

Batik Motif Mathematical Modeling of the Spread of Malaria in Mimika Regency

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Abstract: This study aims to construct a batik motif inspired by the dynamics of malaria transmission through a SEIRS (Susceptible–Exposed–Infected–Recovered–Susceptible) mathematical modeling approach in Mimika Regency. The SEIRS model is used to represent the malaria transmission process, taking into account births, deaths, treatment in the exposed class, and the likelihood of recovered individuals becoming susceptible to infection again. Based on simulation results from the SEIRS model using data from the Mimika Regency Health Office in 2018, the basic reproduction number R_0 was obtained as 0.09, indicating that the spread of malaria tends to decrease and does not significantly cause new infections. This value is then translated into visual elements of batik through a dynamic balance pattern between four population classes (S, E, I, R) depicted as transitions in repetitive shapes and rhythms. The resulting motif represents the relationship between the stability of biological systems and visual harmony in batik art, reflecting the collaboration between science and local culture as an educational approach to public health issues.

Keywords: Basic reproduction number, batik motif, malaria, Mimika Regency, SEIRS model.

Introduction

Malaria is a major communicable disease that remains a significant public health challenge in tropical regions. The disease is transmitted through the bite of the female *Anopheles* mosquito carrying the *Plasmodium* parasite. In Indonesia, while malaria cases tend to decline in most provinces, several eastern regions still exhibit high transmission rates.

Mimika Regency in Papua is one such area characterized by stable and persistent malaria transmission. Environmental factors such as high humidity, heavy rainfall, the abundance of mosquito breeding grounds, and intensive population mobility significantly contribute to the strengthened dynamics of malaria transmission in this region. Therefore, a quantitative understanding of the malaria spread mechanism is essential for developing more effective control strategies.

Mathematical modeling is a widely utilized approach for analyzing the spread of infectious diseases. These models enable researchers to describe the relationships between variables influencing transmission rates, such as the interaction between humans and the vector organism, recovery rates, loss of immunity, and the influence of environmental factors. One model frequently applied in malaria studies is the SEIRS (Susceptible–Exposed–Infectious–Recovered–Susceptible) model. This model partitions the population into several groups based on health status and accommodates the process of immunity loss, allowing recovered individuals to become susceptible to re-infection. This characteristic aligns well with the nature of malaria, which permits repeated infections, particularly in high-endemic areas like Mimika.

The application of the SEIRS model provides an opportunity for a more detailed analysis of malaria transmission dynamics, including the parasite's incubation period in humans, the infectious period,

and the rate of re-susceptibility after recovery. By simulating various parameters, the model can help predict trends in case increases or decreases and assess the effectiveness of interventions. This is crucial because effective malaria control policies require a strong scientific foundation to optimize strategies such as residual spraying, the distribution of insecticide-treated nets (ITNs), or enhancing diagnostic access.

Beyond mathematical analysis, this research integrates a cultural approach through the development of a Batik motif that represents the structure and dynamics of the SEIRS model. Batik, as a strong cultural heritage of Indonesia, possesses powerful symbolic capability to convey ideas and knowledge through geometric patterns and visual repetition. Applying the batik motif in an epidemiological context offers a novel perspective for communicating scientific information to the public in an engaging, contextual, and easily digestible manner. This interdisciplinary approach also holds the potential to strengthen health education and raise public awareness regarding the importance of malaria prevention, particularly in endemic regions.

Based on this background, the objective of this study is to construct and analyze a mathematical model for malaria spread in Mimika Regency using the SEIRS approach, and to further develop a batik motif visualization that represents the model's structure as a culturally relevant medium for education and scientific communication.

Materials And Methods

Study area

The object of study in this research is the dynamics of malaria spread in Mimika Regency, Central Papua Province. The selection of this location is based on the endemic characteristics of malaria, which remains a primary health issue in the region. Although this research is a mathematical modeling study, the geographical and epidemiological context of Mimika Regency is utilized as the foundation for selecting and determining realistic parameters in the numerical simulation

Procedures

This research adopts an interdisciplinary approach by integrating the analysis of epidemiological system dynamics with the application of visual arts, consistent with the paper's title which combines mathematical modeling and Batik motifs.

Qualitative Model Analysis

In this stage, the SEIRS (Susceptible-Exposed-Infectious-Recovered-Susceptible) model is formulated through a system of four first-order non-linear differential equations that describe the population's rate of change over time. This analytical phase includes determining the Existence of Equilibrium Points (Disease-Free and Endemic) and testing the Stability of the DFE point using the Jacobian Matrix. This stability analysis is linked to the Basic Reproduction Number (R_0) as the epidemiological threshold criterion.

Numerical Analysis

Subsequently, the model is validated using numerical simulation. The system of differential equations is computationally integrated using MATLAB software to visualize population dynamics over a 48-month period. The parameters used in the simulation are adjusted to replicate the scenario in Mimika. The simulation results are presented in the form of time series graphs which serve as the visual foundation for the design application stage.

Batik Design Application

The final stage involves implementing the graphical results into a Batik motif. The R (Recovered) curve is selected as the fundamental geometric element of the batik pattern. This curve is chosen because it mathematically demonstrates convergence towards a stable equilibrium point and biologically symbolizes recovery, thus conveying a positive narrative.

The R curve is treated as a geometric function and is manipulated to generate the Batik motif. These manipulations include:

- Rotation (Rotary Symmetries), the R curve is rotated (90° , 180° , 270°) to create a symmetrical pattern around a central point.

- Reflection (Mirroring): the R curve is reflected horizontally and vertically.
- Repetition (Translational Symmetries): the fundamental pattern is periodically repeated to fill the cloth's field, representing the cyclical nature of the mathematical dynamic system.

Results And Discussion

Formulation of the SEIRS Model for Malaria Spread

- In this study, several assumptions were utilized to model the spread of malaria disease, specifically:
- The population undergoes processes of birth and natural death.
- Death can occur in all population classes, namely S , E , I , and R .
- Every newborn individual immediately enters the susceptible class (SS).
- The disease is treatable, allowing recovered individuals to gain temporary immunity.
- All individuals have an equal probability of contracting the infection (homogeneous mixing).
- Treatment or handling efforts are provided to individuals who are in the exposed (SE) stage.

The schema of the Malaria SEIRS model is illustrated in Figure 1.

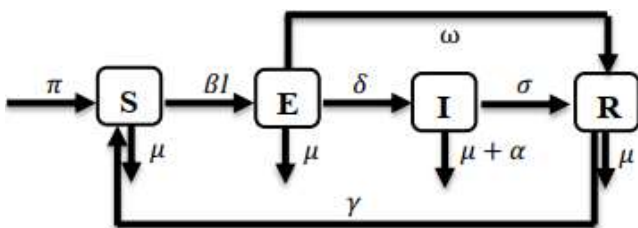


Figure 1. Schema of the Malaria SEIRS Model

Based on Figure 1, the mathematical model can be formulated as a system of differential equations Based on Figure 1.

$$\frac{dS}{dt} = \pi + \gamma R - (\mu + \beta I)S$$

$$\frac{dE}{dt} = \beta IS - (\mu + \omega + \delta)E$$

$$\frac{dI}{dt} = \delta E - (\mu + \alpha + \sigma)I$$

$$\frac{dR}{dt} = \sigma I + \omega E - (\mu + \gamma)R$$

S	:	Number of susceptible individuals
E	:	Number of individuals experiencing symptoms but not yet infected
I	:	Number of infected individuals who can transmit the disease
R	:	Number of recovered individuals
π	:	Birth rate
δ	:	Rate of individuals becoming infected
βI	:	Rate at which individuals become latent due to bites from infected mosquitoes
μ	:	Mortality rate
α	:	Mortality due to malaria
γ	:	Constant rate of immunity loss in humans after recovery
ω	:	Treatment effectiveness in humans
σ	:	Recovery rate

Equilibrium Points

Equilibrium points represent the stable or steady-state of the system and are found by setting the rate of change of every population group in the SEIRS model to zero, $\frac{dS}{dt} = 0, \frac{dE}{dt} = 0, \frac{dI}{dt} = 0, \frac{dR}{dt} = 0$. The system of equations (1) possesses two equilibrium points, the Disease-Free Equilibrium (DFE), denoted by E_0 and the Endemic Equilibrium (EE), denoted by E_1 .

The Disease-Free Equilibrium, denoted by $\mathcal{E}_0$, represents the condition where the disease is completely eliminated from the population. Consequently, there are no exposed, infected, or recovered individuals. Mathematically, this condition is denoted by

A. Disease Free Equilibrium

The Disease-Free Equilibrium, denoted by E_0 , represents the condition where the disease is completely eliminated from the population. Consequently, there are no exposed, infected, or recovered individuals. Mathematically, this condition is denoted by $E = 0, I = 0, R = 0$.

By assuming $E = 0, I = 0, R = 0$ in the $\frac{dS}{dt} = 0$, we obtain:

$$\begin{aligned} \frac{dS}{dt} &= \pi + \gamma R - (\mu + \beta I)S \\ 0 &= \pi + \gamma(0) - (\mu + \beta(0))S \\ 0 &= \pi - \mu S \end{aligned} \quad (1)$$

$$S = \frac{\pi}{\mu}$$

Therefore, the Disease-Free Equilibrium point for Malaria exists at $E_0 = (S, E, I, R) = (\frac{\pi}{\mu}, 0, 0, 0)$.

B. Endemic Equilibrium

The Endemic Equilibrium, denoted by E^* represents the condition where the disease persists (**endemic**) in the population, resulting in a non-trivial number of infected individuals ($I^* \neq 0$). These non-zero equilibrium values are collectively represented as $E^* = (S^*, E^*, I^*, R^*)$.

Existence of Equilibrium Points

This section aims to formally prove the existence of the non-trivial Endemic Equilibrium (E^*). To obtain the explicit solutions for $E^* = (S^*, E^*, I^*, R^*)$, the calculations will be performed using the system of differential equations.

Starting from $\frac{dI}{dt} = 0$, the relationship E^* and I^* is obtained:

$$\delta E^* - (\mu + \alpha + \sigma) I^* = 0$$

$$E^* = \frac{\mu + \alpha + \sigma}{\delta} I^* \quad (2)$$

Next we substitute E^* into the $\frac{dE}{dt} = 0$ equation, which results in:

$$\beta I^* S^* = (\mu + \omega + \delta) \frac{\mu + \alpha + \sigma}{\delta} I^*$$

Since $I^* \neq 0$, both sides of the equation can be divided by I^* yielding the value of the susceptible population S under endemic conditions:

$$S^* = \frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta \delta} \quad (3)$$

Subsequently, we substitute the value of $\frac{dR}{dt} = 0$ equation to obtain the value of the recovered population (R^*) under endemic conditions:

$$\begin{aligned} \sigma I + \omega E - (\mu + \gamma) R &= 0 \\ R^* &= \frac{\sigma I^* + \omega E^*}{\mu + \gamma} \end{aligned} \quad (4)$$

$$\begin{aligned} R^* &= \frac{1}{\mu + \gamma} \left(\sigma I^* + \omega \left(\frac{(\mu + \alpha + \sigma)}{\delta} I^* \right) \right) \\ R^* &= \frac{\sigma \delta + \omega(\mu + \alpha + \sigma)}{(\mu + \gamma) \delta} I^* \end{aligned}$$

The final step is to find I^* by substituting Equations (2), (3), and (4) into the $\frac{dS}{dt} = 0$ equation. This yields the value of the infected population:

$$\begin{aligned} \pi + \gamma R - (\mu + \beta I) S &= 0 \\ \pi + \gamma \cdot \left(\frac{\sigma \delta + \omega(\mu + \alpha + \sigma)}{(\mu + \gamma) \delta} I^* \right) - \mu \cdot \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta \delta} \right) - I^* \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\delta} \right) &= 0 \\ \pi + \gamma \cdot \left(\frac{\sigma \delta + \omega(\mu + \alpha + \sigma)}{(\mu + \gamma) \delta} I^* \right) - \mu \cdot \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta \delta} \right) - I^* \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\delta} \right) &= 0 \\ \left[\frac{\gamma(\sigma \delta + \omega(\mu + \alpha + \sigma))}{\mu + \gamma} - (\mu + \omega + \delta)(\mu + \alpha + \sigma) \right] I^* &= \mu \cdot \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta \delta} \right) - \pi \end{aligned}$$

Next multiply the numerator and the denominator by δ :

$$\begin{aligned} \Rightarrow \left[\frac{\gamma(\sigma \delta + \omega(\mu + \alpha + \sigma))}{\mu + \gamma} - (\mu + \omega + \delta)(\mu + \alpha + \sigma) \right] I^* &= \mu \cdot \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta} \right) - \pi \delta \\ \Rightarrow I^* &= \frac{\mu \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta} \right) - \pi \delta}{\frac{\gamma(\sigma \delta + \omega(\mu + \alpha + \sigma))}{\mu + \gamma} - (\mu + \omega + \delta)(\mu + \alpha + \sigma)} \end{aligned}$$

Thus, the Endemic Equilibrium point for malaria exists at $E^* = (S^*, E^*, I^*, R^*)$ with the following components:

$$S^* = \frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta \delta} \quad (6)$$

$$E^* = \frac{\mu + \alpha + \sigma}{\delta} I^*$$

$$I^* = \frac{\mu \left(\frac{(\mu + \omega + \delta)(\mu + \alpha + \sigma)}{\beta} \right) - \pi \delta}{\frac{\gamma(\sigma \delta + \omega(\mu + \alpha + \sigma))}{\mu + \gamma} - (\mu + \omega + \delta)(\mu + \alpha + \sigma)}$$

$$R^* = \frac{\sigma \delta + \omega(\mu + \alpha + \sigma)}{(\mu + \gamma)\delta} I^*$$

Stability of Equilibrium Points

The stability analysis of an equilibrium point is performed using the **linearization method** around that point. This involves determining the **eigenvalues** (λ) of the **Jacobian Matrix** (J). An equilibrium point is deemed **locally asymptotically stable** if all eigenvalues of the Jacobian matrix evaluated at that point have negative real parts.

The stability of the Disease-Free Equilibrium (E_0) can be expressed using the general Jacobian matrix $J(S, E, I, R)$ [refer to the full matrix here].

$$J(S, E, I, R) = \begin{pmatrix} -\mu - \beta I & 0 & -\beta S & \gamma \\ \beta I & -\mu - \omega - \delta & \beta S & 0 \\ 0 & \delta & -\mu - \alpha - \sigma & 0 \\ 0 & \omega & \sigma & -\mu - \gamma \end{pmatrix}$$

This matrix is then evaluated at the Disease-Free Equilibrium point, $E_0 = (\frac{\pi}{\mu}, 0, 0, 0)$, resulting in the Jacobian Matrix $J(E_0)$:

$$J\left(\frac{\pi}{\mu}, 0, 0, 0\right) = \begin{pmatrix} -\mu & 0 & -\beta \left(\frac{\pi}{\mu}\right) & \gamma \\ 0 & -(\mu + \omega + \delta) & \beta \left(\frac{\pi}{\mu}\right) & 0 \\ 0 & \delta & -(\mu + \alpha + \sigma) & 0 \\ 0 & \omega & \sigma & -(\mu + \gamma) \end{pmatrix}$$

The eigenvalues (λ) of this matrix are obtained by solving the characteristic equation $\det(J - \lambda I) = 0$. This yields four eigenvalues.

$$\lambda_1 = -\mu$$

$$\lambda_2 = -(\mu + \gamma)$$

Since the mortality rate (μ) and the rate of immunity loss (γ) are always positive, these two eigenvalues always have negative real parts. The remaining two eigenvalues ($\lambda_{3,4}$) are obtained by solving the quadratic equation related to the Exposed (E) and Infected (I) population classes:

$$\lambda^2 + (\mu + \omega + \delta + \mu + \alpha + \sigma)\lambda + (\mu + \omega + \delta)(\mu + \alpha + \sigma) - \beta \frac{\pi}{\mu} \delta = 0$$

Based on the Routh-Hurwitz Criterion, since the coefficient $\lambda = (2\mu + \omega + \delta + \alpha + \sigma)$ is positive, the stability is determined by the sign of the constant K , which is defined as:

$$K = (\mu + \omega + \delta)(\mu + \alpha + \sigma) - \beta \frac{\pi}{\mu} \delta$$

The Basic Reproduction Number R_0 is a key parameter in epidemiology. R_0 is defined as the ratio of the new infection rate to the rate of infection loss, which in the SEIRS model is expressed as:

$$R_0 = \frac{\beta \pi \delta}{\mu(\mu + \omega + \delta)(\mu + \alpha + \sigma)}$$

The stability analysis of the DFE shows that the condition R_0 determines the sign of the constant K . If $R_0 < 1$, this condition implies that $K > 0$, such that all eigenvalues ($\lambda_{3,4}$) have negative real parts. This demonstrates that the Disease-Free Equilibrium (E_0) is Locally Asymptotically Stable. Epidemiologically, under this condition, the disease is predicted to fade out from the population over time.

Conversely, if $R_0 > 1$ becomes negative. This results in at least one eigenvalue having a positive real part. Consequently, the Disease-Free Equilibrium (E_0) becomes unstable, which biologically means the disease will spread continuously within the population, and the system will shift towards the Endemic Equilibrium (E^*).

Simulation

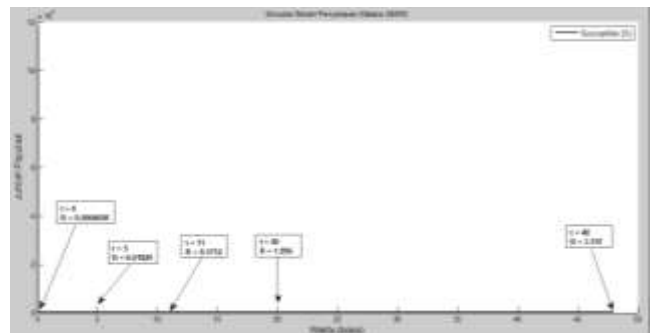


Figure 2. Prediction of Susceptible (S) Population Dynamics in the Malaria SEIRS Model

The model simulation presented in Figure 1 indicates that the Susceptible population (S), or individuals vulnerable to malaria infection, starts

at a very low level at the initial time (month 0), specifically at 0,0004698 individuals. This condition signifies that, at the beginning of the simulation, few individuals were potentially exposed to the disease.

Over time, the susceptible population undergoes a gradual increase, rising to 0,01829 individuals by month 5 and further increasing to 0,1712 individuals by month 11. This increment demonstrates the transition process where individuals move from the infected or recovered states back to being susceptible to the disease.

Entering month 20, the susceptible population increases significantly to reach 1,896 individuals, and by the end of the simulation period (month 48), it reaches 3,197 individuals. This trend indicates that, in the long term, the population vulnerable to malaria experiences an increase until it achieves stability. This condition aligns with the characteristics of the SEIRS model, where individuals who have recovered can lose their immunity over time and revert to the susceptible class, causing the susceptible population to increase and subsequently stabilize towards the end of the simulation period.

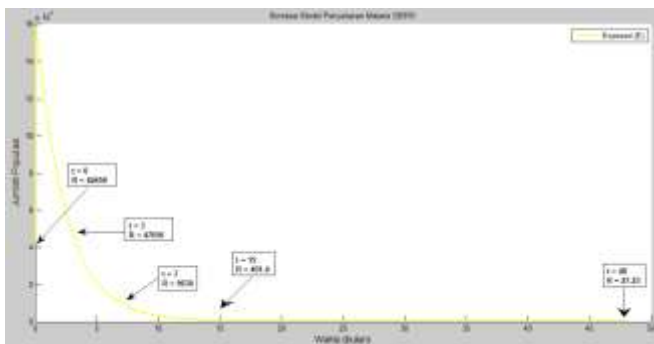


Figure 3. Prediction of Exposed (E) Population Dynamics in the Malaria SEIRS Model

The model simulation presented in Figure 2 shows that the Exposed population (E), or individuals who have been exposed to malaria but are not yet infectious, experiences a very drastic decline in the initial period. At month 0, the exposed population is at its highest value, amounting to 42.650 individuals, indicating a significantly high number of newly exposed individuals at the start of the simulation. However, by month 3, this number sharply decreases to

47.650 individuals, and declines significantly again by month 7, with a population count of 9.630 individuals. This rapid decrease illustrates that most exposed individuals quickly transition to the active infectious stage within a relatively short period.

Subsequently, by month 15, the exposed population is reduced to only 491,4 individuals, which implies that the majority of individuals have moved to other compartments (infected or recovered). By the end of the simulation period, month 48, the exposed population further decreases, reaching 27,23 individuals and tending to stabilize near zero. This indicates that the rate of exposure to malaria drastically declines over time, and in the long term, there are almost no new individuals entering the exposed class.

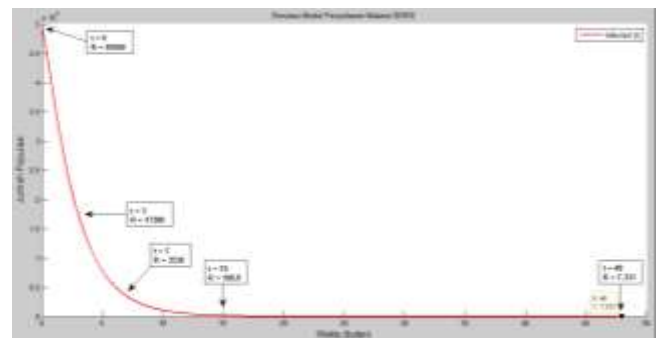


Figure 4. Prediction of Infected (I) Population Dynamics in the Malaria SEIRS Model

The model simulation presented in Figure 3 indicates that the Infected population (I), or individuals currently infected with malaria, experiences a very sharp decline in the initial period. At month 0, the infected population is at its highest value, amounting to 49.500 individuals, signifying a relatively high number of infected individuals at the start of the simulation. However, by month 3, this number drastically decreases to 17.800 individuals, and continues to diminish significantly by month 7, with a population count of 3.530 individuals. This rapid decrease suggests that many infected individuals successfully recover or transition to another stage within a relatively short timeframe.

Subsequently, by month 15, the infected population is reduced to only 168,8 individuals, which indicates that the infection rate continues to decline over time. By the end of the simulation

period, month 48, the infected population becomes increasingly small, reaching 7,331 individuals and tending to stabilize near zero. This illustrates that the spread rate of malaria is continually decreasing, and in the long term, the infection practically ceases to occur within the population.

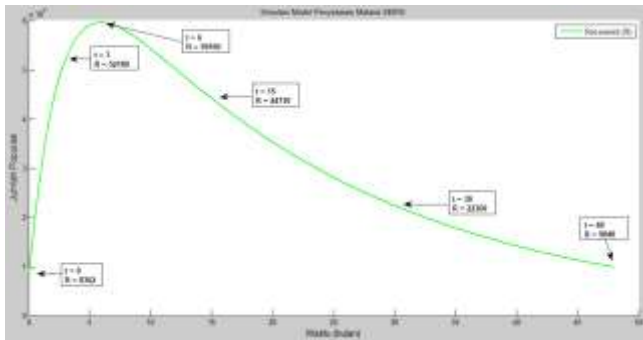


Figure 5. Prediction of Recovered (R) Population Dynamics in the Malaria SEIRS Model

The SEIRS model simulation in Figure 4 illustrates the dynamics of the Recovered population (R), or individuals who have recovered from malaria, over time. At the beginning of the simulation (month 0), the number of recovered individuals is 8,362. Subsequently, the recovered population increases significantly, reaching 52,180 individuals by month 3 and achieving its highest peak at 59,550 individuals by month 6. This rapid increase indicates that in the initial phase of the disease spread, the recovery rate escalated quickly over time.

However, after reaching its peak, the number of recovered individuals begins to experience a gradual decline. By month 15, the number of recovered individuals decreases to 44,110, and continues to decline to 22,360 individuals by month 30. By the end of the simulation period (month 48), the number of recovered individuals reaches 9,848. This pattern suggests that although many individuals initially recovered from the infection, this number diminishes over time, likely due to a lack of new infections or the loss of immunity in the previously recovered population.

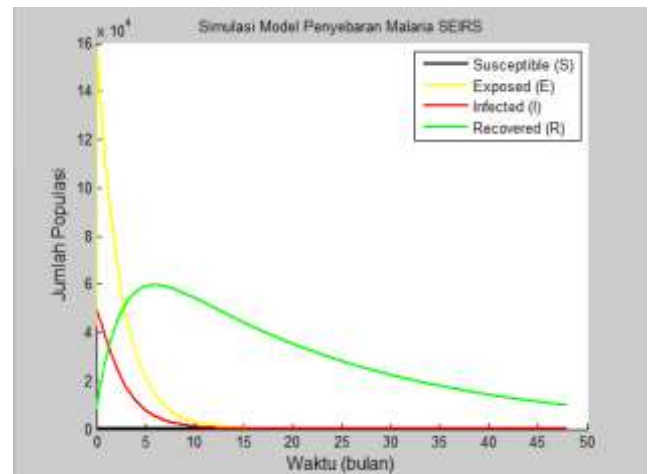


Figure 6. Prediction of Overall SEIRS Model Dynamics for Malaria Spread

Overall, the SEIRS model simulation results illustrate the natural dynamics of malaria transmission, reflecting the transition process between compartments. At the beginning of the simulation, the Exposed (E) and Infected (I) populations were very high, indicating a rapid initial phase of disease spread. However, over time, both populations drastically declined due to a corresponding increase in the Recovered (R) population. The recovered population sharply increased in the initial phase, reaching its peak around month 6, and then gradually decreased because some individuals lost their immunity and reverted to the Susceptible (S) class. This is evident from the increase in the susceptible population towards the end of the simulation period.

In general, the model demonstrates that the malaria transmission rate declines over time until the system reaches a stable condition, where the number of exposed and infected individuals is very small. This implies that the disease tends towards an endemic state with a low spread rate, and the population structure becomes relatively stable in the long term.

and the effectiveness of treatment (ω), both of which work together to transition individuals from the infected group (I) to the recovered group (R). The peak of this pattern symbolizes the point at which the population achieved the highest level of collective immunity during the epidemic.

However, the biological essence of the R curve lies not only in its peak but also in its very slow decline throughout the simulation time. This persistent and gradually descending pattern is a reflection of temporary immunity. The fact that the decline does not immediately drop to zero is biologically interpreted as the constant rate of loss of immunity (γ). This phenomenon is a profound implicit message within the Batik motif: individuals who have recovered will eventually revert to being susceptible (S) and can be re-infected. Therefore, the dominant R curve pattern in the motif serves as a dualistic biological narrative: celebrating the success of recovery while simultaneously warning that the disease cycle will continue to repeat, demanding ongoing vigilance and sustained public health interventions to prevent the recurrence of an outbreak.

Mathematical Meaning

This batik motif originates from the curve of Recovered (R) in the SEIRS mathematical model, which represents the dynamics of malaria transmission. Mathematically, the Recovered (R) compartment is expressed through the following differential equation:

$$\frac{dR(t)}{dt} = \sigma I + \omega E - (\mu + \gamma)R$$

This equation shows that the change in the number of individuals who have recovered (R) is influenced by three main processes, namely:

1. Recovery from infection (σI),
2. Treatment effectiveness on exposed individuals (ωE), and
3. Natural mortality leading to immunity loss $((\mu + \gamma)R)$.

The curve derived from this equation forms a curve that rises and then gradually descends, reflecting an increase in the number of recovered individuals until reaching a stable state (steady state). This serves as the basis for motif formation. Geometrically, the rising part of the curve

represents the recovery phase, while the declining part shows the attainment of equilibrium, where $\frac{dR(t)}{dt} \approx 0$. This condition indicates that the number of recovered individuals has reached dynamic equilibrium between recovery and immunity loss.

In a mathematical context, a curve that stabilizes at a certain value describes a system converging toward a stable equilibrium point. This point is obtained when all compartmental rates of change reach zero, namely:

$$\frac{dS}{dt} = \frac{dE}{dt} = \frac{dI}{dt} = \frac{dR}{dt} = 0$$

This condition represents a balance in the population across susceptible, exposed, infected, and recovered groups. Therefore, the curve used as a motif symbolizes a visual process of convergence from transitional states to a stable state representing system stability.

In creating the motif, the Recovered (R) curve is treated as a geometric representation of logistic growth that ascends and then gradually declines, visually illustrating the value of $R(t)$ as time approaches $t \rightarrow \infty$. This curve is then transformed mathematically through rotations (90° , 180° , 270°), horizontal and vertical reflections, and periodic repetitions. These transformations symbolize the periodic and symmetric properties of the dynamic mathematical system, in which transitions among compartments occur repeatedly and in balance.

Thus, the mathematical meaning of this motif does not lie solely in its visual form, but also in its symbolic representation of the SEIRS differential system, which describes changes in population over time. The rotation and reflection patterns represent the concept of symmetric stability (the system returning to its original form), whereas the descending curve illustrates convergence toward a stable equilibrium point, as achieved when $R_0 < 1$, indicating that the disease no longer spreads significantly and the population reaches equilibrium.

Conclusions

This study integrates the SEIRS mathematical model with cultural visualization through a Batik

motif to illustrate the dynamics of malaria transmission in Mimika Regency. The SEIRS model utilized considers births, deaths, the latent period, infection, recovery, and loss of immunity, thereby providing a quantitative overview of population changes across the S, E, I, and R compartments.

The calculation results indicate a Basic Reproduction Number value of $R_0 = 0,09$ signifying that malaria is in a condition with no potential for an epidemic outbreak. The Disease-Free Equilibrium point is stable, and the numerical simulation demonstrates that the Exposed and Infected classes decline toward zero, while the Susceptible and Recovered populations move toward long-term stability. This suggests that malaria transmission can be effectively controlled.

The developed Batik motif successfully translates the SEIRS curve patterns into an educational and culturally contextual visual form. The symmetry, repetition, and curve patterns within the motif reflect the system's epidemiological journey from infection toward equilibrium. Thus, this research shows that mathematical modeling is not only beneficial for disease analysis but can also be utilized as a medium for education through art and culture, opening opportunities for broader collaboration in malaria control efforts within endemic regions.

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

References

- Hisyam, I., Side, S., & Pagga, M. (2021). Pemodelan Matematika SEIRS Pada Penyebaran Penyakit Malaria di Kabupaten Mimika. *Journal of Mathematics, Computations, and Statistics*, 4(1), 21–29.
- Driessche, P. van den, & Watmough, J. (2002). Reproduction numbers and sub-threshold endemic equilibria for compartmental models of infectious diseases. *Mathematical Biosciences*, 180(1-2), 29–48.
- Bacaër, N., Guernaoui, S., & Oukouiss, A. (2018). *The Basic Reproduction Number R_0 : Some History and Applications*. Springer International Publishing.
- Agusto, F. B., & Khan, M. A. (2020). Mathematical modeling and analysis of malaria dynamics with temperature-dependent parameters. *Infectious Disease Modelling*, 5, 544–557.
- Zhou, Y., Chen, Y., Liu, B., & He, T. (2018). Global analysis of a periodic SEIRS model with time delay and its application to malaria. *Mathematical Methods in the Applied Sciences*, 41(16), 6667–6679.
- Kemenkes RI. (2020). *Laporan Situasi Malaria di Indonesia 2019*. Kementerian Kesehatan Republik Indonesia.
- Hastuti, I., Widyantari, F., & Syafruddin, D. (2019). Molecular Epidemiology of *Plasmodium falciparum* and *Plasmodium vivax* in Mimika, Papua, Indonesia. *Malar J*, 18, 390.
- Prasetyo, A. (2015). The Role of Traditional Indonesian Batik Art in Science Communication. *Journal of Art and Science Integration*, 10(2), 112–125.