

Extensions of the Ross-Macdonald Malaria Model

Abstract

We present a unified account of our development and analysis of a series of increasingly detailed malaria transmission models. Beginning with the classical Ross-Macdonald SIS framework, we first incorporate an extrinsic incubation period and a mosquito treatment branch, derive analytic and numerical expressions for the disease-free and endemic equilibria and the basic reproduction number R_0 . We then generalize the mosquito latent period to an arbitrary Erlang distribution of L_{NM} (untreated) and L_{NT} (treated) stages. Finally, we calibrate the biting rate a so that the no-treatment human prevalence matches a target of 45%.

Default Parameter Set

As a baseline for all simulations we adopt:

Parameter	Description	Value
a	Biting rate (day^{-1})	0.028
b	Human-to-mosquito transmission probability	0.50
c	Mosquito-to-human transmission probability	0.50
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})	0.10
t	Treatment encounter rate (day^{-1})	0.10
L_{NM}	# latent stages, untreated mosquitoes	2
L_{NT}	# latent stages, treated mosquitoes	2
s_M	Total progression rate, untreated latency	0.20
s_T	Total progression rate, treated latency	0.10

Table 1: Default parameter values, calibrated so that in the absence of treatment ($t = 0$) the endemic human prevalence is ≈ 0.45 .

1. Classical Ross-Macdonald SIS Model

The baseline model divides the human population into susceptible S_H and infected I_H (with $S_H + I_H = 1$), and the mosquito population into susceptible S_M and infected I_M . The dynamics are

$$\begin{aligned}\frac{dS_H}{dt} &= -m a b I_M S_H + r I_H, & \frac{dI_H}{dt} &= m a b I_M S_H - r I_H, \\ \frac{dS_M}{dt} &= g - a c I_H S_M - g S_M, & \frac{dI_M}{dt} &= a c I_H S_M - g I_M.\end{aligned}$$

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Disease-Free Equilibrium (DFE) At DFE: $I_H = I_M = 0$, $S_H = 1$, $S_M = 1$.

2. Adding Mosquito Latency and Treatment

To capture the extrinsic incubation period (EIP) we introduce two latent stages for untreated mosquitoes ($E_{1,M}, E_{2,M}$), and similarly ($E_{1,T}, E_{2,T}$) for treated mosquitoes. Susceptible mosquitoes may become treated at rate t , and treated status wanes at rate h . The full system is:

$$\begin{aligned}\frac{dS_H}{dt} &= -m a b (I_M + I_T) S_H + r I_H, & \frac{dI_H}{dt} &= m a b (I_M + I_T) S_H - r I_H, \\ \frac{dS_M}{dt} &= g + h S_T - a c I_H S_M - t S_M - g S_M, \\ \frac{dE_{1,M}}{dt} &= a c I_H S_M - (t + s_{1M} + g) E_{1,M}, \\ \frac{dE_{2,M}}{dt} &= s_{1M} E_{1,M} - (s_{2M} + g) E_{2,M}, \\ \frac{dI_M}{dt} &= s_{2M} E_{2,M} - g I_M, \\ \frac{dS_T}{dt} &= t S_M - a c I_H S_T - h S_T - g S_T, \\ \frac{dE_{1,T}}{dt} &= a c I_H S_T + t E_{1,M} - (s_{1T} + g) E_{1,T}, \\ \frac{dE_{2,T}}{dt} &= s_{1T} E_{1,T} - (s_{2T} + g) E_{2,T}, \\ \frac{dI_T}{dt} &= s_{2T} E_{2,T} - g I_T.\end{aligned}$$

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DFE for Extended Model Setting all infected compartments to zero and $S_H = 1$, we solve

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

giving

$$S_M^* = \frac{h+g}{t+h+g}, \quad S_T^* = \frac{t}{t+h+g}.$$

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Next-Generation Matrix and R_0 Define the infected-state vector

$$\mathbf{x} = [I_H, E_{1,M}, E_{2,M}, I_M, E_{1,T}, E_{2,T}, I_T]^T.$$

The *new-infection* matrix \mathbf{F} and *transition* matrix \mathbf{V} at DFE are

$$F_{1,4} = F_{1,7} = m a b S_H^*, \quad F_{2,1} = a c S_M^*, \quad F_{5,1} = a c S_T^*,$$

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

and

$$R_0 = \rho(F V^{-1}) = \frac{m a^2 b c}{r g} [\pi_M + \pi_T + \pi_{\text{extra}}],$$

with

$$\begin{aligned} \pi_M &= \frac{(h+g) s_{1M} s_{2M}}{(t+h+g)(t+s_{1M}+g)(s_{2M}+g)}, \\ \pi_T &= \frac{t s_{1T} s_{2T}}{(t+h+g)(s_{1T}+g)(s_{2T}+g)}, \\ \pi_{\text{extra}} &= \frac{(h+g) t s_{1T} s_{2T}}{(t+h+g)(t+s_{1M}+g)(s_{1T}+g)(s_{2T}+g)}. \end{aligned}$$

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Endemic Equilibrium

Analytical: Solve for I_H^* from

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

then recover all other compartments.

Numerical: Starting from a perturbed DFE ($I_H = 10^{-3}$), integrate the ODEs in daily steps, store the last N states, fit a linear slope for each variable, and stop when all slopes $< \delta$. The mean of the final states is taken as the equilibrium.

3. Generalization to Erlang-Distributed Latency

To allow an arbitrary number of latent stages, we set

$$s_{M,\text{stage}} = s_M L_{NM}, \quad s_{T,\text{stage}} = s_T L_{NT},$$

so that the mean untreated EIP remains $1/s_M$ and treated EIP remains $1/s_T$. The state vector extends to

$$(S_H, I_H, S_M, E_{1,M}, \dots, E_{L_{NM},M}, I_M, S_T, E_{1,T}, \dots, E_{L_{NT},T}, I_T).$$

The ODEs and NGM construction proceed as before, with sums and progressions over L_{NM} and L_{NT} stages.

4. Calibration of the Biting Rate a

Our initial default $a = 0.2$ yielded $I_H^* \approx 0.90$. To match a target prevalence $I_H^* \approx 0.45$ under no treatment ($t = 0$) we:

1. Fixed all other parameters.
2. Sampled a over $[10^{-5}, 10^{-1}]$ on a log scale.
3. For each a , computed $I_H^*(a)$ via the numerical equilibrium routine.
4. Plotted I_H^* vs. a and selected the value $a \approx 0.028$ satisfying $I_H^* = 0.45$.

Results

We start from a generally used set of parameters and then explore the effects of varying the treatment rate t , the treatment waning rate h , and the latency progression rates. The model we initially developed is the classical Ross-Macdonald SIS model extended to include mosquito latency and treatment. The parameters values are as follows:

Parameter	Description	Value
a	Biting rate (day^{-1})	0.2
b	Human-to-mosquito transmission probability	0.50
c	Mosquito-to-human transmission probability	0.50
m	Mosquito-to-human ratio	20.0
r	Human recovery rate (day^{-1})	0.01
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Table 2: Default parameter values for this stage.

The model dynamics are visualized in following figure:

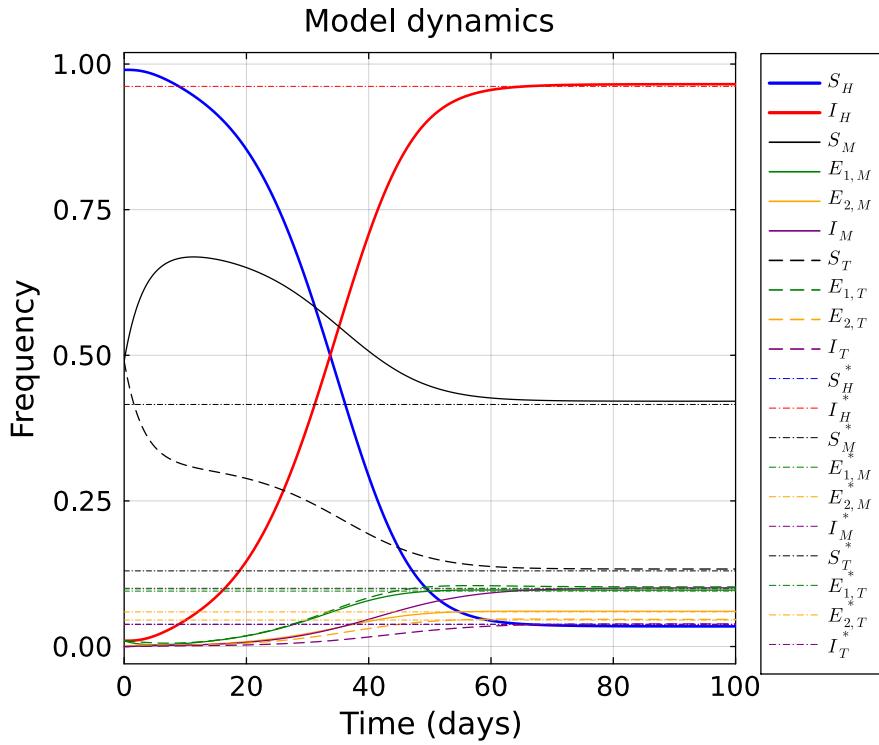


Figure 1: Dynamics of the Ross-Macdonald malaria model with mosquito latency and treatment.

Now we explore the effects of varying the treatment rate t , the treatment waning rate h , and the latency progression rates. The following figures illustrate how these parameters influence the disease dynamics and equilibria.

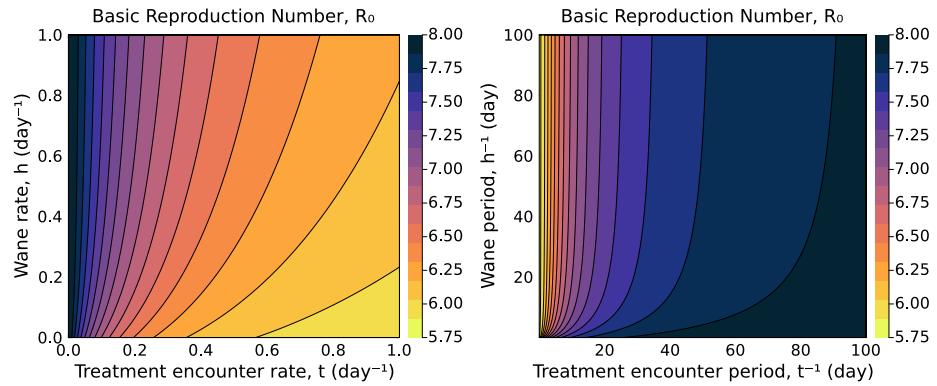


Figure 2: Heatmaps of the basic reproduction number R_0 as a function of treatment rate t and treatment waning rate h or treatment encounter period t and treatment waning period h .

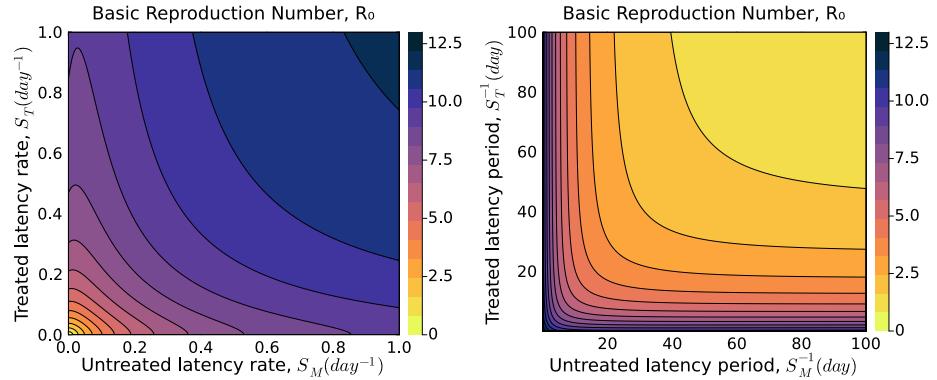


Figure 3: Heatmaps of the basic reproduction number R_0 as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} .

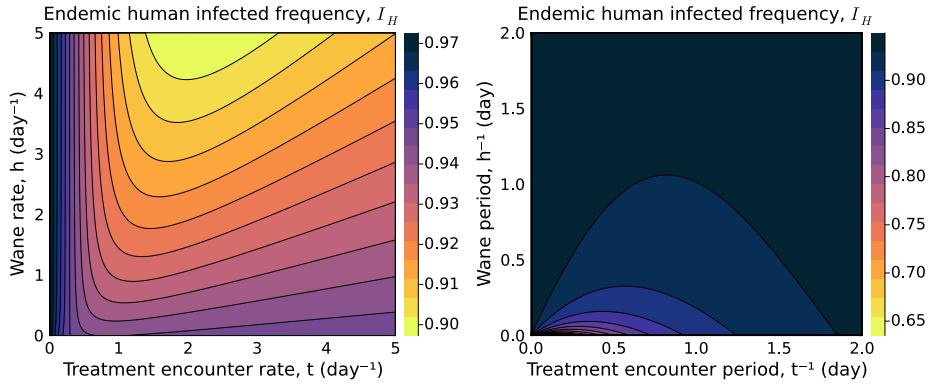


Figure 4: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of treatment rate t and treatment waning rate h or treatment encounter period t and treatment waning period h .

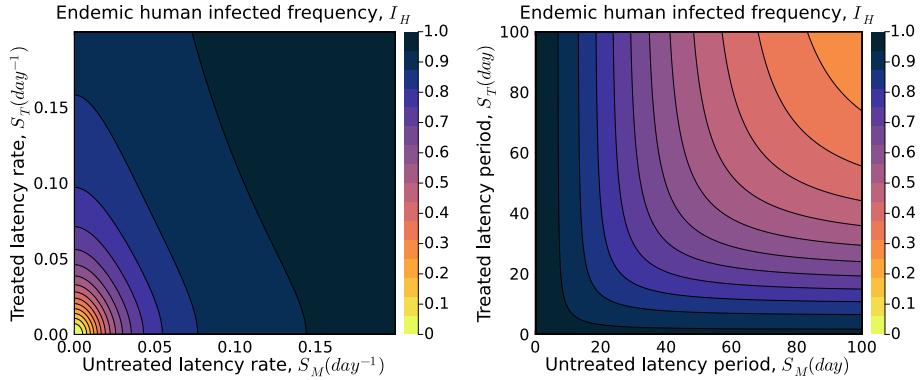


Figure 5: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} .

Now we employ the erlang distribution to generalize the mosquito latency with arbitrary number of stages. The following figures illustrate the effects of varying the number of latent stages for untreated and treated mosquitoes on the basic reproduction number R_0 and the human infected proportion I_H^* at equilibrium.

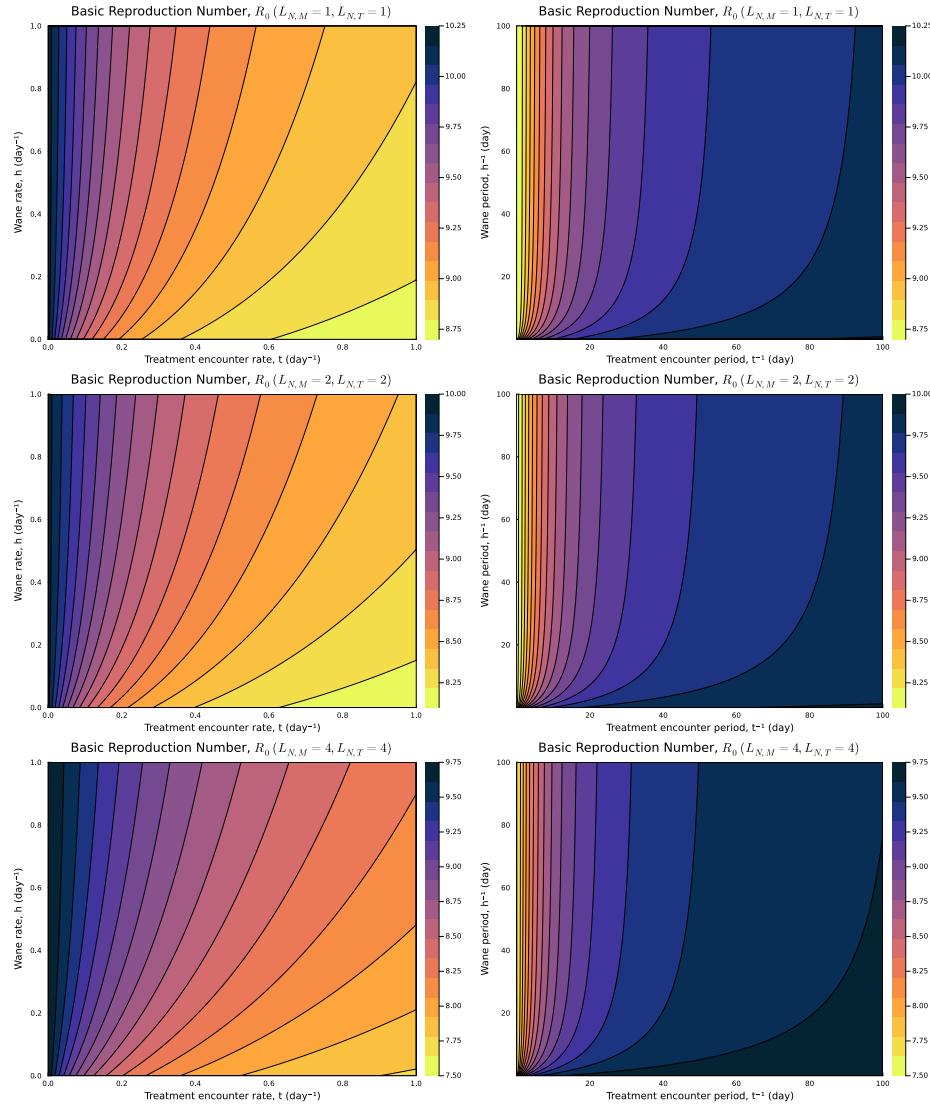


Figure 6: Heatmaps of the basic reproduction number R_0 as a function of treatment rate t and treatment waning rate h or treatment encounter period t and treatment waning period h for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes.

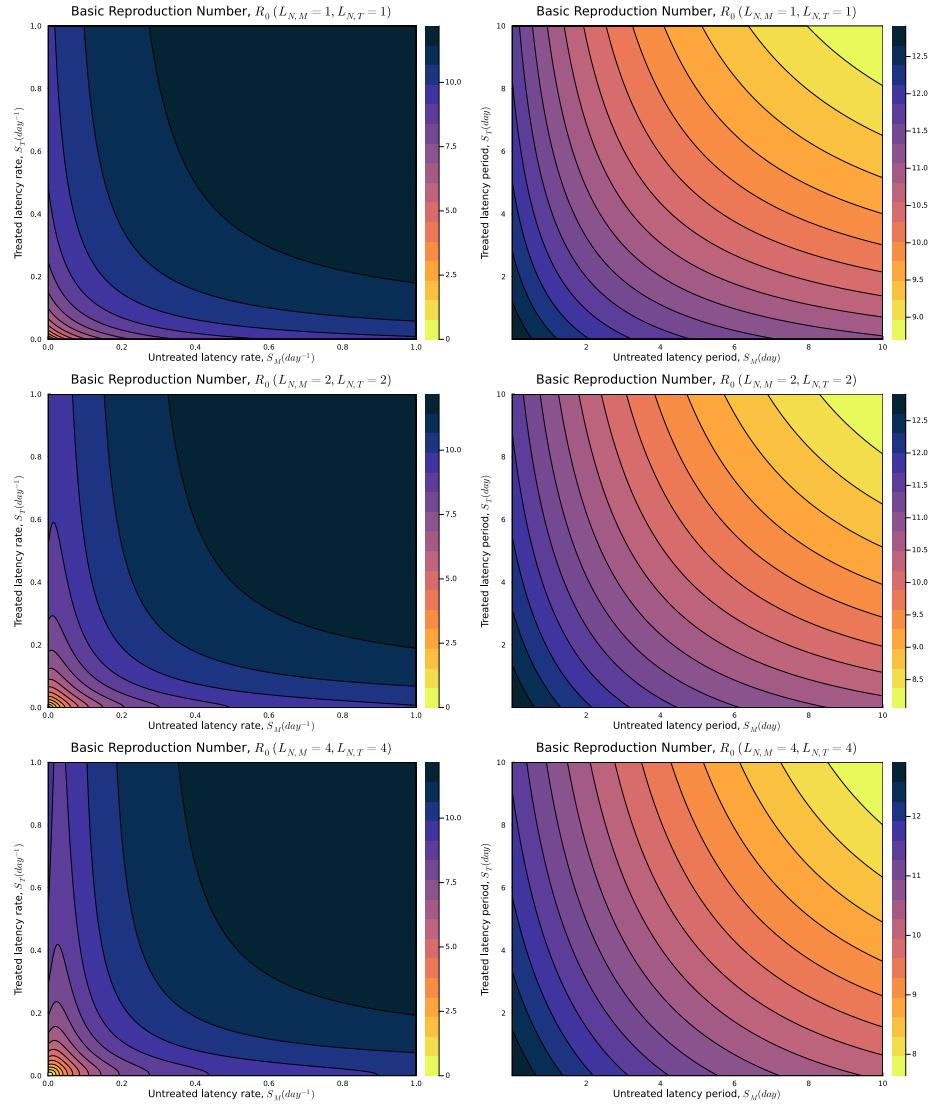


Figure 7: Heatmaps of the basic reproduction number R_0 as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes.

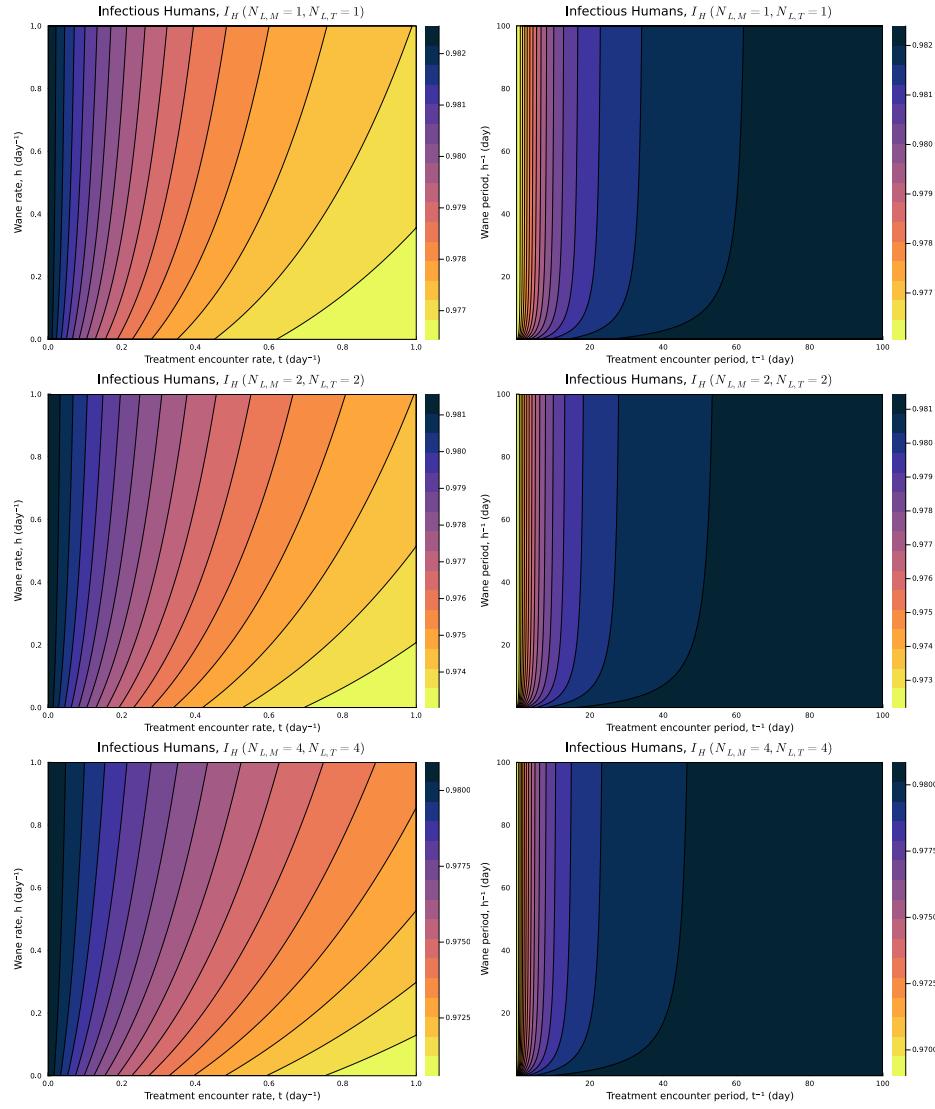


Figure 8: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of treatment rate t and treatment waning rate h or treatment encounter period t and treatment waning period h for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes.

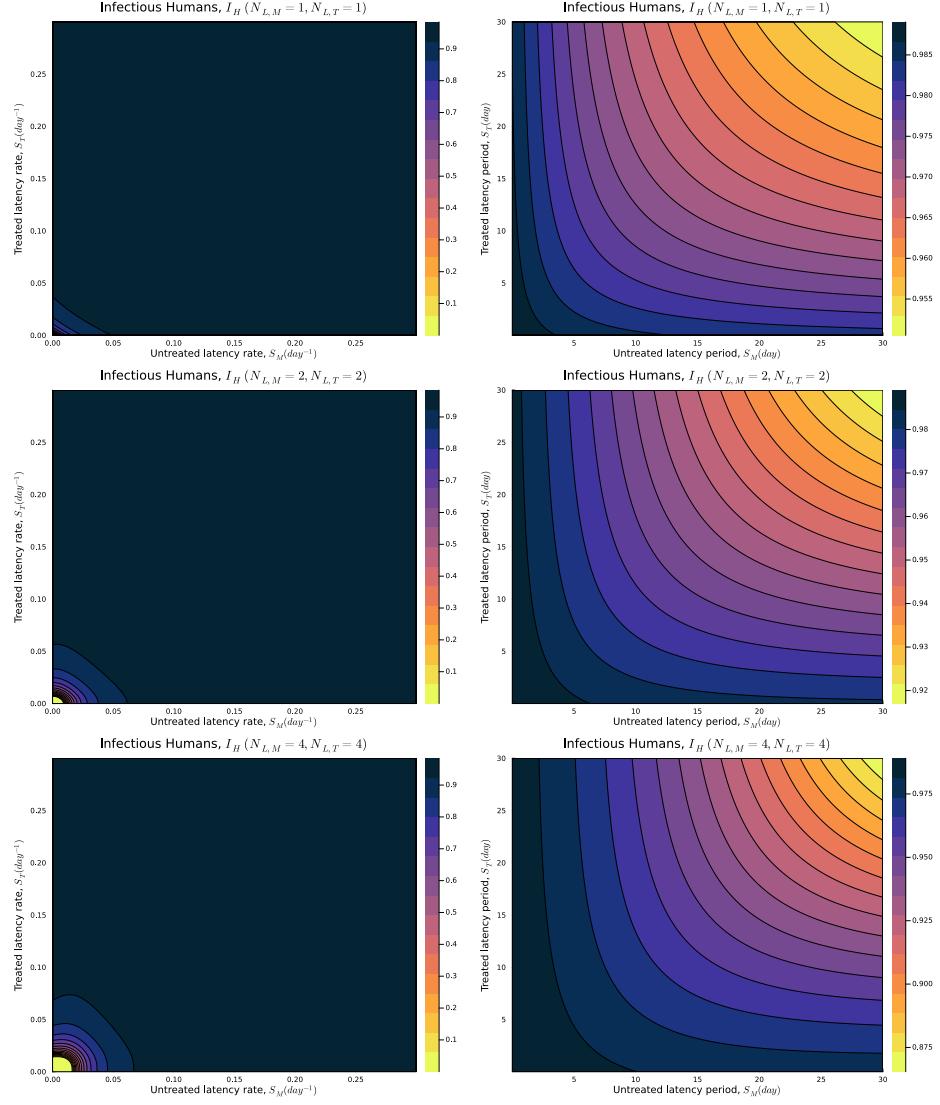


Figure 9: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes.

As it can be seen from the figures, the prevalence is much higher than what we expected, and the basic reproduction number R_0 is also very high. Generally, we expect the prevalence to be around 45% in the absence of treatment, but here it is around 90%. This indicates that

the model parameters need to be adjusted further to achieve a more realistic representation of malaria transmission dynamics. Therefore, we will need to calibrate the biting rate a to achieve the target prevalence of 45% in the absence of treatment. The following illustration shows the calibration process:

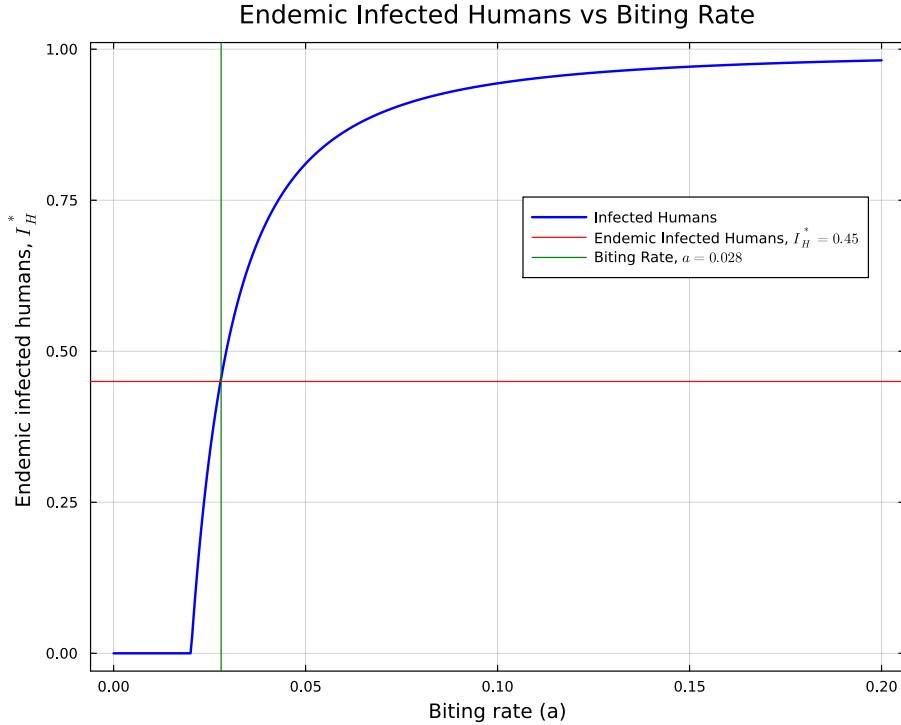


Figure 10: The plot shows the prevalence of malaria in humans as a function of the biting rate a . The red dashed line indicates the target prevalence of 45%. The blue line shows the prevalence calculated from the model, and the green line shows the required biting rate. Therefore, the biting rate a is calibrated to approximately 0.028 to achieve the target prevalence of 45%.

From now on, we will use the calibrated biting rate $a = 0.028$ for all further simulations and analyses. The heatmaps of the basic reproduction number R_0 and the human infected proportion I_H^* at equilibrium will be recalculated with this new value of a and are as follows:

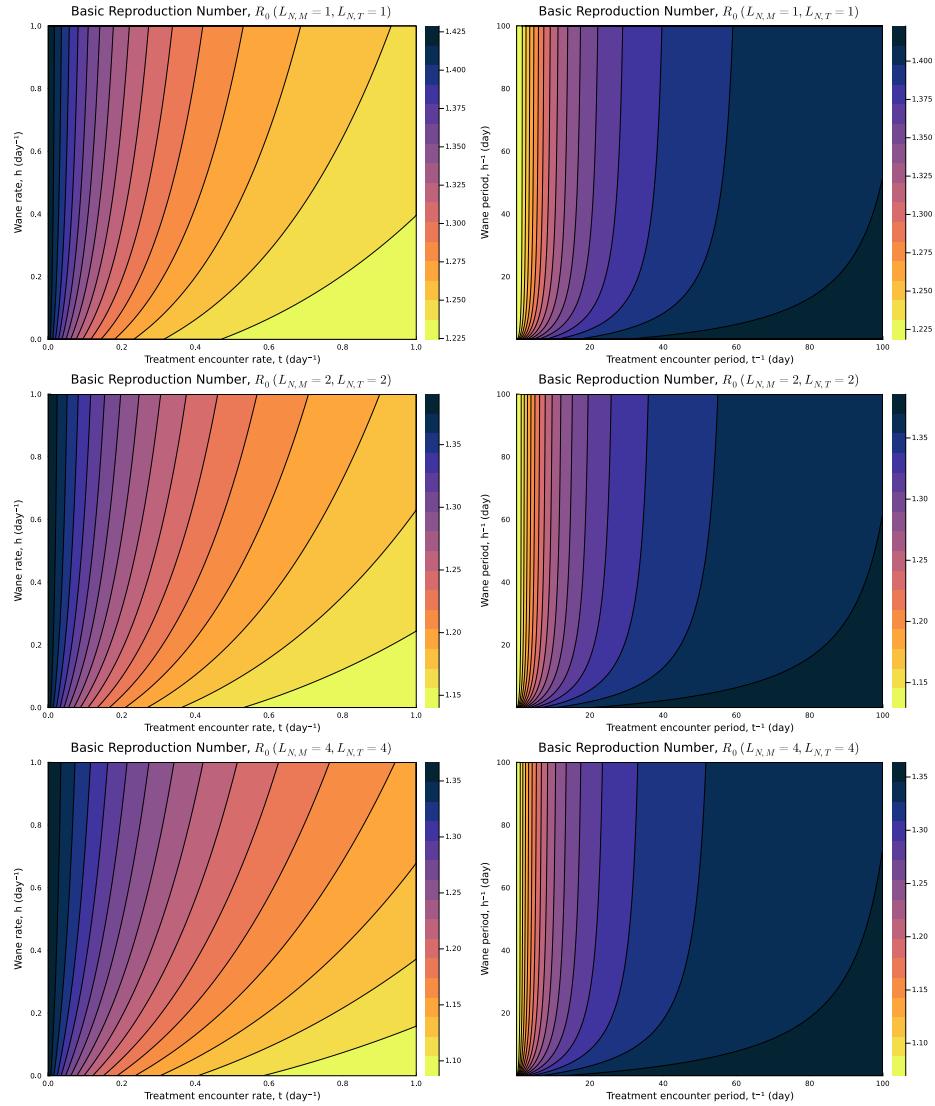


Figure 11: Heatmaps of the basic reproduction number R_0 as a function of treatment rate t and treatment waning rate h or treatment encounter period t^{-1} and treatment waning period h^{-1} for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes with calibrated biting rate $a = 0.028$.

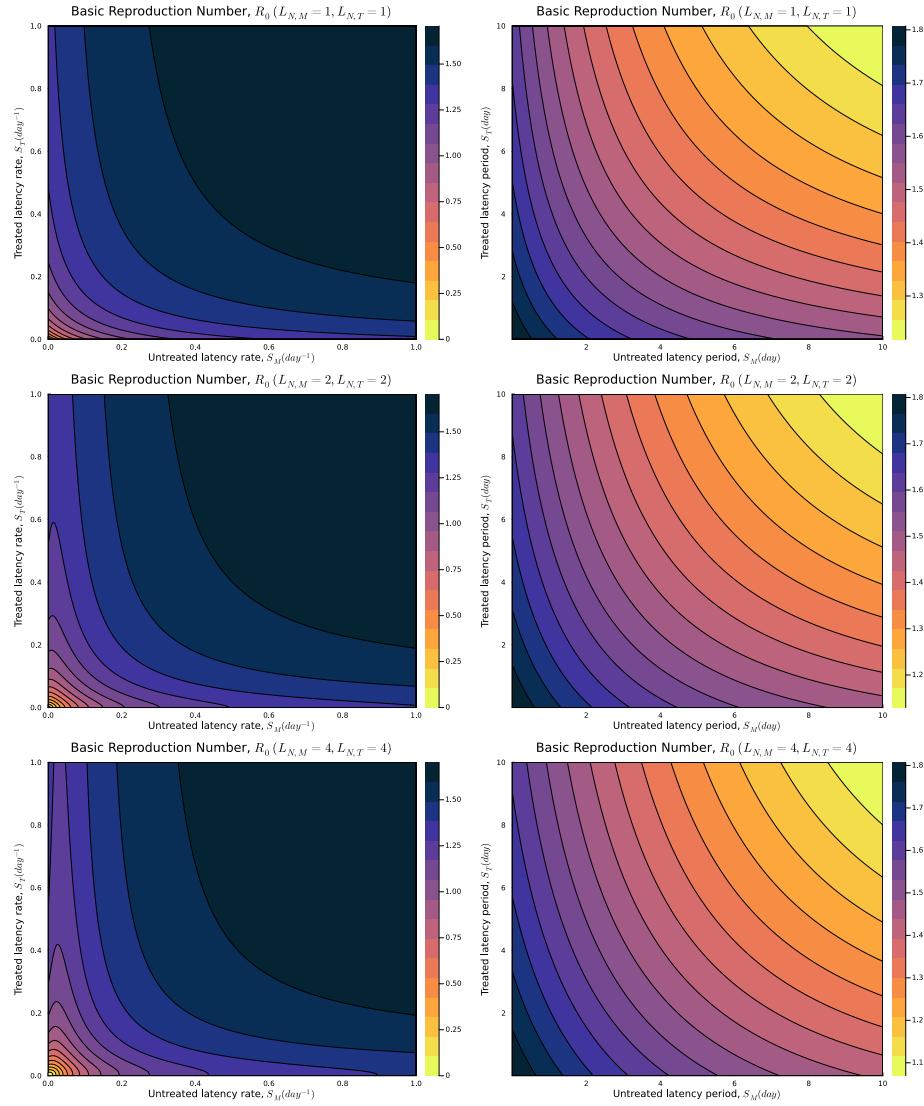


Figure 12: Heatmaps of the basic reproduction number R_0 as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes with calibrated biting rate $a = 0.028$.

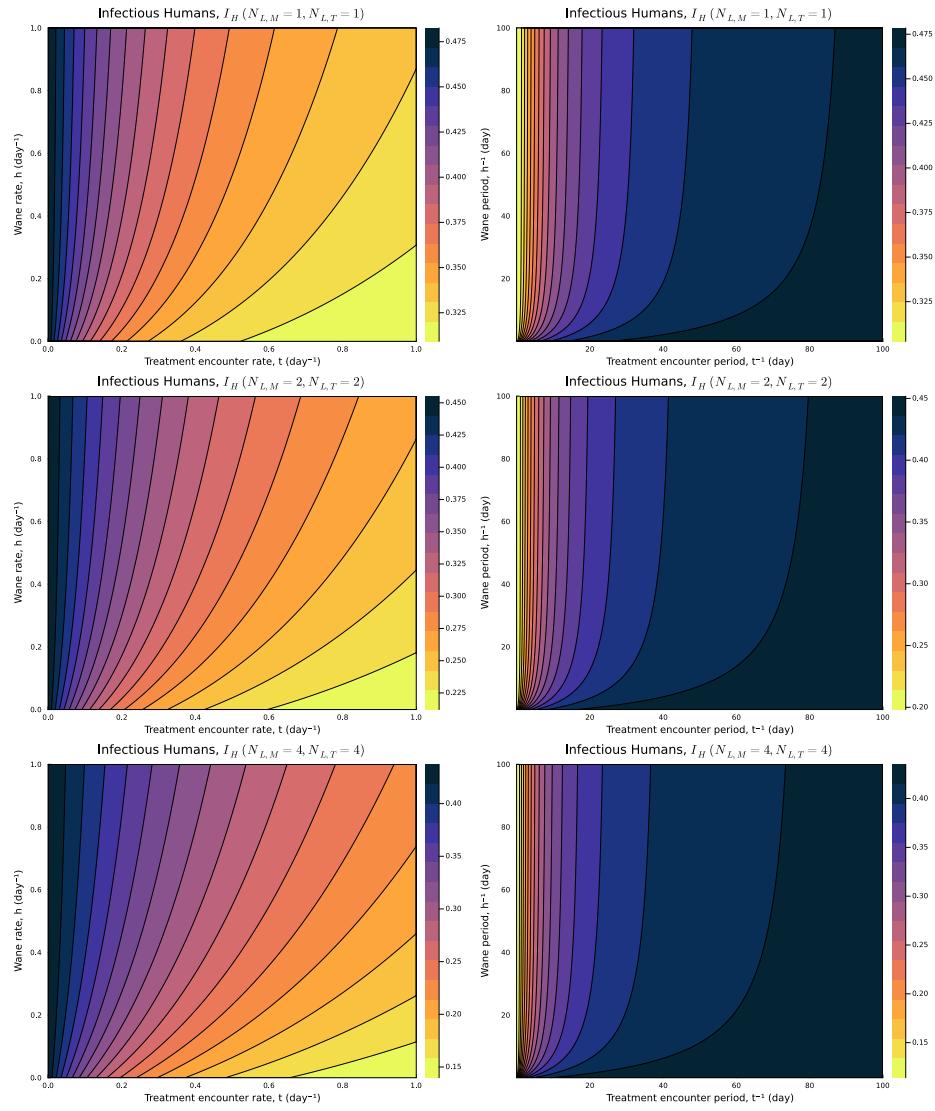


Figure 13: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of treatment rate t and treatment waning rate h or treatment encounter period t and treatment waning period h for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes with calibrated biting rate $a = 0.028$.

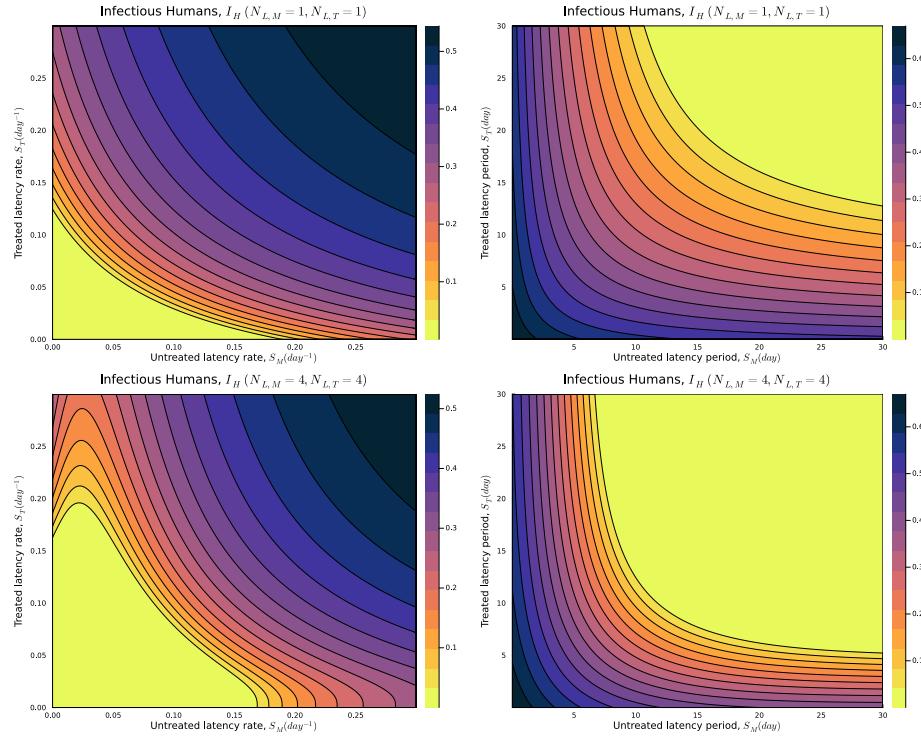


Figure 14: Heatmaps of the human infected proportion I_H^* at equilibrium (prevalence) as a function of untreated mosquito latency progression rate s_M and treated mosquito latency progression rate s_T or untreated mosquito latency period L_{NM} and treated mosquito latency period L_{NT} for the generalized model with erlang-distributed mosquito latency with 1, 2, and 4 latency stages for both untreated and treated mosquitoes with calibrated biting rate $a = 0.028$.