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MATHEMATICS MODEL: DOMINANT FACTORS OF DENGUE HEMORRHAGIC FEVER DISEASE

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Research Paper

***Abstract**: Dengue hemorrhagic fever (DHF) is a disease caused by an arbovirus that enters the human body through the Aedes aegypti or Aedes albopictus mosquito. The spread of dengue fever globally has tended to be higher in the last 50 years, including in Indonesia and Kalimantan, especially the Banjarbaru area. This is a motivation to develop ideas for systematic prevention by involving mathematical models with aquatic and physical factors in the model. Aquatic factors affect water temperature, water pH, COD (Chemical Oxygen Demand), BOD (Biological Oxygen Demand), and DO (Dissolved oxygen). The physical factors include air temperature and humidity. Next, statistical analysis was carried out through correlation and regression analysis involving these factors. This paper aims to determine the most dominant factors in mosquito larvae growth. The water temperature, COD and DO factors were obtained, which were then used in the SIRD-ASI mathematical model in the aquatic compartment. The data collection methodology uses an implicit purposive sampling technique. This method selects samples representing a population by taking primary samples from community locations affected by dengue fever. This preliminary data is essential in forming models, mainly aquatic compartments. Using this model, it is hoped to provide a picture that best suits the existing dengue problem and produce appropriate solutions to prevent the spread of dengue fever by involving aquatic factors.*

***Keywords**: DHF Disease, Aquatic Factors, SIRD-ASI.*

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1. Introduction

Dengue fever is characterized by dengue symptoms such as fever, headache, reddish skin that looks like measles, and muscle and joint pain. Dengue fever can become life-threatening and even cause death in some patients suffering from this disease (Side, Tampa, & Ban, 2018). Data obtained from the 2020 South Kalimantan Province Health Profile (Dinas Kesehatan Provinsi Kalimantan Selatan, 2021). This disease is related to environmental conditions and people's behaviour that is still lacking in PSN (Prevention of Mosquito Nests), which can cause DHF to be endemic in both urban and rural areas (Kementerian Kesehatan, 2019). DHF case data obtained from the Health Service of the South Kalimantan Province from 2015-2019 found that the Banjarbaru area is one of the endemic areas in the Province of South Kalimantan (Sembiring, Setyaningtyas, & Wahyudin, 2017).

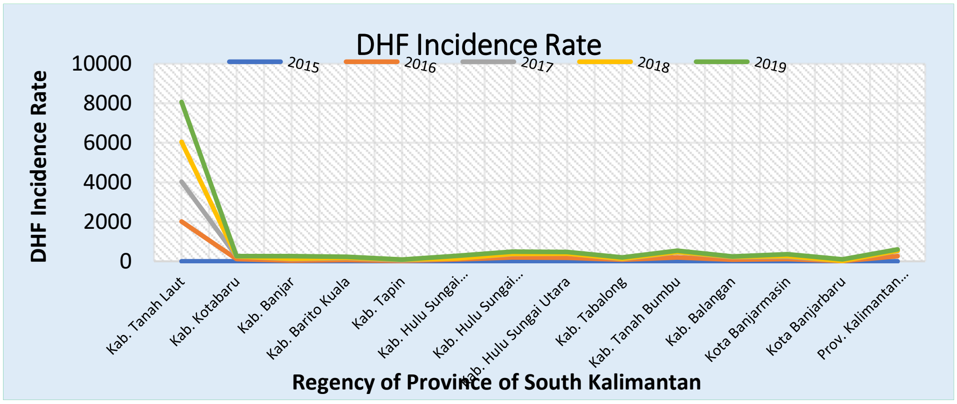

Figure 1.1: DHF Incidence Rate Per 100,000 Population in The Province of South Kalimantan (data.kalselprov.go.id 2021).

At the national level, South Kalimantan Province is also a DHF endemic area, ranking 9th highest Incidence Rate (IR) in Indonesia. With a value of 47.84 per 100,000 residents. Of the 13 urban districts in South Kalimantan Province, Banjarbaru City is one of the areas with high DHF IR for four consecutive years from 2015 to 2019. In 2015, it was 267.07, and in 2016, the highest was 250.26 in South Kalimantan; in 2017, it was 23.2, in third place after Balangan and HSS, while in 2018, it was in second place after HSS Regency with Banjarbaru City DHF IR of 94.5 per 100,000 population. In 2019, it rose to first place with 56.6 per 100,000, with 2,401 cases and 14 DHF deaths. (Kementerian Kesehatan, 2019).

Factors that cause DHF in South Kalimantan, our behaviour and community participation that is still lacking in MNE (Mosquito Nest Eradication) activities (Dinas Kesehatan Provinsi Kalimantan Selatan, 2021). Environmental factors (Kementerian Kesehatan, 2019) are also due to global warming, which can cause climate change; these physical factors have an impact on being one of the causes of the widespread Dengue virus. Climatic factors (Affiandy, Amin, & Ridwan, 2019) like weather, temperature, and humidity also affect parasites and vectors. Rainfall can cause a lot of standing water where mosquitoes breed (AnggrainI & Cahyati, 2017), and humidity affects the life of mosquitoes. Low moisture will shorten the life of mosquitoes. The humidity level of 60% is the lowest limit to allow mosquito life; this is a factor supporting the spread of mosquitoes as a cause of DHF (Kementerian Kesehatan, 2019). Physical and non-physical factors such as density (Kementerian Kesehatan, 2019), climate, rainfall, and humidity influence the incidence of dengue fever (Kementerian Kesehatan, 2019). The temperature factor or air temperature includes environmental factors that directly affect the Aides Aegypti mosquito's life and DHF (Kementerian Kesehatan, 2019).

Efforts to control the Aides Aegypti mosquito continue to be carried out for countermeasures caused by physical and non-physical factors. However, only a few carry out prevention efforts by involving mosquito breeding sites, specifically breeding sites for pre-adult mosquitoes. Aides Aegypti mosquitoes usually live in containers or places filled with clean water. So, observing whether living factors influence pre-adult Aides Aegypti (eggs to larvae) in the water is also necessary. This can be done by following the factors that exist in aquatic such as water temperate and ure, chemical, and chemical Oxygen Demand) the level, which is the dissolved oxygen content in the water, as a parameter to measure water quality. The level of BOD (Biological Oxygen Demand) needs to be observed to determine the amount of dissolved oxygen microorganisms require to decompose organic matter in the water. The level of DO (Dissolved oxygen) also needs to be observed to know the amount of dissolved oxygen in the water that comes from photosynthesis and air absorption. Observation of Aides Aegypti mosquitoes is very important, especially to find out the primary habitat of the larvae, which is the breeding ground for DHF mosquitoes.

Based on the review results of several journals contained in Aguiar et al. (2022) also Affandi, Ahsar K, Suhartono, and Dalle (2022) found that many existing studies involve physical and non-physical factors in efforts to control Aides Aegypti. However, research involving aquatic influences with water content as the primary habitat for Aides Aegypti larvae, specifically COD, BOD and DO factors, still needs to be completed. Existing studies only analyze climate (AnggrainI & Cahyati, 2017), (Affandi et al., 2022), water pH, water temperature, air temperature, and air humidity (Kosnayani & Hidayat, 2018). This study combines the factors COD, BOD, DO (Margarethy, Suryaningtyas, & Asyati, 2017), water pH, water temperature, air temperature, and air humidity, which will be involved in the mathematical model.

Subsequent research related to disease models involves building mathematical models using SIR epidemiological models. (Nuraini, Soewono, & Sidarto, 2007), (Jannah, 2020), (Soleh, Zulpikar, & Desvina, 2019), (Kilicman, 2018) and SEIR (De la Sen, Ibeas, & Alonso-Quesada, 2012), (Syafruddin & Noorani, 2012). The form of the equation uses the SIR-SI model involving the human population as hosts and mosquitoes as vectors (Shim, 2019), using the SIR-SI-SI model involving the human population by administering vaccines (Chanprasopchai, Tang, & Pongsumpun, 2018), (Shim, 2019). Another model used with vaccines and treatments (Affandi, Mahfudz S, Oscar, & Rahim, 2021) is also by (Windawati, Shodiqin, & Aini, 2020), a system of differential equations that represent the epidemiology of dengue hemorrhagic fever (Windawati, Shodiqin, & Aini, 2020). This study discussed the analysis of a mathematical model of the spread of dengue fever with the effect of fogging, which showed a model of the spread of DHF, fixed point, stability analysis, basic reproduction number and simulation results showing the effect of fogging (Windawati, Shodiqin, & Aini, 2020), while in other studies conducted by Side, Tampa, and Ban (2018), discussed the analysis of a mathematical model for the spread of DHF with the Lyapunov function using secondary data from the number of DHF sufferers. Based on the results of Side, Tampa, and Ban (2018), the SIRS mathematical model, fixed point, stability analysis, and primary reproduction number values were obtained (Soleh, Zulpikar, & Desvina, 2019). This paper aims to analyze and model the factors that most influence the COD, BO, DO, water pH, water temperature, air temperature, and air humidity factors involved in mathematical modelling. The analysis of the factors that are most dominant and influential in the model involves statistical analysis. So that the factors involved in the model are only the dominant factors. Furthermore, the model is analyzed by applying mathematical analysis. The reference book published by Kermack and McKendrick (1927) includes primary literature as supporting material. The model introduces the Kermack-McKendrick SIR model flowchart. The model divides the subcompartments into three classes (Susceptible, Infected, and Recovered), known as the SIR model. The emergence of this model greatly influenced the literature related to the spread of diseases that can be detected through mathematical modelling (Pongsumpun, 2008). P. Pongsumpun has extensively studied the Dengue Hemorrhagic Fever model, which began with Fischer D.B.'s writings (Fischer & Halstead, 1970). The development of a DHF mathematical model starts from determining assumptions and parameters and establishing a DHF disease model, with the characteristics of the model involving Aedes aegypti mosquitoes, especially in the aquatic growth phase. The research is organized into five chapters: literature review, methodology, data analysis and discussion, implications, and conclusion.

2. Literature Review

2.1 Mathematical Modeling

It is hoped that mathematical modelling can help with the problem of disease spread DBD so that it is more efficient in dealing with this problem in time and costs. The study of mathematical models began with Kermack and McKendrick, pioneers of epidemiological models. This model can be used to explain, understand and develop strategies related to the spread of infectious diseases by understanding the system's behaviour under various conditions. Models are usually used to simplify complex systems. Mathematical modelling has recently become an attractive tool for understanding infectious disease epidemics (Jannah, 2020). Mathematical modelling became imperative and very influential in understanding the epidemiological dynamics of disease spreading, modelling aspects that can contribute to public health authorities for disease control (Aguiar et al., 2022).

The model from Kermack and McKendrick (1927) divides the human population into three subpopulations: Susceptible, Infected and Recovered. This model is known as the SIR model. Subsequently, this model was modified SEIRP-SEI model was modified SEIRP-SEI by adding the Hospitalized population (Khan, 2021), SIIR-SI model by implementing preventive control, treatment, and insecticide spraying in the model (Jan, Khan, & Gómez-Aguilar, 2020), SIRS model with model simulation SIRS dengue fever can predict the number of dengue fever cases (Sanusi et al., 2021) a lot to solve the spread of disease, including models of dengue fever.

2.2 Dengue Hemorrhagic Fever (Dhf)

H.L. theory Blum (1974) in Green (1986) stated that health is closely related to heredity, environment, behaviour and health services. These four factors have a positive influence on a person's health status. Environmental factors have a significant influence on health status. Environmental factors consist of the physical, biological, and social environments.

According to Chandra and Hamid (2019), the emergence of a disease in a particular community results from interactions between residents and various components in their environment. People interact with food, air, water and insects in everyday life. Suppose various environmental components contain dangerous materials, such as poisonous or microbial materials, that have the potential to cause disease. In that case, humans will fall ill, which can reduce the quality of human resources (Ahmadi, 2005). Usually, at every season transition, especially from the dry season to the rainy season, various health problems arise, including the most common one being Dengue Hemorrhagic Fever.

The dengue fever that occurs indicates how vulnerable the environmental health conditions in society are (Mustafa, 2005). Several factors (Affandi et al., 2022) that can influence diseases transmitted by mosquitoes include air temperature, water temperature, water pH, air humidity, chemical oxygen demand (COD), dissolved oxygen (DO), and biochemical oxygen demand (BOD).

3. Methodology

This paper begins with conducting a literature review in the form of the results of previous papers that can be used as a basis for establishing a Dengue Hemorrhagic Fever (DHF) model (Affandi et al., 2022; Aguiar et al., 2022; Deng et al., 2020), especially the compartmental form and model assumptions that several previous researchers have carried out.

The next stage is data collection using the purposive sampling technique by implicitly selecting samples considered representative of a population by taking samples from locations affected by dengue fever in the Banjarbaru area. Research data related to factors that affect larvae growth, namely air temperature, humidity, water temperature, water pH, COD, BOD, and DO, with primary data collection in several areas around the Banjarbaru area. The next step is to analyze the data using the steps in the statistical method, beginning with determining the existing parameters as a causative factor for Dengue Hemorrhagic Fever (DHF). Correlation and regression methods are also used to obtain several factors that influence the model most. Next, identify the parameters and the formation of a mathematical model.

The following data was collected through direct measurements taken in the field using standard measuring instruments and data measurements obtained at the Laboratory of the Biochemistry and Molecular Department of the Faculty of Medicine. The data, which includes air temperature, humidity, water temperature, water pH, COD, BOD, and DO, can be presented as follows:

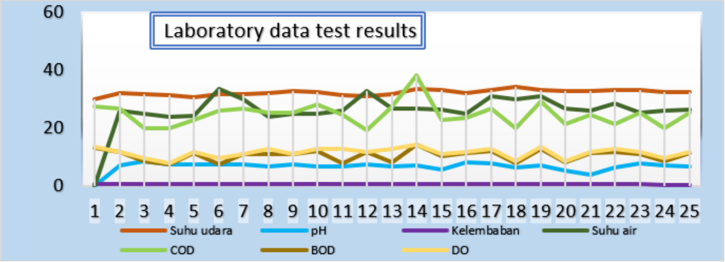

Figure 2: Result Data Primer at Laboratory.

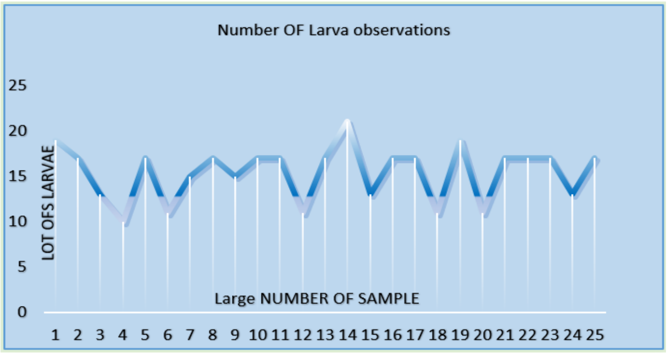

Figure 3: Observation Data on the Number of Larvae.

Then, a Bivariate Correlation Test was carried out from the input data obtained in the form of air temperature, pH, humidity, and water temperature and data measurements at the Laboratory of the Biochemistry and Molecular Department of the Faculty of Medicine in the form of COD, BOD and DO data measurements and their relationship with observational data on the number of larvae.

The purpose of this paper can be achieved by collecting primary data related to water sample data related to COD, BOD, DO, water pH, water temperature, air temperature, and air humidity on the number of larvae using multiple regression. Regression analysis shows that the most dominant factors are COD, DO, and water temperature. These dominant factors are then used to establish an epidemiological mathematical model called SIRD-ASI.

3.1 Data Collection

The initial stage of data collection used in this paper is a data collection technique using Purposive Sampling, which implicitly selects samples considered representative of a population by taking samples at locations where people are affected by DHF. Primary data is in the form of data on the influence of the physical environment, air temperature, and air humidity. Next, take primary data obtained from water sampling around the Banjarbaru area, where the population is affected by D.

3.2 Implementation of data input

The following implementation is data input and compiling the results from primary data. Primary data is obtained by taking water samples and observing the level of water quality by measuring water quality in the form of Oxygen Demand (DO), Chemical Oxygen Demand (COD) and Biological Oxygen Demand (BOD) using the Biochemical and Biomolecular Laboratory services. Humidity, water pH, water temperature, and air temperature are measured using standard instruments. The data analysis method used involves statistics by carrying out the following steps:

1. Initial data collection in primary data (COD, DO, BOD, pH, air temperature, water temperature, and air humidity) about the number of larvae from the water

samples taken. Then, correlation and regression analysis will be performed to determine the factors influencing the number of larvae.
2. Then, carry out a correlation test to measure the level of closeness of the linear relationship between one variable and another by knowing the correlation coefficient, namely the number that shows the direction and strength of the relationship between 2 variables. This direction is expressed in positive and negative relationships. A positive direction occurs if the value of one variable is increased, causing another variable to increase. The negative correlation coefficient means that the value of one variable is increased, causing the value of the other variable to decrease and vice versa. Then, the Bivariate Correlation Test, partial correlation test, and regression test are used to determine the parameters that affect the aquatic factor; the regression analysis aims to obtain a multiple linear regression model used in the regression analysis to be used in the mathematical model formed.
3. Using the most influential factors in forming an epidemiological mathematical model in the form of SIRD-ASI.
4. Determine the parameters affecting the water samples related to COD, BOD, DO, water pH, water temperature, air temperature, and air humidity on the number of larvae using multiple regression.
5. Determine the entry parameters for the aquatic subpopulation based on the influencing parameters to form a SIRD-ASI epidemiological mathematical model.

3.3 Boundary of Research

Data of COD, BOD, DO, water pH, water temperature, air temperature, and air humidity on the number of larvae use primary data taken in the Banjarbaru area, South Kalimantan province. The samples tested were 25 water samples for COD, BOD and DO tests in the ULM Department of Biochemistry and Biomolecular Medicine laboratory. Meanwhile, water pH, water temperature, and air humidity data on the number of larvae were obtained using standard measuring instruments.

4. Results and Discussion

4.1 Data Analysis

From the data in Figure 2 and Figure 3 using multiple regression analysis, the value used is Adjusted R Square = 0.889, which indicates 88.9% of the dependent variable in this paper is the number of larvae present, which has a direct effect on dengue fever; the number of larvae can be explained by the independent variables in this paper, air temperature, air humidity, water temperature, water pH, DO, COD, and BOD. Furthermore, based on the table of Significant Coefficients of the seven coefficients, it can be done with the T-test; it is obtained that the parameters that significantly affect the larvae, which are then used in the Aquatic model compartment, are water temperature, COD and DO.

The temperature factor significantly affects the larvae; this aligns with research conducted (Fitriana & Yudhastuti, 2018; Sufiani, Hayatie, & Djalalluddin, 2021). At high temperatures of around 25-27º, mosquito breeding will increase, resulting in increased cases of DHF. Likewise, in Lahdji., A and Putra. B's research (Lahdji & Putra, 2019) shows that temperatures increasing to 34°C will affect mosquito breeding sites due to warm water temperatures, which can affect the breeding of eggs produced by mosquitoes. In the end, the eggs become larvae quickly.

As for COD and DO, several researchers previously used water pollution parameters (Atima, 2015) and (Kurnianti & Rahman, 2020). This, of course, can affect the life of organisms in the water, including larvae.

4.2 DHF Disease Model Formation Process

The spread of the dengue virus in humans occurs due to the bite of mosquitoes known as vectors that have been infected or mosquitoes that contain the dengue virus in their saliva. The most dominant mosquito in spreading the dengue virus is the female Aedes aegypti mosquito. Apart from the Aedes aegypti mosquito, the Aedes albopictus mosquito can also transmit the dengue virus. So, this mosquito is the primary vector of dengue disease. Without this vector, dengue disease would not spread in humans.

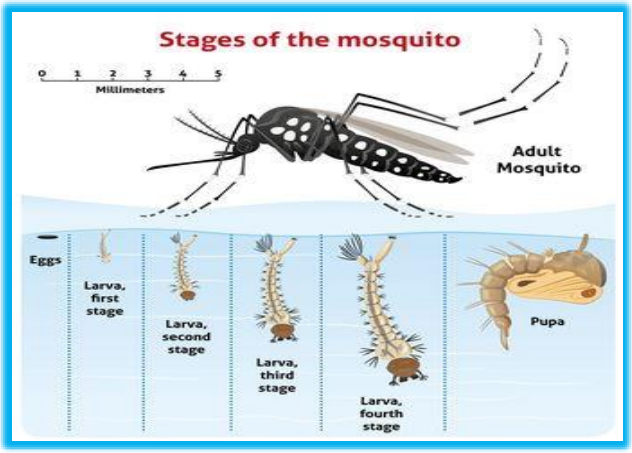

Figure 4: The Life Cycle of the Aedes Aegypti Mosquito, Illustration of the Mosquito Cycle (Kompas.Com/Skola/Image/2022).

The blue dotted line is called the boundary of the aquatic phase (A) indicating that mosquitoes are in the water, this aquatic phase is of concern in the following discussion. Because this phase also affects the growth of mosquitoes before forming adult mosquitoes.

The blue dotted line is called the boundary of the aquatic phase (A), indicating that mosquitoes are in the water; this aquatic phase is of concern in the following discussion. Because this phase also affects the growth of mosquitoes before they form into adult mosquitoes.

The SIRD-ASI mathematical model (susceptible, infected, recovered, death) contains compartment D because some unlucky individuals died, so they were put in compartment D (death). SIRD is found in hosts (human population) and ASI (aquatic, susceptible, and infected) in vectors (mosquitoes).

Based on the Diekmann and Heesterbeek Model, the basis of the known epidemic model is the SIR model. This model divides the population into three sub-populations: susceptible, infectious and removed. From this basic model, the model will develop into models with other variations. The growth process of each sub-population will be modelled by a differential equation so that the growth rate of the sub-population will form a differential system. The mathematical model for the spread of DHF is a mathematical model that describes the dynamics of the spread of DHF between mosquito (vector) and human (host) populations.

3.1.1 Model Assumptions

Vulnerability Before explaining the mathematical model of SIR (susceptible, infected, and recovered) on the host (human population) and ASI (aquatic, susceptible, and infected) on the vector (mosquito) DHF epidemiology by paying attention to the aquatic phase in the Aedes aegypti mosquito, several assumptions must first be stated. Used in the model are as follows:

1. Birth rates in human and mosquito populations are constant.
2. All parameters used in this model are positive constants.
3. The human population is homogeneous, meaning every human has the same opportunity to be infected with DHF.
4. All births to the human population are healthy populations.
5. The model reviews one serotype of the Aedes aegypti mosquito virus.
6. Infected mosquitoes bite healthy humans, which will result in infected humans, so if a healthy mosquito bites an infected human, it will cause mosquitoes to become infected.
7. Each human subpopulation has the same natural mortality rate. Likewise, with mosquitoes, each subpopulation has the same natural death rate.
8. Every mosquito exposed that passes the incubation period becomes an individual infected with the dengue virus so that it enters the infected subpopulation. Likewise, with humans, every exposed individual who passes the incubation period becomes an infected human individual so that he enters the infected subpopulation.
9. Mosquito eggs come from Susceptible Mosquitoes, and the number of infected mosquitoes is α.

The parameters used in the Figure 4 model are stated in Table 1.

Table 1: Parameters In The SIRD-ASI Model.

arameters	Description
τ	Human birth rate per time.
d	Human natural death rate.
m	Mosquito natural death rate.
β	Average bite rate per mosquito per person.
α_v	Possible transmission from infected humans to susceptible mosquitoes.
α_i	Possible transmission from infected mosquitoes to susceptible humans.
ω	The rate of human death due to dengue disease.
y	The recovery rate of humans infected with dengue fever.
θ	The rate of mosquito growth rate from the aquatic process to become Susceptible is influenced by factors θ1, θ2 and θ3.
θ1	The effect of COD on the growth of mosquitoes from the aquatic process to become Susceptible.
θ2	Effect of DO on the growth of mosquitoes from the aquatic process to Susceptible.
θ3	Effect of water temperature on the growth of mosquitoes from the aquatic process to become Susceptible.
α	Mosquito eggs come from Susceptible Mosquitoes and infected mosquitoes.

The variables in the model used in Figure 4 model are stated in Table 2.

Table 2: Variable Definitions in Models.

Variable	Definitions
Si(t)	Number of Individuals in the human subpopulation.
Ii(t)	Healthy and Susceptible at t.
Ri(t)	Number of Individuals in the subpopulation.
Di(t)	human infected / Infected at time t.
Av(t)	Number of individuals in the human subpopulation who recovered from the disease at the time t.
Sv(t)	Number of Individuals in the subpopulation.
Iv(t)	People who died at the time t.

From the assumptions above, an epidemiological model of DHF is derived by taking into account the aquatic phase of the Aedes aegypti mosquito as follows:

For example, N_i is the total human population divided into three sub-populations: the Susceptible S_h sub-population, the Infected I_h sub-population, and the Rh-Recovered human sub-population. The Nm mosquito population was divided into three sub-populations, namely, the aquatic phase sub-population (A_m), the susceptible mosquito sub-population (S_m), and the infected mosquito sub-population (I_m). Schematically, the pattern of dengue spread between hosts (humans) and vectors (mosquitoes).

Based on the grouping above, it can be obtained that the total human population at time t is the sum of the Susceptible, Infectious, Recovered, and Death subpopulations at time t. If the human population at time t is denoted by $N_i(t)$ and the mosquito population is $N_v(t)$, then mathematically, $N_i(t)$ and $N_v(t)$ can be written as follows.

$$Ni(t)=Si(t) + Ii(t) + Ri(t) + Di(t) \text{ and}$$
$$Nv(t)=Av(t) + Sv(t) + Iv(t)$$

Forming a mathematical model for the spread of Dengue Hemorrhagic Fever (DHF) considers two populations: humans as hosts and mosquitoes as vectors. The SIRD-ASI model is an epidemic model for the spread of infectious diseases with the aquatic class in mosquitoes. This model is a development of the SIR model. However, the DHF disease model was developed into a SIRD-ASI model, with four courses in the human population, namely Susceptible (Si(t)), Infectious (Ii(t)), Recovered Ri(t), and Death (Di). Susceptible Si(t) represents the number of individuals who are healthy but susceptible to infection with the DHF virus in the sub-population at time t. Infectious Ii(t) represents the number of individuals in the infected human subpopulation at time t. Recovered Ri(t) means the number of individuals in the human subpopulation who recovered from the disease/recovered at time t. Death (Di) represents the number of individuals in the human subpopulation who died at time t. Some unlucky individuals would die in the process, so they were put in the Di compartment.

Meanwhile, the mosquito population consists of three classes, namely Aquatic Av(t), representing the number of individuals in the mosquito subpopulation in the Aquatic phase at time t. Susceptible Sv(t) states the number of individuals in the Healthy and Susceptible mosquito subpopulation at time t, and infectious (Iv) denotes the number of individuals in the infected mosquito subpopulation at time t.

The SIRD-ASI model is an epidemic model for the spread of infectious diseases with the aquatic class in mosquitoes. This model is called SIRD-ASI and is formed using a system of nonlinear differential equations describing how human and mosquito populations change at the time. Creating a mathematical model for this disease can be explained based on the DHF disease distribution model diagram given in Figure 5. This diagram is formed based on assumptions 1 to 9, the parameters in Table 2, and the variables in Table 3 above. So, based on the assumptions, variables, and parameters described, the process of establishing a DHF SIRD-ASI disease model.

4.2.2 Healthy and Susceptible (Si) Human Subpopulation

Changes in the number of healthy and susceptible human subpopulations over time will increase due to new individuals in the form of births with a birth rate of τi, according to assumption 1. Then, based on assumption 7, changes in the number of susceptible human subpopulations will decrease due to deaths with a natural mortality rate of dSi and the transfer rate to the infected subpopulation based on the assumption that six susceptible human subpopulations will fall due to transmission of the virus through the bite of a virus-infected mosquito to humans so that the human individual will move to the infected subpopulation. Based on this, the changes in the number of healthy human subpopulations classified as susceptible at time t are:

$$\frac{dS_i}{dt} = \tau_i - \beta \frac{\alpha_i S_i I_v}{N_i} - dS_i \qquad (4.1)$$

4.2.3 Infected Human Subpopulation (Ii)

The number of infected human subpopulations will increase because there are healthy human individuals who turn into infected human individuals based on the assumption of 6 $\beta \frac{\alpha_i S_i I_v}{N_i}$ due to transmission of the virus through the bite of a virus-infected mosquito to humans so that the human individual will move to the infected subpopulation. This sub-population will decrease if there are recoveries of yIi. Then, the Infected subpopulation will also reduce due to individuals who die according to assumption seven by ω. Based on this, the changes in the number of infected human subpopulations that can infect over time are:

$$\frac{dI_i}{dt} = \beta \frac{\alpha_i S_i I_v}{N_i} - \omega I_i - yI_i \qquad (4.2)$$

4.2.4 Recovered Human Subpopulation (Ri)

Changes in the number of recovered human subpopulations over time will increase because there are individuals from the Infected class who recover yIi with the individual's natural recovery rate; this is by assumption 8. The number of recovered subpopulations also experiences a reduction, namely due to individuals who die naturally by dRi; this refers to assumption 7. Thus, the change in the number of the Recovered subpopulation over time is:

$$\frac{dR_i}{dt} = \mathrm{yIi} - dR_i \qquad (4.3)$$

4.2.5 Human Subpopulation Death (Di)

Changes in the number of death subpopulations over time will increase because there are infected individuals who die as DHF patients, or in other words, these individuals move into the death class by ωIi, according to assumption 7. Based on this, the change in the number of death subpopulations over time is:

$$\frac{dD_i}{dt} = \omega \mathrm{Ii} \qquad (4.4)$$

4.2.6 Aquatic Mosquito Subpopulation (Av)

Changes in the number of mosquito subpopulations in the aquatic phase increase with the influence of the natural birth factor of α, and there is a reduction in the growth rate of mosquitoes of θ based on assumption 1, which is affected by growth directly proportional to COD (θ1) and DO (θ2) and inversely proportional to there is the influence of water temperature (θ3), and will decrease due to death with a natural mortality rate according to assumption 7 of mAv So that Equation (3.5) of the Aquatic Mosquito subpopulation can be defined as follows:

$$\frac{dA_v}{dt} = \alpha - (1+\theta_1)(1+\theta_2)(1-\theta_3)\theta A_v - mA_v \qquad (4.5)$$

4.2.7 Healthy and Susceptible Mosquito Subpopulation (Sv)

Changes in the number of mosquito subpopulations that are healthy and classified as susceptible to viruses will increase due to the growth rate of mosquitoes of$(1+\theta_1)(1+\theta_2)(1-\theta_3)$ with the influence of COD, DO and water temperature based on assumption 1. Then based on assumption 7, changes in the number of susceptible mosquito subpopulations will reduce due to death with a natural mortality rate of mSv. Furthermore, based on the assumptions, the subpopulation of susceptible mosquitoes will decrease by $\beta\frac{\alpha_v S_v I_i}{N_v}$ due to interactions with infected humans (mosquitoes bite infected humans) so that these individual mosquitoes will move to the infected subpopulation. Based on this, the change in the number of subpopulations of healthy and susceptible mosquitoes to time t is in Equation (3.6) as follows:

$$\frac{dS_v}{dt} = (1+\theta_1)(1+\theta_2)(1-\theta_3)\theta A_v - \beta\frac{\alpha_v S_v I_i}{N_v} - mS_v \qquad (4.6)$$

4.2.8 Infected Mosquito Subpopulation (Iv)

The number of infected mosquito subpopulations that can transmit them to healthy humans and classified as susceptible over time will increase due to individual mosquitoes turning into infected individual mosquitoes as a result of interactions with infected humans (mosquitoes bite infected humans) so that these individual mosquitoes will move to the Exposed subpopulation, according to assumption 6, which is equal to$\beta\frac{\alpha_v S_v I_i}{N_v}$. In addition, according to the assumption that 7 subpopulations of infected mosquitoes will decrease due to natural deaths with a crude mortality rate of mI_v. Based on this, changes in the number of infected mosquito subpopulations that can infect healthy humans and are classified as susceptible over time are:

$$\frac{dI_v}{dt} = \beta\frac{\alpha_v S_v I_i}{N_v} - mI_v \qquad (4.7)$$

Based on Equations (4.1), (4.2), (4.3), (4.4), (4.5), (4.6), and (4.7), it is found that the SIRD-ASI model of the spread of Dengue Hemorrhagic Fever can be approached in the form of a diagram, and an illustration of the diagram can be depicted in compartment form as follows:

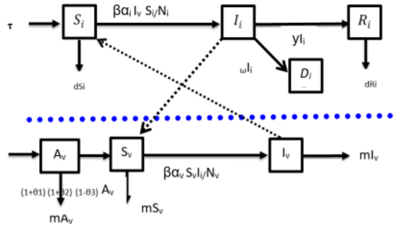

Figure 5: Scheme of DHF Disease SIRD-ASI Model.

The mosquito compartment is not included in the exposed group, because any mosquito that has bitten a human will become infected and will not experience recovery, but will become an infected mosquito ready to spread the dengue virus to humans. Infected mosquitoes will never experience recovery. To create a model for DHF epidemiology by observing the aquatic phase of the Aedes aegypti mosquito by looking at the interactions between humans (hosts) and mosquitoes (vectors) from the compartment diagram above.

The SIRD-ASI model discussed in this paper is in line with the discussion in several previous journals (Nasution, 2016) DHF epidemiological model with attention to the aquatic phase of the Aedes aegypti mosquito. In this aquatic model, the growth rate of mosquitoes in the aquatic phase is influenced by the average rate of oviposition, the proportion of female mosquitoes born, the proportion of mosquitoes moving from oviposition to susceptible mosquitoes and the natural mortality of mosquitoes in the aquatic phase. The SIR-ASI model (Rodrigues et al., 2015) also involves an aquatic phase in a model with egg, larva and pupa stages. The model also includes dengue cases reported in Madeira, with data from October 2012 to February 2013.

4.3. Practical Application of the Model

Based on the SIRD-ASI model obtained, the primary reproduction number can be determined as the number of new infections by typical infective individuals in a population in disease-free equilibrium. According to Driessche & Watmough (Van den Driessche & Watmough, 2002), the Basic Reproduction Number is the number of secondary infected individuals resulting from infection by primary infected individuals who are fully included in the susceptible subpopulation (Susceptible). The value of the direct reproduction number can be less than one, meaning the infection will disappear over time (shallow potential for infecting other people or almost no transmission); it can be equal to one, meaning the infection will become endemic and remain in the population; and if it is more extensive, there will be an epidemic with a high level of death (high potential for infecting other people or it could be said that the epidemic will continue to grow). They were followed by a sensitivity analysis of the primary reproduction number, which was carried out to determine the effect of parameter changes on the direct reproduction number.

From the SIRD-ASI model, a disease-free equilibrium point can also be determined, which is an equilibrium state where no one in the population is infected with an infectious disease and cannot transmit the disease to other subpopulations. The endemic equilibrium point can also be determined, which is a condition where in the population there are individuals infected with infectious diseases, where these individuals can transmit or spread the infection to other individuals, which can cause the disease to become endemic. Furthermore, stability at the disease-free and endemic equilibrium points can be determined, as well as numerical simulations of the SIRD-ASI model using the Runge-Kutta method using initial values and parameters that can be referenced from journal literature.

5. Implications and future Directions

The study of dengue fever involving environmental factors and water quality is expected to produce various theoretical and practical implications that can provide solutions to the dengue problem, especially in the South Kalimantan area. This study underlines the importance of environmental factors in the form of air temperature, air humidity and water quality, which are involved in mathematical models. Water quality factors involve water pH, water temperature, chemical oxygen demand (COD), dissolved oxygen (DO), and biochemical oxygen demand (BOD). Based on statistical tests, it was found that the most influential factors were water temperature, COD and DO. This approach involving the SIRD-ASI model emphasizes the importance of understanding not only environmental factors but also water quality, which is also a very important concern. So, it requires a strategy to regulate water quality, which must also be an important concern.

Practically, the implications emphasize the need for regulatory strategies that can be adjusted to the factors of water temperature, COD and DO. Recommendations for risk reduction efforts can be made by prioritizing the regulation of these water quality factors. This study provides additional insight into the involvement of water quality factors in the mathematical models formed. The application of the findings of this model modification not only has an impact on preventing dengue fever but also functions as a modified model approach that can be utilized in mathematical science.

This study has several limitations that can be addressed in future research to improve generalizability. First, the use of parameters that still use findings from other journals. Future directions may take certain approaches to produce the desired parameters. Second, integrating more powerful predictive models or simulations can increase the accuracy of solving better models.

6. Conclusion

Based on research conducted by analyzing the most influential factors from several test parameters carried out, namely COD, BOD, DO, water pH, water temperature, air temperature and air humidity. The test results showed that COD and DO provided positive factors for the growth of individual larvae in the aquatic phase, while water temperature had the opposite effect on the growth of individual larvae. The three factors obtained were involved in forming a mathematical model of Dengue Hemorrhagic Fever in the form of SIRD-ASI. This model has aquatic characteristics involving COD, DO and water temperature factors. So, this model provides a different style to the dengue disease model.

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