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ANALYSIS OF BASIC REPRODUCTION NUMBER DENGUE FEVER (DBD) SPREAD THE SIR MODEL USING VACCINE IMPACT IN MEDAN CITY

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ABSTRACT

Dengue hemorrhagic fever (DHF) is a dangerous disease that is easily transmitted through mosquito bites of the species Aedes aegypti or Aedes albopictus. Dengue hemorrhagic fever (DHF) in Indonesia is an endemic disease and a serious health problem that causes many deaths. Based on the data obtained, the incidence of DHF is still high, especially in Medan City with its high population density and mobility. It is therefore necessary to have more intensive efforts to prevent DHF, one of which is by administering vaccines. Therefore, vaccination is used as an option that is commonly used to control the spread of dengue hemorrhagic fever (DHF). The purpose of this research is to get a mathematical model with the effect of the vaccine, to find out the analysis of the mathematical model with the effect of the vaccine, and to find out the analysis of the reproduction number () with the effect of the vaccine. TheSIR model was used to analyze the Basic Reproduction Number. According to this study, the basicreproduction number of DHF is $R_0 = \frac{C_{hv}N_v\mu_v(C_{vh}p\mu_h - C_{vh}p^2\mu_h + C_{vh}\mu_h^2 - C_{vh}\mu_h^2 p)}{N_h(\gamma_h+\mu_h)}$

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1. INTRODUCTION

Dengue fever (DBD)) is one of the dangerous diseases that is easily transmitted through the bites of mosquitoes from the Aedes Aegypti or Aedes Albopictus species, the fastest-developing mosquitoes in the world, and has caused

nearly 390 million people to be infected each year [1] [2]. According to the World Health Organization (WHO), Dengue cases increased from 505,430 in 2000 to over 2.4 million in 2010, and 5.2 million in 2019 [3]. Reported deaths between 2000 and 2015 increased from 960 to 4032. In 2020, dengue fever affected several countries, with reports of increased cases in Bangladesh, Brazil, the Cook Islands, Ecuador, India, Indonesia, the Maldives, Mauritania, Nepal, Singapore, Sri Lanka, Sudan, Thailand, Timor-Leste, and Yaman. [4], dengue fever continued to affect Brazil, India, Vietnam, the Philippines, Colombia, Fiji, Kenya, Paraguay, Peru, and the Reunion Islands [5].

DBD cases in Indonesian are still very high, even the highest in Southeast Asia. Based on the Indonesian Health Profile, the reported DBD cases in 2021 amounted to 73,518 cases with a death toll of 705 cases [6]. The incidence rate of dengue fever in 2021 was 27 per 100,000 populations. Medan City is an endemic area for dengue fever. In 2021, the number of reported dengue fever cases was 2,262, with 10 fatalities. There are 3 sub-districts with the highest coverage of DBD cases, namely Medan Helvetia sub-district with 87 cases, Medan Selayang sub-district with 81 cases, and Medan Belawan sub-district with 77 cases [7].

A virus is transmitted to humans through the bite of an infected female mosquito, namely the Aedes Aegypti mosquito [8]. Therefore, in order to prevent the breeding of Aedes Aegypti mosquitoes, efforts have been made to eradicate mosquito breeding sites by draining bathtubs, covering containers that can hold water, and burying used items that can become breeding grounds for mosquito larvae, as well as conducting fogging, larviciding (applying or sprinkling larvicides into water reservoirs), using fish (such as guppies, bettas, and tilapia), and so on [9].

Based on the data obtained, the incidence rate of dengue fever (DBD) is still high, especially in the city of Medan. The number of residents infected with dengue fever and the extent of its spread are increasing, in line with the high population density and mobility of residents [10]. Therefore, more intensive efforts to prevent dengue fever (DBD) are necessary, one of which is through vaccination [11]. Therefore, vaccination is commonly used as a method to control the spread of dengue fever (DF). According to Ramalidan Pamoentjak (2005), a vaccine is a suspension of live pathogens that have been weakened or killed to induce active immunity against a disease, thereby preventing or reducing the impact of infection by natural organisms [12].

Vaccination aims to stimulate effective immunity, resulting in the formation of antibodies and memory cells. The more frequently vaccinations are administered, the greater the number of memory cells that are formed [13]. Successful vaccination will provide protection to the body against infection attacks. It depends on several factors, such as the specificity of the vaccine, the method of administering the vaccine, the vaccine's ability to elicit an immune response, the type of vaccine, and so on. The way vaccine materials are stored greatly determines the effectiveness of the vaccine, especially live vaccines. Relevant research was also conducted by E.N. Bano with the title "Mathematical Model of the Spread of Dengue Hemorrhagic Fever Type Seir Double Infection," and another study was conducted by Duastu with the title "Pediatric Vaccination Model for Dengue Hemorrhagic Fever."

The model used in this research is the SIR Model with Basic Reproduction Number Analysis. The SIR model is a form of a system of differential equations where the population is divided into three groups: the susceptible group, the infected group, and the recovered group. The differential equation will be used to calculate the basic reproduction number [14]. The Basic Reproduction Number, denoted as R_0, is a threshold parameter used to determine the boundary between the extinction and spread of an epidemic disease. Assuming the threshold limit, a model will reach a disease-free equilibrium point and achieve general asymptotic stability, causing the disease to disappear, whereas a value above this limit will result in the disease becoming endemic [15].

2. RESEARCH METHOD

In the research using quantitative methodology in conjuction with a quatitative descriptive litterature apporach. The literature review involves examining relevant books to provide a reference for the research (Siregar, 2021). The quantitative descriptive technique entails the analysis and organization of data in accordance with the researcher's requirements, utilizing numerical data or figures.

3. RESULT AND ANALYSIS

3.1 Model Formulation SIR of DBD Epedemic with vaccinations Mathematical model of peoples population

$$\frac{dS_h}{dt} = \mu_h(1-p)N_h - \left[\frac{C_{vh}l_v}{N_h} + p + \mu_h\right] S_h$$

$$\frac{dI_h}{dt} = \frac{C_{vh}l_v}{N_h} S_h - (\gamma_h + \mu_h) I_h$$

$$\frac{dR_h}{dt} = pS_h + \gamma_h I_h - \mu_h R_h$$

3.2 Mathematical model of mosquito population

$$\frac{dS_v}{dt} = \mu_v N_v - \left[\frac{C_{hv} l_v}{N_h} + \mu_v\right] S_v$$
$$\frac{dI_v}{dt} = \frac{C_{hv} l_h}{N_h} S_v - \mu_v I_v$$

3.3 Case study of DBD Epidemic Model

a. People's Population

In 2021, The number people in the city of Medan who recuperated from dengue fever was 1.582 people's . So R=1.582 people's. The mean infectious duration for dengue fever in humans is 4 days, equivalent to 0.133 per month. The ratio of the transition from infected individuals to recovered individuals.

The period of infectivity is 4 days = 0.133/month. Therefore, the proportion of moving infectious people becoming healthy people $\gamma_h = \frac{1}{\text{period of infectivities}} = \frac{1}{0.133\,\text{month}} = 7.52\,/\text{month} \cdot N_v$, with N_v being the population of Aedes aegypti in City of Medan. The data hasn't been collected, but it is assumed that in 2021, the larvae of Aedes aegypti in City of Medan amounted to 30 tails. So the suspicion of infected people from moving people is $\beta_{vh} = \frac{R_h}{N_v \times D_h} = \frac{1.582}{7.560 \times 0{,}133\ \text{month}} = 1,573\,\text{months}$.

b. Mosquito Population

The rate of death mosquito μ_v as known of the value expectation as below

$\mu_v = \frac{1}{\text{life expectancy}} = \frac{1}{45\ \text{days}} = \frac{1}{1{,}5\ \text{month}} = \frac{0{,}67}{\text{month}}$

The amount of people population in the City of Medan is & 2,460,858 people, or $N_h = 2,460,858$ people. So the suspicion probabilities of infected people to mosquitoes are:

$\beta_{vh} = \frac{R_v}{N_h \times D_v} = \frac{200}{2{,}460{,}858 \times 0{,}866\ \text{month}} = \frac{0{,}000094}{\text{month}}$

The model SIR in the City of Medan can be substituted into the parameters below:

$$\frac{dS_h}{dt} = 0.00114 \times (1 - 0.75) \times 2,460,858 - \left[\frac{11.25 L_v}{2,460,858} + 0.75 + 0.00114\right] S_h \frac{dI_h}{dt}$$
$$= \frac{11.25 L_v}{2,460,858} S_h - (7,52 + 0,00114)\, I_h$$
$$\frac{dR_h}{dt} = 0.75 S_h + 7.52 I_h - 0.00114 R_h$$
$$\frac{dS_v}{dt} = 0.67 \times 7.560 \times \left[\frac{22.5 I_h}{2,460,858} + 0.67\right] S_v$$
$$\frac{dI_v}{dt} = \frac{22.5 I_h}{2,460,858} S_v - 0.67 I_v$$

With $S_h(0) = 2,458,596, \quad I_h(0) = 2,262, \quad R_h(0) = 1,582, \quad S_v(0) = 6,930, \quad I_v(0) = 630$

3.4 The equilibrium point of Epidemic Model in DBD

a Free disease of epidemic Model DBD

Given the equilibrium point of free disease is $E_0 = (S_{v0}, I_{v0}, S_{h0}, I_{h0}) = \left(N_v, 0, \frac{\mu_h (1-p) N_h}{p + \mu_h}, 0\right)$. With $S_v = N_v$ and also $S_h = \frac{\mu_h (1-p) N_h}{p + \mu_h}$ and $I_h,\ I_v$ has value 0.

b The equilibrium point of Epidemic Model in DBD

Given the endemic point DBD as below:

$$\left(\frac{\mu_v N_v}{\frac{c_{hv} I_h}{N_h} + \mu_v}, \frac{c_{hv} I_h S_v}{N_h \mu_v}, \frac{\mu_h (1-\rho) N_h}{\frac{c_{vh} I_v}{N_h} + \rho + \mu_h}, \frac{c_{vh} I_v S_h}{N_h (\mu_h + \gamma_h)}\right)$$

Analysis of Point stability

After obtaining the equilibrium point, a stability analysis of the disease-free equilibrium point will be conducted. The first step is the linearization of the system of linear equations that appear in the DBD epidemic model. The equations used in the linearization process are:

$$f(S_v, I_v, S_h, I_h) = \mu_v N_v - \left(\mu_v + \frac{C_{hv} I_h}{N_h}\right) S_v$$
$$g(S_v, I_v, S_h, I_h) = \frac{C_{hv} I_h}{N_h} S_v - \mu_v I_v$$
$$h(S_v, I_v, S_h, I_h) = \mu_h (1-p) N_h - \left(\mu_h + P + \frac{C_{vh} I_v}{N_h}\right) S_h$$
$$i(S_v, I_v, S_h, I_h) = \frac{C_{vh} I_v}{N_h} S_h - (\mu_h + \gamma_h) I_h$$

From each the derivative result distribution function to Jacobian matrics below:

$$J = \begin{bmatrix} -\left(\mu_v + \frac{C_{hv} I_h}{N_h}\right) & 0 & 0 \\ -\frac{C_{hv} S_v}{N_h} & \frac{C_{hv} I_h}{N_h} & -\mu_v \\ 0 & \frac{C_{hv} S_v}{N_h} & 0 \\ -\frac{C_{vh} S_h}{N_h} & \frac{C_{vh} S_h}{N_h} & -\left(\mu_h + p + \frac{C_{vh} I_v}{N_h}\right) \\ \frac{C_{vh} I_v}{N_h} & 0 & -(\mu_h + \gamma_h) \end{bmatrix}$$

Because point equilibrium free disease $E_0 = (S_{v0}, I_{v0}, S_{h0}, I_{h0}) = \left(N_v, 0, \frac{\mu_h (1-p) N_h}{p+\mu_h}, 0\right)$ so the value of point equilibrium subsitution into distribution function to Jacobian matrics below

$$J_0 = \begin{bmatrix} -\mu_v & 0 & 0 \\ -\frac{C_{hv} N_v}{N_h} & 0 & -\mu_v \\ 0 & \frac{C_{hv} N_v}{N_h} & 0 \\ -\frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & \frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & -(\mu_h + \rho) \\ 0 & 0 & -(\mu_h + \gamma_h) \end{bmatrix}$$

Finding the eigen value λ Jacobian matrices as written bellow $(\lambda I - J) = 0$. With I as identity matrics as λ has eigen value, so the solution doesn't zero of the equation $(\lambda I - J) = 0$. The equation $(\lambda I - J) = 0$ will solution doesn't zero if and only $det(\lambda I - J) = 0$. The equation $det(\lambda I - J) = 0$ is polinom characteristics of J. The characteristics equation of Jacobian matrics as below:

$$\text{Det}\left(\lambda \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix} - \begin{bmatrix} -\mu_v & 0 & 0 \\ -\frac{C_{hv} N_v}{N_h} & 0 & -\mu_v \\ 0 & \frac{C_{hv} N_v}{N_h} & 0 \\ -\frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & \frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & -(\mu_h + \rho) \\ 0 & 0 & -(\mu_h + \gamma_h) \end{bmatrix}\right) = 0$$

$$\text{Det}\left(\begin{bmatrix} \lambda & 0 & 0 & 0 \\ 0 & \lambda & 0 & 0 \\ 0 & 0 & \lambda & 0 \\ 0 & 0 & 0 & \lambda \end{bmatrix} - \begin{bmatrix} -\mu_v & 0 & 0 & 0 \\ -\frac{C_{hv} N_v}{N_h} & 0 & -\mu_v & 0 \\ 0 & \frac{C_{hv} N_v}{N_h} & 0 & 0 \\ -\frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & \frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & -(\mu_h + \rho) & 0 \\ 0 & 0 & 0 & -(\mu_h + \gamma_h) \end{bmatrix}\right) = 0$$

$$\text{Det}\begin{bmatrix} \lambda + \mu_v & 0 & 0 & \frac{C_{hv} N_v}{N_h} \\ 0 & \lambda + \mu_v & 0 & 0 \\ -\frac{C_{hv} N_v}{N_h} & 0 & 0 & \frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} \\ -\frac{C_{vh} \frac{\mu_h (1-p) N_h}{p+\mu_h}}{N_h} & 0 & 0 & \lambda + (\mu_h + \rho) \\ 0 & 0 & 0 & \lambda + (\mu_h + \gamma_h) \end{bmatrix} = 0$$

Therefore the characteristics of equation as below:

$$\lambda^4 + \lambda^3 (2\mu_h + \gamma_h + 2\mu_v + \rho) + \lambda^2 \left({\mu_v}^2 + {\mu_h}^2 + 4\mu_h \mu_v + 2\mu_v \gamma_h + \mu_h \gamma_h + p\mu_h + p\gamma_h + 2p\mu_h\right) +$$
$$+\lambda \left(2\mu_h \mu_v \gamma_h + 2p\mu_h \mu_v + 2p\mu_v \gamma_h + 2{\mu_h}^2 \mu_v + 2\mu_h {\mu_v}^2 + {\mu_v}^2 \gamma_h + {\mu_v}^2 p\right) + {\mu_v}^2 {\mu_h}^2$$
$$+{\mu_v}^2 \mu_h \gamma_h + {\mu_v}^2 p\mu_h + {\mu_v}^2 p\gamma_h$$

Using stability analysis as criteria of *Routh-Hurwitz*

Table 1: *Routh-Hurwitz* Table

λ^4	1	B	d
λ^3	A	C	0
λ^2	$\frac{ab-c}{a}$	$\frac{ad}{a} = d$	
λ^1	$\frac{(\frac{ab-c}{a})c-ad}{\frac{ab-c}{a}} = c - \frac{a^2d}{ab-c}$		
λ^0	D		

Given that all terms are positive, the system exhibits stability, hence satisfying the necessary and sufficient conditions for stability.

3.5 The Basic Reproduction numbers

To determine the basic reproduction number, it is necessary to first know the matrix $\emptyset$ that shows the parameters causing the increase in the class of DBD-infected population and the matrix φ that shows the parameters causing the decrease in the class of DBD-infected. Then it is obtained:

$$\emptyset = \left[\frac{C_{vh} I_v}{N_h} S_h \;\; \frac{C_{hv} I_h}{N_h} S_v \right]$$

$$\varphi = \left[(\gamma_h + \mu_h)\, I_h \;\; \mu_v I_v \right]$$

Then which substitution equilibrium point for free disease DBD as $\left(N_v, 0, \frac{\mu_h(1-p)N_h}{p+\mu_h}, 0\right)$ from before equation:

$$F = \left[0 \;\; \frac{C_{hv} N_v}{N_h} \;\; C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p \;\; 0 \right]$$

$$V = \left[\gamma_h + \mu_h \;\; 0 \;\; 0 \;\; \mu_v \right]$$

Looking for the value of V^{-1}, as below:

$$V^{-1} = \left[\frac{1}{\gamma_h + \mu_h} \;\; 0 \;\; 0 \;\; \frac{1}{\mu_v} \right]$$

The Jacobian matrix comprises derivatives of a nonlinear function, rendering it unsuitable for determining the maximum eigenvalue; hence, the next generation matrix is employed for this purpose. According to the aforementioned equation, the structure of the subsequent generation matrix is derived as follows:

$$K = FV^{-1}$$

$$= \left[0 \;\; \frac{C_{hv} N_v}{N_h} \;\; C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p \;\; 0 \right] \left[\frac{1}{\gamma_h + \mu_h} \;\; 0 \;\; 0 \;\; \frac{1}{\mu_v} \right]$$

$$= \left[0 \;\; \frac{C_{hv} N_v \mu_v}{N_h} \;\; \frac{C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p}{\gamma_h + \mu_h} \;\; 0 \right]$$

The basic reproduction number is the dominant eigenvalue of the matrix $K = FV^{-1}$. To determine the eigenvalue of the matrix K, the characteristic equation will be derived, namely $\det(K - \lambda I) = 0$, where λ represents the eigenvalue and I is the identity matrix. Consequently, we derive:

$$det \left(\left[0 \;\; \frac{C_{hv} N_v \mu_v}{N_h} \;\; \frac{C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p}{\gamma_h + \mu_h} \;\; 0 \right] - \lambda \left[1 \;\; 0 \;\; 0 \;\; 1 \right] \right) = 0$$

$$det \left(\left[0 \;\; \frac{C_{hv} N_v \mu_v}{N_h} \;\; \frac{C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p}{\gamma_h + \mu_h} \;\; 0 \right] - \left[\lambda \;\; 0 \;\; 0 \;\; \lambda \right] \right) = 0$$

$$det \left[-\lambda \;\; \frac{C_{hv} N_v \mu_v}{N_h} \;\; \frac{C_{vh} p\mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p}{\gamma_h + \mu_h} \;\; -\lambda \right] = 0$$

so the charcteristics solution K as:

$$\lambda^2 - \left(\frac{C_{hv} N_v \mu_v}{N_h} \times \frac{C_{vh} p \mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p}{\gamma_h + \mu_h} \right) = 0$$

Therefore given R_0 is

$$R_0 = \frac{C_{hv} N_v \mu_v \left(C_{vh} p \mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p \right)}{N_h \left(\gamma_h + \mu_h \right)}$$

4. CONCLUSION

The conclusion drawn from the discussion that has been conducted is as follows:

The mathematical model of the impact of vaccination on the spread of dengue fever can be expressed as follows:

Mathematical Model of Human Population

$$\frac{dS_h}{dt} = \mu_h (1-p) N_h - \left[\frac{C_{vh} I_v}{N_h} + p + \mu_h \right] S_h$$

$$\frac{dI_h}{dt} = \frac{C_{vh} I_v}{N_h} S_h - \left(\gamma_h + \mu_h \right) I_h$$

$$\frac{dR_h}{dt} = p S_h + \gamma_h I_h - \mu_h R_h$$

Mathematical Model of Mosquito Population

$$\frac{dS_v}{dt} = \mu_v N_v - \left[\frac{C_{hv} I_h}{N_h} + \mu_v \right] S_v$$

$$\frac{dI_v}{dt} = \frac{C_{hv} I_h}{N_h} S_v - \mu_v I_v$$

All parameters has positive value

a Model has two equilibrium point as below

a) Point equilibrium of free disease $E_0 = \left(N_v, 0, \frac{\mu_h (1-p) N_h}{p + \mu_h}, 0 \right)$

b) Point equilibrium of endemic

$$E_1 = (S_{v1}, I_{v1}, S_{h1}, I_{h1}) = \left(\frac{\mu_v N_v}{\frac{c_{hv} I_h}{N_h} + \mu_v}, \frac{c_{hv} I_h S_v}{N_h \mu_v}, \frac{\mu_h (1-\rho) N_h}{\frac{c_{vh} I_v}{N_h} + \rho + \mu_h}, \frac{c_{vh} I_v S_h}{N_h (\mu_h + \gamma_h)} \right)$$

b The effect of vaccine as suspection dengue fever as basic reproduction numbers: $r\,(R_0)$

$$R_0 = \frac{C_{hv} N_v \mu_v \left(C_{vh} p \mu_h - C_{vh} p^2 \mu_h + C_{vh} {\mu_h}^2 - C_{vh} {\mu_h}^2 p \right)}{N_h (\gamma_h + \mu_h)}$$

When, $R_0 < 1$ The disease-free equilibrium point will be asymptotically stable, meaning that the disease will not spread in the population or, in other words, the disease will eventually disappear from the population over a long period. When the endemic fixed point is asymptotically stable, it means that the disease will persist and spread within the population. In order for dengue fever (DF) to be prevented or eliminated over a long period, we need to reduce the basic reproduction number by increasing the chances of vulnerable individuals being vaccinated.

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