Article title: Mathematical Modelling of the Causes, Dynamic Transmission and Control of Malaria Disease
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DOI: 10.14293/PR2199.001252.v1
Preprint first posted online: 04 November 2024
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Mathematical Modelling of the Causes, Dynamic Transmission and Control of Malaria Disease

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Abstract

Malaria is an infectious disease caused by the Plasmodium parasite and spreads between humans via female Anopheles mosquito bites. A mathematical model describes the dynamics of malaria and human population compartments in the form of mathematical equations, which represent the relationships between the compartments' key attributes. The goal of this study id to identify the key parameters involved in the transmission and spread of the endemic malaria disease, as well as to try to discover acceptable solutions and techniques for the prevention and control using mathematical modelling. The malaria model is built on basic mathematical modelling approaches that result in a system of ordinary equations (ODEs). Our study examines the stability of the model's equilibrium points. We found that if the reproduction number R_0 is smaller the 1 ($R_0 < 1$) the disease-free equilibrium point is stable, resulting in disease extinction. If R_0 is greater than 1 ($R_0 > 1$), the disease-free equilibrium becomes unstable. In that situation, the endemic state has a distinct equilibrium, re-invasion is always possible, and the disease remains in the human population. We used the Newton-Raphson method to iterate and successfully find better approximations to the values of the compartments of both the human and vector populations of the model at the endemic equilibrium. Also numerical simulations were carried out using the numerical software Python. These simulations demonstrate the behavior of populations over time as well as the stability of disease-free and endemic equilibrium points.

Keywords: Malaria, Equilibrium Points, Numerical Simulation, Endemic model, Reproduction Number, Epidemiology, Endemic Equilibrium, Disease-Free Equilibrium, Stability, Eigenvalue.

Introduction

An infectious sickness called “malaria” is spread by mosquitoes and affects both humans and other monkey species. Malaria is a parasitic disease caused by plasmodium parasites that are spread by Anopheles mosquitos (Adeniyi, 2023). A fever, chills, sweats, headache, nausea, and vomiting are common signs and symptoms of malaria. Among the deadliest diseases in the world is malaria. Despite being highly treatable and preventive, malaria results in about 881,000 fatalities annually, with sub-Saharan Africa accounting for 85%of all malaria-related deaths (Kokwaro, 2009). This is the same as one child in Africa passing away from malaria every thirty seconds. The parasite Plasmodium falciparum causes the severe forms of the disease. In humans, malaria is caused by Plasmodium vivax, Plasmodium ovale, and Plasmodium malariae causes a milder version of the disease that is usually not fatal (Traore, 2020). According to reports from 2008, there were 109 nations where malaria was prevalent, 45 of which were on Africa. An estimated 228 million case of malaria in 2018 was gotten, with 86% of cases reported in African countries. Africa thereby shares 80% of the cases and 90% of the deaths (Aldila, 2021). Controlling malaria is difficult for a variety of reasons. Some of the challenges include the parasite’s resistance to anti-malaria medications, the cost of the control program. The intricacy of the disease control procedure, and insecticide-resistant vectors. The high prevalence of HIV infection exacerbates malaria cases by weakening the immune system and making HIV-positive individuals more vulnerable to malaria. (Gebremeskel, 2015).

Mathematical modelling of infectious diseases, as well as creative analytical studies and numerical simulations, have made great contributions to understanding disease dynamics and potential control approaches, It is very important for guiding policy and management decisions during disease outbreaks (Dwomoh, 2022). Poverty is a major contributing factor to the spread of malaria, and many at-risk groups reside in isolated, impoverished places (Mojeeb, 2019). In addition to living miles away from the closest medical facility, impoverished, rural families are the least likely to have access to these prophylactic treatments, which are essential to controlling malaria (Rezapour, 2023). As soon as an infection occurs, they are also less able to finance treatment. Malaria has significant economic impact in addition to its human cost. Even though the disease might be handled for a fraction of that amount, it is estimated that malaria costs African countries more than US$12 billion annually in direct damages (Fatmawati, 2021). Malaria currently affects over 87 million countries worldwide and the highest incidence and mortality rates are in sub-Saharan Africa (Mohammed, 2021). In Africa malaria robs the continent’s economy of 1.3% of its annual growth. Malaria mortality have decreased by 50% or more in certain highly endemic countries like Rwanda, Zambia, Zanzibar, Sao Tome and Principle, The Gambia, and Kenya as a result of effective malaria management methods (Zhao 2022). The documented decreases in malaria in these

nations have been attributed to the extensive use of LLINs and IRS as well as the administration of artemisinin-based combination therapy (ACT) for the treatment of simple Plasmodium falciparum malaria (Noeiaghdam, 2021). Vector control is receiving more attention as a result of these advancements. Vector management has been key to the historic and successful eradication of malaria in many regions of the world. This suggests that, in addition to the existing insecticide-based tactics, renewed work in this area should be regarded as a crucial component of any malaria eradiation strategy (Pandey, 2019). Vector control in the World Health Organization's (WHO) Roll Back Malaria (RBM) initiative is mostly reliant on scaling up insecticide-based tactics. The need for the creation of new pesticides is imperative, though, as mosquito resistance to the chemicals already in use is becoming more common (Basir, 2023). Many tools for controlling malaria vectors have been developed recently; some are almost ready for widespread use. (Gwarinda, 2021).

According to reports, there is presently no ideal vaccine to prevent malaria in people, despite widespread efforts worldwide to produce one (Khan, 2022). Intermittent preventive treatment (IPT), mosquito-reduction tactics, self-defense against mosquito bites (with insecticide-treated bed nets; ITNs); and reducing the number of vectors by destroying their breeding grounds are some of the preventive measures used to stop the spread of malaria(Kobe, 2020). Research also uncovered additional intervention tactics, including the use of anti-malarial medications to control malaria and indoor residual spraying (IRS) to eliminate infected indoor mosquitoes using sterile insect technology (Edossa, 2021). Over the years several numbers of mathematical models on the transmission dynamics of malaria have been examined. Following the simple S-I-R malaria model by Ross and Macdonald, many researchers have elaborated these models by incorporating different features associated to malaria transmission dynamics and its control. This includes modelling the effect of age groups on the transmission of malaria, the use of preventive and therapeutic strategies, repeated exposure, impact of climate variables such as temperature and rainfall (Singh, 2020).

Statement of the problem

Malaria has long been seen as a worldwide problem, and numerous experts, including epidemiologists, dedicate their time to understanding the disease's dynamics and preventing its spread. Through their contacts with these scientists, mathematicians have created a valuable and useful tool: mathematical models of malaria. These models provide information on the dynamics of malaria, the interactions between the host and vector populations, how to stop the spread of malaria, and ultimately how to eradicate the disease. Mathematical models offer a powerful tool to understand the causes and transmission of malaria and evaluate the effectiveness of interventions. Identifying the most effective combinations of control interventions (insecticide spraying, bed nets, treatment) for different settings. Optimize resource allocation for malaria control programs, considering

cost-effectiveness and long-term impact, designing targeted interventions for specific demographics or high-risk areas.

Objectives of the study

i. To formulate a malaria disease model showing clearly its flowchart and transmission dynamics.

ii. To derive the human and vector compartmental equations from the model formulated.

iii. To determine the reproduction number, disease-free equilibrium and endemic equilibrium of the model to ascertain the interactions between the human and vector compartments.

iv. To suggest possible solutions to adhere to in order to balance the disease transmission dynamics or wipe out the disease.

Methodology

Model Assumptions

i. No demographic changes

Age distribution, migration, and other demographic shifts within the populations of humans and mosquitoes are not taken into consideration by the model

ii. Homogeneous mixing

Individuals in each compartment (susceptible, exposed, infectious, and recovered) mix together uniformly. All persons have an equal chance of interacting with those from different compartments, according to this description.

iii. Instantaneous transition between compartments

When the necessary conditions are satisfied, transitions between compartments (e.g., from exposed to infectious) occur instantaneously.

iv. Constant population size.

Both the overall human population (N_h) and the overall mosquito population (N_v) remain stable over time. The equilibrium between birth and death rates maintains stable population sizes.

Model Formulation

Table 1: State variables, parameters and descriptions of malaria model.

Parameter	Parameter Description
μ_h	Natural mortality rate of humans
μ_v	Natural mortality rate of mosquitoes
β_h	Transmission rate from infectious mosquitoes to susceptible humans
β_v	Transmission rate from infectious humans to susceptible mosquitoes
σ_h	Rate at which exposed humans become infectious
σ_v	Rate at which exposed mosquitoes become infectious
γ_h	Recovery rate of infectious humans
N_h	Total human population

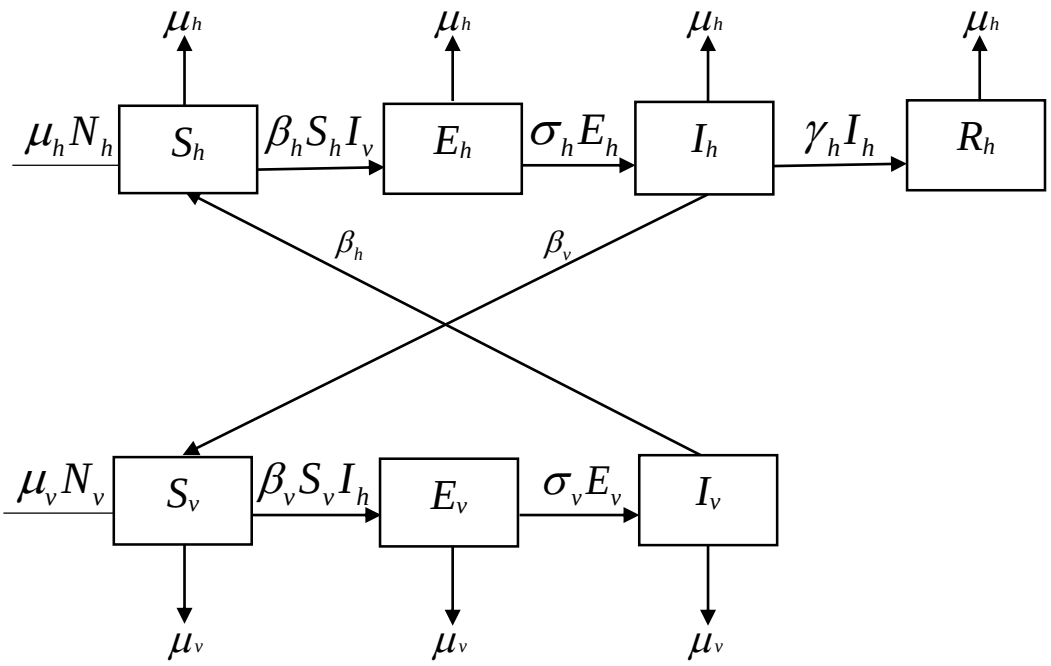

Figure 1: The compartmental model for malaria transmission.

$$\frac{dS_h}{dt} = \mu_h N_h - \beta_h S_h I_v - \mu_h S_h \quad (1)$$

$$\frac{dE_h}{dt} = \beta_h S_h I_v - (\sigma_h + \mu_h) E_h \quad (2)$$

$$\frac{dI_h}{dt} = \sigma_h E_h - (\gamma_h + \mu_h) I_h \quad (3)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h \quad (4)$$

$$\frac{dS_v}{dt} = \mu_v N_v - \beta_v S_v I_h - \mu_v S_v \quad (5)$$

$$\frac{dE_v}{dt} = \beta_v S_v I_h - (\sigma_v + \mu_v) E_v \quad (6)$$

$$\frac{dI_v}{dt} = \sigma_v E_v - \mu_v I_v \quad (7)$$

With initial conditions:

$$S_h(0) = S_{h0},\ E_h(0) = E_{h0},\ I_h(0) = I_{h0},\ R_h(0) = R_{h0} \quad (8)$$

$$S_v(0) = S_{v0},\ E_v(0) = E_{v0},\ I_v(0) = I_{v0} \quad (9)$$

The total population sizes N_h and N_v can be determined by

$$S_h + E_h + I_h + R_h = N_h \quad (10)$$

$$S_v + E_v + I_v + = N_v \quad (11)$$

Determination of Basic Reproduction Number

The reproductive number or index *R*o is a crucial threshold parameter that represents the average number of secondary infections caused by one infected person in a population that is totally susceptible. In this context of the SEIR model that incorporates both human and mosquito populations, the next-generation matrix technique is commonly employed to compute the R_0.

Next-generation matrix approach:

The next-generation matrix defined by *G* is composed of two matrices: *F* (new infections) and *V* (transitions between compartments).

Matrix *F* (New infections):

The elements of F are the partial derivatives of the new infection terms with respect to the infected compartments.

Matrix *V* (Transitions):

The elements of V are the partial derivatives of the transitions (excluding new infections) with respect to the infected compartments.

Defining and evaluating F and V:

We are going to consider the new infections which are:

Infections for humans: $\beta_h S_h I_v$

Infections for mosquitoes: $\beta_v S_v I_h$

For the transitions we have:

Transitions for humans: $(\sigma_h + \mu_h)E_h$, $(\gamma_h + \mu_h)I_h$

Transition for mosquitoes: $(\sigma_v + \mu_v)E_v$, $\mu_v I_v$

Matrices F and V

Let $\chi = (E_h, I_h, E_v, I_v)$

$$F = \begin{pmatrix} 0 & 0 & \beta_h S_h & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \beta_v S_v & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{12}$$

$$V = \begin{pmatrix} \sigma_h + \mu_h & 0 & 0 & 0 \\ -\sigma_h & \gamma_h + \mu_h & 0 & 0 \\ 0 & 0 & \sigma_v + \mu_v & 0 \\ 0 & 0 & -\sigma_v & \mu_v \end{pmatrix} \tag{13}$$

The next generation matrix G is given by:

$G = FV^{-1}$

Then, R_0 is the largest eigenvalue (spectral radius) of G.

Inverse of V

To find V^{-1}

$$V = \begin{pmatrix} \sigma_h + \mu_h & 0 & 0 & 0 \\ -\sigma_h & \gamma_h + \mu_h & 0 & 0 \\ 0 & 0 & \sigma_v + \mu_v & 0 \\ 0 & 0 & -\sigma_v & \mu_v \end{pmatrix} \tag{14}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{\sigma_h + \mu_h} & 0 & 0 & 0 \\ \frac{\sigma_h}{(\sigma_h + \mu_h)(\gamma_h + \mu_h)} & \frac{1}{\gamma_h + \mu_h} & 0 & 0 \\ 0 & 0 & \frac{1}{\sigma_v + \mu_v} & 0 \\ 0 & 0 & \frac{\sigma_v}{(\sigma_v + \mu_v)\mu_v} & \frac{1}{\mu_v} \end{pmatrix} \quad (15)$$

Computing *G*, we have;

$$G = \begin{pmatrix} 0 & 0 & \frac{\beta_h S_h}{\sigma_v + \mu_v} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \frac{\beta_v S_v}{\gamma_h + \mu_h} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \quad (16)$$

The eigenvalues of G can be computed directly. The interest is in the spectral radius of G, which is the largest eigenvalue.

Interpreting the Reproductive number after solving the matrix F and V numerically, we say:

If $R_0 < 1$, the disease will die out in the population.

If $R_0 > 1$, the disease will persist and potentially lead to an epidemic.

The fundamental reproductive number is (R_0) is calculated by multiplying transmission rates and average infectious periods in humans and vectors. This can be simply summarized as stated below;

$$R_0 = \sqrt{\frac{\beta_h S_h \beta_v S_v}{(\sigma_h + \mu_h)(\gamma_h + \mu_h)(\sigma_v + \mu_v)\mu_v}} \quad (17)$$

Existence and stability of disease free equilibrium

Firstly, for a disease-free equilibrium, all the exposed and infected compartments in both the human and vector population are set to zero also the recovered compartment in the human compartment is zero. Thus, we have:

$S_h = N_h$, $E_h = 0$, $I_h = 0, R_h = 0$, $S_V = N_V$, $E_V = 0$, $I_V = 0$

Computing the Jacobian matrix with these partial derivatives, the equilibrium values

$S_h, E_h, I_h, R_h, S_v, E_v, I_v$ are substituted into the partial derivatives the following Jacobian matrix.

$$J_{DFE}=\begin{bmatrix} -\mu_h & 0 & 0 & 0 & 0 & 0 & -\beta_h N_h \\ 0 & -(\sigma_h+\mu_h) & 0 & 0 & 0 & 0 & \beta_h N_h \\ 0 & \sigma_h & -(\gamma_h+\mu_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -\beta_v N_v & 0 & -\mu_v & 0 & 0 \\ 0 & 0 & \beta_v N_v & 0 & 0 & -(\sigma_v+\mu_v) & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_v & -\mu_v \end{bmatrix} \quad (18)$$

Finally, we examine the eigenvalues of *J*. The signs of these eigenvalues influence how stable the DFE is. When all real components of the eigenvalues are negative, the DFE is stable. If a real portion is positive, DFE is unstable.

Existence and stability of disease endemic equilibrium

To determine the stability of this model using the Jacobian matrix, we need to carry out the following steps;

i. Identification of the equilibrium points: By identifying the equilibrium points, we determine the disease-free equilibrium (DFE) where the number of infected humans is zero.

ii. Construction of the Jacobian matrix: We will calculate the Jacobian matrix at the equilibrium point.

iii. Analysis of the eigenvalues: We will determine the stability by analyzing the eigenvalues of the Jacobian matrix.

To determine the endemic equilibrium of this SEIR model, we need to solve for the steady-state values where the derivatives are equal to zero. This implies solving the system of equations where:

$\frac{dS_h^*}{dt} = 0,\ \frac{dE_h^*}{dt} = 0,\ \frac{dI_h^*}{dt} = 0,\ \frac{dR_h^*}{dt} = 0,\ \frac{dS_v^*}{dt} = 0,\ \frac{dE_v^*}{dt} = 0,$ and $\frac{dI_v^*}{dt} = 0.$

From the system of differential equations in (1) – (7) we have;

$$S_h^* = \frac{\mu_h N_h}{\beta_h I_v^* + \mu_h} \quad (19)$$

$$E_h^* = \frac{\beta_h S_h^* I_v^*}{\sigma_h + \mu_h} \quad (20)$$

$$I_h^* = \frac{\sigma_h E_h^*}{\gamma_h + \mu_h} \quad (21)$$

$$R_h^* = \frac{\gamma_h I_h^*}{\mu_h} \quad (22)$$

$$S_v^* = \frac{\mu_v N_v}{\beta_v I_v^* + \mu_v} \tag{23}$$

$$E_v^* = \frac{\beta_v S_v^* I_h^*}{\sigma_v + \mu_v} \tag{24}$$

$$I_v^* = \frac{\sigma_v E_v^*}{\mu_v} \tag{25}$$

$$J_{EE} = \begin{bmatrix} -(\beta_h I_v^* + \mu_h) & 0 & 0 & 0 & 0 & 0 & -\beta_h S_h^* \\ \beta_h I_v^* & -(\sigma_h + \mu_h) & 0 & 0 & 0 & 0 & \beta_h S_h^* \\ 0 & \sigma_h & -(\gamma_h + \mu_h) & 0 & 0 & 0 & 0 \\ 0 & 0 & \gamma_h & -\mu_h & 0 & 0 & 0 \\ 0 & 0 & -\beta_v S_v^* & 0 & -(\beta_v I_h^* + \mu_v) & 0 & 0 \\ 0 & 0 & \beta_v S_v^* & 0 & \beta_v I_h^* & -(\sigma_v + \mu_v) & 0 \\ 0 & 0 & 0 & 0 & 0 & \sigma_v & -\mu_v \end{bmatrix} \tag{26}$$

Numerical Simulations

For basic reproduction number determination, we will be considering the following numerical values to show some numerical results and further discuss the reproduction number;

i. μ_h : 0.02

ii. μ_v : 0.2

iii. β_h : 0.0001

iv. β_v : 0.001

v. σ_h : 0.1

vi. σ_v : 0.2

vii. γ_h : 0.1

viii. N_h : 1000

ix. N_v : 5000

where $S_h = N_h$ and $S_V = N_V$

From equation (17),

Using the reproduction number formula;

$$R_0 = \sqrt{\frac{\beta_h S_h \beta_v S_v}{(\sigma_h + \mu_h)(\gamma_h + \mu_h)(\sigma_v + \mu_v)\mu_v}}$$

Substituting the numerical values into the equation;

$$R_0 = \sqrt{\frac{0.0001 \times 1000 \times 0.001 \times 5000}{(0.1+0.02)(0.1+0.02)(0.2+0.2)0.2}}$$

$R_0 = 20.83333333$

Using the next generation matrix approach to determine the reproduction number R_0;

From equations (12)-(13)

We compute $G = FV^{-1}$

$$F = \begin{bmatrix} 0 & 0.1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 5 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

$$V = \begin{bmatrix} 0.12 & 0 & 0 & 0 \\ -0.1 & 0.12 & 0 & 0 \\ 0 & 0 & 0.4 & 0 \\ 0 & 0 & -0.2 & 0.2 \end{bmatrix}$$

We are going to make use of the python software to complete the simplification of the matrix by generating the inverse of the matrix and furthermore computing the eigenvalues of G given as $/G - \lambda I/ = 0$ where λ represents the eigenvalues and I is the identity matrix.

$$V^{-1} = \begin{bmatrix} 8.33333 & 0 & 0 & 0 \\ 6.94444 & 8.33333 & 0 & 0 \\ 0 & 0 & 2.5 & 0 \\ 0 & 0 & 2.5 & 5 \end{bmatrix}$$

$$G = FV^{-1} \approx \begin{bmatrix} 0.69444 & 0.83333 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 12.5 & 25 \\ 0 & 0 & 0 & 0 \end{bmatrix}$$

From $/G - \lambda I/ = 0$;

$$\lambda I = \begin{pmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{pmatrix}$$

$$/G - \lambda I / = \begin{pmatrix} 0.69444 & 0.83333 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 12.5 & 25 \\ 0 & 0 & 0 & 0 \end{pmatrix} - \begin{pmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{pmatrix}$$

$$= \begin{pmatrix} 0.69444 - \lambda & 0.83333 & 0 & 0 \\ 0 & -\lambda & 0 & 0 \\ 0 & 0 & 12.5 - \lambda & 25 \\ 0 & 0 & 0 & -\lambda \end{pmatrix}$$

$$(0.69444 - \lambda)(-\lambda)(12.5 - \lambda)(-\lambda) = 0$$

$\lambda_1 = 6.94444$

$\lambda_2 = 0$

$\lambda_3 = 12.5$

$\lambda_4 = 0$

$R_0 = 12.5$

Which is the largest eigenvalue of K

The reproduction number R_0, the largest absolute value, indicates unstable disease dynamics and persistence in the population. Zero eigenvalues indicate potential complications. Intervention aims to reduce R_0 to balance disease death.

NB: The formula method simplifies reproduction number R_0 calculation, neglecting all transitions and compartments in the model, while the next generation matrix approach provides a comprehensive analysis, ensuring the most accurate result.

Determination of stability at disease free equilibrium (DFE)

Using the given values below to determine the stability of this model, we will be considering the following steps simultaneously.

i. μ_h : 0.02

ii. μ_v : 0.2

iii. β_h : 0.002

iv. β_v : 0.02

v. σ_h : 0.2

vi. σ_v : 0.4

vii. γ_h : 0.1

viii. N_h : 2000

ix. N_v : 10000

(*)

At the DFE,

(S_h, E_h, I_h, R_h, S_v, E_v,I_v) = (N_h, 0, 0, 0, N_v, 0, 0).

Substituting the given values in the matrix in (3.46) we have;

$$J_{\text{DFE}} = \begin{bmatrix} -0.02 & 0 & 0 & 0 & 0 & 0 & -4 \\ 0 & -0.22 & 0 & 0 & 0 & 0 & 4 \\ 0 & 0.2 & -0.12 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.1 & -0.02 & 0 & 0 & 0 \\ 0 & 0 & -200 & 0 & -0.2 & 0 & 0 \\ 0 & 0 & 200 & 0 & 0 & -0.6 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.4 & -0.2 \end{bmatrix}$$

$$[-0.02 + 0.j \quad -0.02 + 0.j \quad -0.2 + 0.j \quad -3.11980073 + 0.j$$
$$-0.28473047 + 2.82234252j \quad -0.28473047 - 2.82234252j \quad 2.54926161 + 0.j]$$

The eigenvalues of the DFE are the values calculated above.

The eigenvalues determine the stability of the DFE. For the DFE to be stable, all eigenvalues must have negative real parts, meanwhile if any eigenvalue has a positive real part, the DFE is unstable. Considering the eigenvalues above we have a positive real part which clearly indicates the DFE is unstable. It follows thus, if the system is marginally perturbed away from the disease-free condition, the disease will spread and remain in the population rather than being eradicated.

Determination of stability at the endemic equilibrium (EE)

In determining the endemic equilibrium we need to first obtain the values of $S_h^*, E_h^*, I_h^*, R_h^*, S_v^*, E_v^*, I_v^*$ and solve the system iteratively, to do so we will have to assume a value for I_h^*

Assume $I_h^* = 1$

Substituting the given numerical values in equation (*) above into equations (18)-(24) and solving iteratively, we have;

Table 2: Iteration table for the endemic equilibrium values of the model compartments.

	$I_h^* = 1$	$I_h^* = 10$	$I_h^* = 50$	$I_h^* = 100$	$I_h^* = 500$
S_v^*	9091	5000	1667	910	196
S_E^*	303	1667	2778	3030	3267
I_v^*	606	3334	5556	6061	6532
S_h^*	32	6	4	3	0.3
E_h^*	179	181	181	181	18
I_h^*	298	302	302	302	151
R_h^*	1491	1510	1512	1512	757

From the table above we will be making use of the highest of I_h^* to generate or determine the eigenvalues of the endemic equilibrium

We hereby make use of the values in equation (*) and the highest values of I_h^* above to determine the eigenvalues of the endemic equilibrium of the model as earlier mentioned above;

Substituting the values of (*) and I_h^* in equation (18), we have;

$$J_{EE} = \begin{bmatrix} -13.084 & 0 & 0 & 0 & 0 & 0 & -0.0006 \\ 13.064 & -0.22 & 0 & 0 & 0 & 0 & 0.0006 \\ 0 & 0.2 & -0.12 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0.1 & -0.02 & 0 & 0 & 0 \\ 0 & 0 & -3.92 & 0 & -3.22 & 0 & 0 \\ 0 & 0 & 3.92 & 0 & 3.02 & -0.6 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0.4 & -0.2 \end{bmatrix}$$

We will be making use of python software to further compute the eigenvalues of the endemic equilibrium and by satisfying the relation $(J - \lambda I) = 0$

Computing we have;

$$[-0.02 + 0.j \quad -3.73030739 + 0.j \quad -13.08400012 + 0.j \quad -0.09921692 + 0.j$$
$$-0.1198067 + 0.j \quad -0.22006886 + 0.j \quad -0.2 + 0.j]$$

$\lambda_1 = -0.02$

$\lambda_2 = -3.73030739$

$\lambda_3 = -13.08400012$

$\lambda_4 = -0.09921692$

$\lambda_5 = -0.1198067$

$\lambda_6 = -0.22006886$

$\lambda_7 = -0.2$

The Jacobian matrix's eigenvalues define the EE's stability. If all eigenvalues have negative real portions, the EE is stable, implying that the disease will remain in the population without producing huge outbreaks. If any eigenvalue has a positive real portion, the EE is unstable, which means that tiny perturbations can cause huge breakouts or disease die-off. Stability implies that the system will remain at the EE even if disrupted slightly. An unstable EE indicates that the system man deviate from equilibrium, perhaps leading to new outbreaks or disease elimination. This analysis sheds light on the disease's long-term behavior in the community, which can assist inform public health efforts.

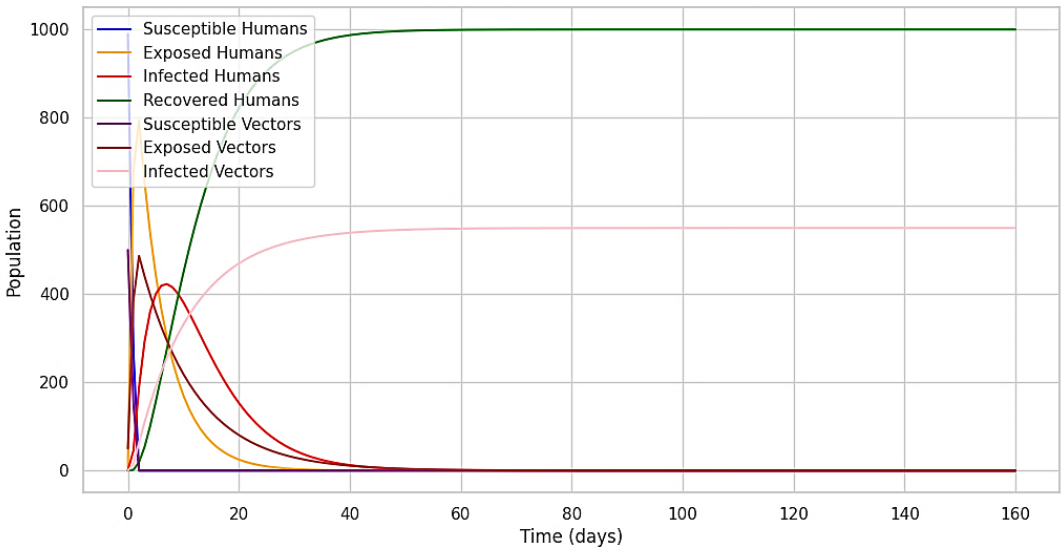

Figure 2: Graphical display of the behavioral relationships and interactions of SEIR model dynamics in both human and vector compartments.

The malaria disease spreads through both human and vector populations over time, with the majority initially susceptible. As the disease spreads, the population declines, and the infected population grows. The line

continues until control is achieved. Understanding the interaction between human and vector compartments helps determine control measures and infections during epidemics. Vector population monitoring is crucial for vector-borne diseases like malaria.

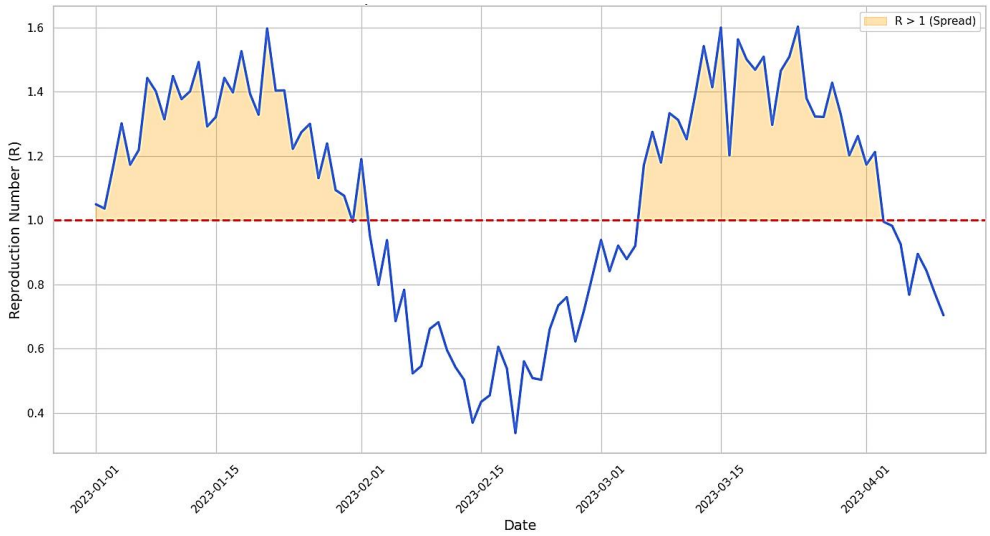

Figure 3: Visualization of the behavior of the reproductive number over time using the computed numerical values.

The graph shows the reproduction number changes over time. The threshold line (R=1) indicates the point at which the illness is seen as having either declined (R<1) or spread (R>1). The shaded area (R>1) is an important zone for public actions to be taken which represents times when the disease is aggressively spreading. Studying this graph helps understand malaria dynamics over time.

Control Strategy

Implementing treatments such as insecticide-treaded bed nets, indoor residual spraying, and public health campaigns can stabilize and reduce disease prevalence by lowering transmission rates $\beta_h \; and \; \beta_v$ respectively. Effective medical therapy increases recovery rates γ_h and reduces the number of infected individuals. The model aids in assessing the possible impact of various control strategies, as well as the significance of ongoing efforts in vector control and medical treatment. The SEIR malaria model offers and organized method for comprehending the dynamics of malaria transmission and the possible outcomes of different interventions. We can forecast the long-term course of the illness within a population and create efficient plans for the control and elimination of malaria by examining the stability of the model. The SEIR malaria model's overall control strategy includes vector control, immunization, treatment, public education, and environmental management, all of which are backed by comprehensive monitoring and surveillance systems. The most effective control

technique is often determined by the specific context, which includes local vector species, human behavior, and ecological factors. Integrating multiple methods (IVM) is often advised for long-term malaria transmission reduction.

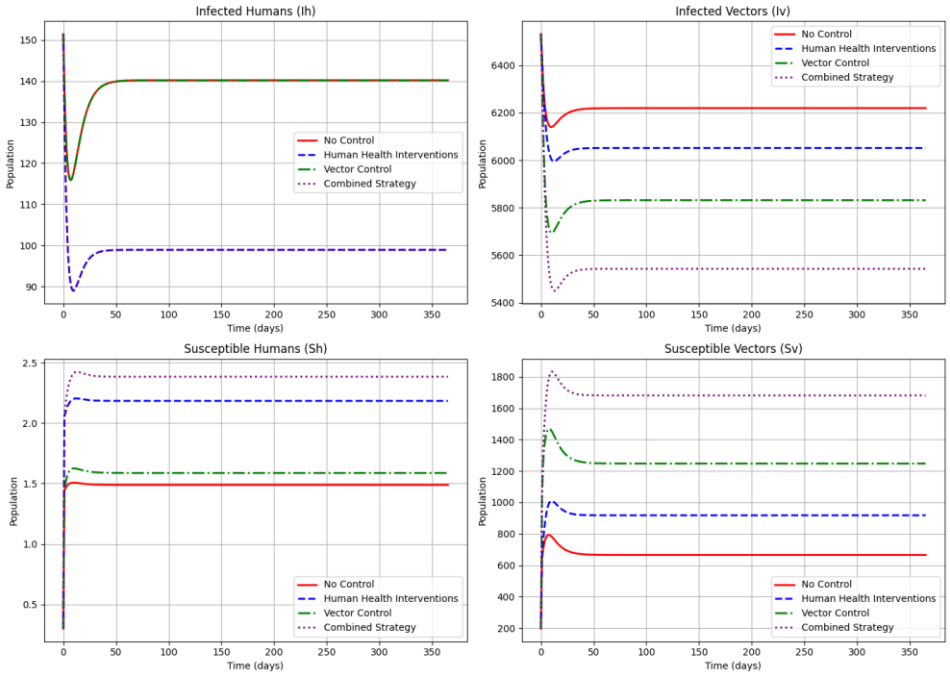

Figure 4: Visualization of the control of the I_h, I_v, S_h and S_v compartments using the computed numerical values.

Above is a visualization of the control of malaria disease using the computed data in the numerical solution. These graphs show how alternative control tactics (no control, human health interventions, vector control and combined strategy) affect the populations of infected and vulnerable humans and vectors over time.

Discussion of Results

From the computed results above we can clearly see that the next generation matrix approach is most accurate in determining the reproduction number R_0 of a population as compared to the formula method. Also we observed that for disease free equilibrium state, all eigenvalues must have negative real parts for the disease free equilibrium to be stable otherwise, DFE will be unstable and this also holds for the endemic equilibrium state. And lastly we observed from the graphical representation that the most effective technique is the combined strategy (which is a combination of both human health interventions and vector control), which drastically reduces infected populations while boosting susceptible populations, showing that disease transmission is successfully prevented.

Conclusion and Recommendations

In this study, we have derived and analyzed a mathematical model in order to better understand the transmission and spread of the malaria disease, and tried to suggest possible ways for its prevention and control. Mathematically, we modelled malaria as a 7-dimensional system of ordinary differential equations. We first defined the domain where the model is epidemiologically and mathematically well-posed. Our analysis encompassed the generation of basic reproduction number for malaria. We computed a reproductive number (R_0), which is epidemiologically accurate. We showed the existence and stabilities of equilibrium points of the model. In the model, we demonstrated that the disease-free equilibrium point DFE, is stable if ($R_0 < 1$) and if the eigenvalues of the Jacobian matrix have negative real parts, so that the disease dies out. If ($R_0 > 1$), disease-free equilibrium is unstable while the endemic state emerges as a unique equilibrium. Reinvasion is always possible and the disease never dies out. One can observe from the simulations that the infected human population increases with larger values of the contact rates from mosquito to human population and human to mosquito population. Clearly, the numerical simulations have shown that the disease-free equilibrium is unstable when the reproduction number lies above 1 and endemic equilibrium points are stable if the reproduction number lies above 1. We observed that in order to reduce the basic reproduction number below 1, intervention strategies need to be focused on treatment and reduction of the contact between mosquito vector and human host. Thus, there is a need for effective drugs, treated bed nets, and insecticides that would reduce the mosquito population and keep the human population stable.

Based on the results determined from the study, the following recommendations are made to be adhered to in order to balance, reduce and curb the spread of malaria disease.

i. Researchers and public health officials can make use of this models with their associated graphical visualizations to better understand the dynamics of infectious disease over time and to guide their decisions on the treatments like lockdowns, social distance and vaccination programs.
ii. Mathematicians, scientist, researchers, etc. can make use of the SEIR model to ascertain the endemic and disease-free equilibriums of infectious diseases in order to reduce the reproduction number thereby balancing the disease in the population or wiping it out entirely.
iii. Advocate for improved malaria management by training healthcare professionals, improving infrastructure, and ensuring enough diagnostic equipment and treatments. Also secure and sustain funds for malaria control programmes to ensure the long-term implementation of effective techniques.

iv. We recommend the use of higher and more compartments in the modelling of diseases by future researches/researchers in order to be able to capture the complex interactions amongst the human and vector compartments more extensively.

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