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Batik Motifs from the Model of Spreading Infectious Diseases with Vaccination

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Abstract: Mathematical modeling not only plays a role in the fields of science and health, but can also provide visual inspiration in the field of art, especially in the making of batik motifs. This research aims to develop a batik pattern inspired by the graph produced through a simulation of a mathematical model of the spread of infectious diseases with vaccination. The model used is SVIR (Susceptible, Vaccinated, Infected, Recovered). The simulation results produce solution graphs and phase portraits that depict changes in population dynamics under various parameter conditions. The lines and shapes formed from the graphic are then adapted into batik motifs. The resulting motifs represent the balance and interconnectedness between the elements, reflecting the dynamics that exist in the mathematical model. These findings show that mathematical approaches can be a new source of inspiration in the development of batik designs that combine aesthetic and scientific values.

Keywords: mathematical model, batik, numerical simulation, system stability, batik pattern.

Introduction

Microorganisms such as bacteria, viruses, and fungi are the cause of various infectious diseases in humans. These types of microorganisms have the ability to adapt and replicate quickly, so they are able to spread widely in a short time and cause outbreaks that have a major impact on the human population. Therefore, a scientific approach is needed to understand the dynamics of disease spread so that control efforts can be carried out more effectively.

One way that can be done to understand the spread of infectious diseases is by mathematical modeling. Through mathematical models, we can describe how diseases spread and change over time in a population. Typically, this model uses differential equation theory, which describes the change in the number of individuals in each group over time (Perasso, 2018).

One of the important components of the infectious disease model is the baseline reproductive number (R_0), which indicates the average number of new individuals infected by a single sick person in a fully vulnerable population (van den Driessche, 2017). If $R_0 < 1$, the disease will disappear from the population because the system is in a stable disease-free state, whereas if $R_0 > 1$, the disease can persist and become endemic. In the context of the SRIR model, vaccination is an important factor to reduce the R_0 value so that the spread of disease can be optimally controlled (Zhu et al., 2024).

Research conducted by (Firmansyah & Prihandono, 2024) discuss the SVIR (Susceptible, Vaccinated, Infected, Recovered) model using the Next Generation Matrix method and perform numerical simulations using Python. Their results show how interactions between vulnerable populations, those who have been vaccinated, and those who are infected can affect the stability of the system under certain conditions. This shows that with a mathematical approach, we can see how vaccination plays an important role in controlling the spread of disease.

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Interestingly, mathematical approaches such as the SVIR model are not only useful in the field of health, but can also be used as inspiration in the art world. The results of numerical simulations that display population dynamics graphs and phase portraits can be adapted into visual forms that have aesthetic value. Several studies in the field of fine arts show that mathematical patterns can be the basis for designing batik motifs. (Yulisetiani & Sutrisno, 2023).

Based on the science and art side, this research tries to combine the two by making the results of the SVIR model simulation as inspiration for the design of batik motifs. Simulations were performed using MATLAB software to generate graphs and phase portraits that represent the dynamics of interactions between compartments. The pattern formed was then adapted into a batik motif that depicted balance and relationships between elements, as well as the relationships between variables in mathematical models. In this way, this research not only shows how mathematics can be used to understand biological phenomena, but also how the results can be a source of aesthetic inspiration in the art world, especially in batik design. So, this approach is not only for the purpose of scientific analysis, but also to show that science and art can complement each other and produce works that have scientific meaning as well as cultural value.

Mathematical Model

This study uses a mathematical modeling approach with reference to the SVIR (Susceptible, Vaccinated, Infected, Recovered) model developed by (Firmansyah & Prihandono, 2024). The model describes changes in the number of individuals in each population group over time, with parameters such as infection rates, vaccination, and recovery based on theoretical assumptions from mathematical epidemiology studies.

The simulation was performed using MATLAB software to obtain graphs and patterns of population dynamics that depict the interactions between groups of individuals in the model. The visual results of the simulation were then adapted into inspiration in the design of batik motifs, by emphasizing the balance of shapes and the interconnectedness between elements as reflected in the mathematical model.

To better understand the mechanism of disease spread described through the SVIR model, an illustration of how individuals in the population can move from one group to another is needed. In the SVIR model, the displacement process is visualized in the flow chart shown in Figure 1.

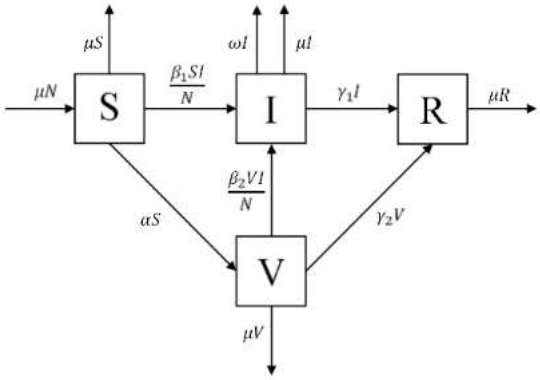

Figure 1 Transfer diagram of the SVIR model (source : (Firmansyah & Prihandono, 2024))

Descriptions :

μ : natural birth and death rate in each sub-population

$\propto$: vactination rate

ω : disease-induced death rate in the infected sub-population

β_1 : disease transmission rate from the susceptible sub-population to the infected sub-population

β_2 : disease transmission rate frome the vaccinated sub-population to the infected sub-population

γ_1 : recovery rate from the infected sub-population to the recovered sub-population

γ_2 : average rate from at which individuals in the vaccinated sub-population acquire immunity

S : number of individuals in the susceptible sub-population at time t

V : number of individuals in the vaccinated sub-population at time t

I : number of individuals in the infected sub-population at time t

R : number of individuals in the recovered sub-population at time t

s : proportion of individuals in the susceptible sub-population relative to the total population at time t

v : proportion of individuals in the vaccinated sub-population relative to the total population at time t

i : proportion of individuals in the infected sub-population relative to the total population at time t

r : proportion of individuals in the recovered sub-population relative to the total population at time t

Based on the flow in Figure 1, the dynamics of the change in the number of individuals in each group can be explained through the equation of the rate of change of individuals in the following SVIR model:

1. Sub-population S : $\frac{dS}{dt} = \mu N - \mu S - \frac{\beta_1 SI}{N} - \propto S$ …(1)
2. Sub-population I : $\frac{dI}{dt} = \frac{\beta_1 SI}{N} + \frac{\beta_2 VI}{N} - \gamma_1 - \omega I - \mu I$ …(2)
3. Sub-population R : $\frac{dR}{dt} = \gamma_2 V + \gamma_1 I - \mu R$ …(3)
4. Sub-population V : $\frac{dV}{dt} = \propto S - \frac{\beta_2 VI}{N} - \gamma_2 V - \mu V$ …(4)

Since the total populations is assumed to be constant, we have $S + V + I + R = N$. By considering prevalence, defined as the proportions of individuals in each sub-population, equations $1, 2, 3, 4$ can be simplified using the sustitutions $s = \frac{S}{N}, i = \frac{I}{N}, v = \frac{V}{N}, r = \frac{R}{N}$ resulting in $s + v + i + r \left(\frac{S}{N} + \frac{V}{N} + \frac{I}{N} + \frac{R}{N} = \frac{N}{N} = 1\right)$. Based on the subtitutions, the system of rate equations can be rewritten in the form :

$$\frac{ds}{dt} = \frac{1}{N}\frac{dS}{dt}$$

$$\frac{ds}{dt} = \frac{1}{N}\left(\mu N - \mu S - \frac{\beta_1 SI}{N} - \propto S\right)$$

$$\frac{ds}{dt} = \mu - \frac{\mu S}{N} - \frac{\beta_1 S}{N}\frac{I}{N} - \frac{\propto S}{N}$$

$$\frac{ds}{dt} = \mu - \mu s - \beta_1 si - \propto s \quad \ldots(5)$$

$$\frac{di}{dt} = \frac{1}{N}\frac{dI}{dt}$$

$$\frac{di}{dt} = \frac{1}{N}\left(\frac{\beta_1 SI}{N} + \frac{\beta_2 VI}{N} - \gamma_1 I - \omega I - \mu I\right)$$

$$\frac{di}{dt} = \frac{\beta_1 S}{N}\frac{I}{N} + \frac{\beta_2 V}{N}\frac{I}{N} - \frac{\gamma_1 I}{N} - \frac{\omega I}{N} - \frac{\mu I}{N}$$

$$\frac{di}{dt} = \beta_1 si + \beta_2 vi - \gamma_1 i - \omega i - vi \quad \ldots(6)$$

$$\frac{dr}{dt} = \frac{1}{N}\frac{dR}{dt}$$

$$\frac{dr}{dt} = \frac{1}{N}(\gamma_2 V + \gamma_1 I - \mu R)$$

$$\frac{dr}{dt} = \frac{\gamma_2 V}{N} + \frac{\gamma_1 I}{N} - \frac{\mu R}{N}$$

$$\frac{dr}{dt} = \gamma_2 v + \gamma_1 i - \mu r \quad \ldots(7)$$

$$\frac{dv}{dt} = \frac{1}{N}\frac{dV}{dt}$$

$$\frac{dv}{dt} = \frac{1}{N}\left(\propto S - \frac{\beta_2 VI}{N} - \gamma_2 V - \mu V\right)$$

$$\frac{dv}{dt} = \frac{\propto S}{N} - \frac{\beta_2 V}{N}\frac{I}{N} - \frac{\gamma_2 V}{N} - \frac{\mu V}{N}$$

$$\frac{dv}{dt} = \propto s - \beta_2 vi - \gamma_2 v - \mu v \quad \ldots(8)$$

Next, the disease-free equilibrium point is obtained by assuming a steady-stease condition, in which $\frac{ds}{dt} = \frac{dv}{dt} = \frac{di}{dt} = \frac{dr}{dt} = 0$. By applying this condition to the system of equation (5) – (8), equation (5) becomes:

$$\mu - \mu s - \propto s = 0$$

$$\mu = \mu s + \propto s$$

$$\mu = (\mu + \propto)s$$

$$s_o = \frac{\mu}{(\mu + \propto)}$$

Equation (8) becomes

$$\propto \frac{\mu}{(\mu + \propto)} - \beta_2 vi - \gamma_2 v - \mu v = 0$$

$$\propto \frac{\mu}{(\mu + \propto)} = \gamma_2 v + \mu v$$

$$\propto \frac{\mu}{(\mu+\propto)} = v(\gamma_2+\mu)$$

$$v_o = \frac{\propto \mu}{(\mu+\propto)(\gamma_2+\mu)}$$

Equation (7) becomes

$$\gamma_2 v + \gamma_1 i - \mu r = 0$$

$$\mu r = \gamma_2 v$$

$$r_o = \frac{\gamma_2 v}{\mu}$$

$$r_o = \frac{\gamma_2 \propto}{(\gamma_2+\mu)(\mu+\propto)}$$

After obtaining the disease-free equilibrium point, the endemic equilibrium point is determined, which is a condition when the disease persists in the population. This endemic equilibrium point occurs when the rate of change of each group of individuals is zero $\frac{ds}{dt} = \frac{dv}{dt} = \frac{di}{dt} = \frac{dr}{dt} = 0$ and $i > 0$ so that equation (5) becomes

$$\mu - \mu s - \beta_1 s i^* - \propto s = 0$$

$$\mu = \mu s + \beta_1 s i^* + \propto s$$

$$\mu = (\mu + \beta_1 i^* + \propto) s$$

$$s^* = \frac{\mu}{\mu + \beta_1 i^* + \propto}$$

Equation (8) becomes

$$\propto s^* - \beta_2 v i^* - \gamma_2 v - \mu v = 0$$

$$\propto s^* = \beta_2 v i^* + \gamma_2 v + \mu v$$

$$\propto s^* = v(\beta_2 i^* + \gamma_2 + \mu)$$

$$v^* = \left(\frac{\propto}{\beta_2 i^* + \gamma_2 + \mu}\right)\left(\frac{\mu}{\mu + \beta_1 i^* + \propto}\right)$$

Equation (7) becomes

$$\gamma_2 v + \gamma_1 i - \mu r = 0$$

$$\mu r = \gamma_2 v^* + \gamma_1 i^*$$

$$r^* = \frac{\gamma_2 v^* + \gamma_1 i^*}{\mu}$$

$$r^* = \frac{\gamma_2 \propto}{(\beta_2 i^* + \gamma_2 + \mu)(\mu + \beta_1 i^* + \propto)} + \mu\gamma_1 i^*$$

So that it is obtained

$$E_*(s^*, v^*, i^*, r^*) = \left(\frac{\mu}{\mu + \beta_1 i^* + \propto}, \left(\frac{\propto}{\beta_2 i^* + \gamma_2 + \mu}\right)\left(\frac{\mu}{\mu + \beta_1 i^* + \propto}\right), i^*, \frac{\gamma_2}{(\beta_2 i^* + \gamma_2 + \mu} + \mu\gamma_1 i^*\right)$$

Next, the value of i^* will be searched. with the substitution of the equation v^*. and s^*. to equation (6) and because $i^* > 0$ so that equation (6) becomes

$$\beta_1 s + \beta_2 v - \gamma_1 - \omega - v = 0$$

$$\beta_1\left(\frac{\mu}{\mu + \beta_1 i^* + \propto}\right) + \beta_2\left(\frac{\propto \mu}{(\beta_2 i^* + \gamma_2 + \mu)(\mu + \beta_1 i^* + \propto)}\right) = \gamma_1 + \omega + \mu$$

$$\beta_1\mu(\beta_2 i^* + \gamma_2 + \mu) + \beta_2 \propto \mu = \gamma_1 + \omega + \mu(\beta_2 i^* + \gamma_2 + \mu)(\mu + \beta_1 i^* + \propto)$$

$$\beta_1\mu\beta_2 i^* + \beta_1\mu(\gamma_2 + \mu) + \beta_2 \propto \mu = \gamma_1 + \omega + \mu(\beta_2 i^* + \gamma_2 + \mu)(\mu + \beta_1 i^* + \propto)$$

$$\beta_1\mu\beta_2 i^* + \beta_1\mu(\gamma_2 + \mu) + \beta_2 \propto \mu = \gamma_1 + \omega + \mu(\beta_2 i^* + (\gamma_2 + \mu))(\beta_1 i^* + (\mu+\propto))$$

$$\beta_1\mu\beta_2 i^* + \beta_1\mu(\gamma_2 + \mu) + \beta_2 \propto \mu = (\gamma_1 + \omega + \mu)[\beta_1\beta_2 i^{*2} + \beta_2 i^*(\mu+\propto) + \beta_1 i^*(\gamma_2 + \mu) + (\gamma_2 + \mu)(\mu+\propto)]$$

$$\beta_1\mu\beta_2 i^* + \beta_1\mu(\gamma_2 + \mu) + \beta_2 \propto \mu = (\gamma_1 + \omega + \mu)\beta_1\beta_2 i^{*2} + (\gamma_1 + \omega + \mu)[\beta_2(\mu+\propto) + \beta_1(\gamma_2 + \mu)]i^* + (\gamma_1 + \omega + \mu)(\gamma_2 + \mu)(\mu+\propto)$$

Move the section so that it becomes

$$0 = [(\gamma_1 + \omega + \mu)\beta_1\beta_2]i^{*2} + \left[(\gamma_1 + \omega + \mu)\left(\beta_2(\mu+\propto) + \beta_1(\gamma_2 + \mu)\right)\right]i^* + [(\gamma_1 + \omega + \mu)(\mu+ \propto)(\gamma_2 + \mu)] - (\beta_1\beta_2\mu)i^* - \beta_1\mu(\gamma_2 + \mu) - \beta_2 \propto \mu$$

$$0 = [(\gamma_1 + \omega + \mu)\beta_1\beta_2]i^{*2} + \left[(\gamma_1 + \omega + \mu)\left(\beta_2(\mu+\propto) + \beta_1(\gamma_2 + \mu)\right) - \beta_1\beta_2\mu\right]i^* + [(\gamma_1 + \omega + \mu)(\mu+\propto)(\gamma_2 + \mu) - \beta_1\mu(\gamma_2 + \mu) - \beta_2 \propto \mu]$$

So that from $A_1 i^{*2} + A_2 i^* + A_3(1 - C) = 0$ with $C > 1$ is obtained

$$A_1 = (\gamma_1 + \omega + \mu)\beta_1\beta_2$$

$$A_2 = (\gamma_1 + \omega + \mu)\left(\beta_2(\mu+\propto) + \beta_1(\gamma_2 + \mu)\right) - \beta_1\beta_2\mu$$

$$A_3 = (\gamma_1 + \omega + \mu)(\mu+\propto)(\gamma_2 + \mu)$$

With a value of $C = \frac{\beta_1 N}{(\gamma_1+\omega+\mu)(\mu+\propto)} + \frac{\beta_2 \propto \mu}{(\gamma_1+\omega+\mu)(\mu+\propto)(\mu+\gamma_2)}$

So the solution for the value of i^*. can be obtained through the ABC formula where

$$i^* = \frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_2(1 - C)}}{2A_1}$$

In order for there to be a positive root $i^* > 0$ then

1) Non-negative discrimination : $D = A_2^2 - 4A_1A_2(1 - C) \geq 0$
2) One of the roots yields a value greater than zero.

Next, the existence condition of the model is determined to assess the stability of the resulting system. The existence of the disease-free equilibrium point, denoted as EP_0, represents a state in which no individuals in the population are infected. This disease-free equilibrium exists and is expressed as:

$$E_0: (s_0, v_0, i_0, r_0) = \left(\frac{\mu}{\mu+\alpha}, \frac{\alpha\mu}{(\mu+\alpha)(\gamma_2+\mu)}, 0, \frac{\gamma_2\alpha}{(\mu+\alpha)(\gamma_2+\mu)}\right)$$

$$s_0 + v_0 + i_0 + r_0 = \frac{\mu}{\mu+\alpha} + \frac{\alpha\mu}{(\mu+\alpha)(\gamma_2+\mu)} + 0 + \frac{\gamma_2\alpha}{(\mu+\alpha)(\gamma_2+\mu)}$$

$$= \frac{\mu}{\mu+\alpha} + \frac{\alpha\mu + \gamma_2\alpha}{(\mu+\alpha)(\gamma_2+\mu)}$$

$$= \frac{\mu + \alpha}{\mu+\alpha}$$

$$= 1$$

Since all parameters are greater than zero, all components lie within the interval [0,1], and their sum equals 1, the existence of E_0 is thus confirmed.

Next, to determine the existence of the endemic equilibrium point, the general form of the following quadratic equation is used:

$$A_1 i^{*2} + A_2 i^* + A_3(1 - C) = 0$$

With the coefficient defined as $A_1 i^{*2} + A_2 i^* + A_3(1 - C) = 0$

$$A_1 = B_2B_1(\gamma_1 + w + \mu)$$

$$A_2 = (\gamma_1 + w + \mu)(B_2(\mu + \alpha) + B_1(\gamma_2 + \mu) - B_1B_2\mu$$

$$A_3 = (\gamma_1 + w + \mu)(\mu + \alpha)(\gamma_2 + \mu)$$

$$C = \frac{B_1\mu}{(\gamma_1 + w + \mu)(\mu + \alpha)} + \frac{B_2\alpha\mu}{(\gamma_1 + w + \mu)(\mu + \alpha)(\mu + \gamma_2)}$$

The square root formula of $i^* = \frac{-A_2 \pm \sqrt{A_2^2 - 4A_1A_3(1-C)}}{2A_1}$, $i > 0$

The existence of endemic equilibrium conditions is determined based on the value of C.

If $C \leq 1$ then $A_3(1 - C) \geq 0$ means that there is no positive root so there is no endemic equilibrium.

If $C > 1$ then $D = A_2^2 - 4\,A_1A_3(1 - C) > 0$ This means that there is exactly one positive root so that an endemic equilibrium exists.

Once the existence conditions are known, the next step is to conduct a system stability analysis in disease-free conditions to determine whether the equilibrium point is stable or not. By lowering each

function over time, the following system is obtained:

$$f_1 : \frac{\partial s}{\partial t} : \mu - \mu s - \beta_1 si - \alpha s$$

$$f_2 : \frac{\partial v}{\partial t} : \alpha s - \beta_2 vi - \gamma_2 v - \mu v$$

$$f_3 : \frac{\partial i}{\partial t} : \beta_1 si + \beta_2 vi - \gamma_1 i - \omega i - \mu i$$

$$f_4 : \frac{\partial r}{\partial t} : \gamma_2 v + \gamma_1 i - \mu r$$

So that :

$\frac{\partial f_1}{\partial s} : -\mu - i - \alpha$ $\frac{\partial f_2}{\partial s} : \alpha$ $\frac{\partial f_3}{\partial s} : \beta_1 i$

$\frac{\partial f_1}{\partial v} : 0$ $\frac{\partial f_2}{\partial v} : -\beta_2 i - \gamma_2 - \mu$ $\frac{\partial f_3}{\partial v} : \beta_2 i$

$\frac{\partial f_1}{\partial i} : -\beta_1 s$ $\frac{\partial f_2}{\partial i} : -\beta_2 v$ $\frac{\partial f_3}{\partial i} : \beta_1 s + \beta_2 v - \gamma_1 - \omega - \mu$

$\frac{\partial f_1}{\partial r} : 0$ $\frac{\partial f_2}{\partial r} : 0$ $\frac{\partial f_3}{\partial r} : 0$

$\frac{\partial f_4}{\partial s} : 0$

$\frac{\partial f_4}{\partial v} : \gamma_2$

$\frac{\partial f_4}{\partial i} : \gamma_1$

$\frac{\partial f_4}{\partial r} : -\mu$

Thus, the jacobian matrix is obtained :

$$\begin{bmatrix} -\mu - \beta_1 i^* - \alpha & 0 & -\beta_1 s & 0 \\ -\alpha & -\gamma_2 - \mu & -\beta_2 v & 0 \\ 0 & 0 & \beta_1 s + \beta_2 v - \gamma_1 - \omega - \mu & 0 \\ 0 & \gamma_2 & 0 & -\mu \end{bmatrix}$$

Then by subtituting E_0 such that $i = 0$, we obtain :

$$J[E_0] : \begin{bmatrix} -\mu - \alpha & 0 & -\beta_1 s_0 & 0 \\ -\alpha & -\gamma_2 - \mu & -\beta_2 v_0 & 0 \\ 0 & 0 & \beta_1 s_0 + \beta_2 v_0 - \gamma_1 - \omega - \mu & 0 \\ 0 & \gamma_2 & 0 & -\mu \end{bmatrix}$$

Looking for $det\ det\ (J[E_0] - \lambda I) = 0$

$$\begin{bmatrix} -\mu - \alpha - \lambda & 0 & -\beta_1 s_0 & \\ -\alpha & -\gamma_2 - \mu - \lambda & -\beta_2 v_0 & \\ 0 & 0 & \beta_1 s_0 + \beta_2 v_0 - \gamma_1 - \omega - \mu - \lambda & \\ 0 & \gamma_2 & 0 & -\mu \end{bmatrix} = 0$$

Obtained :

$$(-\mu - \alpha - \lambda)(-\mu - \gamma_2 - \lambda)(\beta_1 s_0 + \beta_2 v_0 - \gamma_1 - \omega - \mu - \lambda)(-\mu - \lambda) = 0$$

Thus the value of eigen is obtained :

$$\lambda_1 : -(\mu + \alpha) < 0$$

$$\lambda_2 : -(\mu + \gamma_2) < 0$$

$$\lambda_3 : \beta_1 s_0 + \beta_2 v_0 - \gamma_1 - \omega - \mu$$

$$: -(\gamma_1 + \omega + \mu)\left(1 - \frac{\beta_1 \mu}{(\mu + \alpha)(\gamma_1 + \omega + \mu)} + \frac{\beta_2 \alpha \mu}{(\mu + \alpha)(\gamma_2 - \mu)(\gamma_1 + \omega + \mu)}\right) < 0$$

$$: -(\gamma_1 + \omega + \mu)(1 - R_0) < 0$$

$$\lambda_4 : -\mu < 0$$

All eigen values are negative $\rightarrow E_0$ local asymptotic stability.

Next, a system stability analysis was carried out in endemic conditions to determine the behavior of population dynamics when the disease persists in the system. Based on the results of the evaluation around the endemic equilibrium point, the Jacobian value system from a_{11}, a_{22}, a_{33}. can be changed to,

$$-\mu - \beta_1 i^* s^* - \alpha s^* = 0 \leftrightarrow -\mu - \beta_1 i^* - \alpha = -\frac{\mu}{s^*}$$

$$\alpha s^* - \beta_2 v^* i^* - \gamma_2 v^* - \mu v^* = 0 \leftrightarrow -\mu - \gamma_2 - \beta_2 i^* = -\frac{\alpha s^*}{v^*}$$

$$\beta_1 s^* + \beta_2 v^* - \gamma_1 - \omega - \mu = 0$$

So the Jacobian matrix :

$$J(E^*) = \begin{bmatrix} -\frac{\mu}{s^*} & 0 & -\beta_1 s^* & 0 \\ \alpha & -\frac{\alpha s^*}{v^*} & -\beta_2 v^* & 0 \\ \beta_1 i^* & \beta_2 i^* & 0 & 0 \\ 0 & \gamma^* & \gamma_1 i^* & -\mu \end{bmatrix}$$

Looking for $\det [J(E^*) - \lambda I] = 0$

$$\begin{bmatrix} -\frac{\mu}{s^*} - \lambda & 0 & -\beta_1 s^* & 0 \\ \alpha & -\frac{\alpha s^*}{v^*} & -\beta_2 v^* & 0 \\ \beta_1 i^* & \beta_2 i^* & -\lambda & 0 \\ 0 & \gamma^* & \gamma_1 i^* & -\mu - \lambda \end{bmatrix} = 0$$

$$\lambda^4 - a_0\lambda^3 - a_1\lambda^2 + a_2\lambda + a_3 = 0$$

With :

$$a_0 : \frac{\alpha s^*}{v^*} + \frac{\mu}{s^*} + \mu > 0$$

$$a_2 : \frac{\alpha\mu s^*}{v^*} + \frac{\alpha\mu}{\mu^*} + \frac{\mu^2}{s^*} + is^*\beta_1^2 + iv^*\beta_2^2 > 0$$

$$a_3 : \frac{\alpha {s^*}^2 \beta_1^2}{v^*} + \alpha\beta_2\beta_1 s^* + \mu v^*\beta_2^2 s^* > 0$$

With all $a_j > 0$ due to the model parameters and components s^*, v^*, i are all positive.

The criteria for polynomial of orde 4 : $\lambda^2 - b_1\lambda^3 + b_2\lambda^2 + b_3\lambda + b_2 = 0$ the condition is met if :

1. $b_1 > 0\ , b_2 > 0, b_3 > 0, b_4 > 0$
2. $b_1 b_2 > b_3$
3. $b_1 b_2 b_3 > b_3^2 + b_1^2 b_4$

Where, in the solution $b_1 = a_0, b_2 = a_1, b_3 = a_2, b_4 = a_3$, the conditions are satisfied.

Thus, if $i^* > 0$, which corresponds to $c > 1$ the endemic equilibrium exists. In this case, all coefficient a_j are positive and the criteria for a fourth-order polynomial are fulfilled. Consequently, all eigen values are negative, and z^* is locally asymptotically stable.

Matlab Simulases

Numerical simulation was conducted using MATLAB software to visualize the dynamics of disease transmission based on the SVIR (Susceptible–Vaccinated–Infected–Recovered) model. This model was modified from the study by (Firmansyah & Prihandono, 2024), with several parameter adjustments to produce a stable dynamic pattern.

The simulation was conducted using the initial conditions $S(0) = 0{,}85$, $V(0) = 0{,}05$, $I(0) = 0{,}15$, and $R(0) = 0$. The parameters used in the model include the natural birth and death rate ($\mu = 0.08$), vaccination rate ($\alpha = 0.08$), infection rate of susceptible individuals ($\beta_1 = 0.012$), infection rate of vaccinated individuals ($\beta_2 = 0{,}0005$), recovery rate of infected individuals ($\gamma_1 = 0{,}12$), recovery rate of vaccinated individuals ($\gamma_2 = 0{,}28$), and the rate of immunity loss ($\omega = 0{,}015$). All parameters are expressed in units per day.

Based on the parameters adjusted according to the results of the model analysis, the MATLAB code used to simulate the dynamics of disease transmission is as follows:

```
function dy = vaksinasi(t,y)
    % ===== Model SVIR (Modifikasi) =====
    % Model ini dimodifikasi dari Firmansyah dkk. (2024)
    % untuk menghasilkan pola dinamis berbeda namun tetap stabil.

    miu   = 0.08;    % tingkat kelahiran/kematian alami (modifikasi dari 0.1)
    n     = 1;       % total populasi (dikonversi ke proporsi)
    beta1 = 0.012;   % laju infeksi individu rentan (lebih tinggi sedikit)
    alfa  = 0.08;    % laju vaksinasi (lebih rendah)
    beta2 = 0.0005;  % laju infeksi individu divaksinasi (sedikit lebih tinggi)
    gama2 = 0.28;    % tingkat kesembuhan populasi vaksinasi
    gama1 = 0.12;    % tingkat kesembuhan populasi terinfeksi
    omega = 0.015;   % hilangnya imunitas (lebih kecil dari 0.02)

    % Persamaan diferensial model SVIR
    dy = zeros(4,1);
    dy(1) = miu*n - miu*y(1) - beta1*y(1)*y(3)/n - alfa*y(1);          % dS/dt
    dy(2) = alfa*y(1) - beta2*y(2)*y(3)/n - gama2*y(2) - miu*y(2);     % dV/dt
    dy(3) = beta1*y(1)*y(3)/n + beta2*y(2)*y(3)/n - gama1*y(3) ...
            - omega*y(3) - miu*y(3);                                   % dI/dt
    dy(4) = gama2*y(2) + gama1*y(3) - miu*y(4);                        % dR/dt
end
```

Then an SVIR model simulation is run to get visualization in the form of a graph with the following code :

```
clear; clc; close all

% Rentang waktu & kondisi awal
tspan = linspace(0,50,10000);
y0 = [0.85 0.05 0.15 0];

% Jalankan ODE
[t,y] = ode45(@vaksinasi, tspan, y0);

% Buat figure
figure('Name','Dinamika Model SVIR','NumberTitle','off')

%% ---------- (a) Grafik Dinamika Populasi ----------
subplot(2,2,1)
plot(t,y(:,1),'b','LineWidth',1.5); hold on
plot(t,y(:,2),'Color',[1 0.6 0],'LineWidth',1.5);
plot(t,y(:,3),'r','LineWidth',1.5);
plot(t,y(:,4),'g','LineWidth',1.5);
xlabel('Waktu (Hari)')
ylabel('Proporsi Populasi')
legend('S','V','I','R')
title('(a) Dinamika Populasi')
grid on

%% ---------- (b) Potret Fase S-I ----------
subplot(2,2,2)
S0_values = linspace(0,1,10);
for S0 = S0_values
    y0_temp = [S0 0.05 0.15 0];
    [t_temp,y_temp] = ode45(@vaksinasi,tspan,y0_temp);
    plot(y_temp(:,1), y_temp(:,3), 'LineWidth',1.2, 'DisplayName',['S_0 = ' num2str(S0)]);
    hold on

    idx = 1:300:length(y_temp(:,1))-1;
    quiver(y_temp(idx,1), y_temp(idx,3), ...
        y_temp(idx+1,1)-y_temp(idx,1), y_temp(idx+1,3)-y_temp(idx,3), ...
        0, 'r', 'MaxHeadSize',0.5)
end
xlabel('S(t)')
ylabel('I(t)')
title('(b) Potret Fase S-I')
legend show
grid on
```

```
%% ---------- (c) Potret Fase S-V ----------
subplot(2,2,3)
for S0 = S0_values
    y0_temp = [S0 0.05 0.15 0];
    [t_temp,y_temp] = ode45(@vaksinasi,tspan,y0_temp);
    plot(y_temp(:,1), y_temp(:,2), 'LineWidth',1.2, 'DisplayName',['S_0 = ' num2str(S0)]);
    hold on

    idx = 1:300:length(y_temp(:,1))-1;
    quiver(y_temp(idx,1), y_temp(idx,2), ...
        y_temp(idx+1,1)-y_temp(idx,1), y_temp(idx+1,2)-y_temp(idx,2), ...
        0, 'm', 'MaxHeadSize',0.5)
end
xlabel('S(t)')
ylabel('V(t)')
title('(c) Potret Fase S-V')
legend show
grid on

%% ---------- (d) Potret Fase V-I ----------
subplot(2,2,4)
for S0 = S0_values
    y0_temp = [S0 0.05 0.15 0];
    [t_temp,y_temp] = ode45(@vaksinasi,tspan,y0_temp);
    plot(y_temp(:,2), y_temp(:,3), 'LineWidth',1.2, 'DisplayName',['S_0 = ' num2str(S0)]);
    hold on

    idx = 1:300:length(y_temp(:,1))-1;
    quiver(y_temp(idx,2), y_temp(idx,3), ...
        y_temp(idx+1,2)-y_temp(idx,2), y_temp(idx+1,3)-y_temp(idx,3), ...
        0, 'c', 'MaxHeadSize',0.5)
end
xlabel('V(t)')
ylabel('I(t)')
title('(d) Potret Fase V-I')
legend show
grid on
```

And the results of the visualization are obtained as follows :

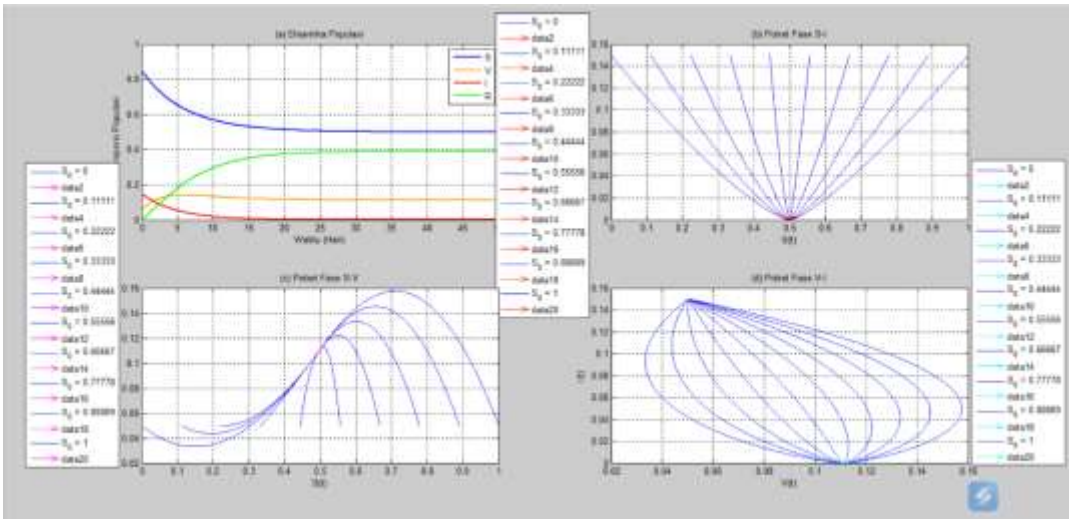

Figure 2 Modified results of SVIR model simulation using MATLAB (source:(Firmansyah & Prihandono, 2024))

Batik Patterns

The batik motif design process in this study is based on the visualization results of the SVIR (Susceptible–Vaccinated–Infected–Recovered) model simulation, which produces graphical images. These graphs display line patterns, curves, and intersections that represent the dynamic

interactions among susceptible, vaccinated, infected, and recovered populations. These visual elements serve as the foundation for developing batik designs that emphasize balance and order.

The initial stage of motif creation involves extracting distinctive shapes from the simulation graphs using screenshots from MATLAB. These patterns are then digitally refined using the Canva graphic design software to aesthetically reconstruct the lines, curves, and surfaces. Each line in the graph is interpreted as a symbol of inter-population relationships, while the intersection points reflect equilibrium or stable interactions within the disease transmission system.

The next stage is the composition of the basic batik pattern, guided by traditional batik aesthetic principles such as symmetry, balance, and repetition. The curves derived from the simulation are transformed into motifs resembling flow or movement, symbolizing the dynamic spread of disease.

The final stage is the refinement of the motif into a complete batik composition ready for visual application. The simulation-based patterns are arranged into a harmonious design while maintaining visual balance. The design process focuses on elements, proportions, and visual equilibrium to achieve a coherent form aligned with traditional batik motifs. Thus, the resulting batik motif not only possesses visual beauty but also carries a profound philosophical meaning about balance, interaction, and harmony in life—as reflected in the dynamics described by the SVIR mathematical model.

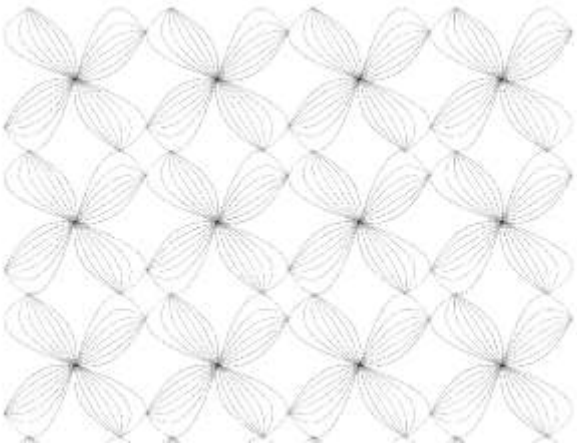

Figure 3 Batik design from SVIR model simulation

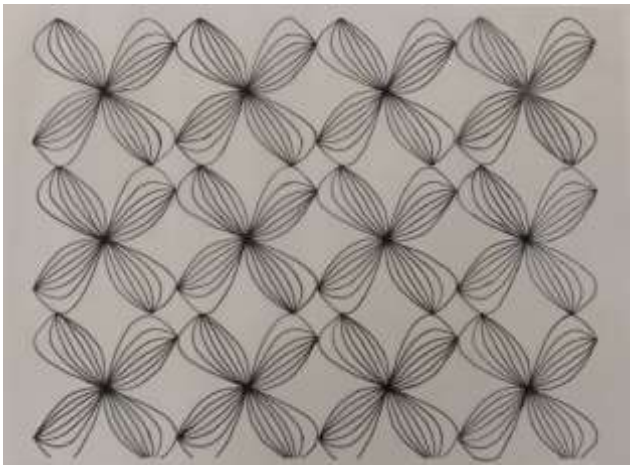

Figure 4 Batik pattern image of the SVIR model simulation on tracing paper

The pattern generated in the image resembles petals or wings arranged in a repetitive and symmetrical manner. From a philosophical perspective, this pattern can be interpreted as a symbol of balance, order, and interconnectedness among the elements of life. Each petal converging toward a central point represents the interrelatedness of various aspects of human existence. The central point symbolizes the origin of life or the source of knowledge, while the radiating lines illustrate development, dissemination, and mutual influence among the elements. The regular repetition of the pattern also reflects the harmony between science and art, affirming that beauty can emerge from scientific order. In the context of batik, this meaning aligns with traditional philosophy, which often emphasizes the balance between humanity, nature, and the divine.

Biologically, the shape of the pattern can be associated with natural structures commonly found in nature, such as the arrangement of flower petals, insect wings, or radial symmetry in microscopic organisms like viruses and cells. This pattern reflects the orderly and repetitive dynamics of biological life, such as growth, cell division, or disease transmission within a population. The central point in the pattern may be likened to the core of life or the origin of spread, while the curved lines extending outward depict biological processes that expand and evolve from a single source in multiple directions. Thus, the pattern symbolizes the continuity of life that perpetually unfolds and develops harmoniously in nature.

Mathematically, the pattern represents the order and symmetry characteristic of periodic functions. Visually, the repeating petal-like shapes can be explained through the concept of a rose curve in polar coordinates, typically expressed by the equations $r = a\sin(n\theta)$ or $r = a\cos(n\theta)$. Each curve illustrates the outcome of trigonometric functions that are periodic and symmetric with respect to the center. In the context of biological mathematical models such as the SVIR model, the central point in the pattern can be interpreted as the equilibrium point of the system, where all population variables are in a stable state. Accordingly, this pattern reflects how mathematical regularity can produce visual forms that are both beautiful and meaningful, highlighting the profound connection between mathematical logic, biological processes, and aesthetic visual expression.

Conclusion

This study shows that the mathematical modeling approach can contribute not only to the fields of science and health but also to the arts and culture. Through the SVIR (Susceptible, Vaccinated, Infected, Recovered) model, an overview of the dynamics of infectious disease spread can be obtained and visualized in the form of graphs. These visualization results are then utilized as a source of inspiration for designing batik patterns.

The process of transforming mathematical data into visual art produces batik patterns that not only possess aesthetic value but also contain scientific meaning. The lines and curves emerging from simulations depict relationships, balance, and interactions among variables in a disease transmission system, which are then translated into harmonious and repetitive visual forms, similar to batik patterns.

Thus, this study proves that the integration of mathematical science and visual arts can produce works that have educational, philosophical, and cultural value. This approach opens new opportunities for the development of modern batik designs based on scientific data, while also enriching the meaning of batik as a cultural heritage capable of adapting to the advancement of knowledge.

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