

Computational model for Malaria

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- Abstract

Malaria is a disease caused by the Plasmodium parasite and remains a global public health challenge. Malaria is one of the Vector-borne diseases so it can not be modeled by a simple model because they are not transmitted directly from individual to individual. As a vector, the mosquito is needed for transmission, modeling of the disease epidemiology will be incomplete without consideration of that population as well. Thus, we introduce the SIS model for the human population and the SI model for the mosquito population for the Malaria disease. We focused on developing a computational model of malaria transmission using a system of differential equations and explored the dynamics between susceptible and infective populations of humans and mosquitoes. Simulations were conducted to analyze the effects of initial infective populations, mosquito feeding rates, and total mosquito population size on disease spread. Results showed that infection dynamics converged more rapidly with higher initial mosquito infections and reducing mosquito feeding rates or total mosquito population size significantly decreased the infective population in both species.

- Introduction

We wanted to make a computational model for Malaria. To make a mathematical model, we need to understand Malaria from the biological perspective.

To simplify our analysis we will begin with a model with fixed population sizes in the stable states. For the human population, we assume that we are interested in relatively short time periods. This is because the Malaria infection period is very short compared to the human life cycle, thus we can ignore births and deaths. We will also ignore disease-related deaths. This is not a perfect assumption because malaria can be a fatal disease, with 881,000 deaths (worldwide) from the disease in 2006. However, there were an estimated 247 million cases in the same period, and thus the mortality rate is

below 0.5 percent. Thus, the effect of disease-related deaths on total population size can reasonably be neglected.

However, as the mosquito's life cycle is much faster than that of humans (typically a week to a month), ignoring mosquito births and deaths will not be reasonable on any timescale of interest to humans. We may still assume a constant population size, by making the birth and death rates the same. Note that we are also presuming that there are no disease-related deaths for mosquitoes and that infected mosquitoes reproduce at the same rate as susceptibles. Again, this may not be a perfect assumption, as there is likely some negative effect on the insect, but the effect is not highly significant.

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 again, ignoring demographic processes among people but explicitly including births and deaths of mosquitoes (but with constant population size).

$$\begin{aligned}
 \text{Human : } \quad \frac{dS_H}{dt} &= -\epsilon_1 \beta \frac{S_H}{N_H} I_M + \gamma I_H & \frac{dI_H}{dt} &= +\epsilon_1 \beta \frac{S_H}{N_H} I_M - \gamma I_H \\
 \text{Mosquito : } \quad \frac{dS_M}{dt} &= \alpha N_M - \epsilon_2 \beta \frac{I_H}{N_H} S_M - \alpha S_M & \frac{dI_M}{dt} &= +\epsilon_2 \beta \frac{I_H}{N_H} S_M - \alpha I_M
 \end{aligned}$$

Here,

Here, β is a mosquito feeding rate, while ϵ_1 and ϵ_2 describe the fraction of bites

involving a susceptible/infective pair that lead to the transfer of the infectious agent; γ is the human recovery rate; α is the mosquito birth/death rate.

- Results and Discussion

Now we implement our SIS and SI model of Malaria in Matlab, using parameters consistent with our understanding of Malaria disease mentioned in the introduction. Now we simulate the expected disease dynamics for 200 days in the condition of no infected individuals existing in both human and mosquito populations. A starting set of

parameters is $\beta=5$, $\epsilon_1=0.01$, $\epsilon_2=0.1$, $\gamma=0.05$, and $\alpha=0.02$, with total population sizes of 10^6 for both mosquitoes and humans.

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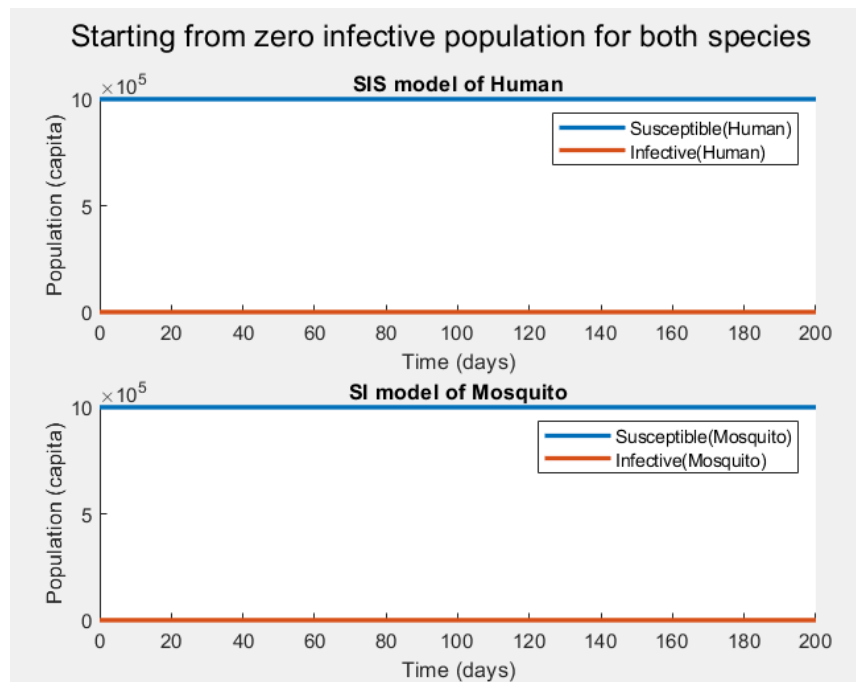
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% SIS model for malaria (begin with no infective population for both species)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% main parameters
alpha = 0.02; % mosquito birth/death rate
beta = 5; % mosquito feeding rate
epsilon1 = 0.01; % fraction of bites that lead to infection(mosquito to human)
epsilon2 = 0.1; % fraction of bites that lead to infection(human to mosquito)
gamma = 0.05; % human recovery rate
total_Hp = 10^6; % total population of human
total_Mp = 10^6; % total population of mosquito
I_I_h = 0; % initial infective human population
I_S_h = total_Hp-I_I_h; % initial susceptible human population
I_I_m = 0; % initial infective mosquito population
I_S_m = total_Mp-I_I_m; % initial susceptible mosquito population
% simulation
dt=0.01; % time step: (one day/100)
timev=0:dt:200; % time vector for 200 days
sim_S_h=zeros(length(timev),1); % vector to store susceptible human population
sim_I_h=zeros(length(timev),1); % vector to store infective human population
sim_S_m=zeros(length(timev),1); % vector to store susceptible mosquito
population
sim_I_m=zeros(length(timev),1); % vector to store infective mosquito
population
k=0; %counter
S_H=I_S_h; % a number
I_H=I_I_h; % a number
S_M=I_S_m; % a number
I_M=I_I_m; % a number
for t=timev
    k=k+1;
    % main equation
    if k~=1
        S_H = S_H + (-epsilon1*beta*S_H/total_Hp*I_M + gamma*I_H)*dt;
        I_H = I_H + (epsilon1*beta*S_H/total_Hp*I_M - gamma*I_H)*dt;
        S_M = S_M + (alpha*total_Mp - epsilon2*beta*I_H/total_Hp*S_M -
alpha*S_M)*dt;
        I_M = I_M + (epsilon2*beta*I_H/total_Hp*S_M-alpha*I_M)*dt;
    end
    if S_H<0 S_H=0; end; % population cannot go below than zero
    if I_H<0 I_H=0; end;
    if S_M<0 S_M=0; end;
    if I_M<0 I_M=0; end;
end

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```

    % store values for plotting
    sim_S_h(k)=S_H;
    sim_I_h(k)=I_H;
    sim_S_m(k)=S_M;
    sim_I_m(k)=I_M;
end
% plot
figure(1); clf
sgtitle('Starting from zero infective population for both species')
subplot(2,1,1)
hold on
plot(timev,sim_S_h,'LineWidth', 2)
plot(timev,sim_I_h,'LineWidth', 2)
hold off
legend('Susceptible(Human)', 'Infective(Human) ')
xlabel('Time (days)');ylabel('Population (capita)')
title('SIS model of Human')
subplot(2,1,2)
hold on
plot(timev,sim_S_m,'LineWidth', 2)
plot(timev,sim_I_m,'LineWidth', 2)
hold off
legend('Susceptible(Mosquito)', 'Infective(Mosquito) ')
xlabel('Time (days)');ylabel('Population (capita)')
title('SI model of Mosquito')

```



If we simulate with zero infective population for both mosquitoes and humans, no infection will occur for either population during the whole simulation. Considering a

situation where only two species exist, since the infected population does not exist in both species, infection will not occur, and the infective population for both will be zero during the whole simulation. This is biologically natural, and in the mathematical model, since all terms of the derivatives of the infective include I_M and I_H , it can be seen that when these parameters become 0, the derivative value becomes 0.

Now, we run three simulations using this model all with an initial population of infective humans of zero and initial populations of infective mosquitoes equal to 10%, 50%, and 90% of the total mosquito population. We plot the populations over time and analyze the dynamics.

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%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% SIS model for malaria (only with initial infective mosquitoes)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% main parameters
alpha = 0.02; % mosquito birth/death rate
beta = 5; % mosquito feeding rate
epsilon1 = 0.01; % fraction of bites that lead to infection(mosquito to human)
epsilon2 = 0.1; % fraction of bites that lead to infection(human to mosquito)
gamma = 0.05; % human recovery rate
total_Hp = 10^6; % total population of human
total_Mp = 10^6; % total population of mosquito
I_I_h = 0; % initial infective human population
I_S_h = total_Hp-I_I_h; % initial susceptible human population
I_I_m = 0; % initial infective mosquito population
I_S_m = total_Mp-I_I_m; % initial susceptible mosquito population
% simulation
dt=0.01; % time step: (one day/100)
timev=0:dt:200; % time vector for 200 days
sim_S_h=zeros(length(timev),1); % vector to store susceptible human population
sim_I_h=zeros(length(timev),1); % vector to store infective human population
sim_S_m=zeros(length(timev),1); % vector to store susceptible mosquito
population
sim_I_m=zeros(length(timev),1); % vector to store infective mosquito
population
k=0; j=0; l=-1;%counter
S_H=I_S_h; % a number
I_H=I_I_h; % a number
S_M=I_S_m; % a number
I_M=I_I_m; % a number
figure(2); clf;
sgtitle('Started with only infected mosquitoes')
for i = 0.1:0.4:0.9

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j=j+2;l=l+2;k=0;
S_H=I_S_h; % a number
I_H=I_I_h; % a number
I_M = i*total_Mp;
S_M = total_Mp - I_M;
for t=timev
    k=k+1;

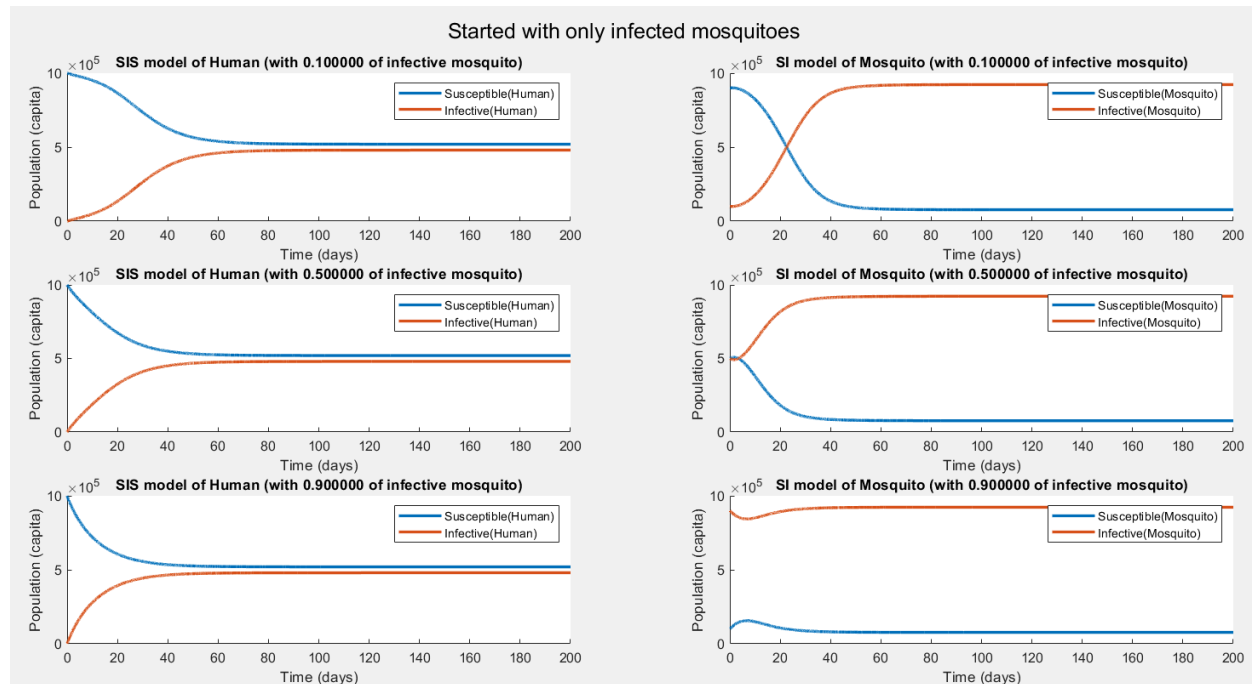
    % main equation
    if k~=1
        S_H = S_H + (-epsilon1*beta*S_H/total_Hp*I_M + gamma*I_H)*dt;
        I_H = I_H + (epsilon1*beta*S_H/total_Hp*I_M - gamma*I_H)*dt;
        S_M = S_M + (alpha*total_Mp - epsilon2*beta*I_H/total_Hp*S_M -
alpha*S_M)*dt;
        I_M = I_M + (epsilon2*beta*I_H/total_Hp*S_M-alpha*I_M)*dt;
    end

    if S_H<0 S_H=0; end; % population cannot go below than zero
    if I_H<0 I_H=0; end;
    if S_M<0 S_M=0; end;
    if I_M<0 I_M=0; end;

    % store values for plotting
    sim_S_h(k)=S_H;
    sim_I_h(k)=I_H;
    sim_S_m(k)=S_M;
    sim_I_m(k)=I_M;
end
% plot
subplot(3,2,1)
hold on
plot(timev,sim_S_h(1:length(timev)),'LineWidth', 2)
plot(timev,sim_I_h(1:length(timev)),'LineWidth', 2)
hold off
legend('Susceptible(Human)', 'Infective(Human) ')
xlabel('Time (days)');ylabel('Population (capita)')
title(sprintf('SIS model of Human (with %f of infective mosquito)', i))

subplot(3,2,j)
hold on
plot(timev,sim_S_m(1:length(timev)),'LineWidth', 2)
plot(timev,sim_I_m(1:length(timev)),'LineWidth', 2)
hold off
legend('Susceptible(Mosquito)', 'Infective(Mosquito) ')
xlabel('Time (days)');ylabel('Population (capita)')
title(sprintf('SI model of Mosquito (with %f of infective mosquito)', i))
end

```



We ran three simulations while increasing the number of initially infected mosquitoes. Overall, we could see that the population dynamics in the simulations stabilized faster as the number of mosquitoes increased. In other words, we could see that the number of people infected with diseases by mosquitoes increased more quickly as the number of initially infected mosquitoes increased. As a result, we could check that the susceptible and the infective population converged more quickly to a specific value. The graph also shows that regardless of the population conditions of initially infected mosquitoes, the susceptible and the infective populations approached each other over time and eventually converged to a ratio of approximately 51:49. But one interesting thing is that in all of the simulations above, the susceptible populations are always larger than the infective population. Similarly, in the case of mosquitoes, we could notice that the susceptible and the infective population converged to each specific value more quickly as the number of initially infected mosquitoes increased. It is noteworthy that regardless of how small the initial mosquito value is, the infective population of mosquitoes eventually occupies most of the total population over time.

Now we run another three simulations using this model all with an initial population of infective mosquitoes of zero and initial populations of infective humans

equal to 10%, 50%, and 90% of the total human population. Again, we plot the populations over time and show the dynamics of simulations.

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%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%% SIS model for malaria (only with initial infective human population)
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% main parameters
alpha = 0.02; % mosquito birth/death rate
beta = 5; % mosquito feeding rate
epsilon1 = 0.01; % fraction of bites that lead to infection(mosquito to human)
epsilon2 = 0.1; % fraction of bites that lead to infection(human to mosquito)
gamma = 0.05; % human recovery rate
total_Hp = 10^6; % total population of human
total_Mp = 10^6; % total population of mosquito
I_I_h = 0; % initial infective human population
I_S_h = total_Hp-I_I_h; % initial susceptible human population
I_I_m = 0; % initial infective mosquito population
I_S_m = total_Mp-I_I_m; % initial susceptible mosquito population
% simulation
dt=0.01; % time step: (one day/100)
timev=0:dt:200; % time vector for 200 days
sim_S_h=zeros(length(timev),1); % vector to store susceptible human population
sim_I_h=zeros(length(timev),1); % vector to store infective human population
sim_S_m=zeros(length(timev),1); % vector to store susceptible mosquito
population
sim_I_m=zeros(length(timev),1); % vector to store infective mosquito
population
k=0; j=0; l=-1;%counter
S_H=I_S_h; % a number
I_H=I_I_h; % a number
S_M=I_S_m; % a number
I_M=I_I_m; % a number
figure(3); clf;
sgtitle('Started with only infected human')
for i = 0.1:0.4:0.9
    j=j+2;l=l+2;k=0;
    I_H=i*total_Hp;
    S_H = total_Hp - I_H;
    S_M=I_S_m; % a number
    I_M=I_I_m; % a number
    for t=timev
        k=k+1;

        % main equation
        if k~=1
            S_H = S_H + (-epsilon1*beta*S_H/total_Hp*I_M + gamma*I_H)*dt;
            I_H = I_H + (epsilon1*beta*S_H/total_Hp*I_M - gamma*I_H)*dt;

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        S_M = S_M + (alpha*total_Mp - epsilon2*beta*I_H/total_Hp*S_M -
alpha*S_M)*dt;
        I_M = I_M + (epsilon2*beta*I_H/total_Hp*S_M-alpha*I_M)*dt;
    end

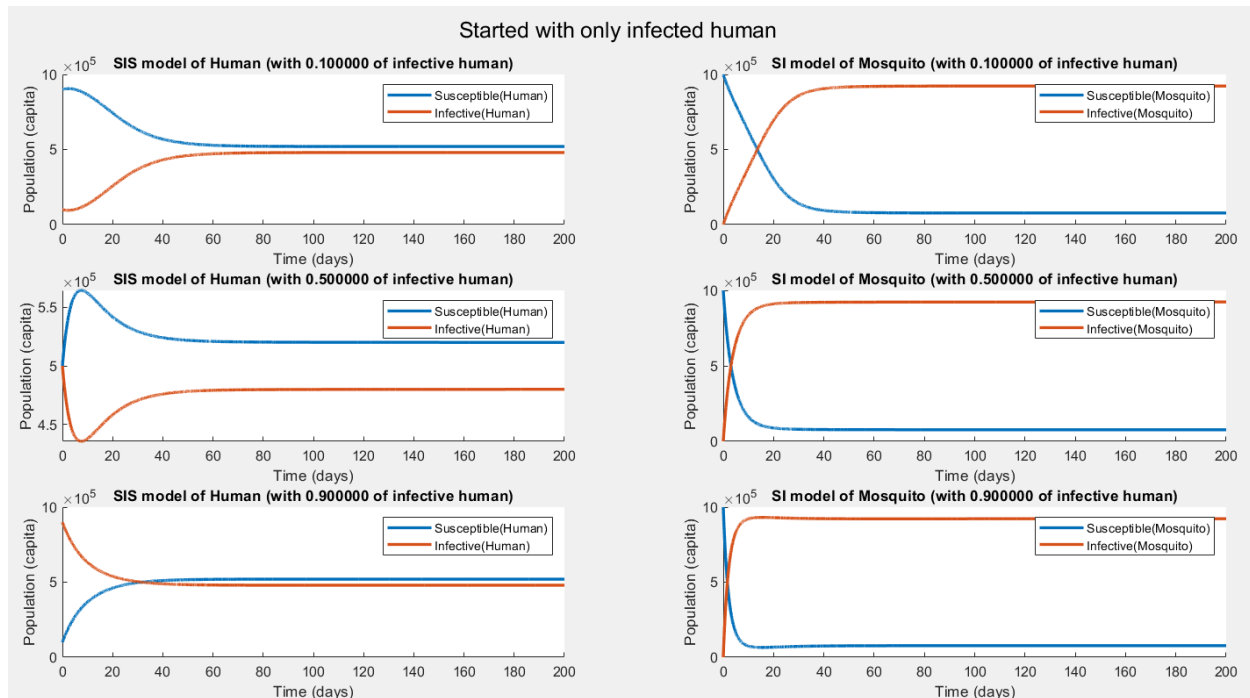
    if S_H<0 S_H=0; end; % population cannot go below than zero
    if I_H<0 I_H=0; end;
    if S_M<0 S_M=0; end;
    if I_M<0 I_M=0; end;

    % store values for plotting
    sim_S_h(k)=S_H;
    sim_I_h(k)=I_H;
    sim_S_m(k)=S_M;
    sim_I_m(k)=I_M;
end
% plot

subplot(3,2,1)
hold on
plot(timev,sim_S_h(1:length(timev)),'LineWidth', 2)
plot(timev,sim_I_h(1:length(timev)),'LineWidth', 2)
hold off
legend('Susceptible(Human)', 'Infective(Human) ')
xlabel('Time (days)');ylabel('Population (capita)')
title(sprintf('SIS model of Human (with %f of infective human)', i))

subplot(3,2,j)
hold on
plot(timev,sim_S_m(1:length(timev)),'LineWidth', 2)
plot(timev,sim_I_m(1:length(timev)),'LineWidth', 2)
hold off
legend('Susceptible(Mosquito)', 'Infective(Mosquito) ')
xlabel('Time (days)');ylabel('Population (capita)')
title(sprintf('SI model of Mosquito (with %f of infective human)', i))
end

```



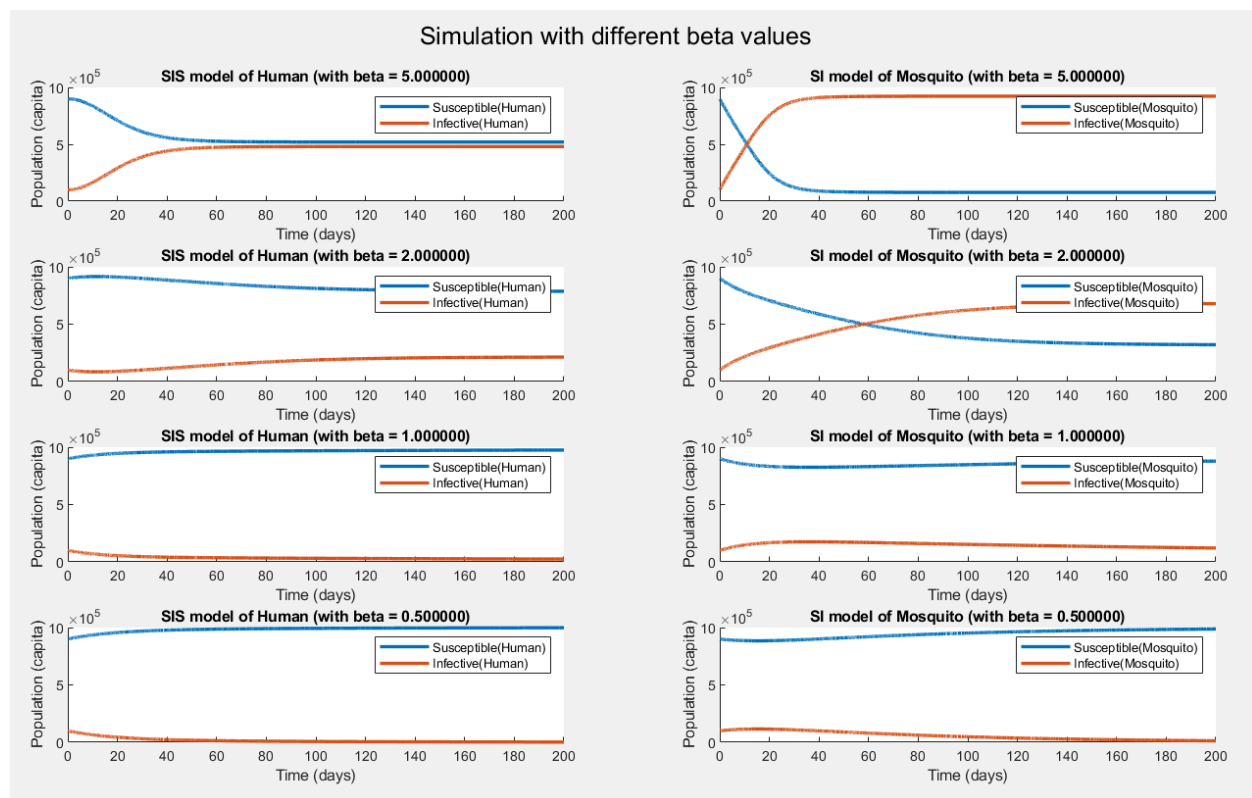
We simulated our model while increasing the number of initially infected humans.

As a result, in the case of mosquitoes, we could see that the number of mosquitoes infected by humans increased more rapidly as the number of initially infected humans increased. In other words, we could see that the susceptible and the infective population of mosquitoes converged more quickly to a specific value. In addition, regardless of the portion of initially infected humans, as long as there are infected people, the infective population of mosquitoes eventually occupied most of the total population over time in all of our simulations.

In the case of humans, we could also see that the susceptible and infective populations stabilized more quickly as we increased the initially infected population. In addition, susceptible and infective populations in all cases converged to similar values. One interesting thing is that when the simulation started with 50% infected, we could see that the graph of susceptible drew a convex upward graph and converged to a specific value, and the graph of infective drew a convex downward graph and converged to a specific value. However, in the 50% simulation, as we can see in the y-axis units, the fluctuation range is actually small. Thus, we can say that the infective

and susceptible populations converged faster than starting with 10% infection, and also both populations eventually have similar values. The thing to note is that under any conditions, the susceptible population always stabilizes at a value greater than the infective population.

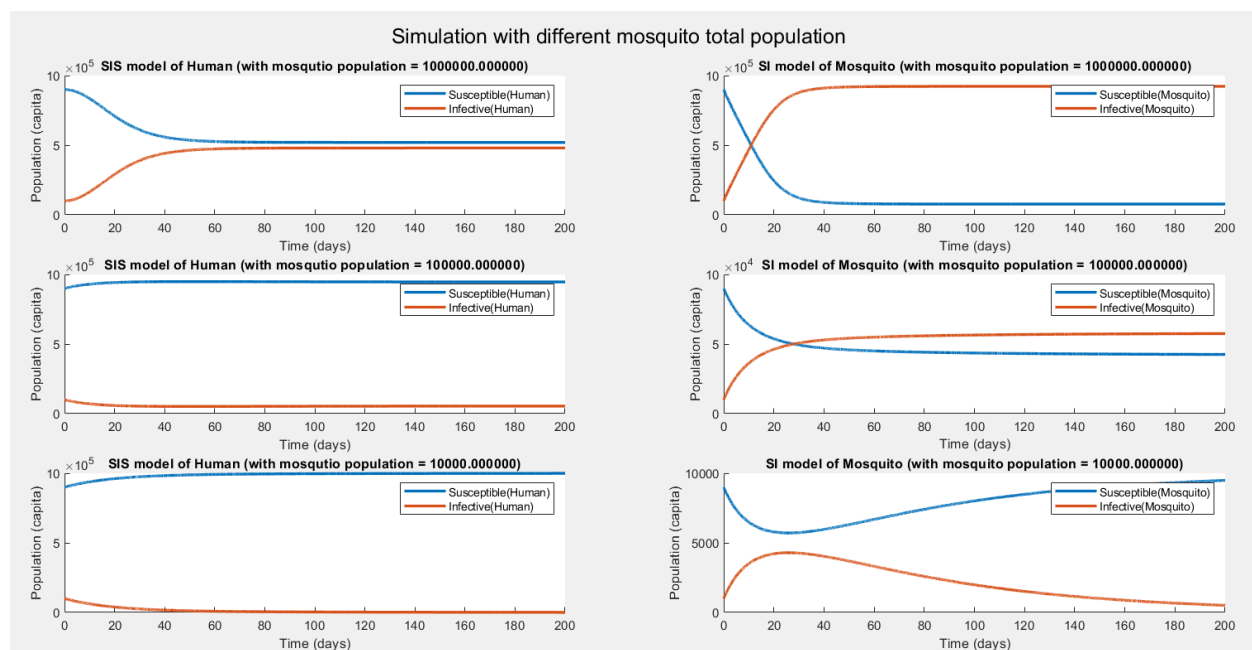
Now we run another four simulations using this model, but with $\beta=5$, $\beta=2$, $\beta=1$, and $\beta=0.5$; We use initial populations of both infective humans and mosquitoes equal to 10% of the total populations in all cases. We also plot the populations over time and analyze the results.



As a result, as the mosquito feeding rate, β , decreased, the speed at which humans were infected with the disease over time decreased, and most importantly, as the beta value decreased, the convergence value of the susceptible population increased and the convergence value of the infective population decreased significantly. In other words, the beta value affected the size of the value strongly at which the susceptible and infective populations of humans stably converge. In particular, we confirmed that when the beta value is 0.5, the convergence value of the infective

population of humans approaches 0. In the case of mosquitoes, it was confirmed that as the beta value decreased, the convergence value of the infective population of mosquitoes decreased and at the same time, the convergence value of the susceptible population increased. In particular, we confirmed that when the beta value is 0.5, the convergence value of the infective population of mosquitoes approaches 0. In all previous experiments, we saw that even if a low initial infection number was given, the infective population eventually occupied most of the population over time. However, this experiment showed that a decrease in the beta value can cause the infectious population of mosquitoes to converge to a lower value than the susceptible population, which can also have a significant impact on increasing human susceptible population. As a result, we confirmed that reducing the beta value significantly reduces the convergence value of the infective population of both humans and mosquitoes, leading to disease eradication.

Finally, we run another set of simulations using the original parameters ($\beta=5$), but with the total mosquito population size equal to 10^6 , 10^5 and 10^4 . We plot the populations over time and discuss the observations.



We experimented with the model while reducing the total mosquito population size. In the case of the mosquito population, as the total population decreased, the population infected with the disease decreased significantly over time. In other words, the convergence value of the infective population gradually decreased, and when the total population was 10^4 , the infective approached zero. Naturally, the susceptible population of mosquitoes increased as the total population decreased. In the case of humans, as the total population of mosquitoes decreased, the population infected with the disease decreased significantly. In other words, it was confirmed that the convergence value of the susceptible population of humans increased and the convergence value of the infective population decreased. In particular, when the total population of mosquitoes was 10^4 , the infective population of humans approached zero. As a result, it was confirmed that reducing the total population of mosquitoes significantly reduced the convergence value of the infective population of both humans and mosquitoes, leading to the eradication of the disease.

From all the results of the simulation and analyses, we know that if the value of beta and the total population of mosquitoes is sufficient, we can confirm that even a small infective population can lead populations of both species to epidemic situations. Since the early outbreak of disease is often beyond our control, we want to focus on reducing mosquito feeding rates and the total mosquito population. Our research results show that reducing mosquito feeding rates and the total population of mosquitoes significantly reduces the incidence of disease in humans as well as mosquitoes, and significantly reduces the over-time convergence value of the infective population. However, simply reducing the incidence of disease does not end the epidemic, but only maintains a low infective population value. To eradicate a disease, the infectious population must be close to zero. This requires either a beta value close to zero or a very small overall population of mosquitoes. Therefore, in order to eradicate malaria, we must make efforts to minimize the feeding rate of mosquitoes in our daily lives. This includes using mosquito nets on beds and spraying mosquito repellents in our daily lives, which will reduce the feeding rate of mosquitoes, thereby affecting the decrease in beta, which will reduce the infective population and effectively control malaria. In

addition, eliminating water sources for breeding sites can be used to control the total population of mosquitoes. Since mosquitoes lay eggs in stagnant water, this method will reduce the total population of mosquitoes, thereby reducing the infective population and effectively controlling malaria. These efforts will require not only individual efforts but also collective efforts with government support, which will statistically significantly reduce the beta value and the total population of mosquitoes.

- Conclusion

This study demonstrated that malaria transmission dynamics are highly sensitive to mosquito feeding rates and total population size. By reducing these factors in our computational model, the spread of malaria can be significantly controlled and, even under certain conditions, it was eradicated. Simulation results also revealed that even minimal infective populations could lead to an epidemic for both human and mosquito populations when mosquito feeding rates and population sizes are sufficiently high. However, We confirmed that we can effectively lower the infective population in both humans and mosquitoes by reducing the feeding rate or total mosquito population. These results highlight the importance of interventions such as using mosquito nets, and mosquito repellents and eliminating breeding sites to control malaria. Achieving disease eradication requires a coordinated effort, thus, we expect that individual practices with the support of the government can minimize mosquito feeding rates and population sizes. Such measures could significantly reduce the prevalence of malaria, contributing to improved public health outcomes.

- References

David Green (2024). *A model of malaria transmission*

I have only used the information inside the homework paper