Research Proposal

Ziyabukwa Mthi (24863831@sun.ac.za)

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Introduction

Malaria is a blood parasite caused by an essential intracellular protozoan parasite of the malaria protozoan species transmitted by infected female anoferin mosquitoes. Among the five species of Plasmodium vivax that cause malaria, Plasmodium vivax and Plasmodium falciparum are widespread around the world [1]. Despite promising efforts to reduce malaria-related mortality and morbidity, malaria is the third leading cause of death among infectious diseases, after HIV/AIDS and tuberculosis. Therefore, malaria remains recognized as one of the existing health threats, causing significant amounts of mortality, morbidity, and financial burden, exacerbating problems in all of sub-Saharan Africa. It is affecting the area [2].

Malaria has historically been a serious human public health issue, and it is still a significant cause of enormous mortality and morbidity worldwide [3]. Malaria occurs mainly in the poor tropical and subtropical regions of the world (sub-Saharan Africa). The burden of malaria has increased in Africa. The reasons for this increase were resistance to commonly used antimalarial drugs, progressively worse primary health care in many areas, and new resistance of mosquitoes to pesticides used for vector control [4]. Although malaria can be a deadly disease, illness and death from malaria can be prevented and it is curable through treatment and vaccination.

In many malaria-affected countries, malaria is a major cause of illness and death. The most vulnerable groups in high-incidence areas are infants who are not yet immune to malaria and pregnant women whose immunity is weakened by pregnancy. The cost of malaria for individuals, families, communities and countries is enormous[5]. In general, severe or complex malaria is the focus of epidemiological studies as it is the leading cause of malaria-related deaths. Malaria remains a globally important disease with 241 million malaria cases and 627 000 malaria deaths worldwide in 2020. This is equivalent to an increase of approximately 14 million cases and 69,000 deaths in 2020 compared to 2019 [6]. Malaria is a imposes substantial costs to both individuals and governments which include social, economic and health burden. Throughout Africa, millions of people still lack access to the tools they need to prevent and treat their diseases [7].

Malaria has long been recognized as a global problem, and many epidemiologists and other scientists are focused on understanding the dynamics of malaria and controlling its transmission. From these interactions with scientists, mathematicians are an important and effective tool for the interaction between host and vector populations, malaria dynamics, control of malaria infection, and ultimately eradication there [8]. Mathematical modeling is a useful method for understanding of how infectious diseases spread through a population. The possible course of an outbreak and procedures to contain an epidemic can also be anticipated using this type of modeling.

We have developed a mathematical model of malaria that provides insights. Numerous epidemiological models have been mathematically formulated. In this study, we look at an SEIR malaria model that combines treatment and vaccination strategies and covers both human and vector populations. The goal is to gain insight into the best interventions to reduce malaria disease transmission within the population and to study the effects of various intervention options, such as vaccination and treatment. The important dynamics are taken into account in this model. We will estimate the character of the vaccination compartment with time using the first-order non-linear equation.

Mathematical Model

Model formulation

Consider SEIR epidemic model, where the compartmental model divides the total human host population, denoted by N_h into four compartments related to the epidemic, the susceptible (S_h), the exposed (E_h), the infectious (I_h) and the recovered (R_h). We formulate the problem based on the SEIR model with vital dynamics and study the effect of Vaccination and epidemiological factors related to it. The individuals in the (Sh) compartment are those who are vulnerable to become infected. An individual is in the (Eh) compartment are exposed to malaria parasites and the individuals in this compartment are not able to spread the disease (a compartment in which the disease is latent; infected but not infectious). Infectious individuals are in the (Ih) compartment and the immune individuals are in the (Rh) compartment. In malaria, there is no possibility of lifelong immunity after recovering from it, despite that the antibodies are developed and during active antibodies, it remains in the recovered compartment for a restricted period and then flows back to the susceptible compartment. We assume that vaccination will give life-long immunity either in one dose or with periodic boosters. The population which does not receive vaccination after recovering shall flow back in the compartment of susceptible S at a rate ρ after completing the recovery period λ^{-1}. The reciprocals ϵ^{-1}, average disease incubation period, and μ^{-1} are average natural deaths. Λ^{-1} and μ^{-1} describe a model with vital dynamics (endemic model), which has an inflow of births into the class Sh at a rate Λ^{-1} and outflow of deceased μ^{-1} S. This model is based on the assumptions proposed by Hethcote; the population size is constant and large enough so that we can consider the population of each compartment as a continuous model. The birth and death rates are equal and the population (fixed) is homogeneously mixed and uniform. The governing differential equations are:

$$\begin{aligned}
\frac{dS_h}{dt} &= \Lambda_h - \beta_h S_h I_v - (\mu_h + \alpha) S_h + \sigma E_h + \rho R_h \\
\frac{dE_h}{dt} &= \beta_h S_h I_v - (\mu_h + \sigma + \epsilon) E_h + \lambda V_h \\
\frac{dI_h}{dt} &= \epsilon E_h - (\delta + \mu_h + \gamma) I_h \\
\frac{dR_h}{dt} &= \gamma I_h - (\mu_h + \rho) R_h \\
\frac{dV_h}{dt} &= \alpha S_h - (\mu_h + \lambda) V_h
\end{aligned}$$

Let S_h(t), V_h(t), E_h(t), I_h(t) and R_h(t) represent the number of individuals in the corresponding compartment at the time t, respectively. Thus, the total population at time t is denoted as N_h(t) satisfying:

$$N_h(t) = S_h(t) + V_h(t) + E_h(t) + I_h(t) + R_h(t)$$

The total vector population, denoted by N_v is divided into three compartment, the susceptible (S_v), the exposed (Ev) and the infectious (I_v). In (S_v) compartment are susceptible mosquitoes. The mosquitoes that are exposed in malaria parasite are in (E_v) compartment. The vector population model is given by the following system of ordinary differential equations:

$$\begin{aligned}
\frac{dS_v}{dt} &= \Lambda_v - \beta_v S_v I_h - \mu S_v \\
\frac{dE_h}{dt} &= \beta_v S_v I_h - (\mu + \omega) E_h \\
\frac{dI_h}{dt} &= \omega E - \mu I_v
\end{aligned}$$

Infected mosquitoes are in (I_v) compartment. The total vector population at time t is denoted as N_v(t) satisfying:

$$N_v(t) = S_v(t) + E_h(t) + I_h(t)$$

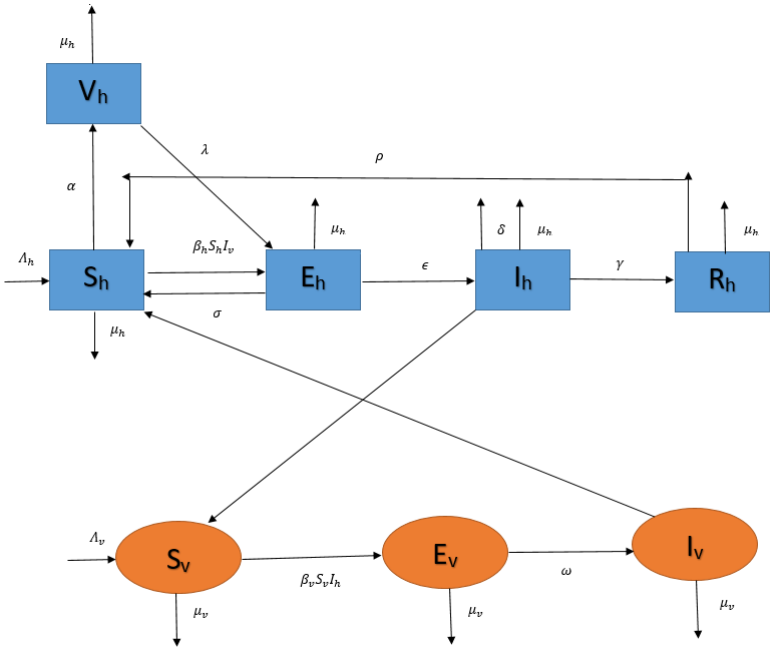

Figure 1: A schematic diagram for malaria transmission

Susceptible individuals are recruited at a rate Λ_h. Susceptible individuals acquire malaria through contact with infectious mosquitoes at a rate β_h. The rate of vaccination is α to the individuals present in Susceptible. The rate of inflow into susceptible from the exposed compartment is σ. Due to waning effect, some vaccinated individuals will move to the exposed class at a rate λ. Exposed individuals move to the infectious class at a rate ϵ. Individuals with malaria are treated under control, and are recovered spontaneously at rate γ. Loss of immunity for humans is ρ.

Susceptible mosquitoes are generated at a rate Λ_v and acquire malaria through contacts with infected humans at a rate β_v. Developing ω rate of exposed (mosquitoes) becoming infectious. Mosquitoes are assumed to suffer death due to natural causes and various control measures (insecticides, destruction of mosquitoes breeding sites, etc.) at a rate μ_v.

The vaccine will be administered to the susceptible individuals so that in addition to their natural immunity they can acquire vaccine-induced immunity too at rate δ. This epidemic disease model predicts a peak of susceptible, exposed, infected, and recovered including vaccinated individuals per day as a function of time. The μ is defined as the rate of mortality, which includes both natural and due to malaria.

Table 1: Parameter and Description for the model

Parameter	Description
Λ_h	Recruitment rate of humans
Λ_v	Recruitment rate of mosquitoes
μ_h	Natural death rate of humans
μ_v	Natural death rate of mosquitoes
β_h	Susceptible individuals acquire malaria through contact with infectious mosquitoes at a rate
β_v	Acquire malaria through contacts with infected humans at a rate
α	The rate of vaccination of individuals present in Susceptible
σ	The rate of inflow into susceptible from the exposed compartment
ρ	Loss of immunity for human
δ	Induce death rate of humans
ϵ	Developing rate of exposed (humans) becoming infectious
γ	Recover rate of humans.(removal rate)
λ	Vaccinated individuals will move to the exposed class
ω	Developing rate of exposed (mosquitoes) becoming infectious

Table 2: Parameter and Values for the model

Parameter	Values	References
Λ_h	0.00099	Mukandavireetal.(2009)
Λ_v	0.0089	Mukandavireetal.(2009)
μ_h	0.00004	Mukandavireetal.(2009)
μ_v	0.1429	Mukandavireetal.(2009)
β_h	0.03	Blayneh et al.(2009)
β_v	0.8333	Blayneh et al.(2009)
α	0.5	Assumed
σ	0.1	Assumed
ρ	0.7902	Nakul et al.(2006)
δ	0.25	Assumed
ϵ	1/17	Blayneh et al.(2009)
γ	0.00656	Mukandavireetal.(2009)
λ	0.6352	Assumed
ω	1/18	Nakul et al.(2006)

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