2) \quad (12)$$

which are derived by adding Equation (6) – (8) for the human population and (9) – (10) for the mosquito vector population.

3. Analysis of the Model

In the model, the term $\frac{abS_H I_V}{N_H}$ denotes the rate at which the human hosts S_H get infected by infected mosquitoes I_V and $\frac{acS_V I_H}{N_H}$ refers to the rate at which the susceptible mosquitoes S_V are infected by infected human hosts I_H. Since it is easier to analyze our model in terms of proportions of quantities instead of actual proportions, we make the transformation $s_h = \frac{S_H}{N_H}$, $i_h = \frac{I_H}{N_H}$, $r_h = \frac{R_H}{N_H}$, $s_v = \frac{S_V}{N_V}$ and $i_v = \frac{I_V}{N_V}$ in the classes S_H, I_H, R_H, S_V and I_V in the population respectively and $m = \frac{N_V}{N_H}$. This is done by differentiating the fractions with respect to time t and simplifying as follows:

$$\begin{aligned}\frac{ds_h}{dt} &= \frac{1}{N_H}\left[\frac{dS_H}{dt} - s_h\frac{dN_H}{dt}\right]\\ &= \lambda_h - abms_h i_v + \gamma r_h - \mu_h s_h - \alpha s_h - s_h\left[(\lambda_h - \mu_h) - \delta i_h\right]\\ &= \lambda_h - abms_h i_v + \gamma r_h - \alpha s_h - \lambda_h s_h + \delta s_h i_h\\ &= \lambda_h(1 - s_h) - abms_h i_v + \gamma r_h - \alpha s_h + \delta s_h i_h \end{aligned} \quad (13)$$

$$\begin{aligned}\frac{di_h}{dt} &= \frac{1}{N_H}\left[\frac{dI_H}{dt} - i_h\frac{dN_H}{dt}\right]\\ &= abms_h i_v - ri_h - \delta_h i_{h-}\mu_h i_h - i_h\left[(\lambda_h - \mu_h) - \delta i_h\right]\\ &= abms_h i_v - ri_h - \delta_h i_{h-}\lambda_h i_h + \delta i_h^2\\ &= abms_h i_v - (r + \delta + \lambda_h)i_h + \delta i_h^2 \end{aligned} \quad (14)$$

Similarly,

$$\frac{dr_h}{dt} = ri_h - (\gamma + \lambda_h)r_h + \alpha s_h + r_h\delta i_h \quad (15)$$

$$\frac{ds_v}{dt} = (1 - s_v)[\lambda_v - s_v(\mu_v + k_1)] - s_v[aci_h + i_v(\mu_v + k_2)] \quad (16)$$

$$\frac{di_v}{dt} = s_v[aci_h + i_v(\mu_v + k_1)] + i_v[(\mu_v + k_2)(i_v - 1) - \lambda_v] \quad (17)$$

subject to the restriction $s_h + i_h + r_h = 1$ and $s_v + i_v = 1$, we note that the population sizes $N_H(t)$ and $N_V(t)$ do not appear in the system. Therefore, using the relations $r_h = 1 - s_h - i_h$ and $s_v = 1 - i_v$ lead to studying the system of differential equations.

$$\frac{ds_h}{dt} = \lambda_h(1 - s_h) - abms_h i_v + \gamma(1 - s_h - i_h) - \alpha s_h + \delta s_h i_h \quad (18)$$

$$\frac{di_h}{dt} = abms_h i_v - (r + \delta + \lambda_h) i_h + \delta i_h^2 \quad (19)$$

$$\frac{di_v}{dt} = (1 - i_v)[aci_h + i_v(\mu_v + k_1)] + i_v[(\mu_v + k_2)(i_v - 1) - \lambda_v] \quad (20)$$

Now we intend to analyze and investigate the existence and stability of the associated equilibrium points. Assuming that all the parameters are non-negative, and solving for the equilibrium points by setting the right-hand sides of Equation (18) - (20) to zero, the system takes the form as shown:

$$\lambda_h(1 - s_h^*) - abms_h^* i_v^* + \gamma(1 - s_h^* - i_h^*) - \alpha s_h^* + \delta s_h^* i_h^* = 0 \quad (21)$$

$$abms_h^* i_v^* - (r + \delta + \lambda_h) i_h^* + \delta i_h^{*2} = 0 \quad (22)$$

$$(1 - i_v)[aci_h + i_v(\mu_v + k_1)] + i_v[(\mu_v + k_2)(i_v - 1) - \lambda_v] = 0 \quad (23)$$

In the absence of infection, $i_v = i_h = 0$, so that Equation (21) yields

$$\lambda_h - \lambda_h s_h^* + \gamma - \gamma s_h^* - \alpha s_h^* = 0$$
$$\lambda_h + \gamma = s_h^*(\lambda_h + \gamma + \alpha)$$
$$s_h^* = \frac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}$$

Hence the model has a steady state, E_0 called the disease-free equilibrium points, where

$$E_0 = \left(\frac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}, 0, 0\right)$$

3.1. Stability of the Disease Free Equilibrium Point

To establish the stability of this equilibrium, the Jacobian matrix of equations (21)–(23) is computed and evaluated at E_0.

Let $F_1 = \lambda_h(1 - s_h^*) - abms_h^* i_v^* + \gamma(1 - s_h^* - i_h^*) - \alpha s_h^* + \delta s_h^* i_h^*$

$F_2 = abms_h^* i_v^* - (r + \delta + \lambda_h) i_h^* + \delta i_h^{*2}$

$F_3 = (1 - i_v)[aci_h + i_v(\mu_v + k_1)] + i_v[(\mu_v + k_2)(i_v - 1) - \lambda_v]$

$$\frac{\partial F_1}{ds_h} = -\lambda_h - abmi_v^* - \gamma - \alpha + \delta i_h^* = -(\lambda_h + abmi_v^* + \gamma + \alpha - \delta i_h^*) \qquad \frac{\partial F_1}{di_h} = -\gamma + \delta s_h^* \quad \frac{\partial F_1}{di_v} = -abms_h^*$$

$$\frac{\partial F_2}{ds_h} = abmi_v^* \qquad \frac{\partial F_2}{di_h} = -r - \delta - \lambda_h + 2\delta i_h^* = -(r + \delta + \lambda_h) + 2\delta i_h^* \quad \frac{\partial F_2}{di_v} = abms_h^*$$

$$\frac{\partial F_3}{ds_h} = 0 \qquad \frac{\partial F_3}{di_h} = ac - aci_v^* \qquad \frac{\partial F_3}{di_v} = -(aci_h^* + \lambda_v) + (k_1 - k_2)(1 - 2i_v^*)$$

At the steady states of the model, the Jacobian matrix at *E* is given by

$$J_E = \begin{bmatrix} -\left(\lambda_h + abmi_v^* + \gamma + \alpha - \delta i_h^*\right) & -\gamma + \delta s_h^* & -abms_h^* \\ abmi_v^* & -Q_T + 2\delta i_h^* & abms_h^* \\ 0 & ac\left(1 - i_v^*\right) & -\left(aci_h^* + \lambda_v\right) + \left(k_1 - k_2\right)\left(1 - 2i_v^*\right) \end{bmatrix} \quad (24)$$

where $Q_T = \left(r + \delta + \lambda_h\right)$

Evaluating the Jacobian in Equation (24) at E_0 gives

$$J_{E_0} = \begin{bmatrix} -\left(\lambda_h + \gamma + \alpha\right) & -\gamma + \dfrac{\delta\lambda_h + \delta\gamma}{\lambda_h + \gamma + \alpha} & -abm\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right) \\ 0 & -Q_T & abm\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right) \\ 0 & ac & -\lambda_v + \left(k_1 - k_2\right) \end{bmatrix} \quad (25)$$

To get the eigenvalues, we obtain the characteristic equation
Thus,

$$\left|J_{E_O} - qI\right| = \begin{vmatrix} -\left(\lambda_h + \gamma + \alpha\right) - q & -\gamma + \dfrac{\delta\lambda_h + \delta\gamma}{\lambda_h + \gamma + \alpha} & -abm\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right) \\ 0 & -Q_T - q & abm\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right) \\ 0 & ac & -\lambda_v + \left(k_1 - k_2\right) - q \end{vmatrix} = 0 \quad (26)$$

$$= -\left(\lambda_h + \gamma + \alpha\right) - q \begin{vmatrix} -Q_T - q & abm\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right) \\ ac & -\lambda_v + \left(k_1 - k_2\right) - q \end{vmatrix} = 0$$

which yields

$$\left[-\left(\lambda_h + \gamma + \alpha\right) - q\right]\left[q^2 + \left[Q_T + \lambda_v - \left(k_1 - k_2\right)\right]q + Q_T\left[\lambda_v - \left(k_1 - k_2\right)\right] - \frac{a^2bcm\left(\lambda_h + \gamma\right)}{\lambda_h + \gamma + \alpha}\right] = 0 \quad (27)$$

The eigenvalues of the characteristic equation are given by

$$-\left(\lambda_h + \gamma + \alpha\right),$$

$$\frac{-\left[Q_T + \lambda_v - \left(k_1 - k_2\right)\right] \pm \sqrt{\left[Q_T + \lambda_v - \left(k_1 - k_2\right)\right]^2 - 4\left\{Q_T\left[\lambda_v - \left(k_1 - k_2\right)\right] - a^2bmc\,\dfrac{\left(\lambda_h + \gamma\right)}{\lambda_h + \gamma + \alpha}\right\}}}{2}$$

i.e $\quad -\left(\lambda_h + \gamma + \alpha\right), \ \dfrac{-\left[Q_T + \lambda_v - \left(k_1 - k_2\right)\right] \pm \sqrt{\left[Q_T + \lambda_V - \left(k_1 - k_2\right)\right]^2 - 4Q_T\left[\lambda_v - \left(k_1 - k_2\right)\right]\left(1 - R_O\right)}}{2}$

where, $R_o = \dfrac{a^2 bmc\left(\dfrac{\lambda_h + \gamma}{\lambda_h + \gamma + \alpha}\right)}{Q_T\left[\lambda_v - (k_1 - k_2)\right]}$, is called the basic reproduction number.

The eigenvalues are hereby analysed
i.e $q_1 = -(\lambda_h + \gamma + \alpha) < 0$

$$q_2 = \frac{-\left[Q_T + \lambda_v - (k_1 - k_2)\right] + \sqrt{\left[Q_T + \lambda_V - (k_1 - k_2)\right]^2 - 4Q_T\left[\lambda_v - (k_1 - k_2)\right](1 - R_O)}}{2}$$

$$q_3 = \frac{-\left[Q_T + \lambda_v - (k_1 - k_2)\right] - \sqrt{\left[Q_T + \lambda_V - (k_1 - k_2)\right]^2 - 4Q_T\left[\lambda_v - (k_1 - k_2)\right](1 - R_O)}}{2}.$$

If $1 - R_O > 0$, then $R_O < 1$ and

$$q_2 < \frac{-\left[Q_T + \lambda_v - (k_1 - k_2)\right]}{2} + \frac{\sqrt{\left[Q_T + \lambda_v - (k_1 - k_2)\right]^2}}{2} = 0$$

$$\text{and } q_3 < \frac{\left[Q_T + \lambda_v - (k_1 - k_2)\right]}{2} - \frac{\sqrt{\left[Q_T + \lambda_v - (k_1 - k_2)\right]^2}}{2} = -\left[Q_T + \lambda_v - (k_1 - k_2)\right]$$

Therefore, $q_2 < 0$ and $q_3 < 0$ thus establishing $q_1 < 0,\ q_2 < 0,\ q_3 < 0$

Using [12], the following theorem holds.

3.1. Theorem

Giving the system of equation in (21)–(23) and that $r, \delta, \lambda_h, \gamma, \lambda_v, k_1, k_2 > 0$ and $R_O < 1$, then the disease-free equilibrium state is locally and asymptotically stable.

4. Results and Discussion

Table 1. Parameter values and references

Experiment	Values				References
Parameters	1	2	3	4	
a	0.05	0.05	0.05	0.05	[8]
b	0.5	0.5	0.5	0.5	[8]
c	0.05	0.05	0.05	0.05	[8]
m	0.10	0.10	0.10	0.10	[1]
λ_h	0.02	0.02	0.02	0.02	[1]
δ	0.33	0.33	0.33	0.33	[9]
r	0.3	0.6	0.9	0.9	Assumed
λ_v	0.071	0.071	0.071	0.071	[8]
γ	0.140	0.140	0.140	0.140	[9]
α	0.3	0.6	0.9	0.9	Assumed
s_h	0.40	0.40	0.40	0.40	[1]
i_h	0.24	0.24	0.24	0.24	[1]
i_v	0.33	0.33	0.33	0.33	[8]
k_1, k_2	0.20, 0.23	0.20, 0.23	0.20, 0.23	0.20, 0.23	Assumed

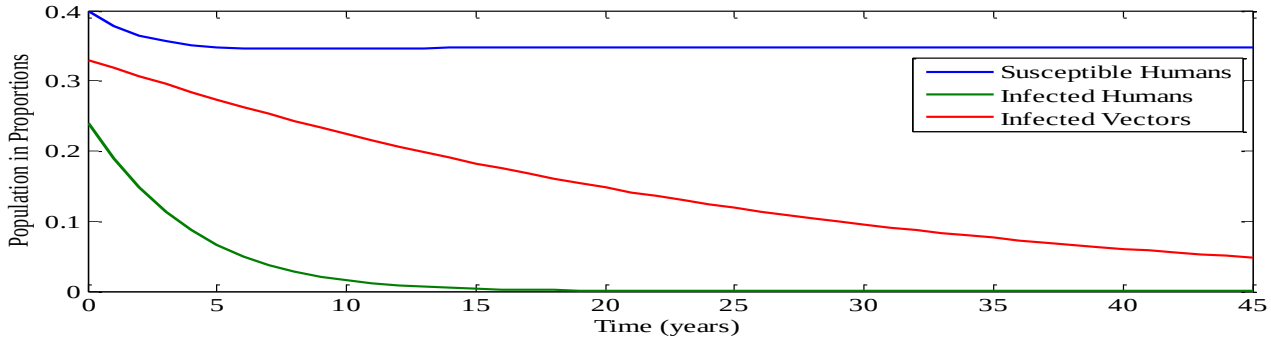

Figure 1: The behaviour of the model when $r = 0.3, \alpha = 0.3$ and $k_1 = 0.20, k_2 = 0.23$

The effect of implementing treatment and vaccination at 30% is shown in Figure 1 with vector control fixed at 20% and 23%. While treatment and vaccination reduces the proportion of susceptible humans we see that the disease is quickly eradicated from the population. We see clearly in Figure 2 that increasing treatment and vaccination rates to 60% significantly reduces the susceptible and infected humans. And a further increase to 90% improves the trend. On the hand, vector control parameter k_1 and k_2 $(k_1 \neq k_2)$ results enhances the pace at which the vector population is eradicated. In particular, when $k_1 < k_2$, the infected vector will continue to reduce as the time progresses. We also see in Figure 2 and Figure 3 that as intervention are increasing deployed, an equilibrium is established in population of the susceptible humans and infected vectors at least once.

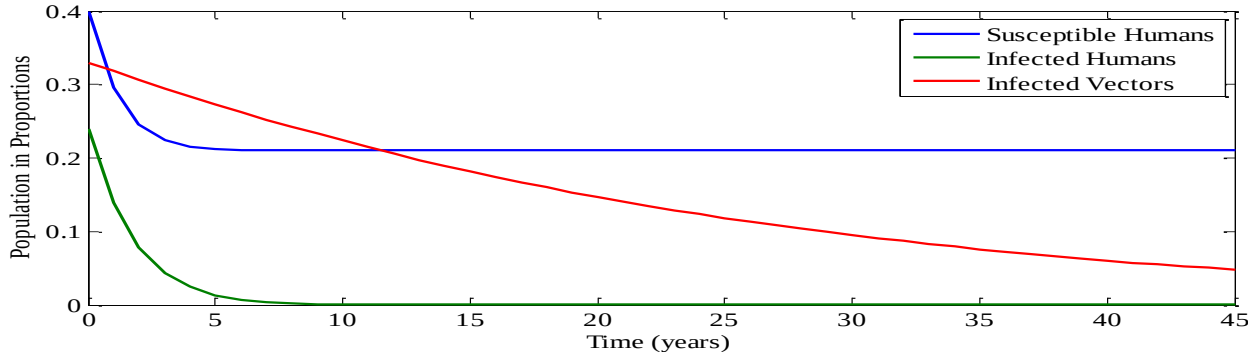

Figure 2: The behaviour of the model when $r = 0.6, \alpha = 0.6$ and $k_1 = 0.20, k_2 = 0.23$

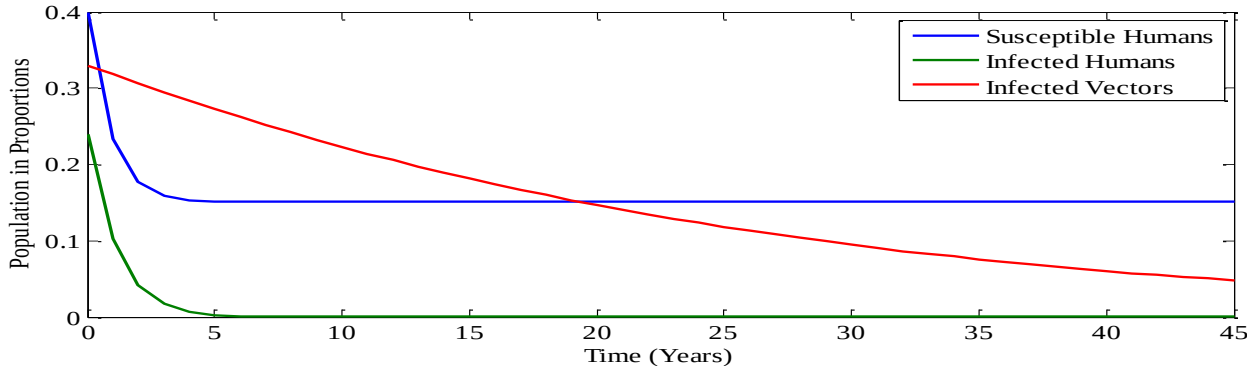

Figure 3: The behaviour of the model when $r = 0.9, \alpha = 0.9$ and $k_1 = 0.20, k_2 = 0.23$

But, when the vector control parameter is suspended as indicated in Figure 4, we see an almost insignificant impact in the rate at which the infected vector is reduced, even though, the treatment and vaccination rates are very high.

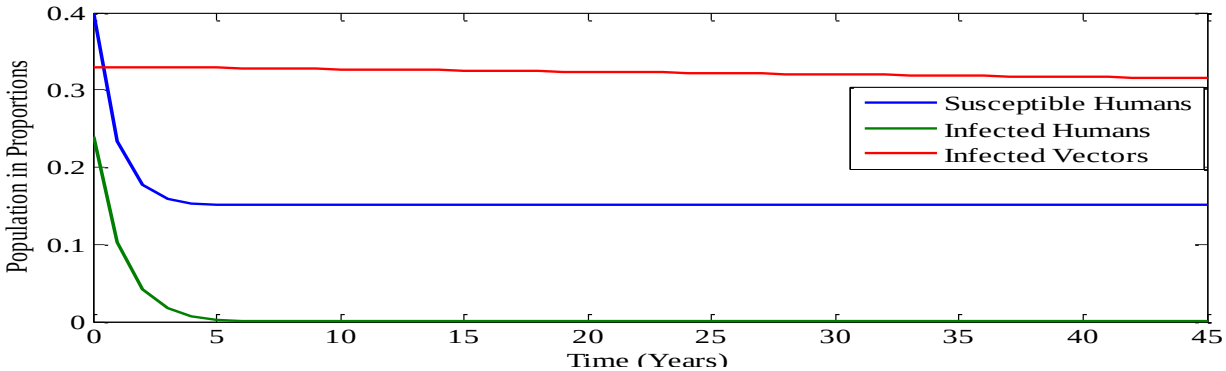

Figure 4: The behaviour of the model when $r = 0.9, \alpha = 0.9$ and $k_1 = 0, k_2 = 0$

4. Conclusion

The host – vector malaria disease model in [11] was modified by including a vector reduction parameter for the dynamics of malaria within human host and mosquito vectors. The model was analyzed in terms of proportion of quantities. The model's basic reproduction number was determined. The stability of the equilibrium point obtained by method of linearization were analyzed and found to be locally asymptotically stable and otherwise if $1 - R_O > 0$. From the result of our simulations, it was observed that treatment and vaccination as a way of controlling the menace of the disease in the human population is quite insufficient but with the combined effect of treatment, vaccination and vector-population reduction as an additional strategy, malaria can be eliminated in the shortest possible time.

Nomenclature

$S_H(t)$	Number of susceptible human hosts at time t
$I_H(t)$	Number of infected human hosts at time t
$R_H(t)$	Number of partially immune human host at time t
$S_V(t)$	Number of susceptible mosquito vectors at time t
$I_V(t)$	Number of infected mosquito vectors at time t
$m = \frac{N_V}{N_H}$	Number of female mosquitoes per human host
a	Average biting rate on man by a single mosquito (infection rate)
b	Proportion of bites on man that produce an infection
c	Probability that a mosquito become infectious
γ	Per capita rate of loss of immunity in human hosts
r	Rate at which human host acquire immunity
δ	Per capita death rate of infected human hosts due to the disease
v	Rate of recovery of human host from the disease
λ_h	Per capita natural birth rate of humans
λ_v	Per capita natural birth rate of the mosquitoes
μ_h	Per capita natural death rate of the humans
μ_v	Per capita natural death rate of the mosquitoes

k_1	Rate at which susceptible mosquitoes are killed
k_2	Rate at which infected mosquitoes are killed

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