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e-ISSN: 2774-2016 - https://journal.itera.ac.id/index.php/indojam/
p-ISSN: 2774-2067

Mathematics Model SIRS-SI of Transmission Dengue Virus Considering Fumigation, Vaccination and Treatment in Case of Tangerang City

Received 14th August 2024
Accepted 4th January 2025
Published 31st January 2025

Open Access

DOI
https://doi.org/10.35472/indojam.v4i2.1913

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Abstract: In this paper, we construct a mathematical model SIRS-SI transmission dengue fever considering fumigation, vaccination and treatment in case Tangerang City. Background why this research has to do because in Tangerang City the case of dengue fever is pretty lot. Method in this research is using compartment model and create differential equation system. We also do some model of analysis like determining free disease equilibrium point and endemic equilibrium point. We also determine basic reproduction number and make analyze stability of the model around equilibrium points. We also do simulation of the model and the result; model is local asymptotic stable in free disease equilibrium area and local asymptotic stable in endemic equilibrium area. When R0 <1 for free disease equilibrium point, then there are no endemic disease, otherwise when R0 > 1 for endemic equilibrium point then situation is in endemic dengue fever.

Keywords: *SIRS, Fumigation, Vaccination, Treatment, Dengue*

Abstrak: Paper ini berisikan hasil penelitian tentang model matematika SIRS-SI transmisi virus dengue dengan melibatkan adanya pengasapan, vaksinasi, dan pengobatan untuk studi kasus Kota Tangerang. Latar belakang dilakukannya penelitian ini dikarenakan kasus wabah penyakit demam berdarah di Kota Tangerang cukup banyak. Metode dalam penelitian ini menggunakan model kompartmen dan dari model tersebut dibentuk sistem persamaan diferensial. Pada penelitian ini, kami juga melakukan analisa mengenai titik kesetimbangan bebas penyakit dan titik kesetimbangan pada saat endemik. Kami juga melakukan simulasi dari model yang telah dibentuk dan hasilnya model stabil asimtotik disekitar titik kesetimbangan bebas penyakit begitu pula disekitar titik ekuilibrium endemik. Karena R0 <1 untuk titik ekuilibrium bebas penyakit, hal demikian menandakan tidak terjadi wabah. Lebih lanjut, karena R0>1 untuk titik ekuilibrium endemik, hal ini menandakan terjadinya wabah demam berdarah.

Kata Kunci: *SIRSI, Pengasapan, Vaksinasi, Pengobatan, Dengue*

Introduction / Pendahuluan

Dengue Fever Disease (DFD) is a disease caused by Dengue Virus (DV) spread by Aedes Aegypti mosquito. Actually, this disease not only caused by Aedes Aegypti mosquito, but also can caused by Aedes albopictus based on research by (Paupy et al., 2009), but the most vector that caused dengue fever disease is Aedes Aegypti. Human that infected by this virus will feel high body temperature, nauseous, and decrease of platelets straightly. *Antara News* reported that through year 2022, in Tangerang Regency there are at least 1322 cases of dengue fever disease. Moreover, *Republika News* reported that since January 2022, at least there are 577 cases of this disease, and in Tangerang, report of *Media Indonesia*; there are 331 cases of fever by caused by aedes Aegypti. All that news informs that Great Tangerang Region is a place with pretty much cases disease caused by Aedes Aegypti bitten include giving information that the dengue virus is so dangerous so we need to take an action to prevent, so that bad impact of this virus does not spread wider.

The spreading dengue virus actually involves interaction of human or host (h) and mosquito as vector

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(v). Host divided by three classes, i.e., Suspect host S_h, Infected host I_h and Recovery host R_h.

Suspect host class means that some people classified as population that risked bitten Aedes Aegypti mosquito. Individual that bitten by this mosquito will be infected dengue virus and we call them as infected host class. Directly, individual that infected of dengue virus called as people with dengue fever disease. Recovery host class mean as population of people that recover from dengue fever disease. People with dengue fever disease can recovered by intensive treatment, but there are no guarantee that people cannot infected dengue virus again. This word says that people in Recovery host class is very possible to come back into Suspect host class or as a whole part of information above we can call this phenomena into mathematics model SIRS.

In class of Aedes Aegypti mosquito or we call as vector, they are divided into two classes, Suspect vector S_v and Infected vector I_v. Suspect vector means as a population of Aedes Aegypti mosquito that very possible to infected by dengue virus. Note that, not all whole of Aedes Aegypti will caused dengue fever disease; only female mosquito of Aedes Aegypti with dengue virus will cause this disease. Infected vector class filled by Aedes Aegypti that has been infected of dengue virus. This mosquito is the main player to spread virus to host body so that they infected dengue fever disease. Based on that information above, classes in vector can created as mathematic model SI. Because the spread of dengue virus involves interactions between host and vector, so that the mathematic model we known as SIRS-SI.

Actually, mathematics model explains the spreading of dengue virus involves interaction between host and vector not only as SIRS-SI. The simpler model can be as SIR-SI expressed that host cannot possible going back to Suspect host class S_h. Sometimes the mathematic model also be more complicated. The researcher often add another human class and vector class named exposed human class E_h and Exposed Vector class E_v so that the mathematic model expressed as SEIR-SEI or SEIRS-SEI if we consider host can be return to Suspect host class S_h after recovery. In this paper, we only focus mathematics model spreading dengue virus SIRS-SI for the reason to restrict the discussion and make the mathematic model simpler.

Mathematic research in epidemic field especially focused in dengue virus actually has been done by many researchers. For example, research by (Khan & Fatmawati, 2021) focused in dengue infection and its optimal control analysis in East Java and research by (Ndii et al., 2020) about optimal vaccination strategy for dengue transmission in Kupang City, Indonesia. Other research done by (Ndii, 2022) about the effect of vaccination, vector controls and media on dengue transmission and research by (Aldila et al., 2023) about impact of social awareness of dengue virus in Jakarta. Mathematics model spreading dengue virus considering vaccination also done by (Chanprasopchai et al., 2018) , and research by (Sanusi et al., 2021) about analysis and simulation of SIRS model dengue fever trasnsmission in South Sulawesi. In other city, we can find research of dengue virus transmission like research SIR model spreading dengue fever in Pekanbaru (Soleh et al., 2018) and spreading pattern dengue fever with SIR model in Madiun during 2020-2022 (Baihaqi et al., 2023). In Bone Regency, research of the transmission dengue virus has been done by (Side et al., 2018) and (Mendoza, 2024) about dengue incidence model in Magalang.

The usage of Fumigation as a part in mathematics model also often carried out by some researchers. Research by (Windawati et al., 2020) tell us the mathematic model of spreading dengue fever considering fumigation. Focused on optimal control of spreading dengue virus considering insecticide and treatment. Using fumigation and considering age structure in research model of transmission dengue virus also done by (*35307-Article Text-78639-1-10-20220213*, n.d.).

Research of dengue virus consider Wolbachia invasion or considering larvicide has been success by (Hu et al., 2019) , (Naikteas Bano et al., 2022) and research of mathematic model to evaluate the role of memory B and T cells in dengue infection has been done by (Rubio & Yang, 2022).

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Based on relevance research above, we look that there is a gap, which is there is no researcher who have researched SIRS-SI model consider three matters fumigation, vaccination and treatment in case in Tangerang City. Based on this fact, we decided to take an research about mathematic transmission dengue virus SIRS-SI consider three matters above in case Tangerang City.

Research of dengue transmission not only around create mathematic SIR-SI, SIRS-SI or SEIR-SEI considering many things like fumigation, vaccination or treatment, but also develop into using many views in mathematics theory to analyze this phenomenon. We can say research by (Hosny et al., 2024) using generalized rough set to enhancing dengue fever, research of vector mosquito image classification using machine learning by (Rustam et al., 2022) and (Side et al., 2022) focused of numerical solution of mathematic model using Runge-Kutta Fourth Order method. Generally, this is the proof that mathematics can be used to explain dengue fever phenomenon and by the mathematic research, we hope dengue virus cannot spreading widely.

Method / Metode

In this research, we combine two methods between theories and applied mathematics. Mathematical theory aimed to create mathematical model of transmission dengue virus refers to mathematical modelling theory. For creating mathematical model, we use some relevance literatures so that we have scientific guide. References, which used in this research, can be seen in reference. Moreover, this is an Applied Mathematics Research. The application reflected as mathematics model of transmission dengue virus considering fumigation, vaccination and treatment in case Tangerang City.

This model can be used as a guide for The Stakeholder to take action to stop and prevent spreading dengue virus in Tangerang. Moreover, steps of this research detailed as follow.

I. Creating mathematics model of transmission dengue virus using compartment SIRS-SI consider fumigation, vaccination and treatment for host infected by this virus.
II. Analyzing the mathematical model SIRS-SI, like determining the equilibrium points. Equilibrium point in the epidemical model usually divided as two forms. The first is free disease equilibrium point and second is endemic equilibrium point. For analyzing the mathematic SIRS-SI model, we also determine basic reproduction number using next generation operator or new generation matrix. We also do local-stable analyzing of the free disease equilibrium point and analysis endemic equilibrium point. For determining the local stable analysis researcher usually analysis the Eigen value of Jacobian matrix. But if the Eigen values cannot be determined, Rough-Hurwitz criterion can be used.
III. Making a simulation of mathematical model SIRS-SI of transmission dengue virus by substituting the number of determined parameters into the model. To make the simulation and resume we use MAPLE software.

Results And Discussion

To create mathematic model that explained the transmission of dengue fever in Tangerang City considering fumigation, vaccination and treatment, we classified host into three classes named Suspect host S_h, infected host I_h and recovery host R_h. By assuming, the recovery host class can return into Suspect host class S_h, then we call our model as SIRS mathematical model.

We classify into two classes, Suspect vector class S_v and infected vector class I_v. The transmission of Dengue virus only happened if there is an interaction between host and vector so that we get compartment model shown in picture 1 below.

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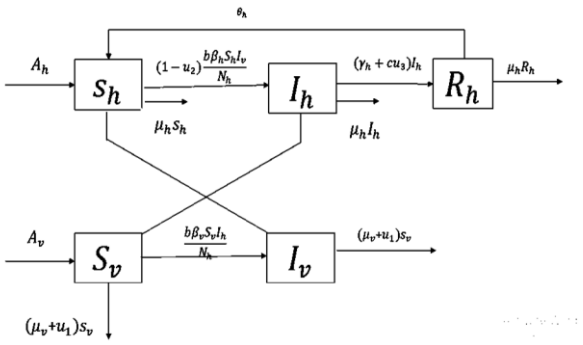

Picture 1. SIRS-SI Model of human and Vector Population considering Fumigation, Vaccination and Treatment.

Compartment model in picture 2 full of notation and parameter. For understanding them, here we delivering the meaning of every notation and parameter that used in the model picture 2.

A_h : Amount of human birth per capita

A_v : Amount of mosquito recruitment

μ_h : Rate of human birth

μ_v : Rate of death mosquitos naturally

u_1 : Rate of death mosquitos caused fumigation

u_2 : Control of vaccination to suspected host

u_3 : Control of treatment of infected host of dengue virus

b : Rate of mosquito bite to host

β_h : Probability of transmission dengue virus from Infected vector to suspected host

β_v : Probability of transmission dengue virus from infected host to suspected vector

γ_h : Rate of host recovery

N_h : Amount of host population.

c : Coefficient of treatment of infected host.

After understanding the meaning of notation and parameter used in compartment model in picture 1, here we delivered model picture 1 into differential equation system as follow

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

Picture 2. Differential Equation System

ANALYSIS MATHEMATICS MODEL SIRS-SI

After constructing the mathematical model delivered in (1), then we do some analysis like determine the equilibrium point of free disease and endemic disease, determining basic reproduction number and local-stable analyze around those equilibrium points. Every single part of discussion will be explained in their own section below.

Equilibrium Point

Equilibrium Point found by creating equation in system (1) then equal by zero, or we can write mathematically as $\frac{dS_h}{dt} = 0$, $\frac{dI_h}{dt} = 0$, $\frac{dR_h}{dt} = 0$, $\frac{dS_v}{dt} = 0$ and $\frac{dI_v}{dt} = 0$. The result of equilibrium point can be as free disease equilibrium point and endemic equilibrium point.

Free Disease Equilibrium Point

Free disease equilibrium Point means condition with no spreading dengue fever in a population. That means, this equilibrium point happened when $I_h = 0$, $I_v = 0$. Free disease equilibrium point delivered as $E_0 = (S_h, I_h, R_h, S_v, I_v) = (\frac{A_h + \theta_h}{\mu_h} 0,0, \frac{A_v}{(\mu_v + u_1)}, 0)$.

Endemic Equilibrium Point

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Endemic equilibrium point is a condition of human population infected by dengue virus.

This condition means that $I_h = 0, I_v = 0$. Based on that, we get an endemic equilibrium point defined as $E_0 = \left(S_h^*, I_h^*, R_h^*, S_v^*, I_v^*\right)$ which every single part defined as:

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

$$R_h^* = \frac{\left(\gamma_h + cu_3\right) I_h}{\mu_h + \theta_h}, \quad S_v^* = \frac{A_v}{\frac{b\beta_v I_h}{N_h} + \left(\mu_v + u_1\right)} \text{ and}$$

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

Alternatively, the complete process to get endemic equilibrium point can be seen as follows. From (1) we get

$$A_h - \left(1-u_2\right)\frac{b\beta_h S_h I_v}{N_h} - \mu_h S_h + \theta_h R_h = 0 \quad (2)$$

$$\left(1-u_2\right)\frac{b\beta_h S_h I_v}{N_h} - \left(\gamma_h + cu_3\right) I_h - \mu_h I_h = 0 \quad (3)$$

$$\left(\gamma_h + cu_3\right) I_h - \mu_h R_h - \theta_h R_h = 0 \quad (4)$$

$$A_v - \frac{b\beta_v S_v I_h}{N_h} - \left(\mu_v + u_1\right) S_v = 0 \quad (5)$$

$$\frac{b\beta_v S_v I_h}{N_h} - \left(\mu_v + u_1\right) I_v = 0 \quad (6)$$

From (2) we get

$$A_h - \mu_h S_h + \theta_h R_h = \left(1-u_2\right)\frac{b\beta_h S_h I_v}{N_h} \quad (7)$$

From (3) we get

$$\left(1-u_2\right)\frac{b\beta_h S_h I_v}{N_h} = \left(\gamma_h + cu_3 + \mu_h\right) I_h \quad (8)$$

From (7) and (8) we get

$$A_h - \mu_h S_h + \theta_h R_h = \left(\gamma_h + cu_3 + \mu_h\right) I_h$$

$$\mu_h S_h = -\left(\gamma_h + cu_3 + \mu_h\right) I_h + A_h + \theta_h R_h$$

$$S_h = \frac{-\left(\gamma_h + cu_3 + \mu_h\right) I_h + A_h + \theta_h R_h}{\mu_h} \quad \textbf{(9)}$$

From (4) we get

$$\left(\gamma_h + cu_3\right) I_h - \left(\mu_h + \theta_h\right) R_h = 0$$

$$\left(\gamma_h + cu_3\right) I_h = \left(\mu_h + \theta_h\right) R_h$$

$$R_h = \frac{\left(\gamma_h + cu_3\right)}{\left(\mu_h + \theta_h\right)} I_h \quad \textbf{(10)}$$

From (9) and (10) we get

$$S_h = \frac{-\left(\gamma_h + cu_3 + \mu_h\right) I_h \left(\mu_h + \theta_h\right) + A_h\left(\mu_h + \theta_h\right) + \theta_h\left(\gamma_h + cu_3\right) I_h}{\mu_h\left(\mu_h + \theta_h\right)}$$

(10a)

From (5) we get

$$A_v - \frac{b\beta_v S_v I_h}{N_h} = \left(\mu_v + u_1\right) S_v$$

$$S_v = \frac{A_v N_h}{b\beta_v I_h + \left(\mu_v + u_1\right) N_h} \quad \textbf{(11)}$$

Notice (6) and Using (11), substitute (6) we get

$$\frac{b\beta_v S_v I_h}{N_h} - \left(\mu_v + u_1\right) I_v = 0$$

$$I_v = \frac{b\beta_v S_v I_h}{N_h\left(\mu_v + u_1\right)} \quad \textbf{(11a)}$$

$$I_v = \frac{b\beta_v I_h}{N_h\left(\mu_v + u_1\right)}\left(\frac{A_v N_h}{b\beta_v I_h + \left(\mu_v + u_1\right) N_h}\right) \quad \textbf{(12)}$$

Substitute (12) to (8) we get:

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

$$\frac{A_v\left(1-u_2\right) b^2 \beta_h S_h \beta_v I_h}{N_h\left(\mu_v + u_1\right) b\beta_v I_h + N_h{}^2\left(\mu_v + u_1\right)^2} = \left(\gamma_h + cu_3 + \mu_h\right) I_h$$

(13)

Remember (10a) substitute (13) we get:

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$$\frac{A_v(1-u_2)b^2\beta_h\beta_v}{N_h(\mu_v+u_1)b\beta_v I_h+N_h{}^2(\mu_v+u_1)^2}\left(\frac{-(\gamma_h+cu_3+\mu_h)I_h(\mu_h+\theta_h)+A_h(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)I_h}{\mu_h(\mu_h+\theta_h)}\right)=(\gamma_h+cu_3+\mu_h)$$

More over

$$\frac{A_v(1-u_2)b^2\beta_h\beta_v}{N_h(\mu_v+u_1)b\beta_v I_h+N_h{}^2(\mu_v+u_1)^2}\left(-\frac{(\gamma_h+cu_3+\mu_h)I_h}{\mu_h}+\frac{A_h}{\mu_h}+\frac{\theta_h(\gamma_h+cu_3)I_h}{\mu_h(\mu_h+\theta_h)}\right)=(\gamma_h+cu_3+\mu_h)$$

More over

$$\frac{-\left((\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)\right)I_h+A_h(\mu_h+\theta_h)}{\left(N_h(\mu_v+u_1)b\beta_v I_h+N_h{}^2(\mu_v+u_1)^2\right)\mu_h(\mu_h+\theta_h)}=\frac{(\gamma_h+cu_3+\mu_h)}{A_v(1-u_2)b^2\beta_h\beta_v}$$

More over

$$\left(\frac{\left(-(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)\right)I_h+A_h(\mu_h+\theta_h)}{\mu_h(\mu_h+\theta_h)\left(N_h(\mu_v+u_1)b\beta_v I_h+N_h{}^2(\mu_v+u_1)^2\right)}\right)=\frac{(\gamma_h+cu_3+\mu_h)}{A_v(1-u_2)b^2\beta_h\beta_v}$$

More over

$$\left(\frac{\left(-TQ+\theta_h(\gamma_h+cu_3)\right)I_h+A_hQ}{Q\mu_h\left(Pb\beta_v I_h+PN_h(\mu_v+u_1)\right)}\right)=\frac{T}{A_v(1-u_2)b^2\beta_h\beta_v}$$

$$\left(-TQ+\theta_h(\gamma_h+cu_3)\right)I_h+A_hQ=\frac{TQ\mu_h(Pb\beta_v I_h)}{A_v(1-u_2)b^2\beta_h\beta_v}+\frac{TQPN_h\mu_h(\mu_v+u_1)}{A_v(1-u_2)b^2\beta_h\beta_v}$$

$$\left(-TQ+\theta_h(\gamma_h+cu_3)\right)I_h-\frac{TQ\mu_h(Pb\beta_v I_h)}{A_v(1-u_2)b^2\beta_h\beta_v}=\frac{TQPN_h\mu_h(\mu_v+u_1)}{A_v(1-u_2)b^2\beta_h\beta_v}-A_hQ$$

$$I_h=\frac{\frac{TQPN_h\mu_h(\mu_v+u_1)}{A_v(1-u_2)b^2\beta_h\beta_v}-A_hQ}{\left(-TQ+\theta_h(\gamma_h+cu_3)\right)-\frac{TQ\mu_h(Pb\beta_v)}{A_v(1-u_2)b^2\beta_h\beta_v}}$$

Where

$$Q=(\mu_h+\theta_h),P=N_h(\mu_v+u_1),T=(\gamma_h+cu_3+\mu_h)$$

$$I_h=\frac{\frac{(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)N_h(\mu_v+u_1)N_h\mu_h(\mu_v+u_1)}{A_v(1-u_2)b^2\beta_h\beta_v}-A_h(\mu_h+\theta_h)}{\left(-(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)\right)-\frac{(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)\mu_h(N_h(\mu_v+u_1)b\beta_v)}{A_v(1-u_2)b^2\beta_h\beta_v}}$$

$$I_h^*=\frac{(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)N_h(\mu_v+u_1)N_h\mu_h(\mu_v+u_1)-A_h(\mu_h+\theta_h)A_v(1-u_2)b^2\beta_h\beta_v}{\left(-(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)\right)A_v(1-u_2)b^2\beta_h\beta_v-(\gamma_h+cu_3+\mu_h)(\mu_h+\theta_h)\mu_h(N_h(\mu_v+u_1)b\beta_v)} \quad (14)$$

Based on (14) then we get

$$S_h^*=\frac{-(\gamma_h+cu_3+\mu_h)I_h^*(\mu_h+\theta_h)+A_h(\mu_h+\theta_h)+\theta_h(\gamma_h+cu_3)I_h^*}{\mu_h(\mu_h+\theta_h)} \quad \textbf{(15)}$$

$$R_h^*=\frac{(\gamma_h+cu_3)}{(\mu_h+\theta_h)}I_h^* \quad \textbf{(16)}$$

$$S_v^*=\frac{A_vN_h}{b\beta_v I_h^*+(\mu_v+u_1)N_h} \quad \textbf{(17)}$$

$$I_v^*=\frac{b\beta_v I_h^*}{N_h(\mu_v+u_1)}\left(\frac{A_vN_h}{b\beta_v I_h^*+(\mu_v+u_1)N_h}\right) \quad \textbf{(18)}$$

After determined free disease and endemic equilibrium point, then we determined basic reproduction number. Basic reproduction number is measurement of seconder infection that will happened because one infection primer in a population substance suspect. For determining basic reproduction number R_0, we can use next generation operator method or next generation matrix method. In this paper, we use New Generation Matrix method to determine basic reproduction number (R_0)as follow.

I. We create Jacobian matrix contain subclass Infected I_h, I_v

$$J(I_h,I_v)=\begin{bmatrix}\frac{\partial\dot{I}_h}{I_h} & \frac{\partial\dot{I}_h}{I_v}\\ \frac{\partial\dot{I}_v}{I_h} & \frac{\partial\dot{I}_v}{I_v}\end{bmatrix}=\begin{bmatrix}-(\gamma_h+cu_3+\mu_h) & (1-u_2)\frac{b\beta_hS_h}{N_h}\\ \frac{b\beta_vS_v}{N_h} & -(\mu_v+u_1)\end{bmatrix} \quad (17)$$

II. Substitute free disease equilibrium

$$E_0=(S_h,I_h,R_h,S_v,I_v)$$

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$= \left(\frac{A_h + \theta_h R_h}{\mu_h} 0,0, \frac{A_v}{(\mu_v + u_1)}, 0 \right)$ into (17) then we get

$$J\left(\frac{A_h + \theta_h R_h}{\mu_h}, 0, 0, \frac{A_v}{(\mu_v + u_1)}, 0 \right) = \begin{bmatrix} -(\gamma_h + cu_3 + \mu_h) & (1-u_2)\frac{b\beta_h (A_h + \theta_h)}{\mu_h N_h} \\ \frac{b\beta_v A_v}{N_h(\mu_v + u_1)} & -(\mu_v + u_1) \end{bmatrix} \quad (18)$$

III. Delivered matrix $J = F - V$ where F is transmission matrix and V is transition. Determine

$$F = \begin{bmatrix} 0 & (1-u_2)\frac{b\beta_h (A_h + \theta_h)}{\mu_h N_h} \\ \frac{b\beta_v A_v}{N_h(\mu_v + u_1)} & 0 \end{bmatrix} \quad (19)$$

$$V = \begin{bmatrix} (\gamma_h + cu_3 + \mu_h) & 0 \\ 0 & (\mu_v + u_1) \end{bmatrix} \quad (20)$$

$$V^{-1} = \begin{bmatrix} \frac{1}{(\gamma_h + cu_3 + \mu_h)} & 0 \\ 0 & \frac{1}{(\mu_v + u_1)} \end{bmatrix} \quad (21)$$

Using matrix (19) and (21) we get

$$FV^{-1} = \begin{bmatrix} 0 & \frac{(1-u_2)(A_h + \theta_h) b\beta_h}{(\mu_h + N_h)(\mu_v + u_1)} \\ \frac{b\beta_v A_v}{N_h(\mu_v + u_1)(\gamma_h + cu_3 + \mu_h)} & 0 \end{bmatrix} \quad (22)$$

IV. Basic reproduction number can be found with way $R_0 = \rho\left(FV^{-1}\right)$. Count $\left|\lambda I - FV^{-1}\right| = 0$, then we get:

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

$$\lambda^2 - \left(\frac{(1-u_2)(A_h + \theta_h) b\beta_h}{(\mu_h + N_h)(\mu_v + u_1)} \right) \left(\frac{b\beta_v A_v}{N_h(\mu_v + u_1)(\gamma_h + cu_3 + \mu_h)} \right) = 0$$

$$\lambda_{1,2} = \pm \sqrt{\left(\frac{(1-u_2)(A_h + \theta_h) b\beta_h}{(\mu_h + N_h)(\mu_v + u_1)} \right) \left(\frac{b\beta_v A_v}{N_h(\mu_v + u_1)(\gamma_h + cu_3 + \mu_h)} \right)} \quad (23)$$

$R_0 = \rho\left(FV^{-1}\right)$ Obtained from spectral radius or the greatest Eigen values of λ_1, λ_2 in (21) so we get

$$R_0 = \sqrt{\left(\frac{(1-u_2)(A_h + \theta_h) b\beta_h}{(\mu_h + N_h)(\mu_v + u_1)} \right) \left(\frac{b\beta_v A_v}{N_h(\mu_v + u_1)(\gamma_h + cu_3 + \mu_h)} \right)}$$

or

$$R_0 = \sqrt{\left(\frac{(1-u_2)(A_h + \theta_h) b^2 \beta_h \beta_v A_v}{N_h(\mu_h + N_h)(\mu_v + u_1)^2 (\gamma_h + cu_3 + \mu_h)} \right)} \quad (24)$$

Next, we do analysis of stability in free disease equilibrium point and endemic point. Look at this Jacobian Matrix

$$J = \begin{bmatrix} -(1-u_2)\frac{b\beta_h I_v}{N_h} - \mu_h & 0 & \theta_h & 0 & -(1-u_2)\frac{b\beta_h S_h}{N_h} \\ (1-u_2)\frac{b\beta_h I_v}{N_h} & -(\gamma_h + \mu_h + cu_3) & 0 & 0 & (1-u_2)\frac{b\beta_h S_h}{N_h} \\ 0 & (\gamma_h + cu_3) & -\mu_h - \theta_h & 0 & 0 \\ 0 & -\frac{b\beta_v S_v}{N_h} & 0 & -(\mu_v + u_1) & 0 \\ 0 & \frac{b\beta_v S_v}{N_h} & 0 & \frac{b\beta_v I_h}{N_h} & -(\mu_v + u_1) \end{bmatrix} \quad (25)$$

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Substitute $E_0 = (S_h, I_h, R_h, S_v, I_v)$ = ($\frac{A_h + \theta_h}{\mu_h}$ 0,0, $\frac{A_v}{(\mu_v + u_1)}$, 0) to (25) and we get

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

(26)

Based on (26), create $|\lambda I - J(f(0))| = 0$ and we get eigen value $\lambda_1, \lambda_2, \lambda_3, \lambda_4, \lambda_5$ sequentially as follow

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

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

$$+2N_h^2\mu_h^2 c u_3\mu_v^2\gamma_h + N_h^2\mu_h^2 c^2 u_3^2 u_1^2 + N_h^2\mu_h^2 u_1^4 - 6\mu_h^3\mu_v^2 N_h^2 u_1$$

$$-6\mu_h^3\mu_v N_h^2 u_1^2 - 2\mu_h^2\mu_v^3 N_h^2\gamma_h - 2\mu_h^2 u_1^3 N_h^2\gamma_h - 6\mu_h^2\mu_v^2 N_h^2\gamma_h u_1 - 6\mu_h^2\mu_v N_h^2\gamma_h u_1^2 - 6\mu_h^2\mu_v N_h^2 c u_3 u_1^2 - 2\mu_h^2\mu_v^3 N_h^2 c u_3 - 6\mu_h^2\mu_v^2 N_h^2 c u_3 u_1$$

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

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

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

$$\Big(N_h\mu_h\gamma_h u_1 + N_h\mu_h^2\mu_v + N_h\mu_h c u_3\mu_v + N_h\mu_h c u_3 u_1 + N_h\mu_h\mu_v^2 + N_h\mu_h^2 u_1$$

$$+N_h\mu_h u_1^2 + 2N_h\mu_h\mu_v u_1 + N_h\mu_h\gamma_h\mu_v + (-2\mu_h^3\mu_v^3 N_h^2 + N_h^2\mu_h^2\mu_v^2\gamma_h^2\mu_v^2 + 4N_h^2\mu_h^2 u_1^3\mu_v + N_h^2\mu_h^2\gamma_h^2 u_1^2 + 6N_h^2\mu_h^2\mu_v^2 u_1^2 + 4N_h^2\mu_h^2\mu_v^3 u_1$$

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

$$+N_h^2\mu_h^2 c^2 u_3^2 u_1^2 + N_h^2\mu_h^2 u_1^4 - 6\mu_h^3\mu_v^2 N_h^2 u_1 - 6\mu_h^3\mu_v N_h^2 u_1^2 - 2\mu_h^2\mu_v^3 N_h^2\gamma_h - 2\mu_h^2 u_1^3 N_h^2\gamma_h - 6\mu_h^2\mu_v^2 N_h^2\gamma_h u_1 - 6\mu_h^2\mu_v N_h^2\gamma_h u_1^2$$

$$-2\mu_h^2\mu_v^3 N_h^2 c u_3 - 6\mu_h^2\mu_v^2 N_h^2 c u_3 u_1 - 6\mu_h^2\mu_v N_h^2 c u_3 u_1^2$$

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

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

$$+4\mu_h^3 N_h^2 c u_3\mu_v u_1 + N_h^2\mu_h^2\mu_v^4)^{(1/2)}\Big) / (\mu_h(\mu_v + u_1)N_h)$$

We can see that all of Eigen values is negative, then the model is local asymptotic stable in free disease equilibrium. With the same way by using Routh-Hurwitz criterion, we will find all of Eigen values is also negative then the model is local asymptotic stable in the area of disease equilibrium point.

SIMULATION OF MODEL SIRS-SI.

To make the simulation, we determine parameters that we used in this paper which presented in table 1

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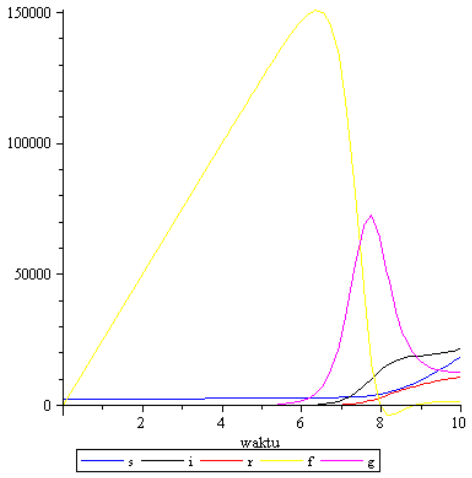
Information	Symbol	Value
Level of birth host per capita	A_h	$\frac{1000}{65(365)}$
Amount of recruitment vector	A_v	25000
Rate birth of host	μ_h	$\frac{1}{65(365)}$
Rate of death vector naturally	μ_v	$\frac{1}{30}$
Rate of death vector because fumigation	u_1	1
Rate of bitten vector on host	b	1
Probability transmission virus from infected vector to suspect host	β_h	0.75
Probability transmission virus infected host to suspect vector	β_v	0.375
Rate recovery infected host	γ_h	$\frac{1}{14}$
Amount of host population	N_h	2274
Control vaccination to suspect host	u_2	0.9
Control treatment to infected host	u_3	0.9
Coefficient treatment control	c	0.55
Rate recovery host come back to suspect host	θ	0.87

Table 1. Parameter of Model SIRS dengue virus transmission.

In this simulation, initial amount of host is 1000 so that initial value suspect host is $S_h(0) = 2274$, more over initial value of host infected $I_h(0) = 0.053$, initial value of host recovery $R_h(0) = 0.083$. Initial value of suspect vector $S_v(0) = 225$ and initial value of infected vector is $I_v(0) = 0.008$. Assumed the rate of recruitment vector is $A_v = 25000$, and substitute parameters in table 1 $R_0 = 0.8385254916 < 1$. Moreover, to simply in this simulation the notation classes S_h, I_h, R_h, S_v, I_v rewrite as s, i, r, f, g. Picture 3 below is the result of simulation showing interaction of host and vector with parameter in table 1 and the initial value delivered at free disease equilibrium point.



Picture 2. Graphic SIRS-SI model interaction between host and vector considering fumigation, vaccination and treatment at the free disease equilibrium point

Picture 2 shows that interaction between host and vector in classes S_h, I_h, R_h, S_v, I_v. Suspect Host class, Infected Host class and Recovery Host class are stable at the initial interval, but as the time increases, they are going to one point (stable asymptotic). Class of Suspect Vector growing up straightly but then decrease straightly and table asymptotic to zero. Infected Vector is increasing at certain interval and decreasing into a point or stable asymptotic. Because suspect vector is going to zero and infected vector decreasing into a point after increasing straightly, then we can say there is no Dengue virus disease.

Next, we continue to make simulation for endemic equilibrium point using parameter in table 1 and several initial conditions except the value of $A_v = 50000$. The value of A_v change from 25000 to 50000, it means that the amount of recruitment vector increasing because of endemic situation. In this simulation, we get $R_0 = 1.185854123 > 1$. Picture 3 below shows the interaction of S_h, I_h, R_h, S_v, I_v at the endemic equilibrium point.

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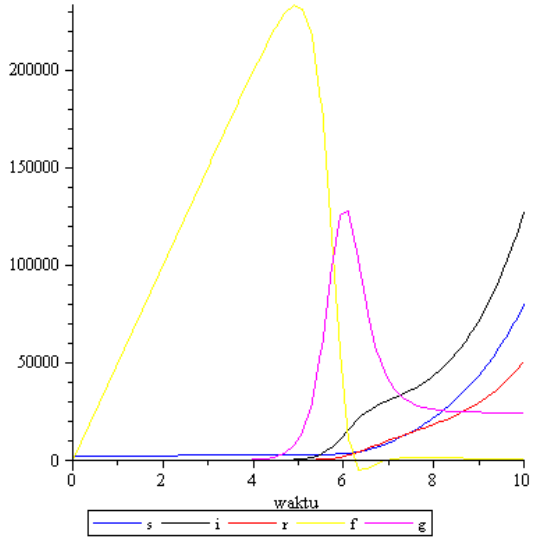

Picture 3. Graphic SIRS-SI model interaction host and vector considering fumigation, vaccination and treatment at the endemic disease equilibrium point

Picture 3 shows both suspect and infected vector are decreasing, or stable asymptotic, yet suspected host, infected host, and recovery host are still increasing. In order words it shows an Endemic Dengue Virus conditions. The value of R0 confirms that conditions, $R_0 = 1.185854123 > 1$.

In this paper, we can give some recommendations to the Government how to control and prevent the Dengue virus.

1. Increase the number of Fumigation to kill mosquito and larva. On the same side increase the value of u_1 the rate death of mosquitos caused fumigation
2. Enhance the vaccination or the value of that control the vaccination to the suspected host.
3. Enhance the treatment for infected host u_3 and coefficient c meaning coefficient treatment of host infection.

Conclusions / Kesimpulan

Some conclusions can be written as follow

1. Model of SIRS-SI transmission dengue virus considering fumigation, vaccination and treatment shown as

$$\frac{dS_h}{dt} = A_h - (1-u_2)\frac{b\beta_h S_h I_v}{N_h} - \mu_h S_h + \theta_h R_h$$

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

$$\frac{dR_h}{dt} = (\gamma_h + cu_3) I_h - \mu_h R_h - \theta_h R_h$$

$$\frac{dS_v}{dt} = A_v - \frac{b\beta_v S_v I_h}{N_h} - (\mu_v + u_1) S_v$$

$$\frac{dI_v}{dt} = \frac{b\beta_v S_v I_h}{N_h} - (\mu_v + u_1) I_v$$

2. Basic reproduction number

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

and $R_0 = 0.8385254916 < 1$ for free disease equilibrium point and $R_0 = 1.185854123 > 1$ for endemic equilibrium point.

3. Free disease equilibrium is local asymptotic stable and meaning there is no endemic dengue fever. On other hand disease, equilibrium point is also local asymptotic stable. It means there is an endemic dengue fever.

Conflicts of interest

There are no conflicts of interest

Acknowledgements

We would like to thank you to Higher Education of Muhammadiyah Board and Universitas Muhammadiyah Tangerang.

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