Transformation of the SITR Mathematical Model into Batik Motifs: Visualization of Tuberculosis Transmission in Makassar City through MATLAB Simulation

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Abstract: Micro, Small, and Medium Enterprises (MSMEs) are the main drivers of Indonesia's economy, particularly in Cirebon City, which is rich in cultural heritage and local wisdom. However, many MSMEs face obstacles in scaling up due to limited digital adoption, traditional management practices, and restricted market access. This study aims to examine digital transformation in the strategic management of MSMEs through the development of a sales application that integrates elements of local wisdom to strengthen competitiveness and support MSMEs in Cirebon to move up to a higher business level. This research applies a mixed-method approach, combining interviews with MSME actors and stakeholders as qualitative data with digital adoption readiness analysis as quantitative data. The application development follows the System Development Life Cycle (SDLC) framework with a user-centered design to ensure relevance to business needs. Key features include sales reports, supplier data, product data, and sales graphs. The findings show that the application improves operational efficiency and supports data-driven decision-making. Moreover, the integration of cultural identity within the digital platform contributes to the preservation of local wisdom while fostering sustainable business growth. This study highlights that digital transformation, when combined with culture-based strategic management, can serve as a pathway for MSMEs to upgrade their business class while aligning with national economic priorities and global sustainable development goals.

Keywords: SITR Model, Tuberculosis, MATLAB Simulation, Batik Motif, Integration of Science and Culture.

Introduction

Micro, Small, and Medium Enterprises (MSMEs) in Cirebon City play an important role in driving the regional economy, particularly in the trade, culinary, and craft sectors based on local wisdom (Abu et al., 2025).

A mathematical model is a framework that uses mathematical language and equations to represent and analyze complex real-world systems (Brauer et al., 2019). This model is built upon a series of assumptions underlying the observed phenomena, with the aim of understanding system behavior, evaluating scenarios, and making predictions (Hethcote, 2000). In various scientific fields, including public health and biology, mathematical modeling has become an essential tool for studying system dynamics (Ma, 2020). One of the most important applications of mathematical modeling is in the field of epidemiology, namely to analyze the transmission mechanisms of infectious diseases. Classic epidemiological models such as SIR (Susceptible-Infected-Recovered) and SEIR (Susceptible-Exposed-Infected-Recovered) have long been used to predict the spread rate of diseases (Hethcote, 2000; Kermack & McKendrick, 1927).

However, for diseases with more complex characteristics, such as tuberculosis (TB), more specific models are required. This research will utilize the SITR (Susceptible-Infective-Treatment-Recovered) epidemic model. The SITR model is a modification of the SIR model that divides the population into four subpopulations: susceptible

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individuals (Susceptible), actively infectious individuals who can transmit the disease (Infective), infected individuals undergoing treatment (Treatment), and individuals who have recovered (Recovered). This model is considered more representative for TB, as the recovery process from TB is highly dependent on the success and adherence of individuals undergoing the long treatment phase (Sama et al., 2019).

Tuberculosis (TB) remains one of the most significant global health challenges. The disease, caused by the bacterium Mycobacterium tuberculosis, is transmitted through the air when an infected person coughs or sneezes (World Health Organization [WHO], 2023). TB continues to be one of the world's deadliest infectious diseases. The latest Global TB Report from WHO (2023) estimates that in 2022, 10.6 million people worldwide fell ill with TB, resulting in 1.3 million deaths (including 167,000 people with HIV).

Indonesia itself faces a very heavy TB burden. According to WHO (2023), Indonesia ranks as the second country with the highest TB burden in the world, after India. It is estimated that there were 1,060,000 new TB cases in Indonesia in 2022, equivalent to 10% of the total global cases. These high incidence and prevalence rates underscore the urgent need for innovative intervention and control strategies to curb the rate of TB transmission in Indonesia (Kementerian Kesehatan RI, 2023; WHO, 2023). Although mathematical analysis and numerical simulations (as conducted in previous studies) are crucial for understanding disease dynamics, their final results are often limited to academic circles. Standard outputs, such as curve graphs and complex numbers, may be difficult to interpret by the general public or even by non-technical policymakers. This creates a "communication gap," where important data regarding the threat of TB fails to be effectively conveyed to increase public awareness.

To bridge this gap, an innovative interdisciplinary approach is needed. This research does not stop at standard numerical simulations. We propose a new method for visualizing epidemiological data by transforming the simulation results of the SITR model into a local arts and cultural medium, namely batik motifs. Batik, as a globally recognized Indonesian cultural heritage, possesses a visual language rich in philosophical meaning and complex pattern structures. By mapping key parameters from the SITR model (such as transmission rate, recovery rate, or number of cases) into design elements—such as color, size, or pattern repetition—this research aims to create a unique science communication medium. Visualization through batik motifs is expected to represent the TB transmission data in Makassar City in a way that is more accessible, memorable, and understandable to the public.

Materials And Methods

SITR Model

The epidemiological model used in this study is the SITR (Susceptible-Infective-Treatment-Recovered) model. This model specifically divides the observed population into four subpopulations (compartments), namely: Susceptible (S) (healthy individuals who are at risk of infection), Infective (I) (infected individuals who can transmit the disease), Treatment (T) (infected individuals who have been diagnosed and are undergoing treatment), and Recovered (R) (individuals who have fully recovered after completing treatment) (Mbara & Omondi, 2023).

The SITR model is an important modification of the classic SIR (Susceptible-Infected-Recovered) model. While the standard SIR model often assumes that infected individuals (I) can recover naturally and move directly to the recovered (R) compartment, the SITR model represents a more accurate dynamic for diseases like tuberculosis (TB). In the case of TB, recovery is highly dependent on medical intervention. Therefore, the SITR model introduces the Treatment (T) compartment as a mandatory intermediate pathway that infected individuals (I) must pass through to reach the recovered (R) status (Gaffar & Usman, 2024; Sama et al., 2019).

The stability of an equilibrium point of a system of differential equations, whether linear or nonlinear, is in the following definition: Given a system of first-order differential equations and x(t,

x_0) is its solution at time t with the initial condition $x(0) = x0$.

1. A vector x that satisfies $f(x) = 0$ is called an equilibrium point
2. The equilibrium point x is said to be stable if, for any $\varepsilon > 0$ there exists a $\delta = \delta(\varepsilon) > 0$ such that if $||x_0 - x|| < \delta$ (where $||.||$ is a norm on R^n), then $||x(t,x_0) - x|| < \varepsilon$ for all $t \geq 0$.
3. The equilibrium point is **asymptotically stable** if it is stable and there exists a $\delta_1 > 0$ such that $\lim_{t\to\infty} ||x(t, x_0) - x|| = 0$, provided that $||x_0 - x|| < \delta_1$.

Procedures

This study is classified as theoretical and applied research. This involves a review of literature related to mathematical modeling that can be used to solve problems, preceded by first developing the required conceptual framework. The data used in this study is secondary data on the number of tuberculosis patients in 2024, obtained from the Makassar City Health Office.

The steps undertaken in this research are as follows:

1. Building the SITR model for tuberculosis transmission
   a. Assuming the variables and parameters of the SITR model
   b. Formulating the SITR model
2. *Analyzing the SITR model for tuberculosis transmission*
   a. Determining the equilibrium points of the SITR model
   b. Determining the stability type of the equilibrium points based on eigenvalues
3. *Implementing the simulation results of tuberculosis* transmission *using MATLAB*
   a. Collecting tuberculosis patient data obtained from the Makassar City Health Office
   b. Inputting the tuberculosis patient data obtained from the Makassar City Health Office
   c. Inputting the model analysis results into the software
   d. Analyzing the simulation results
   e. Drawing conclusions
4. Transforming *the simulation results into batik motif*
   a. The philosophy of the batik motif

Results And Discussion

SITR Model for Tuberculosis Transmission

In this tuberculosis transmission model, the human population is classified into four epidemiological compartments. The first compartment is Susceptible (S), which consists of healthy individuals who are at risk of infection. The second compartment is Infective (I), which includes individuals who have been infected with the Mycobacterium tuberculosis bacterium and can transmit it to susceptible individuals. The third compartment, Treatment (T), represents infected individuals who have been diagnosed and are undergoing medical therapy. Finally, the Recovered (R) compartment contains individuals who have fully recovered from the disease after completing treatment.

The specific assumptions are as follows:

1. All new individuals (recruitment) are assumed to enter the Susceptible (S) compartment.
2. TB infection is hazardous and can cause disease-induced death in individuals within the infected compartment.
3. Individuals who successfully complete treatment (moving from T to R) will acquire permanent immunity and will not return to the Susceptible (S) compartment.
4. The total population $N(t)$ at any given time is defined as the sum $N(t) = S(t) + I(t) + T(t) + R(t)$, where its size can fluctuate over time due to vital dynamics.

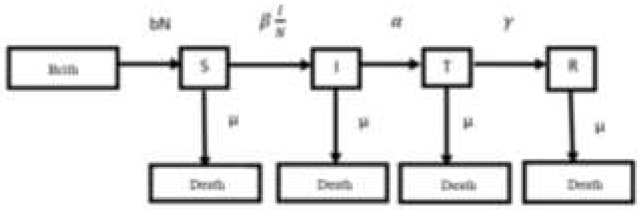

Figure 1. Population Diagram of the SITR Model for Tuberculosis Transmission.

The system illustrated in Figure 1. can be expressed as a mathematical model, which is the following system of nonlinear differential equations:

$$\frac{dS}{dt} = bN - \beta\frac{I}{N}S - \mu S \cdots\cdots (1a)$$
$$\frac{dI}{dt} = \beta\frac{I}{N}S - \alpha I - \mu I \cdots\cdots (2a)$$
$$\frac{dT}{dt} = \alpha I - \gamma T - \mu T \cdots\cdots (3a)$$
$$\frac{dR}{dt} = \gamma T - \mu R \cdots\cdots (4a)$$

Analysis of the SITR Model for Tuberculosis Transmission

The equilibrium points will be found based on equations (1a, 2a, 3a, 4a). The equilibrium point is obtained when $\frac{dS}{dt} = 0, \frac{dI}{dt} = 0, \frac{dT}{dt} = 0\ dan \frac{dR}{dt} = 0.$ Using functional-based software, the equilibrium point (S,I,T,R) = (S*, 0, 0, 0) ... (5a) is obtained, with

$$(S_0, I_0, T_0, R_0) = \left(\frac{bN}{\mu}, 0,0,0\right)$$

The results show that

$$S = \frac{bN^2}{\beta I + \mu N} \cdots\cdots (1b)$$

$$I = 0 \text{ atau } \beta S - \alpha N - \mu N = 0 \cdots\cdots (2b)$$

$$T = \frac{\alpha I}{\gamma + \mu} \cdots\cdots (3b)$$

$$R = \frac{\gamma T}{\mu} \cdots\cdots (4b)$$

The Jacobian Matrix

Suppose the equations (1a, 2a, 3a, 4a) are defined as the following $x = f\ x\ , x \in R4$…..(5a) with $x \in R4$ representing the variables in equation (5a).The Jacobian matrix of equation (5a) is defined as:

$$J(S,I,T,R) = \begin{pmatrix} \frac{df_1}{dS} & \frac{df_1}{dI} & \frac{df_1}{dT} & \frac{df_1}{dR} \\ \frac{df_2}{dS} & \frac{df_2}{dI} & \frac{df_2}{dT} & \frac{df_2}{dR} \\ \frac{df_3}{dS} & \frac{df_3}{dI} & \frac{df_3}{dT} & \frac{df_3}{dR} \\ \frac{df_4}{dS} & \frac{df_4}{dI} & \frac{df_4}{dT} & \frac{df_4}{dR} \end{pmatrix}$$
$$= (S_0, I_0, T_0, R_0) = \left(\frac{bN}{\mu}, 0,0,0\right)$$

$$\begin{pmatrix} -\beta\frac{I}{N} - \mu & -\beta\frac{S}{N} & 0 & 0 \\ \beta\frac{I}{N} & \frac{\beta S}{N} - \alpha - \mu & 0 & 0 \\ 0 & \alpha & -\gamma - \mu & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix}$$

Determination of the Jacobian Matrix for the Disease-Free Equilibrium

The stability of the equilibrium point $(S_0, I_0, T_0, R_0) = \left(\frac{bN}{\mu}, 0,0,0\right)$ can be determined by linearizing the system of differential equations (5a) around x. The resulting Jacobian matrix for the disease-free equilibrium point is obtained as follows:

$$J\left(\frac{bN}{\mu}, 0,0,0\right) = \begin{pmatrix} -\mu & -\beta\frac{\frac{bN}{\mu}}{N} & 0 & 0 \\ 0 & \frac{\beta\left(\frac{bN}{\mu}\right)}{N} - \alpha - \mu & 0 & 0 \\ 0 & \alpha & -\gamma - \mu & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix}$$
$$= \begin{pmatrix} -\mu & -\frac{\beta b}{\mu} & 0 & 0 \\ 0 & \frac{\beta b}{\mu} - \alpha - \mu & 0 & 0 \\ 0 & \alpha & -\gamma - \mu & 0 \\ 0 & 0 & \gamma & -\mu \end{pmatrix}$$

Next, the eigenvalues will be determined λ

$$\left|J\left(\frac{bN}{\mu}, 0,0,0\right) - \lambda I\right| = 0$$

$$\begin{vmatrix} -\mu - \lambda & -\frac{\beta b}{\mu} & 0 & 0 \\ 0 & \frac{\beta b}{\mu} - \alpha - \mu - \lambda & 0 & 0 \\ 0 & \alpha & -\gamma - \mu - \lambda & 0 \\ 0 & 0 & \gamma & -\mu - \lambda \end{vmatrix} = 0$$

$$(-\mu - \lambda)\begin{vmatrix} \frac{\beta b}{\mu} - \alpha - \mu - \lambda & 0 & 0 \\ \alpha & -\gamma - \mu - \lambda & 0 \\ 0 & \gamma & -\mu - \lambda \end{vmatrix} = 0$$

$$(-\mu - \lambda)\left(\frac{\beta b}{\mu} - \alpha - \mu - \lambda\right)\begin{vmatrix} -\gamma - \mu - \lambda & 0 \\ \gamma & -\mu - \lambda \end{vmatrix} = 0$$

$$(-\mu-\lambda)\left(\frac{\beta b}{\mu}-\alpha-\mu-\lambda\right)(-\gamma-\mu-\lambda)(-\mu-\lambda)$$
$$=0$$

As a result, we obtain

$$\lambda_1=-\mu$$
$$\lambda_2=\frac{\beta b}{\mu}-\alpha-\mu$$
$$\lambda_3=-\gamma-\mu$$
$$\lambda_4=-\mu$$

To be stable, all obtained eigenvalues must be negative

- For $\lambda_1=-\mu$, it is already negative because $\mu>0$
- For $\lambda_2=\frac{\beta b}{\mu}-\alpha-\mu$is obtained
$$\lambda_2<0$$
$$\frac{\beta b}{\mu}-\alpha-\mu<0$$
$$\frac{\beta b}{\mu}<\alpha+\mu$$
$$\frac{\beta b}{\mu(\alpha+\mu)}<1$$
- For $\lambda_3=-\gamma-\mu=-(\gamma+\mu)$ it is also negative because $\gamma,\mu>0$
- For $\lambda_4=-\mu$, it is already negative because $\mu>0$

Because the eigenvalues are negative, it implies that if a few infected individuals are introduced into a healthy population, the social/medical system in place (treatment, etc.) is robust enough to eradicate the disease. The population will naturally return to a completely healthy state.

Simulasi Model SITR untuk Penyebaran Penyakit Tuberkulosis

Simulations were conducted to study population dynamics that are difficult to observe empirically. The parameter values used in this model were largely adopted from verified scientific literature. Meanwhile, parameters related to demographic conditions were based on logical assumptions reflecting the general epidemiological scenario. The parameter values used are presented in Table 1.

Table 1. Parameter values of the SITR model for tuberculosis transmission

Simbol	Parameter	Parameter Values
b	Birth rate	0.018
μ	Death rate	0.007
β	Transmission rate	0.75
α	Treatment rate	0.90
γ	Recovery rate	1.33
N	Total population	1

The initial conditions that will be used in this model simulation are as follows: The values of $S(0)$, $I(0)$, $T(0)$, and $R(0)$ for the SITR model are determined as shown in Table 2.

Table 2. Table 2 Initial conditions of the SITR model.

Variabel	Nilai	Sumber
S(0)	$\frac{1.421.247}{1.432.189}=0.99236$	Statistics Indonesia (BPS) of South Sulawesi Province. (2024)
I(0)	$\frac{2.910}{1.432.189}=0.00203$	Makassar City Health Office. (2024)
T(0)	$\frac{2.910}{1.432.189}=0.00203$	Makassar City Health Office. (2024)
R(0)	$\frac{5.122}{1.432.189}=0.00358$	Makassar City Health Office. (2024)

Computer Simulation of the SITR Model

Berdasarkan dari tabel parameter diperoleh lima empat grafik.

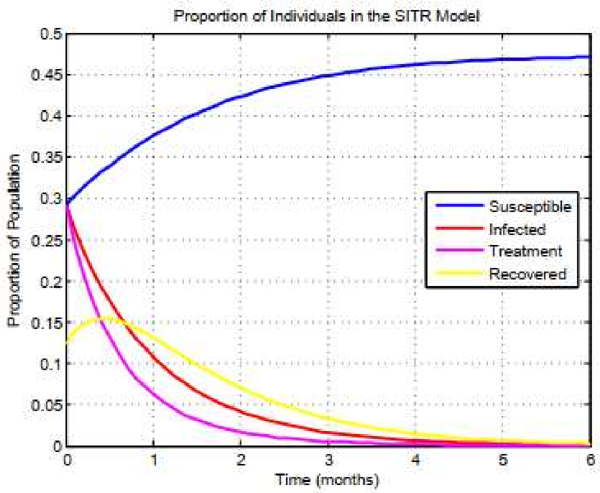

Figure 2. Proportion of individuals in the SITR model.

The numerical simulation results in Figure 2 present the dynamics of individual proportions in the SITR model over a 12-month period, clearly illustrating a disease eradication scenario. The proportion of Susceptible (S) individuals, marked by the blue line, begins as the majority of the population (around 0.9925). After experiencing a very slight, almost imperceptible decrease in the initial period, this proportion steadily increases for the remainder of the simulation, approaching 0.998 by the 12th month, indicating the recovery of the healthy population. This behavior is in stark contrast to the Infective (I) (red line) and Treatment (T) (yellow line) compartments. The proportion of (I) undergoes a drastic decline from the beginning of the simulation and effectively disappears (approaching zero) from the population by around the 4th month. The (T) proportion follows a similar pattern; after a slight increase in the first month as (I) individuals enter therapy, its proportion also drops sharply to zero. Meanwhile, the Recovered (R) compartment (purple line) shows an increase during the first 3 months as patients successfully complete treatment, but then begins to slowly decrease after there is no new influx of individuals from the (T) compartment. Overall, this graph indicates that the intervention parameters used (such as treatment and recovery rates) are highly effective in eliminating the disease from the population, causing the system to move stably towards the Disease-Free Equilibrium.

The philosophy of the batik motif

After the calculation and analysis process, the final step is to translate it into a batik motif.

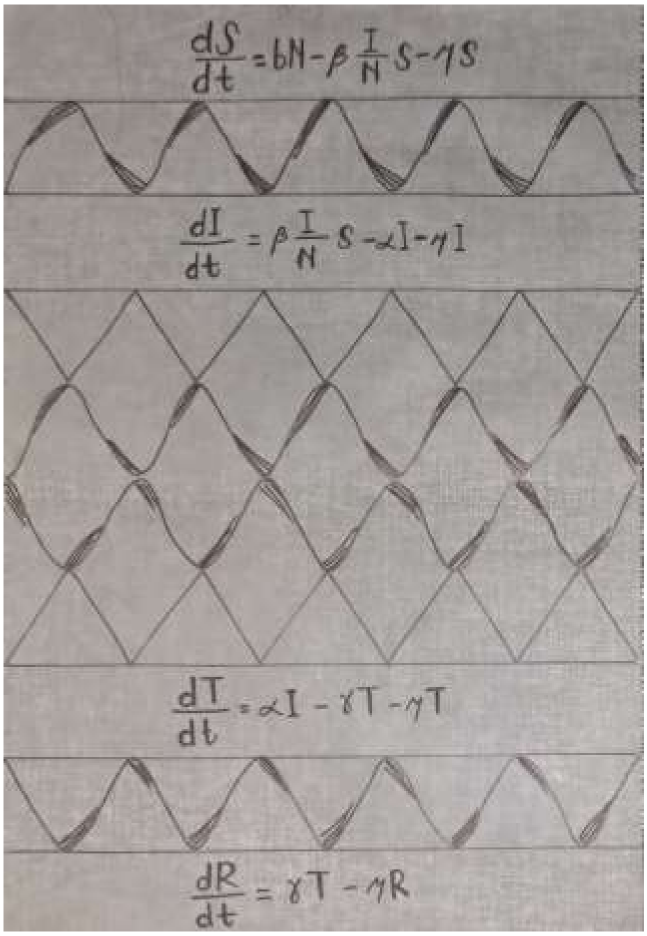

Figure 3. Batik drawing on tracing paper.

This batik is a "modern lontara," inspired by the SITR (Susceptible–Infected–Treatment–Recovered) mathematical model for tuberculosis (TB) transmission in Makassar, closely interweaving modern science with local wisdom. Its central motif is the dynamic wave, adopted directly from the solution graph of the model's system of differential equations. Mathematically, this wave is a visual expression of change over time (Δ), representing the system's search for an equilibrium point; the rising wave symbolizes the chaos of an epidemic, while the falling wave represents the control that leads to stability. Biologically, this same wave motif is a visualization of the flow of life, death, transmission, and recovery. It reflects the infection cycle as a "war" of adaptation between the human host and the Mycobacterium tuberculosis pathogen, where the receding wave symbolizes the struggle of the body and the community to return to a balanced state of health.However, this scientific meaning does not stand alone. Philosophically, the wave represents the phases of the human journey through TB from susceptibility, infection, treatment, to recovery. The interlocking pattern symbolizes an interconnected social destiny, a reminder that community healing is an inseparable "interlocking piece" of individual recovery.This scientific wave is then woven together with the distinctive Makassar Lontara Script. If the mathematical model is a "rational mantra" for understanding the epidemic, the Lontara Script is the symbol of paseng (ancestral teaching) that serves as a moral compass for facing life's trials. Overall, this batik is a symbol of resilience; amidst the rise and fall of the epidemic wave, the Makassar community holds fast to its cultural identity to achieve healing, recording contemporary health struggles on cloth with the same spirit that their ancestors recorded civilization in the past.

Discussion

The numerical simulation results, as described in the analysis of Figure 2, strongly suggest that the modeled intervention strategies are highly effective. The rapid decline of the Infective (I) population, which approaches zero by the fourth month 11, is a direct consequence of the high treatment rate (α) and recovery rate (γ) used in the simulation parameters. This finding empirically validates the analytical stability analysis; the system robustly trends towards the disease-free equilibrium33, implying that the disease can be successfully eradicated from the population under these conditions. This outcome underscores the critical importance of the 'Treatment' (T) compartment, justifying the selection of the SITR model over a standard SIR model for a disease like tuberculosis, where recovery is almost exclusively intervention dependent.

However, the primary contribution of this study lies in its novel approach to science communication, which directly addresses the "communication gap" identified in the introduction. By translating the abstract graphical outputs of the MATLAB simulation into a tangible batik motif, the research successfully bridges the divide between complex quantitative data and public comprehension. The dynamic waves of the simulation, representing the rise and fall of population compartments, are philosophically reinterpreted as the "human journey through TB" and the "interlocking pattern" of social destiny. This fusion of quantitative data and cultural narrative makes the epidemiological threat more accessible, memorable, and culturally resonant for the people of Makassar.

Furthermore, the integration of the distinctive Makassar Lontara script alongside the visual representation of the differential equations in the final design (Figure 3) represents a deep synthesis of modern analytical tools and ancestral wisdom. The mathematical model acts as a "rational mantra" for understanding the epidemic, while the Lontara script provides the paseng (ancestral teaching) for moral resilience. This research, therefore, functions as a "modern lontara", demonstrating that mathematics is not merely a sterile analytical tool but can also serve as a source of artistic inspiration and a creative discipline that aligns with local cultural values.

Conclusions

This research successfully developed and analyzed an SITR (Susceptible-Infective-Treatment-Recovered) mathematical model to simulate the transmission dynamics of tuberculosis (TB) in Makassar City. The analytical study identified the disease-free equilibrium (DFE) point and determined the stability conditions necessary for disease eradication, highlighting that control is achieved when the rates of treatment and recovery outpace the rate of new infections. Numerical simulations using MATLAB, based on local data and verified parameters, confirmed this stability, illustrating a scenario where the infected population is effectively eliminated over time.

The primary contribution of this work is the novel integration of these scientific findings with local culture. The abstract solution graph from the simulation was successfully transformed into a tangible and philosophically rich batik motif. By juxtaposing the dynamic waves of the SITR model with traditional Lontara script , this study creates a "modern lontara" that serves as a unique and accessible medium for science communication.

This interdisciplinary approach demonstrates that complex epidemiological data can be made meaningful to the public, bridging the gap between scientific analysis and cultural understanding, and offering a new pathway for public health education.

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