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Analysis and Application of Mathematical modeling in Malaria Disease Control

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Abstract

In this paper, we develop a mathematical model to analyze malaria transmission dynamics, as malaria is an infectious disease caused by the spread of progenitor parasites to humans through the bite of the female Anopheles mosquito. Mathematical models have long served as a framework for understanding and managing the impact of malaria, which has affected populations for over a century. Our model incorporates infected individuals who may recover and later lose immunity, thus reentering the susceptible class. The purpose of this model is to identify key factors that contribute to the rapid spread or reduction of the disease, and to explore new control strategies using mathematical tools. We employ a standard system of ordinary differential equations (ODEs) and propose a SEIR (Susceptible–Exposed–Infectious–Recovered) model to evaluate the outcomes of disease transmission and progression. A central feature of the model is the basic reproductive number, Ro, which plays a critical role in disease dynamics, if Ro < 1, the disease tends to die out, whereas if Ro > 1, the disease persists in the population. Numerical simulations are presented to illustrate the theoretical findings and validate the model. The results provide valuable insights into how changes in transmission parameters can affect disease control. Overall, this study highlights the importance of mathematical modeling in predicting disease behavior and guiding effective intervention strategies.

Keywords: Malaria, equilibrium points, reproduction number, malaria, equilibrium points, numerical simulation, endemic model, reproduction number

INTRODUCTION

Malaria being as one of the most harmful disease-causing millions of people lives around the world, globally every age people are getting affected by these infectious diseases. This disease is caused by single parasites of genus Plasmodium, these parasites get transmitted to human body when infected female Anopheles mosquito's bites human being. The symptoms seen during the mosquito's bite are mainly fever, headache, chills and nausea but it could lead to some series conditions like affecting your lungs, kidneys and affecting other body organs. One of the major factors of the increment of disease is environmental conditions, the warm temperatures, humidity and water bodies allows mosquitoes reproduce at rapid rate. Climate condition affects the life cycle of vectors and parasites and due to which there is increment of cases in some areas and decline in other. So, it is difficult to control the disease transmission due to many factors, the high cost to control transmission, variations in the disease pattern which also vary from place to place and by environmental conditions. Malaria as affecting a major population of people below poverty line, as due to the

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availability of less resources, hygiene issues and poor sanitization which is the major reason for the growth of mosquitoes and that increase the chances of getting bitten by an infected one. As considering this as a global issue scientists and mathematicians devoted their time and starts analyzing the pattern of host and vector population and developed a tool as mathematical models of malaria, to see how to actually control the transmission. Mathematical modelling is indeed a systematic approach for simulating, analysing, and predicting the spread of malaria in a population. The mathematical models divide a population into other compartments, namely, susceptible, infected, recovered, and exposed, thus enabling exploration on how different biological and environmental factors affect the transmission of the disease. These are usually formulated as systems of ordinary differential equations representing rates of transition across the compartments and using parameters such as mosquito biting rate, human recovery rate, and parasite development time. In this work, a compartmental model of malaria considering both human and mosquito populations is presented, which makes it possible to examine more closely different control strategies such as vector reduction, chemoprevention, and vaccination, from which threshold parameters, like the basic reproduction number R_0 can be derived, as well as the necessary conditions for eradication or persistence of malaria. Analytical and numerical simulations are intended to provide relevant insights to inform policy and optimize malaria interventions. Mathematical modeling simplifies very complicated biological systems into classes or compartments, such as the Suspected-exposed-infected-recovered (SEIR) classification of human and mosquito populations. These models describe movements of individuals among the compartments as differential equations. The rate of transfer between compartments is considered by parameters such as mosquito biting rate, probability of transmission per bite, parasite incubation period, and recovery or death rates among infected individuals, so that the model really simulates reality as best as possible. The major purpose of this type of modelling is to find out the basic reproduction number, R_0 which is the average number of secondary infections caused by a single infected individual in a completely susceptible population. If $R_0 < 1$the disease will come to extinction. If $R_0 >1$it will persist in the population as an endemic. Changing the parameters of the models can show how it increases, programs of vaccination, or seasonal spraying effect (R_0) which helps further control the spread of malaria.

Model Formulation

Parameters	Parameter Description
δ	Natural mortality rate of humans
μ	Natural mortality rate of mosquitoes
ω	Contact rate of infected mosquitoes with humans susceptible
σ	Rate at which exposed mosquitoes become infectious
τ	Transition rate from exposed to infected human population
γ	Transition rate from infected to recovered human population
ε	Recovery rate of infectious humans
P_s	Susceptible human population
P_e	Exposed human population
P_i	Infected human population
P_r	Recovered human population
V_s	Susceptible human population
V_i	Infected human population

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Modal Equation

$$\left.\begin{aligned}
\frac{dP_s}{dt} &= \alpha + \varepsilon P_r - \frac{\omega V_i P_s}{P} - \delta P_s \\
\frac{dP_e}{dt} &= \frac{\omega V_i P_s}{P} - \tau P_e - \delta P_e \\
\frac{dP_i}{dt} &= \tau P_e - \gamma P_i - \delta P_i \\
\frac{d P_r}{dt} &= \gamma P_i - \varepsilon P_r - \delta P_r \\
\frac{dV_s}{dt} &= \beta - \sigma p_e \frac{P_e V_s}{P} - \sigma p_i \frac{P_i V_s}{P} - \mu V_s \\
\frac{dV_i}{dt} &= \sigma p_e \frac{P_e V_s}{P} + \sigma p_i \frac{P_i V_s}{P} - \mu V_i
\end{aligned}\right\} \tag{1}$$

With Initial Conditions:

$$P_s(0) = P_{s_o} > 0, P_e(0) = P_{e_o} > 0, P_i(0) = P_{i_o} > 0, P_r(0) = P_{r_o} > 0,$$

$$V_s(0) = V_{s_o} > 0, V_i(0) = V_{i_o} > 0$$

$$and\ P = P_s + P_e + P_i + P_r$$

Determination of Basic Reproduction Number

The reproduction number commonly referred to as R_o serves as a key epidemiological indicator that reflects the expected number of new infections generated by one infected individual in a fully susceptible population. In the SEIR modeling framework that incorporates both human hosts and mosquito vectors, the calculation of R_o typically involves the application of the next-generation matrix method. The next-generation matrix is defined by K is composed of two matrices which are F (New Infection) and V (Transitions between compartment). We consider a structured malaria transmission modal with Human Population (SEIR) and Mosquito Population (SI)-

P_S : *Susceptible*

P_E : *Exposed* V_S : *Susceptible*

P_I : *Infected* V_I : *Infected*

P_R : Recovered

Only compartments contributing to infection dynamics are:

$$x = (P_E, P_I, V_I)$$

$$F(x) = \begin{pmatrix} 0 & 0 & \frac{\omega P_s}{P} \\ 0 & 0 & 0 \\ \frac{\sigma P_e V_s}{P} & \frac{\sigma P_i V_s}{P} & 0 \end{pmatrix} \qquad V(x) = \begin{pmatrix} -(\tau+\delta) & 0 & 0 \\ \tau & -(\gamma+\delta) & 0 \\ 0 & 0 & -\mu \end{pmatrix}$$

The next-generation matrix K is given as: $K = FV^{-1}$

$$V^{-1}=\begin{pmatrix} \frac{-1}{\tau+\delta} & 0 & 0 \\ \frac{-\tau}{(\tau+\delta)(\gamma+\delta)} & \frac{-1}{\gamma+\delta} & 0 \\ 0 & 0 & \frac{-1}{\mu} \end{pmatrix}$$

Now computing K, we have:

$$K=\begin{pmatrix} 0 & 0 & \frac{-\omega P_s}{\mu P} \\ 0 & 0 & 0 \\ \frac{-\sigma P_e V_s}{P(\tau+\delta)}+\frac{-\tau\sigma P_i V_s}{P(\tau+\delta)(\gamma+\delta)} & \frac{-\sigma P_i V_s}{P(\gamma+\delta)} & 0 \end{pmatrix}$$

Now the eigenvalues of the next-generation matrix G can be computed directly, where the dominant eigenvalue gives the basic reproduction number R_o. This value reflects the average number of secondary infections caused by a single infected individual in a fully susceptible population. If R_o <1, the infection cannot invade and will die out over time. If R_o >1, the disease can spread and may become endemic. This method provides a clear and systematic way to evaluate the potential of disease spread and informs control strategies.

$$R_o=\sqrt{\frac{\omega P_s \sigma V_s}{\mu P^2(\tau+\delta)}\left(P_e+\frac{\tau P_i}{\gamma+\delta}\right)}$$

Existence and stability of disease-free equilibrium

In a disease-free equilibrium, the exposed and infected compartments of both the human and vector populations are set to zero, including the recovered compartment in the human population. Thus, we have:

$$\begin{aligned} &P_S=P, P_E=0, P_I=0 \\ &V_s=V, V_I=0 \end{aligned}, \qquad \text{Let } x=\begin{pmatrix} P_S \\ P_E \\ P_S \\ V_S \\ V_I \end{pmatrix}$$

We'll compute the Jacobian matrix, which consists of partial derivatives for each equation:

$$J=\begin{pmatrix} -\delta & 0 & 0 & 0 & 0 & 0 \\ 0 & -\tau-\delta & 0 & 0 & 0 & 0 \\ 0 & \tau & -\gamma-\delta & 0 & 0 & 0 \\ 0 & 0 & \gamma & -\delta-\varepsilon & 0 & 0 \\ 0 & -\sigma\frac{V_s}{P} & -\sigma\frac{V_s}{P} & 0 & -\mu & 0 \\ 0 & \sigma\frac{V_s}{P} & \sigma\frac{V_s}{P} & 0 & 0 & -\mu \end{pmatrix}$$

Existence and Stability of Disease Endemic Equilibrium

To determining the stability using the Jacobian matrix, firstly by identifying the equilibrium point. In order to derive the endemic equilibrium of the SEIR model it is necessary to determine the accurate steady-state values where all time derivatives will now become zero. This requires solving mathematically the system of equations caused by setting the above derivatives to zero.

$$\frac{dP_s}{dt}=0, \frac{dP_e}{dt}=0, \frac{dP_i}{dt}=0, \frac{dP_r}{dt}=0, \frac{dV_s}{dt}=0, \frac{dV_i}{dt}=0$$

Now from these systems of equation we have

$$P_s=\frac{\alpha+\varepsilon P_r}{\frac{\omega V_i}{P}+\delta},\ P_e=\frac{\frac{\omega V_i P_s}{P}}{\tau+\delta},\ P_i=\frac{\tau P_e}{\gamma+\delta},\ P_r=\frac{\gamma P_i}{\varepsilon+\delta}$$

$$V_s=\frac{\beta}{\sigma p_e\frac{P_e}{P}+\sigma p_i\frac{P_i}{P}+\mu},\ V_i=\frac{\sigma p_e\frac{P_e}{P}+\sigma p_i\frac{P_i}{P}}{\mu}$$

$$J=\begin{bmatrix} -\frac{\omega V_i}{P}-\delta & 0 & 0 & \varepsilon & 0 & -\frac{\omega P_s}{P} \\ \frac{\omega V_i}{P} & -\tau-\delta & 0 & 0 & 0 & \frac{\omega P_s}{P} \\ 0 & \tau & -\gamma-\delta & 0 & 0 & 0 \\ 0 & 0 & \gamma & -\delta-\varepsilon & 0 & 0 \\ 0 & -\sigma\frac{V_s}{P} & -\sigma\frac{V_s}{P} & 0 & -\sigma p_e\frac{p_e}{P}-\sigma p_i\frac{P_i}{P}-\mu & 0 \\ 0 & \sigma\frac{V_s}{P} & \sigma\frac{V_s}{P} & 0 & \sigma p_e\frac{P_e}{P}+\sigma p_i\frac{P_i}{P} & -\mu \end{bmatrix}$$

Numerical Simulations

For calculating Reproduction number, we will now consider some numerical values to show our numerical result: ω: 0.001, σ: 0.01, μ: 0.5, τ: 0.03, δ: 0.02, γ: 0.3, P_s: 3000, V_s: 1000

P: 3000, P_e: 150, P_i: 75

Considering the Reproduction number: $R_o=\sqrt{\frac{\omega P_s\sigma V_s}{\mu P^2(\tau+\delta)}\left(P_e+\frac{\tau P_i}{\gamma+\delta}\right)}$

Now substituting the considered numerical values

$$R_o=\sqrt{\frac{0.001\times3000\times0.01\times1000}{0.5\times3000^2\times(0.03+0.02)}\left(150+\frac{0.03\times75}{0.3+0.02}\right)},\ R_o=0.1447$$

Now using next generation matrix, we compute $K=FV^{-1}$

$$F=\begin{pmatrix}0 & 0 & 0.001\\ 0 & 0 & 0\\ 0.5 & 0.75 & 0\end{pmatrix},\ V=\begin{pmatrix}-0.05 & 0 & 0\\ 0.03 & -0.32 & 0\\ 0 & 0 & -0.5\end{pmatrix}$$

Now we will use MATLAB software to compute the inverse of matrix and further the eigenvalues of K as given $|K-\lambda I|=0$ where I represents the Identity matrix and λ represents the eigenvalues.

$$V^{-1}=\begin{pmatrix}-20 & 0 & 0\\ -1.875 & -3.125 & 0\\ 0 & 0 & -2\end{pmatrix}$$

$$K=FV^{-1}=\begin{pmatrix}0 & 0 & -0.002\\ 0 & 0 & 0\\ -4.40625 & -125 & 0\end{pmatrix}$$

From $|K-\lambda I|=0$, $\lambda I=\begin{pmatrix}\lambda & 0 & 0\\ 0 & \lambda & 0\\ 0 & 0 & \lambda\end{pmatrix}$

$$|K-\lambda I|=\begin{pmatrix}0 & 0 & -0.002\\ 0 & 0 & 0\\ -4.40625 & -125 & 0\end{pmatrix}-\begin{pmatrix}\lambda & 0 & 0\\ 0 & \lambda & 0\\ 0 & 0 & \lambda\end{pmatrix}=\begin{pmatrix}-\lambda & 0 & -0.002\\ 0 & -\lambda & 0\\ -4.40625 & -125 & -\lambda\end{pmatrix}$$

$$-\lambda(\lambda^2)-0.002((0\times-125)-(-\lambda\times-4.4062))=0$$
$$\lambda_1=0,\lambda_2=-0.0938,\lambda_3=0.0938$$

The fundamental reproduction number, R_o is the largest absolute eigenvalue, indicating the potential of disease dynamics to become unstable and for disease transmission to continue in the population. Zero eigenvalues may suggest complications or indeterminate behavior of the system. Public health interventions attempt to reduce R_0 so that a balance may be achieved between disease spread and mortality.

Determination of Stability at disease free equilibrium

Using the given values, we will compute the stability of this model. Now substituting the values in above Disease-free equilibrium matrix

$$J=\begin{pmatrix}-0.02 & 0 & 0 & 0 & 0 & 0\\ 0 & -0.05 & 0 & 0 & 0 & 0\\ 0 & 0.03 & -0.32 & 0 & 0 & 0\\ 0 & 0 & 0.3 & -0.07 & 0 & 0\\ 0 & -0.0033 & -0.0033 & 0 & -0.5 & 0\\ 0 & 0.0033 & 0.0033 & 0 & 0 & -0.5\end{pmatrix}$$
$$\lambda_1=-0.02,\lambda_2=-0.05,\lambda_3=-0.32,\lambda_4=-0.07,\lambda_5=-0.5,\lambda_6=-0.5$$

As we have calculated the eigenvalues of the differential equation above, as we are well known eigenvalues determine the stability of the DFE, as all the eigenvalues have negative parts, so our DFE is stable.

CONCLUSION

The application of mathematical modelling to the study of malaria transmission and control has proven to be an invaluable approach for understanding the complex interplay between host and vector populations, as well as for evaluating potential public health interventions. In this study, we formulated a compartmental model that effectively captures the dynamics between human and mosquito populations by incorporating key epidemiological parameters such as the biting rate, transmission probabilities from mosquito to human and vice versa, as well as human recovery and disease-induced mortality rates. Through analytical investigation and parameter estimation, we derived the basic reproduction number (R0), a fundamental threshold quantity that determines whether the disease will persist or die out in the population. This parameter serves as a critical metric in epidemiology, guiding decisions regarding the intensity and type of control strategies needed to curb transmission. The model provides theoretical insights that can assist in the design and evaluation of vector control programs, treatment strategies, and public health policies aimed at malaria eradication.

Overall, this research highlights the strength of mathematical models not only in deepening our understanding of disease dynamics but also in offering a predictive framework for informed decision-making in malaria control and prevention efforts.

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