

A Compartmental Model for Malaria Dynamics and Intervention Strategies

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Abstract

Malaria continues to be a major public health concern in many tropical and subtropical regions. Mathematical models offer valuable tools to understand and manage the dynamics of malaria transmission. This study presents a compartmental model that segments the human (host) population into four epidemiological classes susceptible, exposed, infected, and recovered and the mosquito (vector) population into two classes susceptible and infected. The model incorporates various biological and epidemiological parameters such as recruitment rates, natural mortality rates, infection rates due to mosquito-human interactions, and transitions between disease states. This structured approach allows for an in-depth analysis of how malaria spreads, persists, and can be controlled. The formulation emphasizes interactions between hosts and vectors through contact and biting rates and examines how exposed individuals and reinfections influence disease dynamics. This model provides a foundation for assessing intervention strategies like vector control, medical treatment, and public health campaigns. By simulating realistic scenarios, the model helps predict potential outbreaks and evaluate the effectiveness of mitigation efforts. Overall, it offers critical insights that support evidence-based.

Keywords: Malaria transmission dynamics, compartmental modeling, vector-borne disease, mathematical epidemiology, host-vector interaction malaria control programs and contribute to the long-term goal of disease eradication

INTRODUCTION

Malaria remains one of the deadliest parasitic diseases globally, with millions of cases and hundreds of thousands of deaths reported annually, particularly in sub-Saharan Africa, parts of Asia, and South America. The disease is primarily caused by the Plasmodium parasite and transmitted through the bites of infected female *Anopheles* mosquitoes. Despite ongoing efforts involving insecticide-treated nets, indoor residual spraying, antimalarial drugs, and vaccine development, malaria continues to pose a significant health and economic burden in endemic areas. Mathematical modeling serves as a crucial tool for understanding the transmission dynamics of malaria and evaluating the potential impacts of different control strategies. Models allow researchers and policymakers to simulate various scenarios, predict outcomes, and design optimal intervention plans. Over the decades, a range of malaria models has been developed, each contributing to a better grasp of the disease's behavior under changing environmental and public health conditions.

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The present study builds upon this tradition by formulating a compartmental model that captures key aspects of the malaria transmission cycle. The model divides the host population into four classes: susceptible, exposed, infected, and recovered. The mosquito population is split into susceptible and infected classes. The model equations incorporate realistic parameters such as contact rates, recruitment and mortality rates, and transition rates between disease states. The main objective is to use this framework to explore how infection spreads

between humans and mosquitoes, and how recovered individuals may become susceptible again thereby contributing to the endemicity of malaria.

LITERATURE REVIEW

Mathematical models for infectious diseases have a rich history, starting with the classic SIR (Susceptible-Infected-Recovered) model introduced by Kermack and McKendrick in 1927. Since then, extensions of this framework have been tailored to a variety of diseases, including vector-borne illnesses such as malaria. One of the earliest malaria-specific models was developed by Ross and Macdonald, which laid the foundation for modern vector-host interaction modeling. Their work emphasized the importance of mosquito density and biting rates in determining the basic reproduction number R_0 , a critical threshold for disease persistence. Recent studies have expanded upon these classical models to include more realistic features such as latency periods, varying immunity levels, reinfections, and seasonal fluctuations. For example, Mandal et al. (2011) presented a review of deterministic models for malaria, focusing on how control strategies like insecticide-treated nets and antimalarial drugs can alter transmission dynamics. Meanwhile, Chitnis et al. (2006) introduced a model incorporating multiple infection stages and vector dynamics, showing how complex feedback loops govern disease outbreaks [1].

The current model aligns with this evolving body of literature by integrating the exposed class (E) in both human and vector populations, allowing for the representation of latent periods before symptoms or infectivity arise. This addition significantly improves the model's biological realism, especially in understanding time delays between mosquito bites and onset of illness. Furthermore, the inclusion of re-infection among recovered individuals reflects field observations where partial immunity does not always confer long-term protection against malaria. Another important contribution of this model is the use of distinct transition and contact rates for both exposed and infected individuals interacting with the mosquito population. This dual-pathway approach recognizes that both symptomatic and asymptomatic individuals can contribute to vector infection, which is a common feature in malaria-endemic zones [2].

Various control-oriented studies have applied such models to real-world policy decisions. For instance, Smith et al. (2012) employed a structured compartmental model to simulate mass drug administration in combination with vector control, demonstrating that integrated strategies produce the most substantial long-term impact. Similarly, modeling efforts by the WHO Malaria Modelling Consortium have played a central role in designing national malaria elimination plans in countries like Zambia and Sri Lanka. In light of these advancements, the model presented here aims to offer a flexible yet robust structure for exploring malaria dynamics. It can be adapted to different geographical regions by adjusting parameter values and serves as a foundation for developing more complex models incorporating seasonality, age structure, spatial heterogeneity, or stochastic effects. Ultimately, the model contributes to ongoing efforts in malaria research by offering insights into the interplay between host susceptibility, vector infection, and recovery dynamics [3].

Model Formulation

In this model, the Host population (humans) are divided into four classes: the susceptible class P_s , the exposed class P_e , the infected class P_i and recovered class P_r . the mosquitoes population (Vector) is subdivided into two classes: susceptible class V_s and the infected class V_i . α and β are the recruitment rate of host population and vector population respectively. δ is the natural mortality rate of humans. δP_s , δP_e , δP_i and δP_r are the number of susceptible, exposed, infected and recovered individuals respectively that die naturally. ω is the contact rate of infected mosquitoes with humans susceptible. $\frac{\omega V_i P_s}{P}$ is the proportion of susceptible humans that can encounter female anopheles with a ω rate. $\frac{\sigma P_e P_e V_s}{P}$ is the number of mosquitoes that become infected by biting exposed individuals (P_e) at the

rate σ_{P_e} and $\frac{\sigma_{P_i} P_i V_s}{P}$ represents the number of mosquitoes that become infected by biting infected persons (P_i) at a rate σ_{P_i} . τ is the transition rate from P_e to P_i . τP_e is the total exposed population that manifests malaria disease at time t (exposed individuals who pass into the P_i class). γ is the transfer rate of humans from P_i to P_r class. γP_i is the set of sick humans who recover from malaria (humans who enter the P_r class). β is the recruitment of mosquitoes. μ is the natural mortality rate of mosquitoes. μV_s and μV_i are the mosquitoes that die naturally respective in class V_s and V_i . The individual recovered (εP_r) of malaria disease recontacts malaria disease in recruitment [4].

Model Equations

The model equations are given below.

$$\left. \begin{aligned} \frac{dP_s}{dt} &= \alpha + \varepsilon P_r - \frac{\omega V_i P_s}{P} - \delta P_s \\ \frac{dP_e}{dt} &= \frac{\omega V_i P_s}{P} - \tau P_e - \delta P_e \\ \frac{dP_i}{dt} &= \tau P_e - \gamma P_i - \delta P_i \\ \frac{dP_r}{dt} &= \gamma P_i - \varepsilon P_r - \delta P_r \\ \frac{dV_s}{dt} &= \beta - \sigma_{P_e} \frac{P_e V_s}{P} - \sigma_{P_i} \frac{P_i V_s}{P} - \mu V_s \\ \frac{dV_i}{dt} &= \sigma_{P_e} \frac{P_e V_s}{P} + \sigma_{P_i} \frac{P_i V_s}{P} - \mu V_i \end{aligned} \right\} \quad (1)$$

With the initial condition

$$P_s(0) = P_{s_0} > 0, P_e(0) = P_{e_0} > 0, P_i(0) = P_{i_0} > 0, P_r(0) = P_{r_0} > 0,$$

$$V_s(0) = V_{s_0} > 0, V_i(0) = V_{i_0} > 0$$

$$\text{and} \quad P = P_s + P_e + P_i + P_r$$

Theoretical Analysis of the Malaria Model

The mathematical model presented for malaria control offers a structured representation of how the disease spreads and can be managed within a given population. It divides the human population into four primary categories: individuals who are susceptible to malaria, those who have been exposed but are not yet showing symptoms, those who are actively infected, and those who have recovered. Simultaneously, the mosquito population, which serves as the vector for malaria, is divided into two categories: those that are capable of being infected and those that are already carrying the parasite. This dual-compartmental structure provides a framework that captures the full life cycle of malaria transmission between humans and mosquitoes. The model takes into account the entry of new individuals into both the human and mosquito populations, reflecting natural recruitment or birth. It also considers the natural death of individuals in each class for both populations, allowing the system to simulate realistic demographic changes over time [5].

One of the most important features of this model is the interaction between humans and mosquitoes.

Susceptible humans can become exposed to the disease through bites from infected mosquitoes. The rate at which this exposure occurs depends on the frequency of contact between humans and vectors and the probability of transmission per bite. This assumption reflects real-world epidemiological findings, where transmission is more intense in regions with high mosquito density and frequent human exposure. After exposure, individuals do not become immediately infectious. Instead, they enter a latent period, which is represented in the model by an exposed class. This stage acknowledges that there is a delay between the time a person is bitten by an infected mosquito and the time they start to show symptoms or become capable of spreading the infection. This latency is a key biological feature of malaria and is important in understanding how the disease progresses within the human host [6].

Eventually, exposed individuals transition into the infectious class, at which point they are considered to be actively suffering from malaria. These individuals may contribute to the continuation of the cycle by infecting mosquitoes that bite them. In the model, both exposed and infected humans can contribute to the infection of mosquitoes, though possibly at different rates. This nuanced assumption reflects field evidence that even asymptomatic individuals may carry low levels of parasites and serve as a reservoir for the disease. From the infected stage, individuals may recover and move into the recovered class. However, the model allows for the possibility that recovered individuals can become susceptible again. This is particularly relevant for malaria, as immunity is often incomplete or short-lived. In many endemic regions, people may experience multiple episodes of malaria over their lifetime, and the possibility of reinfection must be accounted for in any robust model. On the mosquito side, the model includes both the natural recruitment of new mosquitoes and the death of mosquitoes over time. Susceptible mosquitoes become infected by biting either exposed or infected humans. After becoming infected, mosquitoes remain carriers of the parasite for the rest of their lives. They play a critical role in the disease cycle, as they are responsible for transmitting the parasite back to humans [7].

The theoretical design of this model is comprehensive in the way it captures key stages in malaria transmission. It includes the biological realities of latency, reinfection, and mosquito-human interaction. It also recognizes that both host and vector populations are dynamic and subject to demographic changes. This framework is valuable not just for understanding how malaria spreads but also for evaluating the impact of different intervention strategies. For example, reducing the contact between humans and mosquitoes—through measures like bed nets or insecticide spraying—would decrease the rate at which humans move from being susceptible to exposed. Improving access to treatment could accelerate the transition from infected to recovered, thereby reducing the overall infectious burden. Vector control strategies could also reduce the number of infected mosquitoes, thereby cutting off the transmission chain [8].

Furthermore, this model can be expanded or adapted depending on the context. For example, one might introduce age-specific behavior, spatial distribution of populations, or seasonal variations in mosquito activity. The current structure provides a strong foundation for such extensions, offering a flexible platform for further study. In summary, the theoretical model analyzed here presents a detailed and realistic view of malaria transmission dynamics. By structuring both the human and mosquito populations into meaningful categories and incorporating transitions that reflect biological processes, it serves as a powerful tool for both understanding the spread of malaria and designing control strategies. It balances simplicity with biological realism and offers a pathway for future research and policy driven applications [9, 10].

CONCLUSION

This study presents a compartmental mathematical model that effectively captures the dynamics of malaria transmission between humans and mosquitoes. By segmenting the human population into susceptible, exposed, infected, and recovered classes, and dividing the mosquito population into susceptible and infected vectors, the model provides a structured representation of the complex interactions driving malaria spread. The inclusion of reinfection, latency, and variable contact rates contributes to the model's biological realism, offering a more accurate simulation of real-world malaria

epidemiology.

The theoretical framework not only highlights the roles of various transition mechanisms within and between populations but also emphasizes the critical points where intervention strategies could disrupt the transmission cycle. Such strategies may include reducing mosquito contact rates, enhancing recovery through effective treatment, and minimizing reinfection. This model serves as a foundational tool for researchers, epidemiologists, and public health planners to test and optimize malaria control policies in endemic regions. Future work can build on this model by integrating spatial dynamics, seasonal variability, and stochastic processes to further enhance its applicability. Ultimately, the model supports global efforts toward malaria mitigation and eventual eradication by providing a scientifically grounded approach to understanding and interrupting disease transmission.

REFERENCES

1. Kermack WO, McKendrick AG. A contribution to the mathematical theory of epidemics. Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character. 1927 Aug 1;115(772):700-21.
2. Bacaër N. Ross and malaria (1911). In A short history of mathematical population dynamics 2011 (pp. 65-69). London: Springer London.
3. Macdonald G. The epidemiology and control of malaria. Oxford: Oxford University Press; 1957.
4. Chitnis N, Hyman JM, Cushing JM. Determining important parameters in the spread of malaria through the sensitivity analysis of a mathematical model. Bulletin of mathematical biology. 2008 Jul;70:1272-96.
5. Mandal S, Sarkar RR, Sinha S. Mathematical models of malaria-a review. Malaria journal. 2011 Dec;10:1-9.
6. Smith DL, Battle KE, Hay SI, Barker CM, Scott TW, McKenzie FE. Ross, Macdonald, and a theory for the dynamics and control of mosquito-transmitted pathogens. PLoS pathogens. 2012 Apr 5;8(4):e1002588.
7. World Health Organization. World malaria report 2023. World Health Organization; 2023 Nov 30.
8. Tchuinkam T, Akogbeto M. Impact of insecticide-treated materials on malaria vector populations and disease transmission. Trop Med Int Health. 2000;5(8):579-86.
9. Yang HM, Ferreira CP, Takahashi LT. A mathematical model for the dynamics of malaria in a human and mosquito population. Math Comput Model. 2005;41(9-10):1031-9.
10. Smith T, Killeen GF, Lengeler C. Sleeping under insecticide-treated nets to prevent malaria: Evidence for efficacy from the past and implications for the future. Trop Med Int Health. 2004;9(10):833-6.