

Visualization of Batik Patterns from Numerical Simulation of the SVEIQR Measles Model Using the Laplace Adomian Decomposition Method

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Abstract: This study develops a fractional differential equation model of measles transmission using the Susceptible–Vaccinated–Exposed–Infected–Quarantined–Recovered (SVEIQR) framework, which incorporates the fractional Caputo derivative of order $0 < q \leq 1$. The model captures the dynamic behavior of disease spread more accurately by considering memory effects inherent in fractional calculus. The system is analyzed theoretically to determine the existence and uniqueness of solutions, equilibrium points, and basic reproduction numbers, and then solved numerically using the Laplace Adomian Decomposition Method (LADM), which combines Laplace transformation and Adomian decomposition to obtain approximate analytical solutions. Numerical simulations were performed for different fractional orders and parameter variations, showing that smaller fractional orders ($q < 1$) introduce memory-dependent effects, producing smoother transitions between epidemiological compartments. Beyond its numerical results, this study presents an innovative visualization of the SVEIQR simulation data through batik-inspired patterns, where each motif, shape, and color corresponds to specific epidemiological meanings. The resulting batik design transforms mathematical dynamics into an aesthetic representation, integrating scientific order with cultural symbolism. The five-petal flower pattern represents the five main epidemiological phases (S,V,E,I,R), while the central circle depicts quarantine (Q) as a stabilizing force between infection and recovery. Curving tendrils express nonlinear transitions, and leaf motifs symbolize regeneration and healing. Through this integration of mathematics, biology, and traditional art, the research demonstrates how complex epidemiological phenomena can be communicated not only quantitatively but also through artistic and cultural perspectives, promoting an interdisciplinary understanding of epidemic dynamics.

Keywords: Laplace Adomian Decomposition, Fractional Differential Equations, Mathematical Batik, Pattern Visualization, SVEIQR.

Introduction

Mathematical modeling is a fundamental approach for understanding and analyzing complex dynamic phenomena across various scientific disciplines, including physics, biology, economics, and epidemiology. A mathematical model represents a simplified abstraction of real-world phenomena through a set of equations that link independent and dependent variables, with the aim of explaining and predicting system behavior (Lega, 2023). Through such formulations, mathematical models function as a bridge between theoretical

concepts and empirical observations, enabling researchers to gain deeper insights into the underlying mechanisms of a phenomenon.

One of the major challenges in mathematical modeling lies in solving nonlinear differential equation systems that frequently arise in natural and social phenomena. Obtaining an exact analytical solution is often difficult due to the complexity of these equations; therefore, efficient semi-analytical methods are required. One of the widely used approaches is the Laplace Adomian Decomposition Method (LADM), an extension of the Adomian Decomposition Method (ADM) that

integrates the Laplace transform to accelerate convergence and simplify the iterative process. Previous studies, such as that conducted by Bahgat (2016), have demonstrated that LADM is effective in solving various nonlinear differential equation systems with high precision and computational efficiency.

In the field of mathematical epidemiology, numerous compartmental models have been developed to describe the dynamics of infectious disease transmission. One such model is the SVEIQR model (Susceptible-Vaccinated-Exposed-Infected-Quarantined-Recovered), an extension of the classical SEIR model that incorporates the effects of vaccination and quarantine on disease spread. This model captures behavioral differences among population groups under different infection and intervention conditions, making it more realistic for mathematical analysis. The study conducted by Jang et al. (2024) showed that model effectively characterizes the transmission dynamics of infectious diseases, particularly in assessing the effectiveness of vaccination and outbreak control strategies.

Measles remains one of the most persistent infectious diseases, posing ongoing public health challenges in many countries, including Indonesia. Despite the widespread implementation of vaccination programs, outbreaks continue to occur due to disparities in immunization coverage and high population mobility. According to the World Health Organization (WHO, 2024), measles infected approximately 10.3 million people and caused 107,500 deaths worldwide in 2023. This situation underscores the importance of mathematical analysis in understanding disease transmission patterns and identifying parameters that influence infection dynamics. The application of the SVEIQR model using the LADM approach is therefore highly relevant for providing efficient analytical and numerical solutions to describe the evolution of populations affected by measles.

Beyond generating mathematical solutions, this research introduces an innovative visual approach to represent numerical simulation results through batik patterns derived from mathematical models. The concept stems from the idea that the dynamic systems within the SVEIQR model possess not only

scientific meaning but also aesthetic potential, which can be expressed through visual patterns resembling traditional batik motifs. Accordingly, each element of disease dynamics such as fluctuations in susceptibility, infection, or vaccination is translated into motifs and geometric repetitions characteristic of batik, reflecting balance, order, and transformation within the system.

This approach serves not only as a visual interpretation of simulation outcomes but also as an integration of science and cultural art. The batik patterns generated from mathematical representations aim to reveal the inherent order and beauty within dynamic systems, while fostering appreciation for the connection between scientific concepts and Indonesia's cultural heritage. By transforming mathematical model outputs into meaningful visual artworks, this study contributes to the development of scientific batik, which harmoniously blends aesthetic, educational, and scientific values.

Materials And Methods

This study develops a mathematical model of measles transmission using the Susceptible–Vaccinated–Exposed–Infected–Quarantined–Recovered (SVEIQR) framework based on the fractional Caputo differential equation with order $0 < q \leq 1$. The parameter values and initial conditions were adapted from the studies of Farman et al. (2018) dan Aldila & Asrianti (2019), along with several assumptions proposed by the researchers. The model is solved numerically using the Laplace Adomian Decomposition Method (LADM), which combines the Laplace transform and the Adomian decomposition method to obtain an approximate analytical solution.

In addition to producing numerical solutions for population dynamics, this study also performs visualization of the simulation results in the form of batik-inspired patterns. The numerical simulation results of the SVEIQR model obtained through LADM are visualized as population dynamics graphs for compartment: Susceptible (S), Vaccinated (V), Exposed (E), Infected (I),

Quarantined (Q), Recovered (R). The resulting simulation curves are then transformed into batik visual patterns, aiming to integrate mathematical modeling with visual aesthetics so that the simulation results can be interpreted intuitively and artistically.

The descriptions of the initial values for each compartment are presented in Table 1, and the parameters used in the numerical simulation are presented in Table 2

Table 1 Initial Conditions of The Compartments

Compartment	Description	Initial Value
<i>S</i> (Susceptible)	Population susceptible to the disease	600
<i>V</i> (Vaccinated)	Population that received the vaccine	0
<i>E</i> (Exposed)	Population exposed to the disease but not yet infectious	250
<i>I</i> (Infected)	Infected population	100
<i>Q</i> (Quarantined)	Quarantined population	0
<i>R</i> (Recovered)	Recovered population	50

Table 2 SVEIQR Model Parameters

Parameters	Description	Value
Λ	Natural birth rate	0,32
ω	Vaccination rate	0,6

β	Contact rate between susceptible and infected individuals	0,001
α	Transmission rate from <i>E</i> to <i>I</i>	0,01
σ	Direct recovery rate from <i>E</i>	0,25
γ	Recovery rate	0,2
δ	Quarantine rate	0,5
μ	Natural death rate	0,2

Where $S(t) + V(t) + E(t) + I(t) + Q(t) + R(t) = N(t)$ and initial conditions $S(0) = S_0, V(0) = V_0, E(0) = E_0, I(0) = I_0, Q(0) = Q_0, R(0) = R_0$.

Model Assumptions

The assumptions used in the SVEIQR model for the spread of measles are as follows:

1. The natural birth rate (Λ) is assumed to be constant and only increases the susceptible compartment (*S*).
2. Vaccination is carried out once at a rate ω .
3. Infection occurs through contact between susceptible and infected individuals at a rate β .
4. Individuals in the *exposed* compartment (*E*) move to the *infected* compartment (*I*) at a rate α .
5. Some *exposed* individuals (*E*) can recover directly through therapy at a rate of σ .
6. Infected individuals can either recover at a rate (γ) or be quarantined at a rate of (δ).
7. Quarantined individuals (*Q*) recover at a rate γ and do not interact with other individuals.
8. Vaccination provides permanent immunity, preventing reinfection.
9. All compartments have the same natural death rate μ .
10. Recovered individuals (*R*) are assumed to have lifelong immunity and cannot be infected again.

Analysis Method

The fractional differential equation model is formulated as follows:

$$\frac{dS}{dt} = \Lambda - \beta SI - (\omega + \mu)S$$

$$\frac{dV}{dt} = \omega S - \mu V$$

$$\frac{dE}{dt} = \beta SI - (\sigma + \mu + \alpha)E$$

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

$$\frac{dQ}{dt} = \delta I - (\mu + \gamma)Q$$

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

Results And Discussion

Equilibrium Point

The equilibrium point is a condition in a dynamic system where all variables do not change over time, or in other words, the rate of change (time derivative) of each variable is equal to zero.

Mathematically, the equilibrium point is obtained by assuming:

$$\begin{aligned} D^q S(t) = D^q V(t) = D^q E(t) = D^q I(t) = D^q Q(t) \\ = D^q R(t) = 0 \end{aligned}$$

And finding the solution. To find the non-academic equilibrium point, the number of infected individuals is set to $I = I^0 = 0$, while the endemic equilibrium point is found with $I \neq 0$.

• Disease-Free

The non-endemic equilibrium point of the model

$$\begin{aligned} E_0 &= (S^0, V^0, E^0, I^0, Q^0, R^0) \\ &= \left(\frac{\Lambda}{\omega + \mu}, \frac{\Lambda \omega}{\mu(\omega + \mu)}, 0, 0, 0, 0 \right) \end{aligned}$$

• Infected

The endemic equilibrium point of the model

$$E^* = (S^*, V^*, I^*, Q^*, R^*)$$

$$S^* = \frac{\omega \Lambda}{\alpha \beta}, V^* = \frac{\omega \Lambda}{\alpha \beta \mu}, E^* = \frac{\Lambda \alpha \beta - \omega \Lambda}{\alpha \beta \mu}$$

$$I^* = \frac{\Lambda \alpha \beta - \omega \Lambda}{\beta \mu \gamma}, Q^* = \frac{\delta(\Lambda \alpha \beta - \omega \Lambda)}{\beta \mu \gamma \delta}$$

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

Existence

Existence in the context of fractional differential equations refers to the presence (existence) of a solution to a system of differential equations that satisfies certain initial conditions. In other words, existence indicates that there is at least one solution that can describe the behavior of the system over time. It will be shown that the system has a unique solution using the Banach fixed point theorem. The system can be written as:

$$\begin{aligned} D^q S(t) &= k_1(t, S(t)), \\ D^q V(t) &= k_2(t, V(t)), \\ D^q E(t) &= k_3(t, E(t)), \\ D^q I(t) &= k_4(t, I(t)), \\ D^q Q(t) &= k_5(t, Q(t)), \\ D^q R(t) &= k_6(t, R(t)) \end{aligned}$$

The solution to the system of fractional differential equations can be obtained using the Volterra integral. The system can be written as follows:

$$S(t) - S(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_1(\xi, S) d\xi, \quad (1)$$

$$V(t) - V(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_2(\xi, V) d\xi, \quad (2)$$

$$E(t) - E(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_3(\xi, E) d\xi, \quad (3)$$

$$I(t) - I(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_4(\xi, I) d\xi, \quad (4)$$

$$Q(t) - Q(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_5(\xi, Q) d\xi, \quad (5)$$

$$R(t) - R(0) = \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} k_6(\xi, R) d\xi, \quad (6)$$

Assume that S, V, E, I, Q, R a bounded function. Suppose :

$$\begin{aligned} ||S(t)|| \leq \rho_1, ||V(t)|| \leq \rho_2, ||E(t)|| \leq \rho_3, ||I(t)|| \\ \leq \rho_4, ||Q(t)|| \leq \rho_5, ||R(t)|| \leq \rho_6 \end{aligned}$$

where is $\rho_1, \rho_2, \rho_3, \rho_4, \rho_5, \rho_6$ a positive constant. It will be proven that each kernel $k_i, i = 1, 2, 3, 4, 5, 6$ satisfies the Lipschitz and contraction conditions.

The kernel k_1 satisfies the Lipschitz and contraction conditions if it meets the following inequality:

$$\begin{aligned} & \|k_1(t, S) - k_1(t, S_1)\| \\ &= \left\| -\beta(S(t) - S_1(t))I(t) \right. \\ &\quad \left. - (\omega + \mu)(S(t) - S_1(t)) \right\| \\ &\leq (\beta\mu_4 + \omega + \mu)\|S(t) - S_1(t)\|. \end{aligned}$$

Suppose $c_1 = (\beta\mu_4 + \omega + \mu)$ then

$$\|k_1(t, S) - k_1(t, S_1)\| \leq c_1\|S(t) - S_1(t)\|.$$

Thus, k_1 satisfies the Lipschitz condition and since $0 < (\beta\mu_4 + \omega + \mu) < 1$ then is k_1 a contraction.

Similarly, the Lipschitz condition for is obtained $k_i, i = 2, 3, 4, 5, 6$ as follows:

$$\|k_2(t, V) - k_2(t, V_1)\| \leq c_2\|V(t) - V_1(t)\|$$

$$\|k_3(t, E) - k_3(t, E_1)\| \leq c_3\|E(t) - E_1(t)\|$$

$$\|k_4(t, I) - k_4(t, I_1)\| \leq c_4\|I(t) - I_1(t)\|$$

$$\|k_5(t, Q) - k_5(t, Q_1)\| \leq c_5\|Q(t) - Q_1(t)\|$$

$$\|k_6(t, R) - k_6(t, R_1)\| \leq c_6\|R(t) - R_1(t)\|$$

Where $c_2 = \mu, c_3 = (\sigma + \mu + \alpha), c_4 = (\gamma + \mu + \delta), c_5 = (\mu + \gamma), c_6 = \mu$, and since, $0 < c_i < 1, i = 2, 3, 4, 5, 6$ then is $k_i, i = 2, 3, 4, 5, 6$ a contraction.

Based on equations (1) to (6), a recursive formula is formed as follows:

$$\begin{aligned} G_{1n}(t) &= S_n(t) - S_{n-1}(t) \\ &= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_1(\xi, S_{n-1}) - k_1(\xi, S_{n-2})) d\xi, \end{aligned}$$

$$\begin{aligned} G_{2n}(t) &= V_n(t) - V_{n-1}(t) \\ &= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_2(\xi, V_{n-1}) - k_2(\xi, V_{n-2})) d\xi, \end{aligned}$$

$$\begin{aligned} G_{3n}(t) &= E_n(t) - E_{n-1}(t) \\ &= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_3(\xi, E_{n-1}) - k_3(\xi, E_{n-2})) d\xi, \end{aligned}$$

$$G_{4n}(t) = I_n(t) - I_{n-1}(t)$$

$$= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_4(\xi, I_{n-1}) - k_4(\xi, I_{n-2})) d\xi,$$

$$\begin{aligned} G_{5n}(t) &= Q_n(t) - Q_{n-1}(t) \\ &= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_5(\xi, Q_{n-1}) - k_5(\xi, Q_{n-2})) d\xi, \end{aligned}$$

$$\begin{aligned} G_{6n}(t) &= R_n(t) - R_{n-1}(t) \\ &= \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_6(\xi, R_{n-1}) - k_6(\xi, R_{n-2})) d\xi, \end{aligned}$$

With initial condition $S_0(t) = S(0), V_0(t) = V(0), E_0(t) = E(0), I_0(t) = I(0), Q_0(t) = Q(0), R_0(t) = R(0)$. It can be written as:

$$S_n(t) = \sum_{i=1}^n G_{1i}(t),$$

$$V_n(t) = \sum_{i=1}^n G_{2i}(t),$$

$$E_n(t) = \sum_{i=1}^n G_{3i}(t),$$

$$I_n(t) = \sum_{i=1}^n G_{4i}(t),$$

$$Q_n(t) = \sum_{i=1}^n G_{5i}(t),$$

$$R_n(t) = \sum_{i=1}^n G_{6i}(t),$$

For equation (7), then

$$\begin{aligned} \|G_{1n}(t)\| &= \|S_n(t) - S_{n-1}(t)\| \\ &= \left\| \frac{1}{\Gamma(q)} \int_0^t (t - \xi)^{q-1} (k_1(\xi, S_{n-1}) \right. \\ &\quad \left. - k_1(\xi, S_{n-2})) d\xi \right\| \\ &\leq \frac{1}{\Gamma(q)} \int_0^t \|(t - \xi)^{q-1} (k_1(\xi, S_{n-1}) \\ &\quad - k_1(\xi, S_{n-2}))\| d\xi. \end{aligned}$$

With the Lipschitz condition obtained

$$\|G_{1n}(t)\| \leq \frac{1}{\Gamma(q)} c_1 \int_0^t \|G_{1n(n-1)}(\xi)\| d\xi$$

Similarly, it is obtained that

$$\|G_{in}(t)\| \leq \frac{1}{\Gamma(q)} c_i \int_0^t \|G_{in(n-1)}(\xi)\| d\xi, i = 2, 3, 4, 5, 6$$

The solution of the fractional differential equation model SVEIQR for measles transmission exists if there is $t_1 > 0$ such that

$$\frac{1}{\Gamma(q)} c_i t_1 < 1,$$

For $i=1,2,3,4,5,6$

Stability

Stability analysis aims to determine the conditions under which the fractional epidemiological SVEIQR system reaches an equilibrium state, representing either the elimination or persistence of measles within the population. The model equations have been defined in the previous section, therefore this analysis focuses on the disease-free equilibrium (DFE) and the endemic equilibrium (EE) points. The disease-free equilibrium corresponds to a state where no infection exists in the population ($E = I = Q = 0$), while the endemic equilibrium represents a steady state in which the disease persists at a constant level. To assess the system's stability, the Jacobian matrix of the model is evaluated at each equilibrium point, and its eigenvalues will decay (stable) or grow (unstable) over time.

The local stability of the disease-free equilibrium is ensured when the basic reproduction number (R_0) is less than one ($R_0 < 1$), meaning that each infected individual, on average, generates less than one secondary infection. In this case, the infection eventually dies out, and the population returns to a disease-free state. Conversely, when $R_0 > 1$, the disease-free equilibrium becomes unstable, and the system tends toward the endemic equilibrium, indicating sustained disease transmission. The fractional

order q also plays a crucial role in the system's dynamic response: smaller q values reflect stronger memory effects, which may delay convergence toward equilibrium but also produce smoother and more realistic epidemiological transitions. Thus, the stability analysis not only characterizes threshold behavior through R_0 but also illustrates how fractional dynamics influence the temporal evolution and long-term stability of the measles epidemic model.

• Disease-free equilibrium Point (DFE)

The disease-free equilibrium point is obtained by assuming there are no infected individuals, $E = I = Q = 0$. Substitute this into the system, resulting in:

$$S^* = \frac{\Lambda}{\omega + \mu}, V^* = \frac{\omega S^*}{\mu}, \\ E^* = I^* = Q^* = R^* = 0$$

At this point, the spread of disease stops and the population remains in a stable condition without infection.

The basic reproduction number represents the average number of new individuals infected by one infectious individual. Based on the next generation matrix method, it is obtained that:

$$R_0 = \frac{\beta S^* \sigma}{(\sigma + \mu)(\gamma + \delta + \mu)} + \frac{\alpha V^* \sigma}{(\sigma + \mu)(\gamma + \delta + \mu)}$$

If $R_0 < 1$, the disease will disappear from the population. If $R_0 > 1$, the disease will persist and the system will move toward endemic equilibrium.

• Local Stability

Local stability is analyzed by linearizing the system around the equilibrium point:

$$D^q X(t) = J(X^*)[X(t) - X^*],$$

Where is $J(X^*)$ the Jacobian matrix at the equilibrium point. For the Caputo fractional system, local stability is achieved if all eigenvalues satisfy:

$$|\arg(\lambda_i)| > \frac{q\pi}{2}$$

The analysis results show that when , all eigenvalues have negative real parts, so the disease-free equilibrium point is locally

asymptotically stable. Conversely, if , there are positive eigenvalues causing the system to move toward a stable endemic state.

Simulation

Simulation is the process of representing or imitating the behavior of a real system through a mathematical model to study the dynamics and response of the system under various conditions or parameters. In the context of this journal research, simulation is used to describe changes in population in each compartment of the SVEIQR model over time using numerical methods.

Numerical simulation of the fractional SVEIQR model was carried out using the Laplace Adomian Decomposition Method (LADM) to analyze the population dynamics of each compartment over time. The initial conditions used are:

$$\begin{aligned} S(0) &= 600, V(0) = 0, E(0) = 250, I(0) \\ &= 100, Q(0) = 0, R(0) = 50 \end{aligned}$$

The simulation parameters are:

$$\begin{aligned} \Lambda &= 0,32, \quad \omega = 0,6, \beta = 0,001, \alpha = 0,01, \sigma \\ &= 0,25, \gamma = 0,2, \delta = 0,5, \mu = 0,2 \end{aligned}$$

Simulations were carried out for several fractional order values and variations of key parameters such as vaccination rate (ω) and quarantine rate (δ). The simulation results are visualized in graphs showing the population of each compartment over time.

Simulation Results

1. Variation of fractional order (q)

When the value of q approaches 1, the fractional solution increasingly resembles the classical first-order model. Smaller q values accelerate population changes due to a stronger memory effect.

2. Variation of vaccination rate (ω)

An ω increase in causes the number of susceptible $S(t)$ individuals to decrease faster and increases the vaccinated population $V(t)$, thus suppressing the spread of infection.

3. Variation of quarantine rate (δ)

A δ increase in accelerates the movement of individuals from the infectious compartment to

quarantine, thus reducing the number of active infections more quickly.

Numerical Implementation

Using MATLAB software, the graphical results of the solutions obtained by applying the Laplace Adomian Decomposition Method (LADM) with different values of order q are presented as follows:

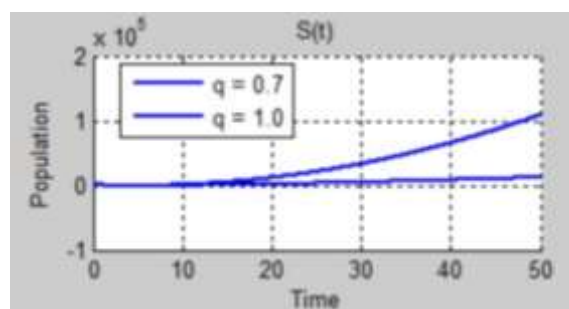


Figure 1. Graph of compartment S.

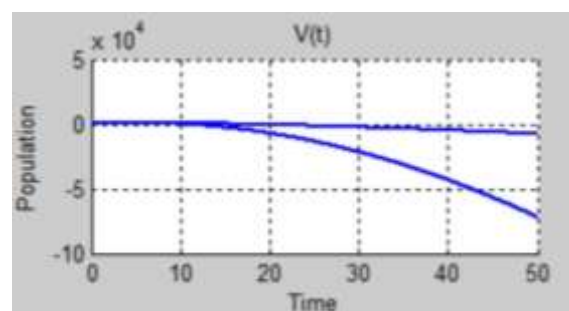


Figure 2. Graph of compartment V.

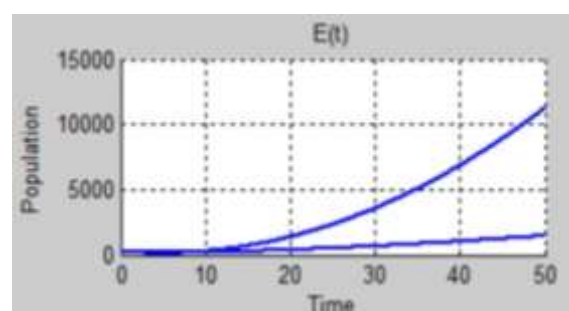


Figure 3. Graph of compartment E.

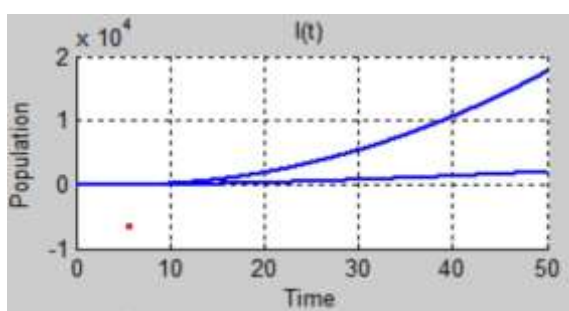
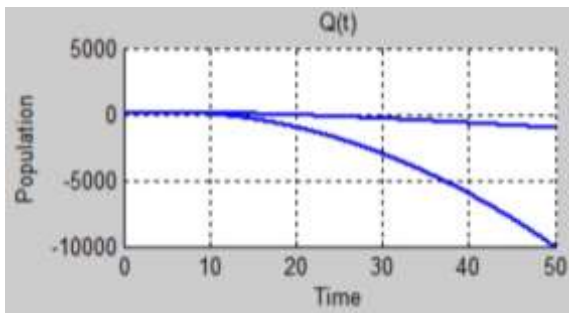
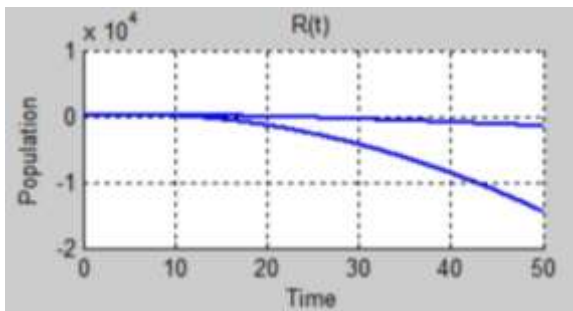


Figure 4. Graph of compartment I.

Figure 5. Graph of compartment Q .Figure 6. Graph of compartment R .

Interpretation of Simulation

The simulation results show that the fractional SVEIQR model can represent the memory effect in the dynamics of disease transmission. The fractional order value plays an important role in determining the system's rate toward stability.

- ✓ The smaller the q , the faster the population changes, but stability is reached more slowly.
- ✓ An increase in vaccination rate (ω) significantly reduces the number of susceptible individuals and accelerates the decrease in infection cases.
- ✓ An increase in quarantine rate (δ) suppresses the infection peak and shortens the duration of disease spread.

Thus, interventions in the form of increased vaccination and quarantine are effective in suppressing disease transmission, while the influence of fractional order provides additional insight into memory effects in fractional epidemiological dynamics.

Furthermore, the simulation highlights how the fractional order q introduces memory-dependent behavior into the system, meaning the current state of each compartment depends not only on its immediate conditions but also on past epidemiological patterns. This memory effects smooths transitions between disease phases and

produces more realistic epidemic curves compared to classical integer-order models. When $q < 1$, the infected and exposed curves decline more gradually, indicating that population behavior and disease progression retain the influence of earlier conditions. Such characteristics align with real-world epidemics where I_u unity development, behavioral changes, and intervention responses evolve gradually rather than instantaneously.

In addition, the combined influence of vaccination (ω) and quarantine (δ) demonstrates a synergistic effect in reducing measles transmission. Higher vaccination rates reduce the susceptible pool, while more effective quarantine measures isolate infectious individuals quickly, resulting in a significantly lower infection peak and shorter epidemic duration. These numerical patterns were later reflected in the batik-inspired visual motifs, where smooth epidemic curves produced harmonious visual structures and sharper variations created more dynamic motif transitions. This shows that the simulation outcomes are not only scientifically meaningful but also visually interpretable, strengthening the interdisciplinary connection between mathematical modeling, public health strategies, and cultural artistic representation.

Batik Model

The following batik motif was obtained from the numerical simulation of the SVEIQR measles model using Laplace Adomian Decomposition Method:

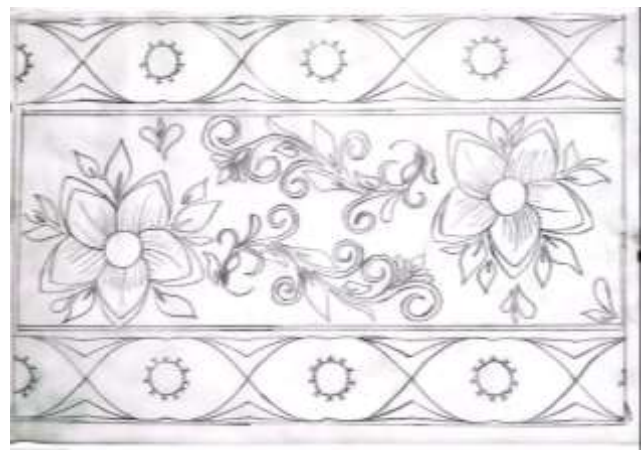


Figure 7. Batik model

The Meaning of the Batik Patterns

This batik pattern is a visual representation of the SVEIQR model (Susceptible-Vaccinated-Exposed-Infected-Quarantined-Recovered) simulated using the Laplace Adomian Decomposition Method (LADM). The design transforms mathematical dynamics of measles transmission into an artistic pattern, combining aesthetic and scientific representation of order and balance.

The five petal flower symbolizes the five main epidemiological phases (S, E, I, V, R), while the central circle represents quarantine (Q) as a control point balancing transmission and recovery. Winding tendrils depict the movement of individuals between compartments, reflecting the non-linear, dynamic nature of disease spread. Budding flowers at tendril ends represent latent (Exposed) individuals, symbolizing the potential for disease development and the importance of early interventions.

Parallel virus motifs highlight that biological phenomena follow predictable scientific patterns, even if they appear random, illustrating how art can communicate complex scientific concepts. Leaves along the tendrils symbolize regeneration and recovery, while visual spacing reflects system balance that can be maintained through public health measures.

Mathematical waves at the top and bottom, derived from the susceptible curve, represent the dynamics of the vulnerable population over time. Overall, this batik integrates mathematics, biology, and art, presenting epidemic dynamics as a structured, interdependent system, and demonstrating that epidemics can be studied not only quantitatively but also through aesthetic and cultural perspectives.

Conclusions

This study successfully developed a fractional differential equation model of measles transmission using the **SVEIQR Susceptible-Vaccinated-Exposed-Infected-Quarantined-Recovered** framework. The model was constructed bases on caputo's fractional derivative of order $0 < q \leq 1$ and solved numeically using the Adomian

Laplace Decomposition Method (ALDM). Through this approach, the model provided analytical approximations that describe the dynamic interactions among the population compartments. The simulation results revealedd that changes in the fractional order q significantly affectt the system's behavior, where the solution for smaller q values capture memory effects and slower transitions between epidemiological states.

Beyond numerical analysis, this research introduced a novel visualization approach by transforming the simulation graphs of the SVEIQR model into batik-inspired patterns. The resulting visualizations bridge the domains of mathematics, epidemiology, and Indonesian cultural art. Each pattern, color, and structure corresponds to specific epidemiological meanings (for instance), the five-petal flower symbolizes the five major phases of disease dynamics, and the central circle represents quarantines as stabilizing force in the system. The batik complex mathematical concepts more accessible and intuitive.

Overall, the study demonstrates that **mathematical modeling can be communicated through cultural and artistic forms**, enriching both scientific understanding and visual storytelling. The batik visualization of the SVEIQR model highlights the interdependence between infection, recovery, and control measures, while emphasizing balance, regeneration, and research contributes a new interdisciplinary framework that connects quantitative science with aesthetic interpretation, offering a creative perspective for communicating the dynamics of infections disease transmission.

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References

- Aldila, D., & Asrianti, D. (2019, May). A deterministic model of measles with imperfect vaccination and quarantine intervention. In *Journal of physics: conference series* (Vol. 1218, No. 1, p. 012044). IOP Publishing.
- Bahgat, M. S. Numerical Solution of Coupled System of Nonlinear Partial Differential Equations Using Laplace-Adomian Decomposition Method. *Journal of Advances in Mathematics*, 12(08).
- Farman, M., Saleem, M. U., Ahmad, A., & Ahmad, M. O. (2018). Analysis and numerical solution of SEIR epidemic model of measles with non-integer time fractional derivatives by using Laplace Adomian Decomposition Method. *Ain Shams Engineering Journal*, 9(4), 3391-3397.
- Jang, G. H., Kim, S. J., Lee, M. J., & Son, S. W. (2024). Effectiveness of vaccination and quarantine policies to curb the spread of COVID-19. *Physica A: Statistical Mechanics and its Applications*, 637, 129580.
- Saharjo BH, Nurhayati AD. 2006. Domination and composition structure change at hemic peat natural regeneration following burning; a case study in Pelalawan, Riau Province. *Biodiversitas* 7: 154-158.
- Lega, J. (2023). Introduction to Mathematical Modeling. The University of Arizona Open Textbooks. <https://opentextbooks.library.arizona.edu/mathematical-modeling>
- World Health Organization. (2024, November 14). Measles cases surge worldwide, infecting 10.3 million people in 2023. <https://www.who.int/news/item/14-11-2024-measles-cases-surge-worldwide--infecting-10.3-million-people-in-2023>