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Modelling the role of prophylaxis in malaria prevention

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***Abstract*—**Malaria is by far the world's most persistent tropical parasitic disease and is endemic to tropical areas where the climatic and weather conditions allow continuous breeding of the mosquitoes that spread malaria. A mathematical model for the transmission of malaria with prophylaxis prevention is analyzed. The stability analysis of the equilibria is presented with the aim of finding threshold conditions under which malaria clears or persists in the human population. Our results suggest that eradication of mosquitoes and prophylaxis prevention can significantly reduce the malaria burden on the human population.

***Keywords*—**prophylaxis prevention, basic reproductive number, stability

I. Introduction

Infectious diseases such as malaria, AIDS and cholera continue to claim millions of lives around the world [1]. Global eradication programmes of these infectious diseases have been implemented for many years with some considerable success [2]. Malaria is by far the world's most persistent tropical parasitic disease, with annual estimates of clinical cases ranging from 300 to 500 million, with 86% being in Africa. In Southern Africa, out of an estimated population of 145 million, about 92 million people live in malarious areas [3]. Long term solutions to combating some of these diseases have eluded researchers, because some of these diseases have no cure. Malaria, an infection of the red blood cells caused by *Plasmodium*, is spread by the bite of an infected female anopheles mosquito and is endemic to tropical areas where the climatic and weather conditions allow continuous breeding of the mosquito. For instance, temperature influences anopheline mosquito feeding intervals, population density and the reproductive potential of the *Plasmodium* parasite [4]. There is no vaccine that can provide permanent immunity against malaria. However drugs can be taken in advance before entering a malaria high-risk area to prevent or reduce the possibility of infection. No drug therapy has been found to be completely effective in preventing the infection. Moreover the drug therapy depends on which type of malaria an individual has. Many factors have influenced the resurgence and spread of malaria in recent years. These include mosquito resistance to the usual insecticides, resistance of some parasite strains to the commonly used anti malaria drugs and economic factors that influence the financing of malaria control operations. Most malaria high-risk areas are located in developing countries where (a), the level of education in generally low and (b), drugs can be purchased without prescriptions. A combination of (a) and (b) generally results in maladministration of the drugs. In particular, Southern Africa is prone to malaria epidemics and the disease is a major cause of mortality with an estimated $200\ 000$ deaths occurring annually. Out of the approximated 139 million people living in Southern Africa, 63% live in malarious areas[5].

A number of studies modeling the effects of vaccination as a disease control mechanism have been carried out by many authors [6], [7], [8]. Kribs-Zaleta and Velasco-Hernandez [8] considered a simple vaccination model in which they found that vaccination may fail to achieve the desired objective of eradicating the epidemic. This conclusion is supported by Blower and Mclean [9] and by Hadeler and Castillo [10]. In these studies, the basic reproductive number, R_0, plays an important role in determining whether a disease can persist or clear in a population. If $R_0 < 1$ the disease can not invade the population and if $R_0 > 1$ invasion is always possible and in many cases ending up with the establishment of an endemic disease in steady state.

In a situation where, several strains of the malaria parasite exist, climate changes favor malaria transmission and drug resistance is common, we ask the question, "what is the role played by prophylaxis prevention in malaria control?" We ask a further question,"what is the effect of loss of immunity on the dynamics of the disease?" Particularily, we want to investigate how the use of preventive drugs affects the dynamics of the disease. The model presented in this paper is an SVIRS model with vectorial transmission. Studies of mathematical models of vector transmitted diseases, especially those involving diseases transmitted by mosquitoes, have been considered in [11], [12], [13]. We formulate a host-vector model that treats in a qualitative and quantitative manner the main features of the transmission process. We note that R_0 is a threshold parameter for the local stability of the disease free equilibrium point and we apply the center manifold theory to determine the existence and stability of the endemic equilibria near R_0.

This paper is arranged as follows; we give the model formulation in the Section II. The model analysis which includes a derivation of the basic reproduction number, stability analysis of the disease free equilibrium point and the endemic equilibrium point is given in Section III. Numerical results are given in Section IV and the discussion and conclusion is Section V.

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II. Model Formulation

The model consists of six ordinary differential equations which specify the rate of change of four categories of individuals in the human population and two categories of the vector population over time. The human population consists of a class susceptible individuals (S), a class of individuals under prophylaxis prevention (V), a class infected individuals (I) and a class of individuals who recover with temporary immunity (R), while the vector population consists of a class of susceptible mosquitoes (S_v) and a class of infected mosquitoes (I_v).

Suppose the human population N_H (where $N_H = S+V+I+R$) and the vector population N_v (where $N_v = S_v + I_v$) have constant mortality rates μ and ν respectively. The mortality rate of the vector population is a sum of the natural and induced (for example by the use of pesticides) mortality rates. A proportion ϵ of the population is under chemotherapy (i.e given malaria prevention drugs) while $(1-\epsilon)$ are not. Furthermore, therapy only reduces the probability of infection when exposed to pathogens, i.e it offers a degree of protection denoted ψ with $(1-\psi)$ measuring the protection failure of the therapy, so that $\psi = 0$ means the therapy is completely ineffective in preventing infection, while $\psi = 1$ means the therapy is very effective i.e no individual under therapy will be infected. We let β_1, β_2 and β_3 be the effective contacts between susceptible individuals and vectors, individuals under prophylaxis prevention and vectors and susceptible vectors and infected individuals respectively. The effective contact rate between the human and vector populations may be defined as the average number of contacts per given time that will lead to the infection of one population if the other population is infectious. It is taken to be the product of the number of bites per vector per host per unit time, the proportion of bites that lead to an infection and the ratio of the vector numbers to the host numbers [14]. Even though the human population under prophylaxis prevention can still be infected and become infections, it will be reasonable to assume that $\beta_1 > \beta_2$. The prophylaxis prevention immunity wanes at a rate θ and thus the average time of prevention is $\frac{1}{\theta}$. We assume a recovery rate γ for infected individuals who loose immunity at a rate σ. The dynamics of the disease is modelled by the following system of differential equations.

$$\begin{aligned}
\dot{S}(t) &= \mu(1-\epsilon)N_H - \mu S(t) - \beta_1 S(t)\frac{I_v(t)}{N_v} + \theta V(t) + \sigma R,\\
\dot{V}(t) &= \mu\epsilon N_H - (1-\psi)\beta_2 V(t)\frac{I_v(t)}{N_v} - (\mu+\theta)V(t)\\
\dot{I}(t) &= \beta_1 S(t)\frac{I_v(t)}{N_v} + (1-\psi)\beta_2 V(t)\frac{I_v(t)}{N_v} - (\gamma+\mu)I(t),\\
\dot{R}(t) &= \gamma I(t) - (\mu+\sigma)R(t) \qquad (1)\\
\dot{S}_v(t) &= \nu N_v - \nu S_v - \beta_3 S_v(t)\frac{I(t)}{N_H}\\
\dot{I}_v(t) &= \beta_3 S_v(t)\frac{I(t)}{N_H} - \nu I_v(t).
\end{aligned}$$

All parameters in the model are positive. Introducing the following fractions $s = \frac{S(t)}{N_H},\ v = \frac{V(t)}{N_H},\ i = \frac{I(t)}{N_H}$, $r = \frac{R(t)}{N_H},\ s_v = \frac{S_v(t)}{N_v}$ and $i_v = \frac{I_v(t)}{N_v}$ and using the relations $r = 1 - v - i - s$ and $s_v = 1 - i_v$ system (1) reduces to

$$\begin{aligned}
\dot{s} &= \pi - (\mu+\sigma)s - \beta_1 s i_v + (\theta-\sigma)v - \sigma i, \qquad (2)\\
\dot{v} &= \mu\epsilon - (1-\psi)\beta_2 v i_v - (\mu+\theta)v, \qquad (3)\\
\dot{i} &= \beta_1 s i_v + (1-\psi)\beta_2 v i_v - (\gamma+\mu)i, \qquad (4)\\
\dot{i}_v &= \beta_3 i(1-i_v) - \nu i_v. \qquad (5)
\end{aligned}$$

where $\pi = \mu(1-\epsilon) + \sigma$, in the region

$$\Omega = \{(s, v, i, i_v)|\ 0 \le s + v + i \le 1, 0 \le i_v \le 1\}.$$

The vector field of system (2) - (5) on the boundary of Ω does not point to the exterior of Ω, the solution of the system remains in Ω for all $t > 0$ and thus the problem is well posed and biologically meaningful. The disease free equilibrium, **DFE**, point for system (2) - (5) is given by $E_0 = (1-\phi, \phi, 0, 0)$ and is determined in Subsection III-B.

III. Model Analysis

A. The reproduction number

We arrange the equations of system (2) - (5)) beginning with the infectives and use the method given in [15] to determine the basic reproductive number. The method is a direct application of lemma 1 in [15]. The decomposition of the model into components $\mathcal{P}$ and $\mathcal{Q}$ leads to a system of the form $\dot{\mathcal{X}} = \mathcal{P} - \mathcal{Q}$ where

$$\mathcal{P} = \begin{pmatrix} \beta_1 s i_v + (1-\psi)\beta_2 v i_v \\ \beta_3 i(1-i_v) \\ 0 \\ 0 \end{pmatrix},$$

$$\mathcal{Q} = \begin{pmatrix} (\gamma+\mu)i \\ \nu i_v \\ \beta_1 s i_v + (\mu+\sigma)s + \sigma i - (\theta-\sigma)v - \pi \\ (1-\psi)\beta_2 v i_v + (\mu+\theta)v - \mu\epsilon \end{pmatrix}$$

and $\mathcal{X} = (i,\ i_v,\ s,\ v)^T$. Since the infected compartments are i and i_v, at the disease free equilibrium point we define

$$P = \left[\frac{\partial \mathcal{P}_i}{\partial x_j}\right] \text{ and } Q = \left[\frac{\partial \mathcal{Q}_i}{\partial x_j}\right] \text{ for } 1 \le i, j \le 2$$

giving

$$P = \begin{pmatrix} 0 & \beta_1(1-\phi) + (1-\psi)\beta_2\phi \\ \beta_3 & 0 \end{pmatrix}, \text{ and}$$

$$Q = \begin{pmatrix} (\gamma+\mu) & 0 \\ 0 & \nu \end{pmatrix} \text{ where } \phi = \frac{\mu\epsilon}{\mu+\theta}.$$

From this expression for ϕ, we note that $\phi = \frac{\mu\epsilon}{\mu+\theta} = \frac{\theta}{\mu+\theta}\frac{\mu\epsilon}{\theta}$. $\frac{\mu\epsilon}{\theta}$ represents the number of individuals successfully protected by chemoprevention with probability $\frac{\theta}{\mu+\theta}$.

Note that P is nonnegative, Q is a nonsingular M-matrix, its inverse, Q^{-1} is nonnegative and PQ^{-1} is nonnegative. According to [16], PQ^{-1} is the next generation matrix and R^0 is the spectral radius of PQ^{-1}. In this case, if

$$\mathcal{A} = PQ^{-1} = \begin{pmatrix} 0 & \frac{1}{\nu}(\beta_1(1-\phi) + (1-\psi)\beta_2\phi) \\ \frac{\beta_3}{\mu+\gamma} & 0 \end{pmatrix}$$

then, the eigenvalues of $\mathcal{A}$ are given by

$$\lambda_{1,2} = \pm\sqrt{\frac{\beta_3(\beta_1(1-\phi) + (1-\psi)\beta_2\phi)}{\nu(\gamma+\mu)}}.$$

Hence the effective reproductive number is given by

$$R = \sqrt{\frac{\beta_3(\beta_1(1-\phi)+(1-\psi)\beta_2\phi)}{\nu(\gamma+\mu)}} = \sqrt{R_v \cdot R_h},$$

where $R_v = \frac{\beta_3}{\nu}$, and

$$R_h = (1-\phi)R_1 + \phi(1-\psi)R_2,$$

with $R_1 = \frac{\beta_1}{\mu+\gamma}$ and $R_2 = \frac{\beta_2}{\mu+\gamma}$.

The geometric mean of the product R_vR_h, defines the mean number of secondary cases generated by a single case of an infection by an infectious mosquito or human being during their infectious period, in a susceptible population in which prophylaxis prevention is in use. Close to the **DFE** point, each infected vector produces R_h newly infected individuals over its expected infectious period and each infected individuals produces R_v newly infected mosquitoes during the period of infectiousness. The reproduction number with a square root is due to the two generations required for an infection to be reproduced [15]. The two terms of R_h measure the influence of individuals not under prophylaxis prevention and those under prophylaxis prevention respectively.

By setting $R = 1$, the critical prophylaxis prevention coverage ϵ^* that would be required to contain malaria can be calculated. The case $\beta_1 = \beta_2$ gives

$$R_vR_h = R_0\left(1-\epsilon\beta\right)$$

where $\beta = \frac{\mu\psi}{\mu+\theta}$, $R_0 = R_vR_1$.

Here $R_0 = R_vR_1$ is the basic reproduction number, i.e the number of new infection cases that result from a single case of an infection in a population that is wholly susceptible when no intervention is in place. We note that β is the impact or efficacy of the vaccine and for the human population, the critical prophylaxis prevention coverage, ϵ^* is given by

$$\epsilon^* = \frac{1}{\beta}\left(1-\frac{1}{R_0}\right). \tag{6}$$

For the case where $\beta_1 \neq \beta_2$, the critical prophylaxis prevention coverage is given by

$$\epsilon_* = \frac{\mu+\theta}{\mu}\left(\frac{1-R_0}{(1-\psi)R_m - R_0}\right) \tag{7}$$

where $R_m = R_vR_2$. The expression (7) collapses to (6) for $\beta_1 = \beta_2$.

To investigate the impact of taking prophylactic vaccines on the permanence of the malaria infection, we consider a limiting case $\psi \to 1$. We note that

$$\lim_{\psi\to 1} R_hR_v = (1-\phi)R_0.$$

We also note that,

$$\frac{\partial R_h}{\partial \psi} < 0.$$

This means that R_h is a decreasing function of ψ and consequently as ψ increases, R decrease. This means that as the protection against malaria improves, the number of secondary infections decreases. In developing countries, governments and non-governmental organisations have been distributing chemically treated mosquito nets in order to increase the level of protection.

In the absence of intervention i.e when $\phi = 0$, we have $R_hR_v = R_0$. A comparison of R_hR_v and R_0 results in the following lemma;

Lemma 1: $R_0 > R_vR_h$ whenever $\psi^* > \left(1-\frac{\beta_2}{\beta_1}\right)$.
We omit the proof of the proposition, which can easily be established.

Remark: ψ^* is thus a threshold parameter, because for intervention to have an impact on the control of malaria, ψ must exceed the ratio $\frac{\beta_1-\beta_2}{\beta_1}$. This ratio is important to public health intervention programs. It sets the minimum value for the degree of protection that a therapy should achieve for an intervention to be effective. We shall now assume that this condition is satisfied in our analysis of the equilibrium point.

B. Disease free equilibrium point

From equations (2), (3) and (5), the equilibrium points must satisfy the following relations in terms of i:

$$i_v = \frac{R_vi}{1+R_vi} \tag{8}$$

$$v = \phi\frac{1+R_vi}{1+\mathcal{U}R_vi} \tag{9}$$

$$s = \frac{(\alpha_1+\alpha_2i+\alpha_3i^2)(1+R_vi)}{(\sigma+\mu)(1+\mathcal{U}R_vi)(1+\mathcal{T}R_vi)} \tag{10}$$

where $\mathcal{U} = 1+\frac{(1-\psi)\beta_2}{\mu+\theta}$, $\mathcal{T} = 1+\frac{\beta_1}{\mu+\sigma}$ and $\alpha_1 = (\mu+\sigma)(1-\phi)$,
$\alpha_2 = (\mu+\sigma)(1-\phi)R_v + \frac{\pi(1-\psi)\beta_2}{(\mu+\theta)}R_v - \sigma$ and $\alpha_3 = -\sigma\mathcal{U}R_v$.
Substituting equations (8), (9) and (10) into (4) and equating to zero, we get $i = 0$ and the quadratic equation

$$F(i) = Ai^2 + Bi + C = 0, \tag{11}$$

where

$$A = -R_v^2\mathcal{U}[\beta_1(\mu+\gamma+\sigma) + (\mu+\gamma)(\mu+\sigma)],$$

$$B = R_v\left[C + \mathcal{U}A + \frac{(\mu+\gamma)(\mu+\sigma)}{\mu+\theta}(1-\psi)\beta_2\left(R_0-1\right)\right],$$

$$C = (\mu+\gamma)(\mu+\sigma)(R-1).$$

Taking $i = 0$ and substituting into (8), (9) and (10) gives the disease free equilibrium point

$$E_0 = (1-\phi, \phi, 0, 0).$$

The case $i \neq 0$ is considered in the next section .

Theorem 1: If $R < 1$, then the **DFE** point, E_0 is locally asymptotically stable in Ω, and unstable for $R > 1$.

Proof: The Jacobian of system (2) - (5) at E_0 has two eigenvalues $l_1 = -(\mu+\sigma)$, $l_2 = -(\mu+\theta)$ and the other two have negative real parts if and only if $R < 1$. Thus the **DFE** point is locally asymptotically stable if $R < 1$ and unstable if $R > 1$. ■

C. The endemic equilibria

A solution i, of (11) corresponds to an endemic equilibrium solution. From (11) it is easy to observe that $A < 0$,

$$C \begin{cases} < 0 & \text{if} \quad R < 1 \\ > 0 & \text{if} \quad R > 1 \end{cases} \quad \text{and} \quad B < 0 \text{ if } R < 1, \ R_0 < 1.$$

Equation (11) has multiple solutions that depend on the parameter values chosen. So, the model has multiple equilibria of coexistence. We draw the following results on the existence of multiple endemic equilibria:

Theorem 2: (a) System (2) - (5) has only one positive equilibrium point if $R > 1$.

(b) If $R < 1$ and $B > 0$ then system (2) - (5) has two positive equilibrium solutions.

(c) If $R < 1$ and $R_0 < 1$, then no positive equilibria exist for system (2) - (5).

Result (b) of the above theorem, suggests the coexistence of the endemic equilibrium point and the disease free equilibrium point, a phenomena known as backward bifurcation.

For $\psi = 1$, we note that $\mathcal{U} = 1$, $\alpha_2 = (\mu+\sigma)(1-\phi)R_v - \sigma$, $\alpha_3 = -\sigma R_v$ and $R_h = (1-\phi)R_1 = \Re$. The system has a unique stable endemic equilibrium whenever $\Re > 1$ given by, $E_1(s^*, v^*, i^*, I_v^*)$, where

$$\begin{aligned} v^* &= \phi \\ i^* &= \eta(\Re - 1), \\ &\quad \text{for } \eta = \frac{(\mu+\gamma)(\mu+\sigma)}{R_v[(\mu+\gamma)(\mu+\sigma) + \beta_1(\mu+\sigma+\gamma)]}, \\ i_v^* &= \frac{R_v i^*}{1 + R_v i^*} \\ s^* &= \frac{(\mu+\sigma)(1-\phi) - \sigma i^*}{\mu + \sigma + \beta_1 i_v^*.} \end{aligned}$$

IV. Numerical Results

In the previous section, the qualitative analysis of the model is presented. The conditions for local and global stability are presented. We now consider numerical results for the model using Matlab and Mathematica.

Malaria is a major cause of mortality if Southern Africa and the burden is greatest among children under the age of five years and pregnant women [3]. Between 10 million and 37 million confirmed cases of malaria occur annually. It is estimated that up to 200 000 malaria deaths occur annually in Southern Africa, with the following estimated percentage distributions in Table I [5].

Country	% distribution	Country	% distribution
Angola	16.4	South Africa	0.2
Botswana	0.1	Swaziland	0.1
Malawi	14.7	Tanzania	32.1
Mozambique	22.3	Zambia	9.3
Namibia	0.1	Zimbabwe	4.6

TABLE I
ESTIMATED DISTRIBUTION OF MALARIA DEATHS IN SOUTHERN AFRICA.

In Southern Africa the human life span is taken to be 14 600 days (40 years) so that $\mu = 0.025$ [17]. The vectors life span is taken to be $2-3$ weeks giving $0.04 \leq \nu \leq 0.06$ years [18]. These values represent the natural death rate of the mosquitoes. It is however apparent that in reality ν is higher that these values and difficult to measure. For the purpose of these simulations we shall consider $\nu \geq 0.06$. The incidence of confirmed malaria cases is between 73 and 266 per 1000 individuals per annum. The death rate due to malaria can be calculated to be 0.0014 [5]. The period of prophylaxis prevention is estimated to be 15-37 days and the duration of protection of temporary immunity is estimated to be 28 days [19]. It is important to note that many of the model parameters are difficult to estimate but indirect parameter estimates can be obtained from the estimates of the quantities that are measured directly. For example, the rate of recovery of infected individuals can be obtained from the confirmed malaria cases and the estimates of deaths. The rate of recovery per annum γ is thus calculated to be approximately 0.98. The effective contact rate of humans to vectors is 0.375 and from vectors to humans is 0.75 [20]. Some authors assume a transmission rate from humans to vectors of about 0.4167 [14]. The parameter values for the model are listed in Table II.

Parameter	Approx. values/year	Parameter	Approx. values/year
ϵ	$0 < \epsilon < 1$	μ	0.0264
ψ	$0 \leq \psi \leq 1$	γ	0.98
β_1	$\beta_1 > 0.375$	θ	$0.04 \leq \theta \leq 0.1$
β_2	$\beta_2 < 0.3$	ν	$\nu \geq 0.06$
β_3	0.75	σ	0.08

TABLE II
PARAMETER VALUES

The following initial conditions are assumed for the proportions; $s(0) = 0.6$, $v(0) = 0.2$, $i(0) = 0.1$ and $z(0) = 0.1$ in our simulations. Simulations were run for different sets of initial conditions and the qualitative form of the solutions were similar.

We begin by looking at the prevalence curve for the human population for the parameter values given in the caption of Figure 1. In this case the vector population plays an important role in the overall disease transmission as seen from the value of the reproduction number R_v. A decrease in the contribution of the vector to the overall transmission of malaria leads to a decrease in the prevalence of malaria. The implications of a declining prevalence are related to the eradication of malaria. The waning duration of a prophylaxis is of great importance in disease prevention. If it is short, then the desired results are likely not to be achieved. If the it is long then individuals are assured of protection for longer periods. Below is a graph showing the corresponding long tern evolution of the prevalence curves for changing values of θ. We note that increasing the values of θ leads to an increase in the reproduction number. For the given values of θ it the table, increasing θ implies reduced duration of protection.

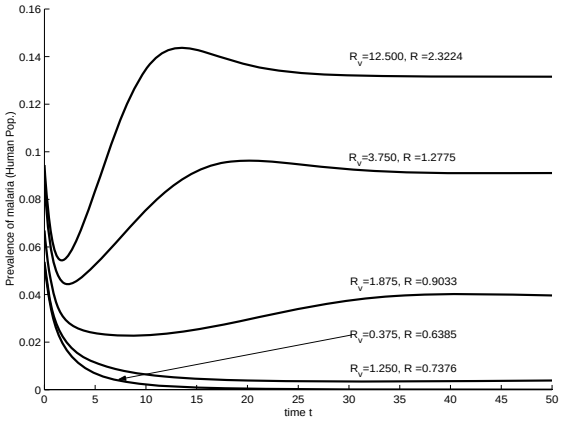

Fig. 1. The evolution of prevalence for the human population over time for the following parameter values, $\pi = 0.2,\ \mu = 0.0264,\ \sigma = 0.08,\ \theta = 0.06,\ \epsilon = 0.2,\ \psi = 0.5,\ \gamma = 0.98,\ \beta_1 = 0.46,\ \beta_2 = 0.2,\ \beta_3 = 0.75$ and $R_h = 0.4352$.

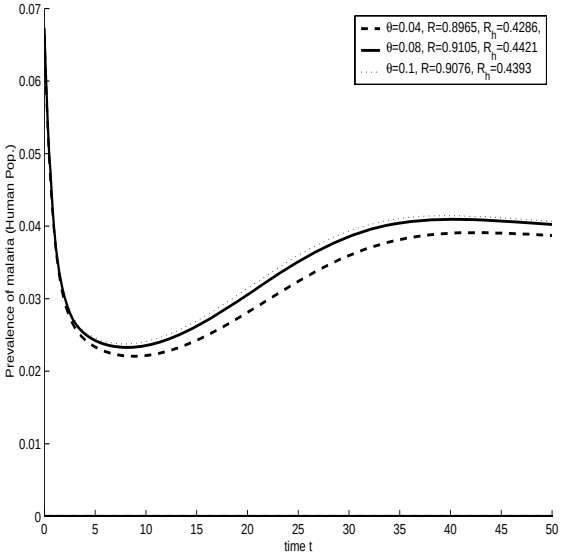

Fig. 2. The evolution of prevalence for the human population over time for the following parameter values, $\pi = 0.2,\ \mu = 0.0264,\ \sigma = 0.08,\ \nu = 0.4,\ \epsilon = 0.2,\ \psi = 0.5,\ \gamma = 0.98,\ \beta_1 = 0.46,\ \beta_2 = 0.2,\ \beta_3 = 0.75$ and $R_v = 1.8750$.

We noted that $\dfrac{\partial R_h}{\partial \psi} < 0$. Consequently, as ψ increases R decreases. The result is supported numerically by the graph below.

V. Conclusion

Presented in this paper is the influence of prophylaxis prevention in the spread of malaria. prophylaxis prevention is meant to reduce susceptibility to infection and like vaccines, it is characterized by two important parameters given in the model: the the degree of protection ψ and the waning period θ. The model presented in this paper is perhaps the simplest caricature possible of a prophylaxis prevention

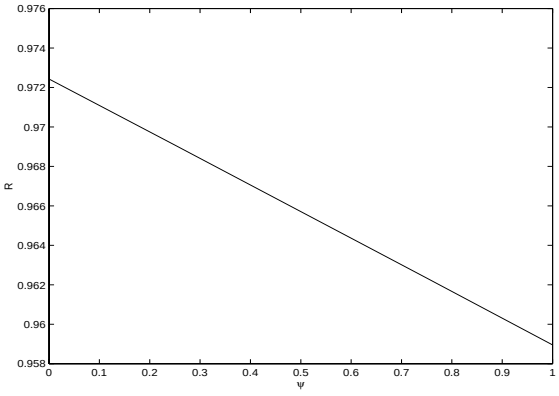

Fig. 3. The relationship between ψ and the reproduction number R for the following parameter values, $\pi = 0.2,\ \mu = 0.0264,\ \sigma = 0.08,\ \theta = 0.06,\ \epsilon = 0.2,\ \gamma = 0.98,\ \beta_1 = 0.46,\ \beta_2 = 0.2,\ \beta_3 = 0.75,\ \nu = 0.35$

program applied to a general population. The results show that prophylaxis are capable of reducing malaria epidemics if issues related to drug/pesticides resistance are seriously taken into consideration. Models that look into the issues of drug resistance were considered in [21].

The model analysis included the determination of equilibrium points and carrying out their stability analysis in terms of the preventive therapy reproduction number R. We note that R is a product of two terms R_v and R_h. From the expression

$$R = (1 - \phi)R_0 + (1 - \psi)\phi R_m,$$

ϕ is the probability that an individual is successfully protected by chemoprevention, R_0 is the mean number of secondary cases of malaria produced by a single case of infection in a population that is wholly susceptible with no chemoprevention intervention in place. R_m is the mean number of secondary cases of malaria that are produced by an individual who is successfully protected by prophylaxis preventionand becomes infected during his or her life time.

This work can provide insights into several aspects of the malaria control. It is important to acknowledge that the dynamics of malaria transmission are not simple. Malaria transmission in Southern Africa has been affected by funding and service delivery, political instability (the cases of Mozambique, Angola and the Democratic Republic of Congo), poverty, drug and insecticide resistance. The evolution of these biological and social systems is complex, making it impossible for mathematical models to provide accurate predictions of the disease dynamics. They can however be used to forecast, but only in fairly gross terms. Modelling should be an integral part of any disease control program and the model system should be easy to use and can beadapted to new results and changes in control policies [22].

Vector control plays a central role in the control of malaria. Problems specific to vector control are insecticide resistance, species identification and control strategy choices. Overall,

mathematical models can assist in determining control strategies with large impacts on outcomes and can provide comprehensive evaluation of model assumptions that influence decisions.

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