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Mathematical Modeling of Hepatitis Transmission Using the SEIR Model and Batik-Inspired Motifs from Simulation

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Abstract: Hepatitis is an infectious disease that remains a major health problem in Indonesia. This study aims to model the spread of hepatitis using the SEIR (Susceptible, Exposed, Infected, Recovered) mathematical model and connect it with the concept of batik patterns as a medium of mathematical visualization. The research employs a literature study and numerical simulation based on secondary data of hepatitis patients from Dr. M. Haulussy Ambon Hospital in 2019. The SEIR model describes the dynamic transitions among subpopulations of susceptible (S), exposed (E), infected (I), and recovered (R) individuals. The concept of batik patterns is used to represent the regularity and interconnectedness among the model's compartments, where each motif symbolizes dynamic and repetitive population interactions—analogous to the rhythm of disease transmission. The analysis results reveal two equilibrium points: the endemic equilibrium and the disease-free equilibrium, with the system being stable according to the Routh–Hurwitz criteria. Integrating mathematical modeling with the philosophy of batik offers an interdisciplinary approach that is both analytical and aesthetic. This study hightlights that the that the harmony between science and culture can enrich the way infectious disease phenomena are understood within society.

Keywords: batik, endemic, hepatitis, mathematical visualization, SEIR model.

Introduction

Hepatitis is one of the diseases of serious concern in global public health due to its significant impact on human quality of life. This disease, especially that caused by viruses, attacks the liver and can cause severe complications such as cirrhosis and liver cancer. Inflammation of the liver that can be caused by various factors, such as excessive alcohol consumption, autoimmune disorders, medications, or toxins.

Hepatitis A was discovered in 1973 by Feinstone, who at the time found spherical particles with a 27-nanometer diameter visible via immune electron microscopy in fecal samples from hepatitis A patients [1]. Hepatitis A is a disease caused by an RNA virus from the *Picornaviridae* family, which is primarily found in high concentrations in the feces of infected individuals. Its transmission generally occurs via the fecal-oral route, which is when a person ingests food, water, or touches objects contaminated by the feces of an infected person, especially at the end of the incubation period when the virus is shed in large quantities.

Hepatitis B is a liver infection caused by a DNA virus from the *Hepadnaviridae* family, which was first identified in 1963 as the *Australian antigen*. This virus has a complex structure with a nucleocapsid containing the viral DNA, core antigen (HBcAg), and DNA polymerase enzyme, and is enveloped by the surface antigen (HBsAg), which plays a role in its infectivity. Furthermore, the gene that encodes HBcAg also produces the e-antigen (HBeAg), which is an important marker of viral replication activity and the level of disease transmissibility. Risk factors for hepatitis B virus (HBV) transmission include a history of blood transfusion, use of injected drugs or shared injection equipment [2], use of contaminated

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piercing or tattoo equipment [3], sexual contact with an infected person, and organ transplantation from an HBV-positive donor [4].

Hepatitis C is a small, enveloped, positive-sense single-stranded RNA virus. This virus was first identified in 1989 and belongs to the *Flaviviridae* family as the sole member of the *Hepacivirus* genus. Its transmission primarily occurs through percutaneous routes, such as contact with infected blood from shared needles or needlestick injuries, and can also occur non-percutaneously through blood transfusions, organ transplants, hemodialysis, tattoos, piercings, or religious procedures involving skin incisions. Meanwhile, transmission through sexual contact or from mother to baby (perinatal) is less common.

Hepatitis D (HDV) is a "defective" single-stranded RNA virus because it requires the presence of the hepatitis B virus (HBV) to replicate and express itself completely. First identified by Rizzetto and colleagues in 1977 in Italy, HDV is the sole member of the *Deltavirus* genus and consists of eight genotypes, with genotype 1 being the most common in North America, Europe, and the Middle East. This virus contains the hepatitis D antigen (HDAg) and RNA, which are enveloped by the HBV surface antigen (HBsAg); therefore, HDV infection only occurs concurrently with HBV infection. Its transmission mechanism is similar to hepatitis B, namely through exposure to contaminated blood or bodily fluids, whereas perinatal transmission is relatively rare [5].

Hepatitis E is an RNA virus and the only species in the *Hepevirus* genus. Its primary transmission route is fecal-oral. Fecally contaminated water is the most common mode of transmission, while direct person-to-person transmission is rare. However, maternal–neonatal transmission (from mother to newborn) can sometimes occur [6].

According to WHO reports, millions of people worldwide are still infected with hepatitis viruses annually, with high mortality rates. In 2022, approximately 61 million people were living with hepatitis B and 9 million with hepatitis C in the Southeast Asia region, which ranks second in hepatitis B cases after Africa. However, diagnosis and treatment rates remain low, at less than 5% for hepatitis B and 14% for hepatitis C [7]. In Indonesia, the prevalence of hepatitis B decreased from 7.1% in 2013 to 2.4% in 2023 thanks to the joint efforts of various parties, showing significant progress in prevention, although challenges in early detection and elimination of this disease still need to be strengthened [8].

Mathematical modeling has long been used as a tool to study the spread of infectious diseases. One widely applied model is the SEIR (Susceptible–Exposed–Infected–Recovered) model, which describes the dynamics of disease transmission by accounting for individuals in the latent stage—that is, individuals who have been exposed but are not yet infectious. Through this model, the dynamics of hepatitis transmission can be analyzed quantitatively, allowing important parameters such as the infection rate, incubation period, and recovery rate to be determined more accurately. This type of analysis is very useful in formulating effective strategies to curb the rate of disease spread.

Previous research modeled the transmission of hepatitis using the SEIR (Susceptible, Exposed, Infected, Recovered) model. Using a literature study method and MATLAB simulations, this study used 2019 hepatitis patient data from Dr. M. Haulussy Regional General Hospital (RSUD) Ambon. The mathematical model formulated yielded two equilibrium points: endemic and disease-free. Stability analysis showed the model to be stable. Numerical simulation results showed that the Susceptible (S) subpopulation decreased sharply, while the Exposed (E), Infected (I), and Recovered (R) subpopulations peaked at different times before eventually declining [9].

This study aims to analyze the transmission process of hepatitis using the SEIR model and to simulate its dynamic behavior through numerical methods. The simulation results are then visualized as batik motifs derived from the model, representing the dynamic patterns of disease transmission transformed into batik designs inspired by the beauty and philosophy of Indonesian traditional art. The integration of mathematical science and batik art is expected to provide an innovative, engaging, and educational way to communicate scientific findings.

Thus, this research not only contributes to the development of mathematical modeling in the field of epidemiology but also introduces an innovative approach that bridges science and culture. Through scientific visualization in the form of batik motifs, it is hoped that greater appreciation will emerge for the role of mathematics in understanding real-world phenomena while simultaneously strengthening Indonesian cultural values in a modern scientific context.

Materials And Methods

Study Area

The scope of this study does not focus on a specific geographical area, but rather on the conceptual domain of epidemiological modeling and the simulation of hepatitis transmission dynamics. The population under consideration is represented through a mathematical framework in which individuals are categorized into the Susceptible, Exposed, Infected, and Recovered compartments according to the SEIR model. This abstraction allows the transmission process to be analyzed systematically without being limited to a particular region or demographic structure.

The epidemiological parameters used in the model—such as transmission rate, incubation period, infectious duration, and recovery rate—were obtained through an extensive review of scientific literature and reports from recognized global health institutions. These parameters serve as the foundation for conducting numerical simulations that reflect the general characteristics of hepatitis transmission.

Furthermore, this study utilizes MATLAB as the computational environment in which the SEIR model is simulated. The resulting curves describing the evolution of each compartment over time become the primary dataset for further interpretation. These curves form the basis for generating batik-inspired motifs that visually represent the dynamic behavior of the model. Thus, the area of study encompasses mathematical modeling, epidemiological data interpretation, and the transformation of scientific results into culturally meaningful artistic visualizations.

Procedures

This research was carried out through the following stages:

1. Literature Study
   A literature study was conducted to obtain a theoretical foundation regarding epidemiological models, specifically the SEIR model, and to understand the transmission characteristics of Hepatitis.
2. Data Collection
   Relevant primary and secondary data related to the spread of Hepatitis were collected for use in the model's development.
3. Model Analysis and Simulation
   The SEIR mathematical model was designed, and simulations were performed using MATLAB software. In this stage, parameters obtained from the literature study and field data were input into the model to visualize the population dynamics in each compartment (S, E, I, R) over a specific time period.
4. Batik Model Development
   A Batik model representation was developed based on the simulation results from MATLAB to visually depict the patterns and distribution of the disease spread.

Data Analysis

This study uses secondary data obtained from previous literature and reports, specifically data on Hepatitis patients at Dr. M. Haulussy Regional Public Hospital (RSUD) in Ambon for the year 2019. The population included in the study consists of 48 patients. The data were then analyzed using the SEIR mathematical model to examine the dynamics of disease transmission. Additional literature sources used in this research include scientific journals, reports from the World Health Organization (WHO), and official data from the Ministry of Health of the Republic of Indonesia.

Results And Discussion

Mathematical Model

The following is a flowchart of the SEIR mathematical model.

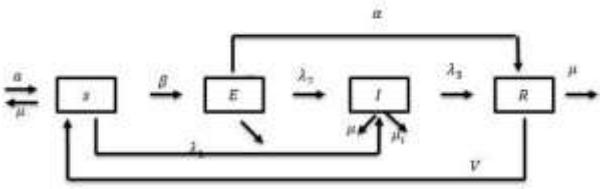

Figure 1 : SEIR Model

Based on the model formulation above, the mathematical model formed for hepatitis disease:

$$\frac{dS}{dt} = a + vR - (\beta + \lambda_1 + \mu)S$$
$$\frac{dE}{dt} = \beta S - (\alpha + \lambda_2 + \mu)E$$
$$\frac{dI}{dt} = \lambda_1 S + \lambda_2 E - (\lambda_3 + \mu + \mu i)I$$
$$\frac{dR}{dt} = aE + \lambda_3 I - (v + \mu)R$$

Description:
S = Susceptible - individuals who are potentially infected
E = Exposed - individuals who show symptoms of infection
I = Infected - individuals who have been infected and are contagious
R = Recovered - individuals who have recovered and are immune
a = Birth rate
v = Rate of individuals becoming immune due to the vaccine
α = Length of treatment (the rate of selection from exposed to recovered)
β = Rate of disease transmission
λ_1 = Rate of infection in susceptible individuals without the vaccine
λ_2 = Rate of congenital disease in susceptible individuals without the vaccine
λ_3 = Rate of recovery of infected individuals after treatment and medical treatment
μ = Natural death rate
μ_i = Rate of death due to infection

In the SEIR model of hepatitis, *existence* refers to the assurance that the system of differential equations possesses well-defined solutions for all $t \geq 0$. This is guaranteed because all epidemiological parameters in the model are positive, ensuring that the state variables $S(t)$, $E(t)$, $I(t)$, and $R(t)$ remain within the non-negative real domain. Moreover, the presence of both the disease-free and endemic equilibrium points confirms that the system admits valid steady-state conditions that can be further examined through stability analysis.

The equilibrium points to be analyzed are the endemic equilibrium point and the disease-free equilibrium point.

1. Disease-Free Equilibrium Point

   $$E = (S^\circ, E^\circ, I^\circ, R^\circ)$$
   $$= \left(\frac{a\mu\alpha + a\mu^2}{\mu^2\beta + \mu^2\alpha - \alpha}, \frac{\beta a u}{\mu^2\beta + \mu^2\alpha - \alpha}, 0, \frac{a\alpha\beta}{\mu v\beta + \mu v a + \mu^2 v + \mu\alpha\beta + \mu^2\beta + \mu^2\alpha + \mu^3}\right)$$

2. Endemic Equilibrium Point

   $$E = (S^*, E^*, I^*, R^*)$$
   $$= \left(\frac{ba}{(\beta+\lambda_1+\mu)b - ve}, \frac{a}{(\beta+\lambda_1+\mu)b - ve}, \frac{ca}{(\beta+\lambda_1+\mu)b - ve}, \frac{ea}{(\beta+\lambda_1+\mu)b - ve}\right)$$

3. SEIR Model Stability Analysis

   Based on the previous system of equations, we obtain:

$$f_1 = \frac{dS}{dt} = a + vR - (\beta + \lambda_1 + \mu)S$$

$$f_2 = \frac{dE}{dt} = \beta S - (\alpha + \lambda_2 + \mu)E$$

$$f_3 = \frac{dI}{dt} = \lambda_1 S + \lambda_2 E - (\lambda_3 + \mu + \mu i)I$$

$$f_4 = \frac{dR}{dt} = aE + \lambda_3 I - (v + \mu)R$$

$\frac{\partial f_1}{\partial S} = -(\beta + \lambda_1 + \mu)$	$; \frac{\partial f_1}{\partial E} = 0$
$\frac{\partial f_1}{\partial I} = 0$	$; \frac{\partial f_1}{\partial R} = v$
$\frac{\partial f_2}{\partial S} = \beta$	$; \frac{\partial f_2}{\partial E} = -(\alpha + \lambda_2 + \mu)$
$\frac{\partial f_2}{\partial I} = 0$	$; \frac{\partial f_2}{\partial R} = 0$
$\frac{\partial f_3}{\partial S} = \lambda_1$	$; \frac{\partial f_3}{\partial E} = \lambda_2$
$\frac{\partial f_3}{\partial I} = -(\lambda_3 + \mu + \mu_1)$	$; \frac{\partial f_3}{\partial R} = 0$

$\frac{\partial f_4}{\partial S} = 0$	$; \frac{\partial f_4}{\partial E} = \alpha$
$\frac{\partial f_4}{\partial I} = \lambda_3$	$; \frac{\partial f_4}{\partial R} = -(v + \mu)$

To simplify the calculation, suppose:

$r_1 = \beta + \lambda_1 + \mu$

$r_2 = \alpha + \lambda_2 + \mu$

$r_3 = \lambda_3 + \mu + \mu_i$

$r_4 = v + \mu$

Next, a Jacobian matrix is formed, namely:

$$(S,E,I,R) = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial E} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial R} \\ \frac{\partial f_2}{\partial S} & \frac{\partial f_2}{\partial E} & \frac{\partial f_2}{\partial I} & \frac{\partial f_2}{\partial R} \\ \frac{\partial f_3}{\partial S} & \frac{\partial f_3}{\partial E} & \frac{\partial f_3}{\partial I} & \frac{\partial f_3}{\partial R} \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial E} & \frac{\partial f_4}{\partial I} & \frac{\partial f_4}{\partial R} \end{bmatrix}$$

$$= \begin{bmatrix} -r_1 & 0 & 0 & v \\ \beta & -r_2 & 0 & 0 \\ \lambda_1 & \lambda_2 & -r_3 & 0 \\ 0 & \alpha & \lambda_3 & -r_4 \end{bmatrix}$$

Jacobian matrix for hepatitis disease freedom

$$J(S^\circ, E^\circ, I^\circ, R^\circ) = J\left(\frac{a\mu\alpha + a\mu^2}{\mu^2\beta + \mu^2\alpha - \alpha}, \frac{\beta a u}{\mu^2\beta + \mu^2\alpha - \alpha}, 0, \frac{a\alpha\beta}{\mu v\beta + \mu v a + \mu^2 v + \mu a\beta + \mu^2\beta + \mu^2\alpha + \mu^3}\right)$$

$$= \begin{bmatrix} -r_1 & 0 & 0 & v \\ \beta & -r_2 & 0 & 0 \\ \lambda_1 & \lambda_2 & -r_3 & 0 \\ 0 & \alpha & \lambda_3 & -r_4 \end{bmatrix}$$

Then, the eigenvalue will be searched for with $|J(S^\circ, E^\circ, I^\circ, R^\circ) - \lambda I| = 0$

Please note:

$$|J(S^\circ, E^\circ, I^\circ, R^\circ) - \lambda I| = 0$$

$$\left| \begin{bmatrix} -r_1 & 0 & 0 & v \\ \beta & -r_2 & 0 & 0 \\ \lambda_1 & \lambda_2 & -r_3 & 0 \\ 0 & \alpha & \lambda_3 & -r_4 \end{bmatrix} - \begin{bmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix} \right| = 0$$

$$\begin{vmatrix} -r_1 - \lambda & 0 & 0 & v \\ \beta & -r_2 - \lambda & 0 & 0 \\ \lambda_1 & \lambda_2 & -r_3 - \lambda & 0 \\ 0 & \alpha & \lambda_3 & -r_4 - \lambda \end{vmatrix} = 0$$

$$(-r_1 - \lambda)\begin{vmatrix} -r_2 - \lambda & 0 & 0 \\ \lambda_2 & -r_3 - \lambda & 0 \\ \alpha & \lambda_3 & -r_4 - \lambda \end{vmatrix} - v\begin{vmatrix} \beta & -r_2 - \lambda & 0 \\ \lambda_1 & \lambda_2 & -r_3 - \lambda \\ 0 & \alpha & \lambda_3 \end{vmatrix} = 0$$

$$(-r_1 - \lambda)(-r_2 - \lambda)(-r_3 - \lambda)(-r_4 - \lambda) - v\left[\beta(\lambda_2\lambda_3 + \alpha(r_3 + \lambda)) + (r_2 - \lambda)\lambda_1\lambda_3\right] = 0$$

$$\lambda^4 + (r_1 + r_2 + r_3 + r_4)\lambda^3 + (r_1r_2 + r_1r_3 + r_1r_4 + r_2r_3 + r_2r_4 + r_3r_4)\lambda^2 + \left(r_1r_2r_3 + r_1r_2r_4 + r_1r_3r_4 + r_2r_3r_4 - v(\alpha\beta + \lambda_1\lambda_3)\right)\lambda + \left(r_1r_2r_3r_4 - v(\beta\lambda_2\lambda_3 + \beta\alpha r_3 + r_2\lambda_1\lambda_3)\right) = 0$$

If expanded, $\det(A - \lambda I) = \lambda^4 + k_1\lambda^3 + k_2\lambda^2 + k_3\lambda + k_4 = 0$, then the following coefficients are obtained:

$$(2)\begin{cases} k_1 = r_1 + r_2 + r_3 + r_4 \\ k_2 = r_1r_2 + r_1r_3 + r_1r_4 + r_2r_3 + r_2r_4 + r_3r_4 \\ k_3 = r_1r_2r_3 + r_1r_2r_4 + r_1r_3r_4 + r_2r_3r_4 - v(\alpha\beta + \lambda_1\lambda_3) \\ k_4 = r_1r_2r_3r_4 - v(\beta\lambda_2\lambda_3 + \beta\alpha r_3 + r_2\lambda_1\lambda_3) \end{cases}$$

From the results (2), Routh Hurwitz will analyze using $\lambda^4 + k_1\lambda^3 + k_2\lambda^2 + k_3\lambda + k_4 = 0$, The following is the Routh-Hurwitz table

λ^4	1	k_2	k_4
λ^3	k_1	k_3	0
λ^2	b_1	b_2	0
λ^1	c_1	c_2	0
λ^0	d_1	0	0

Description:

$$b_1 = \frac{k_1k_2 - k_3}{k_1},\ b_2 = k_4$$

$$c_1 = \frac{b_1k_3 - k_1b_2}{b_1} = \frac{(k_1k_2 - k_3)k_3 - k_1^2k_4}{k_1k_2 - k_3}$$

$$= c_2 = 0$$

$$d_1 = k_4$$

Thus, the first column of the Routh–Hurwitz table is

λ^4	1
λ^3	k_1
λ^2	$\frac{k_1k_2 - k_3}{k_1}$
λ^1	$\frac{(k_1k_2 - k_3)k_3 - k_1^2k_4}{k_1k_2 - k_3}$
λ^0	k_4

Since $1 > 0, k_1 > 0$, dan $k_4 > 0$, the system is stable provided that $b_1 > 0$ and $c_2 > 0$ which leads to the conditions $k_1k_2 > k_3$ and $(k_1k_2 - k_3)k_3 > k_1^2k_4$

Mathematical Model Simulation using MATLAB

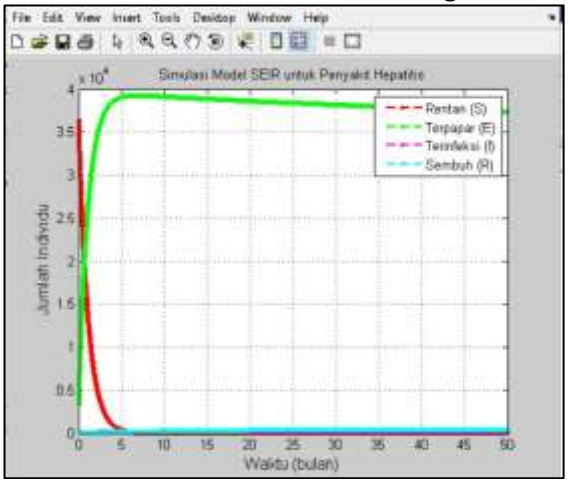

Figure 2 : MATLAB Simulation

Variable	Description	Value
S	Subpopulation of individuals who are susceptible to infection	36,476
E	Subpopulation of individuals who show signs of exposure	3,323
I	Subpopulation of individuals who are infected	48
R	Subpopulation of individuals who have recovered	37

Parameter	Description	Value
a	Birth rate	0.021
v	Rate of individuals becoming immune due to vaccination	0.083
$\propto$	Duration of treatment	0.00092
β	Disease transmission rate	0.91
λ_1	Infection rate for susceptible individuals without vaccination	0.0012
λ_1	Rate of congenital disease among susceptible individuals without	0.00092

	vaccination	
λ_1	Recovery rate of infected individuals after receiving medical treatment	0.00092
μ	Natural mortality rate	0.00012
μ_i	Mortality rate due to infection	0.125

The simulation of the SEIR model for hepatitis shows that the disease spreads rapidly, with the exposed (E) class becoming the dominant population group. At the beginning of the simulation, the susceptible (S) population decreases sharply, dropping to nearly zero within the first four months. This dramatic decline results from the high transmission rate (β = 0.91), which causes most susceptible individuals to quickly move into the exposed class. Meanwhile, the exposed (E) group rises steeply and becomes the largest compartment, reaching close to 40,000 individuals. This indicates that a large number of individuals enter and remain in the latent phase before progressing to the next stages of infection.

In contrast, the number of infected (I) individuals remains very small and shows minimal change over time. This occurs because the transition rate from E to I is relatively low, while the infection-induced mortality rate (μ_i = 0.125) is quite high, resulting in individuals not staying long in the actively infected class. Additionally, some individuals recover through treatment or natural recovery before contributing significantly to the infected population. The recovered (R) population also stays very small and stable. This is due to the relatively high rate of revaccination (v = 0.083), which moves individuals from the recovered class back into the susceptible class, combined with natural mortality that reduces the number of recovered individuals over time.

Overall, the model illustrates that hepatitis spreads rapidly, with a substantial accumulation of individuals in the exposed phase, while the infected and recovered phases remain small due to the high rates of transition out of these compartments. The interplay of key parameters—particularly the high transmission rate, elevated infection-induced mortality, and revaccination—creates dynamics in which the exposed class dominates the population, and the S, I, and R classes stabilize at low levels after only a few months. These results highlight that although many individuals are exposed to the disease, only a small proportion progress to active infection or recovery, reflecting the characteristics of hepatitis transmission and progression within this SEIR framework.

Batik Visualization of the Hepatitis Mathematical Model

After obtaining the simulation results generated using the SEIR model, the following are the batik motifs inspired by those data.

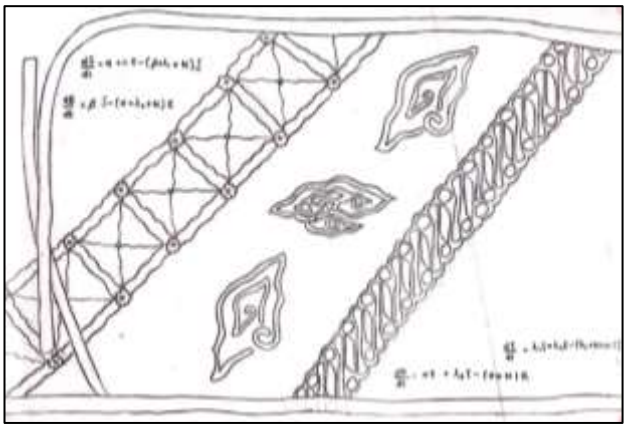

Figure 3 : Batik Model

Philosophical Meaning

In its philosophical dimension, every batik motif carries a profound message. *Batik parang*, with its continuous slanted "S" pattern, symbolically represents continuity and an unyielding fighting spirit. The pattern is often likened to the relentless waves of the ocean striking the rocks an emblem of life's dynamic and never-ending struggles frequently associated with power and agility.

In contrast, *batik megamendung*, which translates to "shaded clouds," is a noble symbol of patience, inner calmness, and compassion. Its philosophy

encourages individuals to embody a soothing presence in any situation, like clouds that bring shade and serenity.

Meanwhile, the hepatitis mathematical batik model presents a unique contemporary philosophy science as a symbol of hope. This motif fundamentally transforms abstract and intimidating disease data into a beautiful work of art. It represents the power of knowledge, where intellectual understanding of an outbreak (through science) becomes a tool for the struggle for health and humanity.

Biological Meaning

Batik fabric often serves as a reflection of the natural and biological world. The intertwined "S" shapes in *batik parang* can be biologically interpreted as a visual representation of the double-helix structure of DNA. In this context, *parang* becomes a fundamental symbol of heredity the blueprint of life itself while also reflecting the constant and interdependent flow of energy within an ecosystem.

The biological meaning of *batik megamendung* is closely related to the hydrological cycle, which is fundamental to life. The cloud shapes visually represent the process of water vapor condensation in the atmosphere. This motif stands as a timeless reminder of the importance of water gathered by clouds before being returned to Earth as rain to sustain all life.

In the hepatitis mathematical batik model, the biological meaning is literal and explicit rather than interpretative. The motif depicted on the fabric is not the imagination of an artist but a visualization of real biological data. The pattern may accurately depict the morphological structure of the Hepatitis virus itself or the complex interactions that occur as it attacks liver cells (hepatocytes).

Mathematical Meaning

Behind its beauty, batik patterns embody structured mathematical principles. *Batik parang* is a perfect visualization of the concept of geometric transformation, particularly translation. The entire motif is constructed on this principle, where a basic pattern unit (*rapet*) is repeated periodically and consistently along diagonal lines to fill the fabric surface harmoniously and orderly.

Batik megamendung, on the other hand, is a stunning visual example of a fractal concept. Its cloud forms exhibit self-similarity a hallmark of fractals in which the main geometric shape (large cloud clusters) is composed of smaller, similarly shaped forms, creating captivating visual depth and complexity.

The greatest uniqueness of the hepatitis mathematical batik model lies in its applied mathematical meaning. These intricate patterns are generated from visualizations of computer simulation data using mathematical disease-spread models. Scientists employ tools such as SEIR differential equations to predict outbreak dynamics, and the simulation results are then translated into batik motifs.

Conclusions

This study demonstrates that the SEIR model provides a comprehensive framework for analyzing the transmission dynamics of hepatitis. By incorporating the exposed compartment, the model effectively captures the latent phase of infection, allowing a more accurate representation of the disease's progression within a population. The numerical simulations performed using MATLAB reveal distinct phases in the transmission process, including the initial increase of exposed individuals, the peak of infection, and the eventual decline as recovery rates surpass transmission rates.

The results also show that variations in key epidemiological parameters significantly influence the shape of the transmission curves. Changes in the incubation period, infection rate, or recovery rate lead to notable shifts in the timing and magnitude of infection peaks, highlighting the importance of precise parameter estimation in disease control strategies. These findings reinforce the relevance of mathematical modeling as a tool for understanding and predicting disease behavior.

Beyond its scientific implications, this study introduces an innovative interdisciplinary approach by transforming the simulation outcomes

into batik-inspired motifs. The curves generated by the SEIR model serve as visual representations that, when stylized into artistic patterns, demonstrate how mathematical structures can be communicated through culturally rooted artistic expressions. This integration of scientific modeling and batik design not only enriches the interpretation of the model but also provides an alternative medium for science communication that is both engaging and culturally meaningful.

In conclusion, this research contributes to the advancement of epidemiological modeling while simultaneously offering a creative bridge between mathematics and Indonesian traditional art. The study emphasizes that mathematical concepts can transcend disciplinary boundaries, inspiring visual forms that communicate scientific ideas in innovative and culturally resonant ways.

Conflict Of Interest: The authors declare that there are no conflicts of interest concerning the publication of this article.

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