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TRANSMISSION MODEL OF DENGUE FEVER IN CASE OF TANGERANG CITY WITH SEVERAL SIMULATIONS

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Abstract: The aim of our research is constructing mathematics model *SIR-SI* transmission of dengue virus in case of Tangerang City consider vaccination, fumigation and treatment. Background of our research is because so many cases of dengue fever in Tangerang at least 577 cases. We use method compartment model and creating differential equation system. The Result tells us that our mathematics model giving two equilibrium points. As the first, we call as disease free equilibrium point E_0 and the second is endemic equilibrium point E_1 (simulation 1). We also success determining basic reproduction number R_0 and we analyze state the conditions for local stable. Local stability around E_0 is asymptotic stable with R_0 =0.7863699062 < 1 and local stable around endemic equilibrium point E_1 is asymptotic stable with R_0 =3.045597501> 1. For simulation 2 with the parameter $\mathbf{u_2}$, $\mathbf{u_3}$ and $\mathbf{c}$, which each meaning control in form of giving vaccination to susceptible individual, control in the form of treatment of infected individual, and coeficcient asociated with treatment control. Those all parameters changed from 0,9 into 1 we get result that the number of infected humans decreased and the number of recoveries is increase for free disease condition. In the disease condition of simulation 2, the result seems like same of free disease condition in simulation 2 but not too significantly for decrease the number of infected human and the number of increase recovery human. Overalls the case of Dengue in Tangerang actually decrease since applied vaccination, fumigation and treatment.

Keywords: *Dengue, Transmission, Model, Several, Simulations*

Abstrak: Tujuan dari penelitian ini yakni mengonstruksi model matematika *SIR-SI* transmisi virus dengue pada kasus DBD di Kota Tangerang dengan melibatkan adanya vaksinasi, penyemprotan dan pengobatan. Latar belakang dari penelitian ini yakni banyaknya kasus DBD di Kota Tangerang. Metode pada penelitian ini yakni model kompartemen *SIR-SI* dan membentuk sistem persamaan diferensial. Hasil penelitian ini memberikan dua titik kesetimbangan yakni titik kesetimbangan bebas penyakit $\boldsymbol{E_0}$ dan titik kesetimbangan endemik $\boldsymbol{E_1}$. Penelitian ini juga menghasilkan bilangan reproduksi dasar $\boldsymbol{R_0}$ dan kami melakukan analisis kestabilan lokal pada tiap titik kesetimbagan. Kestabilan lokal di sekitar titik ekuilibrium $\boldsymbol{E_0}$ yakni stabil asimtotik dengan $\boldsymbol{R_0 = 0,7863699062 < 1}$. Lebih lanjut, kestablilan lokal di sekitar titik di sekitar titik ekulibrium $\boldsymbol{E_1}$ juga stabil asimtotik dengan $\boldsymbol{R_0 = 3,045597501 > 1}$. Dari hasil ini dilakukan simulasi dengan memasukkan nilai parameter yang ada, dan simulasi ini disebut dengan simulasi1. Lebih lanjut simulasi 2 dilakukan dengan mengubah nilai parameter $\boldsymbol{u_2}$, $\boldsymbol{u_3}$ dan *c* dari 0,9 menjadi 1, dan diperoleh hasil yang menunjukkan bahwa grafik *host* yang terinfeksi menurun sebaliknya grafik *host* yang sembuh naik. Hal ini terjadi pada titik kesetimbangan bebas penyakit. Untuk titik kesetimbangan endemik, hasil yang diperoleh juga sama dengan yang diperoleh dari simulasi titik kesetimbangan bebas penyakit. Hanya saja penurunan *host* yang terinfeksi dan *host* yang sembuh tidak terlalu signifikan.

Kata Kunci: *Dengue, Transmisi, Model, Simulasi*

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Introduction

Dengue Haemorrhagic Fever (DHF) is an infectious disease caused by the dengue virus. The dengue virus is transmitted by the Aedes aegypti mosquito, which is infected with the dengue virus through bites. Because of the bite of the Aedes aegypti mosquito, which carries the dengue virus, humans or individuals affected by mosquito bites, will experience high body heat, nausea and a drastic decrease in platelet levels. If it is not treated early, individuals who are infected with the dengue virus or suffer from dengue fever can die. The definition of dengue here server by Alodocter (2024).

Antara News reported that during 2022, as many as 1322 individuals in Tangerang Regency were affected by dengue fever. Furthermore, according to Republika News, since January 2022, there have been at least 577 cases of individuals infected with dengue fever and for the city of Tangerang itself; Media Indonesia recorded that there were 331 individuals affected by dengue fever. Based on the facts above, it can be seen that the number of cases of individuals infected with dengue fever in the Greater Tangerang area is very large, including in the Tangerang City area. This requires serious attention so that the spread of the dengue virus can be controlled so that it does not spread further and demands healing efforts for victims affected by the dengue virus.

Efforts that can be made to prevent the spread of the dengue virus can be done by using the 3 M method, namely closing water reservoirs, which are the media or egg-laying places for the Aedes aegypti mosquito, draining open bathtubs regularly, especially after finding mosquito larvae that breed and throwing away used items in the bathroom. a place where it can be recycled. Apart from 3M's efforts, there are also other efforts that can be made to prevent the spread of the dengue virus, namely by spraying (fumigation). Spraying here means spraying insecticides or poisons that can kill Aedes aegypti mosquito larvae.

Even though it is thought to cause mosquitoes to become immune or resistant, this spraying effort is still widely carried out because it can have a positive impact on stopping the spread of the dengue virus. Another effort that individuals can make to avoid contracting the dengue virus is by vaccinating. This vaccination is carried out on individuals who are susceptible to the dengue virus so that they do not become infected. This effort is justified and better prevents contracting the dengue virus when compared to individuals who do not receive vaccination. As for giving anti-mosquito bite lotion, in this study it is considered the same as giving vaccination because it can prevent individuals from contracting dengue virus.

For individuals who have been infected with the dengue virus, treatment can be carried out in the form of medication. Treatment that can be carried out can be in the form of medical treatment in the form of medicines or herbal remedies, which are considered capable of increasing blood platelet levels, such as consuming red yeast rice. Research to construct mathematical models of the spread of the dengue virus is generally carried out using compartment or class models. This means that individuals (humans) can be grouped into the Suspect (S) or susceptible class, Infected (I) or infected, Recovery (R) or the class of individuals who have completed or recovered from dengue fever.

The Aedes aegypti mosquito can also be classified into Suspect (S) and Infected (I) classes, which respectively indicate mosquito vectors that are susceptible to the dengue virus and mosquito vectors that are infected with the dengue virus. Based on this, the mathematical model can be in the form of SIR-SI. This SIR-SI model has been carried out, for example by Soleh (2018) [1] who examined the spread of dengue fever in Pekanbaru and Baihaqi, et al (2023) [2] who examined the pattern of the spread of dengue fever in Madiun in 2020-2022.

The difference in research between Soleh (2018) and Baihaqi, et al (2023), apart from being in the research area, also lies in the mathematical model, namely for the research conducted by Baihaqi, et al, they used the SIR model for individual classes, but did not include the SI class for mosquitoes. Windawati, et al (2020) [3] which included fumigation or fogging, carried out the SIR model -Another SI. Fogging here can also be interpreted as fumigation.

The SIR-SI model for the spread of the dengue virus was also carried out by Andiraja, et al (2022) [4]

which includes the use of vaccines in individuals who are susceptible to the dengue virus. The SIR-SI model with vaccination was also carried out by Chanprasopchai et al (2018) [5] with the difference being in the Suspect (S) and Infected (I) individual classes which were divided into two other parts. Bano (2018) [6] carried out another research for the SIR-SI model of the spread of the dengue virus with research on the spread of the dengue virus using larvicide. Furthermore, Harianto, et al (2023) [7] which involved the saturation birth ratio factor, carried out another study on the spread of the SIR-SI dengue virus. Novia (2020) [8] which took into account age structure and spraying carried out another SIR-SI model.

A part from the SIR-SI dengue virus spread model, there are other developments of this model, for example carried out by Side, et al (2018) [9] who developed the SIR-SI model into SIRI-SI. This model assumes that a class of individuals who have completed (recovered) from dengue fever can be re-infected with the dengue virus. Sanusi, et al (2021) [10] who developed the SIR-SI model into SIRS-SI, also carried out research on the development of the SIR-SI model. This model assumes that individuals who have recovered from dengue fever can re-enter the vulnerable class. This research was conducted in the South Sulawesi region. Side, et al (2018) [11] who discussed the analysis of the dengue virus spread model using the Lyapunov function, continued the research of Sanusi, et al (2021). Amar, et al (2022) [12] taking into account pesticide spraying and treatment, also carried out the SIRS-SI model.

Development of models for the spread of the dengue virus is also continuing by adding other classes for individuals and mosquito vectors. The addition of this class is the Exposed (E) class, which means, "Exposed". Based on this, the model formed is SEIR-SEI. Researchers who constructed the SEIR-SEI model include Purwanto, et al (2014) [13] who studied the spread of the dengue virus with one dengue virus serotipe. Another research is the SEIRS-SEI dengue virus spread model conducted by Ode Sabran, et al (2020) [14]. This research considers the influence of temperature and assumes that individuals in the Recovery (R) class in the SEIRS-SEI model have the potential to return to the Suspect (S) class.

Another model is Galuh (2023) [15] which divides individual classes into SITR-SI with class T indicating individuals undergoing treatment. Many studies have also been carried out on the topic of this epidemic, such as research by Abidemi, et al (2024) [16] which examined the optimal model for controlling the dengue virus using asymptomatic, isolation and vigilance. Furthermore, there is also research by Liu & Zaenab (2021) [17] on the impact of information intervention on a stochastic dengue fever epidemic model. Then there was research on noninteger models for the Zika and dengue viruses carried out by Iheonu et al (2023) [18]. Further research was carried out by Pandey, et al (2023a) [19], (2023b) [20] on the effect of vaccination on a dynamic model of dengue virus transmission in Nepal and research on reducing dengue virus vectors was carried out by M.A & G.M (2024) [21] using a fractional order approach.

Based on the review of research on the spread of the dengue virus, which has been described above, the author can draw out a common research gap that can be developed, one of which is a mathematical model of the spread of the dengue virus SIR-SI by considering spraying (fumigation), vaccination and treatment. In fact, other higher-level research that can be developed by considering these three factors can be in the form of SIRS-SI, SIRI-SI, SEIR-SI, even SEIRS-SEI models. Research on the SITR-SI model with these three factors can also be carried out, but this research is limited to SIR-SI to make it easier to carry out the mathematical analysis. Research on the SIR-SI mathematical model, taking into account the factors of spraying, vaccination and treatment, carried out a case study of dengue fever in Tangerang City.

Method

To determine the results of this research, it is necessary to first explain the stages or scheme carried out. These stages are necessary so that the process of this research is clear and focused. Furthermore, the research stages in question are described as follows.

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I. Develop a mathematical model of the spread of the SIR-SI dengue virus involving spraying (fumigation), vaccination and treatment for individuals infected with the dengue virus. This stage includes assuming the variables and parameters of the SIR-SI model used
II. Carrying out an analysis of the mathematical model of the spread of the SIR-SI dengue virus that has been formed includes finding the equilibrium point, which consists of a disease-free equilibrium point and an endemic equilibrium point. Analysis of the SIR-SI mathematical model also includes finding the basic reproduction number, analysis of the local stability of the disease-free equilibrium point and analysis of the local stability of the endemic equilibrium point.
III. Simulate the mathematical model that has been produced by entering the existing parameter values. This simulation uses Maple software and analysis is carried out from the simulation that has been carried out. After analyzing the mathematical model simulation, conclusions are drawn.

Results and Discussion

In constructing a mathematical model of the spread of the dengue virus in Tangerang City by including spraying, vaccination and treatment, a compartment or class model for individuals (Host) and mosquitoes (Vector) was used. The compartment model used is in the form of SIR-SI with the information that the class for individuals is SIR and the class for mosquitoes is SI. Class S means Suspect or vulnerable, class I means Infected or infected and class R means Recovery or recovered.

For individuals, class S or Suspect means vulnerable, meaning individuals who are susceptible to being infected with the dengue virus, while for mosquitoes, Suspect also means vulnerable, meaning mosquitoes that are susceptible to carrying the dengue virus. Furthermore, the Infected class for an individual means that the individual is exposed to or infected with the dengue virus and for mosquitoes, it also means the same thing, namely mosquitoes that have carried the dengue virus. The Recovery class only exists in individuals, which means that the individual has recovered from the dengue fever they suffered from, while in mosquitoes there is no Recovery class.

Several assumptions used in this research include the total population of individuals and mosquitoes being considered fixed or constant. This means that there is no possibility of increase either from within in the form of births or from outside in the form of migration for individual aspects and mosquitoes. Apart from natural death, mosquito deaths can also be caused by spraying. Mosquitoes infected with the dengue virus will never recover because the lifespan of mosquitoes is short and mosquitoes exposed to spraying (fumigation) will not become resistant or immune.

There is only one dengue virus serotype in one area, which means that individuals who recover cannot be infected with the dengue virus again. Individuals born are considered individuals who are susceptible to the dengue virus. Susceptible individuals will be vaccinated to minimize infection with the dengue virus and individuals infected with the dengue virus will be treated to cure the disease. Based on the assumptions described above, the SIR-SI compartment model is obtained as follows.

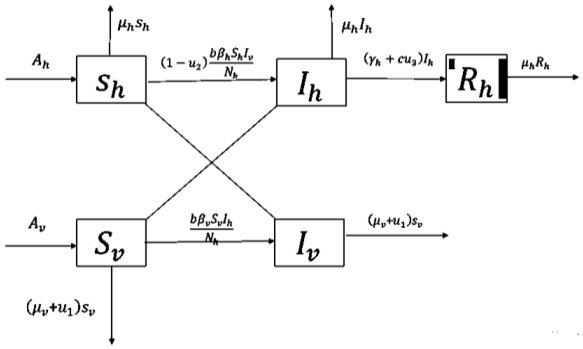

Figure 1. Transfer diagram of the SIR-SI Dengue Fever Spread Model involving Spraying, Vaccination and Treatment.

From the transfer diagram in Figure 2 above, a mathematical model of interaction between Host and Vector is obtained in the form of a system of non-linear differential equations as follows.

$$\begin{aligned}
\frac{dS_h}{dt} &= A_h - (1-u_2)\frac{b\beta_h S_h I_v}{N_h} - \mu_h S_h \\
\frac{dI_h}{dt} &= (1-u_2)\frac{b\beta_h S_h I_v}{N_h} - (\gamma_h + cu_3) I_h - \mu_h I_h \\
\frac{dR_h}{dt} &= (\gamma_h + cu_3) I_h - \mu_h R_h \qquad (1) \\
\frac{dS_v}{dt} &= A_v - \frac{b\beta_v S_v I_h}{N_h} - (\mu_v + u_1) S_v \\
\frac{dI_v}{dt} &= \frac{b\beta_v S_v I_h}{N_h} - (\mu_v + u_1) I_v
\end{aligned}$$

with parameters

A_h	: Human birth rate per capita
A_v	: Number of mosquito recruitment
μ_h	: Human birth rate
μ_v	: Natural mosquito death rate
u_1	: Death rate of mosquitoes due to fumigation
u_2	: Control in the form of giving vaccinations to susceptible individuals
u_3	: Control in the form of treatment of infected individuals
b	: Rate of mosquito bites on humans
c	: Coefficient associated with treatment control
β_h	: The chance of spreading the virus from an infected mosquito to a susceptible individual
β_v	: The chance of spreading the virus from an infected individual to a susceptible mosquito
γ_h	: Recovery rate of infected individuals
N_h	: Total human population

After constructing a mathematical model of the spread of the SIR-SI dengue virus, which involves spraying, vaccination and treatment according to the system of equations (1), the model is then analyzed. This analysis includes determining the equilibrium point, which consists of the disease-free equilibrium point, endemic equilibrium point, determining the basic reproduction number, and local stability analysis at the disease-free and endemic equilibrium points. The results of each analysis are described as follows.

Equilibrium Point

The equilibrium point is obtained by forming each equation in model (1) to be equal to zero, so that the equilibrium point is obtained when $\frac{dS_h}{dt} = 0$, $\frac{dI_h}{dt} = 0$, $\frac{dR_h}{dt} = 0$, $\frac{dS_v}{dt} = 0$, $\frac{dI_v}{dt} = 0$. The resulting equilibrium points are disease-free equilibrium points and endemic equilibrium points.

Disease-Free Equilibrium Point

The disease-free equilibrium point is a condition where there is no spread of infectious disease (DHF) in a population. In this case, the disease-free equilibrium point occurs when $I_h = 0$ and $I_v = 0$.The disease-free equilibrium point is given by $E_o = (S_h, I_h, R_h, S_v, I_v)$ $= \left(\frac{A_h}{\mu_h}, 0, 0\frac{A_v}{(\mu_v + u_1)}, 0\right)$.

Endemic Equilibrium Point

The endemic equilibrium point is a situation where disease infection occurs in the population, in other words when it occurs $I_h \neq 0$ and $I_v \neq 0$. Based on this, the endemic equilibrium point is given by $E_1 = (S_h^*, I_h^*, R_h^*, S_v^*, I_v^*)$ and written as follows.

$$S_h^* = \frac{A_h}{(1-u_2)\frac{b\beta_h S_h I_v}{N_h} + \mu_h},$$

$$I_h^* = \frac{(1-u_2)\frac{b\beta_h S_h I_v}{N_h}}{(\gamma_h + \mu_h + cu_3)},$$

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$$R_h^* = \frac{(\gamma_h + cu_3) I_h}{\mu_h}$$

$$S_v^* = \frac{A_v}{\left(\mu_v + u_1 + \frac{b\beta_v I_h}{N_h}\right)} \text{ and } I_v^* = \frac{\frac{b\beta_v S_v I_h}{N_h}}{(\mu_v + u_1)}$$

Some people perhaps ask why I_h^*contains I_v but on the other hand I_v^*contains I_h?. Actually we can serve those equations independently, but for the simply we serve like that as you can see above.

After determining the disease-free equilibrium point and endemic equilibrium point, the basic reproduction number is then determined. The basic reproduction number is the number of individuals who are susceptible to infection by other infected individuals. The basic reproduction number means that the disease will disappear from the population, whereas the basic reproduction number means that an outbreak will occur in the population. The basic reproduction number is obtained by calculating the eigenvalues of the Jacobian matrix calculated at the disease-free equilibrium point. Furthermore, matrices 2 and 3 below respectively show the Jacobian matrix and the Jacobian matrix, which has been substituted for the disease-free equilibrium, point.

$$J = \begin{bmatrix} -(1-u_2)\frac{b\beta_h I_v}{N_h} - \mu_h & 0 & 0 & 0 & -(1-u_2)\frac{b\beta_h S_h}{N_h} \\ (1-u_2)\frac{b\beta_h I_v}{N_h} & -(\gamma_h + \mu_h + cu_3) & 0 & 0 & (1-u_2)\frac{b\beta_h S_h}{N_h} \\ 0 & (\gamma_h + cu_3) & -\mu_h & 0 & 0 \\ 0 & -\frac{b\beta_v S_v}{N_h} & 0 & -(\mu_v + u_1) & 0 \\ 0 & \frac{b\beta_v S_v}{N_h} & 0 & \frac{b\beta_v I_h}{N_h} & -(\mu_v + u_1) \end{bmatrix} \quad (2)$$

Substitute value of $E_o = (S_h, I_h, R_h, S_v, I_v) = \left(\frac{A_h}{\mu_h}, 0, 0 \frac{A_v}{(\mu_v + u_1)}, 0\right)$ into equation (2) and we get this results.

$$J(f(E_0)) = \begin{bmatrix} -\mu_h & 0 & 0 & 0 & -(1-u_2)\frac{b\beta_h A_h}{\mu_h N_h} \\ 0 & -(\gamma_h + \mu_h + cu_3) & 0 & 0 & (1-u_2)\frac{b\beta_h A_h}{\mu_h N_h} \\ 0 & (\gamma_h + cu_3) & -\mu_h & 0 & 0 \\ 0 & -\frac{b\beta_v A_v}{N_h(\mu_v + u_1)} & 0 & -(\mu_v + u_1) & 0 \\ 0 & \frac{b\beta_v A_v}{N_h(\mu_v + u_1)} & 0 & 0 & -(\mu_v + u_1) \end{bmatrix} \quad (3)$$

Based on the Jacobian matrix in matrix (3) above, linearization is then carried out by forming a characteristic equation so that the eigenvalues are obtained as follows.

$$\lambda_1 = -\mu_h, \lambda_2 = -\mu_h, \lambda_3 = -\mu_v - u_1 \text{ and} \lambda_4 =$$

$$\frac{1}{2}\Big(-N_h \mu_h u_1^2 - N_h \mu_h^2 u_1 - 2N_h \mu_h \mu_v u_1 - N_h \mu_h \gamma_h \mu_v - N_h \mu_h^2 \mu_v - N_h \mu_h \mu_v^2$$
$$- N_h \mu_h c u_3 \mu_v - N_h \mu_h \gamma_h u_1 - N_h \mu_h c u_3 u_1 + (N_h^2 \mu_h^2 \mu_v^4 - 2\mu_h^3 u_1^3 N_h^2$$
$$+ N_h^2 \mu_h^4 \mu_v^2 - 6\mu_h^3 \mu_v^2 N_h^2 u_1 - 6\mu_h^3 \mu_v N_h^2 u_1^2 - 2\mu_h^2 u_1^3 N_h^2 \gamma_h$$

$$+ 2\mu_h^4 N_h^2 \mu_v u_1 + 2\mu_h^3 N_h^2 \gamma_h u_1^2 + 4\mu_h^3 N_h^2 \gamma_h \mu_v u_1 + 2\mu_h^3 N_h^2 c u_3 \mu_v^2$$
$$+ 2\mu_h^3 N_h^2 c u_3 u_1^2 - 6\mu_h^2 \mu_v^2 N_h^2 \gamma_h u_1 - 6\mu_h^2 \mu_v N_h^2 \gamma_h u_1^2 - 2\mu_h^2 \mu_v^3 N_h^2 c u_3$$
$$- 6\mu_h^2 \mu_v^2 N_h^2 c u_3 u_1 - 6\mu_h^2 \mu_v N_h^2 c u_3 u_1^2 - 4\mu_h \mu_v b^2 \beta_v A_v \beta_h A_h u_2$$

$$- 2\mu_h^2 u_1^3 N_h^2 c u_3 + 4\mu_h u_1 b^2 \beta_v A_v \beta_h A_h - 4\mu_h u_1 b^2 \beta_v A_v \beta_h A_h u_2$$
$$+ 4\mu_h^3 N_h^2 c u_3 \mu_v u_1 + 4N_h^2 \mu_h^2 u_1^3 \mu_v + 6N_h^2 \mu_h^2 u_1^2 \mu_v^2 + 4N_h^2 \mu_h^2 \mu_v^3 u_1$$
$$+ N_h^2 \mu_h^2 \gamma_h^2 u_1^2 + 2N_h^2 \mu_h^2 \gamma_h \mu_v^2 c u_3 + 2N_h^2 \mu_h^2 \gamma_h^2 \mu_v u_1$$

$$+ 4N_h^2 \mu_h^2 \gamma_h \mu_v c u_3 u_1 + N_h^2 \mu_h^2 c^2 u_3^2 \mu_v^2 + 2N_h^2 \mu_h^2 c^2 u_3^2 \mu_v u_1$$
$$+ 2N_h^2 \mu_h^2 \gamma_h u_1^2 c u_3 + N_h^2 \mu_h^2 c^2 u_3^2 u_1^2 + \mu_h^4 N_h^2 u_1^2 + N_h^2 \mu_h^2 u_1^4$$
$$- 2N_h^2 \mu_h^3 \mu_v^3 + N_h^2 \mu_h^2 \gamma_h^2 \mu_v^2 - 2N_h^2 \mu_h^2 \gamma_h \mu_v^3 + 2N_h^2 \mu_h^3 \gamma_h \mu_v^2$$

$$+ 4\mu_h \mu_v b^2 \beta_v A_v \beta_h A_h)^{(1/2)}\Big) / (\mu_h (\mu_v + u_1) N_h)$$

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and $\lambda_5 =$

$$-\frac{1}{2}\Big(N_h \mu_h u_1^{\,2} + N_h \mu_h^{\,2} u_1 + 2N_h \mu_h \mu_v u_1 + N_h \mu_h \gamma_h \mu_v + N_h \mu_h^{\,2} \mu_v + N_h \mu_h \mu_v^{\,2}$$
$$+ N_h \mu_h c u_3 \mu_v + N_h \mu_h \gamma_h u_1 + N_h \mu_h c u_3 u_1 + (N_h^{\,2} \mu_h^{\,2} \mu_v^{\,4} - 2\mu_h^{\,3} u_1^{\,3} N_h^{\,2}$$
$$+ N_h^{\,2} \mu_h^{\,4} \mu_v^{\,2} - 6\mu_h^{\,3} \mu_v^{\,2} N_h^{\,2} u_1 - 6\mu_h^{\,3} \mu_v N_h^{\,2} u_1^{\,2} - 2\mu_h^{\,2} u_1^{\,3} N_h^{\,2} \gamma_h$$

$$+ 2\mu_h^{\,4} N_h^{\,2} \mu_v u_1 + 2\mu_h^{\,3} N_h^{\,2} \gamma_h u_1^{\,2} + 4\mu_h^{\,3} N_h^{\,2} \gamma_h \mu_v u_1 + 2\mu_h^{\,3} N_h^{\,2} c u_3 \mu_v^{\,2}$$
$$+ 2\mu_h^{\,3} N_h^{\,2} c u_3 u_1^{\,2} - 6\mu_h^{\,2} \mu_v^{\,2} N_h^{\,2} \gamma_h u_1 - 6\mu_h^{\,2} \mu_v N_h^{\,2} \gamma_h u_1^{\,2} - 2\mu_h^{\,2} \mu_v^{\,3} N_h^{\,2} c$$
$$- 6\mu_h^{\,2} \mu_v^{\,2} N_h^{\,2} c u_3 u_1 - 6\mu_h^{\,2} \mu_v N_h^{\,2} c u_3 u_1^{\,2} - 4\mu_h \mu_v b^2 \beta_v A_v \beta_h A_h u_2$$

$$- 2\mu_h^{\,2} u_1^{\,3} N_h^{\,2} c u_3 + 4\mu_h u_1 b^2 \beta_v A_v \beta_h A_h - 4\mu_h u_1 b^2 \beta_v A_v \beta_h A_h u_2$$
$$+ 4\mu_h^{\,3} N_h^{\,2} c u_3 \mu_v u_1 + 4N_h^{\,2} \mu_h^{\,2} u_1^{\,3} \mu_v + 6N_h^{\,2} \mu_h^{\,2} u_1^{\,2} \mu_v^{\,2} + 4N_h^{\,2} \mu_h^{\,2} \mu_v^{\,3} u_1$$
$$+ N_h^{\,2} \mu_h^{\,2} \gamma_h^{\,2} u_1^{\,2} + 2N_h^{\,2} \mu_h^{\,2} \gamma_h \mu_v^{\,2} c u_3 + 2N_h^{\,2} \mu_h^{\,2} \gamma_h^{\,2} \mu_v u_1$$

$$+ 4N_h^{\,2} \mu_h^{\,2} \gamma_h \mu_v c u_3 u_1 + N_h^{\,2} \mu_h^{\,2} c^2 u_3^{\,2} \mu_v^{\,2} + 2N_h^{\,2} \mu_h^{\,2} c^2 u_3^{\,2} \mu_v u_1$$
$$+ 2N_h^{\,2} \mu_h^{\,2} \gamma_h u_1^{\,2} c u_3 + N_h^{\,2} \mu_h^{\,2} c^2 u_3^{\,2} u_1^{\,2} + \mu_h^{\,4} N_h^{\,2} u_1^{\,2} + N_h^{\,2} \mu_h^{\,2} u_1^{\,4}$$
$$- 2N_h^{\,2} \mu_h^{\,3} \mu_v^{\,3} + N_h^{\,2} \mu_h^{\,2} \gamma_h^{\,2} \mu_v^{\,2} - 2N_h^{\,2} \mu_h^{\,2} \gamma_h \mu_v^{\,3} + 2N_h^{\,2} \mu_h^{\,3} \gamma_h \mu_v^{\,2}$$

$$+ 4\mu_h \mu_v b^2 \beta_v A_v \beta_h A_h)^{(1/2)}\Big) \Big/ (\mu_h (\mu_v + u_1) N_h)$$

Eigen value that we found, we can see that $\lambda_1 = -\mu_h, \lambda_2 = -\mu_h, \lambda_3 = -\mu_v - u_1 \quad \lambda_4, \lambda_5$ as we can see also are negative value. Based on that disease-free equilibrium point called as asymptotical stable. Furthermore, the basic reproduction number will be determined. To determine the basic reproduction number, the next generation matrix method is used with the following stages.

I. Create Jacobian Matrix covered *infected* classes I_h, I_v

$$J(I_h, I_v) = \begin{bmatrix} (-\gamma_h - cu_3 - \mu_h) & \dfrac{(1-u_2) b\beta_h S_h}{N_h} \\ \dfrac{b\beta_v S_v}{N_h} & (-\mu_v - u_1) \end{bmatrix}$$

II. Substitute disease-free equilibrium point $E_0 = \left(\dfrac{A_h}{\mu_h}, 0, 0, \dfrac{A_v}{\mu_v + u_1}, 0\right)$ in

$$J\left(\frac{A_h}{\mu_h}, 0, 0, \frac{A_v}{\mu_v + u_1}, 0\right) = \begin{bmatrix} (-\gamma_h - cu_3 - \mu_h) & \dfrac{(1-u_2) b\beta_h A_h}{\mu_h N_h} \\ \dfrac{b\beta_v A_v}{N_h (\mu_v + u_1)} & (-\mu_v - u_1) \end{bmatrix}$$

III. Define matrix $J = F - V$ with

$$F = \begin{bmatrix} 0 & \dfrac{(1-u_2) b\beta_h A_h}{\mu_h N_h} \\ \dfrac{b\beta_v A_v}{N_h (\mu_v + u_1)} & 0 \end{bmatrix}$$

and $V = \begin{bmatrix} (\gamma_h + cu_3 + \mu_h) & 0 \\ 0 & \mu_v + u_1 \end{bmatrix}$ so that

we get $V^{-1} = \begin{bmatrix} \dfrac{1}{(\gamma_h + cu_3 + \mu_H)} & 0 \\ 0 & \dfrac{1}{\mu_v + u_1} \end{bmatrix}$

IV. Moreover

$$FV^{-1} = \begin{bmatrix} 0 & \dfrac{(1-u_2) b\beta_h A_h}{(\mu_h N_h)(\mu_v + u_1)} \\ \dfrac{b\beta_v A_v}{(N_h)(\mu_v + u_1)(\gamma_h + cu_3 + \mu_H)} & 0 \end{bmatrix}$$

And value of basic reproduction number R_0 decided with $R_0 = \rho\left(FV^{-1}\right)$.

V. Count the value of $\left|\lambda I - FV^{-1}\right| = 0$ and we get

$$\begin{vmatrix} \lambda & -\dfrac{(1-u_2) b\beta_h A_h}{(\mu_h N_h)(\mu_v + u_1)} \\ -\dfrac{b\beta_v A_v}{(N_h)(\mu_v + u_1)(\gamma_h + cu_3 + \mu_H)} & \lambda \end{vmatrix} = 0 \qquad (4)$$

Equation (4) above has values of Eigen numbers are:

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$$\lambda_{1,2} = \pm\sqrt{\frac{(1-u_2)b^2\beta_h\beta_v A_h A_v}{N_h{}^2\mu_h(\mu_v+u_1)^2(\mu_h+\gamma_h+cu_3)}} \qquad (5)$$

We take $R_0 = \sqrt{\frac{(1-u_2)b^2\beta_h\beta_v A_h A_v}{N_h{}^2\mu_h(\mu_v+u_1)^2(\mu_h+\gamma_h+cu_3)}}$ is a spectral radius or the biggest of eigen value from λ_1, λ_2 After analyzing the local stability of the disease-free equilibrium point, then analyzing the local stability of the endemic equilibrium point is carried out. By using the Jacobian matrix in equation (2) and by substituting the endemic equilibrium point in equation (2), the following matrix $J(f(E_1))$ is obtained in equation (6).

$$J(f(E_1)) = \begin{bmatrix} -(1-u_2)\frac{b\beta_h I_v^*}{N_h} - \mu_h & 0 & 0 & 0 & -(1-u_2)\frac{b\beta_h S_h^*}{N_h} \\ (1-u_2)\frac{b\beta_h I_v^*}{N_h} & -(\gamma_h+\mu_h+cu_3) & 0 & 0 & (1-u_2)\frac{b\beta_h S_h^*}{N_h} \\ 0 & (\gamma_h+cu_3) & -\mu_h & 0 & 0 \\ 0 & -\frac{b\beta_v S_v^*}{N_h} & 0 & -(\mu_v+u_1) & 0 \\ 0 & \frac{b\beta_v S_v^*}{N_h} & 0 & \frac{b\beta_v I_h^*}{N_h} & -(\mu_v+u_1) \end{bmatrix} \qquad (6)$$

with $S_h^* = \dfrac{A_h}{(1-u_2)\frac{b\beta_h S_h I_v}{N_h} + \mu_h}$,

$$I_h^* = \frac{(1-u_2)\frac{b\beta_h S_h I_v}{N_h}}{(\gamma_h+\mu_h+cu_3)},\quad R_h^* = \frac{(\gamma_h+cu_3)I_h}{\mu_h}$$

$$S_v^* = \frac{A_v}{\left(\mu_v+u_1+\frac{b\beta_v I_h}{N_h}\right)} \text{ and } I_v^* = \frac{\frac{b\beta_v S_v I_h}{N_h}}{(\mu_v+u_1)}$$

From (6) created characterictic equation $\left|\lambda I - J(f(E_1))\right| = 0$ with matrix $\lambda I - J(f(E_1))$ served into matrix Q in equation (7) bellow.

$$Q := \begin{bmatrix} \lambda + \frac{(1-u_2)\,b\,\beta_h I_v}{N_h} + \mu_h, & 0, & 0, & 0, & \frac{(1-u_2)\,b\,\beta_h S_h}{N_h} \\ -\frac{(1-u_2)\,b\,\beta_h I_v}{N_h}, & \lambda+\mu_h+\gamma_h+c\,u_3, & 0, & 0, & -\frac{(1-u_2)\,b\,\beta_h S_h}{N_h} \\ 0, & -\gamma_h - c\,u_3, & \lambda+\mu_h, & 0, & 0 \\ 0, & \frac{b\,\beta_v S_v}{N_h}, & 0, & \lambda+\mu_v+u_1, & 0 \\ 0, & -\frac{b\,\beta_v S_v}{N_h}, & 0, & -\frac{b\,\beta_v I_h}{N_h}, & \lambda+\mu_v+u_1 \end{bmatrix} \qquad (7)$$

From matrix in equation (7) we search its determinant and equal by zero, then we get this results as follows

$$\begin{aligned} &-(\lambda+\mu_h)(-N_h^3\lambda^3 c\,u_3 - 2N_h^3\lambda^2\gamma_h\mu_v - 2N_h^3\lambda^2\mu_v u_1 - 2N_h^3\lambda\mu_h u_1^2 \\ &-2N_h^3\lambda\mu_h\mu_v^2 - N_h^3\lambda\gamma_h u_1^2 - N_h^3\lambda\gamma_h\mu_v^2 - \mu_h N_h^3\gamma_h u_1^2 - 2N_h^3\lambda^2\gamma_h u_1 \\ &-N_h^3\lambda^4 - 4N_h^3\lambda^2\mu_h u_1 - 4N_h^3\lambda^2\mu_h\mu_v - 2N_h^3\lambda^3\mu_h - \mu_h^2 N_h^3 u_1^2 - \mu_h^2 N_h^3\lambda^2 \\ &-2N_h^3\lambda^3 u_1 - N_h^3\lambda^3\gamma_h - N_h^3\lambda^2\mu_v^2 - 2N_h^3\lambda^3\mu_v - N_h^3\lambda^2 u_1^2 - \mu_h^2 N_h^3\mu_v^2 \\ &-\mu_h N_h^3\gamma_h\mu_v^2 - \mu_h N_h^3\gamma_h\lambda^2 - 2\mu_h^2 N_h^3\lambda\mu_v - 2\mu_h^2 N_h^3\lambda u_1 - 2\mu_h^2 N_h^3\mu_v u_1 \\ &-4N_h^3\lambda\mu_h\mu_v u_1 - 2N_h^3\lambda\gamma_h\mu_v u_1 - N_h^3\lambda c\,u_3\mu_v^2 - N_h^3\lambda c\,u_3 u_1^2 \\ &-2N_h^3\lambda^2 c\,u_3\mu_v - 2N_h^3\lambda^2 c\,u_3 u_1 - 2N_h^3\lambda c\,u_3\mu_v u_1 - \lambda b^3\beta_v^2 S_v\beta_h S_h I_h \\ &+\lambda b^3\beta_v^2 S_v\beta_h S_h I_h u_2 + N_h\lambda^2 b^2\beta_v S_v\beta_h S_h + N_h\lambda b^2\beta_v S_v\beta_h S_h\mu_v \\ &+N_h\lambda b^2\beta_v S_v\beta_h S_h u_1 - N_h\lambda^2 b^2\beta_v S_v\beta_h S_h u_2 - N_h\lambda b^2\beta_v S_v\beta_h S_h u_2\mu_v \\ &-N_h\lambda b^2\beta_v S_v\beta_h S_h u_2 u_1 - b\beta_h I_v N_h^2\lambda u_1^2 - b\beta_h I_v N_h^2\mu_h u_1^2 \\ &-b\beta_h I_v N_h^2\mu_h\mu_v^2 - b\beta_h I_v N_h^2\gamma_h u_1^2 - b\beta_h I_v N_h^2\gamma_h\mu_v^2 - b\beta_h I_v N_h^2\gamma_h\lambda^2 \\ &-b\beta_h I_v N_h^2\lambda\mu_v^2 - b\beta_h I_v N_h^2\mu_h\lambda^2 - 2b\beta_h I_v N_h^2\lambda\mu_v u_1 - 2b\beta_h I_v N_h^2\mu_h\lambda\mu_v \\ &-2b\beta_h I_v N_h^2\mu_h\lambda u_1 - 2b\beta_h I_v N_h^2\mu_h\mu_v u_1 - 2b\beta_h I_v N_h^2\gamma_h\lambda\mu_v \\ &-2b\beta_h I_v N_h^2\gamma_h\lambda u_1 - 2b\beta_h I_v N_h^2\gamma_h\mu_v u_1 - b\beta_h I_v N_h^2 c\,u_3\lambda^2 \\ &-b\beta_h I_v N_h^2 c\,u_3\mu_v^2 - b\beta_h I_v N_h^2 c\,u_3 u_1^2 - 2b\beta_h I_v N_h^2\lambda^2 u_1 - 2b\beta_h I_v N_h^2\lambda^2\mu_v \end{aligned}$$

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\begin{aligned}
&-b\beta_h I_v N_h^2 \lambda^3 - 2b\beta_h I_v N_h^2 c u_3 \lambda \mu_v - 2b\beta_h I_v N_h^2 c u_3 \lambda u_1 \\
&-2b\beta_h I_v N_h^2 c u_3 \mu_v u_1 + b\beta_h I_v u_2 N_h^2 \lambda u_1^2 + b\beta_h I_v u_2 N_h^2 \mu_h u_1^2 \\
&+b\beta_h I_v u_2 N_h^2 \mu_h \mu_v^2 + b\beta_h I_v u_2 N_h^2 \gamma_h u_1^2 + b\beta_h I_v u_2 N_h^2 \gamma_h \mu_v^2
\end{aligned}
$$

$$
\begin{aligned}
&+b\beta_h I_v u_2 N_h^2 \gamma_h \lambda^2 + b\beta_h I_v u_2 N_h^2 \lambda \mu_v^2 + b\beta_h I_v u_2 N_h^2 \mu_h \lambda^2 \\
&+2b\beta_h I_v u_2 N_h^2 \lambda \mu_v u_1 + 2b\beta_h I_v u_2 N_h^2 \mu_h \lambda \mu_v + 2b\beta_h I_v u_2 N_h^2 \mu_h \lambda u_1 \\
&+2b\beta_h I_v u_2 N_h^2 \mu_h \mu_v u_1 + 2b\beta_h I_v u_2 N_h^2 \gamma_h \lambda \mu_v + 2b\beta_h I_v u_2 N_h^2 \gamma_h \lambda u_1
\end{aligned}
$$

$$
\begin{aligned}
&+2b\beta_h I_v u_2 N_h^2 \gamma_h \mu_v u_1 + b\beta_h I_v u_2 N_h^2 c u_3 \lambda^2 + b\beta_h I_v u_2 N_h^2 c u_3 \mu_v^2 \\
&+b\beta_h I_v u_2 N_h^2 c u_3 u_1^2 + 2b\beta_h I_v u_2 N_h^2 \lambda^2 u_1 + 2b\beta_h I_v u_2 N_h^2 \lambda^2 \mu_v \\
&+b\beta_h I_v u_2 N_h^2 \lambda^3 + 2b\beta_h I_v u_2 N_h^2 c u_3 \lambda \mu_v + 2b\beta_h I_v u_2 N_h^2 c u_3 \lambda u_1
\end{aligned}
$$

$$
\begin{aligned}
&+2b\beta_h I_v u_2 N_h^2 c u_3 \mu_v u_1 - 2\mu_h N_h^3 \gamma_h \lambda \mu_v - 2\mu_h N_h^3 \gamma_h \lambda u_1 - 2\mu_h N_h^3 \gamma_h \mu_v u_1 \\
&-\mu_h N_h^3 c u_3 \lambda^2 - \mu_h N_h^3 c u_3 \mu_v^2 - \mu_h N_h^3 c u_3 u_1^2 - 2\mu_h N_h^3 c u_3 \lambda \mu_v \\
&-2\mu_h N_h^3 c u_3 \lambda u_1 - 2\mu_h N_h^3 c u_3 \mu_v u_1 - \mu_h b^3 \beta_v^2 S_v \beta_h S_h I_h
\end{aligned}
$$

$$
\begin{aligned}
&+\mu_h b^3 \beta_v^2 S_v \beta_h S_h I_h u_2 + \mu_h N_h b^2 \beta_v S_v \beta_h S_h \lambda + \mu_h N_h b^2 \beta_v S_v \beta_h S_h \mu_v \\
&+\mu_h N_h b^2 \beta_v S_v \beta_h S_h u_1 - \mu_h N_h b^2 \beta_v S_v \beta_h S_h u_2 \lambda - \mu_h N_h b^2 \beta_v S_v \beta_h S_h u_2 \mu_v \\
&-\mu_h N_h b^2 \beta_v S_v \beta_h S_h u_2 u_1) \Big/ N_h^3 = 0
\end{aligned}
$$

After carrying out a stability analysis for the disease-free equilibrium point and for the endemic equilibrium point, a simulation was then carried out on the SIR-SI model above which was divided into model simulations when disease-free and when endemic. To carry out the simulation, there are values for the parameters used which can be seen in full in table 1 below.

Table 1. Values of parameters transmission dengue virus model SIR-SI considering fumigation, vaccination and treatment

Parameters	Symbol	Value
Individual Birth Rate Per Capita	A_h	$\frac{1000}{65(365)}$
Amount of Mosquito Reqruitment	A_v	5000
Rate of Human Birth	μ_h	$\frac{1}{65(365)}$
Rate of Death Mosquito Naturally	μ_v	$\frac{1}{30}$
Rate of Death Mosquito Caused Fumigation	μ_1	1
Rate of Bites Mosquitos to human	b	1
Probability Transmission Virus from infected mosquitos to suspect human	β_h	0.75
Probability Transmission Virus from infected human to suspect mosquitos	β_v	0.375
Rate of recovery human infected	γ_h	$\frac{1}{14}$
Amount of human population	N_h	2274000
Control of vaccination to suspect human	u_2	0.9
Control of treatment to infected human	u_3	0.9
Coefficient value of treatment control	c	0.5

In this **simulation 1**, number of health human population is 2274000 so that suspect human defined as $S_h(0) = 1850000$. This amount based on the presented the Government of Tangerang City. Moreover, number of initial value of infected human $I_h(0) = 725000$ and initial value of recovery human $R_h(0) = 710000$. This data based on the health board of Tangerang City.

Next, number of suspect mosquitos is 225000 and because of that, the initial value $S_v(0) = 225000$. Initial value of infected mosquito $I_v(0) = 210000$. Assumed reqruitment of mosquitos $A_v = 50000$ and using parameter on Table 1 above we get basic reproduction number $R_0 = 0.7863699062 < 1$ meaning that disease-free equilibrium point is asymptotically stable. Moreover, for the next

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simulation, notations of S_h, I_h, R_h, S_v, I_v are written as s, i, r, f, g. Using parameters above in the table 1, we get graphics shown interaction between human class (S_h, I_h, R_h) and vector class S_v, I_v considering fumigation, vaccination and treatmen bellow.

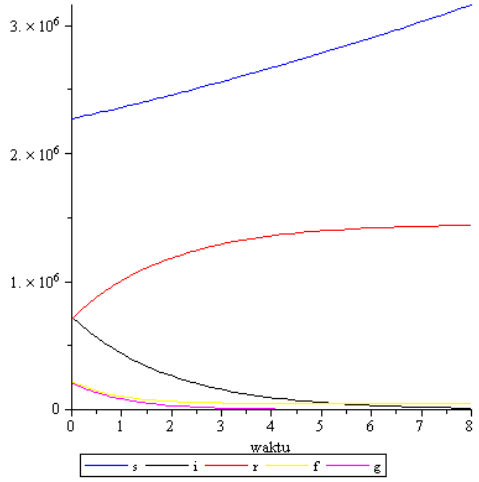

Figure 2. Behavior graphics of model SIR-SI considering fumigation, vaccination and treatment in the disease-free equilibrium point.

Figure 2 above shows class S_h, I_h, R_h, S_v, I_v behavior. The S_h class at the beginning of time is high as it enters the infected class. After experiencing an increase, the class I_h will subside (fall) towards zero or the dengue fever will disappear. A class R_h containing recovered individuals will rise and stabilize to a certain position.

Furthermore, classes S_v appear to have decreased and classes I_v have also decreased and are heading to zero or it could also be said that there are no mosquitoes that will transmit the dengue virus. After carrying out the simulation during disease-free conditions, the simulation is then carried out during endemic conditions. At this time, a change in parameter occurs, and with this, the basic reproduction number becomes. The behavior of the spread of the dengue virus or the interaction between host and vector classes in endemic conditions is depicted in Figure 3 below.

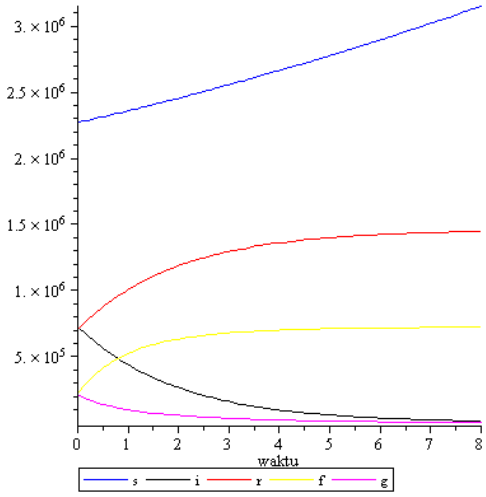

Figure 3. Behaviour graphics of SIR-SI model considering fumigation, vaccination and treatment at endemic equilibrium point.

Figure 3 above provides information that when an endemic occurs; it is characterized by an increase in the number of mosquito recruitment from 50,000 to 75,000, making the basic reproduction number value greater than 1, which indicates that the endemic equilibrium point is locally asymptotically stable.

The striking difference in figure 3 above is that the class of mosquitoes infected with the dengue virus will not decrease for the given time so that there will still be dengue fever because of this.

Simulation 2, actually is the same of simulation 1 but we change some values of parameter shown as Tabel 2 bellow.

Table 2. Values of Parameters Mathematics Model of Dengue Fever

Parameters	**Symbol**	**Value**
Individual Birth Rate Per Capita	A_h	$\frac{1000}{65(365)}$
Amount of Mosquito Reqruitment	A_v	5000
Rate of Human Birth	μ_h	$\frac{1}{65(365)}$
Rate of Death Mosquito Naturally	μ_v	$\frac{1}{30}$
Rate of Death Mosquito Caused Fumigation	μ_1	1

Rate of Bites Mosquitos to human	b	1
Probability Transmission Virus from infected mosquitos to suspect human	β_h	0.75
Probability Transmission Virus from infected human to suspect mosquitos	β_v	0.375
Rate of recovery human infected	γ_h	$\frac{1}{14}$
Amount of human population	N_h	2274000
Control of vaccination to suspect human	u_2	1
Control of treatment to infected human	u_3	1
Coefficient value of treatment control	c	1

In this simulation 2, we change value of u_2 , u_3 and c from 0,9 into 1, and number A_v is 50000 for disease free equilibrium and A_v is 75000 for disease equilibrium. The result of each part in simulation 2 can be seen in figure 4 and 5 bellow.

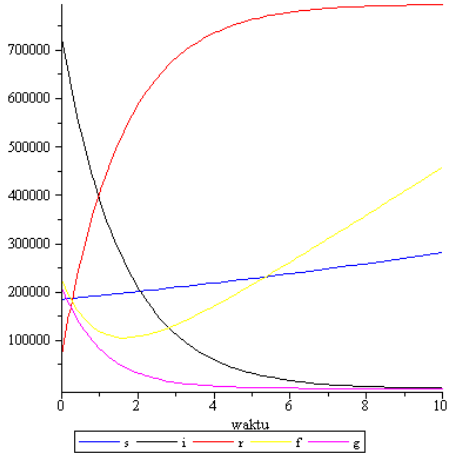

Figure 4. Behavior graphics in the free disease Equilibrium Point

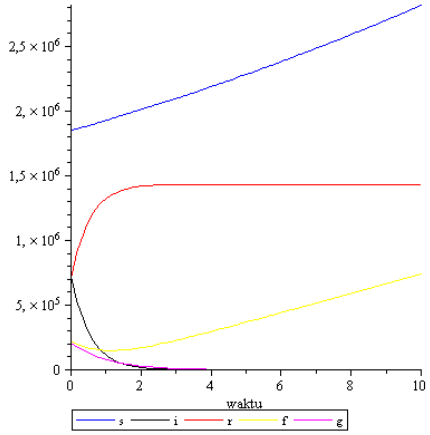

Figure 5. Behaviour graphics in the disease Equilibrium Point

Based on Figure 4, it can be seen that if we change the value of parameter u_2 , u_3 and c from 0,9 into 1, the number of suspect human seems like constant growth, infected human decrease and recovery human enhance. Based on Picture 5, we can see that the behaviour of the model seems like as Picture 4 but with there is some different as you can see, because this simulation in the disease equilibrium point. Based on simulation above, we can say recomendation for the Government to face off dengue fever such as increase the vaccination, fumigation and treatment but based on measurement.

CONCLUTION

Conclusions that can be summarized from the results of this research include:

I. Mathematical model of the spread of the SIR-SI dengue virus or the interaction between host and vector by observing spraying, vaccination and treatment, and tou can see at equation system (1). From equation system (1), we also get the disease free quilibrium point and endemic equilibrium point.

II. Basic reproduction number is

$$R_0 = \sqrt{\frac{(1-u_2)b^2\beta_h\beta_v A_h A_v}{N_h^{\,2}\mu_h(\mu_v+u_1)^2(\mu_h+\gamma_h+cu_3)}}$$ with

$R_0 = 0.7863699062 < 1$ on the disease-free

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situation and $R_0 = 3.045597501 > 1$ on the endemic situation.

III. The disease-free equilibrium point has local asymptotic stability, as does the endemic equilibrium point. This can be seen from the eigenvalue, which is negative. By looking at the basic reproductive value of each disease-free equilibrium point condition and when it is endemic, this means that when the condition is disease-free, there will be no outbreak because humans and mosquitoes infected with the dengue virus will decrease and go towards zero. On the other hand, when it is endemic, there will still be dengue virus outbreaks because mosquitoes will still be alive.

IV. From simulation 1 and 2, we can see that if the parameter u_2, u_3 and c changed from 0.9, 0.9,0.5 into 1,1,1, the suspect virus increased. This is indicated that the doze can't over, eventhough the recovery human increased for those two simulations.

Conflicts of interest

There are no conflicts of interest

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