

Mathematical Modeling of Pneumonia Spread in Toddlers with the Influence of Vaccination in Makassar City and Batik Motifs from the Simulation

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Abstract: Pneumonia remains one of the leading causes of death in children under five years of age in Indonesia, especially in the city of Makassar. This study aims to model the dynamics of pneumonia transmission in toddlers by considering the effect of vaccination as a preventive intervention, using an SEIR (Susceptible–Exposed–Infected Recovered) mathematical model framework. Numerical simulations were conducted to analyze the temporal evolution of the population, with results showing that, without vaccination, the infected population increased sharply before reaching equilibrium. Conversely, the implementation of higher vaccination coverage significantly reduced the peak of infection and accelerated epidemic stabilization, emphasizing the important role of vaccination in controlling the spread of pneumonia. Furthermore, the simulation results were interpreted into batik motifs that adopted layered wave patterns with gradient colors, symbolizing the transition from susceptibility to recovery, and expressing the harmony between science and art.

Keywords: Pneumonia, Vaccination, SEIR Model, Simulation, Batik.

Abbreviations: SEIR: Susceptible-Exposed-Infected-Recovered, R_0 : Basic Reproduction Number

Introduction

Pneumonia is an infectious disease of the lower respiratory tract caused by bacteria, viruses, or fungi, and remains the leading cause of death in children under five years of age. In Indonesia, cases of pneumonia in toddlers are still high, including in the city of Makassar, which is one of the areas with a significant number of pneumonia cases each year. Efforts to combat this disease can be carried out through various strategies, one of which is by increasing vaccination coverage.

Mathematical analysis of the spread of infectious diseases can provide a deeper understanding of the dynamics of transmission and help determine optimal prevention strategies. One approach commonly used in mathematical epidemiology is the SEIR (Susceptible, Exposed, Infected, Recovered) model. This model divides the

population into four compartments according to the individual's health status with regard to the disease. In this study, the SEIR model was developed by incorporating vaccination as a form of protection for vulnerable groups.

Through numerical simulation, the behavior of the disease spread system can be observed over a certain period of time, allowing the effect of vaccination on the dynamics of pneumonia spread to be analyzed. In addition, the simulation results are also interpreted in the form of batik motifs as a mathematical visualization medium that reflects the beauty of the dynamics of disease spread patterns (Madhi et al., 2013).

Materials And Methods

Mathematical modeling aims to describe changes in the number of individuals in each compartment

over time based on realistic assumptions. The total population N is divided into four groups, namely: the number of individuals susceptible to infection ($S_{(t)}$), the number of individuals who have been exposed but are not yet infectious ($E_{(t)}$), the number of individuals who are currently transmitting the disease ($I_{(t)}$) and those who have recovered ($R_{(t)}$), so that $N = S + E + I + R$. This model is formulated in the form of a system of differential equations as follows:

$$\frac{ds}{dt} = \pi(1 - \rho) - \beta si - (\mu + \rho)s,$$

$$\frac{de}{dt} = \beta si - (\gamma + \mu)e,$$

$$\frac{di}{dt} = \gamma e - (\mu + \epsilon)i,$$

$$\frac{dr}{dt} = \rho s + \epsilon i - \mu r$$

Explanation:

π : rate of birth of new individuals per unit time

ρ : proportion of individuals who are immediately immune at birth

β : the rate of disease transmission due to contact between susceptible and infectious individuals

γ : transition rate from exposed to infectious individuals

ϵ : the recovery rate of infected individuals

μ : natural death rate in the population

This model is closed, so that the total population at time t , namely $N_{(t)} = S_{(t)} + E_{(t)} + I_{(t)} + R_{(t)}$, is constant in the long term after scaling. Thus, the variables used in the following analysis are expressed as proportions, namely $s = \frac{S}{N}$, $e = \frac{E}{N}$, $i = \frac{I}{N}$, and $r = \frac{R}{N}$.

Furthermore, equilibrium point analysis aims to determine the conditions of the system when there is no change in the number of individuals in each compartment over time, or in other words, when the system is in a stable state. The equilibrium point is obtained by equating all time derivatives to zero, namely:

$$\frac{ds}{dt} = 0, \quad \frac{de}{dt} = 0, \quad \frac{di}{dt} = 0, \quad \frac{dr}{dt} = 0$$

by solving the above system, two main equilibrium conditions are obtained, namely the disease-free equilibrium point and the endemic equilibrium point.

For the disease-free case, it is assumed that no individuals are exposed or infected, so that $e^* = 0$ and $i^* = 0$. Based on the previous differential system, the disease-free equilibrium point is obtained as follows:

$$E_0 = (s, e, i, r) = \left(\frac{\pi(1 - \rho)}{\mu + \rho}, 0, 0, \frac{\rho s}{\mu} \right)$$

This point represents the condition when the entire population is healthy without any active infection. Meanwhile, for the endemic case, when the disease persists in the population, i.e., $e^* \neq 0$ and $i^* \neq 0$, the endemic equilibrium point is obtained as follows:

$$E_1 = (s^*, e^*, i^*, r^*)$$

with the value of each component depending on model parameters such as $\beta, \gamma, \mu, \epsilon$, and ρ . Analytical solutions for E_1 are generally complex, so the solution is obtained numerically using a computational approach.

To analyze local stability around the equilibrium point, the nonlinear system is linearized using the Jacobian matrix (J), which contains the partial derivatives of each function with respect to each variable. The Jacobian matrix is written as:

$$J = \begin{bmatrix} \frac{\partial f_s}{\partial s} & \frac{\partial f_s}{\partial e} & \frac{\partial f_s}{\partial i} & \frac{\partial f_s}{\partial r} \\ \frac{\partial f_e}{\partial s} & \frac{\partial f_e}{\partial e} & \frac{\partial f_e}{\partial i} & \frac{\partial f_e}{\partial r} \\ \frac{\partial f_i}{\partial s} & \frac{\partial f_i}{\partial e} & \frac{\partial f_i}{\partial i} & \frac{\partial f_i}{\partial r} \\ \frac{\partial f_r}{\partial s} & \frac{\partial f_r}{\partial e} & \frac{\partial f_r}{\partial i} & \frac{\partial f_r}{\partial r} \end{bmatrix}$$

if the Jacobian matrix is evaluated at the disease-free equilibrium point E_0 , then we obtain:

$$J_{E_0} = \begin{bmatrix} -(\mu + \rho) & 0 & -\beta s_0 & 0 \\ 0 & -(\gamma + \mu) & \beta s_0 & 0 \\ 0 & \gamma & -(\mu + \epsilon) & 0 \\ \rho & 0 & \epsilon & -\mu \end{bmatrix}$$

with $s_0 = \frac{\pi(1-\rho)}{\mu+\rho}$

The stability of the system is determined by calculating the eigenvalues of the Jacobian matrix, which are obtained by solving the determinant:

$$\det(J_{E_0} - \lambda I) = 0$$

This equation produces a fourth-order characteristic polynomial that can be analyzed using the Routh–Hurwitz criterion. Based on this criterion, the disease-free equilibrium point E_0 will be asymptotically stable if all real parts of the eigenvalues are negative, which occurs when:

$$R_0 < 1$$

Conversely, if there are eigenvalues with positive real parts, the system becomes unstable, meaning that the disease will spread and the population will move towards an endemic state.

The basic reproduction number (R_0) is an important parameter that describes the average number of new individuals infected by one infectious individual in a fully susceptible population. Its value can be obtained from the ratio between the rate of new infections and the rate of recovery or elimination of infection (Side et al., 2021). Based on the calculation results, it is obtained that:

$$R_0 = \frac{\mu\pi\beta\gamma}{\mu^4 + \mu^3(\rho + \gamma + \epsilon) + \mu^2(\rho\gamma + \rho\epsilon + \gamma\epsilon) + \mu\rho\gamma\epsilon + \mu\pi\beta\rho\gamma}$$

if $R_0 < 1$, then the disease cannot persist in the population, so the system will move toward a disease-free state. However, if $R_0 > 1$, then the disease will persist and the system will reach an endemic equilibrium state.

The analysis of the endemic equilibrium point $E_1 = (s^*, e^*, i^*, r^*)$ is performed in a similar manner, namely by substituting the equilibrium values into the Jacobian matrix. Based on the Routh–Hurwitz criterion, it is obtained that E_1 will

be asymptotically stable if $R_0 > 1$. This indicates that the disease will persist in the population when the transmission rate is high enough to maintain continuous infection, even though interventions such as vaccination have been implemented.

Results And Discussion

Disease Dynamics: Comparison of Control Scenarios

After the analysis of the Endemic Equilibrium Point E_1 is complete, the next step is to perform a numerical simulation to verify the analytical results of stability and test the effect of vaccination intervention (ρ). This simulation aims to visualize the temporal evolution of each population compartment and concretely determine the minimum vaccination rate required to suppress the Basic Reproduction Number (R_0) below one ($R_0 < 1$), thereby eliminating the disease from the population.

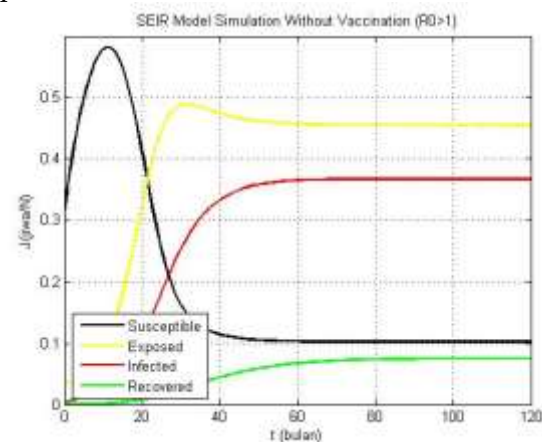


Figure 1. SEIR Model Simulation Without Vaccination ($R_0 > 1$)

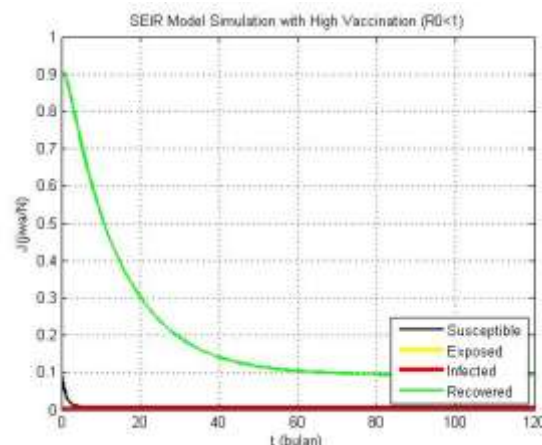


Figure 2. SEIR Model Simulation with High Vaccination ($R_0 < 1$)

The SEIR model simulation shows a clear contrast in the impact of vaccination interventions on disease dynamics. Figure 1, which represents the scenario without vaccination ($\rho = 0\%$), produces $R_0 = 8,756$, indicating that the disease is endemic ($R_0 > 1$). Visually, the infected curve (red) spikes sharply and then settles at a constant value above zero, confirming that the disease remains in the population. In contrast, Figure 2, representing the high vaccination scenario ($\rho = 90\%$ dengan $R = 90\%$), produces $R_0 = 0,274$, which is less than 1 ($R_0 < 1$). In this scenario, the infected and detected curves rapidly decline toward zero, while the recovered curve (green) dominates the population, visualizing the success of the intervention in stabilizing the Disease-Free Equilibrium Point (E_0) and eliminating the disease. Thus, this simulation comparison demonstrates that vaccination plays a crucial role in transforming disease dynamics from an endemic state to an elimination state.

Visualization of Endemic Dynamics: The Batik Motif

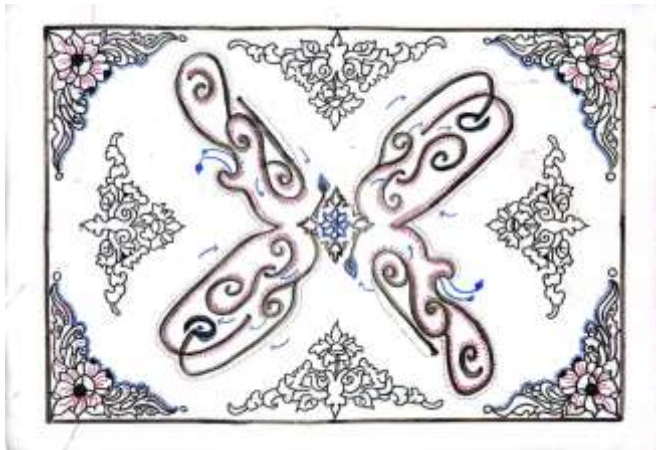


Figure 3. Batik Motif of Pneumonia Endemic Dynamics (SEIR Model)

Interpretation of the Batik Motif

1. Philosophical Meaning

This motif expresses the harmony between science and art:

- Dynamics (Waves and Flows): Curved patterns and flowing lines indicate continuous movement and change in society due to disease.
- Traditional Balance: The use of radial patterns (similar to *Ceplok* or *Kawung*) with floral ornaments as the center (*Ceplok*) and edges gives

an impression of order and balance, even though there is chaotic dynamics within. This reflects that despite the threat of disease, society strives to achieve a balanced and sustainable rhythm.

- Warning: This motif can serve as a reminder (philosophy) of the dangers of disease that remain when preventive measures (vaccination) are neglected, according to the simulation results. $R_0 > 1$.

2. Biological/Epidemiological Meaning

This motif directly represents the phenomenon of the spread of pneumonia among infants in a population:

- Curved Oval Pattern: The main silhouette of the motif symbolizes a towering curve, representing the spike in the number of people infected (I) and detected (E).
- Arrow Direction and Colored Lines: Illustrate the transmission flow and individual disease progression.
- The colors (black, blue, and red) symbolize the transition from susceptibility (*Susceptible*) and detection (*Exposed*) to infection (*Infected*) and recovery (*Recovered*), and the arrows indicate the movement from one compartment to another ($S \rightarrow E \rightarrow I \rightarrow R$).
- Dot and Triangle Ornaments: Can be interpreted as individuals in the population, either newborns (birth rate μ) or those remaining after death (death rate μ).

3. Mathematical Meaning

This motif is a graphical visualization of the solution to the SEIR model's system of differential equations:

- Repetition Pattern ('X' Radial): Symbolizes the time function of the population proportion variables $s_{(t)}$, $e_{(t)}$, $i_{(t)}$, and $r_{(t)}$ over time (t -axis on the simulation graph).
- Flat Curve at the End: The end of the oval pattern that tends to flatten at the end of the simulation time indicates the achievement of the Endemic Equilibrium Point (E_1).
- R_0 : Since this pattern is derived from a simulation without vaccination, it visualizes the condition of $R_0 > 1$, where the disease does not

disappear, and the infected population curve reaches a constant value above zero.

Conclusions

SEIR mathematical modeling of pneumonia spread in toddlers with the influence of vaccination shows that the fate of the epidemic is determined by the Basic Reproduction Number (R_0). Simulation without vaccination intervention results in $R_0 > 1$, which means that the disease is endemic and produces a high spike in infection cases. $R_0 < 1$ This dynamic phenomenon is translated into batik motifs through soaring curved oval patterns, visualizing the peak of an uncontrolled epidemic. Conversely, with vaccination interventions of 50% to 90%, R_0 is successfully achieved, which mathematically means that the disease will disappear from the population. This finding underscores the crucial role of vaccination, with a minimum proportion of 21% to 35% recommended for disease elimination. Thus, the batik motif serves

as an educational medium, blending science with art to tell the story of the pneumonia epidemiology in Makassar City and the importance of achieving balance through vaccination.

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

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