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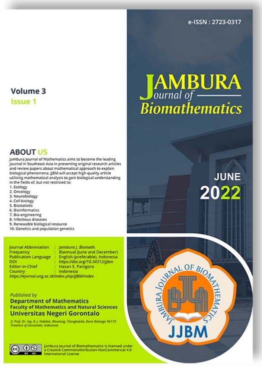

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Research Article

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The Analysis of Epidemic Dynamical Models for Dengue Transmission Considering the Mosquito Aquatic Phase

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ABSTRACT. *This study generalizes the dengue transmission model by considering the dynamics of the human population and the Aedes aegypti mosquito population. The mosquito population is devided into two phases, i.e., the aquatic phase and the adult phase. From the model, we seek the disease-free equilibrium, endemic equilibrium, and basic reproduction number ($\mathcal{R}_0$) points. The model yields a single basic reproduction number which determines the system's behavior. If $\mathcal{R}_0 < 1$, the disease-free equilibrium is locally asymptotically stable, indicating that the disease will die out. Conversely, if $\mathcal{R}_0 > 1$, an endemic equilibrium exists, and the disease may persist in the population. Next, a numerical simulation is performed to geometrically visualize the resulting analysis and also to simulate the dengue transmission in DKI Jakarta Province, Indonesia. The resulting numerical simulation supports our analysis. Meanwhile, the simulation in DKI Jakarta Province suggests that the dengue fever disappears after 60 days from the first case appearance after controlling the mosquito population through fogging and the use of mosquito larvae repellent. Lastly, the sensitivity analysis of $\mathcal{R}_0$ indicates that parameters related to the mosquito's aquatic phase have a strong influence on dengue transmission, meaning that small changes in these parameters can significantly increase or decrease the value of $\mathcal{R}_0$ and thus the potential for an outbreak.*

1. Introduction

Dengue fever (DF) is one of the epidemic diseases which remain an issue to the public health in Indonesia, as it can have the potential to cause extraordinary events. As reported by the the Indonesian Ministry of Health, the death rate caused by dengue fever since 1968 has reached 41.3 % of the total number of sufferers. However, since 1991 the number of mortalities has stabilized below 3 %. As reported in Jakarta and Surabaya in 1968, there were 58 cases of dengue fever with 24 deaths [1], while in 1991 there were 58,501 cases with 1,414 deaths [2]. The data from the Indonesian Ministry of Health [3] indicates that in 2019 the number of dengue patients reached 138,127 cases. This number has increased as compared to 2018, which reported 65,602 cases. Deaths due to DF in 2019 also experienced an increase as compared to 2018, i.e., from 467 to 919 death cases. The dengue transmission has also been evenly distributed to 34 provinces in Indonesia.

DKI Jakarta Province, the capital city of Indonesia, had a population of 10.56 million in 2020 [4]. With its large population and high density, DKI Jakarta faces recurring outbreaks of infectious diseases such as DF. Based on data from the DKI Jakarta Provincial Government through the Health Office, there were 4,541 cases of DF fever in the first quarter of 2019. In 2019, the incidence rate (IR) of DF per 100,000 residents in DKI Jakarta was recorded at 82.45 or greater than the national average of 51.53 [3]. Efforts made by the DKI Jakarta Provincial Government in controlling the dengue outbreak are by fogging and inspection of larvae by the Larva Monitoring Officers (Jumantik) in areas where dengue cases are found.

DF is not transmitted through human-to-human contact but is transmitted through the bite of an Aedes spp mosquito infected with the dengue virus [5]. Female mosquitoes store the virus in their eggs. While male mosquitoes will store the virus in female mosquitoes during sexual contact. The dengue virus enters the human body through the saliva injected by a female Aedes mosquito during a bite. Once inside the body, the dengue virus enters the bloodstream and targets macrophages, its primary host cells. The immune system attempts to block the virus, but it can still replicate within the body [6].

The seasonal factor is one of the factors causing the outbreak of DF in Indonesia [7, 8]. During the rainy season, dengue fever cases generally increase due to a large amount of standing water [9]. Stagnant rainwater or residual flooding are the most ideal places for Aedes mosquitoes to lay eggs. Mosquitoes will breed more easily and quickly in a humid environment. Similarly, during the transition season (transition from dry to rainy season, or vice versa), sometimes the ambient temperature will also feel more humid. This makes the period of virus' incubation

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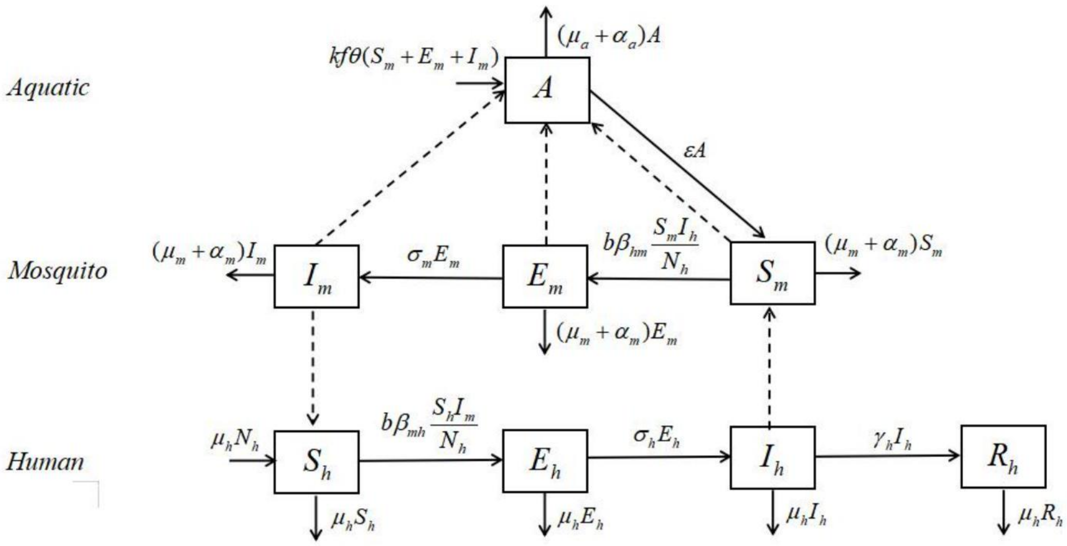


Figure 1. Flowchart diagram of the dengue transmission model

in the mosquito's body faster [10]. This means that mosquitoes will have more chances to infect a large number of people in a short period. In addition, the rate of mosquito bites and the growth rate of mosquitoes will increase in the transition period [10]. These seasonal effects are described as the Aides Aigepty mosquito population which depends on the ambient air temperature [11].

Mathematical modeling plays a crucial role in disease epidemiology, with the Kermack-McKendrick model, introduced in 1927 [12], being a cornerstone of classical theory used in the modeling of disease spread. Traditionally, these models focus on the human population, but more recent studies also consider the role of the vector population in transmitting diseases. For instance, Aldila et al. [13], Esteva and Vargas [14], Ismayasinta et al. [15], and Scott and Morrison [16] explored the impact of mosquito vectors on the transmission of Dengue Fever (DF), while Banni et al. [17], Ahkrizal et al. [18], and Oladapo et al. [18] investigated their role in the transmission of Malaria. Additionally, the environment, particularly water, has been shown to influence the spread of several diseases, such as Cholera [19] and DF [10]. Tien and Earn [20] extended Cholera models by incorporating water as a factor, using the SIWR model. Similarly, the inclusion of water in Dengue models is relevant, as mosquito life stages such as pupae, larvae, and eggs occur in water. While these studies have contributed significantly to understanding disease spread, a key research gap remains in the integration of both vector populations and environmental factors like water and temperature in a unified model, especially in the context of DF.

In this research, the spread of DF is modeled mathematically by taking into account the dynamics of the human population and the Aedes Aegypti mosquito population. The mosquito population is divided into two phases, namely the aquatic phase and the adult phase, with control measures applied through fogging and the use of larvicides, while also considering the influence of temperature on parameters related to mosquito population dynamics. After the model is obtained, we determine the equilibrium point, basic reproduction number, and stability of the equilibrium point. Next, a model simulation is carried out to provide a geometric picture of the solution and to support the obtained theorem, and simulate the spread of DF in DKI Jakarta Province, Indonesia. Finally, a sensitivity analysis is conducted to determine the most important model parameters in affecting the spread of DF.

2. Model Formulation

The mathematical model used to determine the form of the spread of DF is by taking into account the dynamics of the human population and the mosquito population. The mosquito population is devided into two phases, i.e., the pre-adult (immature) phase or the aquatic phase and the adult phase. The adult mosquito divided into the susceptible mosquito $S_m(t)$, latent mosquito $E_m(t)$, and infected mosquito $I_m(t)$ compartments. In addition, a mosquito compartment was added in the aquatic phase $A(t)$. The human population is broken down into the susceptible individuals $S_h(t)$, the latent individuals $E_h(t)$, the infected individuals $I_h(t)$, and the recovered individuals $R_h(t)$ compartments. Without loss of generality, we can re-write as $S_m(t) = S_m, E_m(t) = E_m, I_m(t) = I_m, A(t) = A, S_h(t) = S_h, E_h(t) = E_h, I_h(t) = I_h$, dan $R_h(t) = R_h$.

Figure 1 depicts the scheme for the spread of DF in this study. Every individual born (μ_h) or mosquito born (μ_f) will enter the susceptible compartment. Susceptible mosquitoes can become latent mosquitoes due to biting infected humans with a probability of β_{hm} and assuming the number bites per day is b. Next, susceptible individuals can become latent individuals due to being bitten by an infected mosquito with a probability of β_{mh}. Latent individuals and mosquitoes will then become infected after passing the incubation period with rate of σ_h dan σ_m, respectively. After being infected, the individual will recover from DF at a rate of γ_h. Meanwhile, the mosquito is assumed not to have a recovery phase because of its short life span.

Each compartment will experience a natural death whose rate is assumed to be equal to natural birth for individuals, adult mosquitoes, and mosquitoes in the aquatic phase at the rate of μ_h, μ_m, dan μ_a, respectively. The mortality of mosquito is not only due to natural deaths but also deaths due to human efforts to eradicate mosquitoes through fogging on adult mosquitoes and the administration of mosquito larvae in the aquatic phase, at the rate of α_m dan α_a, respectively. The number of mosquitoes in the aquatic phase increase as the adult female mosquitoes lay their eggs, so let the intrinsic level of female adult mosquitoes be θ. However, not all eggs will hatch into larvae, thus we define k as the ratio of eggs hatching to larvae. Dengue virus disease is transmitted through the bite of the female Aides Aegypti mosquitoes, so let f as the ratio of female mosquitoes that hatch from all eggs that hatch. Furthermore, mosquitoes in the aquatic phase will turn into adult mosquitoes at a rate of ε.

Based on the explanation above, the transmission of DF through the Aides Aegypti mosquito vector taking into account the aquatic phase can be modeled through an ordinary nonlinear differential equations system as follows:

$$\begin{aligned}
\frac{dS_h}{dt} &= \mu_h N_h - b\beta_{mh}\frac{S_h I_m}{N_h} - \mu_h S_h,\\
\frac{dE_h}{dt} &= b\beta_{mh}\frac{S_h I_m}{N_h} - (\sigma_h+\mu_h)E_h,\\
\frac{dI_h}{dt} &= \sigma_h E_h - (\gamma_h+\mu_h)I_h,\\
\frac{dR_h}{dt} &= \gamma_h I_h - \mu_h R_h,\\
\frac{dS_m}{dt} &= \varepsilon A - b\beta_{hm}\frac{S_m I_h}{N_h} - (\mu_m+\alpha_m)S_m,\\
\frac{dE_m}{dt} &= b\beta_{hm}\frac{S_m I_h}{N_h} - (\sigma_m+\mu_m+\alpha_m)E_m,\\
\frac{dI_m}{dt} &= \sigma_m E_m - (\mu_m+\alpha_m)I_m,\\
\frac{dA}{dt} &= kf\theta N_m - (\varepsilon+\mu_a+\alpha_a)A,
\end{aligned} \tag{1}$$

where $N_h = S_h + E_h + I_h + R_h$ and $N_m = S_m + E_m + I_m$. For simplicity, we write the derivative function $\frac{df}{dt} = \dot{f}$. Next, the system model (1) can be formed into a non-dimensional into the following equations:

$$\begin{aligned}
\dot{s}_h &= \mu_h - b\beta_{mh}s_h i_m - \mu_h s_h,\\
\dot{e}_h &= b\beta_{mh}s_h i_m - \sigma_h e_h - \mu_h e_h,\\
\dot{i}_h &= \sigma_h e_h - \gamma_h i_h - \mu_h i_h,\\
\dot{r}_h &= \gamma_h i_h - \mu_h r_h,\\
\dot{s}_m &= \varepsilon a - b\beta_{hm}s_m i_h - (\mu_m+\alpha_m)s_m,\\
\dot{e}_m &= b\beta_{hm}s_m i_h - \sigma_m e_m - (\mu_m+\alpha_m)e_m,\\
\dot{i}_m &= \sigma_m e_m - (\mu_m+\alpha_m)i_m,\\
\dot{a} &= kf\theta - \varepsilon a - (\mu_a+\alpha_a)a,
\end{aligned} \tag{2}$$

where

$$s_h = \frac{S_h}{N_h}, e_h = \frac{E_h}{N_h}, i_h = \frac{I_h}{N_h}, r_h = \frac{R_h}{N_h}, s_m = \frac{S_m}{N_m},$$
$$e_m = \frac{E_m}{N_m}, i_m = \frac{I_m}{N_m}, a = \frac{A}{N_m}.$$

The variable r does not give influence other equations, so the $\dot{r}$ equation can be ignored temporarily from the system. Thus eq. (2) can be written as follows:

$$\begin{aligned}
\dot{s}_h &= \mu_h - b\beta_{mh}s_h i_m - \mu_h s_h,\\
\dot{e}_h &= b\beta_{mh}s_h i_m - \sigma_h e_h - \mu_h e_h,\\
\dot{i}_h &= \sigma_h e_h - \gamma_h i_h - \mu_h i_h,\\
\dot{s}_m &= \varepsilon a - b\beta_{hm}s_m i_h - (\mu_m+\alpha_m)s_m,\\
\dot{e}_m &= b\beta_{hm}s_m i_h - \sigma_m e_m - (\mu_m+\alpha_m)e_m,\\
\dot{i}_m &= \sigma_m e_m - (\mu_m+\alpha_m)i_m\\
\dot{a} &= kf\theta - \varepsilon a - (\mu_a+\alpha_a)a.
\end{aligned} \tag{3}$$

The variables $s_h, e_h, i_h, r_h, s_m, e_m, i_m$ are the susceptible individual proportions, latent individuals, infected individuals, recovery individuals, susceptible mosquitoes, latent mosquitoes, and infected mosquitoes, respectively. Thus, we can define closed sets

$$\begin{aligned}
\Gamma^* &= \{(s_h, e_h, i_h, r_h, s_m, e_m, i_m, a) \in R_+^8 \mid s_h + e_h + i_h + r_h\\
&= 1, s_m + e_m + i_m = 1\},\\
\Gamma &= \{(s_h, e_h, i_h, s_m, e_m, i_m, a) \mid \exists r_h \le 1 \ni (s_h, e_h, i_h, s_m,\\
&\quad e_m, i_m, a) \in \Gamma^*\}.
\end{aligned}$$

3. Analytical Results

The dengue transmission model with Aedes aegypti mosquito vector accounting for aquatic phase is in the form of a nonlinear differential equations system. The system consists of two equilibrium points. The first one is called a disease-free equilibrium point (DFE) and the second one is an endemic equilibrium point (END). Based on the definition, the equilibrium points for the dengue transmission for system (3) is obtained if

$$\dot{s}_h = \dot{e}_h = \dot{i}_h = \dot{s}_m = \dot{e}_m = \dot{i}_m = \dot{a} = 0. \tag{4}$$

The DFE point is fulfilled if no individual is affected by the disease, so that $i_h = i_m = 0$. Next, by substituting $i_h = i_m = 0$ to eq. (4), it is obtained a DFE $E_1 = \left(1, 0, 0, \frac{kf\theta\varepsilon}{(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)}, 0, 0, \frac{kf\theta}{(\varepsilon+\mu_a+\alpha_a)}, 0\right)$. The END is obtained when the infected compartment is not zero, i.e., $i_h^* > 0$ dan $i_m^* > 0$, and thus the END on the system (3) is $E_2(s_h^*, e_h^*, i_h^*, s_m^*, e_m^*, i_m^*, a^*)$,

$$\begin{aligned}
s_h^* &= \frac{\mu_h}{b\beta_{mh}i_m^* + \mu_h},\\
e_h^* &= \frac{b\beta_{mh}i_n^*\mu_h}{(b\beta_{mi}i_m^* + \mu_h)(\sigma_h+\mu_h)},\\
i_h^* &= \frac{b\beta_{mh}i_m^*\mu_h\sigma_h}{(b\beta_{mh}i_m^* + \mu_h)(\sigma_h+\mu_h)(\gamma_h+\mu_h)},\\
s_m^* &= \frac{kf\theta\varepsilon\Psi_1}{(\varepsilon+\mu_a+\alpha_a)\Psi_2},\\
e_m^* &= \frac{(\mu_m+\alpha_m)i_m^*}{\sigma_m},\\
i_m^* &= \frac{(b\beta_{hm})^2 kf\theta\varepsilon\sigma_m\mu_h\sigma_h - \Psi_3}{\Psi_4 + (\mu_m+\alpha_m)(\sigma_h+\mu_h)(\gamma_h+\mu_h)},\\
a^* &= \frac{kf\theta}{(\varepsilon+\mu_a+\alpha_a)},\\
\Psi_1 &= (b\beta_{mi}i_m^* + \mu_h)(\sigma_h+\mu_h)(\gamma_h+\mu_h),\\
\Psi_2 &= (b\beta_{hm})^2 i_m^*\mu_h\sigma_h + (\mu_m+\alpha_m)(b\beta_{mh}i_m^* + \mu_h)(\sigma_h\\
&\quad +\mu_h)(\gamma_h+\mu_h),\\
\Psi_3 &= \mu_h(\mu_m+\alpha_m)^2(\sigma_h+\mu_h)(\gamma_h+\mu_h)(\sigma_m+\mu_m+\alpha_m)(\varepsilon\\
&\quad +\mu_a+\alpha_a),
\end{aligned} \tag{5}$$

$$\Psi_4 = (\mu_m+\alpha_m)(\sigma_m+\mu_m+\alpha_m)(\varepsilon+\mu_a+\alpha_a)(b\beta_{hm})^2\mu_h\sigma_h.$$

3.1. Basic reproduction number

To determine the number of basic reproduction ($\mathcal{R}_0$), the next generation matrices are computed the following steps:

1. Perform linearization for the infected sub-system at E_l. Then, a Jacobian matrix is obtained from equations $\dot{e}_h, \dot{i}_h, \dot{e}_m$, and $\dot{i}_m$.

$$\mathbf{J}\left(1,0,0,\frac{kf\theta\varepsilon}{(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)},0,0,\frac{kf\theta}{(\varepsilon+\mu_a+\alpha_a)}\right).$$

2. Decompose Jacobian matrix $\boldsymbol{J}=\boldsymbol{F}$ - $\boldsymbol{V}$ into matrix of transmission $\boldsymbol{F}$ and matrix of transition V.

$$\mathbf{F}=\begin{pmatrix} 0 & 0 & 0 & b\beta_{mh} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{b\beta_{hm}kf\theta\varepsilon}{(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix},$$

$$\mathbf{V}=\begin{pmatrix} \sigma_h+\mu_h & 0 & 0 & 0 \\ -\sigma_h & \gamma_h+\mu_h & 0 & 0 \\ 0 & 0 & \sigma_m+\mu_m+\alpha_m & 0 \\ 0 & 0 & -\sigma_m & \mu_m+\alpha_m \end{pmatrix}.$$

3. Calculate $\mathcal{R}_0=\rho\left(\boldsymbol{F}\boldsymbol{V}^{-1}\right)$. Then, we get a characteristic equation $\left(\boldsymbol{F}\boldsymbol{V}^{-1}\right)$,

$$-\lambda^2\left(-\lambda^2+\frac{(b\beta_{hm})^2kf\theta\varepsilon\sigma_h\sigma_m}{\Psi_5}\right)=0,$$

and obtain,

$$R_0=\sqrt{\frac{(b\beta_{hm})^2kf\theta\varepsilon\sigma_h\sigma_m}{\Psi_5}},$$

where

$$\Psi_5=(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)^2(\sigma_h+\mu_h)(\gamma_h+\mu_h)(\sigma_m+\mu_m+\alpha_m).$$

Theorem 1. *The existence of DFE E_1 is without any criteria while the END E_2 exists when $\mathcal{R}_0>1$.*

Proof. The existence of an equilibrium point is indicated with each positive element according to the conditions for the formation of this model. Note that $s_h^*, e_h^*, i_h^*, s_m^*, e_m^*$, dan a^* in the $E_2(s_n^*, e_h^*, i_n^*, s_m^*, e_m^*, i_m^*, a^*)$ on eq. (5) are positive if and only if i_m^* positive, so it needs to be shown that $i_m^*>0$. Note that

$$\begin{aligned} i_m^* &= \frac{(b\beta_{hm})^2kf\theta\varepsilon\sigma_m\mu_h\sigma_h-\Psi_6}{(\mu_m+\alpha_m)(\sigma_m+\mu_m+\alpha_m)(\varepsilon+\mu_a+\alpha_a)\Psi_7} \\ &= \frac{\mu_h(\mu_m+\alpha_m)(\sigma_h+\mu_h)(\gamma_h+\mu_h)(R_0^2-1)}{(b\beta_{hm})^2\mu_h\sigma_h+(\mu_m+\alpha_m)(\sigma_h+\mu_h)(\gamma_h+\mu_h)}, \\ \Psi_6 &= \mu_h(\mu_m+\alpha_m)^2(\sigma_h+\mu_h)(\gamma_h+\mu_h)(\sigma_m+\mu_m+\alpha_m)(\varepsilon+\mu_a+\alpha_a), \\ \Psi_7 &= (b\beta_{hm})^2\mu_h\sigma_h+(\mu_m+\alpha_m)(\sigma_h+\mu_h)(\gamma_h+\mu_h). \end{aligned}$$

because $\mathcal{R}_0>1$ then $i_m\geq 0$. □

3.2. Stability Analysis of Equilibrium Points

Theorem 2. *If $\mathcal{R}_0<1$, then the DFE*

$$E_1\left(1,0,0,\frac{kf\theta\varepsilon}{(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)},0,0,\frac{kf\theta}{(\varepsilon+\mu_a+\alpha_a)}\right)$$

is locally asymptotically stable.

Proof. The characteristic equation for $J(E_1)$ is $|J(E_1)-\lambda I|=0$ or equivalently

$$(\mu_h+\lambda)(\varepsilon+\mu_a+\alpha_a+\lambda)(\mu_m+\alpha_m+\lambda)P=0, \quad (6)$$

where

$$\begin{aligned} P &= a_0\lambda^4+a_1\lambda^3+a_2\lambda^2+a_3\lambda+a_4 \quad (7)\\ a_0 &= 1, \\ a_1 &= \sigma_h+2\mu_h+\gamma_h+\sigma_m+2\mu_m+2\alpha_m \\ a_2 &= (\sigma_m+\mu_m+\alpha_m)(\mu_m+\alpha_m)+(\sigma_h+\mu_h)(\gamma_h+\mu_h) \\ &\quad+(\sigma_h+2\mu_h+\gamma_h)(\sigma_m+2\mu_m+2\alpha_m) \\ a_3 &= (\sigma_h+2\mu_h+\gamma_h)(\sigma_m+\mu_m+\alpha_m)(\mu_m+\alpha_m) \\ &\quad+(\sigma_m+2\mu_m+2\alpha_m)(\sigma_h+\mu_h)(\gamma_h+\mu_h) \\ a_4 &= (\sigma_h+\mu_h)(\gamma_h+\mu_h)(\sigma_m+\mu_m+\alpha_m)(\mu_m \\ &\quad+\alpha_m)(1-R_0^2). \end{aligned}$$

Based on eq. (6), we obtain $\lambda_1=-\mu_h$, $\lambda_2=-(\varepsilon+\mu_a+\alpha_a)$, $\lambda_3=-(\mu_m+\alpha_m)$. To examine the sign of the real part of the eigenvalues $\lambda_4,\lambda_5,\lambda_6$ and λ_7, a Routh-Hurwitz criterion is utilized. All parameters used are positive then $0<\mathcal{R}_0<1$, so it is proven

$$\frac{a_1}{a_0}>0,\ \frac{a_2}{a_0}>0,\ \frac{a_3}{a_0}>0,\ \frac{a_4}{a_0}>0. \quad (8)$$

Routh-Hurwitz Matrix for eq. (8) is

$$H=\begin{pmatrix} a_1 & a_0 & 0 & 0 \\ a_3 & a_2 & a_1 & a_0 \\ a_5 & a_4 & a_3 & a_2 \\ 0 & 0 & 0 & a_4 \end{pmatrix}. \quad (9)$$

Based on matrix H, we get the following Hurwitz determinants:

$$\begin{aligned} \Delta_1 &= |a_1|, \\ \Delta_2 &= \begin{vmatrix} a_1 & a_0 \\ a_3 & a_2 \end{vmatrix} \\ &= (\sigma_h+2\mu_h+\gamma_h)\big((\sigma_h+\mu_h)(\gamma_h+\mu_h)+(\sigma_h+2\mu_h \\ &\quad+\gamma_h)(\sigma_m+2\mu_m+2\alpha_m)\big)+(\sigma_m+2\mu_m+2\alpha_m)\big((\sigma_m \\ &\quad+\mu_m+\alpha_m)\big)(\mu_m+\alpha_m)+(\sigma_h+2\mu_h+\gamma_h)(\sigma_m \\ &\quad+2\mu_m+2\alpha_m), \\ \Delta_3 &= \begin{vmatrix} a_1 & a_0 & 0 \\ a_3 & a_2 & a_1 \\ 0 & a_4 & a_3 \end{vmatrix}, \\ &= (\sigma_h+2\mu_h+\gamma_h)(\sigma_m+2\mu_m+2\alpha_m)(\sigma_m+\mu_m \\ &\quad+\alpha_m)(\mu_m+\alpha_m)\big(2(\sigma_h^2+2\mu_h\sigma_h+\gamma_h\sigma_h+\mu_h\sigma_h \end{aligned}$$

Table 1. The model parameters

No	Parameter	Description	Value	Range	Ref.
1.	β_{hm}	The probability of dengue virus transmission vector to humans per bite.	0.5	0.3-0.75	[21]
2.	β_{mh}	The probability of dengue virus transmission humans to vectors per bite.	0.4	0.1-0.75	[22]
3.	σ_h	The rate of transfer from latent to infected mosquito	1/7	0.1-0.25	[23, 24]
4.	γ_h	DF cure rate	1/7	0.1-0.25	[25]
5.	f	The ratio of female mosquitoes hatching from eggs	0.5	0-1	[26]
6.	k	The ratio of hatching eggs to larvae	0.5	0-1	[10]
7.	α_m	The mosquito's rate of mortality due to fogging	0.844 5	0-1	[10]
8.	α_a	The aquatic phase's rate of mortality due to mosquito larvae repellent usage.	0.844 5	0-1	[10]
9.	μ_h	The rate of natural death and birth in the human population	0.77 x 10^{-3}	0-1	[4]

$$+ 3\mu_h^2 + \mu_h\gamma_h + 2\mu_h\gamma_h + \gamma_h^2\big) + (\sigma_m + \mu_m + \alpha_m)\big(\mu_m + \alpha_m)\big) + (\sigma_m + 2\mu_m + 2\alpha_m)(\sigma_h + 2\mu_h + \gamma_h)\big(\sigma_h + \mu_h\big)^2(\gamma_h + \mu_h)^2 + (\sigma_h + 2\mu_h + \gamma_h)^2\big(\sigma_m + 2\mu_m + 2\alpha_m\big)^2(\sigma_h + \mu_h)(\gamma_h + \mu_h)(1 + (\sigma_h + \mu_h)(\gamma_h + \mu_h)) + \frac{(b\beta_{hm})^2 kf\theta\varepsilon\sigma_h\sigma_m}{(\varepsilon + \mu_a + \alpha_a)(\mu_m + \alpha_m)}(\sigma_h + 2\mu_h + \gamma_h + \sigma_m + 2\mu_m + 2\alpha_m)^2$$

$$\Delta_4 = \begin{vmatrix} a_1 & a_0 & 0 & 0 \\ a_3 & a_2 & a_1 & a_0 \\ a_5 & a_4 & a_3 & a_2 \\ 0 & 0 & 0 & a_4 \end{vmatrix} = a_4\Delta_3,$$

then $\Delta_1 > 0$, $\Delta_2 > 0$, $\Delta_3 > 0$, $\Delta_4 > 0$, if $R_0 > 1$. Thus, the Routh-Hurwitz criterion is achieved. It is proven that the sign of the real part of the eigenvalues λ_4, λ_5, λ_6, and λ_7 is negative. Since all eigenvalues from the Jacobian matrix $J(E_1)$ is negative, then it is proven E_1 is locally asymptotically stable. □

4. Numerical Results

A numerical simulation is conducted to support our model analysis shown in the previous section. Simulation for the dengue fever cases in the DKI Jakarta Province is also carried out in this study. The simulation for the dengue transmission model with Aedes Aegypti mosquito vector considering for the aquatic phase is performed by considering various parameters from several studies. The parameters associated with the mosquito vector depend on the temperature (T) and others are constant. The following explains in more detail for each parameter which depend on the temperature (T).

1. Intrinsic oviposition rate for female adult mosquito [11].

$$\theta(T) = -5.4 + 1.8T - 0.2124T^2 + 0.01015T^3 - 1.515 \times 10^{-4}T^4. \tag{10}$$

   To guarantee eq. (10) to be positive, it is assumed $T \geq 12°$C and if $T < 12°$C then the intrinsic oviposition rate is set to zero.
2. Natural mortality and birth rates of adult mosquito population [11].

$$\mu_m(T) = 0.8692 - 0.1599T + 0.01116T^2 - 3.408 \times 10^{-4}T^3 + 3.809 \times 10^{-6}T^4. \tag{11}$$

3. Natural mortality and birth rates of mosquito population in the aquatic phase [11].

$$\mu_a(T) = 2.13 - 0.3797T + 0.02457T^2 - 6.778 \times 10^{-4}T^3 + 6.794 \times 10^{-6}T^4. \tag{12}$$

4. The rate of change from the aquatic phase to the adult phase [11].

$$\varepsilon(T) = 0.131 - 0.05723T + 0.01164T^2 - 0.001341T^3 + 0.00008723T^4 - 3.017 \times 10^{-6}T^5 + 5.153 \times 10^{-8}T^6 - 3.42 \times 10^{-10}T^7. \tag{13}$$

   To ensure eq. (13) to be positive, it is assumed $10.54°\text{C} \leq T \leq 33.41°\text{C}$ and if $T < 10.54°$C or $T > 33.41°$C then the rate of change is set to zero.
5. The daily biting rate [27].

$$b(T) = 0.0043T + 0.0943, 21°C \leq T \leq 32°C. \tag{14}$$

   Daily biting rate increases linearly from 0.18/ day at temperature $T = 21°C$ to 0.23/ day at 32°C.

6. The rate of transfer from latent to infected mosquito.

$$\sigma_m(T) = 24 \times \frac{0.00333 \times \frac{T_k}{298} \times \exp\left(\frac{60513.2}{R}\left(\frac{1}{298} - \frac{1}{T_k}\right)\right)}{1 + \exp\left(\frac{705550}{R}\left(\frac{1}{308.352} - \frac{1}{T_k}\right)\right)}. \tag{15}$$

   The relationship between temperature and extrinsic incubation rate [28] is given by eq. (15) where in $T_k = 273.15 + T$ degrees Kelvin and $R = 1.987\text{caldeg}^{-1}\ \text{mol}^{-1}$ is the ideal gas constant.

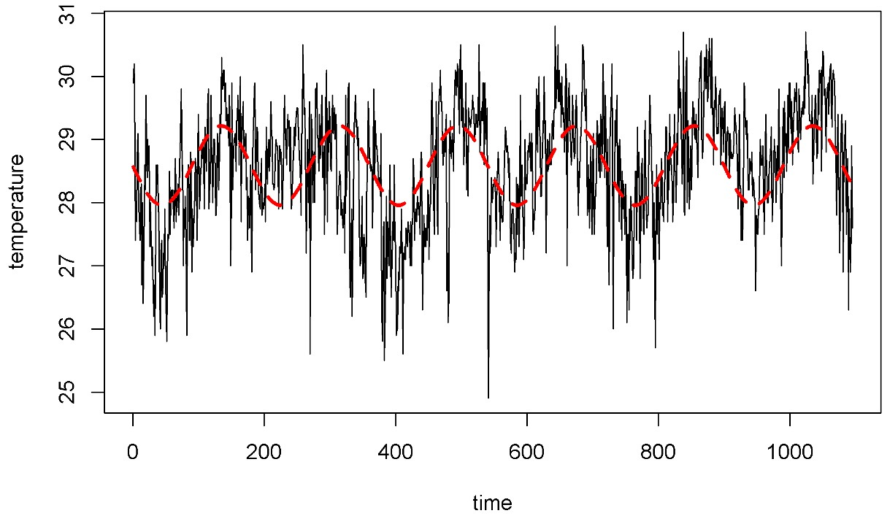


Figure 2. Plot of actual (black line) and predicted (red line) values for the temperature data in DKI Jakarta Province

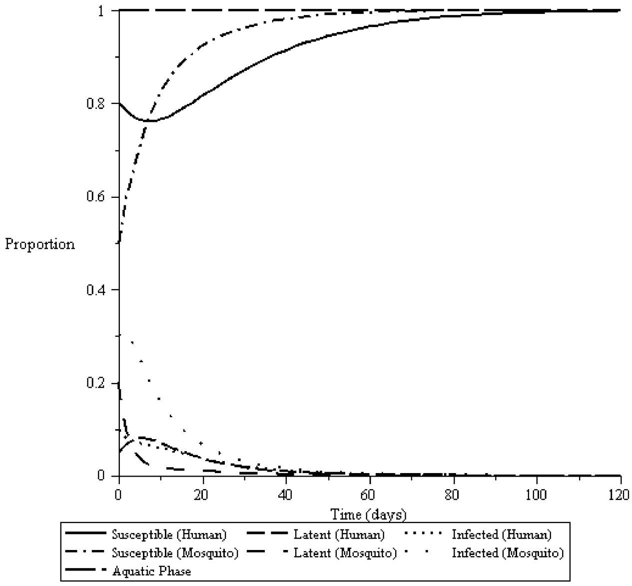


Figure 3. Simulation results from System (3) with disease-free equilibrium point E_1

The constant parameters listed in Table 1, obtained from various sources, include their values and corresponding ranges.

The temperature analysis for DKI Jakarta Province uses temperature data for DKI Jakarta Province from January 2017 to December 2019 obtained from the Meteorology, Climatology and Geophysics Agency (BMKG). Temperature data was collected on a daily period for 3 years from January 2017 to December 2019 with a total of 1095 data, an average of $28.58°$C, a median of $28.60°$C, and a variance of $0.91°$C. The annual pattern of air temperature is predicted using a harmonic model with the help of R software and the result is shown in Figure 2. The prediction values are quite close to the actual periodic temperature pattern with the MAPE value of 2.3% which indicates high accuracy. The prediction equation of the annual air temperature pattern in the DKI Jakarta Province can be written as a time-dependent function as follows:

$$y = 28.58548 - 0.006 \cos t - 0.0208 \sin t. \tag{16}$$

A numerical simulation is performed to support Theorem 1 and 2, and also to simulate the dengue cases in the DKI Jakarta Province. Therefore, three scenarios are considered in the numerical simulation:

4.1. System (4) $\mathcal{R}_0 < 1$

The first scenario uses temperature at $28.58°$C for each parameter value that depends on the temperature, constant parameters in Table 1 (but some of these values were adjusted to fulfill the condition $\mathcal{R}_0 < 1$), and constant population. Some of the parameters that were changes are $\alpha_m = 0.123935468$, $\alpha_a =$

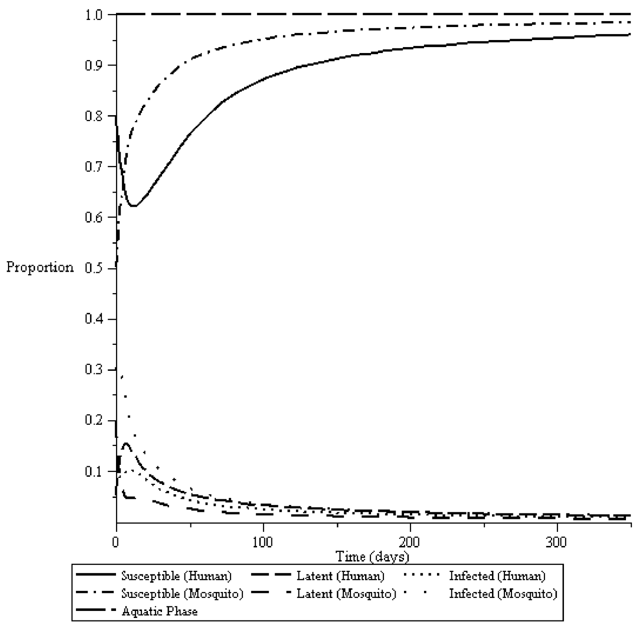


Figure 4. Simulation results from System (3) with endemic equilibrium points E_2

0.861433863, and $\mu_h = 0.057568544$. We obtain the initial reproduction number $R_0 = 0.4779649548$. The simulation results are performed using Maple with initial values $S_h(0) = 0.8, E_h(0) = 0.05, I_h(0) = 0.1, S_m(0) = 0.8, E_m(0) = 0.2, I_m(0) = 0.3, A(0) = 1.$, and are plotted in Figure 3.

Based on Figure 3, the population of susceptible individuals initially decreased until the 10^{th} day, afterward it increased until the 110^{th} day and the population of susceptible individuals reached point 1 and became stable onwards. The population of infected individuals and infected mosquitoes decreased until the 55^{th} day and they reached a point of 0 and ware stable at that point. The population of susceptible mosquitoes increased until the 110^{th} day and it reached point 1 and ware stable onwards. The population of latent individuals and latent mosquitoes declined until the 50^{th} day and 10^{th} day, respectively, and they reached point 0 and was stable onwards. Mosquitoes in the aquatic phase are constant at point 1 . These results suggest that when $R_0 < 1$, the system (4) is stable towards $E_1(1,0,0,1,0,0,1)$. Furthermore, if we substitute the parameter values into $E_1\left(1,0,0,\frac{kf\theta\varepsilon}{(\varepsilon+\mu_a+\alpha_a)(\mu_m+\alpha_m)},0,0,\frac{kf\theta}{(\varepsilon+\mu_a+\alpha_a)}\right)$, we get $E_1(1,0,0,1,0,0,1)$. This indicates that our numerical simulations are in line with Theorem 2, that E_I is asymptotically stable if $R_0 < 1$.

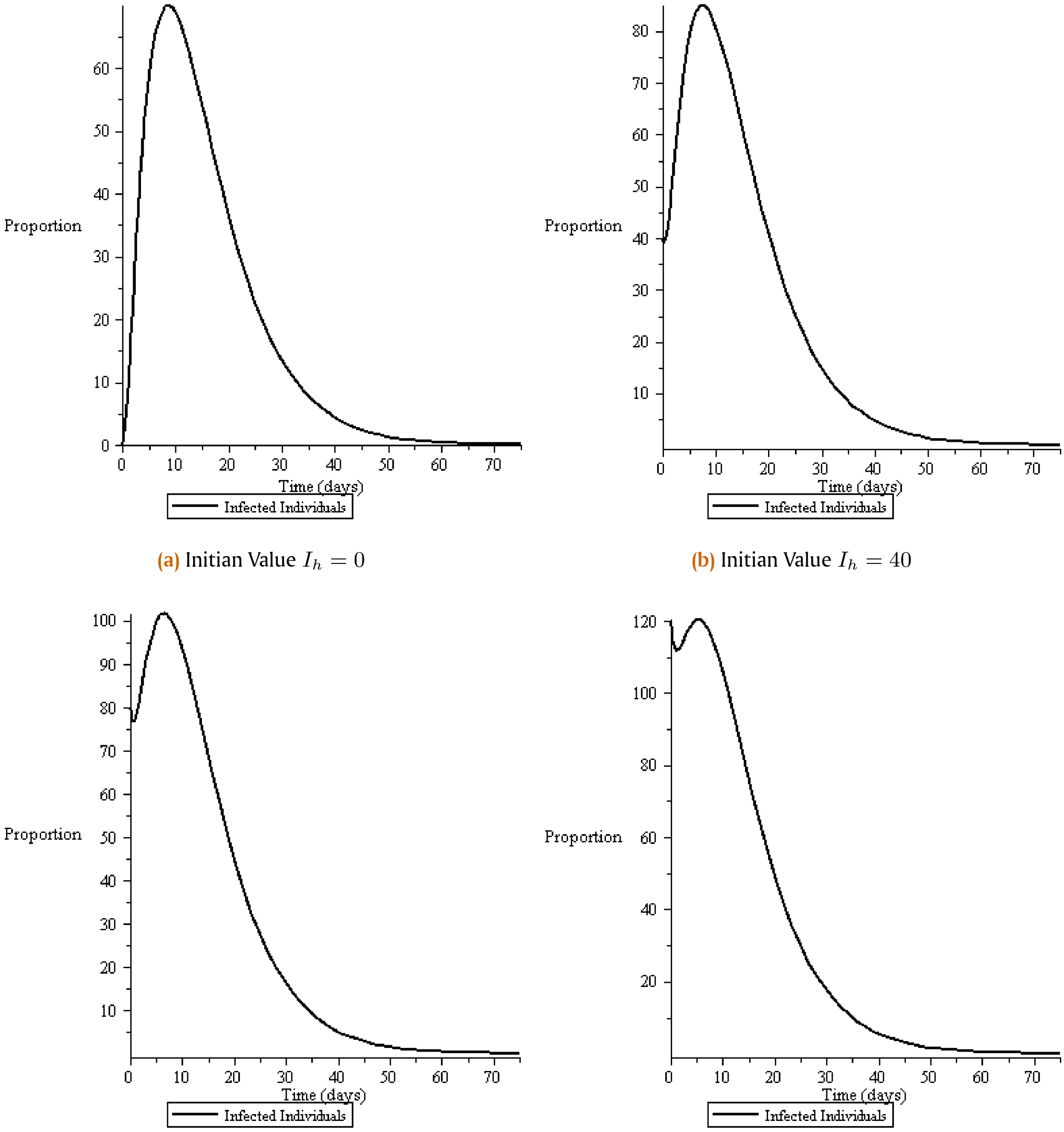
4.2. System (3) ($\mathcal{R}_0 > 1$)

To support Theorem 2, a numerical simulation is carried out for $\mathcal{R}_0 > 1$. The parameter values are the same as in the first simulation but the mosquito biting rate b is increased to 0.5 . We obtain the initial reproduction number $R_0 = 1.10253200$ from the system (3). Since $\mathcal{R}_0 > 1$, then according to [29], the disease will spread and reach the endemic equilibrium point $E_2\left(s_h^*, e_h^*, i_h^*, s_m^*, e_m^*, i_m^*, a^*\right)$. or $E_2 = [0.9548940876, 0.1290573860\text{e}-1, 0.9213138661\text{e}-2, 0.9772267089, 0.5836803545\text{e}-2, 0.1352305708\text{e}-1, 1]$. Figure 4 presents the simulation results using Maple program with initial values $S_h(0) = 0.8$, $E_h(0) = 0.05$, $I_h(0) = 0.1$, $S_m(0) = 0.8$, $E_m(0) = 0.2$, $I_m(0) = 0.3$, $A(0) = 1$.

Based on Figure 4, the susceptible individual population initially decreased until the 10^{th} day, afterward it increased until the 320^{th} day, and the susceptible individual population reached a point of around 0.96 and was stable at that point. The population of infected individuals and infected mosquitoes decreased, until the 250^{th} day it reached a point of around 0.01 and was stable at that point. The population of susceptible mosquitoes increased, until the 320^{th} day it reached a point of 0.98 and was stable at that point. The population of latent individuals and latent mosquitoes decreased, until the 250^{th} day they reached a point of 0.01 and were stable at that point. Mosquitoes in the aquatic phase are constant at point 1 . These results suggest that when $R_0 > 1$, the equilibrium points E_2 is exists.

4.3. System (1) with dengue cases in the DKI Jakarta Province

The third simulation uses the parameter values that depend on the temperature and also constant parameter values in Table 1. Next, the annual pattern of air temperature in the DKI Jakarta Province is presented in eq. (10). The simulation results use initial value $S_h(0) = 1.057 \times 10^7$, according to data on the population of DKI Jakarta province in 2020. We use $S_m(0) = 1.057 \times 10^7, A(0) = 1.057 \times 10^8$ based on the assumption that the adult mosquitoes population is ten times the human population and the number of mosquitoes in the phase of aquatic is ten times the population of adult mosquitoes. This assumption is based on previous studies that consider mosquito populations to be significantly larger than the human population in endemic areas, with a typical adult-to-human ratio ranging from 5:1 to 10:1 [30, 31]. The aquatic mosquito population is also assumed to be an order of magnitude larger than the adult mosquito population, reflecting their life cycle dynamics [32]. Meanwhile, the initial number of infected individuals $I_h(0)$ is made into four cases, $0, 40, 80,$ dan 120 individuals. The initial number of infected adult mosquitoes is assumed to be $I_m(0) = 1000$ and the



(a) Initian Value $I_h = 0$

(b) Initian Value $I_h = 40$

(c) Initian Value $I_h = 80$

(d) Initian Value $I_h = 120$

Figure 5. Simulation results from System (1) in DKI Jakarta Province with four different initial values of the infected population

subpopulation for latent and recovery individuals are assumed to be zero $E_h(0) = 0, E_m(0) = 0, R_h(0) = 0$.

Based on Figure 5 for each initial condition, the population of infected individuals will initially increase until the 10^{th} day and then decrease until the 60^{th} day to zero and stabilize at that point. The peak number of infected individuals for the initial values $I_h(0) = 0, I_h(0) = 40, I_h(0) = 80$, are $70, 80, 100$, and 120 , respectively. This means that DF cases in DKI Province are expected to peak on the 10^{th} day, with the total number of patients depending on the initial conditions. Afterward, the DF patients will gradually decline and disappear around the 60^{th} day assuming a routine fogging and eradication of mosquito larvae are carried out in the community.

5. Sensitivity Analysis on the Number of Basic Reproduction

Parameters with a significant effect on R_0 indicate that these parameters are the most important factors in the DHF spread. The sensitivity analysis in this study refers to studies [33, 34]. The following is an example for the sensitivity index R_0 calculation for β_{hn}.

$$C_{\beta}^{R_0} = \frac{\partial R_0}{\partial \beta_{hm}} \times \frac{\beta_{hm}}{R_0}.$$

Other parameters can be calculated in the same way. Next, it is applied to the constant parameter values in Table 1 and the time-dependent parameters eqs. (10) to (15) by taking a temperature at $28.58°$C, i.e., average daily temperature in the DKI Jakarta Province.

Table 2. The result of sensitivity indices

No.	Model Parameter	Sensitivity Index	No.	Model Parameter	Sensitivity Index
1.	β_{hm}	1.145093555	8.	b	0.3833094673
2.	f	0.5725467778	9.	γ_h	0.1916547340
3.	k	0.5725467778	10.	σ_m	0.1431562764
4.	θ	0.5725467778	11.	μ_a	- 0.03138208481
5.	ε	-0.5690004724	12.	μ_h	- 0.002214573938
6.	α_m	- 0.5262114976	13.	σ_h	0.001027481063
7.	α_a	-0.4628655262	14.	μ_m	-0.0002542464532

Table 2 shows the sensitivity indices for all parameters, sorted from highest to lowest. The results indicate that the most influential factor in the spread of dengue is the transmission rate from mosquitoes to humans, represented by β_{hm}. In practical terms, this means that the more easily mosquitoes can infect people through their bites, the more quickly dengue can spread. In addition, several parameters related to the mosquito's aquatic phase such as the egg-laying rate (f), the hatching success rate (k), the maturation rate from larvae to adults (θ), and the mortality rates of aquatic mosquitoes (ε, α_a, and μ_a) also have a considerable effect on the basic reproduction number R_0. This highlights the importance of targeting mosquito breeding and development stages, not just adult mosquitoes, when designing dengue prevention strategies.

Eight sensitivity index parameters are positive including the bite rate (b) and egg-laying (θ) of mosquitoes. This means that if the value of these parameters increases, the spread of DF will also increase, and vice versa. Furthermore, there are six parameters with negative sensitivity indices, including the mortality rate of mosquitoes due to fogging (α_m) and the mortality rate of mosquitoes in the aquatic phase due to mosquito larvae (α_a). This suggests that if the parameter is increased (or decreased) by 10% and other parameters are held constant, the value of R_0 will decrease (or increase) by 11.4%.

Based on this discussion, the spread of dengue fever (DF) can be prevented through the following measures. Reducing the level of contact of susceptible individuals with infected mosquitoes (β_{hm}). For example, using anti-mosquito lotion and putting mosquito nets on the bed and immediately isolating dengue patients. Increase the rate of mosquito mortality due to fogging (α_m) and mosquito mortality in the aquatic phase (α_a) by intensifying fogging activities and administering mosquito larvae repellent. Increase the healing rate of infected individuals. For example, by immediately bringing DF patients to the hospital to get immediate treatment or by making new drugs that can reduce the rate of dengue virus infection in the body.

6. Conclusion

Based on the assumptions used in this study, the model for the DF spread is obtained by taking into account the dynamics of both the human and mosquito populations. Ordinary differential equations with eight equations and eight dependent variables are constructed to model the DF spread in this study. The model for the spread of dengue fever (DF) with the Aedes aegypti mosquito vector, including its aquatic phase, shows that the disease-free equilibrium (DFE) is locally asymptotically stable when $\mathcal{R}_0 < 1$. Based on the parameter values used in the simulation, the basic reproduction number was found to be $\mathcal{R}_0 = 0.4779$, indicating that the disease will eventually die out under these conditions. Conversely, when the biting rate was increased, $\mathcal{R}_0$ rose to 1.1025, resulting in an endemic equilibrium (END) where the infection persists in the population. The data from the DKI Jakarta Province is used in the numerical simulation. It reveals that the outbreak will reach its peak on the 10^{th} day with the number of sufferers depends on the initial conditions. Afterwards, the DF patients will gradually decrease and disappear on the 60^{th} day assuming routine fogging activities and the use of mosquito larvae repellent are carried out in the community. The sensitivity analysis suggests that the most influential parameters on the spread of dengue disease are β_{hm} (transmission rate vector to humans). In addition, it can be seen that parameters related to mosquitoes in the aquatic phase such as $f, k, \theta, \varepsilon, \alpha_a$, and μ_a have pretty significant effect on R_0.

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Abbreviations.

DF	:	Dengue Fever.
DKI	:	Daerah Khusus Ibukota.
IR	:	Incidence Rate.
SIWR	:	Susceptible, Infected, Water, and Recovery.
DFE	:	Disease Free Equilibrium Point .
END	:	Endemic Equilibrium Point.
BMKG	:	Meteorology, Climatology, and Geophysics Agency.

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