# Malaria Transmission Dynamics with Mosquito Treatment: Reproduction Number Analysis

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March 5, 2025

## 1 Model Description

### 1.1 Ordinary Differential Equations

The model consists of 10 coupled ODEs tracking human and mosquito populations:

**Human Dynamics (SIS):**

$$\frac{dS_H}{dt} = -mab(I_M + I_T)S_H + rI_H$$
$$\frac{dI_H}{dt} = mab(I_M + I_T)S_H - rI_H$$

**Untreated Mosquito Dynamics:**

$$\frac{dS_M}{dt} = g + hS_T - acI_H S_M - tS_M - gS_M$$
$$\frac{dE_{1,M}}{dt} = acI_H S_M - tE_{1,M} - s_{1M}E_{1,M} - gE_{1,M}$$
$$\frac{dE_{2,M}}{dt} = s_{1M}E_{1,M} - s_{2M}E_{2,M} - gE_{2,M}$$
$$\frac{dI_M}{dt} = s_{2M}E_{2,M} - gI_M$$

**Treated Mosquito Dynamics:**

$$\frac{dS_T}{dt} = tS_M - acI_H S_T - hS_T - gS_T$$
$$\frac{dE_{1,T}}{dt} = acI_H S_T + tE_{1,M} - s_{1T}E_{1,T} - gE_{1,T}$$
$$\frac{dE_{2,T}}{dt} = s_{1T}E_{1,T} - s_{2T}E_{2,T} - gE_{2,T}$$
$$\frac{dI_T}{dt} = s_{2T}E_{2,T} - gI_T$$

### 1.2 Parameter Values

Default parameter values used in simulations:

| Parameter | Description | Default Value |
|---|---|---|
| $a$ | Biting rate (day$^{-1}$) | 0.2 |
| $b$ | Human-to-mosquito transmission probability | 0.5 |
| $c$ | Mosquito-to-human transmission probability | 0.5 |
| $m$ | Mosquito-to-human ratio | 20.0 |
| $r$ | Human recovery rate (day$^{-1}$) | 0.01 |
| $g$ | Mosquito death rate (day$^{-1}$) | 0.12 |
| $h$ | Treatment waning rate (day$^{-1}$) | 0.1 |
| $t$ | Treatment encounter rate (day$^{-1}$) | 0.1 |
| $s_{1M}$ | Untreated $E_1 \to E_2$ rate (day$^{-1}$) | 0.2 |
| $s_{2M}$ | Untreated $E_2 \to I$ rate (day$^{-1}$) | 0.2 |
| $s_{1T}$ | Treated $E_1 \to E_2$ rate (day$^{-1}$) | 0.1 |
| $s_{2T}$ | Treated $E_2 \to I$ rate (day$^{-1}$) | 0.1 |

- All rates expressed per day (day$^{-1}$)
- Human population normalized to 1 ($S_H + I_H = 1$)
- Mosquito populations tracked as proportions

## 2 Methods

### 2.1 Reproduction Number Theory

The basic ($R_0$) and effective ($R_{\text{eff}}$) reproduction numbers are calculated using the Next Generation Matrix (NGM). This approach linearizes the system around equilibrium points and quantifies infection spread potential.

#### 2.1.1 Disease-Free Equilibrium (DFE)

The DFE is characterized by:

$$I_H = E_{1,M} = E_{2,M} = I_M = E_{1,T} = E_{2,T} = I_T = 0$$
$$S_H = 1, \quad S_M = S_M^*, \quad S_T = S_T^*$$

where $S_M^*$ and $S_T^*$ solve:

$$\begin{bmatrix} -(t+g) & h \\ t & -(h+g) \end{bmatrix} \begin{bmatrix} S_M^* \\ S_T^* \end{bmatrix} = \begin{bmatrix} -g \\ 0 \end{bmatrix}$$

### 2.1.2 Endemic Equilibrium (EE)

The EE satisfies:

$$\frac{dS_H}{dt} = \frac{dI_H}{dt} = \cdots = \frac{dI_T}{dt} = 0$$
$$I_H > 0, \quad I_M + I_T > 0$$

Numerically found by solving the ODE system until convergence ($\|du/dt\| < 10^{-6}$).

## 2.2 Next Generation Matrix Construction

For infected compartments $\mathbf{x} = [I_H, E_{1,M}, E_{2,M}, I_M, E_{1,T}, E_{2,T}, I_T]^\top$:

### 2.2.1 New Infections Matrix ($F$)

$$F = \begin{bmatrix} 0 & 0 & 0 & mabS_H^* & 0 & 0 & mabS_H^* \\ acS_M^* & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ acS_T^* & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 \end{bmatrix}$$

Where entries represent:

- $F_{1,4}, F_{1,7}$: Mosquito-to-human transmission
- $F_{2,1}, F_{5,1}$: Human-to-mosquito transmission

### 2.2.2 Transition Matrix ($V$)

$$V = \begin{bmatrix} r & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & t + s_{1M} + g & 0 & 0 & 0 & 0 & 0 \\ 0 & -s_{1M} & s_{2M} + g & 0 & 0 & 0 & 0 \\ 0 & 0 & -s_{2M} & g & 0 & 0 & 0 \\ 0 & -t & 0 & 0 & s_{1T} + g & 0 & 0 \\ 0 & 0 & 0 & 0 & -s_{1T} & s_{2T} + g & 0 \\ 0 & 0 & 0 & 0 & 0 & -s_{2T} & g \end{bmatrix}$$

Key components:

- Diagonal entries: Outflow from each compartment
- $V_{3,2}, V_{4,3}$: Untreated mosquito progression
- $V_{6,5}, V_{7,6}$: Treated mosquito progression
- $V_{5,2}$: Treatment transition $E_{1,M} \to E_{1,T}$

## 2.3 Reproduction Number Calculation

### 2.3.1 Basic Reproduction Number ($R_0$)

$$R_0 = \rho(FV^{-1}) \quad \text{at DFE}$$

where $\rho$ denotes spectral radius. This represents expected secondary infections in a fully susceptible population.

### 2.3.2 Effective Reproduction Number ($R_{\text{eff}}$)

$$R_{\text{eff}} = \rho(\tilde{F}\tilde{V}^{-1}) \quad \text{at EE}$$

where $\tilde{F}$ and $\tilde{V}$ use equilibrium values:

- $S_H^{\text{EE}} < 1$, $S_M^{\text{EE}} < S_M^*$, $S_T^{\text{EE}} < S_T^*$
- Maintains same matrix structure as $F$ and $V$

## 2.4 Numerical Implementation

- Matrix inversion via LU decomposition
- Eigenvalue calculation using QR algorithm
- DFE validation: $\|S_H + I_H - 1\| < 10^{-8}$
- EE convergence: Slope $< 10^{-6}$ over 50 iterations

# 3 Results

## 3.1 Model Dynamics

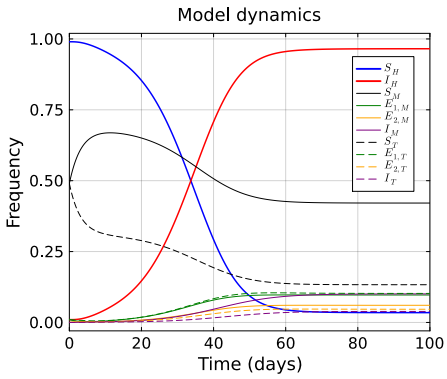


Figure 1: Convergence to endemic equilibrium with default parameters: $R_0 \approx 7.1$, $R_{eff} \approx 1.00005$.

## 3.2 Basic Reproduction Number Analysis

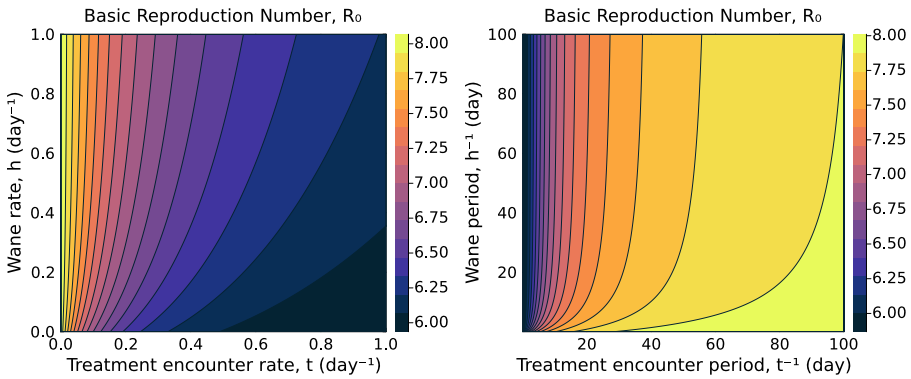


Figure 2: $R_0$ vs treatment rates $(t, h)$ and treatment periods $(1/t, 1/h)$.

## 3.3 Effective Reproduction Number

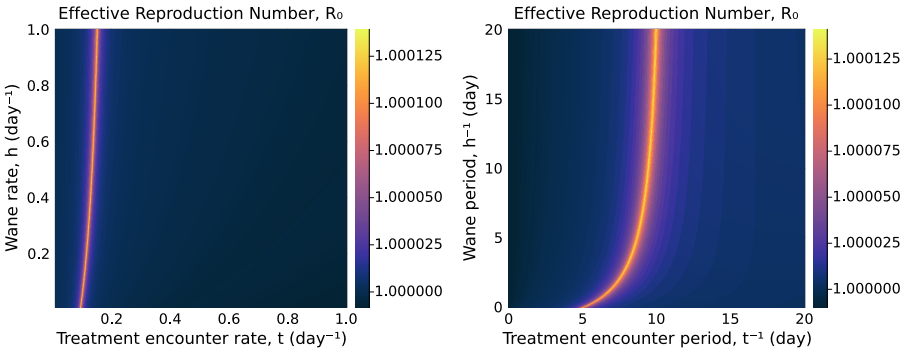


Figure 3: $R_{eff}$ vs treatment rates $(t, h)$ and treatment periods $(1/t, 1/h)$.