MATHEMATICAL MODELING OF THE SPREAD OF DENGUE HEMORRHAGIC FEVER WITH LARVICIDE AS INTERVENTION PARAMETER

(Case Study: West Kalimantan)

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FINAL YEAR PROJECT

DEPARTMENT OF MATHEMATICS
FACULTY OF MATHEMATICS AND NATURAL SCIENCES
UNIVERSITAS TANJUNGPURA
PONTIANAK
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Final year project
as one of the requirements to obtain a degree
in Bachelor of Mathematics at the Department of Mathematics

DEPARTMENT OF MATHEMATICS
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Mita Ekaristi

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Pemodelan Matematika Penyebaran Penyakit Demam Berdarah Dengue dengan Larvasida sebagai Parameter Intervensi (Studi Kasus: Kalimantan Barat)

Abstrak

Demam Berdarah Dengue (DBD) merupakan penyakit menular yang disebabkan oleh virus dengue dan ditularkan melalui gigitan nyamuk *Aedes aegypti*. Penyakit ini menjadi masalah kesehatan masyarakat di daerah tropis, termasuk Kalimantan Barat. Penggunaan larvasida telah menjadi salah satu strategi pengendalian vektor untuk menekan populasi nyamuk pada fase akuatik, sehingga dapat mengurangi penyebaran penyakit. Penelitian ini bertujuan untuk memodelkan penyebaran penyakit DBD dengan menggunakan larvasida sebagai parameter intervensi. Model yang digunakan dalam penelitian ini adalah model SIR-ASI yang mencakup populasi manusia dan vektor nyamuk. Metode analisis dilakukan dengan menentukan titik ekuilibrium, menghitung bilangan reproduksi dasar (R_0) menggunakan metode *Next Generation Matrix*, serta melakukan analisis kestabilan menggunakan matriks Jacobian. Hasil penelitian menunjukkan bahwa sistem memiliki dua titik ekuilibrium, yaitu titik ekuilibrium bebas penyakit dan endemik penyakit. Jika $R_0 < 1$, penyakit akan menghilang dari populasi, sedangkan jika $R_0 > 1$ penyakit akan tetap ada atau menyebar lebih luas. Hasil simulasi numerik menunjukkan bahwa intervensi larvasida (u) dapat menurunkan R_0 secara signifikan. Pada penelitian ini, data yang digunakan adalah data DBD di Kalimantan Barat pada tahun 2023. Dengan parameter simulasi yang digunakan, penerapan larvasida maksimal $(u = 1)$ mengurangi R_0 sebesar 30% dibandingkan tanpa intervensi $(u = 0)$, artinya dari setiap kelompok orang yang sehat, kasus DBD turun dari 100 menjadi 70 jika menerapkan larvasida maksimal. Berdasarkan hasil tersebut, dapat disimpulkan bahwa penggunaan larvasida secara optimal mampu menekan laju penyebaran DBD melalui pengurangan populasi vektor pada fase akuatik. Dengan demikian, intervensi larvasida terbukti efektif sebagai strategi pengendalian vektor untuk menurunkan transmisi DBD di wilayah endemik seperti Kalimantan Barat.

Kata kunci: Model SIR-ASI, Bilangan Reproduksi Dasar, *Aedes aegypti*, Matriks Generasi Berikutnya

Mathematical Modeling of the Spread of Dengue Hemorrhagic Fever with Larvicide as Intervention Parameter (Case Study: West Kalimantan)

Abstract

Dengue Hemorrhagic Fever (DHF) is an infectious disease caused by the dengue virus and transmitted through the bite of Aedes aegypti mosquitoes. This disease is a public health concern in tropical regions, including West Kalimantan. The use of larvicides has been one of the vector control strategies to suppress mosquito populations in the aquatic phase, thereby reducing disease transmission. This study aims to model the spread of DHF using larvicides as an intervention parameter. The model used in this research is the SIR-ASI model, which incorporates human and mosquito vector populations. The analysis method involves determining equilibrium points, calculating the basic reproduction number (R_0) using the Next Generation Matrix method, and conducting stability analysis using the Jacobian matrix. The results show that the system has two equilibrium points: the disease-free equilibrium and the endemic equilibrium. If $R_0 < 1$, the disease will disappear from the population, whereas if $R_0 > 1$, the disease persists or spreads further. Numerical simulations demonstrate that larvicide intervention (u) can significantly reduce R_0. This study uses DHF data from West Kalimantan in 2023. With the applied simulation parameters, the maximum larvicide application $(u = 1)$ reduces R_0 by 30% compared to no intervention $(u = 0)$. This means that for every group of healthy individuals, the number of DHF cases decreases from 100 to 70 when maximum larvicide is applied. Based on these findings, it can be concluded that optimal larvicide use can suppress the spread of DHF by reducing the vector population in the aquatic phase. Thus, larvicide intervention proves effective as a vector control strategy to lower DHF transmission in endemic regions such as West Kalimantan.

Keywords: *SIR-ASI Model, Basic Reproduction Number, Aedes aegypti, Next Generation Matrix*

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In conclusion, I sincerely hope that my final year project can contribute meaningfully to the understanding of Dengue Hemorrhagic Fever and the role of larvicides as an intervention strategy. My goal is for this work to serve as a valuable resource for those interested in public health and mathematical modeling, as we strive to make a positive impact in our communities.

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Pontianak, June 2025

Mita Ekaristi

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LIST OF SYMBOLS

$\frac{dx_n}{dt}$	:	derivative of the function x_n to t
t	:	time
$\boldsymbol{x}$	:	eigenvector
L	:	eigenvalue of the Jacobian matrix ($\boldsymbol{J}$)
$\boldsymbol{J}$	:	Jacobian matrix
$\boldsymbol{I}$	:	identity matrix
$\dot{x}$	:	the rate of change of variable x over time
$\bar{x}$	:	equilibrium point
$\frac{\partial f_m}{\partial x_n}$	:	partial derivative of the function f_m against the variable x_n
R_0	:	basic reproduction number
$\mathcal{F}_i$	:	rate of new infections
$\mathcal{V}_i$	:	transition rate
$\frac{dS_h}{dt}$	:	the rate of change in human subpopulations is susceptible to time t (people per day)
$\frac{dI_h}{dt}$	:	the rate of change in human subpopulations is infected to time t (people per day)
$\frac{dR_h}{dt}$	:	the rate of change in human subpopulations is recovered to time t (people per day)
$\frac{dA_v}{dt}$	:	rate of change in the subpopulation of mosquitoes in the aquatic phase over time t (individuals per day)
$\frac{dS_v}{dt}$	:	rate of change in the subpopulation of susceptible mosquitoes over time t (individuals per day)
$\frac{dI_v}{dt}$	:	rate of change in the subpopulation of infected mosquitoes over time t (individuals per day)
N_h	:	total human population in West Kalimantan (people)
N_v	:	total mosquito population (mosquitoes)
S_h	:	susceptible human subpopulation (people)

I_h : infected human subpopulation (people)

R_h : recovered human subpopulation (people)

A_v : subpopulation of mosquitoes in the aquatic phase (individual/larvae)

S_v : subpopulation of susceptible mosquitoes (individuals/mosquitoes)

I_v : subpopulation of infected mosquitoes (individuals/mosquitoes)

A_h : human birth rate per capita (people per day)

b : average number of mosquito bites against humans (number of bites per mosquito per day)

β_h : average of successful transmission in humans (individuals per mosquito as many days)

β_v : average of successful transmission to mosquitoes (per mosquito as many individuals and as many days)

μ_h : human death rate (per day)

μ_v : mosquito death rate (per day)

μ_A : larvae death rate (larvae per day)

δ_h : the rate of change from R_h to S_h (per day)

γ_h : human recovery rate (per day)

ϕ : average number of eggs produced by a female mosquito (number of eggs per each spawning)

η_v : transition rate from A_v to S_v (per day)

u : larvae mortality rate due to larvicide (abate) (control/intervention)

CHAPTER I
INTRODUCTION

1.1 Research Background

Dengue hemorrhagic fever (DHF) is a viral infection that spreads from mosquitoes to humans. This disease is more common in tropical and subtropical climates. Dengue cases have increased dramatically worldwide in recent decades, with cases reported to the World Health Organization (WHO) increasing from 505,430 cases in 2000 to 5.2 million in 2019. The highest number of dengue cases was recorded in 2023, affecting more than 80 countries in all WHO regions. Since the beginning of 2023, transmission has continued, coupled with an unexpected surge in dengue cases, resulting in record highs of more than 6.5 million cases and more than 7,300 dengue-related deaths reported.

Indonesia is a dengue endemic area and experiences an epidemic once every 4-5 years, with a peak of recurrent epidemics every 9-10 years (Kaligis et al., 2023). The first case of dengue was reported in Surabaya in 1968, with 58 patients, and 24 of them died (41.3%). Dengue disease then spread throughout Indonesia with a total of 158,912 cases in 2009. According to a report by the Indonesian Ministry of Health, all provinces in Indonesia are currently infected with this disease. Diseases with an incidence of more than 10 per 100,000 population, among others, are the provinces of West Sumatra, Riau, Jambi, South Sumatra, DKI, West Java, Central Java, East Java, West Kalimantan, South Kalimantan, and East Nusa Tenggara. Mortality rate (Case Fatality Rate-CFR) occurred in 1968 (41.3%), then in 2009 decreased to 0.89%, but the number increased from 24 in 1968 to 1,420 in 2009 (Ratna Rosita & Jane Soepardi, 2010). In West Kalimantan in particular, from 2019 to 2021, there was a decrease in dengue cases, although for CFR, the movement went up and down. Successively starting in 2019, there were 2,798 cases (CFR: 0.8%), in 2020 there were 784 cases (CFR: 0.5%), in 2021 there were 664 cases (CFR: 0.9%), and in 2022 there were 1394 cases (CFR: 1.1%). However, in 2023, there was a significant increase in cases compared to the previous year, namely 9,006 cases (CFR: 1.1%) (Dinas Kesehatan Provinsi Kalimantan Barat, 2023b)

Dengue epidemics are influenced by the environment with a lot of standing water or containers, which is a breeding ground for mosquitoes Aedes aegypti and Aedes albopictus, which a vectors of dengue transmission (Srifati, 2020). According to Dinas Kesehatan Provinsi Kalimantan Barat (2023a) the rainy season can increase mosquito populations, Aedes aegypti, because the puddles that occur when it rains become a breeding ground for these mosquitoes. Even though in the dry season waterlogging is reduced, water reservoirs that are not properly covered can still be a breeding ground for mosquitoes, Aedes, which allows dengue cases to persist. Due to the complexity of dengue and dengue epidemiology, it is necessary to prevent dengue cases, namely by controlling mosquitoes, which are the main vectors of dengue disease. Eradication of dengue vectors for adult mosquitoes can be carried out by spraying the home environment with insecticides, as well as the use of larvicides using abate to control dengue vectors in the form of larvae (Handiny et al., 2020).

To understand more about the spread of dengue and evaluate interventions, the SIR-ASI mathematical model (Susceptible-Infected-Recovered-Aquatic-Susceptible-Infected) was used. This model describes the dynamics of disease through human-mosquito interaction, taking into account the aquatic phases of vectors (eggs, larvae, pupae). The SIR-ASI model was chosen because it can model complex interactions between human and mosquito populations, allows evaluation of the impact of larvicide interventions on the aquatic phase to reduce adult mosquitoes, is flexible for modifications such as eliminating vaccination subpopulations, and provides predictions based on nonlinear differential equations for control strategies (Binsasi et al., 2021). Larvicides in this context are chemicals used to kill mosquito larvae in the aquatic phase in nesting sites, such as puddles, thereby preventing the development of mosquitoes into adults (Meidiawati et al., 2024). This study modifies the SIR-ASI model from (Bustamam et al., 2018) by eliminating subpopulations vaccinated and related parameters, and focuses on the analysis of the impact of larvicides on the reduction of vector populations. This approach supports the design of effective dengue control strategies in endemic areas such as West Kalimantan.

1.2 Problem Statements

Based on the existing background, the formulation of the problem in this study is how to model the spread of dengue disease and analyze the stability of the mathematical model of the spread of dengue disease in West Kalimantan with larvicide intervention.

1.3 Research Aims

The objectives of this study are as follows.

1. Modeling the spread of dengue disease in West Kalimantan using the SIR-ASI model with larvicide intervention.
2. Determine the equilibrium point of the mathematical model of the spread of dengue disease.
3. Determine the basic reproduction number from a mathematical model of the spread of dengue disease.
4. Analyze the local stability around the equilibrium point of the mathematical model of dengue disease spread.
5. Interpretation of the mathematical model of the spread of dengue disease.

1.4 The Scope of the Study

This study has several limitations to maintain the focus of the research, namely:

1. The model used only included the SIR model for the human population and the ASI model for the Aedes aegypti mosquito population as a vector, without taking into account interactions with other mosquito species.
2. The strategy used is limited to the use of larvicide powder, namely abate powder, without considering other strategies such as fogging or vaccination.

1.5 Literatur Review

This study discusses the analysis of the mathematical model of the spread of dengue disease in West Kalimantan with larvicide. Before analyzing the mathematical model of disease spread, the first thing to do is to understand the

concept of mathematical modeling. Ndii, (2022) explained that mathematical modeling is one of the techniques to represent a complex system in a mathematical model. Mathematical models consist of variables, parameters, and functions that express the relationship between variables and parameters. Lesh (2003) and Werner Blum & Mogens Niss (1991) explain that the problem-solving process in mathematical modeling involves understanding and simplifying problems by understanding information that can be draw conclusions from the problem. It is followed by manipulating problems and developing mathematical models by identifying variables. Then assumptions and model development are prepared, and then interpret or analyze the system and propose new solutions, and verify problems.

Bustamam et al. (2018) researched modelling the spread of dengue and identified intervention strategies that can be used to effectively control dengue disease. The results of this study developed a mathematical model to understand and control the spread of dengue disease by considering various interventions, such as vaccination for adults and infants, the use of insecticides and larvicides, and mechanical control of mosquito populations. The model divides the human and mosquito populations into compartments, including susceptible, infected, and vaccinated individuals, and calculates baseline reproductive rates that are key indicators of potential disease spread. The study found that local stability can be achieved through certain equilibrium points in the model, which are important for determining whether the disease will spread within the population. Through numerical analysis, the study compared the dynamics between infected humans and mosquito populations, showing that the application of appropriate interventions can significantly reduce the number of infected individuals, both in humans and mosquitoes, as well as prevent outbreaks that can transform into endemic diseases.

Agustina & Affandi (2023) are researching the analysis of the SIR-ASI model (Susceptible-Infected-Recovered-Aquatic-Susceptible-Infected) in dengue disease. The purpose of this study is to determine the mathematical model of the spread of dengue disease, reconstruct the model by determining the equilibrium point and basic reproduction number, determine the optimal form of control in dengue

disease, and perform numerical simulations. The result of this study is the formation of the SIR-ASI model for dengue disease. Based on the model formed, two equilibrium points were obtained, namely the disease-free equilibrium point (E_0) and the endemic equilibrium point (E_1). Then, the basic reproduction number (R_0) is obtained through the next generation matrix which is $R_0 = \sqrt{\frac{kB^2\beta_{mh}\beta_{hm}(\varphi\eta_A-\eta_A\mu_m-\mu_A\mu_m)}{\varphi\mu_m^2(\eta_h+\mu_h)}}$

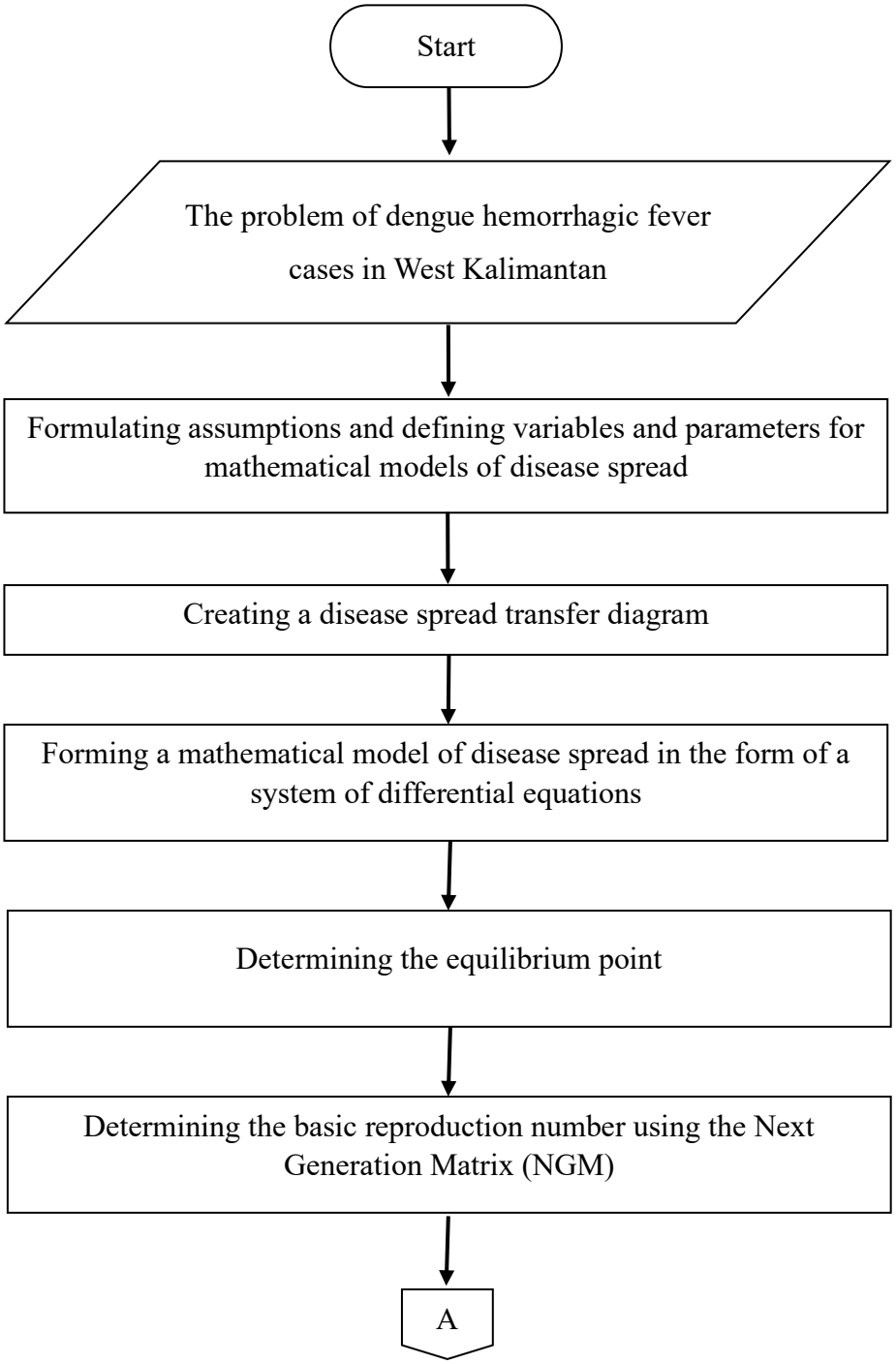
Bano et al. (2022) conducted research on the model of the spread of SIR-type dengue disease with larvicide. Human population groups (Hosted) are sorted into three classes, namely Susceptible, Infected, and Recovered, while mosquito populations (vectors) are also in three classes, namely Aquatic-Susceptible-Infected. Furthermore, from the model, the equilibrium point, the basic reproduction number, the stability analysis of the disease-free equilibrium point, and the simulation were determined. The results of the analysis showed that in the $R_0 < 1$ condition, the equilibrium point without disease was a stable asymptote. The results of the simulation of the effect of larvicide use on the spread of dengue disease also show that the increasing number of larval deaths due to the influence of larvicide use causes the basic reproduction number to decrease or even become very small, so this can help reduce the rate of spread of dengue disease in the population.

1.6 Research Methodology

In this study, the method used is a literature study obtained from books, journals, and other literature related to the problems discussed in this study. This study was conducted to analyse the stability and behaviour of mathematical models in the spread of dengue disease with larvicide. The first thing to do is to compile basic assumptions used in the mathematical modelling of the spread of dengue disease. After that, the variables and parameters to be used in the model are defined. Next, a transfer diagram was created to illustrate the relationship between variables in the spread of the disease. Based on the assumptions and transfer diagrams that have been compiled, the mathematical model is then formed in the form of a system

of non-linear differential equations. After the model was formed, equilibrium point analysis was carried out by evaluating a differential equation system under stationary conditions to determine the disease-free equilibrium point and the endemic equilibrium point. After determining the equilibrium point, this study calculated the basic reproduction number (R_0) using the Next Generation Matrix (NGM) method. This basic reproduction number is the main indicator in determining whether a disease will spread or be controlled in a population.

Furthermore, a system stability analysis was carried out using the Jacobian matrix. The model that has been formed is linearized, and the eigenvalue of the Jacobian matrix is calculated to determine the stability around the equilibrium point. The eigenvalue is determined from the characteristic equation obtained using the Routh-Hurwitz criterion. After the stability analysis was carried out, this study conducted a numerical simulation to solve the differential equation system using the Runge-Kutta Order 4 (RK4) method. This simulation was carried out to analyze the dynamics of disease spread under two conditions, namely, without larvicide intervention $(u = 0)$ and with maximum larvicide intervention $(u = 1)$. The final step in this study was to analyze the impact of larvicide intervention on the dynamics of DHF disease spread through numerical simulation. The analysis was conducted by comparing the trends in changes across all subpopulations, including human populations and mosquitoes in the aquatic phase and adult mosquitoes, under two conditions: maximum larvicide intervention $(u = 1)$ and without intervention $(u = 0)$. The results of this analysis were used to evaluate the effectiveness of larvicides in reducing disease transmission by decreasing vector populations and human cases.


Start
The problem of dengue hemorrhagic fever cases in West Kalimantan
Formulating assumptions and defining variables and parameters for mathematical models of disease spread
Creating a disease spread transfer diagram
Forming a mathematical model of disease spread in the form of a system of differential equations
Determining the equilibrium point
Determining the basic reproduction number using the Next Generation Matrix (NGM)
A

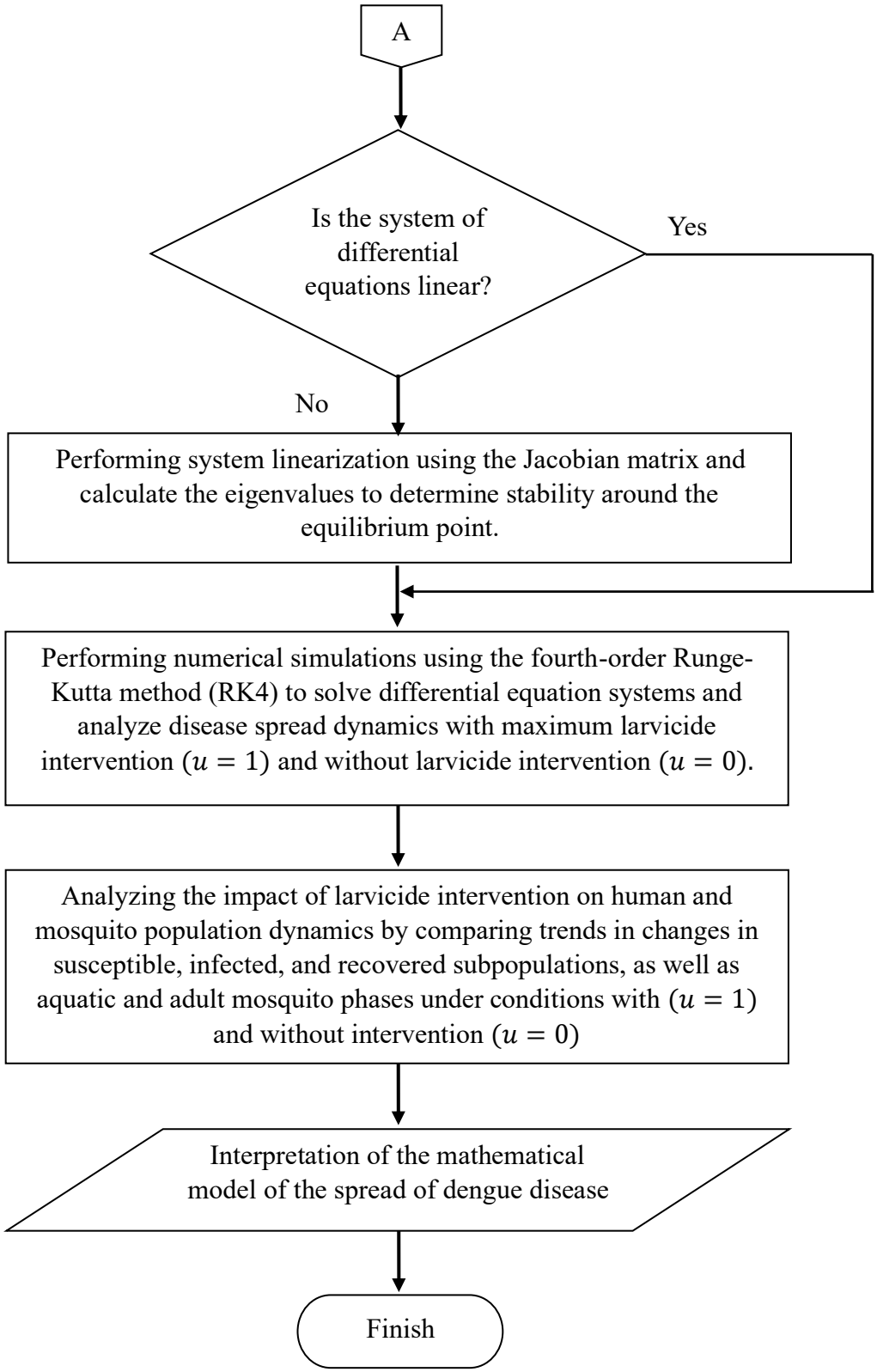


Figure 1.1 Flowchart of Mathematical Modeling of DHF Disease Spread in West Kalimantan with Larvicide