D.5 Malaria Transmission Model

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Abstract

Vector-borne diseases like malaria rely on vectors such as mosquitoes to transmit infections between humans. This study uses a mathematical model, based on differential equations, to explore the dynamics of malaria transmission. The model incorporates mosquito birth rates, death rates and human recovery rates, simulating scenarios under varying initial infection conditions, mosquito bite rates, and total mosquito populations.

Simulations reveal that while the initial infected human or mosquito populations influence the time to equilibrium, they do not affect the stable equilibrium point of the system. Bite rate (β) significantly impacts both the equilibrium infection levels and the speed at which equilibrium is reached, with lower bite rates reducing the infected population size. Similarly, a decrease in the total mosquito population drastically reduces human infections, underscoring the critical role of vector control in disease mitigation.

Introduction

Vector-borne diseases are infectious diseases that require a vector, such as a mosquito or tick, to transmit the infectious agent to humans. A good example of such a disease is malaria. Humans (and other mammals) contract malaria by being bitten by infected Anopheles mosquitoes, and the mosquitoes similarly become infected when they bite an infected mammal. Transmission doesn't occur directly from individual to individual; as such, any model that doesn't include the vector is incomplete. The following differential equations can be used as a model for malaria, treating the illness

as SIS in the human population and SI in the mosquito, and ignoring demographic processes among people but explicitly including "births" and deaths of mosquitoes (but with constant population size).

Human:

$$\frac{dS_H}{dt} = -\epsilon_1 \beta \frac{S_H}{N_H} I_M + \gamma I_H$$

$$\frac{dI_H}{dt} = +\epsilon_1 \beta \frac{S_H}{N_H} I_M - \gamma I_H$$

Mosquito:

$$\frac{dS_M}{dt} = \alpha N_M - \epsilon_2 \beta \frac{I_H}{N_H} S_M - \alpha S_M$$

$$\frac{dI_M}{dt} = +\epsilon_2 \beta \frac{I_H}{N_H} S_M - \alpha I_M$$

Parameter Definitions:

- β: Mosquito feeding rate.

- ϵ_1 and ϵ_2: Fractions of bites involving a susceptible/infective pair that lead to transfer of the infectious agent.

- γ: Human recovery rate.

- α: Mosquito birth/death rate.

For the baseline model, the simulation will be implemented in MATLAB using the Forward Euler algorithm with a total simulation length of 200 days and a time step of 0.01. Our baseline parameters include $\beta = 5$, $\epsilon_1 = 0.01$, $\epsilon_2 = 0.1$, $\gamma = 0.05$, and $\alpha = 0.02$. The total population sizes for both humans and mosquitoes are set to 10^6. We will change these parameters to observe how each parameter affects the infection rate and the total infected individuals at the end of the simulation. Figures 1 and 2 show the code for our model:

```
global beta epsilon1 epsilon2 gamma alpha N_H N_M
beta = 5;
epsilon1 = .01;
epsilon2 = .1;
gamma = .05;
alpha = .02;

N_H = 10^6;
N_M = 10^6;
I_H0 = N_H * 0;
S_H0 = N_H - I_H0;
I_M0 = N_M * .1;
S_M0 = N_M - I_M0;

total_time = 200; % days
h = .01; % time step
num_steps = total_time/h;

function dS_H = H_dS_dt(S_H, I_M , I_H)
    global beta epsilon1 gamma N_H
    dS_H = -epsilon1 * beta * (S_H / N_H) * I_M + gamma * I_H;
end

function dI_H = H_dI_dt(S_H, I_M, I_H)
    global beta epsilon1 gamma N_H
    dI_H = epsilon1 * beta * (S_H / N_H) * I_M - gamma * I_H;
end

function dS_M = M_dS_dt(I_H, S_M)
    global alpha N_M epsilon2 beta N_H
    dS_M = alpha * N_M - epsilon2 * beta * (I_H / N_H) * S_M - alpha * S_M;
end

function dI_M = M_dI_dt(I_H, S_M, I_M)
    global alpha N_H epsilon2 beta
    dI_M = epsilon2 *  beta * (I_H / N_H) * S_M - alpha * I_M;
end
```

Figure 1: Initial variables to our code

```matlab
H_I = zeros(1, 1 + num_steps);
H_S = zeros(1, 1 + num_steps);
M_I = zeros(1, 1 + num_steps);
M_S = zeros(1, 1 + num_steps);
t_values = zeros(1, num_steps+1); %initializing array to store each step
H_I(1) = I_H0;
H_S(1) = S_H0;
M_I(1) = I_M0;
M_S(1) = S_M0;
t = 0;
for i = 1:num_steps
    t = t + h;

    dS_H = H_dS_dt(H_S(i), M_I(i), H_I(i));
    H_S(i+1) = H_S(i) + dS_H * h;

    dI_H = H_dI_dt(H_S(i), M_I(i), H_I(i));
    H_I(i+1) = H_I(i) + dI_H * h;

    dS_M = M_dS_dt(H_I(i), M_S(i));
    M_S(i+1) = M_S(i) + dS_M * h;

    dI_M = M_dI_dt(H_I(i), M_S(i), M_I(i));
    M_I(i+1) = M_I(i) + dI_M * h;

    t_values(i+1) = t;
end

plot(t_values, H_S, 'b-', 'DisplayName', 'Susceptible Humans')
hold on
plot(t_values, H_I, 'r-', 'DisplayName', 'Infected Humans')
plot(t_values, M_S, 'g-', 'DisplayName', 'Susceptible Mosquitoes')
plot(t_values, M_I, 'k-', 'DisplayName', 'Infected Mosquitoes')
xlabel('Time (days)')
ylabel('Population')
title('Malaria Model Simulation')
legend('show')
grid on
hold off
```

Figure 2: Euler function in our code

Results and Discussion

We run three simulations on our model, all with an initial population of infective humans of 0 and initial population of infective mosquitoes equal to 10%, 50%, and 90% of the total mosquito population. The results are shown in Figure 3, 4, and 5.
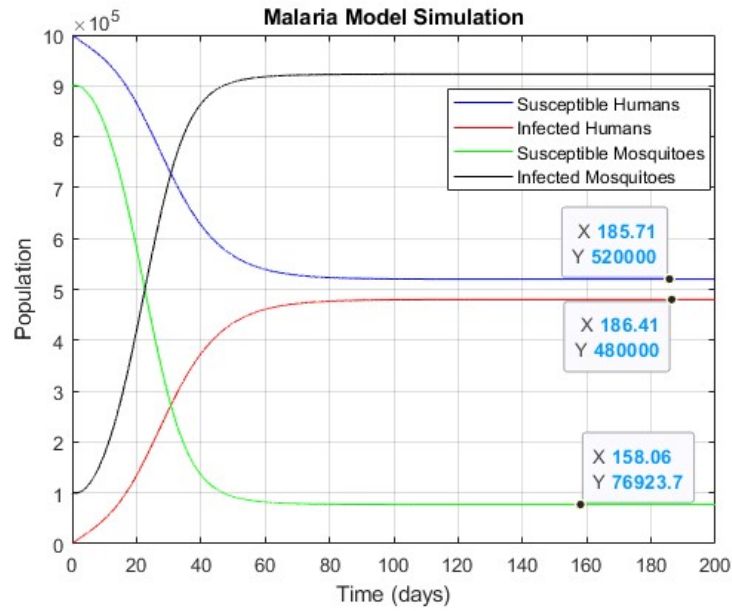

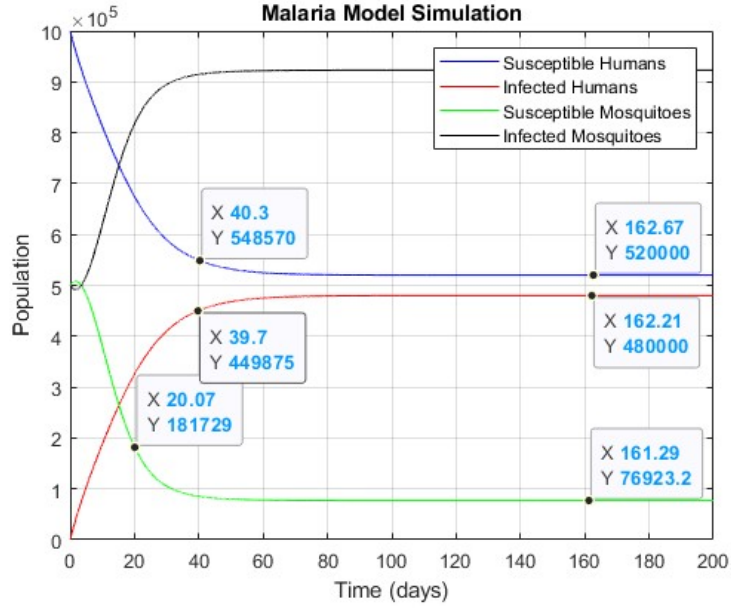Figure 3: Initial infected mosquito population = 10%

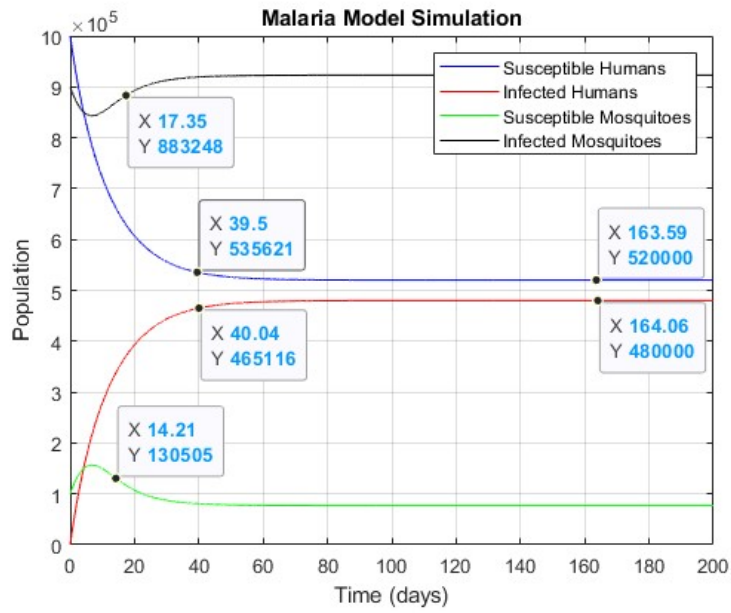Figure 4: Initial infected mosquito population = 50%

Figure 5: Initial infected mosquito population = 90%

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As we see in the Figures above, as we increase the initial infected mosquito population, we reach equilibrium in a shorter period of time. However, changing the infected mosquito population has no impact on the equilibrium point of the model. All 3 results show that we reach a stable point when there are 520,000 susceptible individuals and 76,923 susceptible mosquitoes.

We conduct three additional simulations to examine the impact of varying initial infected human populations. In these simulations, the initial infected mosquito population was set to 0, while the initial infected human populations were set to 10%, 50%, and 90% of the total human population.The results of these simulations are presented in Figures 6, 7, and 8, respectively.
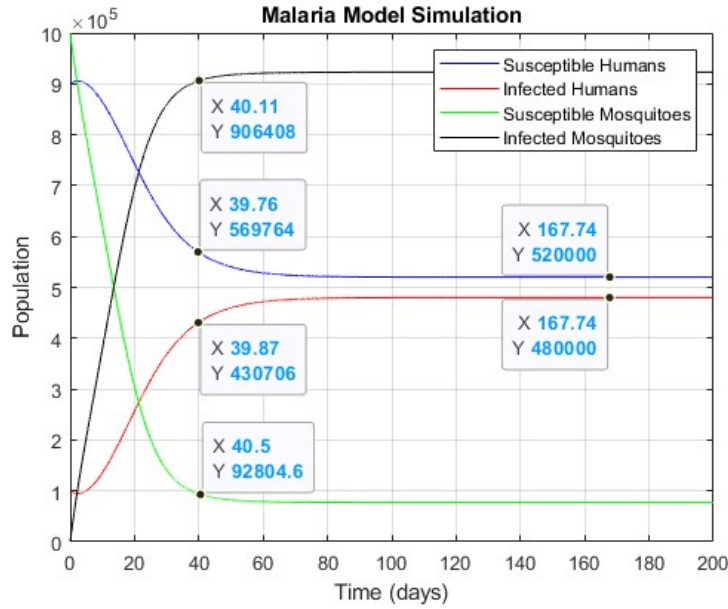

Figure 6: Initial infected human population = 10%
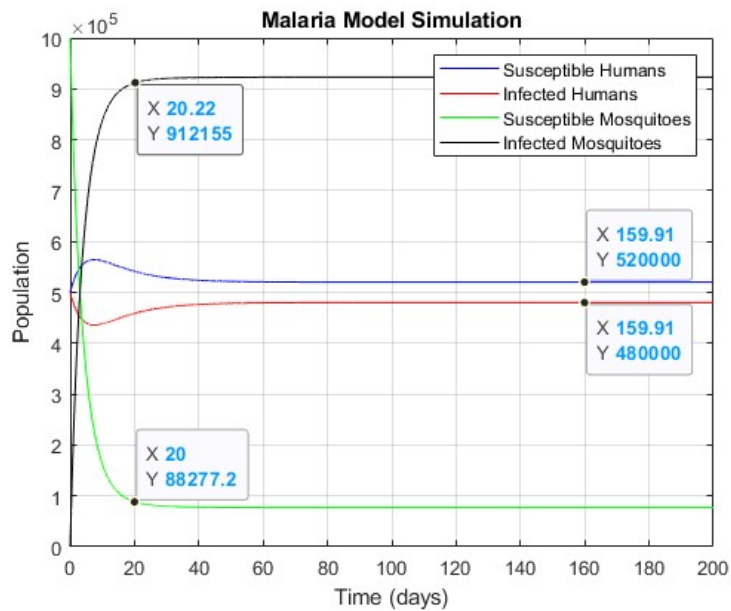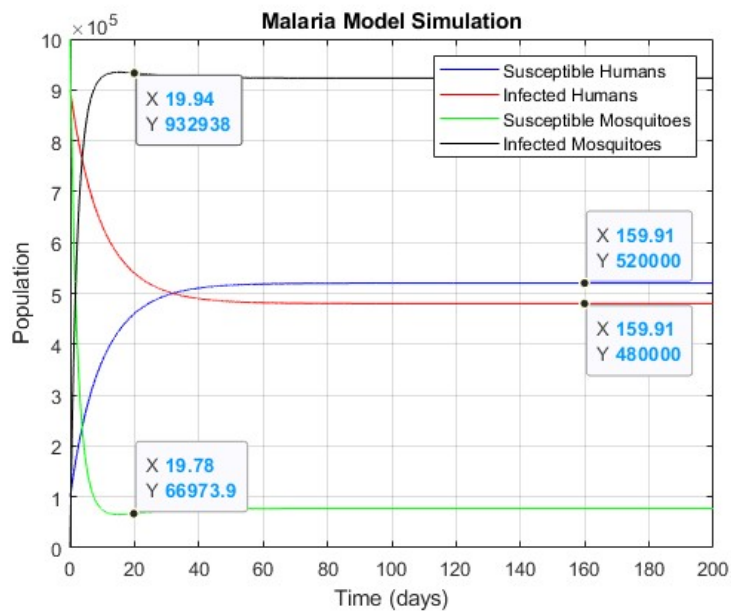
Figure 7: Initial infected human population = 50%

Figure 8: Initial infected human population = 90%

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Regardless of the initial infected human population, the simulations consistently reach the same stable equilibrium. This suggests that neither human nor mosquito initial infected population conditions have any impact on the equilibrium state.

To test the impact of bite rate on our model we run 4 simulations on our model with varying bite rates. Figures 9, 10, 11, 12 show the results with $\beta = 5$, $\beta = 2$, $\beta = 1$ and $\beta = .5$ respectively. In all cases, we set initial populations of both infective humans and mosquitoes equal to 10% of the total populations.
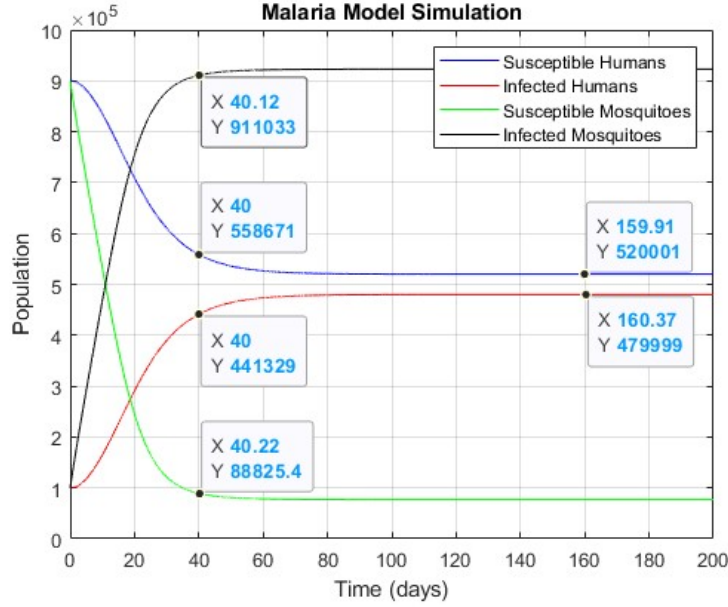

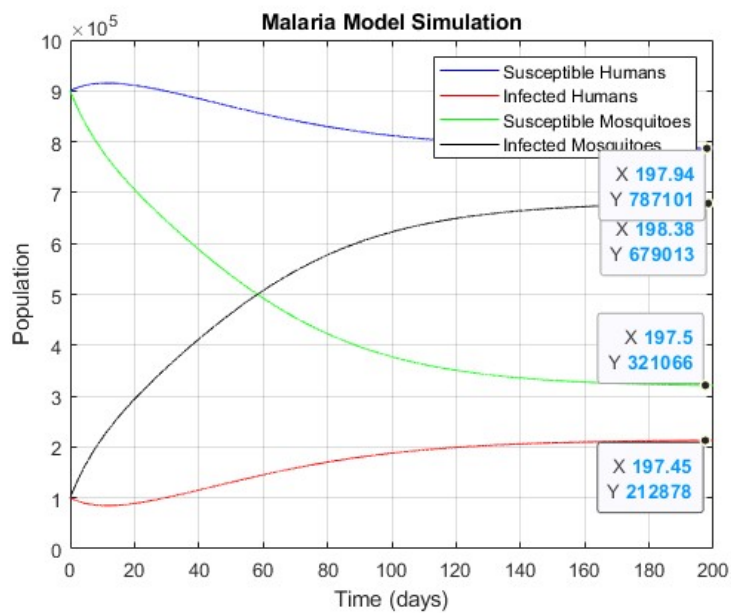Figure 9: Bite rate $\beta = 5$

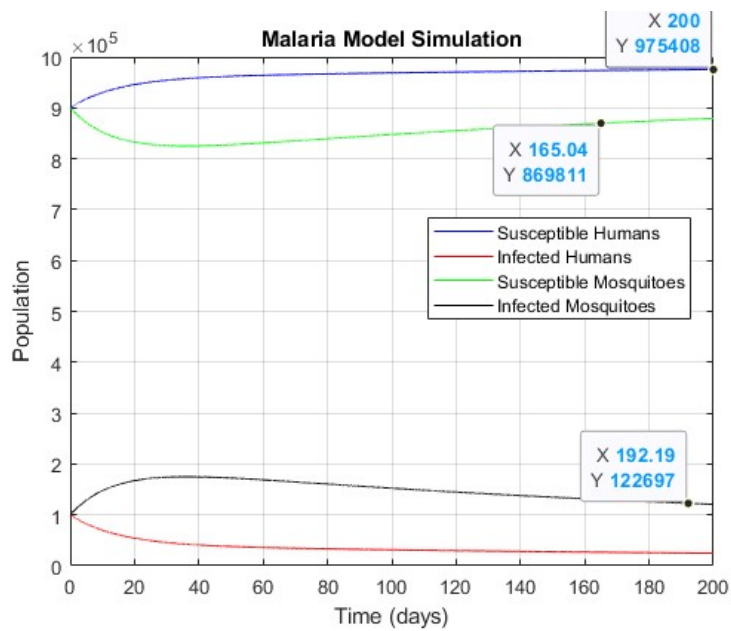Figure 10: Bite rate $\beta = 2$
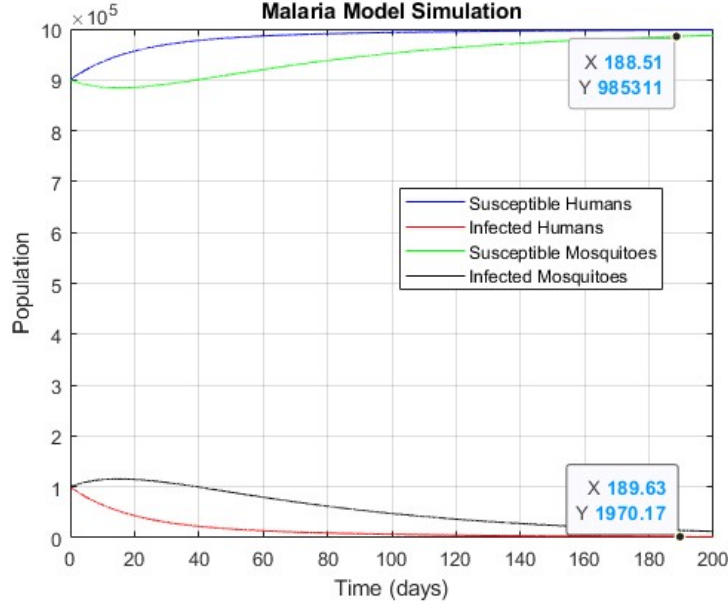

Figure 11: Bite rate $\beta = 1$

Figure 12: Bite rate $\beta = 0.5$

From the results in the figures above we see that as the bite rate decreases, the equilibrium point shifts. We see that the infected population for both mosquitoes and humans at equilibrium decrease every time we reduce β. At $\beta = 5$ equilibrium is at 480,000 infected humans and 920,000 infected mosquitoes. At $\beta = 2$, equilibrium is around 679,000 mosquitoes and 212,900 humans. At $\beta = 1$, the simulation is not long enough for us to see the equilibrium but we can tell that the mosquito infected population is decreasing below 120,000 and human infected population is decreasing below 50,000. At $\beta = 0.5$, both human and mosquito infected population keeps decreasing towards less than 20,000.

Finally, to test the impact of total mosquito population on our model we run 3 simulations with varying total mosquito population. Figures 13, 14 and 15 show the results with 10^6, 10^5 and 10^6 total mosquitoes respectively. In all cases, we set the initial population of infective humans to 0 and initial population of infective mosquitoes equal to 10%.
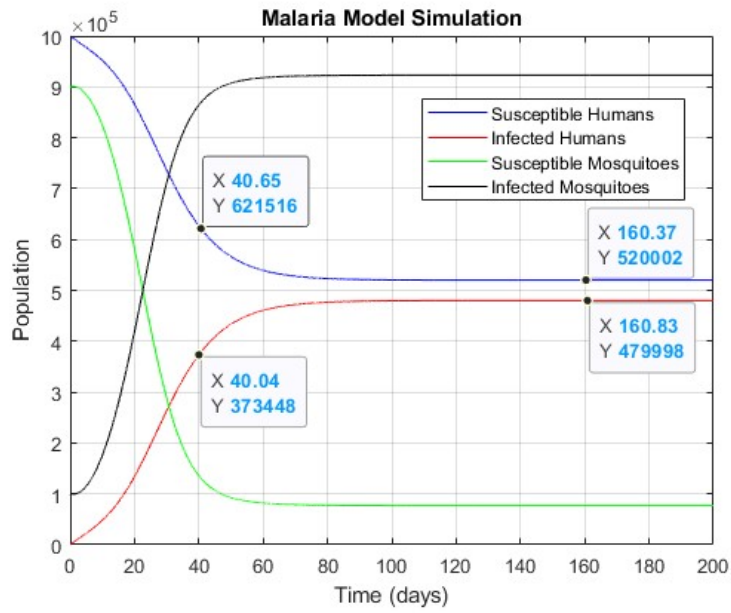
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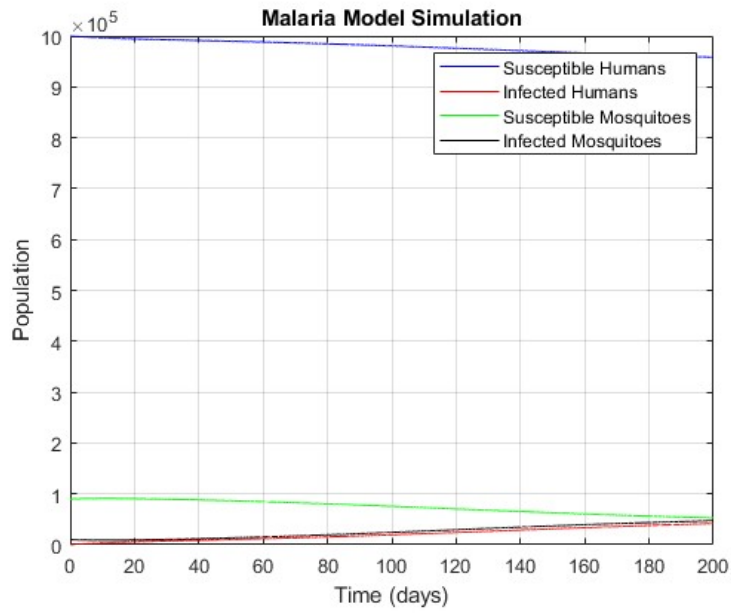Figure 13: Total mosquito population $= 10^6$

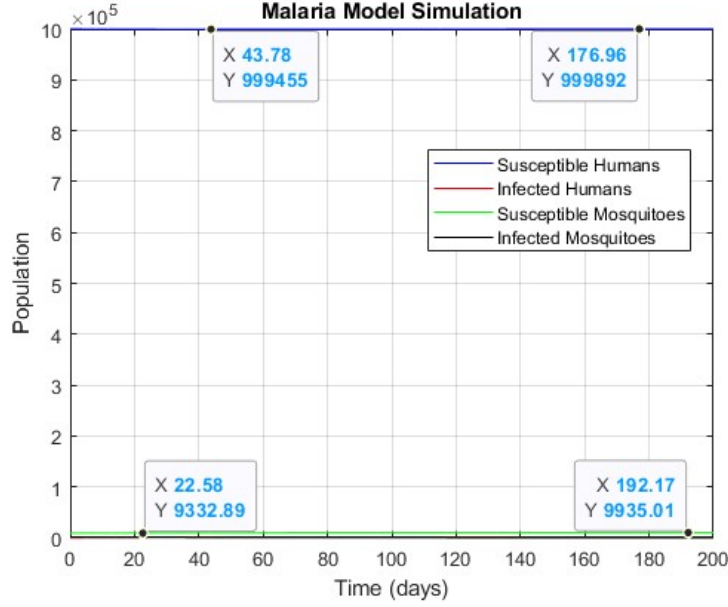Figure 14: Total mosquito population $= 10^5$

Figure 15: Total mosquito population $= 10^4$

From the results in the figures above, at 200 days, in Figure 13 we see that the total infected humans is 520,002 and in Figure 14 the total infected humans is around 50,000. Even decreasing the total mosquito population by an order of magnitude from 10^6 to 10^5, the number of infected individuals is significantly lower. Figure 15, which is a total mosquito population of 10^4, the number of infected humans is not noticeable on the graph.

Conclusion

From our experiments we find that the initial populations of infected humans or mosquitoes affect the speed to equilibrium but not the equilibrium state itself.The bite rate (β) significantly influences both the time to equilibrium and the equilibrium infection levels, with lower bite rates leading to fewer infections. Reducing the total mosquito population drastically decreases the number of infected humans, even when scaled by an order of magnitude, indicating that vector control is a highly effective strategy for mitigating disease spread.

Demographic differences, such as age, sex, and race, can influence sus-

ceptibility to infection, while localized environmental factors affect mosquito populations. Capturing these complexities would require a more sophisticated model tailored to specific scenarios. As such any future model trying to capture a real ongoing situation needs to account for these factors and many more.