

Mathematical Modeling of Measles Disease Spread with Treatment Factors and Batik Motifs from the Simulation

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Abstract: This study analyzes the application of batik motif concepts in mathematical modeling of measles disease spread using the SMEIUR (Susceptible–Exposed–Medicated–Infected–Untreated–Recovered) model, which takes into account treatment aspects. The SMEIUR model was chosen to describe the dynamics of disease spread more comprehensively and in detail by distinguishing between individuals who receive treatment and those who do not, thus providing a more accurate epidemiological picture in the community. The batik motif approach was applied as a medium for mathematical visualization, where batik patterns symbolize order, symmetry, and relationships between compartments in a dynamic population system. Each motif represents the interaction between groups of individuals who are susceptible, exposed, receiving treatment, and recovering from infection. The results of the study show that an increase in the level of treatment can significantly reduce the number of infected individuals and accelerate the achievement of endemic equilibrium. The integration of traditional batik motifs with epidemiological mathematical models is expected to be an interesting innovation in combining cultural values and science, helping the community not only to understand the dynamics of infectious disease spread, such as measles, scientifically, but also to enrich visual communication approaches that are closer to local culture. This interdisciplinary approach opens up opportunities for a more comprehensive understanding of epidemiology through art, while providing new alternatives in public health education that are culturally sensitive and easily accepted. This study proves that the combination of mathematics, art, and culture can be an effective strategy in promoting awareness and control of infectious diseases.

Keywords: SMEIUR model, batik motifs, measles, treatment, mathematical modeling.

Introduction

Mathematical modeling is a quantitative approach that can describe and analyze events by simplifying them into easily understandable assumptions with a measurable system of equations. Through modeling, complex processes such as the spread of infectious diseases can be simplified into a form that is easier to understand and analyze scientifically. One infectious disease that remains a concern for global health is measles. This disease is caused by the Morbillivirus and is known to be highly contagious, especially among preschool and elementary school children. According to a report by the Indonesian Ministry of Health (2019), measles cases are still widespread throughout Indonesia, with an incidence rate of

3.18 per 100,000 population. This high rate indicates the need for a more effective scientific approach to understand the dynamics of its spread and control strategies.

Several previous studies have developed mathematical models to describe the spread of measles by considering various factors such as vaccination, treatment, and individual behavior. A commonly used classical model is the SVEIR (Susceptible Vaccinated Exposed Infected Recovered) model introduced by Edward et al. (2015), which divides the human population into five compartments based on health status. However, this model does not fully describe the real conditions because it does not consider individuals undergoing treatment and the effects

of therapy on disease spread. Therefore, research conducted by Hubu, Achmad, and Nurwan (2020) introduced the SMEIUR (Susceptible–Immunized–Exposed–Infected–Under Treatment–Recovered) model, which is a modification of the SVEIR model by adding the factors of treatment and the treated population (U). The addition of this compartment represents the effect of treatment in reducing infection rates and increasing the proportion of recoveries.

In the SMEIUR model, disease spread is described through a nonlinear differential equation system involving six main population variables. This model was then analyzed to find disease-free and endemic equilibrium points and determine the basic reproduction number. Stability analysis was performed to determine the conditions under which the disease would disappear or persist in the population. Based on the results of this study, it was found that when, the system tends toward a stable disease-free equilibrium point, while when, the system tends toward a stable endemic condition. Through numerical simulation, Hubu et al. showed that increasing the rate of follow-up immunization, the rate of treatment in infected individuals, and the proportion of cured individuals can significantly reduce the value of R_0 , thus playing an important role in suppressing the spread of measles.

In this context, a visual approach through batik motifs can be used as a representative medium to clarify the dynamics of the model and the simulation results. Batik motifs are not only aesthetically valuable, but also rich in philosophical meaning that reflects balance, order, and interconnection between elements of concepts that are in line with the characteristics of dynamic systems in mathematical modeling. The patterns of repetition and interconnection between parts in batik motifs can be analogized with the relationship between compartments in the SMEIUR model. Thus, the integration of batik motifs in the interpretation of simulation results can provide an interdisciplinary perspective between cultural arts and mathematical science.

In addition, the use of batik motifs as a visual approach can also help communicate research results to the wider community. In numerical

simulations, the initially random pattern of measles spread can form structures that resemble regular geometric patterns such as parang or kawung motifs. These patterns reflect the dynamics of disease spread, which moves, spreads, and can ultimately be controlled through medical intervention and immunization. This shows that mathematical models not only have analytical value, but can also be translated visually to strengthen conceptual understanding of the dynamics of disease spread.

The main objective of this study is to develop a more encouraging understanding of mathematical modeling of measles spread with treatment factors and link it to the representation of batik motifs as a dynamic visualization of simulation results. By combining these two approaches, it is hoped that a new interdisciplinary and comprehensive understanding will emerge, namely between mathematics, public health, and visual arts. The analysis resulting from the SMEIUR model is expected to strengthen immunization and treatment policies by providing a quantitative picture of the effectiveness of control parameters, such as the rate of further immunization (ξ), the rate of treatment (ω), and the proportion.

In general, this study confirms that mathematical modeling is not only a numerical analysis tool, but also a medium of scientific communication that can be linked to local cultural values such as batik motifs. This integration fosters awareness that mathematics can synergize with art and socio-culture in addressing real-world problems, including the spread of infectious diseases. Through the visualization of batik motifs that illustrate the dynamics of the SMEIUR model, simulation results can be presented in a more meaningful and contextual form, making mathematics not only rational but also aesthetic and relevant to the lives of Indonesians.

Methods

1. Mathematical Model

This model models the spread of measles, which consists of six population components, namely:

a. S (Susceptible): susceptible individuals,

- eliminated from the population ($R_0 < 1$) or become endemic ($R_0 > 1$). Therefore, with this model, it is necessary to understand the effect of the rate of booster immunization, the rate of treatment, and the recovery rate of individuals who receive treatment on the spread of measles in the community.

From the above assumptions illustrated by the compartment diagram in Figure 1, the following system of differential equations is obtained:

$$\frac{dE}{dt} = \beta \frac{1}{N} S - a\delta E - (1-a)\delta E - \mu E \quad (1)$$

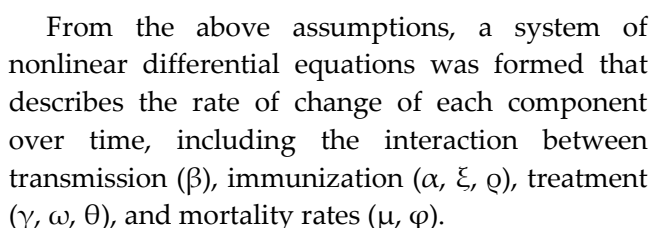
$$\frac{dR}{dt} = \xi M + \theta \gamma U - \mu R$$

Scaling of variables to facilitate the model analysis process. This is done by defining new variables as follows:

Obtained

$$\frac{de}{dt} = \beta \frac{1}{n} s - a \delta e - (1 - a) \delta e - \mu e \quad (2)$$

$$\frac{di}{dt} = (1 - a)\delta e + (1 - \theta)\gamma u - \omega i - \phi i - \mu i$$



This model is then normalized by dividing each variable by the total population ($N = S + M + E + I + U + R$), resulting in six equations in the form of proportions (s, m, e, i, u, r). This step forms the basis for equilibrium point analysis, calculation of the basic reproduction number (R_0), and discussion of model stability in the next section. The purpose of this model is to observe the dynamics of measles spread when immunization and treatment programs are in place, and to determine the conditions under which the disease can be

$$\frac{du}{dt} = \alpha\delta e + \omega i - (1 - \theta)\gamma u - \theta\gamma u - \mu u$$

$$\frac{dr}{dt} = \xi m + \theta\gamma u - \mu r$$

2. Model Analysis

A. Equilibrium Point

An equilibrium point is the solution to a system of differential equations whose value remains constant or unchanged over time. This point is often referred to as a critical point or equilibrium point in a dynamic system. In the case of measles disease spread, equilibrium points can be divided into two types, namely disease-free equilibrium points and endemic equilibrium points. Based on the system used, these two types of points will show the condition of the population when the disease is completely eradicated or when the disease persists in the community. From this system: $\frac{ds}{dt} = \frac{dm}{dt} = \frac{de}{dt} = \frac{di}{dt} = \frac{du}{dt} = \frac{dr}{dt} = 0$ two equilibrium points are obtained, namely:

1. Disease-free equilibrium point

$$E_0^* = (s_0, m_0, e_0, i_0, u_0, r_0)$$

With:

$$s_0 = \frac{q(\xi + \rho + \mu)}{(\alpha + \mu)(\xi + \mu)\mu\rho}, m_0 = \frac{\alpha q}{(\alpha + \mu)(\xi + \mu)\mu\rho},$$

$$e_0 = i_0 = u_0 = 0, \text{ dan } r_0 = \frac{\xi \alpha q}{\mu((\alpha + \mu)(\xi + \mu)\mu\rho)}.$$

(3)

2. Endemic equilibrium point

$$E_1^* = (s_1, m_1, e_1, i_1, u_1, r_1)$$

Dengan

$$s_1 = \frac{(\delta + \mu)(\mu(\mu + \phi + \omega))}{\beta\delta(\gamma(-1 + a\theta) + (-1 + a)\mu)},$$

$$m_1 = \frac{\alpha(\delta + \mu)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega))}{\beta\delta(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho)},$$

$$e_1 = \frac{q}{\delta + \mu''}$$

$$i_1 = -\frac{(\alpha + \mu)(\mu + \xi) + \mu\rho}{\beta(\mu + \xi + \rho)} + \frac{q\delta(\gamma - \alpha\gamma\theta + \mu - \alpha\mu)}{(\delta + \mu)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega))},$$

$$u_1 = \frac{((\alpha(\mu + \phi + \omega)(q\beta\delta(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho) + (\delta + \mu)((\alpha + \mu)(\mu + \xi) + \mu\rho)) - (\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega)))}{(\beta(\delta + \mu)(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho))},$$

$$r_1 = (b_1 + b_2 + b_3),$$

and

b=

$$\frac{\alpha^2 q \beta \gamma \delta^2 \theta (\gamma \theta + \mu)(\mu + \xi + \rho) - \alpha(\delta + \mu)((\gamma + \mu)(\delta + \mu)\xi(\mu + \phi) + \mu((\delta + \mu)\xi + \gamma\theta(-\delta + \xi))\omega)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega))}{(\beta\delta\mu(\delta + \mu)(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega)))},$$

$$b_2 = \frac{\gamma\delta\theta(\mu + \xi + \rho)\omega(-q\beta\delta(\gamma + \mu) + \mu(\delta + \mu)((\gamma + \mu)(\mu + \phi) + (\gamma\theta + \mu)\omega))}{(\beta\delta\mu(\delta + \mu)(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega)))},$$

b3

=

$$\frac{\alpha\gamma\delta\theta(q\beta\delta(\mu + \xi + \rho) - (\gamma + \mu)(\mu + \phi) + (\gamma\theta + \mu)\omega) + (\delta + \mu)((\alpha + \mu)(\mu + \xi) + \mu\rho)(\mu + \phi + \omega) + (\gamma\theta + \mu)\omega)}{(\beta\delta\mu(\delta + \mu)(\gamma(-1 + a\theta) + (-1 + a)\mu)(\mu + \xi + \rho)(\mu(\mu + \phi + \omega) + \gamma(\mu + \phi + \theta\omega)))},$$

B. Basic Reproduction Number

According to Hethcote, the basic reproduction number (R_0) is a ratio that describes the number of susceptible individuals who can contract a disease from one infected individual. To determine the value of R_0 , two matrices are used, namely the φ and ψ matrices. The φ matrix describes the rate of infection that causes an increase in the number of individuals in the infected class, while the ψ matrix shows the rate of infection that causes a decrease in the number of individuals in the infected class. Based on system (2), these two matrices are used to obtain the value of the basic reproduction number.

$$\varphi = \begin{bmatrix} \beta si \\ 0 \\ 0 \end{bmatrix}$$

$$\psi = \begin{bmatrix} a\delta e + (1 - a)\delta e + \mu e \\ -(1 - a)\delta e - (1 - \theta)\gamma u + \omega i + \phi i + \mu i \\ -a\delta e - \omega i + (1 - \theta)\gamma u + \mu u \end{bmatrix}$$

Next, F is the Jacobi matrix of ϕ calculated at the disease-free point and V is the Jacobi matrix of ψ , so that we obtain

$$F = \begin{bmatrix} 0 & \frac{\beta q(\xi + \rho + \mu)}{(\alpha + \mu)(\xi + \mu) + \mu\rho} & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix} \quad (5)$$

V =

$$\begin{bmatrix} a\delta + (1 - a)\delta + \mu & 0 & 0 \\ -(1 - a)\delta & \omega + \phi + \mu & -(1 - \theta)\gamma \\ -a\delta & -\omega & (1 - \theta)\gamma + \theta\gamma + \mu \end{bmatrix} \quad (6)$$

The basic reproduction number is obtained from the largest eigenvalue of [FV-1], resulting in

$$Ro = \frac{q\beta\delta(\gamma(1-\theta)+(1-a)(\theta\gamma+\mu))(\mu+\xi+\rho)}{((\delta+\mu)((\alpha+\mu)(\mu+\xi)+\mu\rho)(\gamma(1-\theta)(\mu+\phi)(\theta\gamma+\mu)(\mu+\phi+\omega)))} \quad (7)$$

C. Stability Analysis

Stability analysis is performed by examining each eigen value obtained. To determine the local stability of the model's equilibrium point, the steps taken are to substitute the equilibrium points into the linearized system. In determining the stability of the disease-free equilibrium point, the point E_0^* is substituted into the Jacobian matrix to obtain the following Jacobian matrix form:

$$\begin{bmatrix} A_{11} & A_{12} & 0 & A_{14} & 0 & 0 \\ A_{21} & A_{22} & 0 & 0 & 0 & 0 \\ 0 & 0 & A_{33} & A_{34} & 0 & 0 \\ 0 & 0 & A_{43} & A_{44} & A_{45} & 0 \\ 0 & 0 & A_{53} & A_{54} & A_{55} & 0 \\ 0 & A_{62} & 0 & 0 & A_{65} & A_{66} \end{bmatrix}$$

(8)

With

$$\begin{aligned} A_{11} &= -(\alpha + \mu) < 0, & A_{12} &= \rho > 0, \\ A_{21} &= \alpha > 0, & A_{22} &= -\xi - \rho - \mu < 0, \\ A_{34} &= \frac{q\beta(\xi+\rho+\mu)}{(\alpha+\mu)(\xi+\mu)+\mu\rho} > 0, & A_{43} &= (1-a)\delta > 0, \\ A_{45} &= (1-\theta)\gamma > 0, & A_{53} &= a\delta > 0, \\ A_{55} &= -(1-\theta)\gamma - \theta\gamma - \mu < 0, & A_{62} &= \xi > 0, \end{aligned}$$

Next, find the characteristic equation of equation (8) by finding $\det(\lambda I - J(E_0^*)) = 0$, so that we obtain

$$(A_{66} - \lambda)(A_{12}A_{21} + (A_{11} - \lambda)(-A_{22} + \lambda)) \quad (9)$$

$$(-A_{34}(A_{45}A_{53} + A_{43}(-A_{55} + \lambda)) + (A_{33} - \lambda)(A_{45}A_{54} + (A_{44} - \lambda)(-A_{55} + \lambda))) = 0.$$

Based on equation (9), six eigenvalues are obtained. The first eigenvalue is obtained as $\lambda_1 = A_{66} = -\mu$. Since all parameter values are positive, $\lambda_1 < 0$. The other five eigenvalues are obtained by solving the following equation.

$$\lambda^2 + (-A_{11} - A_{22})\lambda + (A_{11}A_{22} - A_{12}A_{21}) = 0, \quad (10)$$

$$\lambda^3 + (-A_{33} - A_{44} - A_{55})\lambda^2 + (-A_{34}A_{43} + A_{33}A_{44} - A_{45}A_{54} + A_{33}A_{55} + A_{44}A_{55}\lambda + (-A_{34}A_{45}A_{54} + A_{44}A_{45}A_{54} + A_{34}A_{43}A_{55} - A_{33}A_{44}A_{55})) = 0 \quad (11)$$

Theorem 1. The disease-free equilibrium point E_0^* for system (2) is locally asymptotically stable if: $\alpha + 2\mu + \xi + \rho > 0$,

$$(\alpha + \mu)(\mu + \xi + \rho) - \alpha > 0,$$

$$\lambda_4 + \lambda_5 + \lambda_6 = -a_1,$$

$$\lambda_4\lambda_5 + \lambda_4\lambda_6 + \lambda_5\lambda_6 = a_2$$

$$\lambda_4 + \lambda_5 + \lambda_6 = -a_3$$

Proof.

Equation (10) can be rewritten in the form

$$a_0\lambda^2 + a_1\lambda + a_2 = 0, \quad (12)$$

$$\text{With } A_{14} = \frac{q\beta(\xi+\rho+\mu)}{(\alpha+\mu)(\xi+\mu)+\mu\rho} < 0,$$

$$a_0 = 1, a_1 = -A_{11} - A_{22}, a_2 = (\alpha + \mu)(\mu + \xi + \rho) - \alpha. \quad A_{44} = -\omega - \phi - \mu < 0, \quad A_{54} = \omega > 0,$$

To ensure that all roots in equation (12) have a negative real part, it will be shown that $a_1 > 0$ and $a_2 > 0$

i. Showing $a_1 > 0$

Since $A_{11} < 0$ and $A_{22} < 0$ then $a_1 = -A_{11} - A_{22} > 0$

ii. Showing $a_2 > 0$

Since all parameters are positive, $a_2 > 0$ if $(\alpha+\mu)(\mu+\xi+\rho)-\alpha>0$

Since $a_1 > 0$ and $a_2 > 0$, it is proven that both eigenvalues are negative ($\lambda_2 < 0, \lambda_3 < 0$).

Furthermore, equation (11) can be rewritten in the form:

$$a_0\lambda^3 + a_1\lambda^2 + a_3 = 0, \quad (13)$$

With $a_0 = 1, a_1 = -A_{33} - A_{44} - A_{55}, a_1 = c_1 - c_2, a_3 = c_3 - c_4$, dan

$$c_1 = \left(\delta(2\mu + \phi + \omega) + \gamma(\delta + 2\mu + \phi + \theta\omega) + \mu \right) + \frac{aq\beta\delta(\mu + \xi + \rho)}{(\alpha + \mu)(\mu + \xi) + \mu\rho},$$

$$c_2 = \frac{q\beta\delta(\mu + \xi + \rho)}{(\alpha + \mu)(\mu + \xi) + \mu\rho},$$

$$c_3 = (\mu(\delta + \mu)(\mu + \phi + \omega) + \gamma(\delta + \mu)(\mu + \phi + \theta\omega) + \frac{aq\beta\delta(\gamma\theta + \mu)(\mu + \xi + \rho)}{(\alpha + \mu)(\mu + \xi) + \mu\rho}).$$

The roots of equation (13) are other eigenvalues of the characteristic equation (9), namely λ_4, λ_5 , and λ_6 . Based on the properties of the roots of cubic equations, the following equation is obtained.

$$\lambda_4 + \lambda_5 + \lambda_6 = -a_1$$

$$\lambda_4\lambda_5 + \lambda_4\lambda_6 + \lambda_5\lambda_6 = a_2$$

(14)

$$\lambda_4 + \lambda_5 + \lambda_6 = -a_3$$

Table 1. Parameter values for conditions $R_0 < 1$ and $R_0 > 1$

Parameter	$R_0 < 1$	$R_0 > 1$	Source
q	0,6	0,6	Assumption
α	0,5	0,4	Assumption
ξ	0,4	0,2	Assumption
ρ	0,2	0,5	Assumption
β	0,2	0,4	Assumption
δ	0,7	0,6	Assumption
ω	0,012	0,012	[7]
θ	0,7	0,6	Assumption
ϕ	0,125	0,125	[6]
γ	0,143	0,143	[7]
a	0,5	0,1	Assumption

μ	0,25	0,15	Assumption
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- Objective a_1

Since $A_{33} < 0, A_{44} < 0$, and $A_{55} < 0$, then $a_1 = -(A_{33} + A_{44} - A_{55}) > 0$, so that $\lambda_4 + \lambda_5 + \lambda_6 < 0$

Based on equation (15), it can be seen that the sum of the three eigenvalues is negative. This indicates that at least one eigenvalue is negative.

Assume $\lambda_4 < 0$.

- Consider a_2 . It is clear that $a_2 > 0$ jika $c_1 > c_2$.
- Consider a_3 . It is clear $a_3 > 0$ jika $a_3 > c_4$.

Since $a_2 > 0$ and $a_3 > 0$, both values satisfy the following conditions

$$\lambda_4(\lambda_5 + \lambda_6) + \lambda_5\lambda_6 > 0, \quad (16)$$

$$\lambda_4\lambda_5\lambda_6 < 0 \quad (17)$$

Since $\lambda_4 < 0$ and equation (17) is satisfied, then

$$\lambda_5\lambda_6 > 0 \quad (18)$$

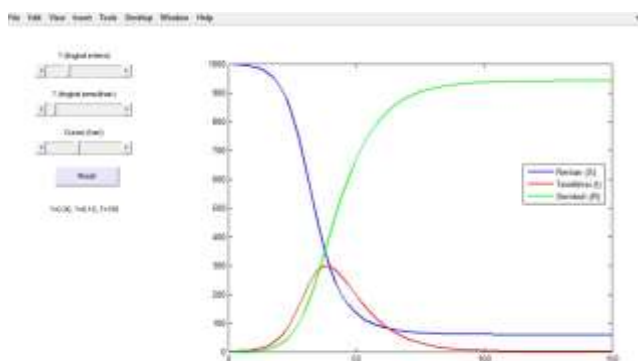
Based on equations (16) and (18), then

$$\lambda_5 + \lambda_6 < 0 \quad (19)$$

Equations (18) and (19) are satisfied if and only if ($\lambda_5 < 0$ dan $\lambda_6 < 0$). This condition indicates that all eigenvalues are negative ($\lambda_1 < 0, \lambda_2 < 0, \lambda_3 < 0, \lambda_4 < 0, \lambda_5 < 0$ dan $\lambda_6 < 0$). Thus, all eigenvalues of characteristic equations (12) and (13) are also negative, namely ($\lambda_1 < 0, \lambda_2 < 0, \lambda_3 < 0, \lambda_4 < 0, \lambda_5 < 0$ dan $\lambda_6 < 0$). Therefore, it can be concluded that the free measles equilibrium point is asymptotically stable.

D. Simulation

Simulation on the modified model was performed using MATLAB software to show the stability properties of each equilibrium point by entering the parameter values listed in Table 1. Furthermore, simulations were run to analyze the dynamics of the human population in a dynamic system by varying several parameters, namely the rate of the population receiving follow-up immunization (x), the rate of treatment in infected individuals (w), and the proportion of individuals who recovered after undergoing treatment (q). The following graphical output was obtained from the simulations:



Results And Discussion

Based on the simulation results using Matlab software, a graph was obtained that illustrates the dynamics of measles spread in a population. The graph shows changes in the number of individuals in three main groups, namely susceptible, infected, and recovered. In general, the system shows a transition of the population from individuals who are susceptible to the measles virus to infected, then recovered and immune to the disease. This pattern shows that measles can eventually be controlled and disappear from the population, allowing the system to reach a disease-free equilibrium point.

The explanation for each curve is as follows:

1. Blue curve (susceptible – S)

- Shows the number of individuals who are still susceptible to measles virus infection.
- At the beginning of the simulation, the number of susceptible individuals is very

high because most of the population does not yet have immunity.

- Over time, the number of susceptible individuals decreases due to the transmission process, then stabilizes at a low point when most of the population has recovered or become immune.

2. Red curve (infected – I)

- Describes the number of individuals currently infected with the measles virus.
- This curve increases sharply at the beginning of the simulation, indicating a peak in the spread of measles.
- After reaching its maximum point, the curve gradually decreases to near zero as more individuals recover and gain natural immunity.

3. Green curve (recovered – R)

- Shows the number of individuals who have recovered from measles.
- At the beginning of the simulation, the number is low, but it increases as more individuals recover from infection.
- The curve then reaches a high stable point, indicating that most of the population is immune to the measles virus.

Overall, the simulation results show that the system is moving towards disease-free stability, where the number of infected individuals decreases until it eventually disappears. This is in line with the results of research by Hubu, Achmad, and Nurwan (2020) in the Jambura Journal of Biomathematics, which states that when the basic reproduction number ($R_0 < 1$), the disease-free equilibrium point is asymptotically stable. This means that measles can disappear from the population within a certain period of time if immunization programs, treatment, and efforts to increase individual recovery are carried out optimally.

Batik Motif



1. Philosophical Meaning

Philosophically, this batik pattern depicts the balance and harmony of life, which is in line with the concept of stability in the measles disease spread model. The shape resembles interconnected petals or leaves, reflecting the reciprocal relationship between individuals in society, as well as the interaction between susceptible, infected, and recovered populations in the SMEIUR model.

The regularity of the shapes and colors in this pattern symbolizes the process towards disease-free stability, as described in the journal, where the system will reach equilibrium when the basic reproduction number ($R_0 < 1$). This can be interpreted to mean that beauty and tranquility in life can only be achieved when balance and harmony are maintained, just as population stability occurs when measles is successfully controlled through immunization and treatment.

2. Biological Meaning

From a biological perspective, this batik motif resembles interconnected cell or tissue structures, depicting a continuous life system. The repeating pattern symbolizes the biological process of measles transmission and recovery as described in the journal, namely the movement of individuals from the susceptible (S) group, exposed (E), infected (I), to recovered (R).

Each interrelated shape depicts the interaction between human populations in the spread of disease. This shows that a person's health affects others around them. This meaning is in line with

the content of Hubu et al. (2020) research, which emphasizes the importance of further immunization, treatment, and the recovery rate of treated individuals in maintaining population balance and suppressing the spread of measles. Thus, this motif depicts the unity between biological life and human efforts to maintain health through prevention and treatment.

3. Mathematical Meaning

Mathematically, this batik pattern reflects the regularity and stability of dynamic systems as found in the SMEIUR model. The repetitive and symmetrical arrangement of shapes depicts the system of differential equations in the measles disease spread model, where each variable (S, M, E, I, U, R) is interrelated and influences one another.

As explained in the journal, system stability is achieved when all eigenvalues are negative ($\lambda < 0$) and ($R_0 < 1$), indicating that the disease will disappear from the population. This harmonious pattern represents this mathematical balance, where each component works in harmony until the system achieves disease-free stability.

Conclusion

Based on the entire content of this study, it can be concluded that the incorporation of batik motifs as a medium of visualization in mathematical models of measles disease spread provides an innovative, interesting, and culturally valuable approach. By applying batik motifs that symbolize order and harmony, this study not only helps to understand the dynamics of disease spread scientifically through the SMEIUR model, but also strengthens the communication of research results to the general public. The simulation results show that increased treatment and immunization are very effective in suppressing the spread of disease and accelerating the achievement of a healthy, disease-free condition. The integration of mathematics, public health, and cultural arts opens up opportunities for more interesting and understandable educational strategies and health campaigns, while preserving local cultural values.

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