A SIMULATION OF SIMV HOST - VECTOR DENGUE MODEL

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Abstract. Dengue is an endemic infectious disease of the tropical countries. Moreover, dengue disease is a major problem in Indonesia, especially in North Kalimantan. This disease is caused by dengue virus. In this paper, we epidemic modeling to analyze the spread of dengue disease by choosing parameters that influence the transmission rate of dengue disease. SI model is a method that rewrite a real-world phenomena into a system of differential equations. We use Euler method to discretize the model. The resulted dynamical behavior of the discrete model is then analyzed, specifically we determine the existence and stability of equilibrium points. We found that this model is converged to its equilibrium points, so its consistent its the exact solution. We use computer simulation to show the trajectories of the numerical solutions plotted into the 2D planes. We found that the numerical simulation is not only illustrate the results, but also exhibit rich dynamics such as periodic solution and bifurcation.

Keywords: discretize; Euler Method; stability.

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1. INTRODUCTION

Dengue disease is a viral infection caused by virus known as DEN-1, DEN-2, DEN-3, and DEN-4. This disease is widely spread in tropical countries [1]. The virus is transmitted to human by the bite of the female mosquitoes of the subgenus Stegomyia.Aedes aegypti has been the most important epidemic vector in the tropical and subtropical regions [2]. The life cycle of Aedes aegypti depending upon the extent of feeding. They lasts for 8 to 10 days at room temperature [3]. It consists of two phases: aquatic (larvae, pupae) and terrestrial (eggs, adults) phase. Mathematical models have been widely used to quantitatively analyse the transmissions of various infectious diseases [4]. These models are compartmental models. In compartemental model, a population is divided into different compartments. We know that there are so many mathematical models for describing and analyzing the behaviors of dengue disease, such as [5, 6]. In this paper, we use SIS and SI model to represent the condition of the host and vector respectively. We divide host population into two groups, those are Susceptible (S) (having potentially to get infected) and Infected (I) (have been infected by the virus) [7]. Similary, we also partitioned vector population into two subclasses, those are susceptible vector and infected vector. In this paper, we use numerical approach to find the solution of the model. The method that we use is Euler Method. This method need a specific step-size in order to make the solution dynamically consistent with its exact solution, otherwise it will blow-up [8]. The model we proposed in this article is as follow.

$$
(1) \quad
\begin{cases}
\dot{S} & = \mu - \mu S - \alpha m S V - \beta S I + \gamma I \\
\dot{I} & = \alpha m S V + \beta S I - (\mu + \gamma) I \\
\dot{M} & = \delta - \delta M - \upsilon M I \\
\dot{V} & = \upsilon M I - \delta V
\end{cases}
$$

where S, I, M, and V denote susceptible host, infected host, susceptible vector, and infected vector respectively. We assume that birth and mortality rate are equal, that is μ. α denote the bitting rate of the vector has to susceptible host S, while β is the rate of direct transmission, and γ is the host recovery rate. The proportion of total vector to total host is denote by m, δ is the mortality rate of vector, and the host infectious to vector susceptible transmission rate is υ. We

also assume that the total population of host and vector remain constant. It can be shown that the basic reproduction number of Equation (1) is $R_0 = \frac{\alpha \upsilon m}{\delta(\mu+\gamma)} + \frac{\beta}{(\mu+\gamma)}$.

2. MATERIALS AND METHODS

Finite difference method, such as Euler method has been use widely to discretize continuous epidemiological model. Euler method has been applied to various model, such as [9], [10], and [11]. This discrete model version shows rich dynamics of the continuous model. However, aside from its simplicity, this technique has disadvantage that is divergent approximation may be reach. In order to minimize the disadvantage, it is necessary to choose the correct step-size to avoid them. We use Euler method to discretize model (1), so we have

(2)
$$\begin{cases} \frac{S_{n+1}-S_n}{h} &= \mu - \mu S_n - \alpha m S_n V_n - \beta S_n I_n + \gamma I_n \\[2mm] \frac{I_{n+1}-I_n}{h} &= \alpha m S_n V_n + \beta S_n I_n - (\mu+\gamma)I_n \\[2mm] \frac{M_{n+1}-M_n}{h} &= \delta - \delta M_n - \upsilon M_n I_n \\[2mm] \frac{V_{n+1}-V_n}{h} &= \upsilon M_n I_n - \delta V_n \end{cases}$$

where h denote step-size we use in model (2). By using simple algebraic manipulation, we rewrite Equation (2) as follow.

(3)
$$\begin{cases} S_{n+1} &= S_n + h\mu - h\mu S_n - h\alpha m S_n V_n - h\beta S_n I_n + h\gamma I_n \\[2mm] I_{n+1} &= I_n + h\alpha m S_n V_n + h\beta S_n I_n - h(\mu+\gamma)I_n \\[2mm] M_{n+1} &= M_n + h\delta - h\delta M_n - h\upsilon M_n I_n \\[2mm] V_{n+1} &= V_n + h\upsilon M_n I_n - h\delta V_n \end{cases}$$

In the following section, we discuss about equilibrium point and simulation of its stability.

3. RESULTS AND DISCUSSION

3.1. Equilibrium Points. Suppose that $(\hat{S}, \hat{I}, \hat{M}, \hat{V})$ denote equilibrium point of Equation (3), then we have

$$
(4) \quad
\begin{cases}
\hat{S}_n &= \hat{S}_n + h\mu - h\mu\hat{S}_n - h\alpha m\hat{S}_n\hat{V}_n - h\beta\hat{S}_n\hat{I}_n + h\gamma\hat{I}_n \\[2mm]
\hat{I}_n &= \hat{I}_n + h\alpha m\hat{S}_n\hat{V}_n + h\beta\hat{S}_n\hat{I}_n - h(\mu + \gamma)\hat{I}_n \\[2mm]
\hat{M}_n &= \hat{M}_n + h\delta - h\delta\hat{M}_n - h\upsilon\hat{M}_n\hat{I}_n \\[2mm]
\hat{V}_n &= \hat{V}_n + h\upsilon\hat{M}_n\hat{I}_n - h\delta\hat{V}_n
\end{cases}
$$

It is easy to show that solution of Equation (4) are $E_0 = (1,0,1,0)$ and $E_1 = (S_e, I_e, M_e, V_e)$ where $S_e = \frac{(\mu+\gamma)(\delta+\upsilon I_e)}{\beta(\delta+\upsilon I_e)+\alpha\upsilon m}$, $M_e = \frac{\delta}{\delta+\upsilon I_e}$, $V_e = \frac{\upsilon I_e}{\delta+\upsilon I_e}$ and I_e is a unique positive solution of $\psi(I_e) = p_2(I_e)^2 + p_1 I_e + p_0$, where $p_2 = \beta\upsilon$, $p_1 = \beta\delta + \alpha\upsilon m - \beta\upsilon + \upsilon(\mu + \gamma)$, and $p_0 = -\delta(\mu + \gamma)(R_0{-}1)$.

3.2. Stability Analysis. Since total population of host and vector remain constant, letting $S = 1{-}I$ and $M = 1{-}V$. We define

$$
(5) \quad
\begin{cases}
F(I,V) &= I + h\alpha m(1-I)V + h\beta(1-I)I - h(\mu + \gamma)I \\[2mm]
G(I,V) &= V + h\upsilon(1-V)I - h\delta V
\end{cases}
$$

then we have $\frac{\partial F}{\partial I} = 1 - h\alpha mV - h\beta I + h\beta(1-I) - h(\mu + \gamma) = 1 - h\alpha mV - 2h\beta I + h(\beta - (\mu + \gamma))$, $\frac{\partial F}{\partial V} = h\alpha m(1-I)$, $\frac{\partial G}{\partial I} = h\upsilon(1-V)$ and $\frac{\partial G}{\partial V} = 1 - h\upsilon I - h\delta$, so the Jacobian matrix of Equation (5) is

$$
(6) \quad
J =
\begin{pmatrix}
\frac{\partial F}{\partial I} & \frac{\partial F}{\partial V} \\[3mm]
\frac{\partial G}{\partial I} & \frac{\partial G}{\partial V}
\end{pmatrix}
$$

Subtituting disease free equilibrium $(0,0)$ to Equation (6) lead us to

$$
(7) \quad
J_0 =
\begin{pmatrix}
1 - h((\mu + \gamma) - \beta) & h\alpha m \\[3mm]
h\upsilon & 1 - h\delta
\end{pmatrix}
$$

Notice that if $R_0 < 1$ then we have $R_0 = \frac{\alpha\upsilon m}{\delta(\mu+\gamma)} + \frac{\beta}{(\mu+\gamma)} < 1$. It means that $\frac{\beta}{\mu+\gamma} < 1$, in other word $(\mu + \gamma) - \beta > 0$. Also notice that if $R_0 < 1$ then $1 - R_0 = 1 - \frac{\alpha\upsilon m}{\delta(\mu+\gamma)} + \frac{\beta}{(\mu+\gamma)} = \frac{\delta((\mu+\gamma)-\beta)-\alpha\upsilon m}{\delta(\mu+\gamma)} > 0$ that lead to the fact that $\delta((\mu + \gamma) - \beta) - \alpha\upsilon m > 0$. Trace and determinant of Jacobian in Equation (7) are $\tau = -[((\mu + \gamma) - \beta) + \delta]h + 2$ and $\Delta = [\delta((\mu + \gamma) - \beta) - \alpha\upsilon m]h^2 - [((\mu + \gamma) - \beta) + \delta]h + 1$ respectively. Let $A = \delta((\mu + \gamma) - \beta) -$

$\alpha \upsilon m > 0$ and $B = ((\mu + \gamma) - \beta) + \delta > 0$. We use the following lemma to observe stability of model (5).

Lemma 1. *If $R_0 < 1$ and $h < \frac{B}{A}$ then $\Delta < 1$.*

Proof. It is easy to show that $h < \frac{B}{A}$ is equivalent with $Ah^2 - Bh + 1 = \Delta < 1$. $\square$

Lemma 2. *If $R_0 < 1$ and $h < \frac{B}{A}$ then $1 - \tau + \Delta > 0$.*

Proof. It is clear that $1 - \tau + \Delta = 1 + [((\mu + \gamma) - \beta) + \delta]h + 2 + [\delta((\mu + \gamma) - \beta) - \alpha \upsilon m]h^2 - [((\mu + \gamma) - \beta) + \delta]h + 1 = [\delta((\mu + \gamma) - \beta) - \alpha \upsilon m]h^2 = Ah^2 > 0$. $\square$

Lemma 3. *If $R_0 < 1$ and $h < \frac{B}{A}\left[1 - \sqrt{1 - \frac{4A}{B^2}}\right]$ or $h > \frac{B}{A}\left[1 + \sqrt{1 - \frac{4A}{B^2}}\right]$ then $1 + \tau + \Delta > 0$.*

Proof. Notice that $h < \frac{B}{A}\left[1 - \sqrt{1 - \frac{4A}{B^2}}\right]$ or $h > \frac{B}{A}\left[1 + \sqrt{1 - \frac{4A}{B^2}}\right]$ are solutions of $Ah^2 - 2Bh + 4 = 1 + \tau + \Delta > 0$. $\square$

Lemma 4. *If $R_0 < 1$ and $h < \frac{B}{A}\left[1 - \sqrt{1 - \frac{4A}{B^2}}\right]$ then Model (5) is locally asymptotically stable.*

Proof. Since Lemma 1, Lemma 2, and Lemma 3 are condition for $|\lambda_i| < 1, i = 1, 2$ where λ_i is characteristic root of Equation (7) then we have the conclusion. $\square$

In other hand, if $R_0 > 1$ then $\frac{\beta}{\mu + \gamma} > 1$, in other word $(\mu + \gamma) - \beta < 0$, also $R_0 - 1 = \frac{\alpha \upsilon m + \beta \delta - \delta(\mu + \gamma)}{\delta(\mu + \gamma)} > 0$ that lead to $\alpha \upsilon m + \beta \delta - \delta(\mu + \gamma) > 0$. Since $\psi(I_e) = p_2(I_e)^2 + p_1 I_e + p_0$, where $p_2 = \beta \upsilon > 0, p_1 = \beta \delta + \alpha \upsilon m - \beta \upsilon + \upsilon(\mu + \gamma) = \alpha \upsilon m + \beta \delta + \upsilon((\mu + \gamma) - \beta), p_0 = -\delta(\mu + \gamma)(R_0 - 1) < 0$. Since $p_1^2 - 4p_2 p_0 = (\alpha \upsilon m + \beta \delta + \upsilon((\mu + \gamma) - \beta))^2 + 4(\beta \upsilon)(\delta(\mu + \gamma)(R_0 - 1)) > 0$, we can conclude that $I_e = -\frac{1}{2(\beta \upsilon)}\left(\alpha \upsilon m + \beta \delta + \upsilon((\mu + \gamma) - \beta) + \sqrt{(\alpha \upsilon m + \beta \delta + \upsilon((\mu + \gamma) - \beta))^2 + 4(\beta \upsilon)(\delta(\mu + \gamma)(R_0 - 1))}\right)$.
Jacobian matrix for endemic equilibrium (I_e, V_e) is

$$(8) \qquad J_e = \begin{pmatrix} 1 - h\left(\frac{\alpha m \upsilon I_e}{\delta + \upsilon I_e}\right) + h\beta(1 - I_e) - h(\beta I_e + (\mu + \gamma)) & h\alpha m(1 - I_e) \\ h\upsilon\left(1 - \frac{\upsilon I_e}{\delta + \upsilon I_e}\right) & 1 - h(\delta + \upsilon) \end{pmatrix}$$

Next we use software to simulate model (3) in various parameter and step-size.

3.3. Numerical Simulation. Now we simulate model (3) with respect to $R_0 < 1$. We use the following parameters: $\mu = 0.7; \alpha = 0.02; m = 0.02; \beta = 0.1; \gamma = 0.1; \upsilon = 0.2; \delta = 0.1$ with step-size $h = 0.1$. Clearly, reproduction number is $R_0 = 0.126 < 1$. Absolute values of this case are $|\lambda_1| = 0.99$ and $|\lambda_2| = 0.93$. We obtain the following numerical solution
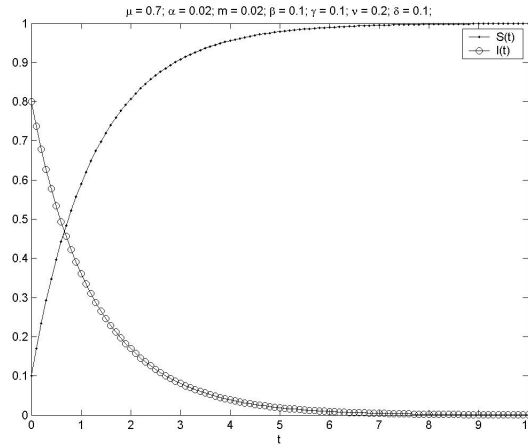

FIGURE 1. Numerical simulation of dengue model with $R_0 < 1$ and $h = 0.1$.

From Figure 1, we found that numerical solution of model (3) converge to its equilibrium points $(\hat{S}, \hat{I}) = (1, 0)$. In this figure, we use $h = 0.1 < 2.8566$. If we use h that tend to 2.8566, the solution become unstable. For illustration, see Figure 2 below.
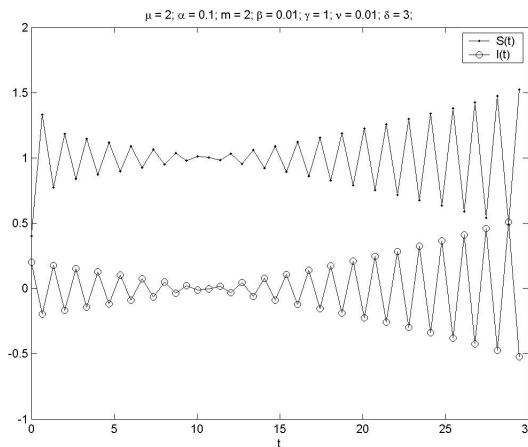

FIGURE 2. Numerical simulation of dengue model with $R_0 < 1$ and $h = 0.67$ become saddle.

In Figure 2, we use $\mu = 2; \alpha = 0.1; m = 2; \beta = 0.01; \gamma = 1; \upsilon = 0.01; \delta = 3$ and $h = 0.67 > 0.6579$. We found that the numerical solution become saddle with $|\lambda_1| = 0.98$ and $|\lambda_2| = 1.04$. It means that choosing the step-size is necessary.

Next we observe case of $R_0 > 1$. We use $\mu = 0.7; \alpha = 0.5; m = 0.9; \beta = 0.1; \gamma = 0.1; \upsilon = 0.9; \delta = 0.1$ with step-size $h = 0.1$. We get $R_0 = 5.188 > 1$ and $|\lambda_1| = 0.971$ and $|\lambda_2| = 0.882$ (see figure below)
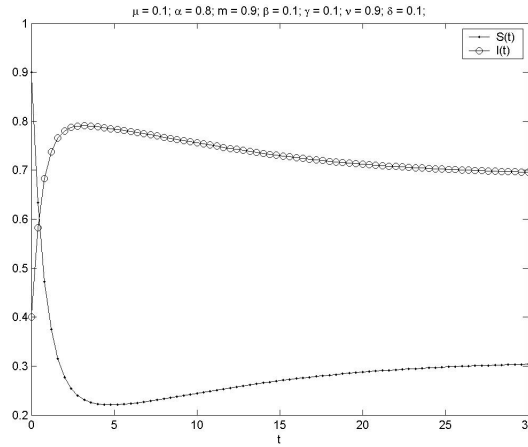

FIGURE 3. Numerical simulation of dengue model with $R_0 > 1$ and $h = 0.1$.

Figure 3 shows that numerical solution converge to endemic equilibrium point $(\hat{S}, \hat{I}) = (0.312, 0.6961)$ with $|\lambda_1| = 0.93$ and $|\lambda_2| = 0.9$.

4. CONCLUSIONS

In this paper, we discuss about host – vector dengue model behaviour. We found that the model has two equilibrium point, named disesase free equilibrium point and endemic equilibrium point. We observe that discretize continous model has a consequences in choosing step size value. We showed that choosing an appropriate step size is a must to obtain consistency between continous and its discrete version. Further work should be focused on bifurcation analysis of the model.

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CONFLICT OF INTERESTS

The author(s) declare that there is no conflict of interests.

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