Report 3: Generalized Malaria Transmission Model with Arbitrary Erlang-Distributed Latent Stages

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Abstract

This report presents a generalized malaria transmission model extending the Ross-Macdonald framework by incorporating an arbitrary number of latent compartments for both treated and untreated mosquito populations, with transitions governed by Erlang distributions. The model explicitly tracks human and mosquito compartments, accounting for treatment coupling and sequential progression through latent stages. We formulate the corresponding system of ordinary differential equations (ODEs), derive the structure of the Next Generation Matrix (NGM) for computing the basic reproduction number R_0, and outline methods for determining both analytical and numerical endemic equilibria. This framework provides a flexible platform to explore the impact of latent period distributions on malaria dynamics.

1 Introduction

Classical malaria transmission models typically adopt a Ross-Macdonald structure with a fixed number of latent stages in mosquito populations, often assuming exponential or Erlang-distributed latent periods via two compartments. To generalize this framework and better capture variability in mosquito latency, we extend the model to support arbitrary numbers of latent stages in both treated and untreated mosquito subpopulations. The per-stage progression rates are now adjusted by multiplying the total rate with the number of stages so that the overall mean latent period remains constant.

This generalization allows investigation into how the shape of the latent period distribution affects key epidemiological quantities such as the basic reproduction number R_0 and the endemic equilibrium.

2 Model Structure and Dynamics

2.1 Compartments and Notation

The model divides the host and mosquito populations into the following compartments:

- **Humans:**

$$S_H \text{ (susceptible)}, \quad I_H \text{ (infected)}.$$

- **Untreated Mosquitoes:**

$$S_M,\, E_{1,M},\, E_{2,M},\, \ldots,\, E_{L_{NM},M},\, I_M.$$

- **Treated Mosquitoes:**

$$S_T,\, E_{1,T},\, E_{2,T},\, \ldots,\, E_{L_{NT},T},\, I_T.$$

The numbers L_{NM} and L_{NT} represent the number of latent stages for untreated and treated mosquitoes, respectively.

2.2 Disease-Free Equilibrium (DFE)

At the DFE, $I_H = 0$ and all infected mosquito compartments are zero. The susceptible mosquito compartments are determined by solving:

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

yielding the equilibrium values S_M^* and S_T^*.

2.3 Generalized ODE System

The dynamics are governed by the following ODEs.

Humans (SIS):

$$\frac{dS_H}{dt} = -mab\,(I_M + I_T)\,S_H + r\,I_H,$$
$$\frac{dI_H}{dt} = mab\,(I_M + I_T)\,S_H - r\,I_H.$$

Untreated Mosquitoes:

$$\begin{aligned}
\frac{dS_M}{dt} &= g + h\, S_T - ac\, I_H\, S_M - tS_M - gS_M, \\
\frac{dE_{1,M}}{dt} &= ac\, I_H\, S_M - \Big(t + s_M\, L_{NM} + g\Big) E_{1,M}, \\
\frac{dE_{i,M}}{dt} &= s_M\, L_{NM}\, E_{i-1,M} - \Big(s_M\, L_{NM} + g\Big) E_{i,M}, \quad i = 2, \ldots, L_{NM}, \\
\frac{dI_M}{dt} &= s_M\, L_{NM}\, E_{L_{NM},M} - g\, I_M.
\end{aligned}$$

Treated Mosquitoes:

$$\begin{aligned}
\frac{dS_T}{dt} &= tS_M - ac\, I_H\, S_T - hS_T - gS_T, \\
\frac{dE_{1,T}}{dt} &= ac\, I_H\, S_T + t\, E_{1,M} - \Big(s_T\, L_{NT} + g\Big) E_{1,T}, \\
\frac{dE_{i,T}}{dt} &= s_T\, L_{NT}\, E_{i-1,T} - \Big(s_T\, L_{NT} + g\Big) E_{i,T}, \quad i = 2, \ldots, L_{NT}, \\
\frac{dI_T}{dt} &= s_T\, L_{NT}\, E_{L_{NT},T} - g\, I_T.
\end{aligned}$$

3 Basic Reproduction Number $\mathbf{R_0}$

The Next Generation Matrix (NGM) method is used to compute R_0. The infected state vector is defined as

$$\mathbf{x} = \Big[I_H,\, E_{1,M},\, \ldots,\, E_{L_{NM},M},\, I_M,\, E_{1,T},\, \ldots,\, E_{L_{NT},T},\, I_T\Big]^\top.$$

3.1 F and V Matrices

The matrices **F** and **V** represent, respectively, new infections and transitions between infected compartments.

New infections arise from:

- Transmission from infectious mosquitoes to humans.
- Transmission from infectious humans to the first latent compartments in both untreated and treated branches.

Transitions (in $\mathbf{V}$) include recovery, death, progression through latent stages (with per-stage progression rates now $s_M\, L_{NM}$ or $s_T\, L_{NT}$), and treatment transfer.

The NGM is:

$$\mathbf{NGM} = \mathbf{F}\,\mathbf{V}^{-1},$$

and the basic reproduction number is given by:

$$R_0 = \rho(\mathbf{NGM}),$$

where ρ denotes the spectral radius.

4 Endemic Equilibrium Calculation

4.1 Analytical Approximation

Analytical expressions for mosquito compartments at endemic equilibrium are derived as functions of I_H, based on the steady-state balance of flows. A consistency equation is then formed:

$$\frac{I_H}{1 - I_H} = \frac{m\,a\,b\,\big(I_M(I_H) + I_T(I_H)\big)}{r},$$

which is solved numerically for I_H^*. Other compartmental values then follow directly.

4.2 Numerical ODE Integration

Alternatively, the endemic equilibrium can be obtained by perturbing the DFE (by seeding a small infection) and iteratively integrating the ODE system. Convergence is assessed by fitting linear regressions to the last N iterates of the state variables. When the slopes fall below a specified tolerance, the average of the final set of iterates is taken as the endemic equilibrium.

5 Results

5.1 R0 for treatment rate/period parameters

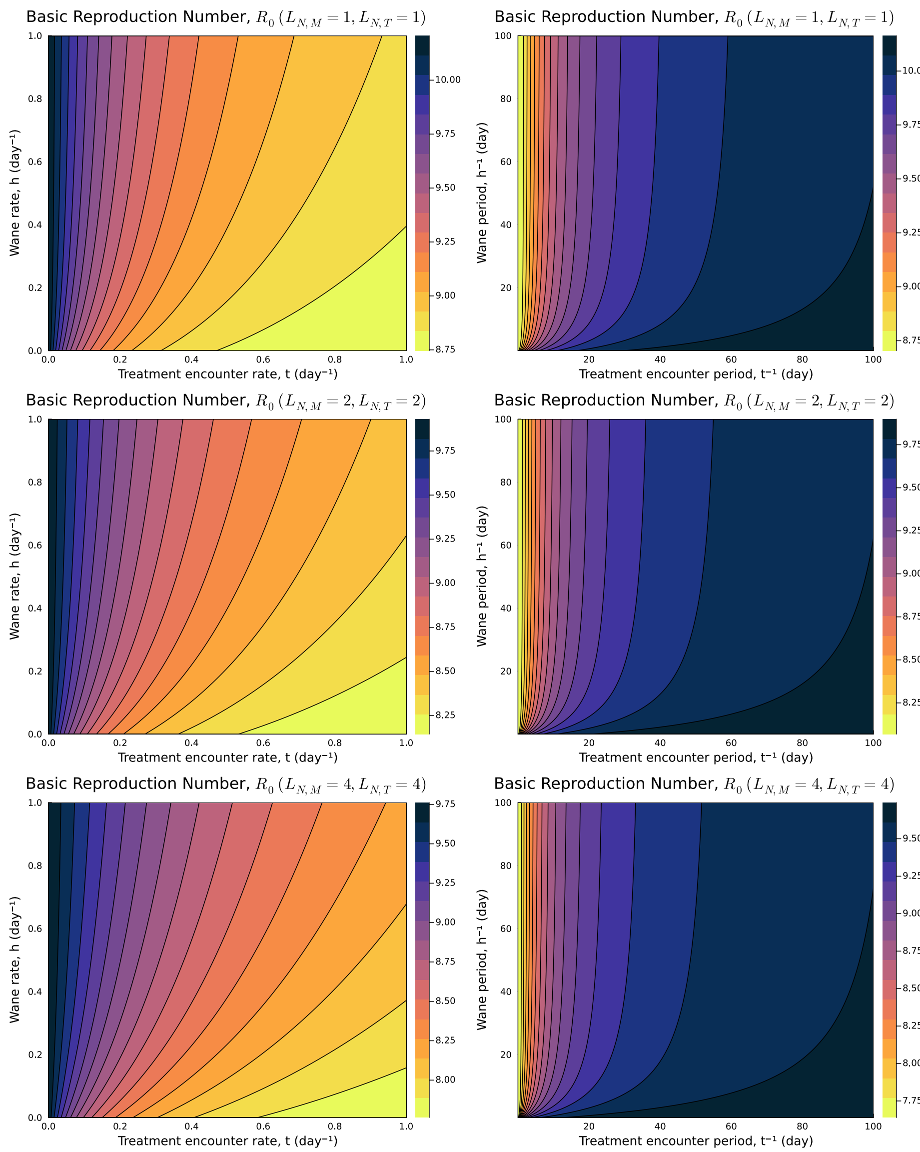

Figure 1: **R0 for treatment rate/period parameters.** The left panels show the basic reproduction number R_0 as a function of the treatment rate, while the right panels show R_0 as a function of the treatment period.

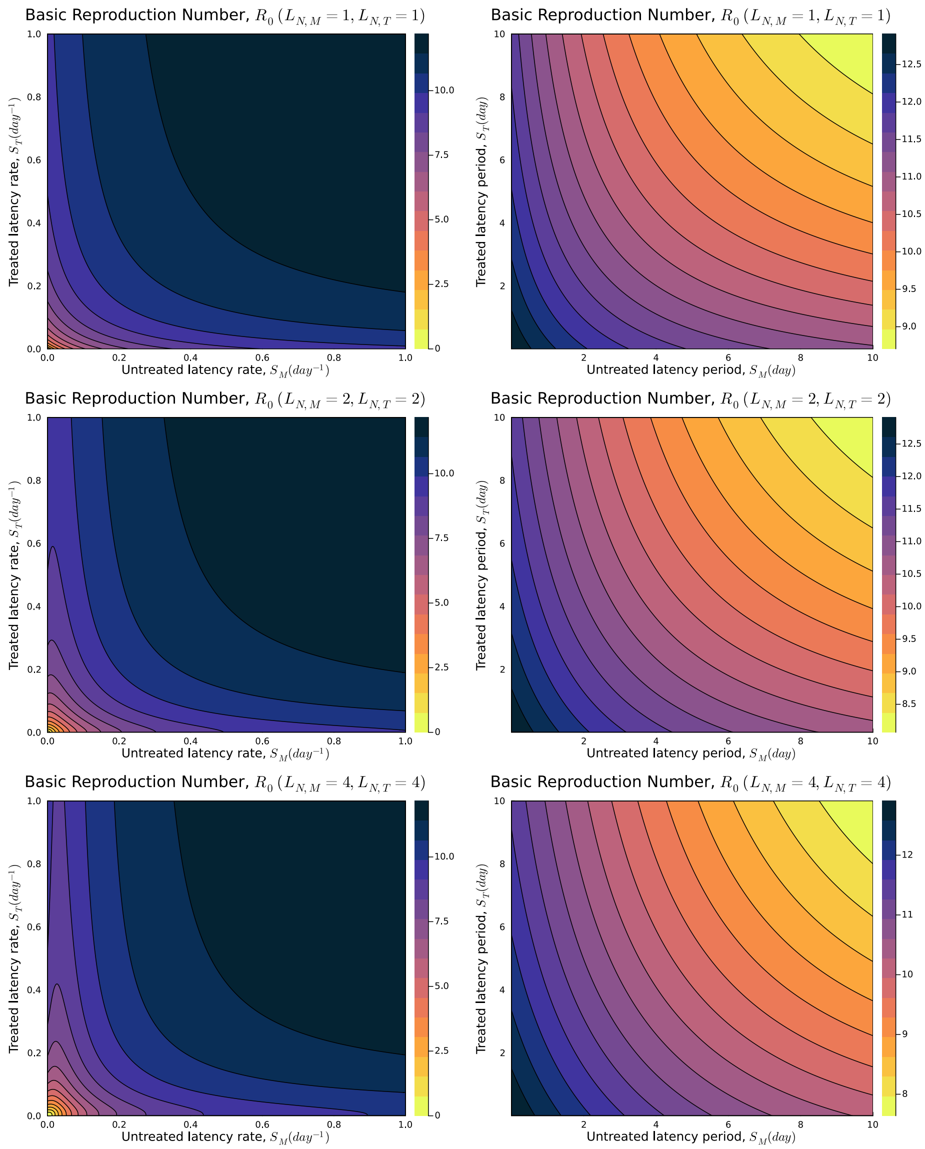

Figure 2: **R0 for latency rate/period parameters.** The left panels show the basic reproduction number R_0 as a function of the latency rate, while the right panels show R_0 as a function of the latency period.

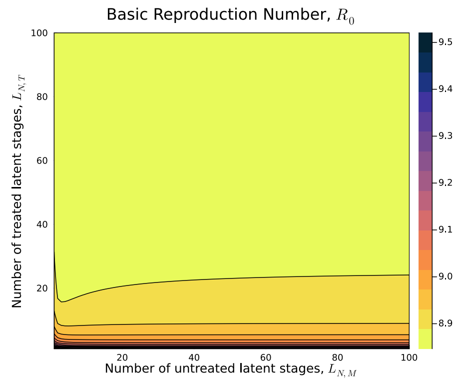

Figure 3: **R0 for number of latent stages.** The basic reproduction number R_0 as a function of the number of latent stages in untreated and treated mosquitoes.

5.2 Infections Humans at endemic equilibrium

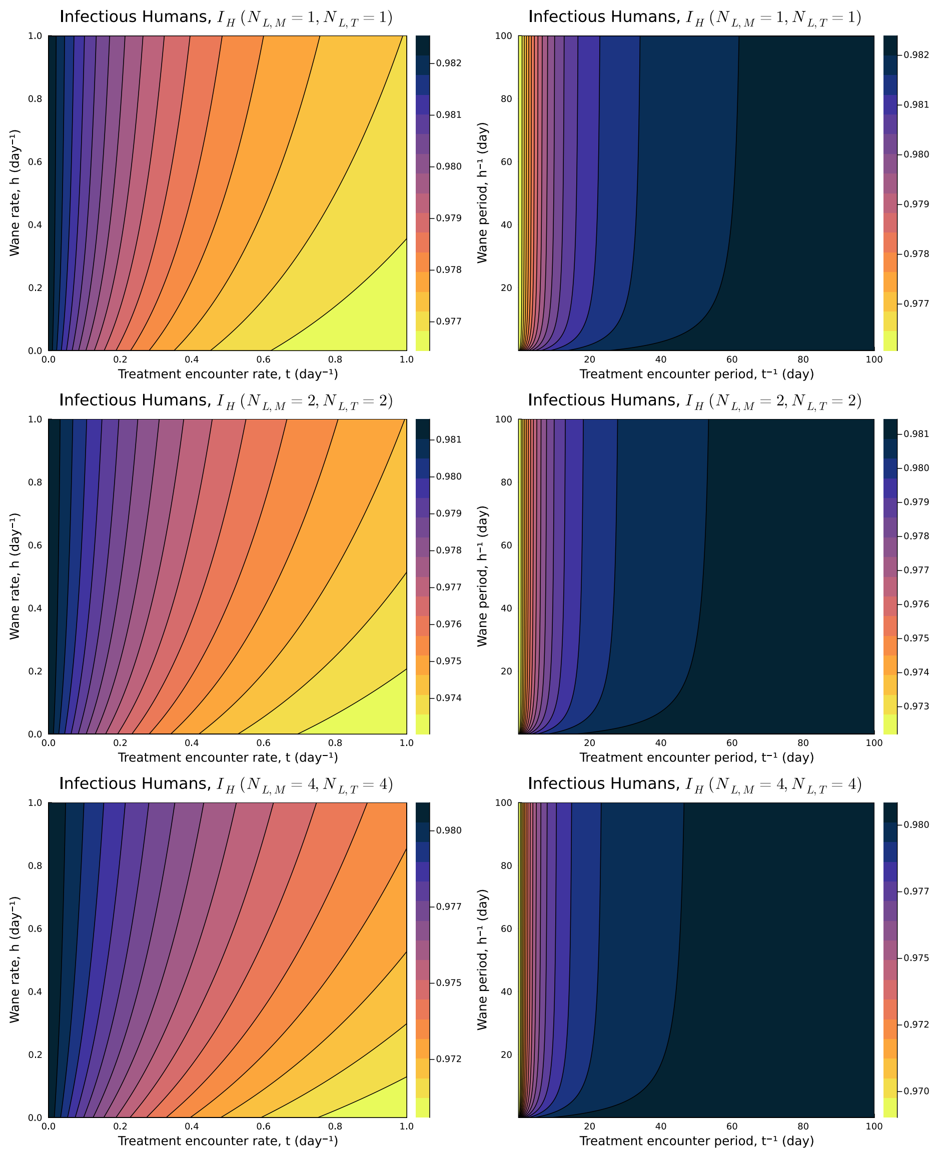

Figure 4: **Infections Humans at endemic equilibrium.** The left panels show the infected humans I_H as a function of the treatment rate, while the right panels show I_H as a function of the treatment period.

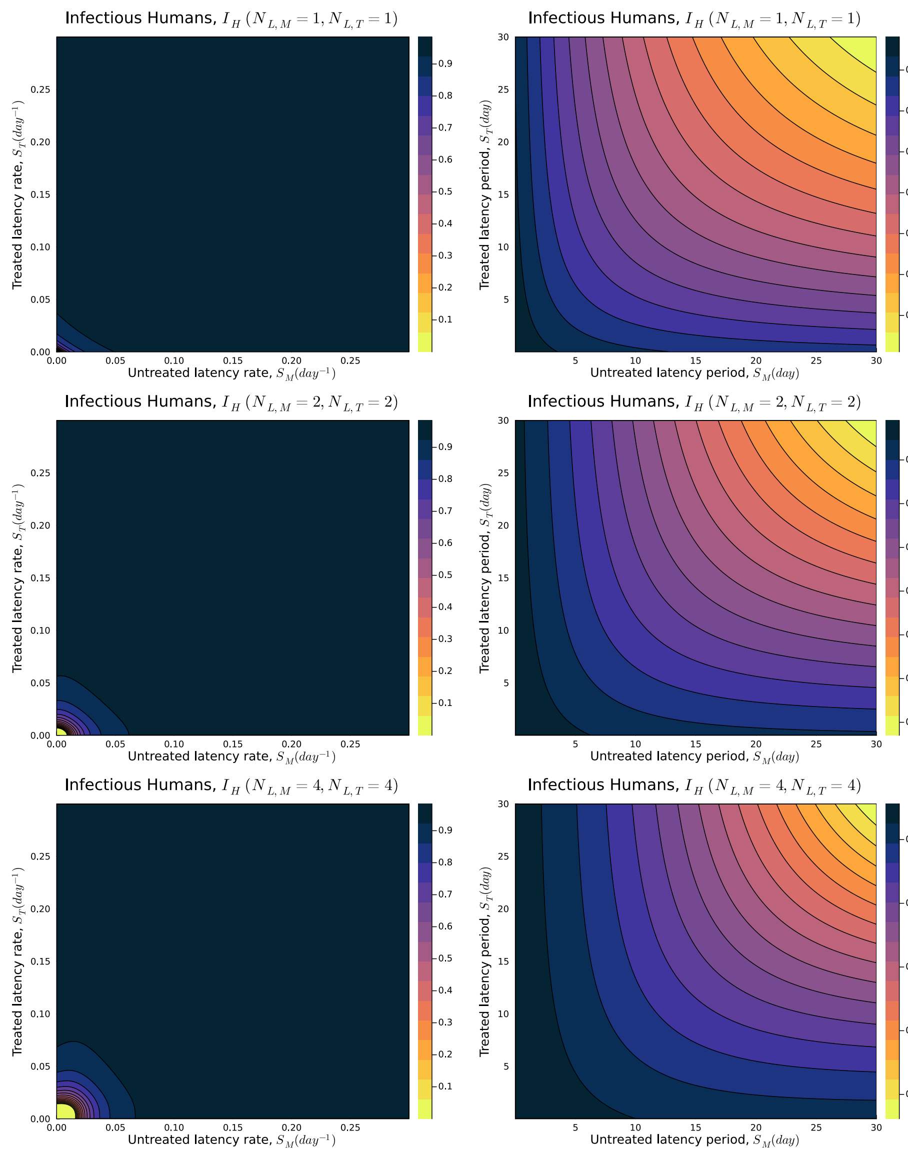

Figure 5: **Infections Humans at endemic equilibrium.** The left panels show the infected humans I_H as a function of the latency rate, while the right panels show I_H as a function of the latency period.