

Batik Motifs: Dynamic Stability Patterns in a Mathematical Model of Malaria Transmission with Asymptomatic Infection and Superinfection

Alifiya Aziza, Nurul Hanin Azzahra Supriyono, Putri Fadhillah, Sugiyanto

Mathematics Department, Faculty of Science and Technology, UIN Sunan Kalijaga,
Jl. Marsda Adisucipto No 1 Yogyakarta 55281, Indonesia. Tel. +62-274-540971, Fax. +62-274-519739.

Corresponding author*

alifiyaaziza5@gmail.com

Abstract: This study discusses the mathematical modeling of malaria transmission, considering the presence of asymptomatic infection and superinfection. The model used is an extension of the SIA-SI (Susceptible–Infected–Asymptomatic in humans and Susceptible–Infected in mosquitoes) model. Each compartment is represented by a system of differential equations based on the principle of the rate of change, reflecting the dynamics of individuals moving between health statuses. An analysis was conducted to determine the disease-free equilibrium and the endemic equilibrium points. The results of the analysis show that in the disease-free state, the entire human and mosquito populations are in a susceptible state with no infected individuals, namely $S_h=N_h$ and $S_m=N_m$. Meanwhile, the endemic equilibrium occurs when a number of human and mosquito individuals remain infected, depending on infection, recovery, and mortality parameters. This model provides a quantitative overview of the dynamics of malaria transmission and can serve as a basis for formulating more effective disease control strategies.

Keywords: Asymptomatic Infection, Differential System, Malaria, Mathematical Modeling, Superinfection.

Introduction

Malaria remains one of the most pressing global public health problems to date. According to the latest report from the World Health Organization (WHO), in 2022 there were an estimated 249 million cases of malaria worldwide with 608,000 resulting deaths. The African region bears the largest burden, accounting for about 94% of total cases and 95% of global deaths (World Health Organization, 2023). This fact underscores that malaria control efforts require an approach that is continuously updated and based on a deep understanding of the disease's transmission dynamics.

However, the dynamics of malaria transmission are highly complex and influenced by various biological factors. One of the main challenges in malaria control is the presence of asymptomatic infection, a condition where individuals are

infected with malaria parasites without showing clinical symptoms, but remain capable of transmitting it to mosquitoes. This condition makes them a hidden reservoir in the transmission chain. Additionally, there is the phenomenon of superinfection, where a person can be reinfected by a new strain before the previous infection has completely cleared. Both of these factors complicate malaria elimination efforts because they affect the patterns of spread and the persistence of the disease in a population (Abdy et al., 2022).

To understand such complex dynamics, mathematical modeling becomes a crucial analytical tool. Mathematical models allow researchers to simulate and predict the behavior of malaria spread under various conditions. Various models have been developed, from simple models like SIS-SI (Fajri et al., 2016) or the addition of special compartments (Maryam et al., 2021). One model relevant to describing the biological reality

above is the SIAS-SI model (*Susceptible–Infected–Asymptomatic–Susceptible* for humans and *Susceptible–Infected for mosquitoes*), which explicitly includes an asymptomatic compartment and accounts for the possibility of superinfection (Abdy et al., 2022). Analysis of such models, especially determining equilibrium points and the Basic Reproduction Number (R_0), is vital for understanding disease stability and determining effective intervention strategies.

Interestingly, the concepts of order and pattern that form the basis of mathematical modeling can also be found in Indonesian visual culture, particularly in the art of batik. Batik is not just a textile work, but a representation of philosophy, symbolism, and patterned structures that reflect local wisdom. Through ethnomathematical studies, researchers have found that traditional batik motifs contain mathematical concepts such as geometry, symmetry, and transformation (Prahmana & D'Ambrosio, 2020). Thus, the process of creating batik actually involves the application of mathematical principles carried out intuitively by the batik artisans.

From this perspective, batik can be seen as a form of "generative art". It is an art that emerges from the application of a set of rules or algorithms to produce complex aesthetic patterns. Previous research has shown that batik patterns can be modeled through an algorithmic approach based on visual rules (Saputro et al., 2022). On the other hand, in the realm of computational art, scientific models, including epidemiological models, have been used as inspiration in creating generative art (Dorin, 2005).

The novelty of this research lies in the attempt to bridge two seemingly different domains—namely, the epidemiological modeling of malaria and the art of batik—through an integrated mathematical and aesthetic approach. Although many ethnomathematical studies of batik have been conducted (Prahmana & D'Ambrosio, 2020) and epidemiological models have been used in the context of generative art (Dorin, 2005), no research has directly linked epidemiological parameters, such as the Basic Reproduction Number (R_0) from the SIAS-SI malaria model, as basic rules or algorithms for generating new batik motifs.

Based on this, this research has two main objectives. First, to analyze the SIAS-SI mathematical model of malaria transmission by considering asymptomatic infection and superinfection to understand the stability of the system and to derive the formula for the Basic Reproduction Number (R_0). Second, to utilize the results of this analysis—particularly the value and dynamics of R_0 as an algorithmic inspiration in the process of creating new batik motifs.

SIAS-SI Mathematical Modeling of the spread of Malaria with Asymptomatic and Superinfection

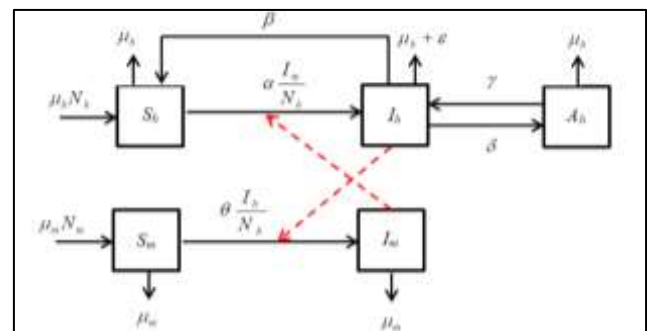


Figure 1. Transmission scheme of the SIAS-SI mathematical model for malaria.

The following are the variables and parameters in the SIAS-SI model for the spread of malaria with asymptomatic and superinfection:

Table 1. Variables in the SIAS-SI Model for the Spread of Malaria with Asymptomatic and Superinfection.

Variable	Description
S_h	Number of Susceptible individuals in humans
I_h	Number of Infected individuals in humans
A_h	Number of Asymptomatic infected individuals in humans
S_m	Number of Susceptible individuals in mosquitoes
I_m	Number of Infectious individuals in mosquitoes

Table 2. Parameters in the SIAS-SI Model for the Spread of Malaria

Parameter	Description
N_h	Human birth rate
α	Rate of infection in humans
γ	Constant rate of superinfection from undetected infected individuals (asymptomatic infected).
δ	Rate of transfer from infected individuals

β	to the asymptomatic group Constant rate of human recovery from the malaria parasite
θ	Rate of transfer from exposed mosquitoes to infected mosquitoes
μ_h	Constant rate of natural human death
ϵ	Constant rate of human death due to malaria
N_m	Mosquito birth rate
μ_m	Constant rate of natural mosquito death

Based on the flow diagram above, for disease transmission, the differential equation for each compartment is obtained by the principle: rate of change = inflow rate – outflow rate. The rate is calculated based on the inflow and outflow arrows in the diagram.

For susceptible humans S_h

Inflow rate: Recruitment of new humans $\mu_h N_h$

Outflow rate:

$$\begin{aligned} \text{Naturan death} &= \mu_h S_h \\ \text{Infected by mosquito} &= \alpha \frac{I_m}{N_h} S_h \end{aligned}$$

$$\begin{aligned} \frac{dS_h}{dt} &= \mu_h N_h - \mu_h S_h - \alpha \frac{I_m}{N_h} S_h + \beta I_h \\ &= \mu_h N_h - \left(\left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h \right) + \beta I_h \\ &= \mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h \quad (1) \end{aligned}$$

Note: There is an addition of $+\beta I_h$ because some infected can return to susceptible.

For infected humans

Inflow rate: Infected from S_h , which is $\alpha \frac{I_m}{N_h} S_h$; from the asymptomatic group A_h who become symptomatic, which is γA_h

Outflow rate:

$$\text{Natural death + death from illness} = (\mu_h + \epsilon) I_h$$

$$\text{Returning to susceptible/recovered} = \beta I_h$$

$$\text{Moving to asymptomatic} = \delta I_h$$

$$\begin{aligned} \frac{dI_h}{dt} &= \alpha \frac{I_m}{N_h} S_h + \underbrace{\gamma A_h}_{\text{from } A_h} - \underbrace{(\beta + \delta + \mu_h + \epsilon) I_h}_{\text{Outflow Rate}} \quad (2) \end{aligned}$$

Compartment A_h (Asymptomatic humans / carriers)

Inflow rate: From I_h who move to asymptomatic = δI_h

Outflow rate:

Becoming symptomatic again (or recovering to another status) = γA_h

Natural death = $\mu_h A_h$

Thus,

$$\begin{aligned} \frac{dA_h}{dt} &= \delta I_h - \gamma A_h - \mu_h A_h \\ &= \underbrace{\delta I_h}_{\text{Masuk}} - \underbrace{(\gamma + \mu_h) A_h}_{\text{Keluar}} \quad (3) \end{aligned}$$

Compartment S_m (susceptible mosquitoes)

Inflow rate: Recruitment/birth of new mosquitoes = $\mu_m N_m$

Outflow rate:

Natural death of mosquitoes = $\mu_m S_m$

Infected by infected humans I_h : Rate of infection in mosquitoes = $\theta \frac{I_h}{N_h} S_m$

Thus,

$$\begin{aligned} \frac{dS_m}{dt} &= \mu_m N_m - \mu_m S_m - \theta \frac{I_h}{N_h} S_m \\ &= \mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m \quad (4) \end{aligned}$$

Compartment I_m (infected mosquitoes)

Inflow rate: Susceptible mosquitoes infected by humans = $\theta \frac{I_h}{N_h} S_m$

Outflow: Natural death of mosquitoes = $\mu_m I_m$

Thus,

$$\frac{dI_m}{dt} = \theta \frac{I_h}{N_h} S_m - \mu_m I_m \quad (5)$$

The equilibrium point of system (1 – 5) is obtained by solving the equations:

$$\begin{aligned} \frac{dS_h}{dt} &= 0, & \frac{dI_h}{dt} &= 0, & \frac{dA_h}{dt} &= 0, & \frac{dS_m}{dt} &= 0, \\ & & & & & & \frac{dI_m}{dt} &= 0 \end{aligned}$$

Thus, from equation (1), substitute $\frac{dS_h}{dt} = 0$

$$\frac{dS_h}{dt} = \mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h$$

$$\mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h = 0 \quad (6)$$

From equation (2), substitute $\frac{dI_h}{dt} = 0$

$$\begin{aligned} \frac{dI_h}{dt} &= \alpha \frac{I_m}{N_h} S_h + \gamma A_h - (\beta + \delta + \mu_h + \epsilon) I_h \\ \alpha \frac{I_m}{N_h} S_h + \gamma A_h - (\beta + \delta + \mu_h + \epsilon) I_h &= 0 \end{aligned} \quad (7)$$

From equation (3), substitute $\frac{dA_h}{dt} = 0$

$$\begin{aligned} \frac{dA_h}{dt} &= \delta I_h - (\gamma + \mu_h) A_h \\ \delta I_h - (\gamma + \mu_h) A_h &= 0 \end{aligned} \quad (8)$$

From equation (4), substitute $\frac{dS_m}{dt} = 0$

$$\begin{aligned} \frac{dS_m}{dt} &= \mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m \\ \mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m &= 0 \end{aligned} \quad (9)$$

From equation (5), substitute $\frac{dI_m}{dt} = 0$

$$\begin{aligned} \frac{dI_m}{dt} &= \theta \frac{I_h}{N_h} S_m - \mu_m I_m \\ \theta \frac{I_h}{N_h} S_m - \mu_m I_m &= 0 \end{aligned} \quad (10)$$

Disease-Free Equilibrium Point (x_{dfe})

The disease-free equilibrium point is a state where the infectious disease does not spread in a population, and it occurs when:

$$I_h = A_h = I_m = 0$$

Substitute the above conditions into equations (6)–(10).

Equation (6) with $I_h = I_m = 0$:

$$\mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h = 0$$

$$\mu_h N_h + \beta \cdot 0 - (\mu_h + \alpha \cdot 0) S_h = 0$$

$$\mu_h (N_h - S_h) = 0$$

Since $\mu_h > 0$, meaning the natural death rate of humans is always positive, not zero, then for this equation to be true, it must be that:

$$N_h - S_h = 0 \quad \Rightarrow \quad S_h = N_h$$

Equation (9) with $I_h = 0$:

$$\mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m = 0$$

$$\mu_m N_m - (\mu_m + \theta \cdot 0) S_m = 0$$

$$\mu_m N_m - \mu_m S_m = 0$$

$$\mu_m (N_m - S_m) = 0$$

Since $\mu_m > 0$, we obtain

$$N_m - S_m = 0$$

$$S_m = N_m$$

To solve equation (7).

Substitute $I_h = A_h = I_m = 0$ and $S_h = N_h$ into the left side of equation (7):

$$\alpha \frac{I_m}{N_h} S_h + \gamma A_h - (\beta + \delta + \mu_h + \epsilon) I_h = 0$$

$$\alpha \frac{0}{N_h} N_h + \gamma \cdot 0 - (\beta + \delta + \mu_h + \epsilon) 0 = 0$$

If we calculate each term:

$$\begin{aligned} \alpha \frac{0}{N_h} N_h &= 0, & \gamma \cdot 0 &= 0, \\ (\beta + \delta + \mu_h + \epsilon) 0 &= 0 \end{aligned}$$

So the entire side becomes $0 + 0 - 0 = 0$. Thus equation (7) is satisfied.

Substitute into equation (8).

Substitute $I_h = 0$, $A_h = 0$, we obtain:

$$\delta I_h - (\gamma + \mu_h) A_h = 0$$

$$\delta \cdot 0 - (\gamma + \mu_h) 0 = 0$$

$$0 = 0$$

Thus equation (8) is satisfied.

Substitute into equation (10).

Substitute $I_h = 0$, $S_m = N_m$, and $I_m = 0$, we obtain:

$$\theta \frac{I_h}{N_h} S_m - \mu_m I_m = \theta \frac{0}{N_h} N_m - \mu_m \cdot 0 = 0 - 0 = 0$$

Verify equation (9) to determine

For equation (9) we want to find S_m at DFE condition. Set $I_h = 0$, so we obtain:

$$\begin{aligned}\mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h}\right) S_m &= \mu_m N_m - (\mu_m + \theta \cdot 0) S_m \\ &= \mu_m N_m - \mu_m S_m = 0\end{aligned}$$

Simplify, it becomes:

$$\mu_m (N_m - S_m) = 0$$

Then, since $\mu_m > 0$, we obtain $N_m - S_m = 0 \Rightarrow S_m = N_m$

Analogous to S_h (obtained from equation (6) when $I_h = 0, = I_h = 0$), we get $S_h = N_h$

By substituting, $I_h = A_h = I_m = 0$ and the results $S_h = N_h$, $S_m = N_m$, all equations (6) – (10) are zero. Therefore, the point

$$x_{dfe} = (S_h, I_h, A_h, S_m, N_m) = (N_h, 0, 0, N_m, 0)$$

fulfills the disease-free equilibrium condition.

Using the Jacobian method for the malaria spread equations

To analyze the stability of the equilibrium point, the first step is to derive (find the derivative) of the system of differential equations to form the Jacobian Matrix. This matrix contains all the first-order partial derivatives of the system. We define our system as $F = [f_1, f_2, f_3, f_4, f_5]$, where each f_i represents the equations $\frac{dS_h}{dt}, \frac{dI_h}{dt}, \frac{dA_h}{dt}, \frac{dS_m}{dt}, \frac{dI_m}{dt}$.

The Jacobian Matrix J will have the form:

$$J = \begin{bmatrix} \frac{\partial F_1}{\partial S_h} & \frac{\partial F_1}{\partial I_h} & \frac{\partial F_1}{\partial A_h} & \frac{\partial F_1}{\partial S_m} & \frac{\partial F_1}{\partial I_m} \\ \frac{\partial F_2}{\partial S_h} & \frac{\partial F_2}{\partial I_h} & \frac{\partial F_2}{\partial A_h} & \frac{\partial F_2}{\partial S_m} & \frac{\partial F_2}{\partial I_m} \\ \frac{\partial F_3}{\partial S_h} & \frac{\partial F_3}{\partial I_h} & \frac{\partial F_3}{\partial A_h} & \frac{\partial F_3}{\partial S_m} & \frac{\partial F_3}{\partial I_m} \\ \frac{\partial F_4}{\partial S_h} & \frac{\partial F_4}{\partial I_h} & \frac{\partial F_4}{\partial A_h} & \frac{\partial F_4}{\partial S_m} & \frac{\partial F_4}{\partial I_m} \\ \frac{\partial F_5}{\partial S_h} & \frac{\partial F_5}{\partial I_h} & \frac{\partial F_5}{\partial A_h} & \frac{\partial F_5}{\partial S_m} & \frac{\partial F_5}{\partial I_m} \end{bmatrix}$$

Here are the partial derivative calculations for each row of the matrix:

Derivative of the susceptible human equation S_h .

The first equation f_1 , is $\frac{dS_h}{dt} = \mu_h N_h + \beta I_h - (\mu_h + \alpha \frac{I_m}{N_h}) S_h$. We find the partial derivative of f_1 with respect to each variable $(S_h, I_h, A_h, S_m, I_m)$:

$$\frac{\partial F_1}{\partial S_h} = -N_h - \alpha \frac{I_m}{N_h}$$

$$\frac{\partial F_1}{\partial I_h} = \beta$$

$$\frac{\partial F_1}{\partial A_h} = 0$$

$$\frac{\partial F_1}{\partial S_m} = 0$$

$$\frac{\partial F_1}{\partial I_m} = \alpha \frac{S_h}{N_h}$$

Derivative of the infected human equation I_h .

The second equation f_2 , is $\frac{dI_h}{dt} = \alpha \frac{I_m}{N_h} S_h + \gamma A_h - \beta I_h - \delta I_h - (\mu_h + \epsilon) I_h$. We find the partial derivative of f_2 with respect to each variable:

$$\frac{\partial F_2}{\partial S_h} = \alpha \frac{I_m}{N_h}$$

$$\frac{\partial F_2}{\partial I_h} = -(\beta + \delta + N_h + \epsilon)$$

$$\frac{\partial F_2}{\partial A_h} = \gamma$$

$$\frac{\partial F_2}{\partial S_m} = 0$$

$$\frac{\partial F_2}{\partial I_m} = \frac{\alpha}{N_h}$$

Derivative of the asymptomatic/carrier human equation

The third equation f_3 , is $f_3 = \frac{dA_h}{dt} = \delta I_h - (\gamma + \mu_h) A_h$. We find the partial derivative of f_3 with respect to each variable:

$$\frac{\partial F_3}{\partial S_h} = 0$$

$$\frac{\partial F_3}{\partial I_h} = \delta$$

$$\frac{\partial F_3}{\partial A_h} = -(\gamma + N_h)$$

$$\frac{\partial F_3}{\partial S_m} = 0$$

$$\frac{\partial F_3}{\partial I_m} = 0$$

Derivative of the susceptible mosquito equation

The fourth equation f_4 , is $f_4 = \frac{dS_m}{dt} = \mu_m N_m - (\mu_m + \theta \frac{I_h}{N_h}) S_m$. We find the partial derivative of f_4 with respect to each variable:

$$\frac{\partial F_4}{\partial S_h} = 0$$

$$\frac{\partial F_4}{\partial I_h} = -\theta \frac{S_m}{N_h}$$

$$\frac{\partial F_4}{\partial A_h} = 0$$

$$\frac{\partial F_4}{\partial S_m} = -\theta \frac{I_h}{N_h}$$

$$\frac{\partial F_4}{\partial I_m} = 0$$

Derivative of the infected mosquito equation

The fifth equation f_5 , is $f_5 = \frac{dI_m}{dt} = \theta \frac{I_h}{N_h} S_m - \mu_m I_m$.

We find the partial derivative of f_5 with respect to each variable:

$$\frac{\partial F_5}{\partial S_h} = 0$$

$$\frac{\partial F_5}{\partial I_h} = \theta \frac{S_m}{N_h}$$

$$\frac{\partial F_5}{\partial A_h} = 0$$

$$\frac{\partial F_5}{\partial S_m} = \theta \frac{I_h}{N_h}$$

$$\frac{\partial F_5}{\partial I_m} = -\mu_m$$

By combining all these partial derivative results into the matrix, we obtain the general Jacobian Matrix for this system:

$$J = \begin{bmatrix} -\left(N_h + \alpha \frac{I_m}{N_h}\right) & \beta & 0 & 0 & \alpha \frac{S_h}{N_h} \\ \alpha \frac{I_m}{N_h} & -(\beta + \delta + N_h + \epsilon) & \gamma & 0 & \frac{\alpha}{N_h} \\ 0 & \delta & -(\gamma + N_h) & 0 & 0 \\ 0 & -\theta \frac{S_m}{N_h} & 0 & -\theta \frac{I_h}{N_h} & 0 \\ 0 & \theta \frac{S_m}{N_h} & 0 & \theta \frac{I_h}{N_h} & -\mu_m \end{bmatrix}$$

Stability analysis of the disease-free point (DFE)

Next, we evaluate the stability of the system at the Disease-Free Equilibrium (DFE) point, which we call E_0 . At this point, there is no infection in the population, so: $I_h = 0, S_m = 0$ and $I_m = 0$. The susceptible population is at its natural equilibrium value: $S_h = N_h$.

We substitute these DFE values into the Jacobian Matrix J to get $J(E_0)$:

$$J(E_0) = \begin{bmatrix} -\mu_h & \beta & 0 & 0 & -\alpha \\ 0 & -(\beta + \delta + N_h + \epsilon) & \gamma & 0 & \alpha \\ 0 & \delta & -(\gamma + N_h) & 0 & 0 \\ 0 & -\theta \frac{N_m}{N_h} & 0 & -\mu_m & 0 \\ 0 & \theta \frac{N_m}{N_h} & 0 & 0 & -\mu_m \end{bmatrix}$$

It is known

$$R_0 = \rho(FV^{-1})$$

Where the DFE will be stable if $R_0 < 1$, and unstable if $R_0 > 1$. With F and V being:

$$F = \begin{bmatrix} 0 & 0 & \alpha \\ 0 & 0 & 0 \\ \theta \frac{N_m}{N_h} & 0 & 0 \end{bmatrix}, \quad V = \begin{bmatrix} \beta + \delta + N_h + \epsilon & -\gamma & 0 \\ -\delta & \gamma + \mu_h & 0 \\ 0 & 0 & \mu_m \end{bmatrix}$$

Endemic Equilibrium Point (X_{ee})

The non-disease-free equilibrium point, or endemic equilibrium point, is the state where the disease persists in the population (number of infected individuals $I_h, A_h, I_m \neq 0$). To find it, we must substitute the stationary conditions ($dS_h/dt = dI_h/dt = dA_h/dt = dS_m/dt = dI_m/dt = 0$) into the systems (1) – (5).

From equation (8) for A_h :

$$\frac{dA_h}{dt} = \delta I_h - (\gamma + \mu_h)A_h = 0$$

The inflow rate to compartment A_h comes from I_h individuals moving to asymptomatic (δI_h), while the outflow rate comes from returning to symptomatic (γA_h) and natural death ($\mu_h A_h$).

Then,

$$\begin{aligned} \delta I_h - (\gamma + \mu_h)A_h &= 0 \\ \Rightarrow A_h &= \frac{\delta}{\gamma + \mu_h} I_h \end{aligned} \quad (11)$$

This means the number of asymptomatic individuals is proportional to the number of infected individuals.

From equation (9) for S_m :

$$\frac{dS_m}{dt} = \mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m = 0$$

The inflow rate to S_m comes from mosquito births ($\mu_m N_m$), the outflow rate from natural mosquito death ($\mu_m S_m$) and infection from contact with infected humans ($\theta \frac{I_h}{N_h} S_m$).

Then,

$$\begin{aligned} \mu_m N_m - \left(\mu_m + \theta \frac{I_h}{N_h} \right) S_m &= 0 \\ \Rightarrow S_m &= \frac{\mu_m N_m}{\mu_m + \theta \frac{I_h}{N_h}} \end{aligned} \quad (12)$$

From equation (10) for I_m :

$$\frac{dI_m}{dt} = \theta \frac{I_h}{N_h} S_m - \mu_m I_m = 0$$

The inflow rate to I_m comes from susceptible mosquitoes becoming infected ($\theta \frac{I_h}{N_h} S_m$), the outflow rate from mosquito death ($\mu_m I_m$).

Thus,

$$\begin{aligned} \theta \frac{I_h}{N_h} S_m - \mu_m I_m &= 0 \\ \Rightarrow I_m &= \frac{\theta}{\mu_m} \frac{I_h}{N_h} S_m \end{aligned} \quad (13)$$

Substitute S_m from (12), then

$$\begin{aligned} I_m &= \frac{\theta}{\mu_m} \frac{I_h}{N_h} \cdot \frac{\mu_m N_m}{\mu_m + \theta \frac{I_h}{N_h}} \\ &= \frac{\theta N_m}{\mu_m} \cdot \frac{\frac{I_h}{N_h}}{1 + \frac{\theta}{\mu_m} \frac{I_h}{N_h}} \end{aligned} \quad (14)$$

From equation (6) for S_h :

$$\begin{aligned} \frac{dS_h}{dt} &= \mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h \\ &= 0 \end{aligned}$$

The inflow rate to S_h comes from new human births ($\mu_h N_h$) and recovery from infection (βI_h), while the outflow rate is from natural human death ($\mu_h S_h$) and infection from infected mosquito bites ($\alpha \frac{I_m}{N_h} S_h$).

Thus,

$$\begin{aligned} \mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h &= 0 \\ \Rightarrow S_h &= \frac{\mu_h N_h + \beta I_h}{\mu_h + \alpha \frac{I_m}{N_h}} \end{aligned} \quad (15)$$

From equation (7) for I_h :

$$\begin{aligned} \frac{dI_h}{dt} &= \alpha \frac{I_m}{N_h} S_h + \gamma A_h \\ &\quad - (\beta + \delta + \mu_h + \epsilon) I_h \\ &= 0 \end{aligned}$$

The inflow rate to I_h comes from susceptible individuals infected by mosquitoes ($\alpha \frac{I_m}{N_h} S_h$) and from asymptomatic individuals who become symptomatic (γA_h). The outflow rate is due to recovery (βI_h), moving to asymptomatic (δI_h), natural death ($\mu_h I_h$), and death from the disease (ϵI_h).

Thus,

$$\alpha \frac{I_m}{N_h} S_h + \gamma A_h - (\beta + \delta + \mu_h + \epsilon) I_h = 0 \quad (16)$$

Substitute (11), (14), and (15) into (16)

$$\text{Substitute } A_h = \frac{\delta}{\gamma + \mu_h} I_h$$

Substitute I_m dari (14)

Substitute S_h dari (15)

Thus equation (16) becomes:

$$\alpha \frac{I_m}{N_h} \left(\frac{\theta N_m}{\mu_m} \cdot \frac{\frac{I_h}{N_h}}{1 + \frac{\theta}{\mu_m} \frac{I_h}{N_h}} \right) \cdot \frac{\mu_h N_h + \beta I_h}{\mu_h + \alpha \frac{I_m}{N_h} \left(\frac{\theta N_m}{\mu_m} \cdot \frac{\frac{I_h}{N_h}}{1 + \frac{\theta}{\mu_m} \frac{I_h}{N_h}} \right)} + \frac{\delta}{\gamma + \mu_h} I_h - (\beta + \delta + \mu_h + \epsilon) I_h = 0$$

Interpretation

If $I_h = 0$, we return to the disease-free equilibrium (DFE).

If $I_h > 0$, satisfying (16), then the endemic equilibrium point $(S_h^*, I_h^*, A_h^*, S_m^*, I_m^*)$ is obtained.

After I_h^* is found (usually by numerical solution), the other compartments can be calculated from:

$$A_h^* = \frac{\delta}{\gamma + \mu_h} I_h^*, S_m^* = \frac{\mu_m N_m}{\mu_m + \theta \frac{I_h^*}{N_h}}, I_m^* = \frac{\theta}{\mu_m} \frac{I_h^*}{N_h} S_m^*, S_h^* = \frac{\mu_h N_h + \beta I_h^*}{\mu_h + \alpha \frac{I_m^*}{N_h}}$$

Determination of the model's basic reproduction number (R_0)

Determining R_0

R_0 is the dominant eigenvalue (the largest positive value), so we take the positive root of the result above. This yields the Equation:

$$R_0 = \frac{\sqrt{c_1 \mu_m c_6 S_m c_4 S_h}}{c_1 \mu_m} \quad (17)$$

Where parameters c_1 , c_4 and c_6 :

$$c_1 = (\beta + \delta + \mu_h + \epsilon)$$

$$c_4 = \frac{\alpha}{N_h}$$

$$c_6 = \frac{\theta}{N_h}$$

Substitution of the Disease-Free Fixed Point (DFE)

Evaluating R_0 at the disease-free fixed point (DFE). At the DFE condition, there is no infection, so the susceptible population is at its maximum capacity.

Susceptible human population: $S_h = N_h$

Susceptible mosquito population: $S_m = N_m$

We will substitute the c values and the DFE values (S_h, S_m) into Equation (17):

$$R_0 = \frac{\sqrt{(\beta + \delta + \mu_h + \epsilon) \cdot \mu_m \cdot \left(\frac{\theta}{N_h}\right) \cdot N_m \cdot \left(\frac{\alpha}{N_h}\right) \cdot S_h}}{(\beta + \delta + \mu_h + \epsilon) \cdot \mu_m}$$

Note that N_h in the denominator $\left(\frac{\alpha}{N_h}\right)$ and N_h from S_h cancel each other out.

$$\sqrt{(\beta + \delta + \mu_h + \epsilon) \cdot \mu_m \cdot \left(\frac{\theta}{N_h}\right) \cdot N_m \cdot \alpha}$$

Regroup the terms:

$$\sqrt{[(\beta + \delta + \mu_h + \epsilon) \mu_m] \cdot \left[\frac{\theta N_m \alpha}{N_h}\right]}$$

Substitute back into R_0 :

$$R_0 = \frac{\sqrt{[(\beta + \delta + \mu_h + \epsilon) \mu_m] \cdot \left[\frac{\theta N_m \alpha}{N_h}\right]}}{(\beta + \delta + \mu_h + \epsilon) \mu_m}$$

Use the algebraic property $\frac{\sqrt{A \cdot B}}{A} = \sqrt{\frac{B}{A}}$:

Let $A = (\beta + \delta + \mu_h + \epsilon) \mu_m$ and $B = \frac{\theta N_m \alpha}{N_h}$, then R_0 becomes

$$R_0 = \sqrt{\frac{B}{A}} = \sqrt{\frac{\frac{\theta N_m \alpha}{N_h}}{(\beta + \delta + \mu_h + \epsilon) \mu_m}}$$

Thus we obtain

$$R_0 = \sqrt{\frac{\theta N_m \alpha}{N_h (\beta + \delta + \mu_h + \epsilon) \mu_m}}$$

Numerical Simulation

In this section, a numerical simulation is performed to observe the long-term population dynamics of the SIAS-SI model. The simulation is divided into two main scenarios based on the value of the Basic Reproduction Number (R_0), which is calculated based on the equation:

$$R_0 = \sqrt{\frac{\theta \alpha N_m}{N_h (\beta + \delta + \mu_h + \epsilon) \mu_m}}$$

The first scenario is the disease-free case ($R_0 < 1$) which uses the set of parameters from the following table:

Table 3. Parameter values for $R_0 < 1$ in the SIAS-SI model for malaria

Parameter	Value	Unit	Reference
N_h	1700	People/time	Assumption
α	0,010	Time ⁻¹	Chitnis et al.,2006
γ	0,005	Time ⁻¹	Cai L, 2017
β	0,09	Time ⁻¹	Cai L, 2017
δ	0,91	Time ⁻¹	Aumsi
μ_h	0,004	Time ⁻¹	Agusto et al., 2012
ε_h	0,005	Time ⁻¹	Agusto et al., 2012
N_m	7700	Mosquitoes/time	Assumption
θ	0,072	Time ⁻¹	Chitnis et al., 2006
μ_m	0,11	Time ⁻¹	Traore B, 2017

Then, the second scenario (simulation) is the endemic case ($R_0 > 1$), which uses the parameters from the following table:

Table 4. Parameter values $R_0 > 1$ in the SIAS-SI model for malaria

Parameter	Value	Unit	Reference
N_h	1700	People/time	Assumption
α	0,70	Time ⁻¹	Assumption
γ	0,005	Time ⁻¹	Cai L, 2017
β	0,09	Time ⁻¹	Cai L, 2017
δ	0,91	Time ⁻¹	Assumption
μ_h	0,0016	Time ⁻¹	Traore B, 2017
ε_h	0,005	Time ⁻¹	Agusto et al., 2012
N_m	7700	Mosquitoes/time	Assumption
θ	0,09	Time ⁻¹	Cai L, 2017
μ_m	0,11	Time ⁻¹	Traore B, 2017

Both simulations use the same initial population conditions, as presented in table 3, and are run for a time range of $t = 30$ hari.

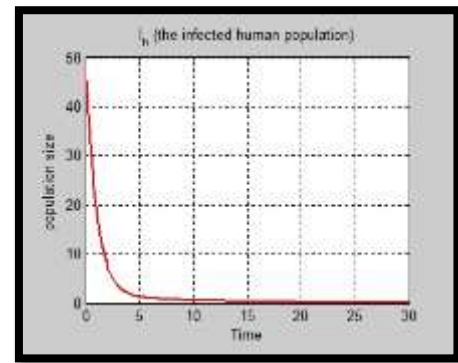
Table 5. Variable values for the SIAS-SI model for malaria

Variable	Nilai	Referensi
S_h	1000	Assumption
I_h	50	Assumption
A_h	10	Assumption
S_m	10000	Assumption
I_m	250	Assumption

Analysis of Scenario 1: Disease-Free Case ($R_0 < 1$)

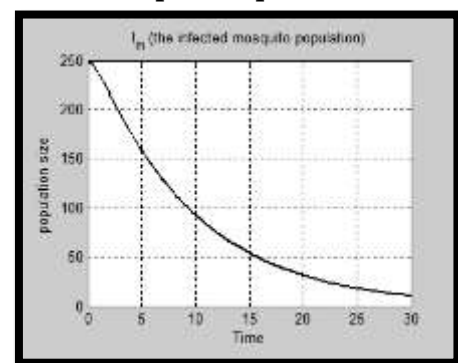
The core of this scenario is that the basic reproduction number R_0 is less than 1. This means, on average, one infected individual transmits the disease to less than one new susceptible individual before they recover or die. This makes the spread of the disease unsustainable.

I_h : Infected Human Population

**Figure 2.** Graph of Infected Human Population for Disease-Free Case ($R_0 < 1$)

The graph starts from the new initial condition, which is 50 individuals, then decreases drastically towards zero. This happens because with $R_0 < 1$, the rate of individuals recovering (or moving to asymptomatic) is faster than the rate of new infections. The disease cannot find new "hosts" fast enough to survive, so the number of active infections collapses.

I_m : Infected Mosquito Population

**Figure 3.** Graph of Infected Mosquito Population for Disease-Free Case ($R_0 < 1$)

The graph starts at 250 and consistently decreases towards zero. This is due to the follow-on effect of the collapse of I_h . Because fewer humans are infected (I_h), susceptible mosquitoes (S_m) have fewer targets to bite and become infected. Without

a source of human infection, the infected mosquito population also disappears.

A_h : Asymptomatic Human Population

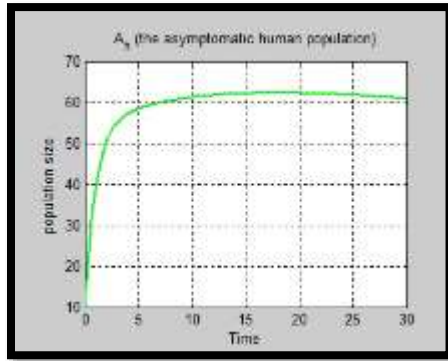


Figure 4. Graph of Asymptomatic Human Population for Disease-Free Case ($R_0 < 1$)

This graph is unique. It starts at 10, rises first (peaking around 60), and then slowly decreases (stabilizing around 60). [Note: As time goes on longer, this will also drop to zero]. This happens because the initial increase occurs as individuals from the infected I_h group (initially 50 people) move to the A_h (at rate δ). However, because there are no significant new infections (as I_h and I_m collapse), the "supply" of people moving to A_h stops, and the A_h population begins to decrease as they recover or die.

S_h : Susceptible Human Population

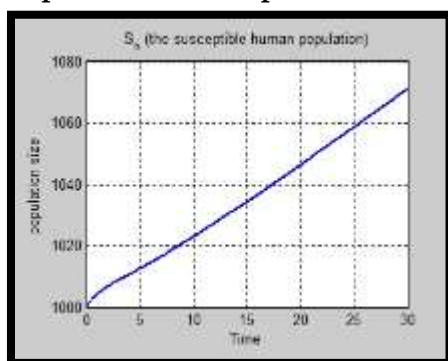


Figure 5. Graph of Susceptible Human Population for Disease-Free Case ($R_0 < 1$)

The graph starts at 1000 and increases steadily. This happens because it is the clearest sign of a recovering population. Since the rate of new infections is almost zero, the susceptible population is no longer decreasing. Instead, it grows back towards its natural equilibrium

(determined by the parameter $N_h = 1700$), driven by the birth rate.

S_m : Susceptible Mosquito Population

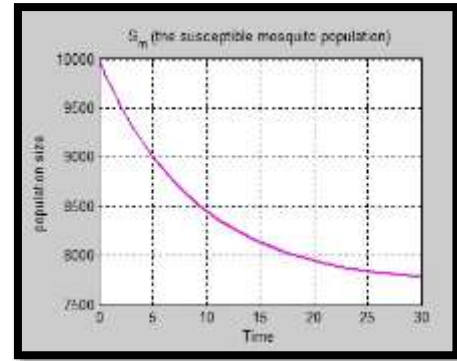


Figure 6. Susceptible Mosquito Population for Disease-Free Case ($R_0 < 1$)

The graph starts at 10,000 and decreases steadily. This happens because, similar to S_h , this population is moving towards its natural equilibrium (determined by the parameter $N_m = 7700$). Since the initial assumption (10,000) was higher than its equilibrium, this population naturally declines.

Analysis of Scenario 2: Endemic Case ($R_0 > 1$)

The core of this scenario is that the basic reproduction number R_0 is greater than 1. This means, on average, one infected individual successfully transmits the disease to more than one new susceptible individual. This allows the disease to spread and persist in the population.

I_h : Infected Human Population

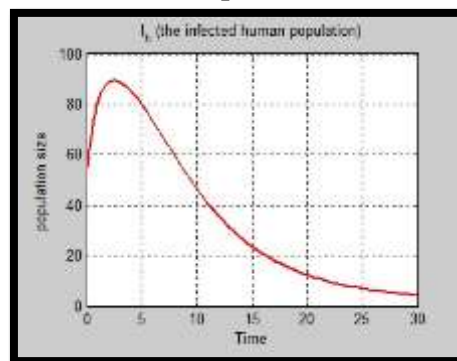


Figure 7. Graph of Infected Human Population for Endemic Case ($R_0 > 1$)

The graph starts at 50, but does not immediately drop. Instead, it first rises to a peak (around 90) before finally decreasing and stabilizing at a non-

zero level (around 5-10). This is because this initial increase is a classic sign of $R_0 > 1$. The rate of new transmission is faster than the rate of recovery, so the number of active infections grows. Eventually, it reaches an equilibrium (balance) when the number of susceptible people has decreased sufficiently.

I_m : Infected Mosquito Population

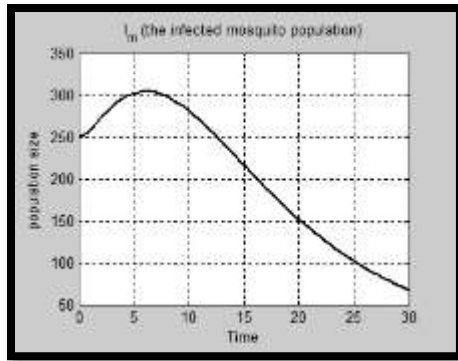


Figure 8. Graph of Infected Mosquito Population for Endemic Case ($R_0 > 1$)

Similar to I_h , this graph starts at 250, rises to a peak (around 320), and then stabilizes at a non-zero level (around 50). This occurs because the I_h population (infected humans) does not disappear, mosquitoes have a constant source of infection to bite. This allows the infection to persist and circulate within the mosquito population.

A_h : Asymptomatic Human Population

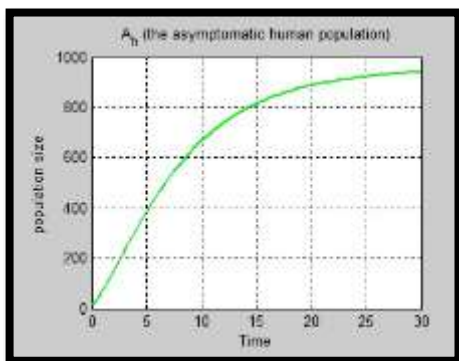


Figure 9. Graph of Asymptomatic Human Population for Endemic Case ($R_0 > 1$)

The graph starts at 10 and increases dramatically, stabilizing at a very high level (approaching 1000). This happens as a direct consequence of the persistent I_h infection. There is a constant "supply" of infected individuals moving

into the asymptomatic compartment, creating a large and stable "reservoir" of infection in the population.

S_h : Susceptible Human Population

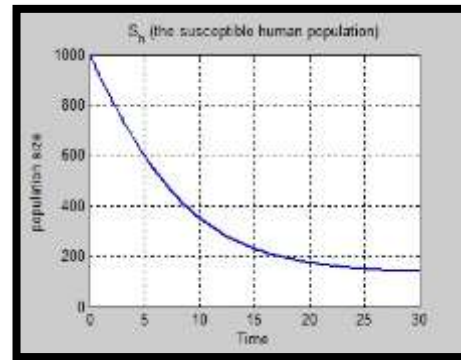


Figure 10. Graph of Susceptible Human Population for Endemic Case ($R_0 > 1$)

The graph starts at 1000 and decreases drastically, stabilizing at a very low level (around 150). This graph is the opposite of the $R_0 < 1$ simulation. Because the disease continues to spread, the "fuel" of the epidemic—the susceptible population—is continuously "consumed" and moved to the I_h and A_h compartments. The susceptible population remains low due to the high rate of new infections.

S_m : Susceptible Mosquito Population

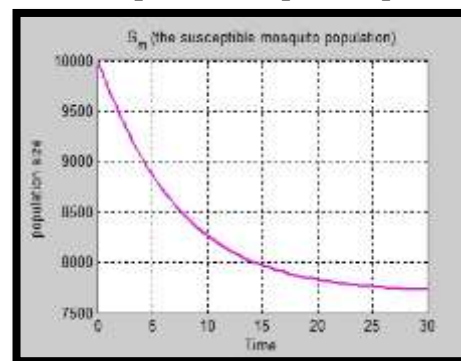


Figure 11. Graph of Susceptible Mosquito Population for Endemic Case ($R_0 > 1$)

The graph starts at 10,000 and decreases, stabilizing at its equilibrium (around 7700). Where, this graph is similar to scenario $R_0 < 1$, it moves from its initial assumption towards its natural equilibrium ($N_m = 7700$).

BATIK OF the spread of Malaria with Asymptomatic and Superinfection

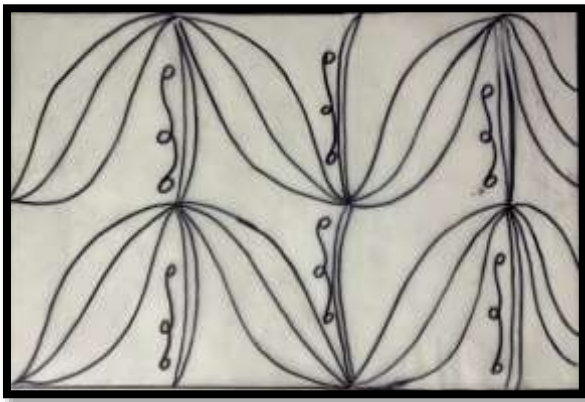


Figure 12. Batik of the Spread of Malaria with Asymptomatic and Superinfection

1. Philosophical Meaning

The batik motif formed from the graph of the malaria spread model consists of winding, long, and repeating lines with an impression of waves, smoke, or plant tendrils. Although the motif seems simple, it can be associated with several philosophies of traditional batik motifs.

Winding, unbroken lines, like ocean waves, are often found in motifs like Batik Parang. Its philosophy symbolizes a spirit that never dies, a continuous struggle, and not easily giving up in facing life's challenges (like waves that continuously hit the rocks).

The form of waves or flow can also symbolize the wheel or flow of life, which is dynamic, full of twists and turns, and ebbs and flows. Like the flow of water or waves, the wearer is expected to have patience, perseverance, and persistence to keep moving forward and find a way out of every problem.

These lines can also be interpreted as plant tendrils or fern leaves (for example, as in the Kaluak Daun Pakis motif from Padang). Tendrils symbolize growth, development, and the ability to adapt flexibly (winding) in different environments. This motif encourages the wearer to have a strong, resilient soul, and to be able to control themselves in living a life that is constantly moving and changing.

2. Biological Meaning in Batik based on the Endemic Case ($R_0 > 1$) Scenario Graph

a) S_h : Susceptible Humans

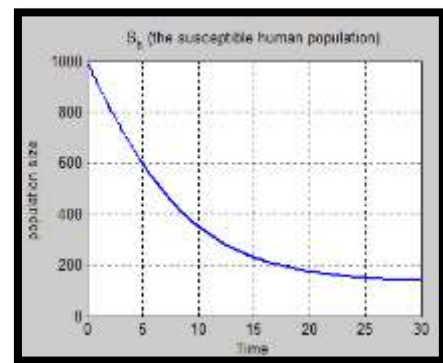


Figure 13. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Susceptible Humans.

This batik motif reflects the biological condition where the number of humans still susceptible to malaria continuously decreases due to a high transmission rate. This decrease occurs as more individuals become infected through the bites of mosquitoes carrying the Plasmodium parasite, so the susceptible group becomes smaller and the system reaches a stable state at an endemic level. Biologically, this illustrates a situation where the disease can persist in the population because the basic reproduction number (R_0) is greater than one, meaning each infected individual can transmit the disease to more than one other person.

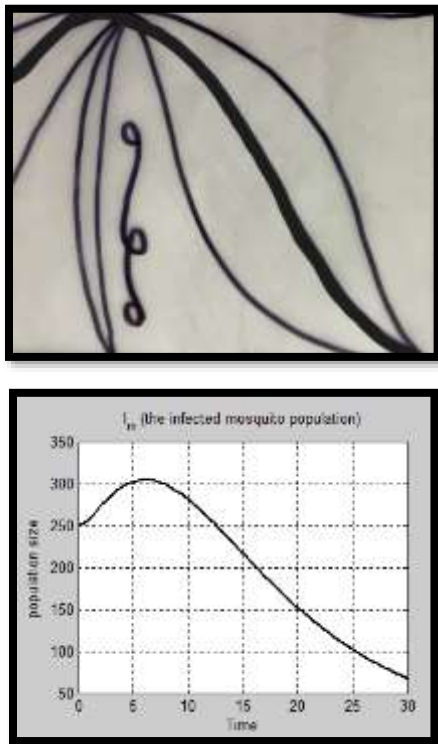
b) I_m : Infected Mosquitoes

Figure 14. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Infected Mosquitoes.

The biological meaning of this batik image illustrates the dynamics of infected mosquitoes (I_m) in the disease spread process. The motif of a line that curves up and then down reflects the change in the number of mosquitoes carrying the parasite. Initially, the number of infected mosquitoes increases due to the large number of infected humans who are a source of parasites for the mosquitoes when they bite. After reaching a peak, the number of infected mosquitoes decreases because some mosquitoes die or no longer find enough humans to transmit the infection to. Nevertheless, the presence of a small number of infected mosquitoes maintains the circulation of the disease in the environment. This visual pattern reflects the biological balance between infection, transmission, and death in the life cycle of the mosquito and the disease it transmits.

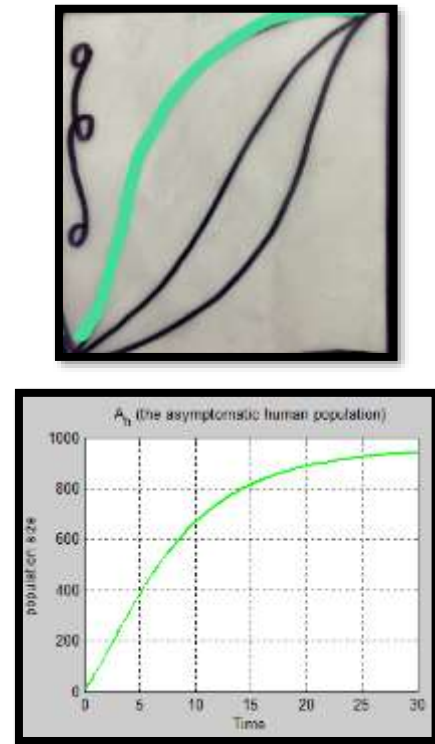
c) A_h : Asymptomatic Humans

Figure 15. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Asymptomatic Humans.

The biological meaning of this batik image illustrates the increase in the number of asymptomatic humans (A_h) which continues to grow until it reaches a high level of stability. The batik line pattern that curves and thickens upwards reflects the population growth of individuals who are infected but show no symptoms. Biologically, this indicates that as more humans are exposed to the disease and remain in a symptom-free state, they become "carriers" or reservoirs of infection that allow transmission to continue in the community. This condition describes an endemic situation, where the disease persists due to a balance between new infections and asymptomatic individuals who continue to carry the parasite in their bodies.

3. Mathematical Meaning in Batik based on the Endemic Case ($R_0 > 1$) Scenario Graph

a) S_h : Susceptible Humans

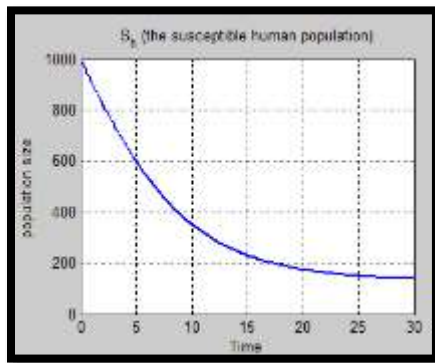
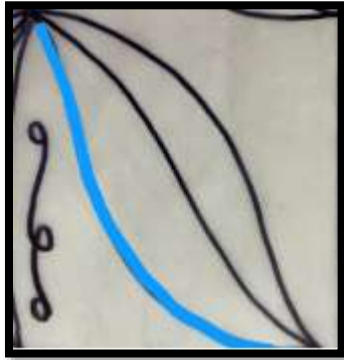


Figure 16. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Susceptible Humans.

$$\mu_h N_h + \beta I_h - \left(\mu_h + \alpha \frac{I_m}{N_h} \right) S_h = 0$$

This equation describes the equilibrium of the susceptible human population (S_h) in a disease spread model involving humans and mosquitoes.

- $\mu_h N_h$: the birth rate of new humans (since it is assumed the total human population is relatively stable, birth $\approx$ death).
- βI_h : the rate of addition of healthy humans who become infected, influenced by the number of infected humans (I_h) — this could also represent the rate of internal exposure among humans.
- $(\mu_h + \alpha \frac{I_m}{N_h}) S_h$: the rate of decrease of healthy humans, either due to natural death ($\mu_h S_h$) or transmission from infected mosquitoes ($\alpha \frac{I_m}{N_h} S_h$).
- The equals zero sign ($= 0$) indicates an equilibrium condition, i.e., the rate of increase of susceptible humans equals the rate of decrease.

When values are inserted:

$$0,0016 \cdot 1700 + 0,09 I_h - \left(0,0016 + 0,7 \frac{I_m}{1700} \right) 1000 = 0$$

Simplifying, it becomes:

$$0,09 I_h = \frac{700 I_m}{1700} - 0,67$$

This shows that the number of infected humans (I_h) increases as the number of infected mosquitoes (I_m) increases. However, the value -0.67 indicates that if the number of infected mosquitoes is too small, transmission to humans will be very low or even non-existent.

b) I_m : Infected Mosquitoes

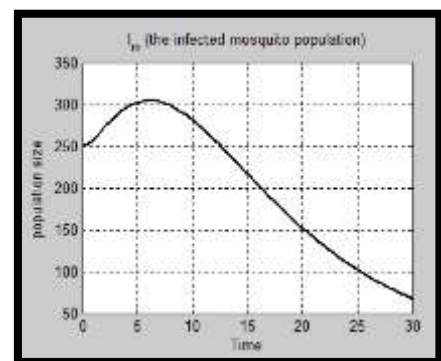


Figure 16. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Infected Mosquitoes.

$$\theta \frac{I_h}{N_h} S_m - \mu_m I_m = 0$$

The equation above shows the dynamic equilibrium of the infected mosquito population (I_m)

- $\theta \frac{I_h}{N_h} S_m$ describes the infection rate of healthy mosquitoes (S_m) that are infected by infected humans (I_h). The more infected humans there are, the

greater the chance of healthy mosquitoes becoming infected.

- $\mu_m I_m$ is the death rate of infected mosquitoes, where μ_m represents the mosquito death rate per unit of time.

When specific values are inserted:

$$0,09 \cdot \frac{I_h}{N_h} S_m - \mu_m \cdot 250 = 0$$

shows that at the moment $I_m = 250$, this equilibrium holds. After rearranging it becomes:

$$0,09 \frac{I_h}{N_h} S_m = 250 \mu_m$$

meaning the number of infected mosquitoes depends directly on the infection rate ($0,072 \frac{I_h}{N_h} S_m$) and the mosquito death rate (μ_m). If the infection rate increases, I_m tends to rise, and if the death rate rises, I_m decreases.

c) A_h : Asymptomatic Humans

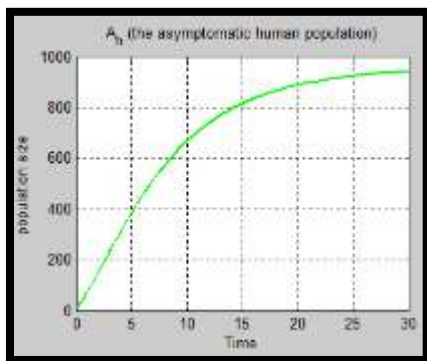


Figure 17. Biological Meaning based on the Endemic Case ($R_0 > 1$) Scenario Graph for Asymptomatic Humans.

$$\delta I_h - (\gamma + \mu_h) A_h = 0$$

The equation above shows the equilibrium of the number of asymptomatic humans (A_h) in a

disease spread model (e.g., malaria or dengue). Its meaning is as follows:

- δI_h : the rate of individuals entering the asymptomatic human group, i.e., individuals previously infected (I_h) who do not show symptoms afterward.
- $(\gamma + \mu_h) A_h$: the rate of individuals leaving the asymptomatic group, either due to recovery (γ) or natural death (μ_h).

When values are inserted:

$$0,91 \cdot I_h - (0,005 + \mu_h) 10 = 0$$

Simplifying, it becomes:

$$0,91 I_h = 10 \mu_h + 0,05$$

This can be interpreted that the number of infected individuals (I_h) is directly proportional to the human death rate (μ_h) and the recovery rate ($\gamma = 0,005$). Meaning, the greater μ_h , the higher the value of I_h needed for the asymptomatic group to remain in equilibrium.

Conclusions

This study has successfully developed and analyzed the SIAS-SI mathematical model for malaria transmission, which specifically includes the complexities of asymptomatic infection and superinfection. This model is represented by a system of five differential equations that describe the dynamics of the susceptible, infected, and asymptomatic populations in humans, as well as the susceptible and infected populations in mosquitoes.

The results of the model analysis identify two main equilibrium points:

1. Disease-Free Equilibrium (DFE) Point: Occurs at the condition $x_{dfj} = (N_h, 0, 0, N_m, 0)$, where the entire human and mosquito populations are in a susceptible state. Numerical simulation for the $R_0 < 1$ scenario validates this, showing that the infected population (I_h) and infected mosquitoes (I_m) decrease drastically towards zero, causing the disease to disappear from the population.
2. Endemic Equilibrium (Xee) Point: Occurs when the disease persists in the population

($I_h, A_h, I_m \neq 0$). Numerical simulation for the $R_0 > 1$ scenario shows that the disease spreads and persists. This is characterized by the stabilization of the infected populations (I_h, I_m) and a drastic increase in the asymptomatic population (A_h), which creates a large and stable infection reservoir.

The novelty of this research lies in the utilization of the model's dynamic analysis results, particularly the graph patterns from the endemic scenario ($R_0 > 1$) as algorithmic inspiration for creating new batik motifs. The resulting patterns, such as the graphs of S_h, A_h and I_m , are interpreted for their biological meaning as visual representations of the decline in the susceptible population, the formation of an asymptomatic reservoir, and the circulation of parasites by mosquitoes. Furthermore, the resulting winding line motifs are also linked to traditional batik philosophies such as Parang, which symbolizes struggle, continuity, and the dynamics of life.

Conflict of Interest: The author declares that there are no conflicts of interest concerning the publication of this article.

References

- Abdy M, Maryam H, Sanusi W. 2022. Pemodelan Matematika SIAS-SI pada Penyebaran Penyakit Malaria Asimtomatik dan Super Infeksi. SAINTIFIK: Jurnal Matematika, Sains, dan Pembelajarannya 8(1): 1–9. <https://doi.org/10.31605/saintifik.v8i1.360>
- Fajri N, Sianturi P, Bakhtiar T. 2016. Model Matematika SIS-SI Dalam Penyebaran Penyakit Malaria dengan Vaksinasi Taksempurna. Jurnal Manajemen dan Agribisnis 15(2): 51–62.
- Maryam H, Abdy M, Alimuddin, Side S. 2021. SEIAS-SEI model on asymptomatic and super infection malaria with imperfect vaccination. Journal of Physics: Conference Series 1918(4). <https://doi.org/10.1088/1742-6596/1918/4/042028>
- Prahmana RCI, D'Ambrosio U. 2020. Learning geometry and values from patterns: Ethnomathematics on the batik patterns of Yogyakarta, Indonesia. Journal on Mathematics Education 11(3): 439–456. <https://doi.org/10.22342/jme.11.3.12949.439-456>
- Saputro DRS, Widyaningsih Y, Wibowo A. 2022. Javanese Batik Motifs and Ornamentation as Objects of Aesthetics and Generative Art with Pseudo-Algorithm. Jurnal Javanologi: International Journal of Javanese Studies 6(1): 1139–1145. <https://doi.org/10.20961/javanologi.v6i1.71408>
- Dorin A. 2005. Artificial Life, Death and Epidemics in Evolutionary, Generative Electronic Art. In: LNCS 3449: 448–457.
- World Health Organization. 2023. World Malaria Report. World Health Organization. <https://www.who.int>