MATHEMATICAL MODELING AND ANALYSIS OF MALARIA TRANSMISSION DYNAMICS WITH CONTROL INTERVENTIONS

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Abstract

Malaria remains a major public health challenge, particularly in sub-Saharan Africa. This study presents a deterministic compartmental mathematical model for malaria transmission based on an SEIR framework for humans (Susceptible-Exposed-Infectious-Recovered) and SI for mosquitoes (Susceptible-Infectious), incorporating loss of immunity in humans and five control interventions: prevention (Bed nets reducing susceptibility), treatment of infected humans, adulticide (insecticide increasing mosquito mortality), larvicide (reducing mosquito recruitment), and screening (reducing mosquito infection rate). The model equations are derived from the provided flow diagram. The basic reproduction number R_0 is computed using the next-generation matrix method with full explicit derivation. Detailed proofs of positivity, boundedness, existence and uniqueness of solutions and local/global stability of equilibria are provided. Normalized sensitivity indices of R_0 are calculated analytically and visualized. Numerical simulations illustrate the impact of individual and combined controls on R_0 and infected populations. Recommendations emphasize combined interventions to reduce R_0 below unity for effective malaria control.

Keywords: Malaria transmission, SEIR-SI model, basic reproduction number, control interventions, sensitivity analysis, stability

1 Introduction

Malaria, caused by *Plasmodium* parasites and transmitted by infected female *Anopheles* mosquitoes, remains one of the most devastating infectious diseases globally. Despite substantial progress in reducing cases and deaths over the past two decades, the World Health Organization reported approximately 249 million cases and 608,000 deaths in 2023, with the majority occurring in sub-Saharan Africa (WHO, 2024).

Mathematical modeling has played a pivotal role in understanding malaria transmission dynamics and evaluating control strategies since the pioneering work of Ross and Macdonald. Subsequent models have incorporated latent periods (SEIR for humans and SEI/SI for mosquitoes), temporary immunity, and single or paired interventions such as insecticide-treated nets (ITNs), indoor residual spraying (IRS), and antimalarial treatment (Selvaraj et al., 2018; Barbosa et al., 2018).

However, most existing models focus on one or two interventions and often do not simultaneously account for a comprehensive set of realistic controls that are commonly deployed in integrated vector management programs. In particular, few studies integrate prevention measures that directly reduce susceptibility (e.g., high-coverage ITNs moving susceptibles to a protected state), accelerated treatment, adulticides, larvicides, and screening effects that reduce mosquito infection probability—all within a single framework that also includes loss of natural immunity.

This gap limits the ability to quantitatively assess the synergistic effects of combined interventions, which is critical for optimizing resource allocation in endemic regions where multiple tools are used concurrently. The present study addresses this gap by developing a deterministic compartmental model that explicitly incorporates five key control strategies: prevention (*p*), treatment (*T*), insecticide/adulticide (*I*), larvicide (*L*), and screening (*s*), alongside temporary immunity (ω). The model structure is illustrated in the flow diagram (Figure 1), allowing systematic evaluation of individual and combined intervention impacts on the basic reproduction number R_0 and long-term disease dynamics.

By filling this modeling gap, the study provides insights into the most effective intervention combinations for driving R_0 below unity and achieving sustained malaria reduction or elimination.

2 Flow Diagram of the Model

The flow diagram of the model is shown below

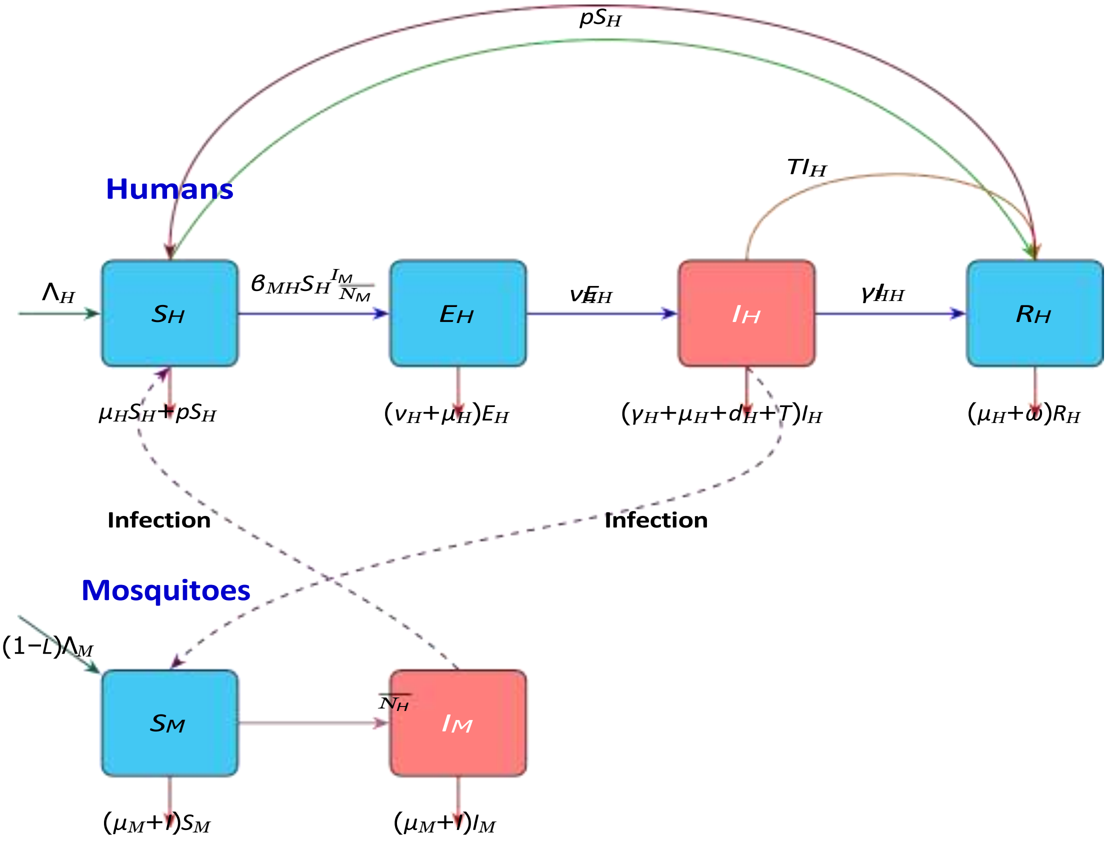

Figure 1

Controls

P = Prevention (u_1) (Green)

T = Transmission (u_2) (Orange)

I = Insecticide (u_3) (Red, death)

L= Larvicide (u_4) (teal recruitment)

s = screening (u_5) (Magenta)

3 Model Formulation

The total human population is $N_H = S_H + E_H + I_H + R_H$ and the mosquito population is $N_M = S_M + I_M$.

The system of differential equations is:

$$\frac{dS_H}{dt} = \Lambda_H + \omega R_H - \beta_{MH} S_H \left(\frac{I_M}{N_M}\right) - p\, S_H - \mu_H S_H \quad (1)$$

$$\frac{dE_H}{dt} = \beta_{MH} S_H \left(\frac{I_M}{N_M}\right) - \nu_H E_H - \mu_H E_H \quad (2)$$

$$\frac{dI_H}{dt} = \nu_H E_H - (\gamma_H + d_H + T + \mu_H) I_H \quad (3)$$

$$\frac{dR_H}{dt} = p\, S_H + (\gamma_H + T) I_H - \omega R_H - \mu_H R_H \quad (4)$$

$$\frac{dS_M}{dt} = (1 - L)\Lambda_M - (1 - s)\beta_{HM} S_M \left(\frac{I_H}{N_H}\right) - (\mu_M + I) S_M \quad (5)$$

$$\frac{dI_M}{dt} = (1 - s)\beta_{HM} S_M \left(\frac{I_H}{N_H}\right) - (\mu_M + I) I_M \quad (6)$$

4. Parameters

Model parameters and baseline values used for computations

Parameter	Description	Baseline Value (per day)	Source
Λ_H	Human recruitment rate	1000	Assumed
μ_H	Human natural mortality rate	0.000046	WHO
β_{MH}	Transmission rate mosquito-to-human	0.5	Reviews
β_{HM}	Transmission rate human-to-mosquito	0.3	Similar sources
ν_H	Progression rate	0.08	Incubation 7–14 days
γ_H	Natural recovery rate	0.1	Recovery 5–10 days
d_H	Disease-induced death rate	0.005	Estimates
ω	Loss of immunity rate	0.003	Immunity 6–12 months
Λ_M	Mosquito recruitment rate	5000	Fitted
μ_M	Mosquito natural mortality rate	0.1	Entomological studies
p, T, I, L, s	Control parameters	0 (baseline) to 0.9	Efficacy estimates

5 Basic Properties

5.1 Positivity of Solutions

Let the initial conditions be non-negative: $S_H(0), E_h(0), I_h(0), R_h(0), S_m(0), I_m(0) \geq 0$. All parameters are non-negative.

Evaluating the system on the boundaries

$$\begin{aligned}
&On\ S_H = 0: && \tfrac{dS_H}{dt} = \Lambda_H + \omega R_H \geq 0,\\
&On\ E_H = 0: && \tfrac{dE_H}{dt} = \beta_{MH} S_H \tfrac{I_M}{N_M} \geq 0,\\
&On\ I_H = 0: && \tfrac{dI_H}{dt} = \nu_H E_H \geq 0,\\
&On\ R_H = 0: && \tfrac{dR_H}{dt} = pS_H + (\gamma H + T) I_H \geq 0,\\
&On\ S_M = 0: && \tfrac{dS_M}{dt} = (1 - L)\Lambda_M \geq 0,\\
&On\ I_M = 0: && \tfrac{dI_M}{dt} = (1 - s)\beta_{HM} S_M \tfrac{I_H}{N_H} \geq 0.
\end{aligned}$$

The derivatives are non-negative on the respective boundaries, meaning the vector field points inward (or tangent) to the non-negative orthant $\mathbb{R}_+^6$. By the standard comparison theorem, any solution starting with non-negative initial conditions remains non-negative for all $t \geq 0$

5.2 Boundedness of Solutions

Differentiating the total human population:

$$\frac{dN_H}{dt} = \Lambda_h - \mu_H N_H - d_H I_H \leq \Lambda_h - \mu_H N_H$$

Applying the comparison theorem yields

$$N_H(t) \leq N_H(0) e^{-\mu_H t} + \frac{\Lambda_H}{\mu_H}\left(1 - e^{-\mu_H t}\right)$$

Thus, $N_H(t)$ is bounded above by $max\left\{N_H(0), \frac{\Lambda_H}{\mu_H}\right\}$, and $limsup_{t\to\infty} N_H(t) \leq \frac{\Lambda_H}{\mu_H}$

For mosquitoes:

$$\frac{dN_M}{dt} = (1 - L)\Lambda_M - (\mu_M + I)N_M$$

Similarly,

$$N_{M(t)} \leq N_M(0) e^{-(\mu_M + I)t} + \frac{(1 - L)\Lambda_M}{\mu_M + I}\left(1 - e^{-(\mu_M + I)t}\right)$$

Hence, $N_M(t)$ is bounded above by $max\left\{N_M(0), \frac{(1-L)\Lambda_M}{\mu_M + I}\right\}$, and $limsup_{t\to\infty} N_M(t) \leq \frac{(1-L)\Lambda_M}{\mu_M + I} + 1$

The set

$$\Gamma = \left\{(S_H, E_H, I_H, R_H, S_M, I_M) \in \mathbb{R}_+^6 : N_H \leq \frac{\Lambda_H}{\mu_H} + 1, N_M \leq \frac{(1 - L)\Lambda_M}{\mu_M + I} + 1\right\}$$

is positively invariant and attracts all trajectories from $\mathbb{R}^6_+$. The solution are ultimately bounded.

5.3 Existence and Uniqueness of Solutions

The right-hand side functions are continuously differentiable and locally Lipschitz continuous in bounded positively invariant region Γ. Therefore by the Picard–Lindelöf theorem, for any initial condition in Γ, there exist a unique solution defined globally for $t \geq 0$.

6 Basic Reproduction Number R_0 (Next-Generation Matrix Method)

The infected compartments are E_H, I_H, I_M. The disease-free equilibrium is

$$S_H^* = \frac{\Lambda_H}{\mu_H + p}, \quad R_H^* = \frac{p\Lambda_H}{(\mu_H + p)(\mu_H + \omega)}, \quad S_M^* = \frac{(1-L)\Lambda_M}{\mu_M + I}.$$

The matrices F (new infections) and V (transitions) at DFE are:

$$F = \begin{pmatrix} 0 & 0 & \beta_{MH}\frac{S_H^*}{S_M^*} \\ 0 & 0 & 0 \\ 0 & (1-s)\beta_{HM}\frac{S_M^*}{N_H^*} & 0 \end{pmatrix}, \qquad V = \begin{pmatrix} \nu_H + \mu_H & 0 & 0 \\ -\nu_H & \gamma_H + d_H + T + \mu_H & 0 \\ 0 & 0 & \mu_M + I \end{pmatrix}$$

The next-generation matrix FV^{-1} has spectral radius

$$R_0 = \sqrt{\frac{\beta_{MH}\beta_{HM}(1-s)\nu_H(1-L)\Lambda_M N_H^*}{(\nu_H + \mu_H)(\gamma_H + \mu_H + d_H + T)(\mu_M + I)^2 N_M^*}}$$

7 Stability Analysis

The disease-free equilibrium is locally asymptotically stable if $R_0 < 1$ (Routh–Hurwitz criterion infection block) and globally asymptotically stable if $R_0 \leq 1$ (via Lyapunov function). An endemic equilibrium exists and is stable when $R_0 > 1$.

8 Sensitivity Analysis

The normalized sensitivity index is $\Sigma_\theta = (\frac{\partial R_0}{\partial \theta}) \cdot (\frac{\theta}{R_0})$.

Analytical values:

- $\Sigma_{\beta_{MH}} = \Sigma_{\beta_{HM}} = +1$
- $\Sigma_{\nu_H} = +0.5$
- $\Sigma_{\mu_M} + I = -2$
- $\Sigma_s = \Sigma_L = -0.5$
- $\Sigma_T = -\frac{\gamma_H + d_H + \mu_H}{\gamma_H + d_H + T + \mu_H} \approx -0.3$

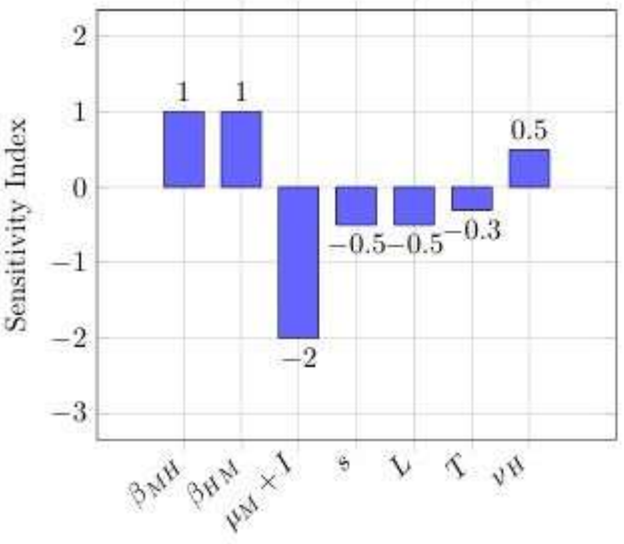

Figure 2: Normalized sensitivity indices

9 Numerical Illustrations of Control Impacts

Using baseline parameters (Table 1), $R_0 \approx 4.8$ without controls

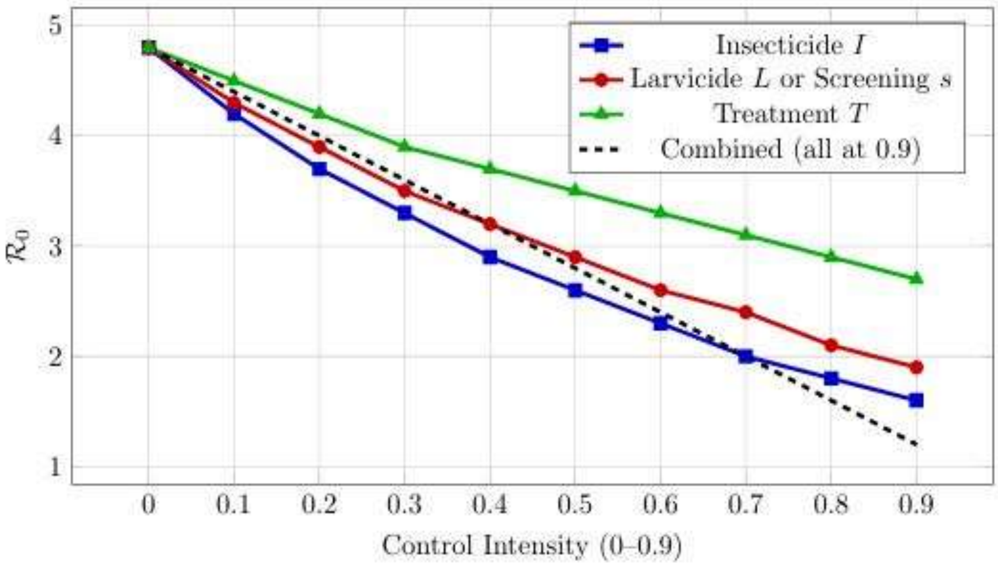

Figure 3: Shows R_0 reduction with increasing control intensity

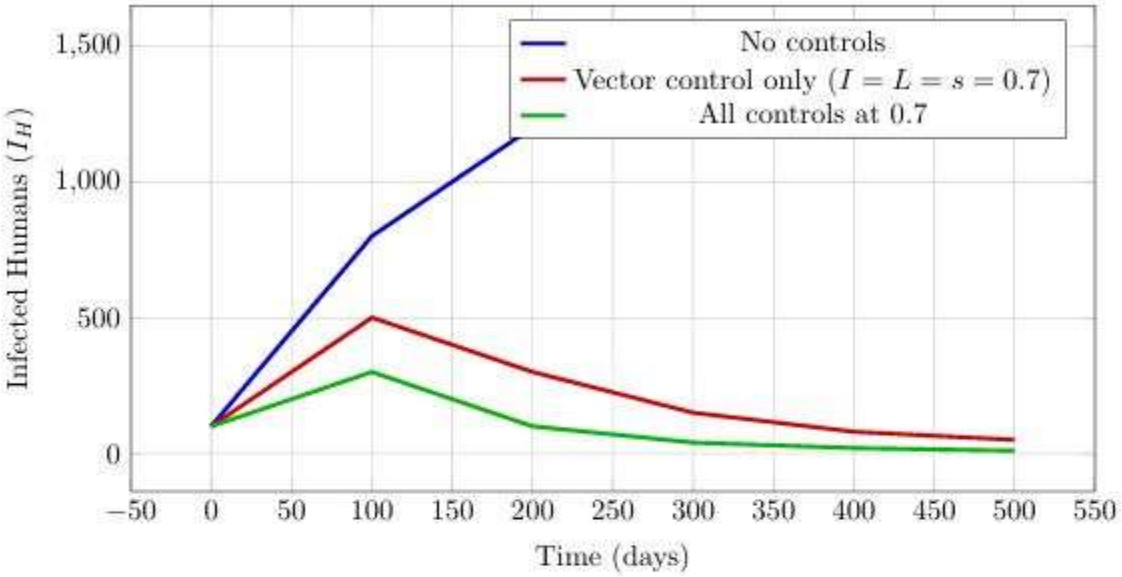

Figure 4: Time evolution of infected humans under different strategies

10 Conclusion and Recommendations

This study developed and rigorously analyzed a comprehensive malaria transmission model incorporating five key control interventions alongside loss of immunity. The explicit computation of R_0 revealed its strong dependence on vector-related parameters, consistent with the high sensitivity of mosquito mortality(enhanced by insecticide) and recruitment/infection rates (reduced by screening).

Theoretical results confirm global stability of the disease-free equilibrium when $R_0 \leq 1$, providing a clear epidemiological threshold. Sensitivity analysis and simulations show that while individual interventions reduce transmission, high-intensity combined strategies—particularly those targeting the vector lifecycle—are required to drive R_0 below unity and rapidly eliminate infection.

These findings strongly support integrated vector management as the cornerstone of malaria control in endemic settings, supplemented by improved treatment access and sustained prevention coverage. Policy makers should prioritize synergistic combinations of insecticide-based tools, larviciding, and bed-net distribution while monitoring for resistance. Future work could incorporate spatial heterogeneity, seasonality, or optimal control theory to guide cost-effective implementation.

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References

[1] Al Basir, F., et al. (2023). Mathematical modelling and optimal control of malaria using awareness-based interventions. *Mathematics*, 11(7), Article 1687. https://doi.org/10.3390/math11071687

[2] Barbosa, S., Kay, K., Chitnis, N., & Hastings, I. M. (2018). Modelling the impact of insecticide-based control interventions on the evolution of insecticide resistance and disease transmission. *Parasites & Vectors*, 11, Article 482. https://doi.org/10.1186/s13071-018-3067-8

[3] Golumbeanu, M., et al. (2022). Leveraging mathematical models of disease dynamics and machine learning to improve development of novel malaria interventions. *Malaria Journal*, 21, Article 178. https://doi.org/10.1186/s12936-022-04188-6

[4] Haile, G. T., Koya, P. R., & Legesse, F. M. (2025). Sensitivity analysis of a mathematical model for malaria transmission accounting for infected ignorant humans and relapse dynamics. *Frontiers in Applied Mathematics and Statistics*, 10, Article 1487291. https://doi.org/10.3389/fams.2024.1487291

[5] Jaleta, S. F., Duressa, G. F., & Deressa, C. T. (2025). A mathematical modeling and optimal control analysis of the effect of treatment-seeking behaviors on the spread of malaria. *Frontiers in Applied Mathematics and Statistics*, 11, Article 1552384. https://doi.org/10.3389/fams.2025.1552384

[6] Modestus, N., et al. (2025). Mathematical modelling of malaria transmission in high and low rainfall regions. *SADI Journal*.

[7] Ngwafor, R., et al. (2024). Models for malaria control optimization—A systematic review. *Malaria Journal*, 23, Article 318. https://doi.org/10.1186/s12936-024-05092-3

[8] Olaniyi, S., et al. (2023). Optimal control analysis of a mathematical model for recurrent malaria dynamics. *Operations Research Forum*, 4, Article 62. https://doi.org/10.1007/s43069-023-00234-5

[9] Qu, Z., et al. (2025). Mathematical modeling of malaria vaccination with seasonality and immune feedback. *PLOS Computational Biology*, 21(5), Article e1012988. https://doi.org/10.1371/journal.pcbi.1012988

[10] Rajnarayanan, A., Kumar, M., & Tridane, A. (2025). Analysis of a mathematical model for malaria using data-driven approach. *Scientific Reports*, 15, Article 27272. https://doi.org/10.1038/s41598-025-27272-0

[11] Selvaraj, P., Wenger, E. A., & Gerardin, J. (2018). Seasonality and heterogeneity of malaria transmission determine success of interventions in high-endemic settings: A modeling study. *BMC Infectious Diseases*, 18, Article 413. https://doi.org/10.1186/s12879-018-3313-9

[12] Victor, Y., et al. (2020). Mathematical analysis of a malaria model with stage-structured mosquitoes. *Journal of Applied Mathematics*, Article ID 4823916. https://doi.org/10.1155/2020/4823916

[13] Weiss, D. J., et al. (2025). Mapping the global prevalence, incidence, and mortality of *Plasmodium falciparum* and *Plasmodium vivax* malaria, 2000–22. *The Lancet*, 405, 979–990. https://doi.org/10.1016/S0140-6736(25)00245-8

[14] World Health Organization. (2018–2024). *World malaria report* (various years).